assignment1

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

```
## Rattle: A free graphical interface for data science with R.
## Version 5.1.0 Copyright (c) 2006-2017 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
```

```
##
## Attaching package: 'rattle'
```

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

```
set.seed(1234)
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!",""))
inTrain <- createDataPartition(y=training$classe, p=0.6, list=FALSE)
myTraining <- training[inTrain, ]; myTesting <- training[-inTrain, ]
dim(myTraining); dim(myTesting)
```

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

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

```
myDataNZV <- nearZeroVar(myTraining, saveMetrics=TRUE)
myNZVvars <- names(myTraining) %in% c("new_window", "kurtosis_roll_belt", "kurtosis_picth_belt",
                                      "kurtosis_yaw_belt", "skewness_roll_belt", "skewness_roll_belt.1", "skewn
ess_yaw_belt",
                                      "max_yaw_belt", "min_yaw_belt", "amplitude_yaw_belt", "avg_roll_arm", "st
ddev_roll_arm",
                                      "var_roll_arm", "avg_pitch_arm", "stddev_pitch_arm", "var_pitch_arm", "av
g_yaw_arm",
                                      "stddev_yaw_arm", "var_yaw_arm", "kurtosis_roll_arm", "kurtosis_picth_ar
m",
                                      "kurtosis_yaw_arm", "skewness_roll_arm", "skewness_pitch_arm", "skewness_
yaw_arm",
                                      "max_roll_arm", "min_roll_arm", "min_pitch_arm", "amplitude_roll_arm", "a
mplitude_pitch_arm",
                                      "kurtosis_roll_dumbbell", "kurtosis_picth_dumbbell", "kurtosis_yaw_dumbe
ll", "skewness_roll_dumbbell",
                                      "skewness_pitch_dumbbell", "skewness_yaw_dumbbell", "max_yaw_dumbbell",
"min_yaw_dumbbell",
                                      "amplitude_yaw_dumbbell", "kurtosis_roll_forearm", "kurtosis_picth_forear
m", "kurtosis_yaw_forearm",
                                      "skewness_roll_forearm", "skewness_pitch_forearm", "skewness_yaw_forearm"
, "max_roll_forearm",
                                      "max_yaw_forearm", "min_roll_forearm", "min_yaw_forearm", "amplitude_roll
_forearm",
                                      "amplitude_yaw_forearm", "avg_roll_forearm", "stddev_roll_forearm", "var_
roll_forearm",
                                      "avg_pitch_forearm", "stddev_pitch_forearm", "var_pitch_forearm", "avg_ya
w_forearm",
                                      "stddev_yaw_forearm", "var_yaw_forearm")

myTraining <- myTraining[!myNZVvars]
myTraining <- myTraining[c(-1)]
trainingV3 <- myTraining #creating another subset to iterate in loop
for(i in 1:length(myTraining)) { #for every column in the training dataset
  if( sum( is.na( myTraining[, i] ) ) /nrow(myTraining) >= .6 ) { #if 60% NAs > 60% of total observations
    for(j in 1:length(trainingV3)) {
      if( length( grep(names(myTraining[i]), names(trainingV3)[j]) ) ==1)  { #if the columns are the same:
        trainingV3 <- trainingV3[ , -j] #Remove that column
      }
    }
  }
}
#To check the new N?? of observations
dim(trainingV3)
```

```
## [1] 11776    58
```

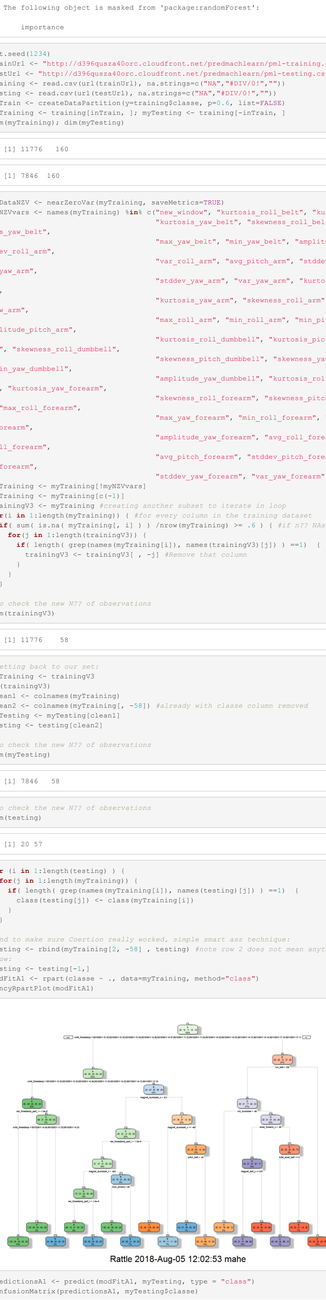
```
#Getting back to our set:
myTraining <- trainingV3
rm(trainingV3)
clean1 <- colnames(myTraining)
clean2 <- colnames(myTraining[, -58]) #already with classe column removed
myTesting <- myTesting[clean1]
testing <- testing[clean2]

#To check the new N?? of observations
dim(myTesting)
```

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

```
#To check the new N?? of observations
dim(testing)
```

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

```
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])
    }
  }
}
#And to make sure Coertion really worked, simple smart ass technique:
testing <- rbind(myTraining[2, -58] , testing) #note row 2 does not mean anything, this will be removed right..
now:
testing <- testing[-1,]
modFitA1 <- rpart(classe ~ ., data=myTraining, method="class")
fancyRpartPlot(modFitA1)
```




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

```
## Confusion Matrix and Statistics
##
##          Reference
## Prediction    A    B    C    D    E
##          A 2161   61    5    3    0
##          B   50 1271   95   64    0
##          C   21  177 1242  203   65
##          D    0    9   19  899   92
##          E    0    0    7  117 1285
##
## Overall Statistics
##
##                Accuracy : 0.8741
##                  95% CI : (0.8665, 0.8813)
##     No Information Rate : 0.2845
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.8407
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            0.9682   0.8373   0.9079   0.6991   0.8911
## Specificity            0.9877   0.9670   0.9281   0.9817   0.9806
## Pos Pred Value         0.9691   0.8588   0.7272   0.8822   0.9120
## Neg Pred Value         0.9874   0.9612   0.9795   0.9433   0.9756
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2754   0.1620   0.1583   0.1146   0.1638
## Detection Prevalence   0.2842   0.1886   0.2177   0.1299   0.1796
## Balanced Accuracy      0.9779   0.9021   0.9180   0.8404   0.9359
```

```
modFitB1 <- randomForest(classe ~. , data=myTraining)
predictionsB1 <- predict(modFitB1, myTesting, type = "class")
confusionMatrix(predictionsB1, myTesting$classe)
```

```
## Confusion Matrix and Statistics
##
##          Reference
## Prediction    A    B    C    D    E
##          A 2232    2    0    0    0
##          B    0 1516    3    0    0
##          C    0    0 1363    5    0
##          D    0    0    2 1280    1
##          E    0    0    0    1 1441
##
## Overall Statistics
##
##                Accuracy : 0.9982
##                  95% CI : (0.997, 0.999)
##     No Information Rate : 0.2845
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9977
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: A Class: B Class: C Class: D Class: E
## Sensitivity            1.0000   0.9987   0.9963   0.9953   0.9993
## Specificity            0.9996   0.9995   0.9992   0.9995   0.9998
## Pos Pred Value         0.9991   0.9980   0.9963   0.9977   0.9993
## Neg Pred Value         1.0000   0.9997   0.9992   0.9991   0.9998
## Prevalence             0.2845   0.1935   0.1744   0.1639   0.1838
## Detection Rate         0.2845   0.1932   0.1737   0.1631   0.1837
## Detection Prevalence   0.2847   0.1936   0.1744   0.1635   0.1838
## Balanced Accuracy      0.9998   0.9991   0.9978   0.9974   0.9996
```

```
predictionsB2 <- predict(modFitB1, testing, type = "class")
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(predictionsB2)

dim(myTraining)
```

```
## [1] 11776    58
```