Prediction Assignment

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```
knitr::opts_chunk$set(echo = TRUE)
###knitr::opts_chunk$set(out.width="400px", dpi=120)
options(width=80)
```

Synopsis

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. These type of devices are part of the quantified self movement – a group of enthusiasts who take measurements about themselves regularly to improve their health, to find patterns in their behavior, or because they are tech geeks. One thing that people regularly do is quantify how much of a particular activity they do, but they rarely quantify how well they do it. 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://web.archive.org/web/20161224072740/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

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

The data for this project come from this source: http://web.archive.org/web/20161224072740/http:/groupware.les.inf.puc-rio.br/har.

LIBRARY'S

```
options(warn=-1)
library(caret)
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
library(randomForest)
```

```
## randomForest 4.6-14
```

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

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

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

```
library(Hmisc)
```

```
## Loading required package: survival
```

```
##
## Attaching package: 'survival'
```

```
## The following object is masked from 'package:caret':
##
##     cluster
```

```
## Loading required package: Formula
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(foreach)
library(doParallel)
```

```
## Loading required package: iterators
```

```
## Loading required package: parallel
```

```
library(rattle)
```

```
## Loading required package: tibble
```

```
## Loading required package: bitops
```

```
## Rattle: A free graphical interface for data science with R.
## Versión 5.4.0 Copyright (c) 2006-2020 Togaware Pty Ltd.
## Escriba 'rattle()' para agitar, sacudir y  rotar sus datos.

##
## Attaching package: 'rattle'

## The following object is masked from 'package:randomForest':
##
##     importance
```

```
library(rpart)
library(rpart.plot)
library(RColorBrewer)
library(gbm)
```

```
## Loaded gbm 2.1.8
```

```
library(plyr)
```

```
##
## Attaching package: 'plyr'

## The following objects are masked from 'package:Hmisc':
##
##     is.discrete, summarize
```

```
set.seed(21243)
```

DATA LOAD

```
train_url <- "https://d396qusza40orc.cloudfront.net/predmachlearn/pml-training.csv"
test_url  <- "https://d396qusza40orc.cloudfront.net/predmachlearn/pml-testing.csv"


training_data <- read.csv(url(train_url), na.strings = c("NA", "#DIV/0!", ""))
testing_data <- read.csv(url(test_url), na.strings = c("NA", "#DIV/0!", ""))

dim(training_data)
```

```
## [1] 19622   160
```

```
dim(testing_data)
```

```
## [1]  20 160
```

Data Cleaning train_url

```r
### Removing Variables which are having nearly zero variance

cData <- training_data
for(i in c(8:ncol(cData)-1)) {cData[,i] = as.numeric(as.character(cData[,i]))}

#### First look at the data for each column and remove variables unrelated to exercise (column number a
featuresnames <- colnames(cData[colSums(is.na(cData)) == 0])[-(1:7)]
features <- cData[featuresnames]
```

Data Partitioning

```r
#### in this course it is recommended to make a partition of 60%-40% but in other documents it is 70%-3

inTrain <- createDataPartition(features$classe, p=0.60, list=FALSE)
training <- features[inTrain,]
testing <- features[-inTrain,]

dim(training)
```

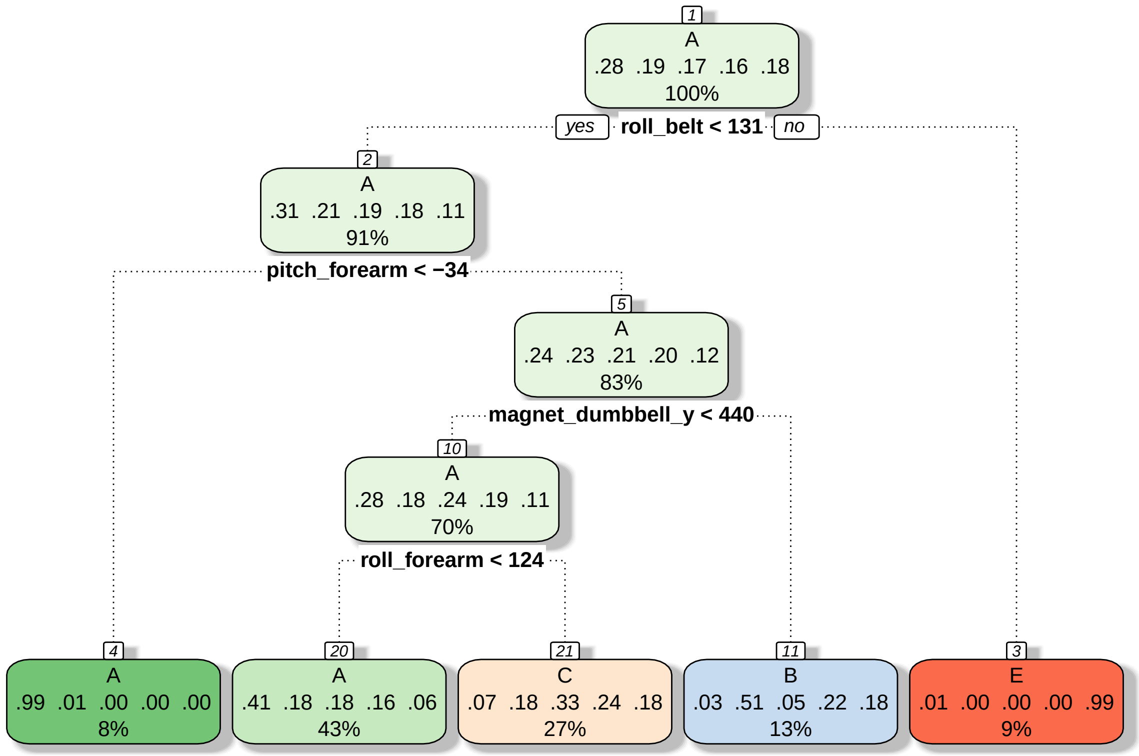
```
## [1] 11776    53
```

```r
dim(testing)
```

```
## [1] 7846   53
```

Decision Tree Model and Prediction

```r
DT_model<- train(classe ~. , data=training, method= "rpart")
fancyRpartPlot(DT_model$finalModel)
```



Rattle 2021−sep.−10 12:03:14 ED

```
DT_prediction<- predict(DT_model, newdata=testing)
identical(DT_prediction , testing$classe)
```

```
## [1] FALSE
```

```
confusionMatrix(table(DT_prediction, testing$classe)) ##
```

```
## Confusion Matrix and Statistics
##
##
## DT_prediction    A    B    C    D    E
##             A 2029  659  643  620  207
##             B   28  495   35  226  206
##             C  171  364  690  440  399
##             D    0    0    0    0    0
##             E    4    0    0    0  630
##
## Overall Statistics
##
##                Accuracy : 0.4899
##                  95% CI : (0.4788, 0.5011)
##     No Information Rate : 0.2845
##     P-Value [Acc > NIR] : < 2.2e-16
##
```

```
##                   Kappa : 0.3325
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9091  0.32609  0.50439   0.0000  0.43689
## Specificity            0.6208  0.92178  0.78790   1.0000  0.99938
## Pos Pred Value         0.4880  0.50000  0.33430      NaN  0.99369
## Neg Pred Value         0.9450  0.85079  0.88274   0.8361  0.88741
## Prevalence             0.2845  0.19347  0.17436   0.1639  0.18379
## Detection Rate         0.2586  0.06309  0.08794   0.0000  0.08030
## Detection Prevalence   0.5300  0.12618  0.26306   0.0000  0.08081
## Balanced Accuracy      0.7649  0.62393  0.64614   0.5000  0.71813
```

GBM model and Prediction

```
gbm_model<- train(classe ~. , data=training, method= "gbm", trControl=trainControl(method="cv",allowPara

gbm_prediction<- predict(gbm_model, newdata=testing)
identical(gbm_prediction , testing$classe)
```

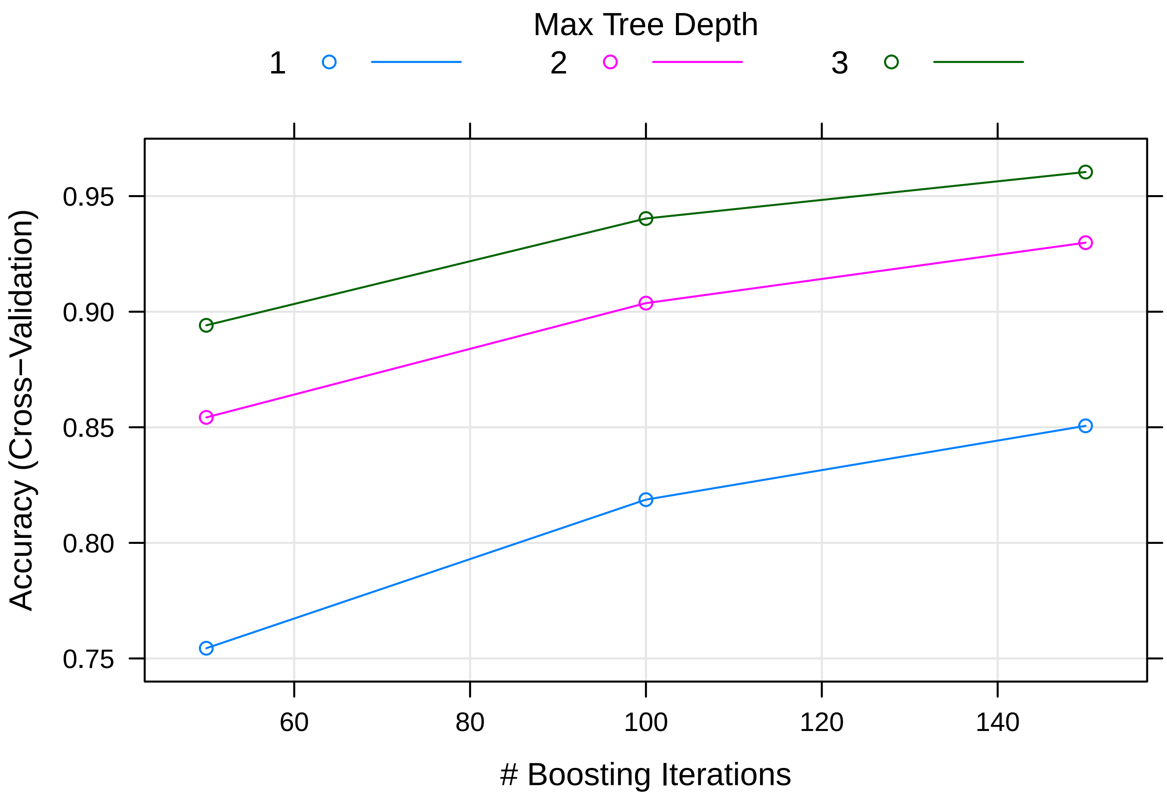
```
## [1] FALSE
```

```
confusionMatrix(table(gbm_prediction, testing$classe)) ##
```

```
## Confusion Matrix and Statistics
##
##
## gbm_prediction    A    B    C    D    E
##              A 2194   62    0    2    3
##              B   30 1409   36    6   11
##              C    4   41 1306   57   19
##              D    3    6   25 1212   18
##              E    1    0    1    9 1391
##
## Overall Statistics
##
##                Accuracy : 0.9574
##                  95% CI : (0.9527, 0.9618)
##     No Information Rate : 0.2845
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9461
##
##  Mcnemar's Test P-Value : 4.825e-09
##
## Statistics by Class:
##
```

```
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9830   0.9282   0.9547   0.9425   0.9646
## Specificity            0.9881   0.9869   0.9813   0.9921   0.9983
## Pos Pred Value         0.9704   0.9444   0.9152   0.9589   0.9922
## Neg Pred Value         0.9932   0.9828   0.9903   0.9888   0.9921
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2796   0.1796   0.1665   0.1545   0.1773
## Detection Prevalence   0.2882   0.1902   0.1819   0.1611   0.1787
## Balanced Accuracy      0.9855   0.9575   0.9680   0.9673   0.9815
```

```
plot(gbm_model)
```



Random Forest Model and Prediction

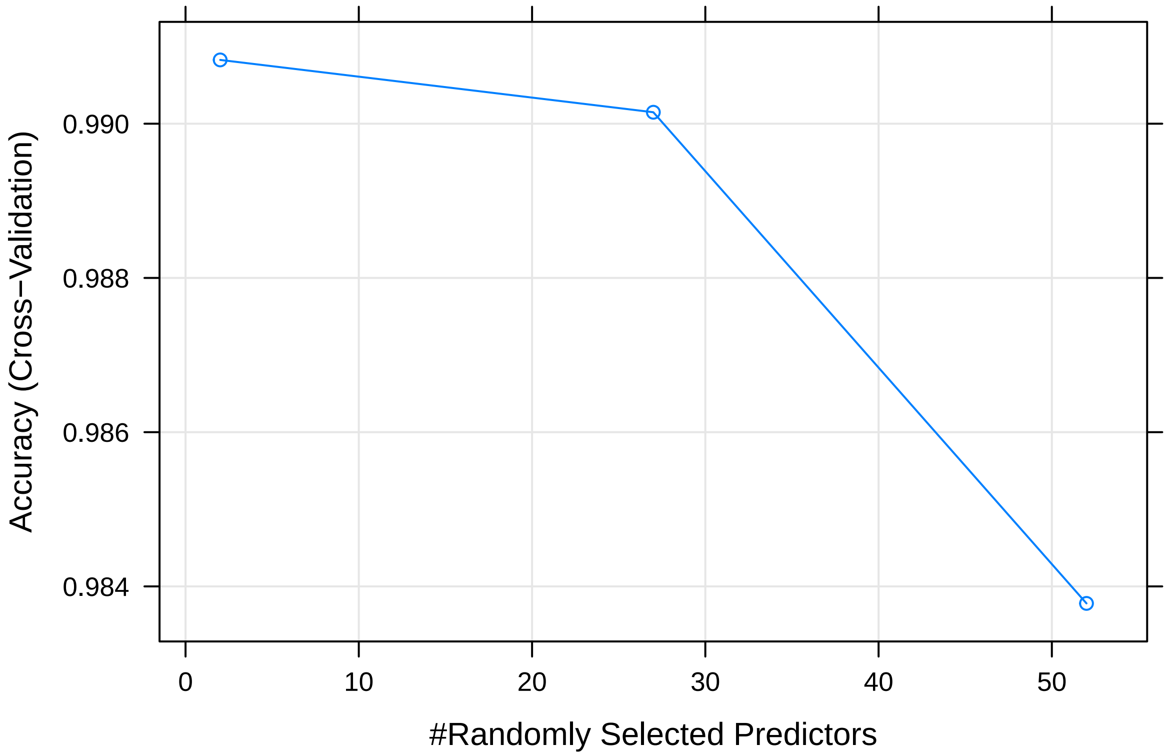
```
RForest <- train(classe~., data=training, method="rf",
        trControl=trainControl(method="cv", classProbs=TRUE,savePredictions=TRUE,allowParallel=TRUE, nu

predRF<-predict(RForest, testing)
CMatrixRF <- confusionMatrix(table(predRF, testing$classe))
CMatrixRF
```

```
## Confusion Matrix and Statistics
##
```

```
##
## predRF    A    B    C    D    E
##      A 2232   17    0    0    0
##      B    0 1491   17    0    0
##      C    0   10 1349   33    1
##      D    0    0    2 1252    3
##      E    0    0    0    1 1438
##
## Overall Statistics
##
##                Accuracy : 0.9893
##                  95% CI : (0.9868, 0.9915)
##     No Information Rate : 0.2845
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9865
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            1.0000   0.9822   0.9861   0.9736   0.9972
## Specificity            0.9970   0.9973   0.9932   0.9992   0.9998
## Pos Pred Value         0.9924   0.9887   0.9684   0.9960   0.9993
## Neg Pred Value         1.0000   0.9957   0.9971   0.9948   0.9994
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2845   0.1900   0.1719   0.1596   0.1833
## Detection Prevalence   0.2866   0.1922   0.1775   0.1602   0.1834
## Balanced Accuracy      0.9985   0.9898   0.9897   0.9864   0.9985
```

```
plot(RForest)
```



Data Cleaning testing

```
### Removing Variables which are having nearly zero variance

cData_t <- testing_data
for(i in c(8:ncol(cData_t)-1)) {cData_t[,i] = as.numeric(as.character(cData_t[,i]))}

#### First look at the data for each column and remove variables unrelated to exercise (column number a
featuresnames <- colnames(cData_t[colSums(is.na(cData_t)) == 0])[-(1:7)]
features_t <- cData_t[featuresnames]
```

Prediction on testing dataset

```
##prediction on Test dataset
predict_Test <- predict(RForest, newdata=features_t)
predict_Test
```

```
##  [1] 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
```

```r
print(as.data.frame(predict_Test))
```

```
##    predict_Test
## 1             B
## 2             A
## 3             B
## 4             A
## 5             A
## 6             E
## 7             D
## 8             B
## 9             A
## 10            A
## 11            B
## 12            C
## 13            B
## 14            A
## 15            E
## 16            E
## 17            A
## 18            B
## 19            B
## 20            B
```

Conclusion

As we can see from the three methods used, each one is improving in its precision but it also has to take into account the time it takes in each of its internal calculations. therefore we stick with rainforest for 99% accuracy.
