PRACTICAL MACHIN LEARNING PROJECT

Background

Using devices such as Jawbone Up, Nike FuelBand, and Fitbit it is now possible to collect a large amount of data about personal activity relatively inexpensively. In this project, your goal will be to use data from accelerometers on the belt, forearm, arm, and dumbell of 6 participants. They were asked to perform barbell lifts correctly and incorrectly in 5 different ways. More information is available from the website here: http://groupware.les.inf.puc-rio.br/har (http://groupware.les.inf.puc-rio.br/har) (see the section on the Weight Lifting Exercise Dataset).

Data

The training data for this project are available here: https://d396qusza40orc.cloudfront.net/predmachlearn/pml-training.csv (https://d396qusza40orc.cloudfront.net/predmachlearn/pml-training.csv)

The test data are available here: https://d396qusza40orc.cloudfront.net/predmachlearn/pml-testing.csv (https://d396qusza40orc.cloudfront.net/predmachlearn/pml-testing.csv)

The data for this project come from this source: http://groupware.les.inf.puc-rio.br/har (http://groupware.les.inf.puc-rio.br/har). If you use the document you create for this class for any purpose please cite them as they have been very generous in allowing their data to be used for this kind of assignment.

Goal

The goal of your project is to predict the manner in which they did the exercise. This is the “classe” variable in the training set. You may use any of the other variables to predict with. You should create a report describing how you built your model, how you used cross validation, what you think the expected out of sample error is, and why you made the choices you did. You will also use your prediction model to predict 20 different test cases.

Getting and loading the data

```
set.seed(12345)

trainUrl <- "http://d396qusza40orc.cloudfront.net/predmachlearn/pml-training.csv"
testUrl <- "http://d396qusza40orc.cloudfront.net/predmachlearn/pml-testing.csv"

training <- read.csv(url(trainUrl), na.strings=c("NA","#DIV/0!",""))
testing <- read.csv(url(testUrl), na.strings=c("NA","#DIV/0!",""))
```

Partioning the training set into two

```
inTrain <- createDataPartition(training$classe, p=0.6, list=FALSE)
myTraining <- training[inTrain, ]
myTesting <- training[-inTrain, ]
dim(myTraining); dim(myTesting)
```

```
## [1] 11776   160
```

```
## [1] 7846  160
```

Cleaning the data

Remove NearZeroVariance variables

```
nzv <- nearZeroVar(myTraining, saveMetrics=TRUE)
myTraining <- myTraining[,nzv$nzv==FALSE]

nzv<- nearZeroVar(myTesting,saveMetrics=TRUE)
myTesting <- myTesting[,nzv$nzv==FALSE]
```

Remove the first column of the myTraining data set

```
myTraining <- myTraining[c(-1)]
```

Clean variables with more than 60% NA

```
trainingV3 <- myTraining
for(i in 1:length(myTraining)) {
    if( sum( is.na( myTraining[, i] ) ) /nrow(myTraining) >= .7) {
        for(j in 1:length(trainingV3)) {
            if( length( grep(names(myTraining[i]), names(trainingV3)[j]) ) == 1)  {
                trainingV3 <- trainingV3[ , -j]
            }
        }
    }
}

# Set back to the original variable name
myTraining <- trainingV3
rm(trainingV3)
```

Transform the myTesting and testing data sets

```
clean1 <- colnames(myTraining)
clean2 <- colnames(myTraining[, -58])  # remove the classe column
myTesting <- myTesting[clean1]         # allow only variables in myTesting that are also
in myTraining
testing <- testing[clean2]             # allow only variables in testing that are also in
myTraining

dim(myTesting)
```

```
## [1] 7846   58
```

```
dim(testing)
```

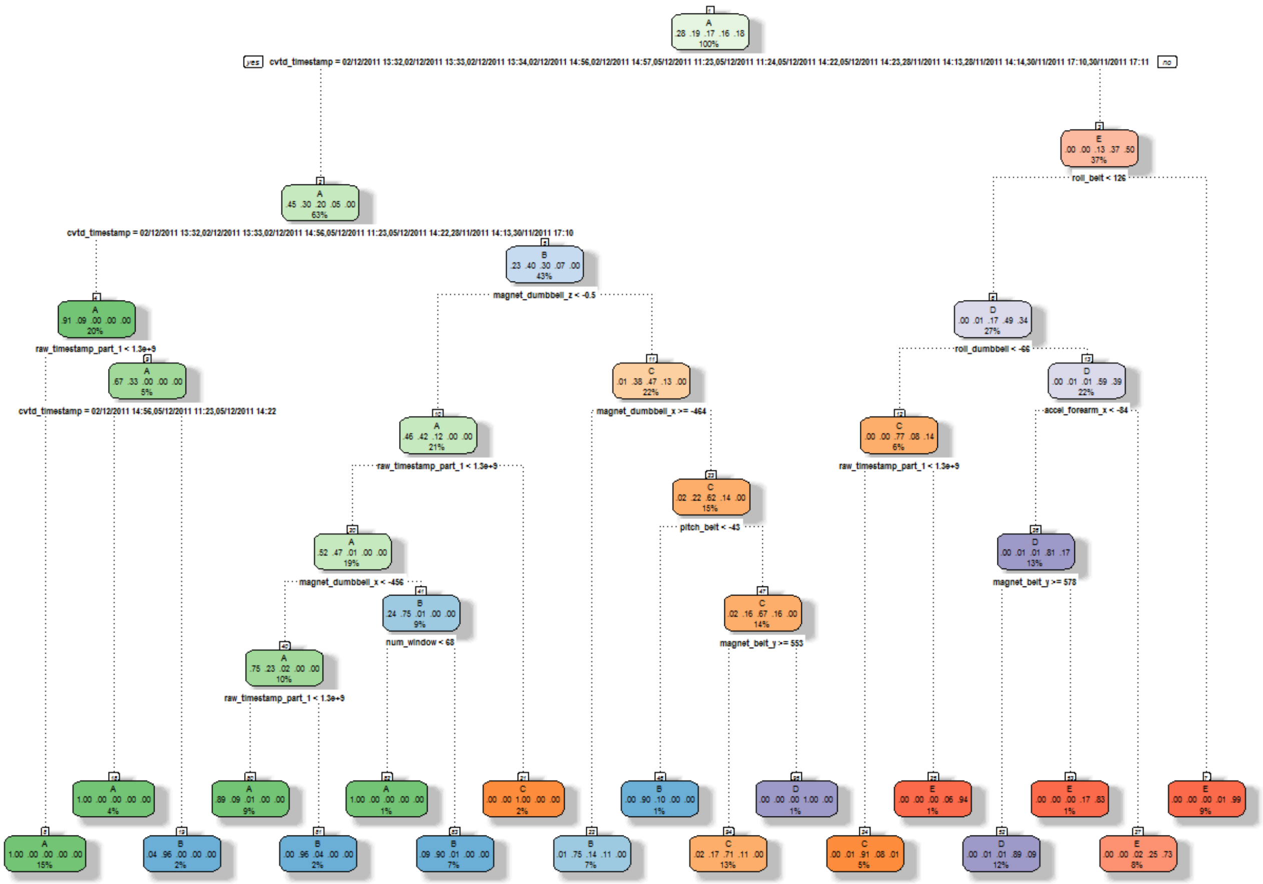
```
## [1] 20 57
```

Coerce the data into the same type

```
for (i in 1:length(testing) ) {
    for(j in 1:length(myTraining)) {
        if( length( grep(names(myTraining[i]), names(testing)[j]) ) == 1)  {
            class(testing[j]) <- class(myTraining[i])
        }
    }
}

# To get the same class between testing and myTraining
testing <- rbind(myTraining[2, -58] , testing)
testing <- testing[-1,]
```

Prediction with Decision Trees

```
set.seed(12345)
modFitA1 <- rpart(classe ~ ., data=myTraining, method="class")
fancyRpartPlot(modFitA1)
```

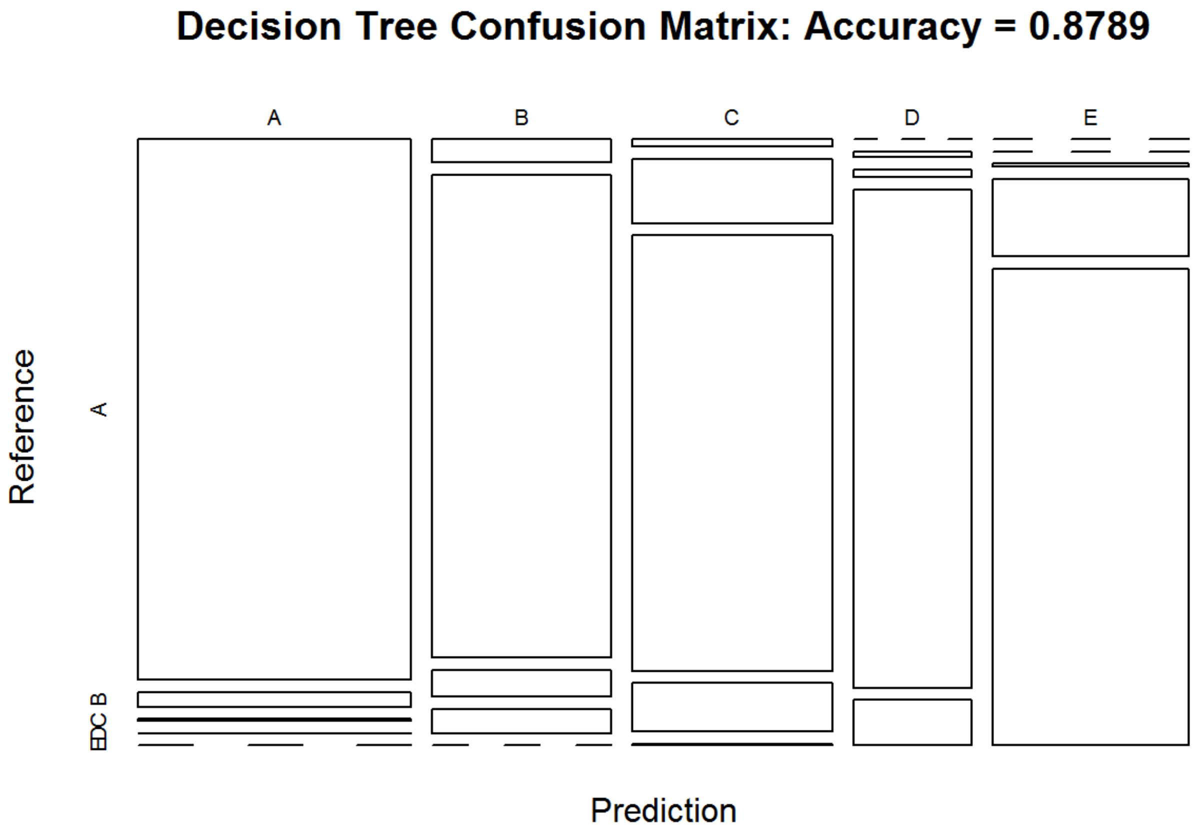


Rattle 2015-Nov-22 00:54:57 ashvini

```
predictionsA1 <- predict(modFitA1, myTesting, type = "class")
cmtree <- confusionMatrix(predictionsA1, myTesting$classe)
cmtree
```

```
## Confusion Matrix and Statistics
## 
##           Reference
## Prediction    A    B    C    D    E
##          A 2150   60    7    1    0
##          B   61 1260   69   64    0
##          C   21  188 1269  143    4
##          D    0   10   14  857   78
##          E    0    0    9  221 1360
## 
## Overall Statistics
##                                          
##                Accuracy : 0.8789         
##                  95% CI : (0.8715, 0.8861)
##     No Information Rate : 0.2845         
##     P-Value [Acc > NIR] : < 2.2e-16      
##                                          
##                   Kappa : 0.8468         
##  Mcnemar's Test P-Value : NA             
## 
## Statistics by Class:
## 
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9633   0.8300   0.9276   0.6664   0.9431
## Specificity            0.9879   0.9693   0.9450   0.9845   0.9641
## Pos Pred Value         0.9693   0.8666   0.7809   0.8936   0.8553
## Neg Pred Value         0.9854   0.9596   0.9841   0.9377   0.9869
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2740   0.1606   0.1617   0.1092   0.1733
## Detection Prevalence   0.2827   0.1853   0.2071   0.1222   0.2027
## Balanced Accuracy      0.9756   0.8997   0.9363   0.8254   0.9536
```

```
plot(cmtree$table, col = cmtree$byClass, main = paste("Decision Tree Confusion Matrix: Accuracy =", round(cmtree$overall['Accuracy'], 4)))
```

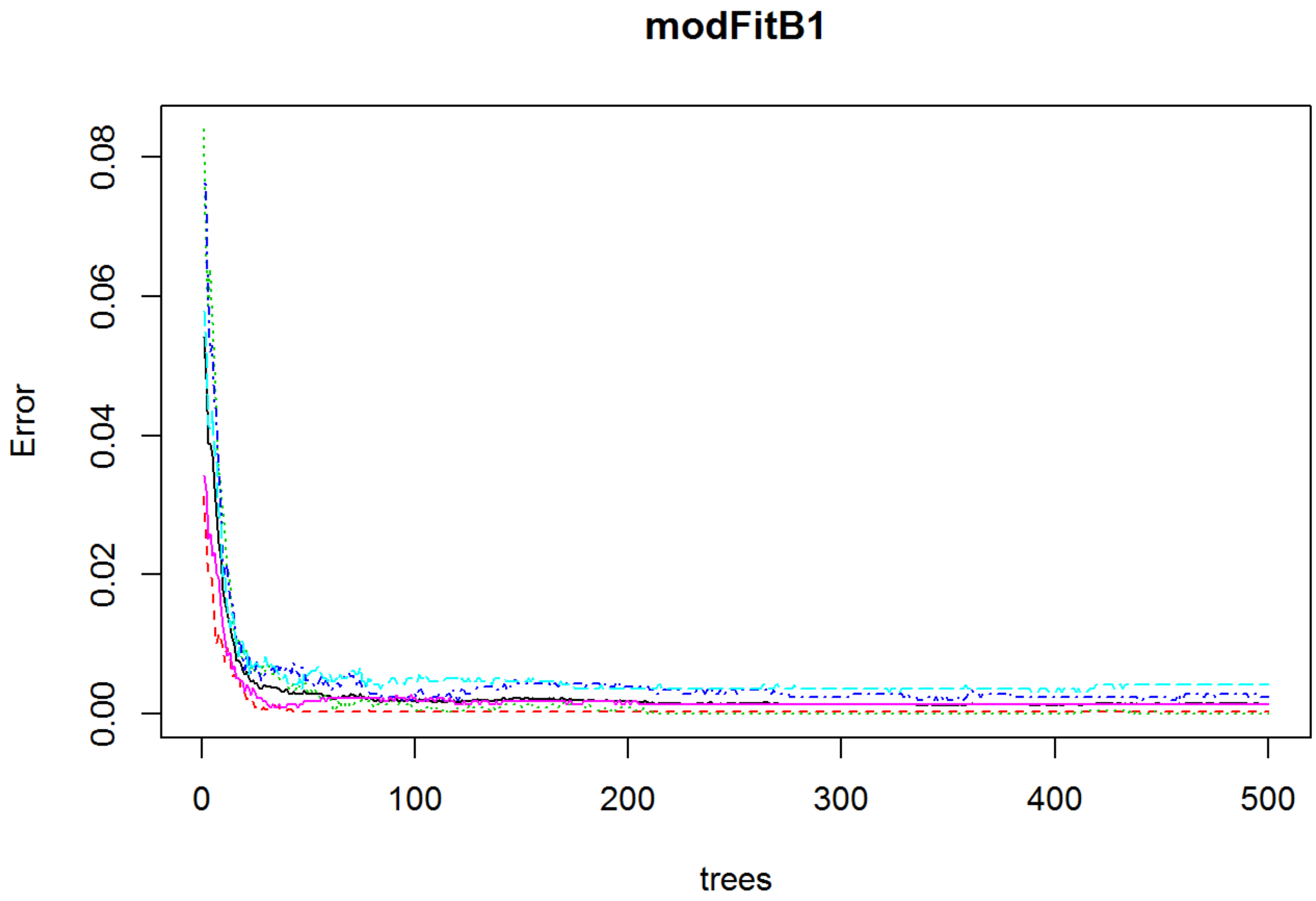


Prediction with Random Forests

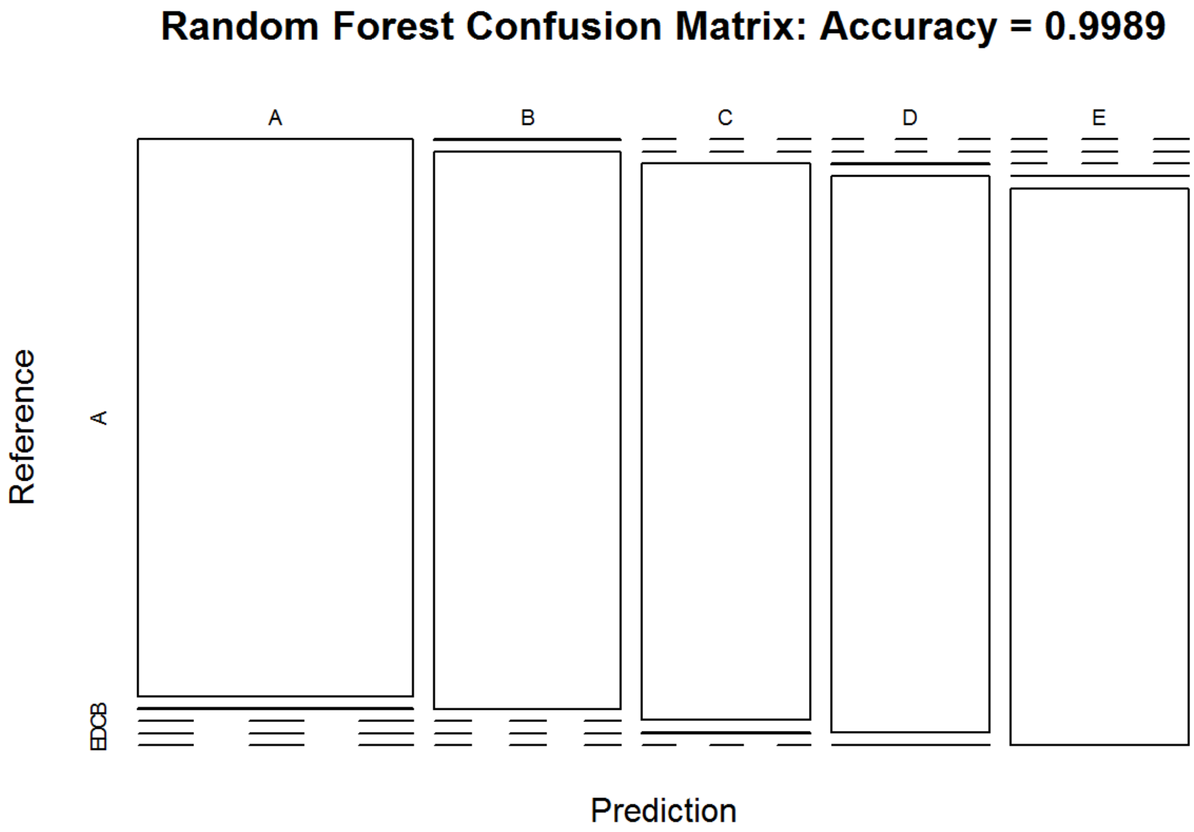
```
set.seed(12345)
modFitB1 <- randomForest(classe ~ ., data=myTraining)
predictionB1 <- predict(modFitB1, myTesting, type = "class")
cmrf <- confusionMatrix(predictionB1, myTesting$classe)
cmrf
```

```
## Confusion Matrix and Statistics
## 
##           Reference
## Prediction    A    B    C    D    E
##          A 2231    2    0    0    0
##          B    1 1516    0    0    0
##          C    0    0 1367    3    0
##          D    0    0    1 1282    1
##          E    0    0    0    1 1441
## 
## Overall Statistics
##                                           
##                Accuracy : 0.9989          
##                  95% CI : (0.9978, 0.9995)
##     No Information Rate : 0.2845          
##     P-Value [Acc > NIR] : < 2.2e-16       
##                                           
##                   Kappa : 0.9985          
##  Mcnemar's Test P-Value : NA              
## 
## Statistics by Class:
## 
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9996   0.9987   0.9993   0.9969   0.9993
## Specificity            0.9996   0.9998   0.9995   0.9997   0.9998
## Pos Pred Value         0.9991   0.9993   0.9978   0.9984   0.9993
## Neg Pred Value         0.9998   0.9997   0.9998   0.9994   0.9998
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2843   0.1932   0.1742   0.1634   0.1837
## Detection Prevalence   0.2846   0.1933   0.1746   0.1637   0.1838
## Balanced Accuracy      0.9996   0.9993   0.9994   0.9983   0.9996
```

```
plot(modFitB1)
```



```
plot(cmrf$table, col = cmtree$byClass, main = paste("Random Forest Confusion Matrix: Accu
racy =", round(cmrf$overall['Accuracy'], 4)))
```

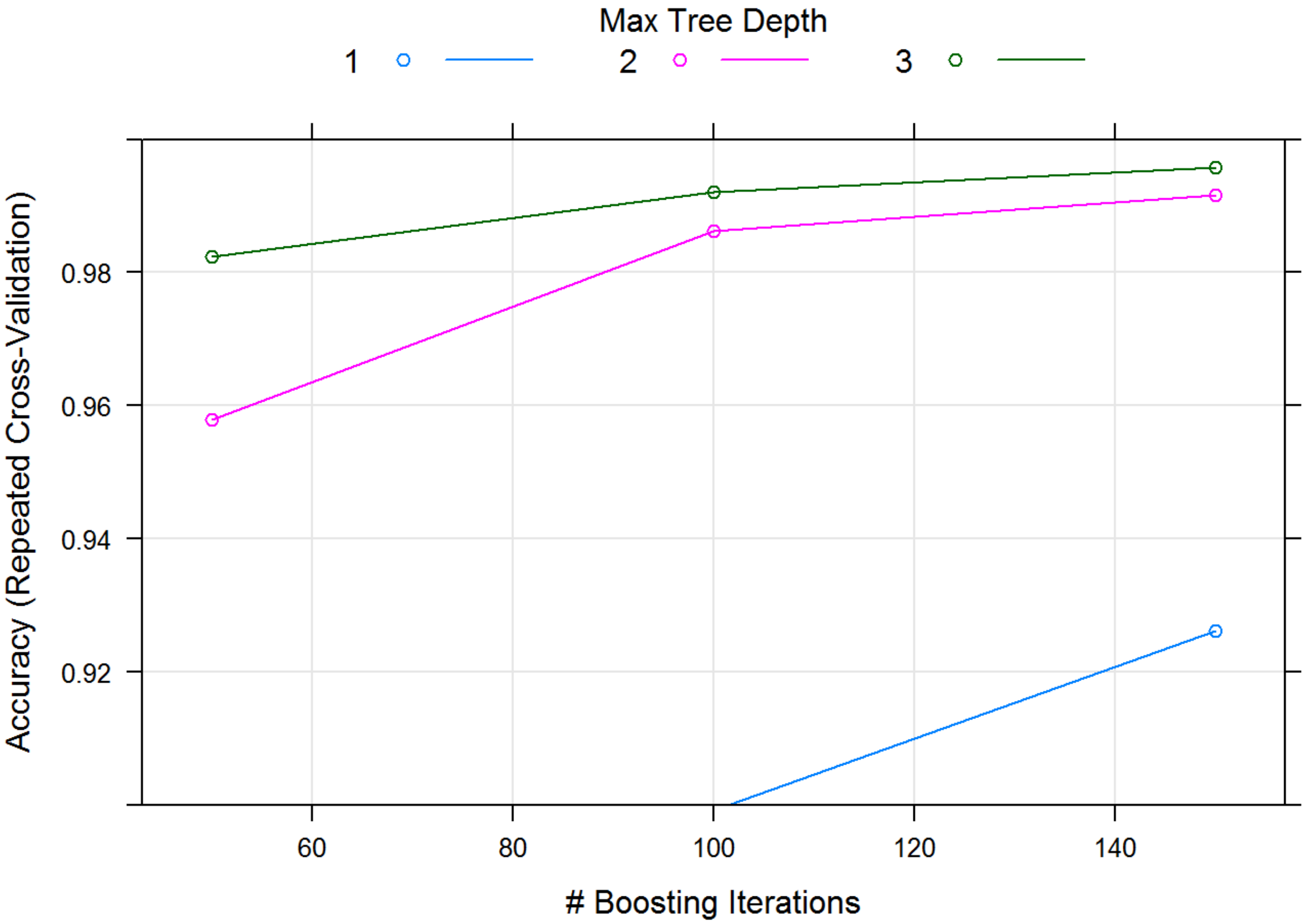


Prediction with Generalized Boosted Regression

```
set.seed(12345)
fitControl <- trainControl(method = "repeatedcv",
                           number = 5,
                           repeats = 1)

gbmFit1 <- train(classe ~ ., data=myTraining, method = "gbm",
                 trControl = fitControl,
                 verbose = FALSE)


gbmFinMod1 <- gbmFit1$finalModel

gbmPredTest <- predict(gbmFit1, newdata=myTesting)
gbmAccuracyTest <- confusionMatrix(gbmPredTest, myTesting$classe)
gbmAccuracyTest
```

```
## Confusion Matrix and Statistics
## 
##           Reference
## Prediction    A    B    C    D    E
##          A 2230    4    0    0    0
##          B    2 1509    1    0    0
##          C    0    4 1361    3    0
##          D    0    1    6 1274    1
##          E    0    0    0    9 1441
## 
## Overall Statistics
##                                           
##                Accuracy : 0.996           
##                  95% CI : (0.9944, 0.9973)
##     No Information Rate : 0.2845          
##     P-Value [Acc > NIR] : < 2.2e-16       
##                                           
##                   Kappa : 0.995           
##  Mcnemar's Test P-Value : NA              
## 
## Statistics by Class:
## 
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9991   0.9941   0.9949   0.9907   0.9993
## Specificity            0.9993   0.9995   0.9989   0.9988   0.9986
## Pos Pred Value         0.9982   0.9980   0.9949   0.9938   0.9938
## Neg Pred Value         0.9996   0.9986   0.9989   0.9982   0.9998
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2842   0.1923   0.1735   0.1624   0.1837
## Detection Prevalence   0.2847   0.1927   0.1744   0.1634   0.1848
## Balanced Accuracy      0.9992   0.9968   0.9969   0.9947   0.9990
```

```
plot(gbmFit1, ylim=c(0.9, 1))
```



Predicting Results on the Test Data

Random Forests gave an Accuracy in the myTesting dataset of 99.89%, which was more accurate that what I got from the Decision Trees or GBM. The expected out-of-sample error is 100-99.89 = 0.11%.

```
predictionB2 <- predict(modFitB1, testing, type = "class")
predictionB2
```

```
##  2 31  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21
##  B  A  B  A  A  E  D  B  A  A  B  C  B  A  E  E  A  B  B  B
## Levels: A B C D E
```

```
# Write the results to a text file for submission
pml_write_files = function(x){
    n = length(x)
    for(i in 1:n){
        filename = paste0("problem_id_",i,".txt")
        write.table(x[i],file=filename,quote=FALSE,row.names=FALSE,col.names=FALSE)
    }
}

# pml_write_files(predictionB2)
```