Course Project

Load stuff

```
require(caret)
require(ggplot2)
require(reshape2)
require(plyr)

#set.seed(42)  # make results reproducible

ds <- read.csv('data/pml-training.csv')
test <- read.csv('data/pml-testing.csv')
```

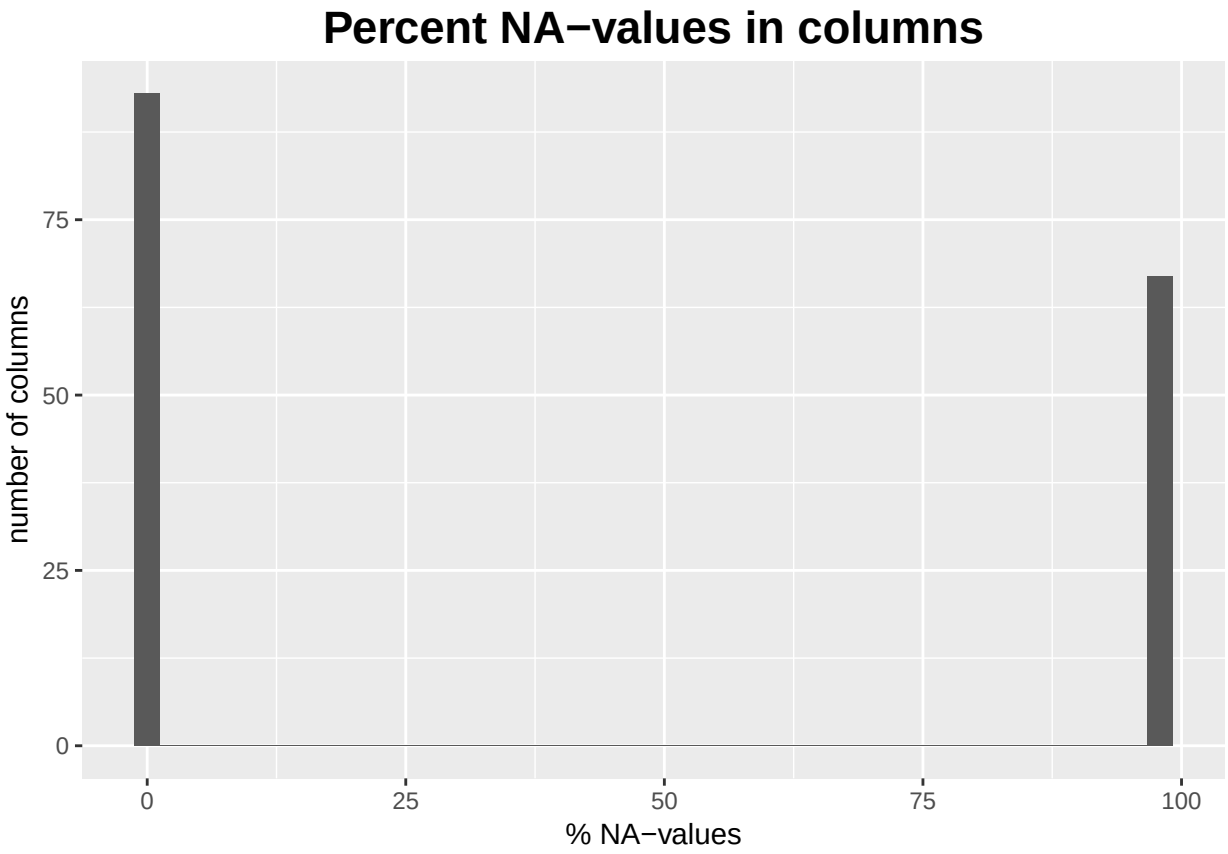
Exploratory data analysis

```
ds_complete <- na.omit(ds)

na_count <- apply(ds, 2, function(x) sum(is.na(x)))  # count number of missing values per column
na_cols <- names(na_count[na_count != 0])
complete_cols <- names(na_count[na_count == 0])

na_per_col <- data.frame(na_count)
na_per_col$colname <- rownames(na_per_col)
na_per_col$percent <- (na_per_col$na_count / nrow(ds)) * 100

g <- ggplot(data=na_per_col) +
  geom_histogram( aes(x=percent), bins=40 ) +
  xlab('% NA-values') +
  ylab('number of columns') +
  ggtitle('Percent NA-values in columns') +
  theme(plot.title = element_text(size=17, face='bold', hjust=0.5))
g
```



There are 19622 observations of barbell exercises in the dataset (one observation being one repetition). The number of features is 158. However, the data is not complete. All except 406 observations contain missing values.

The missing values are not distributed uniformly over the columns. 93 columns have no missing values at all. On the other hand, 67 columns have close to 100% of missing values (almost as if they were deleted on purpose... :-)). With such a high fraction of missing values, one can already suspect that 67 of the features will not be of much use for the prediction. Nevertheless, for the sake of gathering experience, I decided to analyze all features.

It has to be noted that the dataset is ordered, with all the class-A observations at the top of the dataset, followed by class-B observations and so on. Therefore, when fitting a preliminary model, the index-variable X - which just indicates the position of the observation in the dataframe - was identified as the most important 'feature'. Of course, in the test-set or a real-word dataset, the data will not be ordered by class. Therefore, I make sure not to include index variable 'X' in the feature list. For the same reason, I excluded the timestamp-columns from the features. The name of the person performing the exercise was also not used as a feature. It is possible that the name is a useful feature for prediction of the test set, because the test set was collected with the same people as the training set. However, the study aims to identify general patterns which do not depend on the person doing the exercise. Therefore, the information who performed the exercise is intentionally ignored in the model.

Functions for fitting and evaluating random forest models

```
trainRF <- function(trainingdata, features) {
  cv_params <- trainControl(method = 'repeatedcv',
                            number = 4,  # number of folds
```

```
                          repeats = 1,  # number of times, the cv is repeated
                          allowParallel = TRUE)
  RFmodel <- train(classe ~ .,
                   data = trainingdata[,c(features, 'classe')],  # only features and outcome variable (no
                   method = 'rf',
                   trControl = cv_params,
                   importance = TRUE,  # for feature importance
                   verbose = FALSE)
  return(RFmodel)
}

get_probabilities <- function(testdata, features, my_model) {
  prob <- predict(my_model,
                  newdata = testdata[,features],
                  type = 'prob')
  prob$id <- rownames(prob)
  long <- melt(prob, id.vars='id')
  return(long[order(long$id),])
}

get_predictions <- function(probabilities) {  # long format dataframe of probabilities
  pred <- ddply(probabilities, 'id', function(x) {  # get prediction from probability
    return(head(subset(x, value == max(x$value)), 1))  # in case of equal probabilites: take first
  })
  colnames(pred) <- c('id', 'prediction', 'probability')
  return(pred)
}

evaluate <- function(predictions, testdata) {  #
  truth <- data.frame(rownames(testdata), testdata[,'classe'])
  colnames(truth) <- c('id', 'classe')
  compare <- merge(predictions, truth, by='id')
  accuracy <- nrow(subset(compare, prediction == classe)) / nrow(compare)
  return(list(compare, accuracy))
}

get_accuracy <- function(testdata, features, my_model) { # just calculate accuracy (predictions not ret
  prob <- get_probabilities(testdata, features, my_model)
  pred <- get_predictions(prob)
  return(evaluate(pred, testdata)[[2]])
}
```

Feature importance

A runtime of about 5 minutes on this small dataset (using 4-fold cross-validation) revealed it wouldn't be computationally feasible to use all observations and all features for fitting a model. Hence, even if the whole dataset was complete, I would have to select a subset of features.

The feature selection process below is very simple. Fist, a preliminary random forest model was fitted using all features and the importance of the features was determined using the varImp-function. Then, a model was fit to the small training set using only the top 5, top 10, top 15, etc. features.

```
# Split the small, complete dataset of 406 rows into a training set and a test set:
inTraining_mini <- createDataPartition(ds_complete$classe, p = .75, list = FALSE)
minitrain <- ds_complete[ inTraining_mini,]
minitest  <- ds_complete[-inTraining_mini,]
```

good link about runtime: https://www.quora.com/What-is-the-time-complexity-of-Random-Forest-both-building-the-model-a

Fit preliminary model to analyze feature importance

```
RFmodel_prelim <- trainRF(minitrain, feat)
```

```
feat_imp <- data.frame(varImp(RFmodel_prelim)$importance)
feat_imp['average'] <- rowMeans(feat_imp[,c('A', 'B', 'C', 'D', 'E')])
feat_imp <- feat_imp[with(feat_imp, order(average, decreasing=TRUE)),]

top50 <- rownames(head(feat_imp, 50))
top30 <- rownames(head(feat_imp, 30))
top20 <- rownames(head(feat_imp, 20))
top10 <- rownames(head(feat_imp, 10))

head(feat_imp, 10)
```

```
##                            A          B         C        D        E
## var_accel_dumbbell   64.35182 100.000000 86.629836 81.09161 42.37485
## min_roll_forearm     61.49832  30.909220 45.891617 87.92709 13.72594
## var_roll_belt        40.40543  42.631203 39.817772 45.33585 51.24219
## stddev_roll_belt     39.97822  38.357106 38.865720 42.28720 48.12444
## avg_roll_dumbbell    43.98174  23.779371 54.586875 52.21827 12.91149
## avg_roll_belt        37.17181  33.564879 34.315505 33.39768 43.43468
## var_total_accel_belt 34.97033  29.361843 32.434529 36.29284 40.56569
## magnet_dumbbell_z    40.23184  11.480189 33.849589 41.30093 34.76522
## accel_forearm_z      17.99265   9.466516  9.436073 56.61032 50.86930
## avg_pitch_dumbbell   33.33080   9.751794 40.469331 18.85087 10.69826
##                       average
## var_accel_dumbbell   74.88962
## min_roll_forearm     47.99044
## var_roll_belt        43.88649
## stddev_roll_belt     41.52254
## avg_roll_dumbbell    37.49555
## avg_roll_belt        36.37691
## var_total_accel_belt 34.72505
## magnet_dumbbell_z    32.32555
## accel_forearm_z      28.87497
## avg_pitch_dumbbell   22.62021
```

Plot accuracy as a function of feature importance

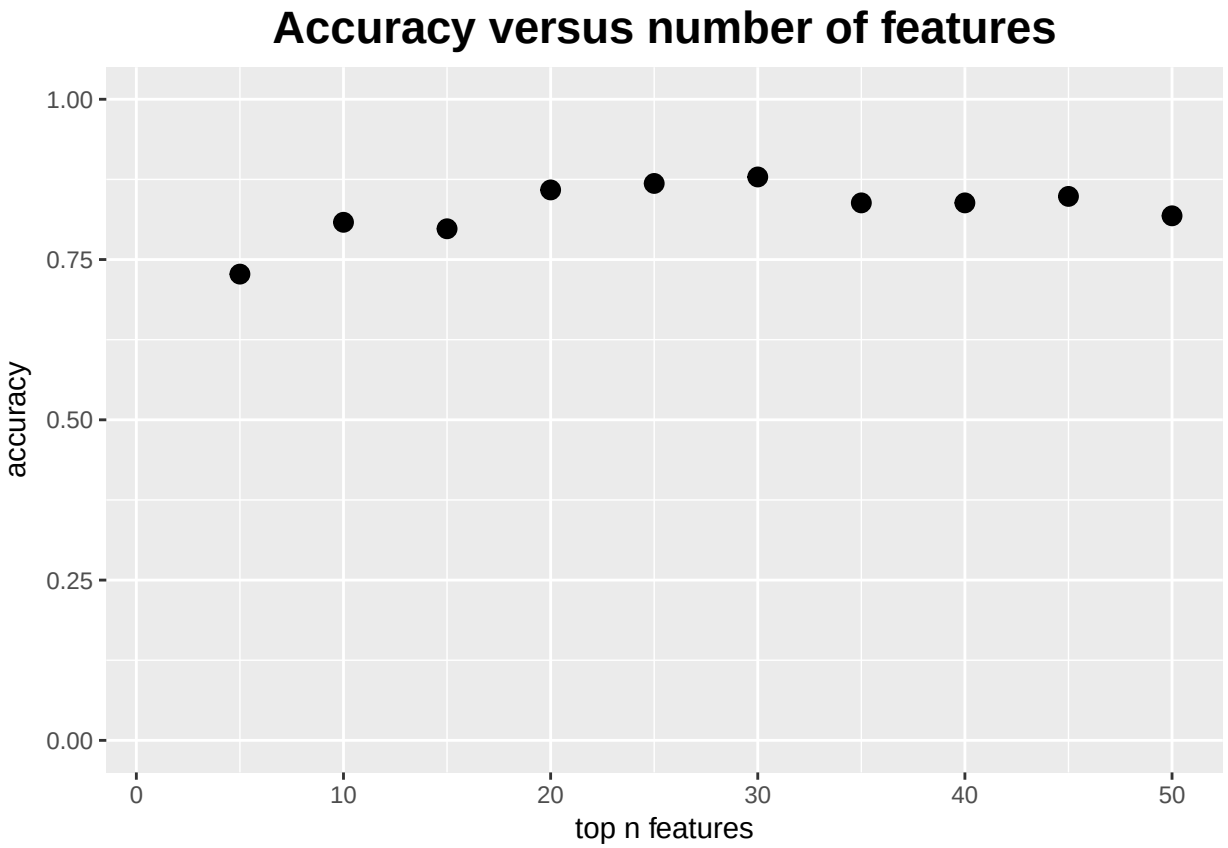
```
get_accuracy_for_feature_subsets <- function(trainingdata, testdata, feature_importance) {
  top_n_features <- (1:10)*5  # which top n features to test
  accuracy <- c()
  for (i in top_n_features) {
    top_features <- rownames(head(feature_importance, i))
```

```
    RFmodel <- trainRF(trainingdata, top_features)
    accuracy <- c(accuracy, get_accuracy(testdata, top_features, RFmodel))
  }
  return(data.frame(top_n_features, accuracy))
}
```

```
feat_acc <- get_accuracy_for_feature_subsets(minitrain, minitest, feat_imp)
feat_acc
```

```
##    top_n_features  accuracy
## 1               5 0.7272727
## 2              10 0.8080808
## 3              15 0.7979798
## 4              20 0.8585859
## 5              25 0.8686869
## 6              30 0.8787879
## 7              35 0.8383838
## 8              40 0.8383838
## 9              45 0.8484848
## 10             50 0.8181818
```

```
g <- ggplot(data=feat_acc, aes(x=top_n_features, y=accuracy)) +
  geom_point(size=3) +
  scale_y_continuous(limits = c(0, 1)) +
  scale_x_continuous(limits = c(1, 50)) +
  xlab('top n features') +
  ggtitle('Accuracy versus number of features') +
  theme(plot.title = element_text(size=17, face='bold', hjust=0.5))
g
```



The plot above shows, that the accuracy increases with the use of more features until about 20 features. Then, the addition of more features does not increase the accuracy. The small differences in accuracy when using 20 or more features represent only the random fluctuations during fitting of a random forest model and can be safely ignored.

k-nearest neighbour imputation

Due large fraction of missing values in many features, imputation cannot be expected to work very well. Nevertheless, out of curiosity, a k-nearest neigbor imputation model was fitted on the small dataset of complete values (406 rows). Then, using this model, the missing value in the whole dataset (19622 rows) were imputed.

```
knn_imp_model <- preProcess(ds_complete, method = 'knnImpute')
ds_imp <- predict(knn_imp_model, ds)
```

Split whole dataset into training and validation set

```
inTraining <- createDataPartition(ds$classe, p = .75, list = FALSE)  # split the training data-set

training_imp <- ds_imp[inTraining,]  # training data with imputed values
validation_imp  <- ds_imp[-inTraining,]

training <- ds[inTraining,]  # training data with missing values
validation  <- ds[-inTraining,]
```

Fit model with imputed features

```
top_imputed_features <- top20

RFmodel_imp <- trainRF(training_imp, top_imputed_features)
prob <- get_probabilities(validation_imp, top_imputed_features, RFmodel_imp)
pred <- get_predictions(prob)
eval <- evaluate(pred, validation_imp)
acc <- eval[[2]]
acc
```

```
## [1] 0.9249592
```

Using the top 20 features - including 7 with mostly imputed values- gives a worse accuracy than just using the best 12 complete features (see next section). The reason for this is mostly the fact that all columns with missing values consist of 99% missing values and only 1% real values. Therefore, the KNN-imputation model is likely to be inaccurate due to a lack of training data. If the missing values were more sparse, it is conceivable that imputation would improve prediction accuracy. In a real-word dataset it would be more likely to find at least a few missing values in every feature and (column) and maybe even a few missing values for each data point (row). In such cases, imputation is not only likely perform better but also necessary because because excluding all data points with missing values would leave only a fraction of the original dataset.

Fit model with real values only

```
feat_complete <- feat[feat %in% complete_cols]  # features without missing values
top_complete_features <- top50[top50 %in% complete_cols]

RFmodel <- trainRF(training, top_complete_features)
prob <- get_probabilities(validation, top_complete_features, RFmodel)
pred <- get_predictions(prob)
eval <- evaluate(pred, validation)
acc <- eval[[2]]
acc
```

```
## [1] 0.9877651
```