Question 10.1

Using the same crime data set `uscrime.txt` as in Questions 8.2 and 9.1, find the best model you can using

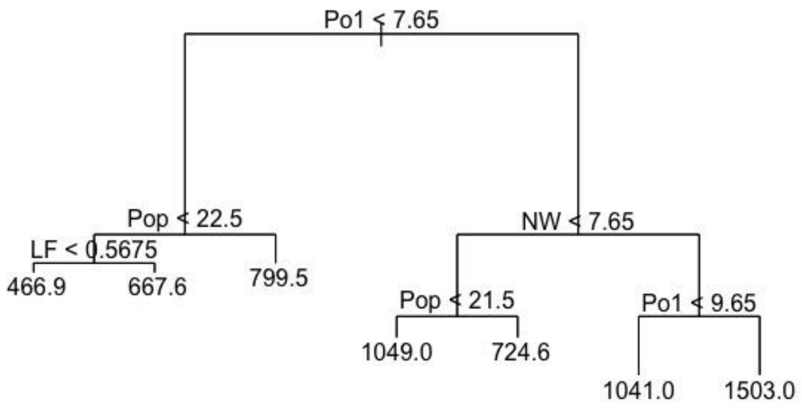
(a) a regression tree model, and

(b) a random forest model.

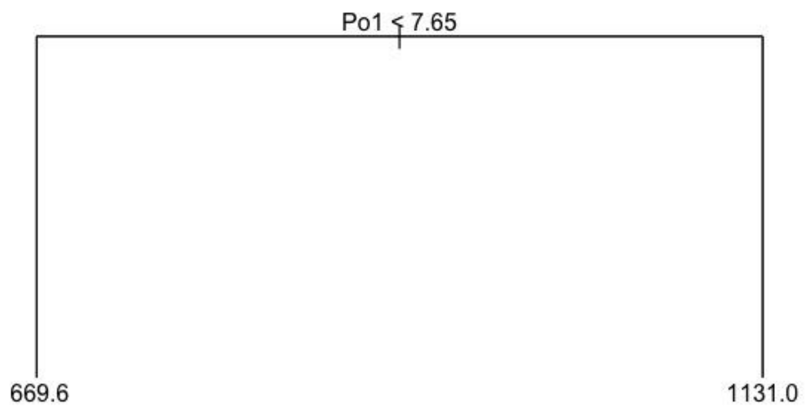
In R, you can use the `tree` package or the `rpart` package, and the `randomForest` package. For each model, describe one or two qualitative takeaways you get from analyzing the results (i.e., don't just stop when you have a good model, but interpret it too).

Summary :

1. Build Simple tree with 7 nodes
    a. R^2 = 0.7244962
    b. Adj R^2 = 0.6750468



2. Build tree with Sample Data 1:1000
    a. R^2 = 0.3629629
    b. AdjR62 = 0.3340067



Observation 1:

insample adjusted R^2 has dropped significantly from .67 to .334. However we are expecting cross validated R^2 to be less than the full model.

3. Build Random Forest Model

Number of Trees built from 500

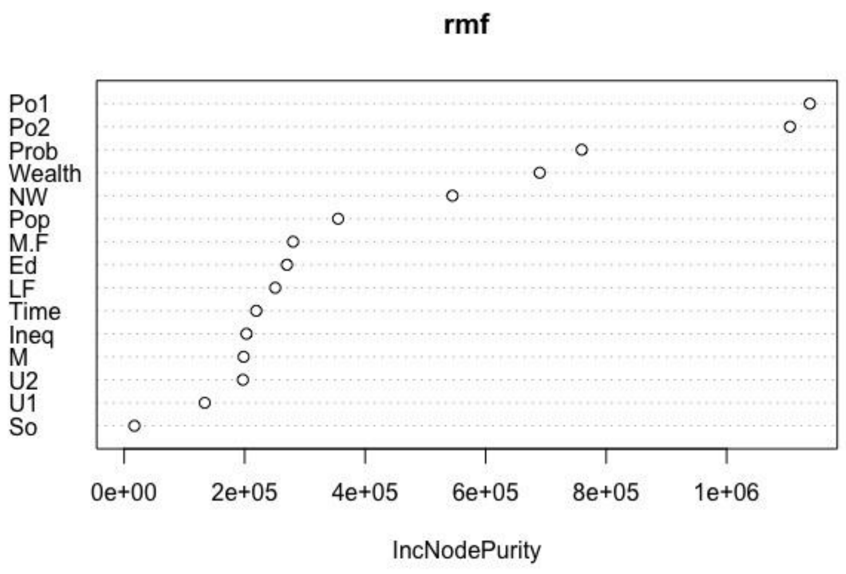
RMSE is 278.7323 0.5181691 213.7942.

Number of Trees built from 400

RMSE is 278.8589, rsquared is 0.5187796, and MAE is 214.4396

Number of Trees built from 300

RMSE is 278.0788 , rSquared is 0.5212120 and MAE is 212.4929



Observation 2 :

small improvement in cross validated performance by limiting the number of trees grown to 400

And no improvement with trees built from 300 so use the previous model with 400 trees constructed.

RSCRIPT :

```
# --------------------------- Data manipulation ------------------------------------


#First, Read in the data

#

data_crime = read.table("uscrime.txt",sep = "",header=TRUE)


#

# optional check to make sure the data is read correctly

#


head(data_crime)
```

```
# It appears the data has a varying scale from hundreth and thousanth decimal place



# Load in library tree, perform tree regression

#and use cross validation to find the optimal size of tree

#

library(tree)

crimetree<-tree(Crime~.,data=data_crime)


# examine the tree we built first


#

summary(crimetree)


# there are actually 7 terminal nodes with Residual mean deviance of 47390


# Check if the splits make sense

plot(crimetree)

text(crimetree ,pretty =0)

crimetree


# From the result, Po1 is the most important variable and therefore used as the first split


#

# calculate R^2 and adjusted R^2 for the tree model

#

SST<-sum((data_crime$Crime-mean(data_crime$Crime))^2)

SSE<-sum((data_crime$Crime-predict(crimetree,newdata=data_crime))^2)
```

```
SST

SSE

r12<-1-SSE/SST

r12


#adjusted R^2 Value


n=nrow(data_crime)

k=7#number of terminal nodes

adjR12<-1-(1-r12)*(n-1)/(n-k-1)

adjR12




#

# build a better tree with less sum of squared residuals

#

sample(1:1000,1)

set.seed(555)

crvs<-cv.tree(crimetree, FUN = prune.tree, K=5)

crvs

plot(crvs$size ,crvs$dev ,type="b")


#

# 5 fold cross validation indicates that optimal size is 2 since dev of 6456140 is the lowest error.

# apply this limit to tree.contol option if tree is bigger than 2 terminal nodes to prevent overfit.

# Try rebuilding the tree with mincut =23 which will give us 2 terminal nodes.

#


crimetree2<-tree(Crime~.,data=data_crime, control = tree.control(nobs = 47, mincut = 23))
```

```
crimetree2

plot(crimetree2)

text(crimetree2 ,pretty =0)



#

#we see that this give the treee with 2 terminal nodes or leaves.

#


summary(crimetree2)


#in-sample residual mean deviance is now 97410 which is twice as high as

#it was with all 7 leaves which makes sense

#since we now have a much simpler model that is not able to explain the training data

#as well so residual deviance is higher.


#Calculate R^2 for the pruned model

#

SSE2<-sum((data_crime$Crime-predict(crimetree2,newdata=data_crime))^2)

SSE2

r22<-1-SSE2/SST

r22

n=nrow(data_crime)

k=2#number of terminal nodes

adjR22<-1-(1-r22)*(n-1)/(n-k-1)

adjR22

#

#insample adjusted R^2 has dropped significantly frkm .67 to .334.

#However we are expecting cross validated R^2 to be less than the full model.
```

```
#use the randomForest package to build a randomForest model

#using first the recommended number of variables to split on

# Try mtry =4 - sqrt( number of predictors)


#

library(randomForest)

rmf<-randomForest(Crime~., data=data_crime, mtry=4)

rmf

#

#we see here that squared is 43.13% which is higher than

#our selected tree model r squared of 0.3629626.

#Find the importance of the predictors using the Importance function and VarImpPlot

#


importance(rmf)

varImpPlot(rmf)

#


#Increase in node purity for Random Forest regression is just the increase

#in RSS averaged over all trees that occurs from splitting over that variable.

#Again we see that Po1 is the most important variable.


#USe cross validation to see if we can improve the model with different mtry levels


library(caret)

set.seed(555)

crvrm<-train(Crime~., data=data_crime,

        trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),

        tuneGrid=expand.grid(mtry=1:15))
```

```
crvrm


SSErm<-sum((crvrm$pred[,2]-crvrm$pred[,1])^2)

SSErm

SSTrm<-sum((crvrm$pred[,2]-mean(crvrm$pred[,2]))^2)

SSTrm

r32<-1-(SSErm/SSTrm)

r32


#

#The mtry level that corresponds to the highest cross validated R^2 is 4 just as we hypothsized.

#It appears that the random forest model has outperformed the single decision tree  pruned tree model.

#Cross validated r squared is 0.4435946.

#this result is not suprising because we are creating many tree to explain the data.


#try lowering the number of trees built from 500 to 400 and compare cross validated performance
perhaps we can prevent overfit

#

set.seed(555)

crvrm2<-train(Crime~., data=data_crime,

        trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),

        tuneGrid=expand.grid(mtry=1:15), ntree=400)

crvrm2

SSErm<-sum((crvrm2$pred[,2]-crvrm2$pred[,1])^2)

SSErm

SSTrm<-sum((crvrm2$pred[,2]-mean(crvrm2$pred[,2]))^2)

SSTrm

r42<-1-(SSErm/SSTrm)

r42
```

```
#

#small improvement in cross validated performance by limiting the number of trees grown to 400

#since RMSE is 278.8589, rsquared is 0.5187796, and MAE is 214.4396 and was 278.7323  0.5181691
213.7942.


#

#try lowering the number of trees built from 400 to 300

#and compare cross validated performance perhaps we can still prevent overfit

#

set.seed(555)

crvrm3<-train(Crime~., data=data_crime,

          trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),

          tuneGrid=expand.grid(mtry=1:15), ntree=300)

crvrm3

SSErm<-sum((crvrm3$pred[,2]-crvrm3$pred[,1])^2)

SSErm

SSTrm<-sum((crvrm3$pred[,2]-mean(crvrm3$pred[,2]))^2)

SSTrm

r52<-1-(SSErm/SSTrm)

r52

#no improvement so use the previous model crvrm2 instead with 400 trees constructed.
```

RSCRIPT with Results

```
> # --------------------------- Data manipulation -----------------------------------
>
> #First, Read in the data
> #
> data_crime = read.table("uscrime.txt",sep = "",header=TRUE)
>
> #
> # optional check to make sure the data is read correctly
> #
>
> head(data_crime)
     M So   Ed  Po1  Po2    LF   M.F Pop   NW    U1  U2 Wealth Ineq     Prob    Time Crime
1 15.1  1  9.1  5.8  5.6 0.510  95.0  33 30.1 0.108 4.1   3940 26.1 0.084602 26.2011   791
2 14.3  0 11.3 10.3  9.5 0.583 101.2  13 10.2 0.096 3.6   5570 19.4 0.029599 25.2999  1635
3 14.2  1  8.9  4.5  4.4 0.533  96.9  18 21.9 0.094 3.3   3180 25.0 0.083401 24.3006   578
4 13.6  0 12.1 14.9 14.1 0.577  99.4 157  8.0 0.102 3.9   6730 16.7 0.015801 29.9012  1969
5 14.1  0 12.1 10.9 10.1 0.591  98.5  18  3.0 0.091 2.0   5780 17.4 0.041399 21.2998  1234
6 12.1  0 11.0 11.8 11.5 0.547  96.4  25  4.4 0.084 2.9   6890 12.6 0.034201 20.9995   682
>
> # It appears the data has a varying scale from hundreth and thousanth decimal place
>
```

```
>
> # Load in library tree, perform tree regression
> #and use cross validation to find the optimal size of tree
> #
> library(tree)
> crimetree<-tree(Crime~.,data=data_crime)
>
> # examine the tree we built first
>
> #
> summary(crimetree)

Regression tree:
tree(formula = Crime ~ ., data = data_crime)
Variables actually used in tree construction:
[1] "Po1" "Pop" "LF"  "NW"
Number of terminal nodes:  7
Residual mean deviance:  47390 = 1896000 / 40
Distribution of residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-573.900  -98.300   -1.545    0.000  110.600  490.100
>
> # there are actually 7 terminal nodes with Residual mean deviance of 47390
>
> # Check if the splits make sense
> plot(crimetree)
> text(crimetree ,pretty =0)
> crimetree
node), split, n, deviance, yval
```

```
      * denotes terminal node

1) root 47 6881000  905.1
   2) Po1 < 7.65 23  779200  669.6
     4) Pop < 22.5 12  243800  550.5
       8) LF < 0.5675 7   48520  466.9 *
       9) LF > 0.5675 5   77760  667.6 *
     5) Pop > 22.5 11  179500  799.5 *
   3) Po1 > 7.65 24 3604000 1131.0
     6) NW < 7.65 10  557600  886.9
      12) Pop < 21.5 5  146400 1049.0 *
      13) Pop > 21.5 5  147800  724.6 *
     7) NW > 7.65 14 2027000 1305.0
      14) Po1 < 9.65 6  170800 1041.0 *
      15) Po1 > 9.65 8 1125000 1503.0 *
>
> # From the result, Po1 is the most important variable and therefore used as the first split
>
> #
> # calculate R^2 and adjusted R^2 for the tree model
> #
> SST<-sum((data_crime$Crime-mean(data_crime$Crime))^2)
> SSE<-sum((data_crime$Crime-predict(crimetree,newdata=data_crime))^2)
> SST
[1] 6880928
> SSE
[1] 1895722
> r12<-1-SSE/SST
> r12
```

```
[1] 0.7244962

>

> #adjusted R^2 Value

>

> n=nrow(data_crime)

> k=7#number of terminal nodes

> adjR12<-1-(1-r12)*(n-1)/(n-k-1)

> adjR12

[1] 0.6750468

>

>

> #

> # build a better tree with less sum of squared residuals

> #

> sample(1:1000,1)

[1] 940

> set.seed(555)

> crvs<-cv.tree(crimetree, FUN = prune.tree, K=5)

> crvs

$size

[1] 7 6 5 4 3 2 1


$dev

[1] 6985079 6920884 6754652 6790966 6469270 6456140 7308121


$k

[1]      -Inf  117534.9  263412.9  355961.8  731412.1 1019362.7 2497521.7


$method
```

```
[1] "deviance"


attr(,"class")
[1] "prune"         "tree.sequence"
> plot(crvs$size ,crvs$dev ,type="b")
>
> #
> # 5 fold cross validation indicates that optimal size is 2 since dev of 6456140 is the lowest error.
> # apply this limit to tree.contol option if tree is bigger than 2 terminal nodes to prevent overfit.
> # Try rebuilding the tree with mincut =23 which will give us 2 terminal nodes.
> #
>
> crimetree2<-tree(Crime~.,data=data_crime, control = tree.control(nobs = 47, mincut = 23))
> crimetree2
node), split, n, deviance, yval
      * denotes terminal node


1) root 47 6881000  905.1
  2) Po1 < 7.65 23  779200  669.6 *
  3) Po1 > 7.65 24 3604000 1131.0 *
> plot(crimetree2)
> text(crimetree2 ,pretty =0)
>
>
> #
> #we see that this give the treee with 2 terminal nodes or leaves.
> #
>
> summary(crimetree2)
```

```
Regression tree:
tree(formula = Crime ~ ., data = data_crime, control = tree.control(nobs = 47,
    mincut = 23))
Variables actually used in tree construction:
[1] "Po1"
Number of terminal nodes:  2
Residual mean deviance:  97410 = 4383000 / 45
Distribution of residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-622.800 -193.200   -5.609    0.000  147.300  862.200
>
> #in-sample residual mean deviance is now 97410 which is twice as high as
> #it was with all 7 leaves which makes sense
> #since we now have a much simpler model that is not able to explain the training data
> #as well so residual deviance is higher.
>
> #Calculate R^2 for the pruned model
> #
> SSE2<-sum((data_crime$Crime-predict(crimetree2,newdata=data_crime))^2)
> SSE2
[1] 4383406
> r22<-1-SSE2/SST
> r22
[1] 0.3629629
> n=nrow(data_crime)
> k=2#number of terminal nodes
> adjR22<-1-(1-r22)*(n-1)/(n-k-1)
> adjR22
```

```
[1] 0.3340067
> #
> #insample adjusted R^2 has dropped significantly frkm .67 to .334.
> #However we are expecting cross validated R^2 to be less than the full model.
> #use the randomForest package to build a randomForest model
> #using first the recommended number of variables to split on
> # Try mtry =4 - sqrt( number of predictors)
>
> #
> library(randomForest)
> rmf<-randomForest(Crime~., data=data_crime, mtry=4)
> rmf


Call:
randomForest(formula = Crime ~ ., data = data_crime, mtry = 4)
               Type of random forest: regression
                     Number of trees: 500
No. of variables tried at each split: 4


          Mean of squared residuals: 83266.41
                    % Var explained: 43.13
> #
> #we see here that squared is 43.13% which is higher than
> #our selected tree model r squared of 0.3629626.
> #Find the importance of the predictors using the Importance function and VarImpPlot
> #
>
> importance(rmf)
Error in UseMethod("importance") :
  no applicable method for 'importance' applied to an object of class "c('randomForest.formula',
'randomForest')"

> #First, Read in the data

> #

> data_crime = read.table("uscrime.txt",sep = "",header=TRUE)

>

> #

> # optional check to make sure the data is read correctly

> #

>

> head(data_crime)

     M So   Ed  Po1  Po2    LF   M.F Pop   NW    U1  U2 Wealth Ineq     Prob    Time Crime

1 15.1  1  9.1  5.8  5.6 0.510  95.0  33 30.1 0.108 4.1   3940 26.1 0.084602 26.2011   791

2 14.3  0 11.3 10.3  9.5 0.583 101.2  13 10.2 0.096 3.6   5570 19.4 0.029599 25.2999  1635

3 14.2  1  8.9  4.5  4.4 0.533  96.9  18 21.9 0.094 3.3   3180 25.0 0.083401 24.3006   578

4 13.6  0 12.1 14.9 14.1 0.577  99.4 157  8.0 0.102 3.9   6730 16.7 0.015801 29.9012  1969

5 14.1  0 12.1 10.9 10.1 0.591  98.5  18  3.0 0.091 2.0   5780 17.4 0.041399 21.2998  1234

6 12.1  0 11.0 11.8 11.5 0.547  96.4  25  4.4 0.084 2.9   6890 12.6 0.034201 20.9995   682

>

> # It appears the data has a varying scale from hundreth and thousanth decimal place

>

>

> # Load in library tree, perform tree regression

> #and use cross validation to find the optimal size of tree

> #

> library(tree)

> crimetree<-tree(Crime~.,data=data_crime)

>

> # examine the tree we built first
```

```
>
> #
> summary(crimetree)

Regression tree:
tree(formula = Crime ~ ., data = data_crime)
Variables actually used in tree construction:
[1] "Po1" "Pop" "LF"  "NW"
Number of terminal nodes:  7
Residual mean deviance:  47390 = 1896000 / 40
Distribution of residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-573.900  -98.300   -1.545    0.000  110.600  490.100
>
> # there are actually 7 terminal nodes with Residual mean deviance of 47390
>
> # Check if the splits make sense
> plot(crimetree)
> text(crimetree ,pretty =0)
> crimetree
node), split, n, deviance, yval
      * denotes terminal node

1) root 47 6881000  905.1
   2) Po1 < 7.65 23  779200  669.6
     4) Pop < 22.5 12  243800  550.5
       8) LF < 0.5675 7   48520  466.9 *
       9) LF > 0.5675 5   77760  667.6 *
     5) Pop > 22.5 11  179500  799.5 *
   3) Po1 > 7.65 24 3604000 1131.0
     6) NW < 7.65 10  557600  886.9
      12) Pop < 21.5 5  146400 1049.0 *
      13) Pop > 21.5 5  147800  724.6 *
     7) NW > 7.65 14 2027000 1305.0
      14) Po1 < 9.65 6  170800 1041.0 *
      15) Po1 > 9.65 8 1125000 1503.0 *
>
> # From the result, Po1 is the most important variable and therefore used as the first split
>
> #
> # calculate R^2 and adjusted R^2 for the tree model
> #
> SST<-sum((data_crime$Crime-mean(data_crime$Crime))^2)
> SSE<-sum((data_crime$Crime-predict(crimetree,newdata=data_crime))^2)
> SST
[1] 6880928
> SSE
[1] 1895722
> r12<-1-SSE/SST
> r12
[1] 0.7244962
>
> #adjusted R^2 Value
>
> n=nrow(data_crime)
> k=7#number of terminal nodes
> adjR12<-1-(1-r12)*(n-1)/(n-k-1)
> adjR12
```

```
[1] 0.6750468
>
>
> #
> # build a better tree with less sum of squared residuals
> #
> sample(1:1000,1)
[1] 328
> set.seed(555)
> crvs<-cv.tree(crimetree, FUN = prune.tree, K=5)
> crvs
$size
[1] 7 6 5 4 3 2 1

$dev
[1] 6985079 6920884 6754652 6790966 6469270 6456140 7308121

$k
[1]      -Inf  117534.9  263412.9  355961.8  731412.1 1019362.7 2497521.7

$method
[1] "deviance"

attr(,"class")
[1] "prune"         "tree.sequence"
> plot(crvs$size ,crvs$dev ,type="b")
>
> #
> # 5 fold cross validation indicates that optimal size is 2 since dev of 6456140 is the lowest error.
> # apply this limit to tree.contol option if tree is bigger than 2 terminal nodes to prevent overfit.
> # Try rebuilding the tree with mincut =23 which will give us 2 terminal nodes.
> #
>
> crimetree2<-tree(Crime~.,data=data_crime, control = tree.control(nobs = 47, mincut = 23))
> crimetree2
node), split, n, deviance, yval
      * denotes terminal node

1) root 47 6881000  905.1
  2) Po1 < 7.65 23  779200  669.6 *
  3) Po1 > 7.65 24 3604000 1131.0 *
> plot(crimetree2)
> text(crimetree2 ,pretty =0)
>
>
> #
> #we see that this give the treee with 2 terminal nodes or leaves.
> #
>
> summary(crimetree2)

Regression tree:
tree(formula = Crime ~ ., data = data_crime, control = tree.control(nobs = 47,
    mincut = 23))
Variables actually used in tree construction:
[1] "Po1"
Number of terminal nodes:  2
Residual mean deviance:  97410 = 4383000 / 45
```

```
Distribution of residuals:
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-622.800 -193.200   -5.609    0.000  147.300  862.200
>
> #in-sample residual mean deviance is now 97410 which is twice as high as
> #it was with all 7 leaves which makes sense
> #since we now have a much simpler model that is not able to explain the training data
> #as well so residual deviance is higher.
>
> #Calculate R^2 for the pruned model
> #
> SSE2<-sum((data_crime$Crime-predict(crimetree2,newdata=data_crime))^2)
> SSE2
[1] 4383406
> r22<-1-SSE2/SST
> r22
[1] 0.3629629
> n=nrow(data_crime)
> k=2#number of terminal nodes
> adjR22<-1-(1-r22)*(n-1)/(n-k-1)
> adjR22
[1] 0.3340067
> #
> #insample adjusted R^2 has dropped significantly frkm .67 to .334.
> #However we are expecting cross validated R^2 to be less than the full model.
> #use the randomForest package to build a randomForest model
> #using first the recommended number of variables to split on
> # Try mtry =4 - sqrt( number of predictors)
>
```

```
> #
> library(randomForest)
> rmf<-randomForest(Crime~., data=data_crime, mtry=4)
> rmf

Call:
randomForest(formula = Crime ~ ., data = data_crime, mtry = 4)
               Type of random forest: regression
                     Number of trees: 500
No. of variables tried at each split: 4

          Mean of squared residuals: 83266.41
                    % Var explained: 43.13
> #
> #we see here that squared is 43.13% which is higher than
> #our selected tree model r squared of 0.3629626.
> #Find the importance of the predictors using the Importance function and VarImpPlot
> #
>
> #importance(rmf)
> varImpPlot(rmf)
> #
>
> #Increase in node purity for Random Forest regression is just the increase
> #in RSS averaged over all trees that occurs from splitting over that variable.
> #Again we see that Po1 is the most important variable.
>
> #USe cross validation to see if we can improve the model with different mtry levels
>
```

```
> library(caret)

> set.seed(555)

> crvrm<-train(Crime~., data=data_crime,

+           trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),

+           tuneGrid=expand.grid(mtry=1:15))

> crvrm

Random Forest


47 samples

15 predictors


No pre-processing

Resampling: Cross-Validated (5 fold)

Summary of sample sizes: 36, 38, 38, 38, 38

Resampling results across tuning parameters:


  mtry  RMSE      Rsquared   MAE

   1    282.2148  0.5109789  232.2553

   2    270.4879  0.5399055  222.0057

   3    267.9380  0.5543635  214.3942

   4    268.5870  0.5537980  212.0183

   5    270.1196  0.5464426  213.2321

   6    274.4155  0.5359920  213.7011

   7    274.1235  0.5295017  211.8640

   8    272.5812  0.5394876  212.9723

   9    277.0303  0.5270595  214.4619

  10    279.2353  0.5187866  214.7263

  11    275.0933  0.5389526  212.4839

  12    276.8314  0.5332234  212.7497
  13    279.1010  0.5258992  213.4738
  14    275.2154  0.5376047  210.8170
  15    278.7323  0.5181691  213.7942

RMSE was used to select the optimal model using the smallest value.
The final value used for the model was mtry = 3.
>
> SSErm<-sum((crvrm$pred[,2]-crvrm$pred[,1])^2)
> SSErm
[1] 65521786
> SSTrm<-sum((crvrm$pred[,2]-mean(crvrm$pred[,2]))^2)
> SSTrm
[1] 103213915
> r32<-1-(SSErm/SSTrm)
> r32
[1] 0.3651846
>
> #
> #The mtry level that corresponds to the highest cross validated R^2 is 4 just as we hypothsized.
> #It appears that the random forest model has outperformed the single decision tree  pruned tree
model.
> #Cross validated r squared is 0.4435946.
> #this result is not suprising because we are creating many tree to explain the data.
>
> #try lowering the number of trees built from 500 to 400 and compare cross validated performance
perhaps we can prevent overfit
> #
> set.seed(555)
> crvrm2<-train(Crime~., data=data_crime,
+            trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),
+            tuneGrid=expand.grid(mtry=1:15), ntree=400)
> crvrm2
Random Forest

47 samples
15 predictors

No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 36, 38, 38, 38, 38
Resampling results across tuning parameters:

  mtry  RMSE      Rsquared   MAE
   1    281.3281  0.5107555  231.0260
   2    271.2270  0.5397441  222.5078
   3    267.8948  0.5577242  213.9204
   4    269.2855  0.5510344  212.6778
   5    270.2207  0.5441216  213.7219
   6    273.4922  0.5414202  213.5780
   7    276.6178  0.5247428  213.2216
   8    273.3596  0.5407124  213.7767
   9    277.1620  0.5291552  215.0050
  10    278.3759  0.5275974  214.2065
  11    275.1091  0.5436061  211.9783
  12    279.2716  0.5226313  213.9776
  13    278.5464  0.5326273  213.3096
  14    273.9128  0.5434945  210.1580
  15    278.8589  0.5187796  214.4396
```

```
RMSE was used to select the optimal model using the smallest value.

The final value used for the model was mtry = 3.

> SSErm<-sum((crvrm2$pred[,2]-crvrm2$pred[,1])^2)

> SSErm

[1] 65591805

> SSTrm<-sum((crvrm2$pred[,2]-mean(crvrm2$pred[,2]))^2)

> SSTrm

[1] 103213915

> r42<-1-(SSErm/SSTrm)

> r42

[1] 0.3645062

> #

> #small improvement in cross validated performance by limiting the number of trees grown to 400

> #since RMSE is 278.8589, rsquared is 0.5187796, and MAE is 214.4396 and was 278.7323  0.5181691
213.7942.

>

> #

> #try lowering the number of trees built from 400 to 300

> #and compare cross validated performance perhaps we can still prevent overfit

> #

> set.seed(555)

> crvrm3<-train(Crime~., data=data_crime,

+           trControl=trainControl(method = 'cv', number = 5, savePredictions = TRUE),

+           tuneGrid=expand.grid(mtry=1:15), ntree=300)

> crvrm3

Random Forest


47 samples
```

```
15 predictors

No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 36, 38, 38, 38, 38
Resampling results across tuning parameters:

  mtry  RMSE      Rsquared   MAE
   1    281.1145  0.5120530  230.1269
   2    269.3940  0.5389937  220.3498
   3    267.6460  0.5604548  213.8100
   4    268.5961  0.5506388  212.5859
   5    270.3770  0.5426735  212.7279
   6    273.8725  0.5389338  213.5581
   7    274.4479  0.5294671  211.6421
   8    273.9322  0.5412890  215.0722
   9    275.6087  0.5401420  213.6776
  10    278.5269  0.5232155  213.8719
  11    274.7225  0.5513087  211.6254
  12    283.1814  0.5060676  217.5156
  13    278.1487  0.5325734  213.6487
  14    273.2436  0.5471932  209.0589
  15    278.0788  0.5212120  212.4929

RMSE was used to select the optimal model using the smallest value.
The final value used for the model was mtry = 3.
> SSErm<-sum((crvrm3$pred[,2]-crvrm3$pred[,1])^2)
> SSErm
[1] 65635355
```

```
> SSTrm<-sum((crvrm3$pred[,2]-mean(crvrm3$pred[,2]))^2)

> SSTrm

[1] 103213915

> r52<-1-(SSErm/SSTrm)

> r52

[1] 0.3640842

> #no improvement so use the previous model crvrm2 instead with 400 trees constructed.
```