#### 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, <u>but interpret it too</u>).

### **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<sup>2</sup> has dropped significantly from .67 to .334. However we are expecting cross validated R<sup>2</sup> 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)</pre> # 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)</pre>
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] 7654321
$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))
```

```
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
```

> crimetree2

```
> #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
```

> #it was with all 7 leaves which makes sense

```
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] 7654321
```

```
[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)
```

\$dev

```
> 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.