Practical Machine Learning Assignment

Executive summary

Analyze the device data from Jawbone Up, Nike FuelBand, and Fitbit for 6 participants, from their accelerometers on the belt, forearm, arm, and dumbelldata for 5 dataset using linear regression models. This learning will quantify how much of a particular activity they do, but they rarely quantify how well they do it.

Reading the data

The Raw Data - Download the file if does not exist in local system

Load the training and testing data

```
trainingdata = read.csv("./Data/pml-training.csv", na.strings = c("NA", ""))
dim(trainingdata); summary(trainingdata$classe)

## [1] 19622    160

## A B C D E
## 5580 3797 3422 3216 3607

testingdata = read.csv("./Data/pml-testing.csv", na.strings = c("NA", ""))
```

Load the library

```
library(ggplot2); library(caret); library(randomForest)
```

Removing near Zero covariates

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

nzv <- nearZeroVar(testingdata,saveMetrics=TRUE)
testingdata <- testingdata[,nzv$nzv==FALSE]</pre>
```

Partioning the training datset

[1] 7846 117

```
inTrain <- createDataPartition(y=trainingdata$classe, p=0.6, list=FALSE)
projTraining <- trainingdata[inTrain, ]; projTesting <- trainingdata[-inTrain, ]
dim(projTraining); dim(projTesting)</pre>
## [1] 11776 117
```

Killing first column of Dataset(ID Removing first ID variable) so that it does not interfer with ML Algorithms.

```
projTraining <- projTraining[c(-1)]</pre>
```

Remove the columns / Variables has too many NAs (keep only the variable > 60% threshold of NA's)

```
subprojTraining <- projTraining</pre>
for(i in 1:length(projTraining)) {
  if( sum( is.na( projTraining[, i] ) ) /nrow(projTraining) >= .6 ) {
    for(j in 1:length(subprojTraining)) {
      if( length( grep(names(projTraining[i]), names(subprojTraining)[j]) ) ==1) {
        subprojTraining <- subprojTraining[ , -j]</pre>
    }
 }
}
projTraining <- subprojTraining</pre>
rm(subprojTraining)
clean1 <- colnames(projTraining)</pre>
clean2 <- colnames(projTraining[, -58]) # Remove the classe column</pre>
projTesting <- projTesting[clean1]; # set/allow same variabels which are in Training</pre>
testing <- testingdata[clean2] # allow same variables which are in training
dim(projTesting); dim(testing)
```

```
## [1] 7846 58
## [1] 20 57
```

Coerce the data into the same type

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

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

Model Builinding \sim Train model with random forest due to its highly accuracy rate.

```
set.seed(12345)
modFit1 <- randomForest(classe ~. , data=projTraining)
plot(modFit1)</pre>
```

modFit1

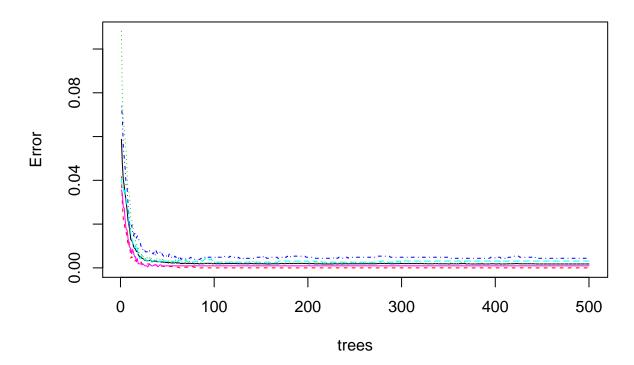


Figure 1:

```
predict1 <- predict(modFit1, projTesting, type = "class")
confMatrix <- confusionMatrix(predict1, projTesting$classe)
confMatrix</pre>
```

```
## Confusion Matrix and Statistics
##
##
            Reference
                     В
                          С
                               D
                                   Ε
## Prediction
               Α
##
           A 2232
                     1
                          0
                               0
                0 1517
##
           В
                          1
           С
##
                0
                     0 1363
                               7
                                   0
##
                     0
                          4 1276
                                    2
           D
                0
           Ε
##
                0
                     0
                          0
                               3 1440
##
## Overall Statistics
##
##
                 Accuracy : 0.9977
##
                   95% CI: (0.9964, 0.9986)
##
      No Information Rate: 0.2845
##
      P-Value [Acc > NIR] : < 2.2e-16
##
##
                    Kappa: 0.9971
  Mcnemar's Test P-Value : NA
##
##
## Statistics by Class:
##
##
                       Class: A Class: B Class: C Class: D Class: E
## Sensitivity
                         1.0000 0.9993
                                         0.9963
                                                  0.9922
                                                            0.9986
## Specificity
                         0.9998 0.9998
                                         0.9989
                                                  0.9991
                                                           0.9995
## Pos Pred Value
                         0.9996 0.9993
                                         0.9949
                                                  0.9953
                                                           0.9979
## Neg Pred Value
                         1.0000 0.9998
                                         0.9992
                                                  0.9985
                                                            0.9997
## Prevalence
                         0.2845 0.1935
                                         0.1744
                                                 0.1639
                                                            0.1838
## Detection Rate
                         0.2845 0.1933
                                          0.1737
                                                   0.1626
                                                            0.1835
## Detection Prevalence
                         0.2846 0.1935
                                          0.1746
                                                  0.1634
                                                            0.1839
## Balanced Accuracy
                         0.9999 0.9996
                                          0.9976
                                                  0.9957
                                                           0.9991
```

Let's have a look at the accuracy

confMatrix\$overall[1]

```
## Accuracy ## 0.9977058
```

It looks very good, it is more then 99.00%. Random Forests yielded better Results, as expected!

Predicting Results on the Test Data

Random Forests gave an Accuracy in the myTesting dataset of 99.7%, which was more accurate than other models. The expected out-of-sample error is 100-99.77=0.23%

```
prediTest <- predict(modFit1, testing, type = "class")
prediTest

## 2 3 41 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</pre>
```

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)
    }
}
# Write the output for all 20 test cases
pml_write_files(prediTest)
```

Conclusion

The estimate the out of sample error is less than 1% (1 - accuracy). This is a promising result to detect exercise form to quantify how much of a particular activity they do and effective.