# **Weight Exsercise Prediction**

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## **Executive Summary**

In this project, the goal will be to use data from accelerometers on the belt, forearm, arm, and dumbell of 6 participants to predict the manner in which an exercise is done.

In particular, we will:

Get and clean the data set:

- Train data is from here (https://d396qusza40orc.cloudfront.net/predmachlearn/pml-training.csv)
- Test data is found at here (https://d396qusza40orc.cloudfront.net/predmachlearn/pml-testing.csv)

Perform Exploratory data analysis to identify patterns

Pre-process data to split and validate, reduce dimentionality with PCA and remoe zero covariates

Fit models on different predictors

Assess model metrics

Summary

## **Getting and Cleaning Data**

#### Data

## [1] 19622 160

#### **Data Cleaning**

Checking for NAs, it looks like some columns have NAs of more than 50% the size of the dataset, therefore columns with NAs more than 20% of the size of the data will be droped, which then reduce the number of columns. Also we will remove timestamp columns since we don't need them as prediction

```
size <- nrow(df.train)
perc <- 20
Na_thresh <- floor(size/100 * perc)

## Drop columns with more than 20% na
dropped_cols <- which(colSums(is.na(df.train) | df.train == "") > Na_thresh)

train_val_set <- df.train[, -c(1, dropped_cols)]

test_set <- df.test[, -c(1, dropped_cols)]

## Drop all columns having timestamp
dropped_time_cols <- grep('timestamp', names(train_val_set))
train_val_set <- train_val_set[, -dropped_time_cols]

test_set <- test_set[, -dropped_time_cols]

## Make classe a factor
train_val_set$classe <- factor(train_val_set$classe)
train_val_set$user_name <- factor(train_val_set$user_name)
test_set$user_name <- factor(test_set$user_name)</pre>
```

#### Split training set to train and validation

3/4 for training and 1/4 for validation

```
partition <- createDataPartition(y = train_val_set$classe, p = 3/4, list = F)

train_data <- train_val_set[partition, ]
validation_data <- train_val_set[-partition, ]

response <- which(names(train_data) == c("classe"))</pre>
```

## **Exploratory Analysis**

### Removing zero covariates

zero or near zero covariates predictors will be removed

```
nsv <- nearZeroVar(train_data, saveMetrics=TRUE)

train_data = train_data[, !nsv$nzv]
validation_data = validation_data[, !nsv$nzv]
test_set = test_set[, !nsv$nzv]

nsv</pre>
```

##	freqRatio	percentUnique	zeroVar	nzv
## user_name	1.104766	0.04076641	FALSE	FALSE
## new_window	47.255738	0.01358880	FALSE	TRUE
## num_window	1.034483	5.82280201	FALSE	FALSE
## roll_belt	1.110429	7.91547765	FALSE	FALSE
## pitch_belt	1.013514	11.80866966	FALSE	FALSE
## yaw_belt	1.060686	12.55605381	FALSE	FALSE
## total_accel_belt	1.064262	0.19024324	FALSE	FALSE
## gyros_belt_x	1.026188	0.90365539	FALSE	FALSE
## gyros_belt_y	1.146927	0.44163609	FALSE	FALSE
## gyros_belt_z	1.057678	1.11428183	FALSE	FALSE
## accel_belt_x	1.119171	1.10748743	FALSE	FALSE
## accel_belt_y	1.155203	0.95121620	FALSE	FALSE
## accel_belt_z	1.098935	1.94319880	FALSE	FALSE
## magnet_belt_x	1.130112	2.08588123	FALSE	FALSE
## magnet_belt_y	1.168421	1.95678761	FALSE	FALSE
## magnet_belt_z	1.020000	3.00312542	FALSE	FALSE
## roll_arm	46.163636			FALSE
## pitch_arm	79.375000	19.35724963	FALSE	FALSE
## yaw_arm	32.974026			FALSE
## total_accel_arm	1.022422			FALSE
## gyros_arm_x	1.114441	4.27367849	FALSE	FALSE
## gyros_arm_y	1.496021			FALSE
## gyros_arm_z	1.121588			FALSE
## accel_arm_x	1.088000			FALSE
## accel arm y	1.200000	3.60782715		FALSE
## accel arm z	1.144330			FALSE
## magnet_arm_x	1.000000			FALSE
## magnet arm y	1.074627			FALSE
## magnet arm z	1.000000			FALSE
## roll dumbbell	1.000000			FALSE
## pitch_dumbbell	2.382353	83.93124066		FALSE
## yaw_dumbbell	1.120879	85.58907460	FALSE	FALSE
## total_accel_dumbbell		0.29215926		FALSE
## gyros dumbbell x	1.015217			FALSE
## gyros dumbbell y	1.287671			FALSE
## gyros dumbbell z	1.055679		FALSE	FALSE
## accel dumbbell x	1.044355		FALSE	FALSE
## accel dumbbell y	1.081967		FALSE	FALSE
## accel dumbbell z	1.171271		FALSE	FALSE
## magnet dumbbell x	1.058824	7.33795353	FALSE	FALSE
## magnet dumbbell y	1.192593	5.60538117	FALSE	FALSE
## magnet dumbbell z	1.027972	4.52507134	FALSE	FALSE
## roll forearm	11.641434		FALSE	FALSE
## pitch_forearm	64.911111	18.21579019	FALSE	FALSE
## yaw forearm	15.455026	12.22312814	FALSE	FALSE
## total_accel_forearm				FALSE
## gyros forearm x	1.062189			FALSE
## gyros_forearm_y	1.062718			FALSE
## gyros_forearm_z	1.092643			FALSE
## accel forearm x	1.169231			FALSE
## accel forearm y	1.040000			FALSE
## accel_forearm_z	1.008403			FALSE
			<b>-</b>	

```
## magnet_forearm_x
                                     10.00815328
                          1.064516
                                                    FALSE FALSE
## magnet_forearm_y
                          1.206349
                                     12.44734339
                                                    FALSE FALSE
## magnet forearm z
                          1.106383
                                     11.02731349
                                                    FALSE FALSE
## classe
                          1.469452
                                      0.03397201
                                                    FALSE FALSE
```

#### Check for correlation between predictors and response variable

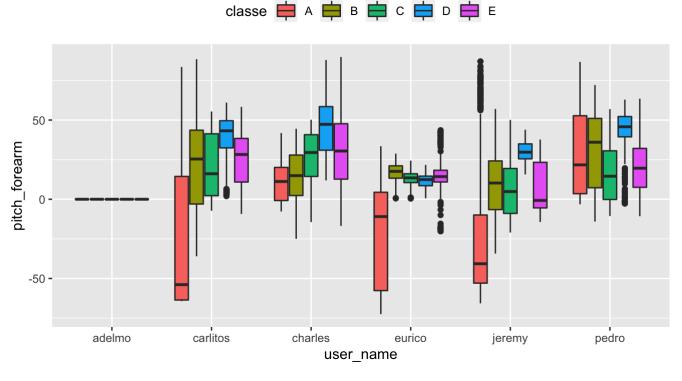
The table below shows all variables have less correlation with the response varible

```
## Remove non numeric columns before calculating correlation
df <- train_data %>% select(-c("user_name", "classe"))

corr <- cor(df, as.numeric(train_data$classe))

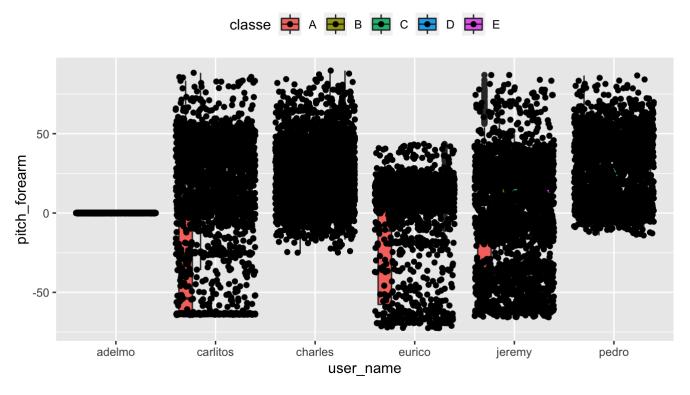
## Convert to dataframe and arrange in decreasing order
coor_df = data.frame(name= row.names(corr) ,pos_cor = abs(corr))
coor_df[coor_df$pos_cor >0.3,]
```

We can now visualize this for a better pespertive



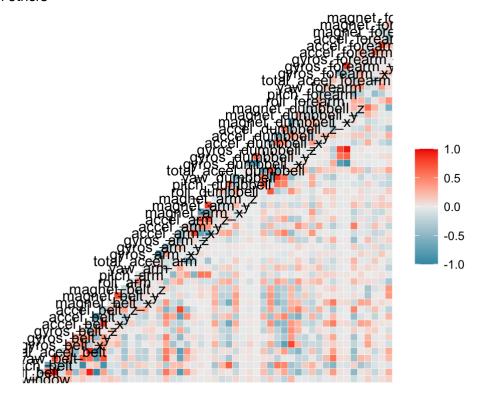
### Plot with points overlayed

This plot shows the number of data-points in each category of user-name, it can be inferred that each person is well represented in the dataset



### Check for correlation between predictors

This plot is not very informational as we have several variable but we can infer that some variables are strongly correlated with others



Now is a better tim to eliminate highly correlated columns

```
high_cor = findCorrelation(cor(df), cutoff = 0.8)
exclude_cols = c(response, high_cor)
```

## **Pre-processing for training**

To reduce overfitting and also dimentionality, we will use PCA with a thresh of 0.9

```
## USe pca to reduce highly correlated variables
pca.all <- preProcess(train_data[, -response], method = 'pca', thresh = 0.9)
train_data.pca.all <- predict(pca.all, train_data[, -response])
validation_data.pca.all <- predict(pca.all, validation_data[, -response])
test_set.pca.all <- predict(pca.all, test_set[, -response])

## remove highly correlated columns and fit pca
pca.excluded <- preProcess(train_data[, -exclude_cols], method = 'pca', thresh = 0.9)
train_data.pca.excluded <- predict(pca.excluded, train_data[, -exclude_cols])
validation_data.pca.excluded <- predict(pca.excluded, validation_data[, -exclude_cols])
#test_set.pca.excluded <- predict(pca.excluded, test_set[, -exclude_cols])</pre>
```

### Model

- Before pca model The next model will be fit on predictors after removing highly correlated variables.
- The train function takes a almost 10x time to train relative to the specific randomForest function but highly efficient.

user system elapsed 3955.071 67.123 4067.016

```
rf.all <- randomForest::randomForest(x = train data[, -response], y = train data$classe,
                                 ntree = 100,
                                  ytest =validation data$classe, xtest = validation data
        [, -response])
rf.excluded <- randomForest::randomForest(x = train_data[, -exclude_cols], y = train_dat
        a$classe,
                                 ntree = 100,
                                  ytest =validation data$classe, xtest = validation data
        [, -exclude cols])
rf.pca <- randomForest::randomForest(x = train_data.pca.all, y = train_data$classe,
                                 ntree = 200,
                                 xtest =validation data.pca.all, ytest =validation data$
        classe )
rf.pca.excluded <- randomForest::randomForest(x = train data.pca.excluded, y = train dat
        a$classe,
                                 ntree = 200, ytest =validation data$classe ,
                                 xtest = validation data.pca.excluded)
```

### **Metrics**

### **Train Accuracy**

```
## [1] "All Predictors acc: 1 Predictors with no high cor acc: 1 PCA acc: 1 PCA with h
igh corr removed acc: 1"
```

### Validation Accuracy

```
## [1] "All Predictors acc: 1 Predictors with no high cor acc: 0.999 PCA acc: 1 PCA wi th high corr removed acc: 1"
```

## **Summary**

- PCA reduces computational time and also gives a good parsimonious model
- Train function is over 10x slower than specific function randomForest
- Removing highly correlated predictors before PCA does not change model performance significantly as PCA takes care of the same thing
- An Accuracy of 99.7% and 87% was achieved on validation set using all predictors and PCA respectively