

# Project 4 - Main Script for Naive Bayes

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*4/14/2017*

This file is an attempt to the Naive Bayes algorithm from “Two Supervised Learning Approaches for Name Disambiguation in Author Citations” Han(2004).

## Step 0: Load the packages, specify directories

```
if (!require("pacman")) install.packages("pacman")

## Loading required package: pacman
pacman::p_load(text2vec, dplyr, qmcMatrix, kernlab, knitr)

if (!require("splitstackshape")) install.packages("splitstackshape")

## Loading required package: splitstackshape
## Loading required package: data.table
## -----
## data.table + dplyr code now lives in dtplyr.
## Please library(dtplyr)!
## -----
##
## Attaching package: 'data.table'
##
## The following objects are masked from 'package:dplyr':
##
##   between, first, last
library(splitstackshape)

if (!require("matrixStats")) install.packages("matrixStats")

## Loading required package: matrixStats
##
## Attaching package: 'matrixStats'
##
## The following object is masked from 'package:dplyr':
##
##   count
library(matrixStats)

if (!require("reshape2")) install.packages("reshape2")

## Loading required package: reshape2
```

```
##
## Attaching package: 'reshape2'

## The following objects are masked from 'package:data.table':
##
##      dcast, melt

library(reshape2)
```

## Step 1: Load and process the data

Please run “data cleaner.Rmd” first so that the .txt files are all in .csv format for processing.

```
dat = read.csv("../data/naameset/A Kumar.csv")
test = data.frame()
train = data.frame()

# sample the dataset by author ID
for (i in 1:max(dat$author.ID))
{
  sub = subset(dat, author.ID == i)
  sam_index = sample(nrow(sub), floor(nrow(sub)/2))
  sam = sub[sam_index, ]
  train = rbind(train, sam)
  antisam = sub[-sam_index, ]
  test = rbind(test, antisam)
}
rm(sub, sam, i, sam_index, antisam)
```

## Step 2: Setting up variable names for Naive Bayes

These are placeholder variables used for the subsequent calculations.

```
# number vectors

# calculate the number of authors in the dataset
numauthor = max(train$author.ID)
# to count the number of paper for each author
numpaper = rep(0, numauthor)
# to count the number of paper authored with coauthors
numpapercoauthor = rep(0, numauthor)
# number of paper the author writes alone
numpapernocoauthor = rep(0, numauthor)
# number of coauthors each author has
numcoauthor = rep("", numauthor)

# probability vectors

# initialize P(xi), prior probabilities vector
p_xi = rep(0, numauthor)
# P(seen|Co, Xi)
p_seen.co = rep(0, numauthor)
```

```

# initialize  $P(A_{1k}/x_i)$ , likelihood vector
p_A1k.X = data.frame()
#  $P(A_{1k}/co, seen, X_i)$ 
p_A1k.seen = data.frame()
#  $P(A_{1k}/co, unseen, X_i)$ 
p_A1k.unseen = data.frame()
#  $P(A_1/X)$ 
p_A1.X = data.frame()

```

### Step 3: Calculate the likelihood of seeing feature one, coauthors.

These values are the log of conditional probabilities of author  $X_i$  collaborating with each and every one of the coauthors.

```

# calculate number of paper each author.ID writes
for (i in 1:numauthor)
{
  numpaper[i] = sum(train$author.ID==i)
}

# number of coauthor an author has
numpapercoauthor = numpaper - numpapernocoauthor

# find the number of paper author writes alone
for (i in 1:numauthor)
{
  numpapernocoauthor[i] = sum(train$coauthor.names=="&train$author.ID==i)
}

# extract all coauthors and put them into a list
coauthor.count = data.frame(cbind(train$author.ID, as.character(train$coauthor.names)))

colnames (coauthor.count) = c("author.ID", "coauthor.names")

coauthor.count = cSplit(coauthor.count, "coauthor.names", ",", "long")[
  , list(collaboaration.times = .N), .(author.ID, coauthor.names)][]

# create a complete coauthor matrix
coauthor.matrix = dcast(coauthor.count, author.ID~...)

```

## Using collaboaration.times as value column: use value.var to override.

```

if("NA" %in% colnames(coauthor.matrix))
{
  coauthor.matrix$`NA`=NULL
}

coauthor.matrix[is.na(coauthor.matrix)]=0

```

```

# calculate  $P(\text{seen}/\text{Co}, x_i)$  and store in coauthor.matrix$seen
for (i in 1: numauthor)
{
  p_seen.co[i] = sum(as.numeric(coauthor.matrix[i,-1])>1) / sum(as.numeric(coauthor.matrix[i,-1])>0)
}

# filter only coauthors with collaboration times >1
seen <- coauthor.count[coauthor.count$collaboaration.times!=1,]
# convert this count list to a dataframe
coauthor.seen.matrix <- dcast(seen, author.ID~...)

## Using collaboaration.times as value column: use value.var to override.

# change NAs to zero
coauthor.seen.matrix[is.na(coauthor.seen.matrix)]<- 0
if("NA" %in% colnames(coauthor.seen.matrix))
{
  coauthor.seen.matrix$`NA`=NULL
}

# do the same for unseen coauthors:
# unseen coauthors
unseen = coauthor.count[coauthor.count$collaboaration.times==1, ]
# convert list to df
coauthor.unseen.matrix <- dcast(unseen, author.ID~...)

## Using collaboaration.times as value column: use value.var to override.

# change NAs to zero
coauthor.unseen.matrix[is.na(coauthor.unseen.matrix)]<- 0
if("NA" %in% colnames(coauthor.unseen.matrix))
{
  coauthor.unseen.matrix$`NA`=NULL
}

# calculate  $P(x_i)$ 
p_xi = table(train$author.ID)/sum(table(train$author.ID))

#  $P(N/x_i)$ , probability of writing next paper alone
p_numpapernocoauthor = numpapernocoauthor/numpaper

# generate an empty matrix with same dim with coauthor.seen.matrix
p_A1k.seen <- data.frame(matrix(rep(0,ncol(coauthor.seen.matrix)*numauthor),nrow = numauthor))

ID <- coauthor.matrix$author.ID
p_A1k.seen <- data.frame(ID, p_A1k.seen)
colnames(p_A1k.seen) <- colnames(coauthor.seen.matrix)
row.names(p_A1k.seen) <- coauthor.matrix$author.ID

# calculate  $P(A_{ik}/\text{Seen}, \text{Co}, x_i)$  and store in A

```

```

# remove column titled "NA"
p_A1k.seen <- p_A1k.seen[!is.na(names(p_A1k.seen))]
coauthor.seen.matrix = coauthor.seen.matrix[!is.na(names(coauthor.seen.matrix))]

p_A1k.seen=as.data.frame(p_A1k.seen, stringsAsFactors = False)

for (i in 1:nrow(coauthor.seen.matrix)) {
  for (j in 2:ncol(coauthor.seen.matrix)) {

    if(coauthor.seen.matrix[i,j] !=0)
      p_A1k.seen[i,j] <- as.numeric(coauthor.seen.matrix[i,j])/sum(as.numeric(coauthor.seen.matrix[i,
      else p_A1k.seen[i,j] = (1/(ncol(coauthor.seen.matrix)-1))/(1+sum(as.numeric(coauthor.seen.matrix

  }
}

# calculate P(A1k/co, unseen, xi)

author.coauthor.total = ncol(coauthor.matrix) + numauthor

for (i in 1:numauthor)
{
  numcoauthor[i] = sum(coauthor.matrix[i,-1]!=0)
}

p_A1k.unseen = 1/(author.coauthor.total - as.numeric(numcoauthor))

## Caculate P(A1k|Xi)

# P(A1k/Seen,Co,Xi)
p_A1k.seen <- as.matrix(p_A1k.seen)
# P(Co|Xi)
p_coauthor <- 1-p_numpapernocoauthor #26*1

# P(A1k/Unseen,Co,Xi)
#dim(p_A1k.unseen) # 26*1
p_A1k.unseen <- as.matrix(p_A1k.unseen)
# P(Unseen/Co,Xi)
p_unseen.co <- 1-p_seen.co

#####

# Caculate P(A1k|Xi)
p_A1k.X <- data.frame (matrix(rep(0,(ncol(p_A1k.seen)-1)*numauthor),nrow = numauthor))# 26*245
p_A1k.seen <- data.frame(p_A1k.seen)
ID <- coauthor.matrix$ author.ID
#ID <- p_A1k.seen$author.ID
p_A1k.X <- data.frame(ID,p_A1k.X)
colnames(p_A1k.X) <- colnames(p_A1k.seen)

```

```

for (i in 1:max(numauthor))
{
  if(!(i %in% as.numeric(coauthor.unseen.matrix$author.ID)))
  {
    coauthor.unseen.matrix = rbind(coauthor.unseen.matrix, rep(1/sum(as.numeric(numcoauthor)), ncol(coauthor.unseen.matrix), 1] = i
  }
}
# creating unseen coauthor probability matrix
for(i in 2:ncol(coauthor.unseen.matrix))
{
  coauthor.unseen.matrix[, i] = p_A1k.unseen
}

#coauthor.unseen.matrix$author.ID = coauthor.seen.matrix$author.ID

p_A1k.X.unseen <- data.frame (matrix(rep(0.1/ncol(coauthor.unseen.matrix), (ncol(coauthor.unseen.matrix) * nrow(coauthor.unseen.matrix))), nrow(coauthor.unseen.matrix), ncol(coauthor.unseen.matrix))
ID <- coauthor.matrix$ author.ID
p_A1k.X.unseen <- data.frame(ID,p_A1k.X.unseen)
colnames(p_A1k.X.unseen) <- colnames(coauthor.unseen.matrix)

for (i in 2: ncol(coauthor.unseen.matrix))
{
  p_A1k.X.unseen[, i] <- as.numeric(as.matrix(coauthor.unseen.matrix[, i])) * p_unseen.co * p_coauthor
}

for (i in 2: ncol(p_A1k.X))
{
  p_A1k.X[,i] <- as.numeric(as.matrix(p_A1k.seen[,i]))*p_seen.co * p_coauthor #+ p_A1k.unseen * p_unseen
}

p_A1k.X.final = cbind(p_A1k.X.unseen, p_A1k.X[, -1])

# get rid of leading and trailing white space
## Caculate P(A1|Xi) = P(A11|Xi)...P(A1k|Xi)...P(A1K|Xi)

# the result from A1
p_A1k.X.logged = log(p_A1k.X.final[, -1])

p_A1.X.logged <- rowSums(p_A1k.X.logged)

p_A1.X.logged <- data.frame(ID,p_A1.X.logged)
colnames(p_A1.X.logged) <- c('ID', 'log(P(A1|Xi))')

```

#### Step 4: Calculate the likelihood of seeing feature two, keywords in paper title.

These values are the log of conditional probabilities of author Xi writing a paper with a specific keyword in the title.

```

# extract all paper titles and put them into a list
paper.count <- data.frame(cbind(train$author.ID, as.character(train$paper.title)))
colnames (paper.count) = c("author.ID", "Paper.title")

# clean paper title
library(tm)

## Loading required package: NLP

library(tidytext)
str(paper.count$Paper.title)

## Factor w/ 118 levels "A Case Study of an Adaptive Load Balancing Algorithm ",...: 90 25 112 11 50 78

corpus <- Corpus(VectorSource(paper.count$Paper.title))
corpus <- tm_map(corpus, tolower)
corpus <- tm_map(corpus, removePunctuation)
corpus <- tm_map(corpus, PlainTextDocument)
#corpus <- tm_map(corpus, removeWords, stopwords('english'))
#corpus <- tm_map(corpus, stemDocument)

paper.count[,2] <- data.frame(corpus$content$content)

# caculate number of words in sentence and store in paper.count
library(stringr)

word.count <- data.frame(matrix(rep(0,nrow(paper.count)),nrow = nrow(paper.count)))
for(i in 1:nrow(paper.count)){
  word.count[i,] <- str_count(paper.count[i,2], '\\s+')+1
}
colnames(word.count) <- 'word.count'
paper.count <- data.frame(paper.count, word.count)

# split sentence into word and store in voc.count
List <- strsplit(as.character(paper.count$Paper.title), " ")
voc.count <- data.frame(author.ID=rep(paper.count$author.ID, sapply(List, length)), Words=unlist(List))

# generate a paper matrix
library(reshape2)
paper.matrix <- dcast(voc.count, author.ID~Words)

## Using Words as value column: use value.var to override.
## Aggregation function missing: defaulting to length

paper.matrix[is.na(paper.matrix)]=0

## calculate P(A2k| Xi)
# generate an empty matrix with same dim with paper.matrix

p_A2k.X <- data.frame(matrix(rep(0,ncol(paper.matrix)*nrow(paper.matrix)),nrow = nrow(paper.matrix)))
author.ID <- paper.matrix$author.ID
p_A2k.X <- data.frame(author.ID, p_A2k.X)
colnames(p_A2k.X) <- colnames(paper.matrix)

p_A2k.X <- p_A2k.X[!is.na(names(p_A2k.X))]

```

```

paper.matrix <- paper.matrix[!is.na(names(paper.matrix))]

# lol
for (i in 1: nrow(p_A2k.X)) {
  for (j in 2: ncol(p_A2k.X)) {

    if(paper.matrix[i,j] != 0)
      p_A2k.X[i,j] <- as.numeric(paper.matrix[i,j])/sum(as.numeric(paper.matrix[i,]))
    else p_A2k.X[i,j] <- (1/(ncol(paper.matrix)-1))/(1+sum(as.numeric(paper.matrix[i,])))
  }
}
# lol

p_A2k.X.logged = log(p_A2k.X[, -1])

p_A2.X.logged <- rowSums(p_A2k.X.logged)

p_A2.X.logged <- data.frame(ID,p_A2.X.logged)
colnames(p_A2.X.logged) <- c('ID', 'log(P(A2|Xi))')

```

## Step 5: Calculate the likelihood of seeing feature two, keywords in journal title.

These values are the log of conditional probabilities of author Xi publishing in a journal with a name that includes a keyword.

```

# extract all paper titles and put them into a list
paper.count <- data.frame(cbind(train$author.ID, as.character(train$journal.title)))
colnames(paper.count) = c("author.ID", "journal.title")

# clean journal title
str(paper.count$journal.title)

```

## Factor w/ 103 levels " APPROX"," at the Workshop Space Telerobotics Jet Propulsion Laboratory",... :

```

corpus <- Corpus(VectorSource(paper.count$journal.title))
corpus <- tm_map(corpus, tolower)
corpus <- tm_map(corpus, removePunctuation)
corpus <- tm_map(corpus, PlainTextDocument)
#corpus <- tm_map(corpus, removeWords, stopwords('english'))
#corpus <- tm_map(corpus, stemDocument)

paper.count[,2] <- data.frame(corpus$content$content)

# caculate number of words in sentence and store in paper.count
library(stringr)

word.count <- data.frame(matrix(rep(0,nrow(paper.count)),nrow = nrow(paper.count)))
for(i in 1: nrow(paper.count)){
  word.count[i,] <- str_count(paper.count[i,2], '\\s+') + 1
}
colnames(word.count) <- 'word.count'

```



```

paper.count <- data.frame(paper.count,word.count)

# split sentence into word and store in voc.count
List <- strsplit(as.character(paper.count$journal.title), " ")
voc.count <- data.frame(author.ID=rep(paper.count$author.ID, sapply(List, length)), Words=unlist(List))

# generate a paper matrix
journal.matrix <-dcast(voc.count, author.ID~Words)

```

## Using Words as value column: use value.var to override.

## Aggregation function missing: defaulting to length

```

journal.matrix[is.na(journal.matrix)]=0

## calculate P(A2k| Xi)
# generate an empty matrix with same dim with journal.matrix

p_A3k.X <- data.frame(matrix(rep(0,ncol(journal.matrix)*nrow(journal.matrix)),nrow = nrow(journal.matrix),
author.ID <- journal.matrix$author.ID
p_A3k.X <- data.frame(author.ID, p_A3k.X)
colnames(p_A3k.X) <- colnames(journal.matrix)

p_A3k.X <- p_A3k.X[!is.na(names(p_A3k.X))]
journal.matrix <- journal.matrix[!is.na(names(journal.matrix))]

for (i in 1: nrow(p_A3k.X)) {
  for (j in 2: ncol(p_A3k.X)) {
    if(journal.matrix[i,j] != 0)
      p_A3k.X[i,j] <- as.numeric(journal.matrix[i,j])/sum(as.numeric(journal.matrix[i,]))
    else p_A3k.X[i,j] <- (1/(ncol(journal.matrix)-1))/(1+sum(as.numeric(journal.matrix[i,])))
  }
}

p_A3k.X.logged = log(p_A3k.X[, -1])

p_A3.X.logged <- rowSums(p_A3k.X.logged)

p_A3.X.logged <- data.frame(ID,p_A3.X.logged)
colnames(p_A3.X.logged) <- c('ID', 'log(P(32|Xi))')

```

## Step 6: Combining results into one dataframe

Here the dataframe “df” has author ID as rows, and the three features: coauthor, paper title, and journal title as columns.

```

df = cbind(p_A1k.X.logged, p_A2k.X.logged, p_A3k.X.logged)

trim.leading <- function (x) sub("^\\s+", "", x)
trim.trailing <- function (x) sub("\\s+$", "", x)

```

```

colnames(df) = trim.leading(trim.trailing(colnames(df)))
colnames(df) <- sub("\\s+", ".", colnames(df))
colnames(df)

df = cbind(df, p_xi)

i = 1
while (i < ncol(df))
{
  if(-Inf %in% df[,i])
  {
    df[, i]=NULL
  }
  i = i+1
}

```

## Step 7: Testing the model

We feed the features one at a time into the dataframe “df” and look up the corresponding conditional probability. We then sum the log of conditional probabilities across all the rows, resulting in a value corresponding to each author ID. Lastly, we find the maximum of the sum, and find the corresponding author ID with which.max function.

```

# this vector holds the final result of the test: rows correspond to author ID, and columns correspond to author ID
final.result = data.frame(matrix(ncol = 0, nrow = max(test$author.ID)))
# actual author ID of the papers
truth = test$author.ID

## Testing with feature one: coauthors
for( i in 1:nrow(test))
{
  # this holds the result from one paper: row corresponds to author ID, columns correspond to logged probability of feature (A1, A2, A3, but so far only A1 is there)
  current.result = data.frame(matrix(ncol = 0, nrow = max(test$author.ID)))
  # this holds one paper
  current = test[i, ]
  if(current$coauthor.names != "" & !is.na(current$coauthor.names))
  {
    coauthor.list = trim.trailing(trim.leading(unlist(strsplit(as.character(current$coauthor.names), " "))))
    coauthor.list = sub("\\s+", ".", coauthor.list)
    # for each coauthor, get the logged probability
    for (j in 1:length(coauthor.list))
    { # 489 unique coauthors
      not_null = !(coauthor.list[j] == "")
      in_colnames = ifelse(not_null, (coauthor.list[j] %in% colnames(df)), FALSE)
      in_colnames = ifelse(is.na(in_colnames), FALSE, coauthor.list[j] %in% colnames(df))

      if(in_colnames)
      {
        current.result = cbind(current.result, as.data.frame(df[, coauthor.list[j]]))
      }
    }
  }
}
# rind the transposed column sum of "current.result". This is the probability for A1.

```

```

        final.result = rbind(final.result, t(rowSums(current.result)))

    }
    # get the prior probability in the result
    final.result = rbind(final.result, t(rowSums(current.result)), t(df$Freq))

## Testing with feature two: paper title
for( i in 1:nrow(test))
{
    current.result = data.frame(matrix(ncol = 0, nrow = max(test$author.ID)))
    current = test[i, ]
    if(current$paper.title!="" & !is.na(current$paper.title))
    {
        paper.list = trim.trailing(trim.leading(unlist(strsplit(as.character(current$paper.title), ","))))
        # for each paper keyword, get the logged probability
        for (j in 1:length(paper.list))
        {
            not_null = !(paper.list[j] != "")
            in_colnames = ifelse(not_null, (paper.list[j] %in% colnames(df)), FALSE)
            in_colnames = ifelse(is.na(in_colnames), FALSE, paper.list[j] %in% colnames(df))

            if(in_colnames)
            {
                current.result = cbind(current.result, as.data.frame(df[, paper.list[j]]), df$Freq)
            }
        }
    }
    # rind the transposed column sum of "current.result". This is the probability for A2.
    final.result = rbind(final.result, rowSums(current.result))
}

## Testing with feature three: journal title

for( i in 1:nrow(test))
{current.result = data.frame(matrix(ncol = 0, nrow = max(test$author.ID)))
  current = test[i, ]
  if(current$journal.title!="" & !is.na(current$journal.title))
  {
      journal.list = trim.trailing(trim.leading(unlist(strsplit(as.character(current$journal.title), ","),
      # for each journal keyword, get the logged probability
      for (j in 1:length(journal.list))
      {not_null = !(journal.list[j] != "")
        in_colnames = ifelse(not_null, (journal.list[j] %in% colnames(df)), FALSE)
        in_colnames = ifelse(is.na(in_colnames), FALSE, journal.list[j] %in% colnames(df))
        if(in_colnames)
        {
            current.result = cbind(current.result, as.data.frame(df[, journal.list[j]]), df$Freq)
        }
      }
  }
}
# rind the transposed column sum of "current.result". This is the probability for A3.

```

```

    final.result = rbind(final.result, rowSums(current.result))
  }

## Combining the results
answer = matrix()
for(i in 1:nrow(test))
{
  answer[i] = which.max(as.numeric(final.result[i, ]))
}

# this variable pits predicted value with the actual value.
presentation = cbind(as.data.frame(answer), as.data.frame(truth))

```

## Step 8: Evaluation

```

source('../lib/evaluation_measures.R')
matching_matrix_NB <- matching_matrix(test$author.ID, answer)
performance_NB <- performance_statistics(matching_matrix_NB)
compare_df <- data.frame(method=c("Naive Bayes"),
                        precision=performance_NB$precision,
                        recall=performance_NB$recall,
                        f1=performance_NB$f1,
                        accuracy=performance_NB$accuracy)
kable(compare_df, caption="Comparision of performance for Naive Bayes", digits = 2)

```

Table 1: Comparision of performance for Naive Bayes

method	precision	recall	f1	accuracy
Naive Bayes	0.27	0.68	0.38	0.54