Weight Lifting Project Code

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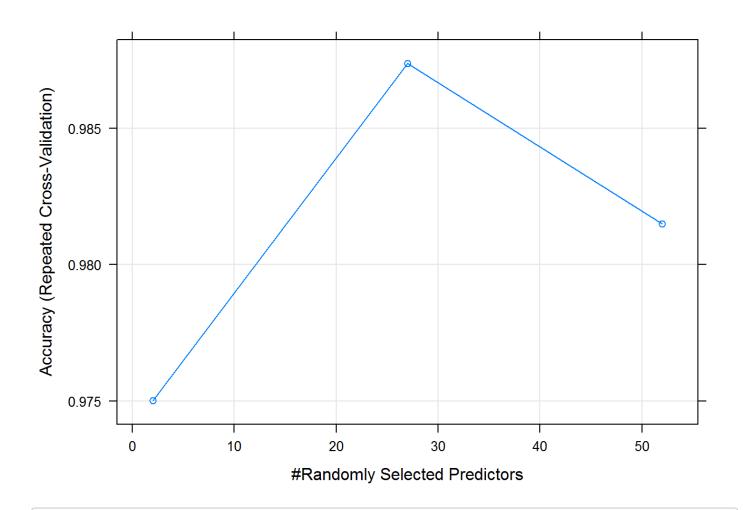
IN THE COMPILED HTML I reduced the number of trees in the random forest from 1000 to 10, because it took several hours to run the 1000 trees I used to build my random forest models; thus the results in this document are different from the results presented in the project write-up.

```
setwd('C:/Rrepos/Rdata/PML')
getwd()
#install.packages('caret', dependencies=c('Depends', 'Suggests'))
require(caret)
## Loading required package: caret
## Warning: package 'caret' was built under R version 3.1.3
## Loading required package: lattice
## Loading required package: ggplot2
# IN THE COMPILED HTML I reduced the number of trees in the random forest from
# 1000 to 10, because it took several hours to run the 1000 trees; thus the results
# in this document are different from the results presented in the project write-up.
# Loading the data
test <- read.csv('C:/Rrepos/Rdata/PML/testing.csv', stringsAsFactors=T, header = T)</pre>
train <- read.csv('C:/Rrepos/Rdata/PML/training.csv', stringsAsFactors=T, header = T)</pre>
# preparing the data; since goal was to predict, eliminated data that did not seem relevan
t (some of initial
# columns, including individual names, and then data that had no values or NAs in the tes
ting dataset; this corresponded to similar but not
# completely equivalent data in the training set (i.e., were some values for kurtosis, et
c.)); note that Adelmo
# had "0" for roll, pitch and yaw forearm
train1 <- train[,-c(1, 3:7,12:36,50:59,69:83,87:101,103:112,125:139,141:150)]
test1 <- test[,-c(1, 3:7,12:36,50:59,69:83,87:101,103:112,125:139,141:150)]
train1 <- train1[,c(2:53,1,54)]
test1 <- test1[,c(2:53,1,54)]
# subsetting the data into training and test data
```

```
inTrain <- createDataPartition(y=train1$class, p=0.7, list=FALSE)</pre>
training <- train1[inTrain,]</pre>
testing <- train1[inTrain,]</pre>
#looking for complete cases
train2 <- complete.cases(train1)</pre>
train3 <-train1[train2,]</pre>
nrow(train3)
# look at distribution of samples among classes in all three data sets
prop.orig <- prop.table(table(train1[54]))</pre>
original_Proportions <- prop.orig</pre>
prop.train <- prop.table(table(training[54]))</pre>
training Proportions <- prop.train
prop.test <- prop.table(table(testing[54]))</pre>
testing Proportions <- prop.test
Table1 <- rbind(original Proportions, training Proportions, testing Proportions)</pre>
Table1
# check for near zero varaiance predictors
training1 <- nearZeroVar(training)</pre>
training1
# check for highly correlated variables and remove
Corr <- cor(training[-c(53:54)])</pre>
highCorr <- findCorrelation(Corr, 0.90)</pre>
names(training[highCorr])
training <- training[,-highCorr]</pre>
testing <- testing[,-highCorr]</pre>
test2 <- test1[,-highCorr]</pre>
# fitting a model and detemining variable importance using random forest
cvCtrl <- trainControl(method='repeatedcv', repeats=3, classProbs=TRUE)</pre>
modFit <- train(class~., data=training, method='rf', ntree=10, trControl=cvCtrl)</pre>
```

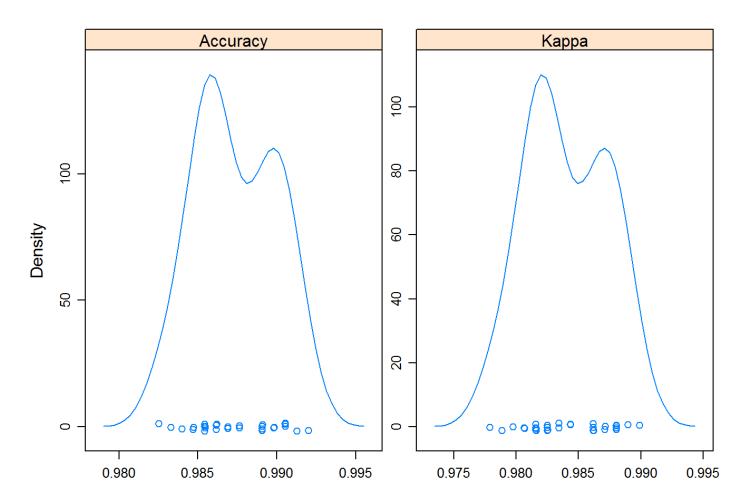
```
## Loading required package: randomForest
## randomForest 4.6-10
## Type rfNews() to see new features/changes/bug fixes.
```

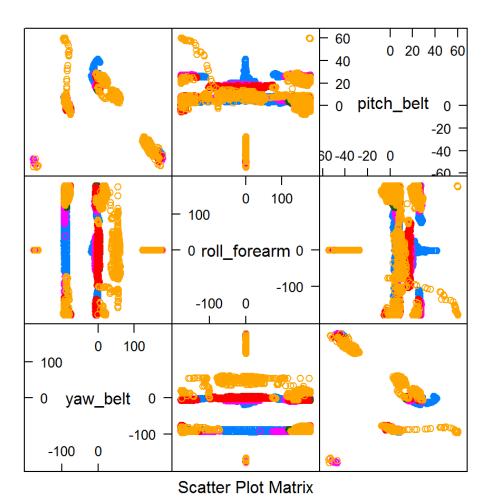
```
modFit
#looking at plots of results and variable importance
Y <- plot(modFit)
Y</pre>
```

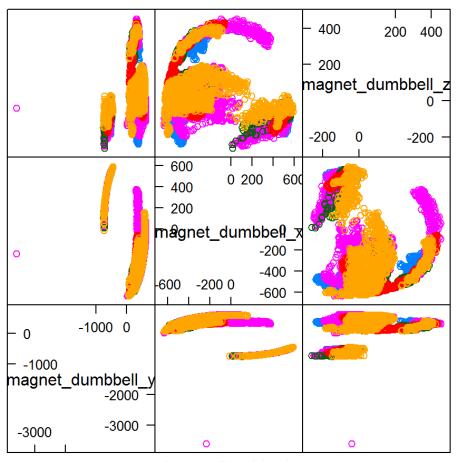


p <- resampleHist(modFit)
p</pre>

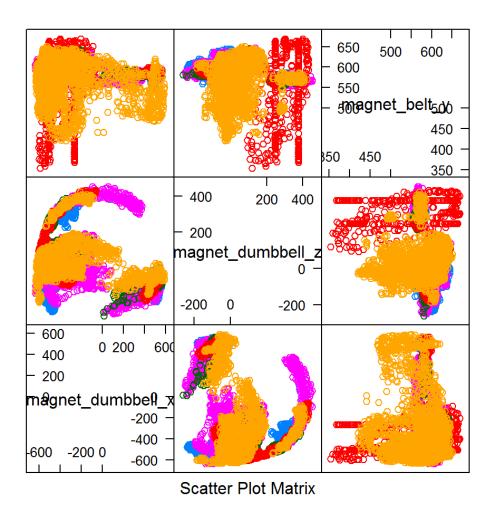
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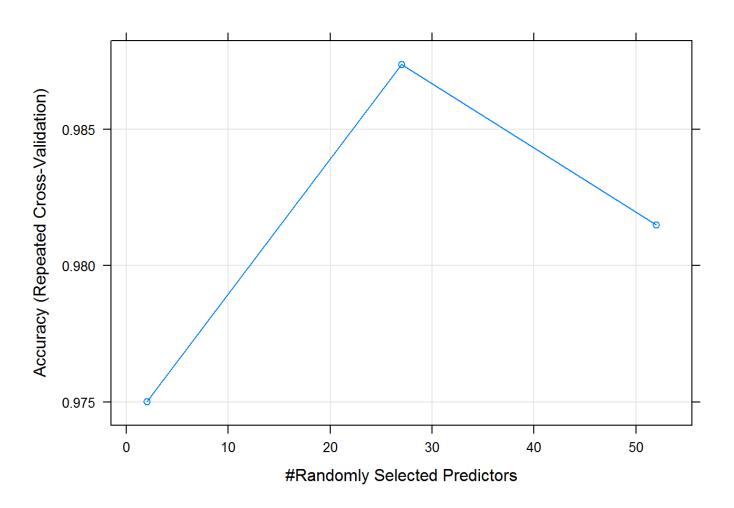




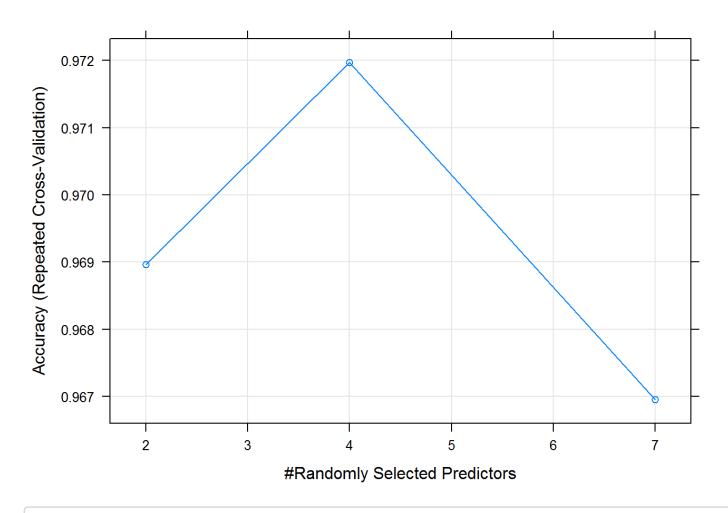
Scatter Plot Matrix



plotting number of predictors vs. accuracy
plot(modFit)

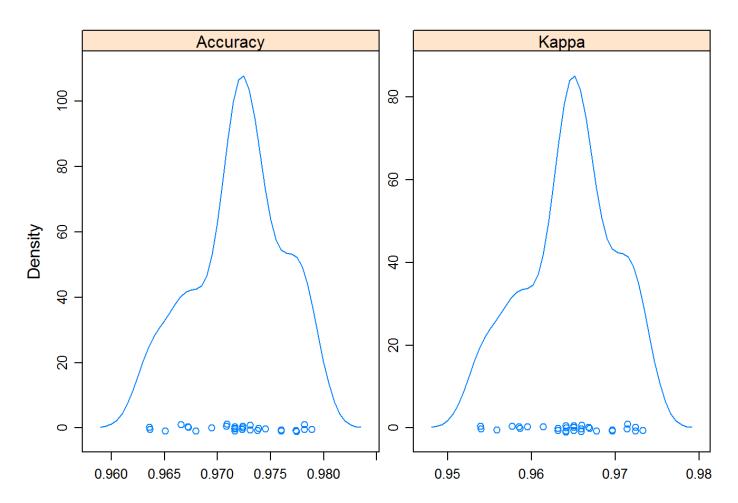


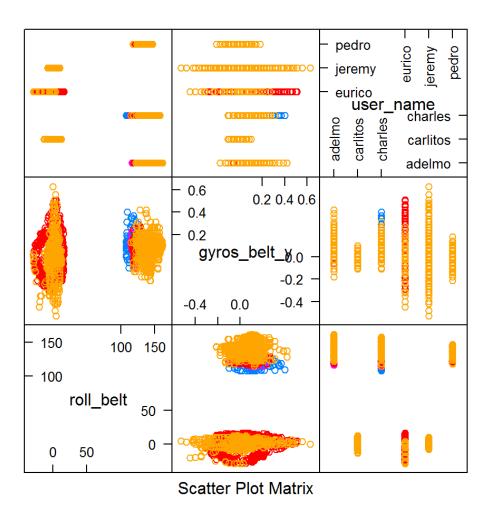
```
# (some of initialcolumns, including individual names, and then data that had no values o
# NAs in the testing dataset; this corresponded to similar but not completely equivalent
# data in the training set (i.e., were some values for kurtosis, etc.)); note that Adelmo
# had "0" for roll, pitch and yaw forearm
train1 <- train[,-c(1, 3:7,12:36,50:59,69:83,87:101,103:112,125:139,141:150)]
test1 <- test[,-c(1, 3:7,12:36,50:59,69:83,87:101,103:112,125:139,141:150)]
# subsetting the data into training and test data
inTrain <- createDataPartition(y=train1$class, p=0.7, list=FALSE)</pre>
training <- train1[inTrain,]</pre>
testing <- train1[-inTrain,]</pre>
#looking for complete cases
train2 <- complete.cases(train1)</pre>
train3 <-train1[train2,]</pre>
nrow(train3)
which(colnames(training)=='yaw_belt')
which(colnames(training)=='pitch forearm')
which(colnames(training)=='pitch_belt')
which(colnames(training)=='magnet dumbbell z')
which(colnames(training)=='magnet_dumbbell_y')
which(colnames(training)=='roll forearm')
which(colnames(training)=='magnet belt y')
# creating subsets of data that had just the 7 most important variables
trainSub <- training[,c(3:4, 13, 39:42, 54)]
testSub <- testing[,c(3:4, 13, 39:42, 54)]
test1Sub <- test1[,c(3:4, 13, 39:42, 54)]
# fitting a model and detemining variable importance using random forest
cvCtrl <- trainControl(method='repeatedcv', repeats=3, classProbs=TRUE)</pre>
modFit <- train(class~., data=trainSub, method='rf', ntree=10, trControl=cvCtrl)</pre>
modFit
Y <- plot(modFit)
Υ
```



p <- resampleHist(modFit)</pre>

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plotting number of predictors vs. accuracy
plot(modFit)

