Assignment 4

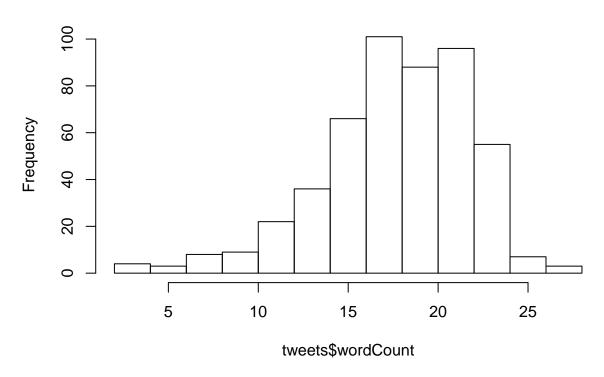
Loic Roldan Waals
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Question 2

First the data is imported

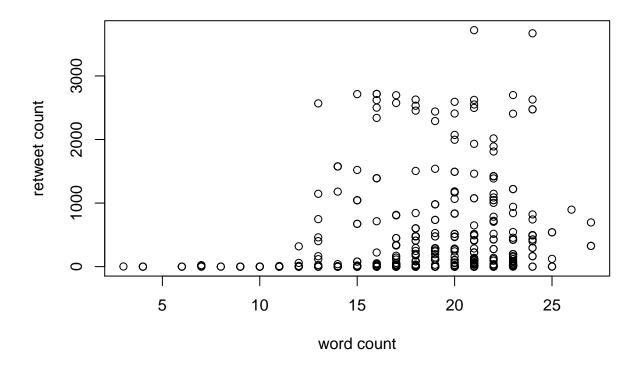
```
#determine where files are read and written
setwd("C:/Users/Loic RW/Google Drive/Big Data and Business Analytics/Assignments/Assignment 4")
#read all the data
library(readr)
tweets <- read_delim("C:/Users/Loic RW/Google Drive/Big Data and Business Analytics/Assignments/Assignm
                     ";", escape_double = FALSE, col_types = cols(favorited = col_skip(),
                                                                   favoriteCount = col_skip(), isRetweet
                                                                   latitude = col_skip(), longitude = co
                                                                   replyToSID = col_skip(), replyToSN =
                                                                   replyToUID = col_skip(), retweeted =
                                                                   statusSource = col_skip(), truncated
                     trim_ws = TRUE)
## Warning in rbind(names(probs), probs_f): number of columns of result is not
## a multiple of vector length (arg 1)
## Warning: 4 parsing failures.
## row # A tibble: 4 x 5 col
                              row col
                                            expected
                                                       actual
                                                                  file
tweets$retweetCount <- as.numeric(tweets$retweetCount)</pre>
## Warning: NAs introduced by coercion
#delete 4 NA's for "retweetcount"
tweets <- tweets[complete.cases(tweets),]</pre>
Next we make a histogram of the number of words of the tweets.
library(ngram)
for (i in 1:nrow(tweets)) {
  tweets$wordCount[i] <- as.numeric(wordcount(tweets$text[i], sep = " ", count.function = sum))</pre>
}
## Warning: Unknown or uninitialised column: 'wordCount'.
```

Histogram of tweets\$wordCount



Next we plot number of words and number of retweets

plot(tweets\$wordCount, tweets\$retweetCount, xlab = "word count", ylab = "retweet count")

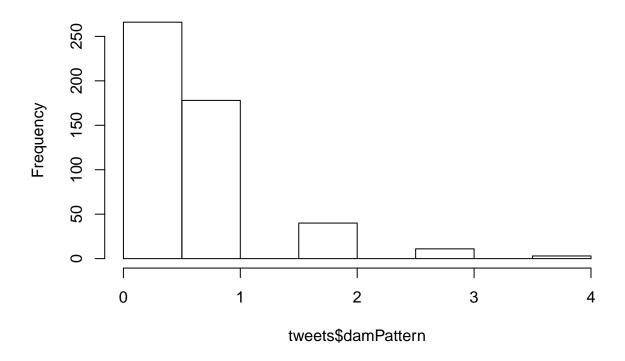


Next we calculate the frequency of the pattern "dam" per tweet. As we can see there are only two instances where the pattern "dam" is used. As this would not make for an exciting graph, we used the string "ing" instead for plotting it against time

```
library(stringr)

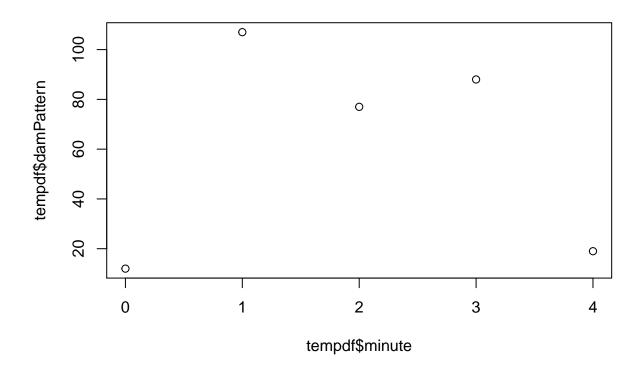
tweets$damPattern <- str_count(tweets$text, "ing")
hist(tweets$damPattern)</pre>
```

Histogram of tweets\$damPattern



```
tweets$realTime <- as.POSIXct(tweets$created, format = "%y-%m-%d %H:%M:%S")
tweets$minute <- as.POSIXlt(tweets$realTime)$min

tempdf <- tweets[,c("damPattern", "minute")]
tempdf <- aggregate(cbind(damPattern)~minute, data = tempdf, FUN = sum)
plot(tempdf$minute,tempdf$damPattern)</pre>
```



Question 3

First we import the data

Then we perform the analysis

```
library(C50)
library(e1071)
mdl <- Survived ~ .
#Xval
#cross validation
nFolds = 10
myFolds <- cut(seq(1,nrow(trainTitanic)),</pre>
               breaks = nFolds,
                labels = FALSE)
#initialise accuracy variables
accNB <- rep(NA, nFolds)
accSVM <- rep(NA, nFolds)</pre>
specNB <- rep(NA, nFolds)</pre>
specSVM <- rep(NA, nFolds)</pre>
sensNB <- rep(NA, nFolds)</pre>
sensSVM <- rep(NA, nFolds)</pre>
AUCNB <- rep(NA, nFolds)
AUCSVM <- rep(NA, nFolds)
library(caret)
## Loading required package: lattice
## Loading required package: ggplot2
library(pROC)
## Type 'citation("pROC")' for a citation.
## Attaching package: 'pROC'
## The following objects are masked from 'package:stats':
##
       cov, smooth, var
for (i in 1:nFolds) {
  cat("Analysis of fold", i, "\n")
  #define training and test set (print commands are to help troubleshoot
  #and determine where the programme aborted during errors)
  testIndex <- which(myFolds == i, arr.ind = TRUE)</pre>
  crossTest <- trainTitanic[testIndex, ]</pre>
  crossTrain <- trainTitanic[-testIndex, ]</pre>
  print("data allocated")
```

```
#train the models
rsltNB <- naiveBayes(mdl, data = crossTrain)</pre>
print("Naive Bayes trained")
rsltSVM <- svm(mdl, data = crossTrain)</pre>
print("svm trained")
#predict values
pdNB <- as.ordered(predict(rsltNB, crossTest, type = "class"))</pre>
print("nb predicted")
pdSVM = as.ordered(predict(rsltSVM, crossTest))
print("svm predicted")
pdNB
pdSVM
#measure accuracy
accNB[i] = mean(pdNB == crossTest$Survived)
print("nb accuracy saved")
accSVM[i] = mean(pdSVM == crossTest$Survived)
print("SVM accuracy saved")
confMatrix <- table(pdNB, crossTest$Survived)</pre>
specNB[i] = specificity(confMatrix)
sensNB[i] = sensitivity(confMatrix)
print("nb other measures done")
confMatrix <- table(pdSVM, crossTest$Survived)</pre>
specSVM[i] = specificity(confMatrix)
sensSVM[i] = sensitivity(confMatrix)
print("svm other measures done")
#AUC
crossTrain$Survived <- as.numeric(crossTrain$Survived)</pre>
crossTest$Survived <- as.numeric(crossTest$Survived)</pre>
rsltNB <- naiveBayes(mdl, data = crossTrain)</pre>
print("Naive Bayes trained")
rsltSVM <- svm(mdl, data = crossTrain)</pre>
print("svm trained")
pdNB <- predict(rsltNB, crossTest, type = "raw")</pre>
pdNB <- pdNB[,2]</pre>
print("nb predicted")
pdSVM = predict(rsltSVM, crossTest)
print("svm predicted")
AUCNB[i] = as.numeric(auc(crossTest$Survived, pdNB))
AUCSVM[i] = as.numeric(auc(crossTest$Survived, pdSVM))
```

```
## Analysis of fold 1
## [1] "data allocated"
```

- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 2
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 3
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 4
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"

- ## Analysis of fold 5
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 6
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 7
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## Analysis of fold 8
- ## [1] "data allocated"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"
- ## [1] "nb predicted"
- ## [1] "svm predicted"
- ## [1] "nb accuracy saved"
- ## [1] "SVM accuracy saved"
- ## [1] "nb other measures done"
- ## [1] "svm other measures done"
- ## [1] "Naive Bayes trained"
- ## [1] "svm trained"

```
## [1] "nb predicted"
## [1] "svm predicted"
## Analysis of fold 9
## [1] "data allocated"
## [1] "Naive Bayes trained"
## [1] "svm trained"
## [1] "nb predicted"
## [1] "svm predicted"
## [1] "nb accuracy saved"
## [1] "SVM accuracy saved"
## [1] "nb other measures done"
## [1] "svm other measures done"
## [1] "Naive Bayes trained"
## [1] "svm trained"
## [1] "nb predicted"
## [1] "svm predicted"
## Analysis of fold 10
## [1] "data allocated"
## [1] "Naive Bayes trained"
## [1] "svm trained"
## [1] "nb predicted"
## [1] "svm predicted"
## [1] "nb accuracy saved"
## [1] "SVM accuracy saved"
## [1] "nb other measures done"
## [1] "svm other measures done"
## [1] "Naive Bayes trained"
## [1] "svm trained"
## [1] "nb predicted"
## [1] "svm predicted"
#determine the average accuracy over the 10 folds for each model
avgAccNB = mean(accNB)
avgAccSVM = mean(accSVM)
avgSpecNB = mean(specNB)
avgSpecSVM = mean(specSVM)
avgSensNB = mean(sensNB)
avgSensSVM = mean(sensSVM)
avgAUCNB = mean(AUCNB)
avgAUCSVM = mean(AUCSVM)
#print all the results
avgAccNB
## [1] 0.7761747
avgAccSVM
```

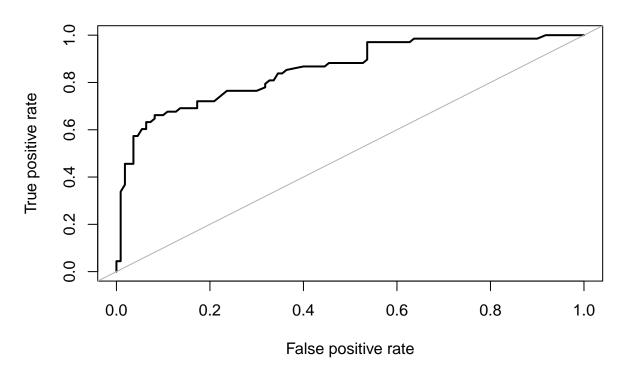
[1] 0.8245148

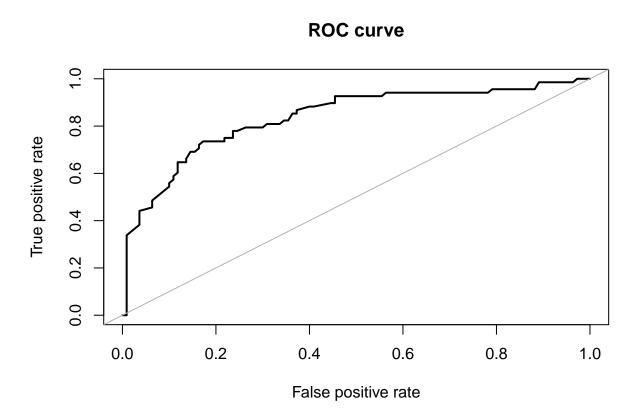
```
{\tt avgSpecNB}
## [1] 0.5849951
avgSpecSVM
## [1] 0.7150887
{\tt avgSensNB}
## [1] 0.8963486
avgSensSVM
## [1] 0.8898537
avgAUCNB
## [1] 0.823757
avgAUCSVM
## [1] 0.8396036
Now we will examine the ROC
#Xval
library(caret)
library(ROSE)
## Loaded ROSE 0.0-3
library(caTools)
set.seed(12345)
trainTitanic$Survived <- as.numeric(trainTitanic$Survived)</pre>
sample <- sample.split(trainTitanic$Survived, SplitRatio = 0.8)</pre>
train = subset(trainTitanic, sample == TRUE)
test = subset(trainTitanic, sample == FALSE)
nrow(test)
```

[1] 178

```
#train the models
rsltNB <- naiveBayes(mdl, data = train)</pre>
print("Naive Bayes trained")
## [1] "Naive Bayes trained"
rsltSVM <- svm(mdl, data = train)</pre>
print("svm trained")
## [1] "svm trained"
#predict values
pdNB <- predict(rsltNB, test, type = "raw")</pre>
pdNB <- pdNB[,2]</pre>
print("nb predicted")
## [1] "nb predicted"
pdSVM = predict(rsltSVM, test)
print("svm predicted")
## [1] "svm predicted"
roc.curve(test$Survived, pdNB)
```

ROC curve





Area under the curve (AUC): 0.837