

R Notebook

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

```
library(tidyverse) # metapackage of all tidyverse packages

## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.3.2      v purrr   0.3.4
## v tibble  3.0.4      v dplyr  1.0.3
## v tidyr   1.1.2      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(tokenizers)
library(stopwords)
library(tm)

## Loading required package: NLP

##
## Attaching package: 'NLP'

## The following object is masked from 'package:ggplot2':
##
##   annotate
##
## Attaching package: 'tm'

## The following object is masked from 'package:stopwords':
##
##   stopwords

library(text2vec)

library(NbClust)
library(cluster)
library(factoextra)
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
library(dbscan)
```

Wczytanie i przetworzenie danych

```
data = read.csv("mbti_1.csv")

n <- 1000 #sample from data

data <- data[sample(nrow(data), n), ]

INTJ <- data[data$type=="INTJ",]
INTP <- data[data$type=="INTP",]
ENTJ <- data[data$type=="ENTJ",]
ENTP <- data[data$type=="ENTP",]
INFJ <- data[data$type=="INFJ",]
INFP <- data[data$type=="INFP",]
ENFJ <- data[data$type=="ENFJ",]
ENFP <- data[data$type=="ENFP",]
ISTJ <- data[data$type=="ISTJ",]
ISFJ <- data[data$type=="ISFJ",]
ESTJ <- data[data$type=="ESTJ",]
ESFJ <- data[data$type=="ESFJ",]
ISTP <- data[data$type=="ISTP",]
ISFP <- data[data$type=="ISFP",]
ESTP <- data[data$type=="ESTP",]
ESFP <- data[data$type=="ESFP",]

#replaces URLs with word "link"
data$posts <- gsub('http[s]?://(?:[a-zA-Z]|[0-9]|[$-_@.&+]|(?:%[0-9a-fA-F][0-9a-fA-F]))+', 'link', data$posts)

#removes all noise from text
data$posts <- gsub('[^a-zA-Z]', " ", data$posts)

#removes more than 1 space
data$posts <- gsub('[ ]{2,}', " ", data$posts)

#word tokenization and stemming
data$posts <- tokenize_word_stems(data$posts, stopwords = stopwords::stopwords("en"))

#create dictionary
iterator = itoken(data$posts)
vocab = create_vocabulary(iterator)
pruned_vocab = prune_vocabulary(vocab,
                                term_count_min = 5,
                                doc_proportion_max = 0.7,
                                doc_proportion_min = 0.1)

pruned_vocab

## Number of docs: 1000
## 0 stopwords: ...
## ngram_min = 1; ngram_max = 1
## Vocabulary:
```

```
##      term term_count doc_count
##  1:  spent         106      100
##  2:   plus         108      100
##  3:   warm         109      100
##  4:   upon         110      100
##  5: brought         111      101
##  ---
## 831:  thank        1625      640
## 832:   intj        1750      489
## 833:  infp         1847      500
## 834:  infj         1857      466
## 835:   link        3527      678
```

Wektoryzacja

```
#document term matrix
vectorizer = vocab_vectorizer(pruned_vocab)
dtm = create_dtm(iterator, vectorizer)

 #(Term Co-occurrence Matrix)
tcm = create_tcm(iterator, vectorizer, skip_grams_window = 5L)

#tf_idf
tf_idf = TfIdf$new()
# fit tf-idf to training data
dt_tfidf = fit_transform(dtm, tf_idf)

# apply pre-trained tf-idf transformation to testing data
#doc_term_test_tfidf = transform(doc_term_test, tf_idf)

vectors.dtm <- dtm
vectors.tfidf <- dt_tfidf
dim(dtm)
```

```
## [1] 1000 835
```

```
#####
# glove #
#####
```

```
glove = GlobalVectors$new(rank = 50, x_max = 10)
wv_main = glove$fit_transform(tcm, n_iter = 100, convergence_tol = 0.01, n_threads = 8)
```

```
## INFO [20:47:49.654] epoch 1, loss 0.1706
## INFO [20:47:49.852] epoch 2, loss 0.1066
## INFO [20:47:50.048] epoch 3, loss 0.0942
## INFO [20:47:50.219] epoch 4, loss 0.0877
## INFO [20:47:50.363] epoch 5, loss 0.0837
## INFO [20:47:50.514] epoch 6, loss 0.0809
## INFO [20:47:50.654] epoch 7, loss 0.0788
## INFO [20:47:50.797] epoch 8, loss 0.0772
## INFO [20:47:50.939] epoch 9, loss 0.0758
## INFO [20:47:51.084] epoch 10, loss 0.0748
## INFO [20:47:51.234] epoch 11, loss 0.0739
## INFO [20:47:51.366] epoch 12, loss 0.0732
```

```

## INFO [20:47:51.510] epoch 13, loss 0.0726
## INFO [20:47:51.511] Success: early stopping. Improvement at iteration 13 is less than convergence_

wv_context = glove$components
word_vectors = wv_main + t(wv_context)
#wv = glove$get_word_vectors()
#dim(wv)
#wv

#If your goal is to classify documents - I doubt any doc2vec approach will beat bag-of-words/ngrams.
#If you still want to try - common simple strategy short documents (< 20 words) is to represent documents
#test= word_vectors["link", , drop=F]
#cos_sim_rom = sim2(x = word_vectors, y = test, method = "cosine", norm = "l2")
#head(sort(cos_sim_rom[,1], decreasing = T), 10)

common_terms = intersect(colnames(dtm), rownames(word_vectors) )
dtm_averaged = normalize(dtm[, common_terms], "l1")
# you can re-weight dtm above with tf-idf instead of "l1" norm
sentence_vectors = dtm_averaged %*% word_vectors[common_terms, ]
vectors.glove <- sentence_vectors

#split rows into single post not 50
library(tidyr)
library(dplyr)

data2 = read.csv("mbti_1.csv")
data2 <- data2[sample(nrow(data2), 50), ] # do 200 jakoś idzie

#replaces URLs with word "link"
data2$posts <- gsub('http[s]?://(?:[a-zA-Z]|[0-9]|[$-_@.&+]|(?:%[0-9a-fA-F][0-9a-fA-F]))+', 'link', data2$posts)

data2 <- data2 %>%
  mutate(posts = strsplit(as.character(posts), "\\|\\|\\|\\|")) %>%
  unnest(posts)

data2$posts <- gsub('[^a-zA-Z]', " ", data2$posts)

#removes more than 1 space
data2$posts <- gsub('[ ]{2,}', " ", data2$posts)

data2 <- subset(data2, sapply(strsplit(posts, " "), length) >= 8)

#word tokenization and stemming
data2$posts <- tokenize_word_stems(data2$posts, stopwords = stopwords::stopwords("en"))

#create dictionary
iterator2 = itoken(data2$posts)
vocab2 = create_vocabulary(iterator2)

pruned_vocab2 = prune_vocabulary(vocab2,
                                term_count_min = 5,
                                doc_proportion_max = 0.8,
                                doc_proportion_min = 0.001)

```

```

#document term matrix
vectorizer2 = vocab_vectorizer(pruned_vocab2)
dtm2 = create_dtm(iterator2, vectorizer2)
 #(Term Co-occurrence Matrix)
tcm2 = create_tcm(iterator2, vectorizer2, skip_grams_window = 5L)

glove2 = GlobalVectors$new(rank = 50, x_max = 10)
wv_main2 = glove2$fit_transform(tcm2, n_iter = 100, convergence_tol = 0.01, n_threads = 8)

```

```

## INFO [20:47:52.800] epoch 1, loss 0.1302
## INFO [20:47:52.833] epoch 2, loss 0.0738
## INFO [20:47:52.868] epoch 3, loss 0.0596
## INFO [20:47:52.904] epoch 4, loss 0.0516
## INFO [20:47:52.941] epoch 5, loss 0.0462
## INFO [20:47:52.974] epoch 6, loss 0.0420
## INFO [20:47:53.019] epoch 7, loss 0.0386
## INFO [20:47:53.052] epoch 8, loss 0.0358
## INFO [20:47:53.087] epoch 9, loss 0.0334
## INFO [20:47:53.127] epoch 10, loss 0.0313
## INFO [20:47:53.162] epoch 11, loss 0.0295
## INFO [20:47:53.202] epoch 12, loss 0.0280
## INFO [20:47:53.239] epoch 13, loss 0.0266
## INFO [20:47:53.272] epoch 14, loss 0.0254
## INFO [20:47:53.306] epoch 15, loss 0.0242
## INFO [20:47:53.344] epoch 16, loss 0.0232
## INFO [20:47:53.378] epoch 17, loss 0.0223
## INFO [20:47:53.417] epoch 18, loss 0.0215
## INFO [20:47:53.458] epoch 19, loss 0.0208
## INFO [20:47:53.503] epoch 20, loss 0.0201
## INFO [20:47:53.542] epoch 21, loss 0.0194
## INFO [20:47:53.579] epoch 22, loss 0.0188
## INFO [20:47:53.614] epoch 23, loss 0.0183
## INFO [20:47:53.656] epoch 24, loss 0.0178
## INFO [20:47:53.691] epoch 25, loss 0.0173
## INFO [20:47:53.727] epoch 26, loss 0.0169
## INFO [20:47:53.780] epoch 27, loss 0.0165
## INFO [20:47:53.823] epoch 28, loss 0.0161
## INFO [20:47:53.872] epoch 29, loss 0.0158
## INFO [20:47:53.920] epoch 30, loss 0.0154
## INFO [20:47:53.968] epoch 31, loss 0.0151
## INFO [20:47:54.015] epoch 32, loss 0.0148
## INFO [20:47:54.056] epoch 33, loss 0.0145
## INFO [20:47:54.104] epoch 34, loss 0.0142
## INFO [20:47:54.144] epoch 35, loss 0.0140
## INFO [20:47:54.188] epoch 36, loss 0.0137
## INFO [20:47:54.226] epoch 37, loss 0.0135
## INFO [20:47:54.262] epoch 38, loss 0.0133
## INFO [20:47:54.297] epoch 39, loss 0.0131
## INFO [20:47:54.333] epoch 40, loss 0.0129
## INFO [20:47:54.366] epoch 41, loss 0.0127
## INFO [20:47:54.403] epoch 42, loss 0.0125
## INFO [20:47:54.442] epoch 43, loss 0.0123

```

```
## INFO [20:47:54.485] epoch 44, loss 0.0122
## INFO [20:47:54.526] epoch 45, loss 0.0120
## INFO [20:47:54.571] epoch 46, loss 0.0119
## INFO [20:47:54.616] epoch 47, loss 0.0117
## INFO [20:47:54.658] epoch 48, loss 0.0116
## INFO [20:47:54.693] epoch 49, loss 0.0114
## INFO [20:47:54.733] epoch 50, loss 0.0113
## INFO [20:47:54.770] epoch 51, loss 0.0112
## INFO [20:47:54.807] epoch 52, loss 0.0110
## INFO [20:47:54.842] epoch 53, loss 0.0109
## INFO [20:47:54.877] epoch 54, loss 0.0108
## INFO [20:47:54.915] epoch 55, loss 0.0107
## INFO [20:47:54.956] epoch 56, loss 0.0106
## INFO [20:47:54.996] epoch 57, loss 0.0105
## INFO [20:47:54.996] Success: early stopping. Improvement at iteration 57 is less than convergence_
```

```
wv_context2 = glove2$components
word_vectors2 = wv_main2 + t(wv_context2)
#wv = glove$get_word_vectors()
#dim(wv)
#wv

#If your goal is to classify documents - I doubt any doc2vec approach will beat bag-of-words/ngrams.
#If you still want to try - common simple strategy short documents (< 20 words) is to represent documents
#test= word_vectors["link", , drop=F]
#cos_sim_rom = sim2(x = word_vectors, y = test, method = "cosine", norm = "l2")
#head(sort(cos_sim_rom[,1], decreasing = T), 10)

common_terms = intersect(colnames(dtm2), rownames(word_vectors2) )
dtm_averaged = normalize(dtm2[, common_terms], "l1")
# you can re-weight dtm above with tf-idf instead of "l1" norm
sentence_vectors2 = dtm_averaged %*% word_vectors2[common_terms, ]
vectors.glove_post <- sentence_vectors2
```

Grupowanie

K-medoids

```
pam.dtm = pam(dtm, 16, metric = "euclidean", stand = FALSE)
pam.tfidf = pam(dt_tfidf, 16, metric = "euclidean", stand = FALSE)
pam.glove = pam(sentence_vectors, 16, metric = "euclidean")
pam.glove2 = pam(sentence_vectors2, 16, metric = "euclidean", stand = FALSE)
```

K-medoids DTM

```
pam_results_dtm <- data %>%
mutate(cluster = pam.dtm$clustering) %>%
group_by(cluster)

pam_results <- subset(pam_results_dtm, select = c(type, cluster))
t <- table(pam_results)
print ("Wyniki ilosciowe grupowania dla dtm")
```

```
## [1] "Wyniki ilosciowe grupowania dla dtm"
print (t)

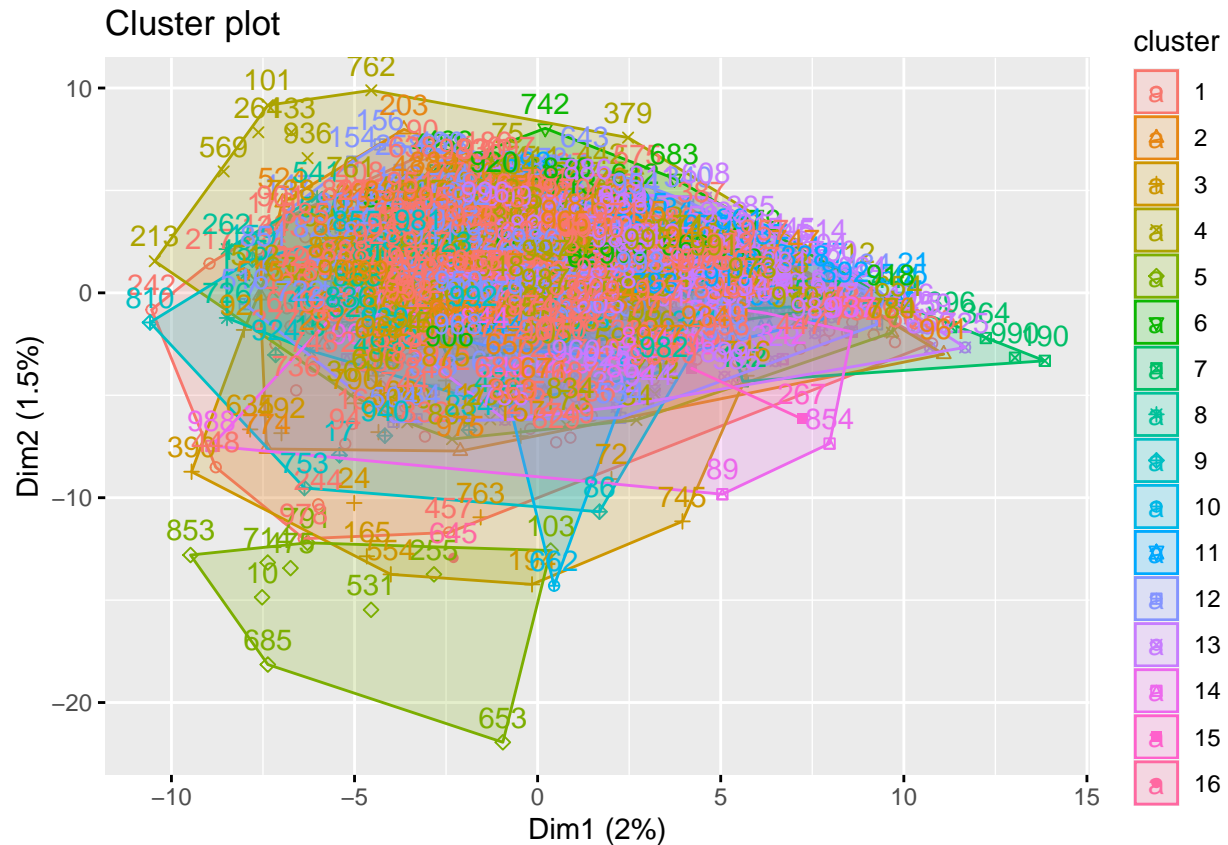
##          cluster
## type      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ      8  6  0  6  0  1  0  1  0  0  0  4  3  1  0  0
## ENFP     17 10  8 13  1  5  0  3  0  3  2  9  7  2  0  0
## ENTJ     14  5  1  4  0  0  0  0  0  0  1 13  5  0  0  0
## ENTP     16  8  8 27  1  3  0  0  1  0  0  3 13  1  1  1
## ESFJ      1  1  1  0  1  0  0  0  0  0  0  2  0  0  0  0
## ESFP      2  1  0  2  0  0  0  0  0  0  0  0  0  0  0  0
## ESTJ      0  1  0  3  0  0  0  0  0  0  0  1  0  1  0  0
## ESTP      2  1  1  4  0  1  0  0  0  0  0  1  2  1  0  0
## INFJ     92  8  9 11  0  5  2  5  1  0  4  7 13  2  0  0
## INFP     51 35  2 18  3  8  3  2  0  0 12 25 36  5  0  0
## INTJ     34  6  2 20  1  1  1 17  2  0  1 15 15  2  0  0
## INTP     31  3  3 29  3  3  0  0 15  0  3 15 28  2  0  0
## ISFJ      2  7  4  2  0  2  1  0  1  0  1  8  2  0  0  0
## ISFP      2  2  0  5  0  0  0  0  1  0  1  9  6  2  1  0
## ISTJ      6  1  1  8  0  0  0  0  0  0  0  3  2  0  0  0
## ISTP     18  3  1  3  0  2  2  0  1  0  3  4  5  1  0  0

t2 <- round(t/rowSums(t)*100)
t2 <- cbind(t2,rowSums(t))
print ("Wyniki procentowe grupowania dla dtm")

## [1] "Wyniki procentowe grupowania dla dtm"
print (t2)

##          1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ     27 20  0 20  0  3  0  3  0  0  0 13 10  3  0  30
## ENFP     21 12 10 16  1  6  0  4  0  4  2 11  9  2  0  80
## ENTJ     33 12  2  9  0  0  0  0  0  0  2 30 12  0  0  43
## ENTP     19 10 10 33  1  4  0  0  1  0  0  4 16  1  1  83
## ESFJ     17 17 17  0 17  0  0  0  0  0  0 33  0  0  0  6
## ESFP     40 20  0 40  0  0  0  0  0  0  0  0  0  0  0  5
## ESTJ      0 17  0 50  0  0  0  0  0  0  0 17  0 17  0  6
## ESTP     15  8  8 31  0  8  0  0  0  0  0  8 15  8  0  13
## INFJ     58  5  6  7  0  3  1  3  1  0  3  4  8  1  0 159
## INFP     26 18  1  9  2  4  2  1  0  0  6 12 18  2  0 200
## INTJ     29  5  2 17  1  1  1 15  2  0  1 13 13  2  0 117
## INTP     23  2  2 21  2  2  0  0 11  0  2 11 21  1  0 135
## ISFJ      7 23 13  7  0  7  3  0  3  0  3 27  7  0  0  30
## ISFP      7  7  0 17  0  0  0  0  3  0  3 31 21  7  3  29
## ISTJ     29  5  5 38  0  0  0  0  0  0  0 14 10  0  0  21
## ISTP     42  7  2  7  0  5  5  0  2  0  7  9 12  2  0  43

fviz_cluster(pam.dtm)
```



K-medoids TFIDF

```
pam_results_tfidf <- data %>%
mutate(cluster = pam.tfidf$clustering) %>%
group_by(cluster)

pam_results <- subset(pam_results_tfidf, select = c(type, cluster))
t <- table(pam_results)
print("Wyniki ilosciowe grupowania dla tf-idf")
```

```
## [1] "Wyniki ilosciowe grupowania dla tf-idf"
```

```
print(t)
```

```
##      cluster
## type   1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ    6  5  1  6  0  0  0  4  0  5  1  2  0  0  0  0
## ENFP   18  5 22 12  0  0  0 10  0  8  3  2  0  0  0  0
## ENTJ    7  2  9  7  0  1  0 10  0  7  0  0  0  0  0  0
## ENTP   18  4  7 23  1  0  1 11  0 13  2  2  0  1  0  0
## ESFJ    0  1  1  3  0  0  0  1  0  0  0  0  0  0  0  0
## ESFP    1  0  2  0  0  0  0  0  0  2  0  0  0  0  0  0
## ESTJ    1  0  0  3  0  0  0  0  0  1  1  0  0  0  0  0
## ESTP    3  0  2  0  0  0  0  5  0  0  1  2  0  0  0  0
## INFJ   24 15  9 33  0  1  6  7  1 55  1  6  0  0  1  0
## INFP   42  9 16 41  0  2 18 13  0 49  4  5  0  0  1  0
```



```
## INTJ 17 3 11 19 0 2 2 41 0 20 1 1 0 0 0 0
## INTP 24 7 10 24 0 0 7 24 1 34 2 2 0 0 0 0
## ISFJ 2 12 2 2 0 0 1 4 0 4 0 1 1 0 0 1
## ISFP 4 4 6 4 0 0 2 3 0 4 0 1 0 1 0 0
## ISTJ 14 1 3 1 0 0 0 2 0 0 0 0 0 0 0 0
## ISTP 11 0 3 7 0 0 5 3 0 10 1 2 1 0 0 0
```

```
t2 <- round(t/rowSums(t)*100)
t2 <- cbind(t2,rowSums(t))
print ("Wyniki procentowe grupowania dla tf-idf")
```

```
## [1] "Wyniki procentowe grupowania dla tf-idf"
```

```
print (t2)
```

```
##      1  2  3  4 5 6  7  8 9 10 11 12 13 14 15 16
## ENFJ 20 17  3 20 0 0  0 13 0 17  3  7  0  0  0  30
## ENFP 22  6 28 15 0 0  0 12 0 10  4  2  0  0  0  80
## ENTJ 16  5 21 16 0 2  0 23 0 16  0  0  0  0  0  43
## ENTP 22  5  8 28 1 0  1 13 0 16  2  2  0  1  0  83
## ESFJ  0 17 17 50 0 0  0 17 0  0  0  0  0  0  0  6
## ESFP 20  0 40  0 0 0  0  0 0 40  0  0  0  0  0  5
## ESTJ 17  0  0 50 0 0  0  0 0 17 17  0  0  0  0  6
## ESTP 23  0 15  0 0 0  0 38 0  0  8 15  0  0  0  13
## INFJ 15  9  6 21 0 1  4  4 1 35  1  4  0  0  1  159
## INFP 21  4  8 20 0 1  9  6 0 24  2  2  0  0  0  200
## INTJ 15  3  9 16 0 2  2 35 0 17  1  1  0  0  0  117
## INTP 18  5  7 18 0 0  5 18 1 25  1  1  0  0  0  135
## ISFJ  7 40  7  7 0 0  3 13 0 13  0  3  3  0  0  30
## ISFP 14 14 21 14 0 0  7 10 0 14  0  3  0  3  0  29
## ISTJ 67  5 14  5 0 0  0 10 0  0  0  0  0  0  0  21
## ISTP 26  0  7 16 0 0 12  7 0 23  2  5  2  0  0  43
```

```
fviz_cluster(pam.tfidf)
```



```
## INTJ 31 4 11 17 13 3 1 1 8 0 6 9 0 4 9 0
## INTP 16 3 17 15 19 7 6 0 7 1 9 15 1 7 12 0
## ISFJ 3 5 2 4 2 1 0 1 3 0 0 3 1 0 4 1
## ISFP 3 5 2 4 0 0 0 0 1 1 1 5 0 2 5 0
## ISTJ 3 4 1 1 4 1 0 0 0 0 2 1 0 2 2 0
## ISTP 3 1 8 5 4 0 2 1 5 2 2 3 0 0 6 1
```

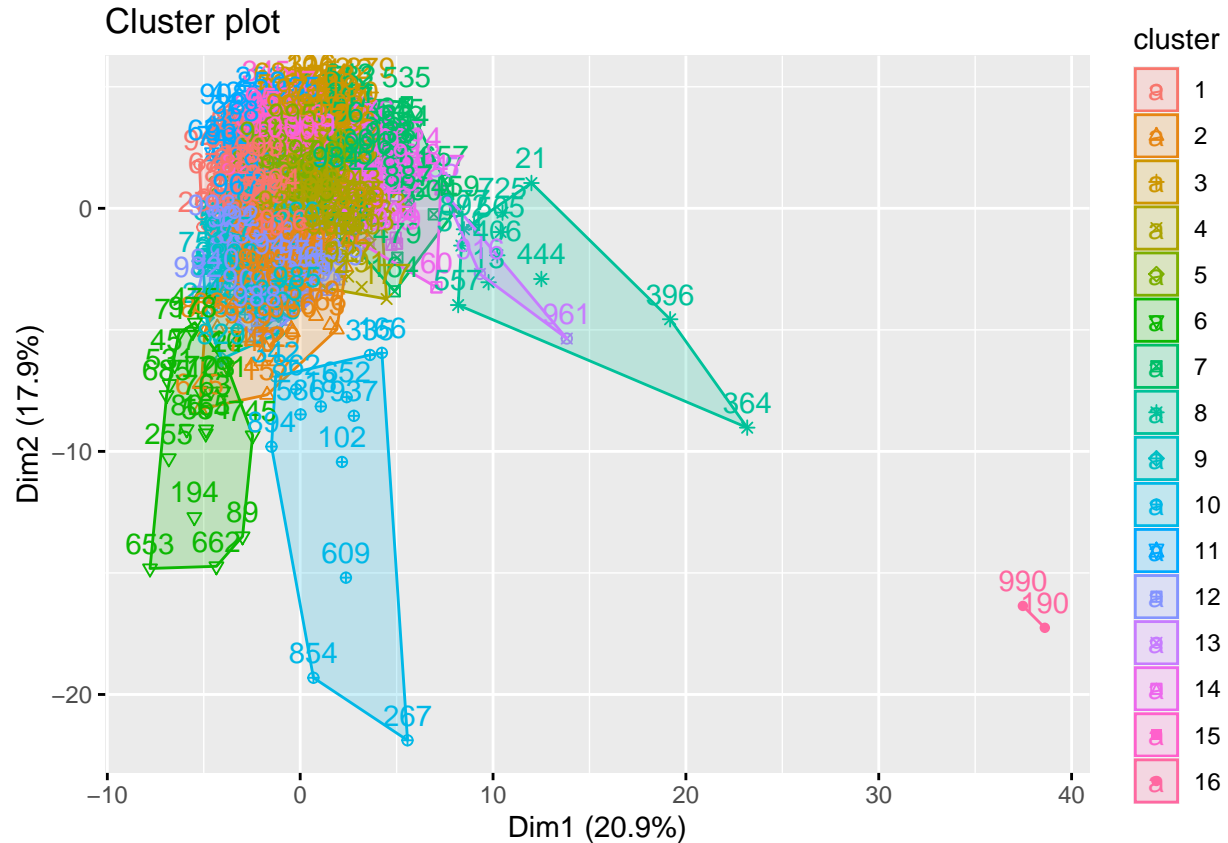
```
t2 <- round(t/rowSums(t)*100)
t2 <- cbind(t2,rowSums(t))
print ("Wyniki procentowe grupowania dla glove1")
```

```
## [1] "Wyniki procentowe grupowania dla glove1"
```

```
print (t2)
```

```
##      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ 13  3  0 17 10  0  0  0  7  0  7  3  0 30 10  0 30
## ENFP 10 15  5 28  6  4  1  0  1  4  4  2  0 12  8  0 80
## ENTJ 21  7  2 19  9  2  0  2  7  0  7  9  0  9  5  0 43
## ENTP 16  7  6 14  8  1  4  0  8  2  6 10  0  6 11  0 83
## ESFJ 50  0  0 33  0 17  0  0  0  0  0  0  0  0  0  0  6
## ESFP  0 60 20  0  0  0  0  0 20  0  0  0  0  0  0  0  5
## ESTJ  0 17  0 17 50  0  0  0  0 17  0  0  0  0  0  0  6
## ESTP 15  8 15 23  8  0  8  0  0  8  0  8  0  0  8  0 13
## INFJ 16 11 11 15 11  0  4  1  5  0  4  7  1  4 10  0 159
## INFP  8  6 14 16  7  2 14  3  4  1  6  4  0  7  9  0 200
## INTJ 26  3  9 15 11  3  1  1  7  0  5  8  0  3  8  0 117
## INTP 12  2 13 11 14  5  4  0  5  1  7 11  1  5  9  0 135
## ISFJ 10 17  7 13  7  3  0  3 10  0  0 10  3  0 13  3 30
## ISFP 10 17  7 14  0  0  0  0  3  3  3 17  0  7 17  0 29
## ISTJ 14 19  5  5 19  5  0  0  0  0 10  5  0 10 10  0 21
## ISTP  7  2 19 12  9  0  5  2 12  5  5  7  0  0 14  2 43
```

```
fviz_cluster(pam.glove)
```



K-medoids Glove(oddzielne posty)

```
pam_results_glove2 <- data2 %>%
mutate(cluster = pam.glove2$clustering) %>%
group_by(cluster)

pam_results <- subset(pam_results_glove2, select = c(type, cluster))
t <- table(pam_results)
print("Wyniki ilosciowe grupowania dla glove2")
```

```
## [1] "Wyniki ilosciowe grupowania dla glove2"
```

```
print(t)
```

```
##      cluster
## type    1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ    9 21 12  1  3  8  1  3  4  3  6 10  2  3  6  0
## ENFP   12 28  3  2  0  8  7  6  5  2  2  8  4  1  1  1
## ENTJ    8 11  2  0  1  1  2  2  3  2  0  5  3  2  1  0
## ENTP   17 18  3  4  3  2  5  4  3  2  1  5  4  1  2  1
## ESFP   10 11  5  1  0  2  3  2  0  3  2  2  3  0  0  0
## ESTJ    7 18  4  0  0  3  3  4  0  1  1  4  2  2  0  0
## INFJ   65 144 37 21 16 40 44 36 25 27 11 38 41 30 24  0
## INFP   33 104 22 24 17 29 26 34 23 19 13 33 28  8 16  1
## INTJ   34 121 15 22 12 19 21 23 18 10 13 33 13 12 15  3
## INTP    8 25  5  5  2  9  5  5  2  2  1  8  7  3  4  0
```

```
##   ISFP  2  7  2  1  3  2  2  5  1  2  5  4  5  0  1  0
##   ISTJ  1  9  0  1  0  1  1  1  0  0  0  0  0  1  0  0
##   ISTP 12 40  7  6  3 13  7  9  3  3  1 10 11  3  4  0
```

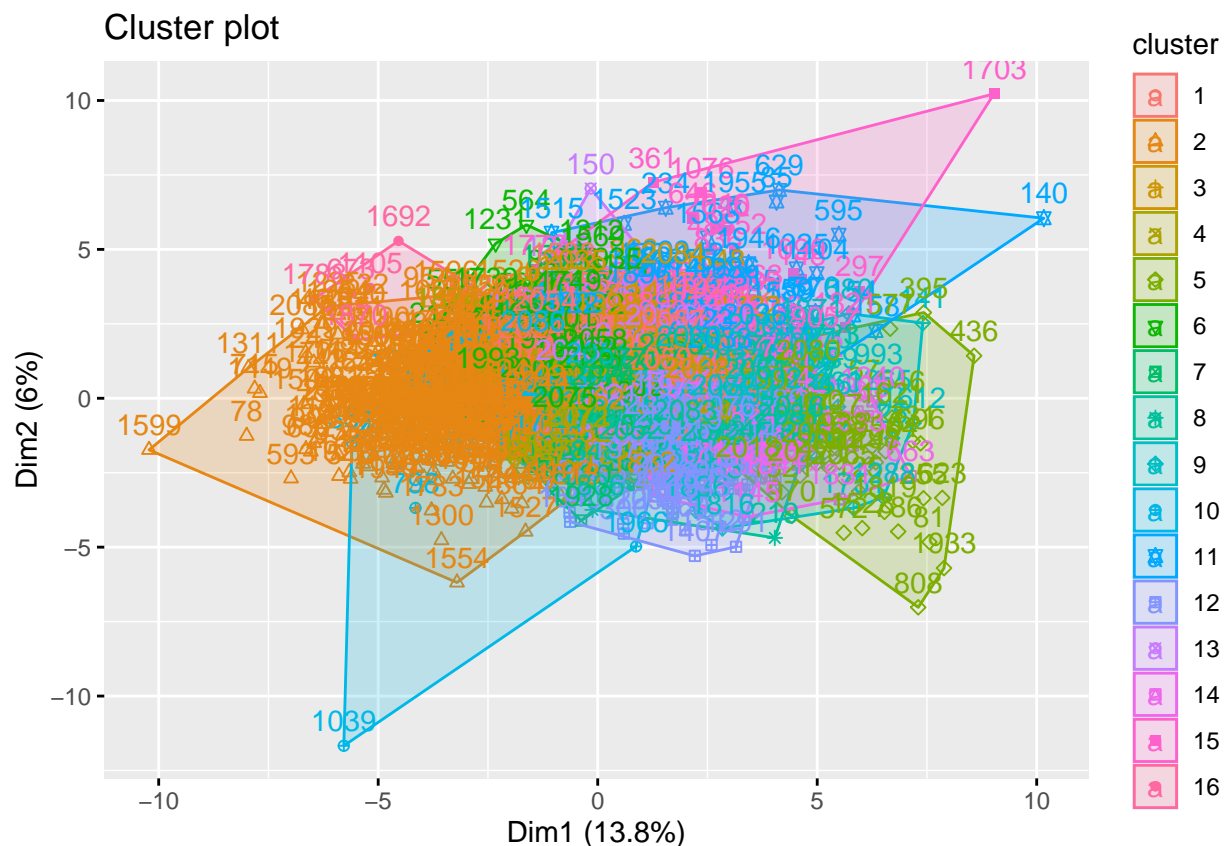
```
t2 <- round(t/rowSums(t)*100)
t2 <- cbind(t2,rowSums(t))
print ("Wyniki procentowe grupowania dla glove2")
```

```
## [1] "Wyniki procentowe grupowania dla glove2"
```

```
print (t2)
```

```
##      1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
## ENFJ 10 23 13 1 3  9 1  3  4  3  7 11  2  3  7  0 92
## ENFP 13 31  3 2 0  9 8  7  6  2  2  9  4  1  1  1 90
## ENTJ 19 26  5 0 2  2 5  5  7  5  0 12  7  5  2  0 43
## ENTP 23 24  4 5 4  3 7  5  4  3  1  7  5  1  3  1 75
## ESFP 23 25 11 2 0  5 7  5  0  7  5  5  7  0  0  0 44
## ESTJ 14 37  8 0 0  6 6  8  0  2  2  8  4  4  0  0 49
## INFJ 11 24  6 4 3  7 7  6  4  5  2  6  7  5  4  0 599
## INFP  8 24  5 6 4  7 6  8  5  4  3  8  7  2  4  0 430
## INTJ  9 32  4 6 3  5 5  6  5  3  3  9  3  3  4  1 384
## INTP  9 27  5 5 2 10 5  5  2  2  1  9  8  3  4  0 91
## ISFP  5 17  5 2 7  5 5 12  2  5 12 10 12  0  2  0 42
## ISTJ  7 60  0 7 0  7 7  7  0  0  0  0  0  7  0  0 15
## ISTP  9 30  5 5 2 10 5  7  2  2  1  8  8  2  3  0 132
```

```
fviz_cluster(pam.glove2)
```



DBSCAN

```
# metric = "euclidean", "manhattan", "gower"
dissimilarity.dtm <- daisy(as.matrix(vectors.dtm), metric = "euclidean")
dissimilarity.tfidf <- daisy(as.matrix(vectors.tfidf), metric = "euclidean")
dissimilarity.glove <- daisy(as.matrix(vectors.glove), metric = "euclidean")
dissimilarity.glove_post <- daisy(as.matrix(vectors.glove_post), metric = "euclidean")
```



USTALENIE OPTIMALNEGO PARAMETRU EPS

Metoda polega na obliczeniu odległości kNN w macierzy punktów.

Wartość k jest określona przez użytkownika i odpowiada MinPts.

Następnie te odległości k są nanoszone w kolejności rosnącej na wykres. Celem jest określenie "kolana", które odpowiada optymalnemu parametrowi eps.

Kolano odpowiada progowi, w którym następuje ostra zmiana wzdłuż krzywej k-odległości.

Funkcji `kNNdistplot()` można użyć do narysowania wykresu odległości k:

>kNNdist - Calculate and plot the k-Nearest Neighbor Distance – pozwala na szybkie wyznaczenie odległości k-najbliższych sąsiadów w macierzy punktów. Wykres stworzony na bazie funkcji może być używany do pomocy w znalezieniu odpowiedniej wartości parametru eps dla funkcji DBSCAN (szukanie „kolana” w wykresie).

`kNNdistplot(dane, k = 5)`

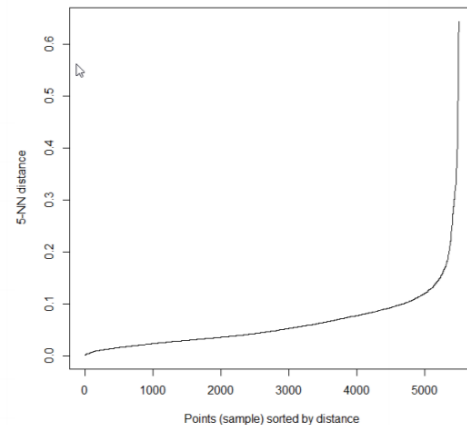


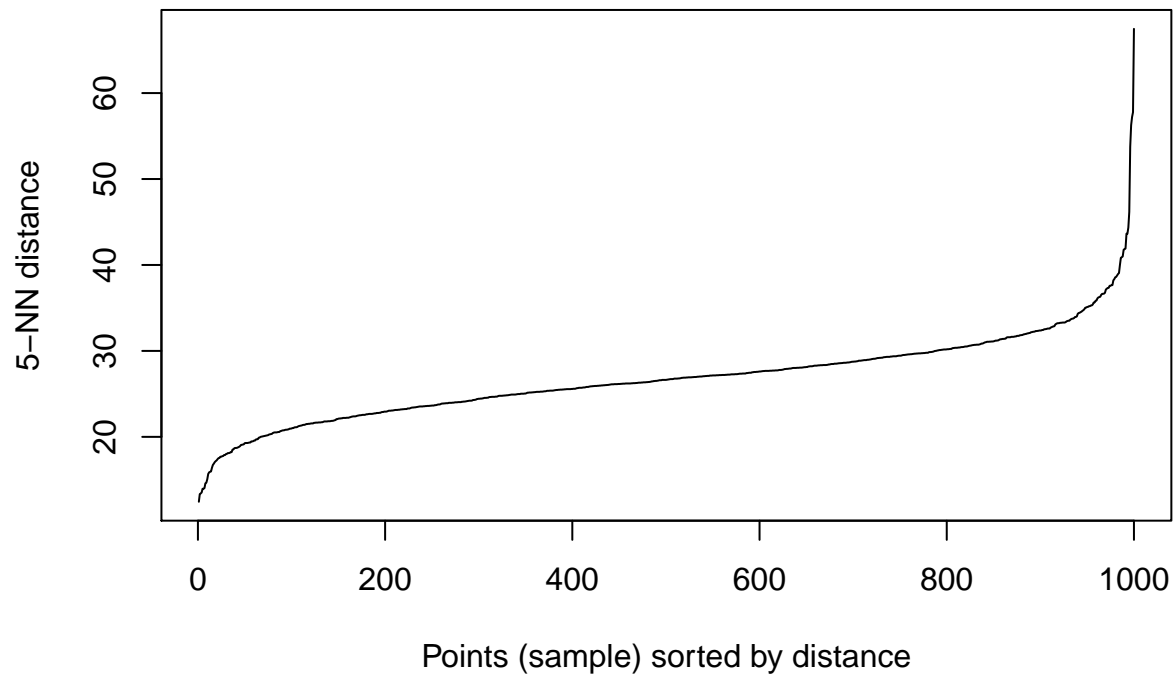
Figure 1: ESP

```
plot_desity <- function(desity, dissimilarity, method) {
  points <- cmdscale(dissimilarity, k = 2)
  plot(points,
    main = method,
    col = as.factor(desity$cluster),
    mai = c(0, 0, 0, 0),
    mar = c(0, 0, 0, 0),
    xaxt = 'n', yaxt = 'n',
    xlab = '', ylab = '')
}
```

DTM

Należy odczytać gdzie na wykresie jest tak zwane kolano, czyli punkt, po którym wykres zaczyna ustawiać się w pionie. Wartość tego punktu zostaje zastosowana jako eps.

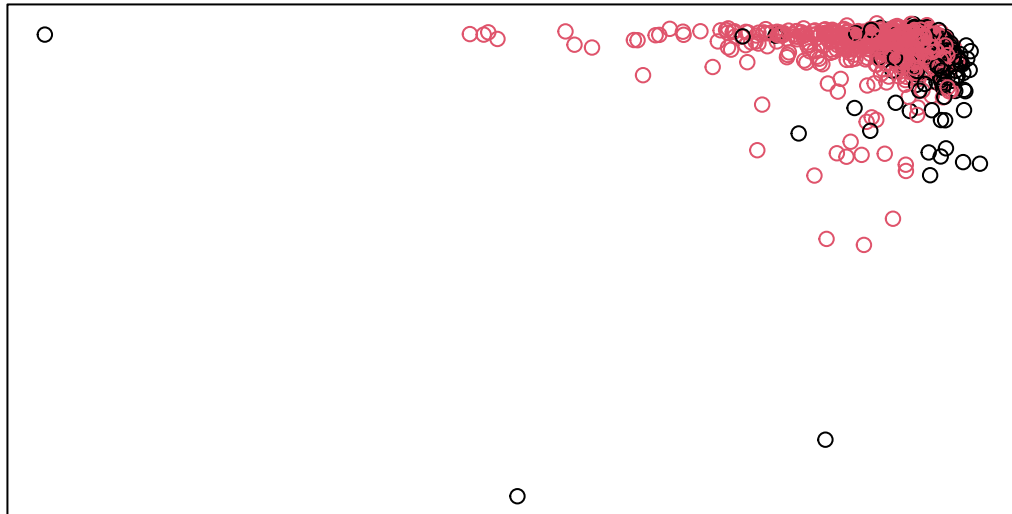
```
kNNdistplot(vectors.dtm, k = 5)
```



```
eps = 30
dbscan.dtm <- dbscan(vectors.dtm, eps = eps, minPts = 5)
dbscan.dtm

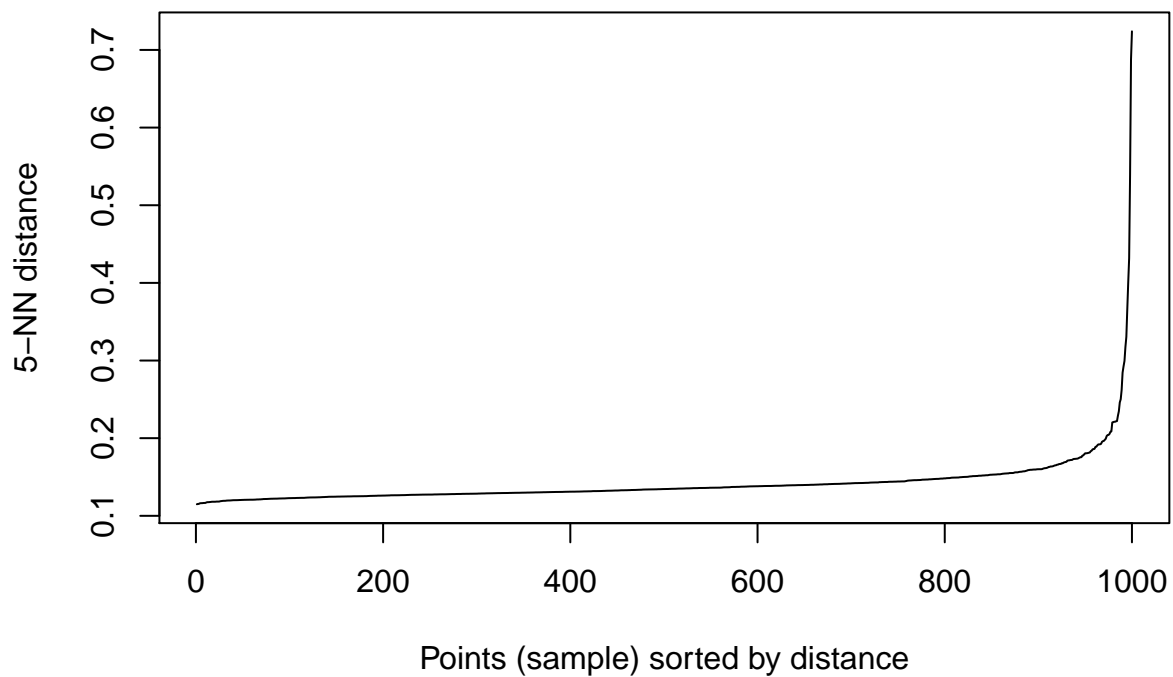
## DBSCAN clustering for 1000 objects.
## Parameters: eps = 30, minPts = 5
## The clustering contains 1 cluster(s) and 160 noise points.
##
##    0    1
## 160 840
##
## Available fields: cluster, eps, minPts
plot_desity(dbscan.dtm, dissimilarity.dtm, "DTM")
```

DTM



TFID

```
kNNdistplot(vectors.tfidf, k = 5)
```

```
eps = 0.15
dbscan.tfidf <- dbscan(vectors.tfidf, eps = eps, minPts = 5)
dbscan.tfidf

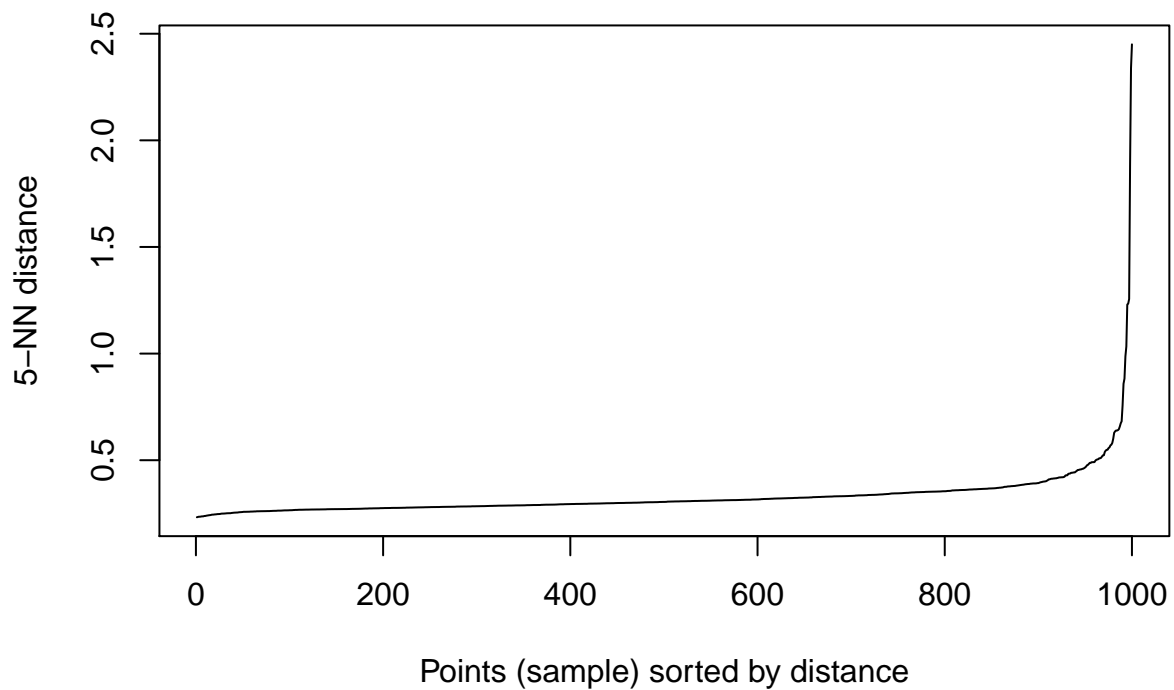
## DBSCAN clustering for 1000 objects.
## Parameters: eps = 0.15, minPts = 5
## The clustering contains 1 cluster(s) and 133 noise points.
##
##    0    1
## 133 867
##
## Available fields: cluster, eps, minPts
plot_desity(dbscan.tfidf, dissimilarity.tfidf, "TFIDF")
```

TFIDF



GLOVE

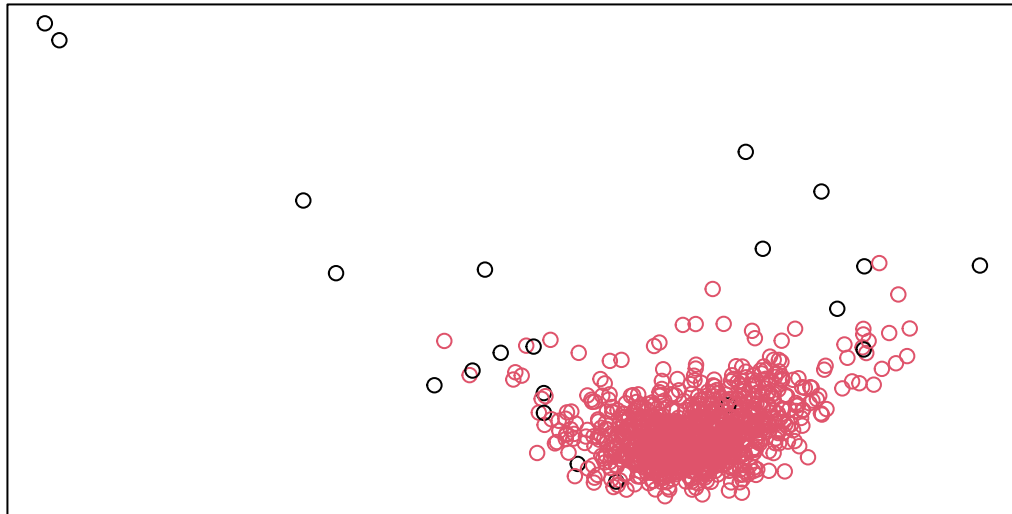
```
kNNdistplot(vectors.glove, k = 5)
```



```
eps = 0.5
minPts = 5
dbscan.glove <- dbscan(vectors.glove, eps = eps, minPts = minPts)
dbscan.glove
```

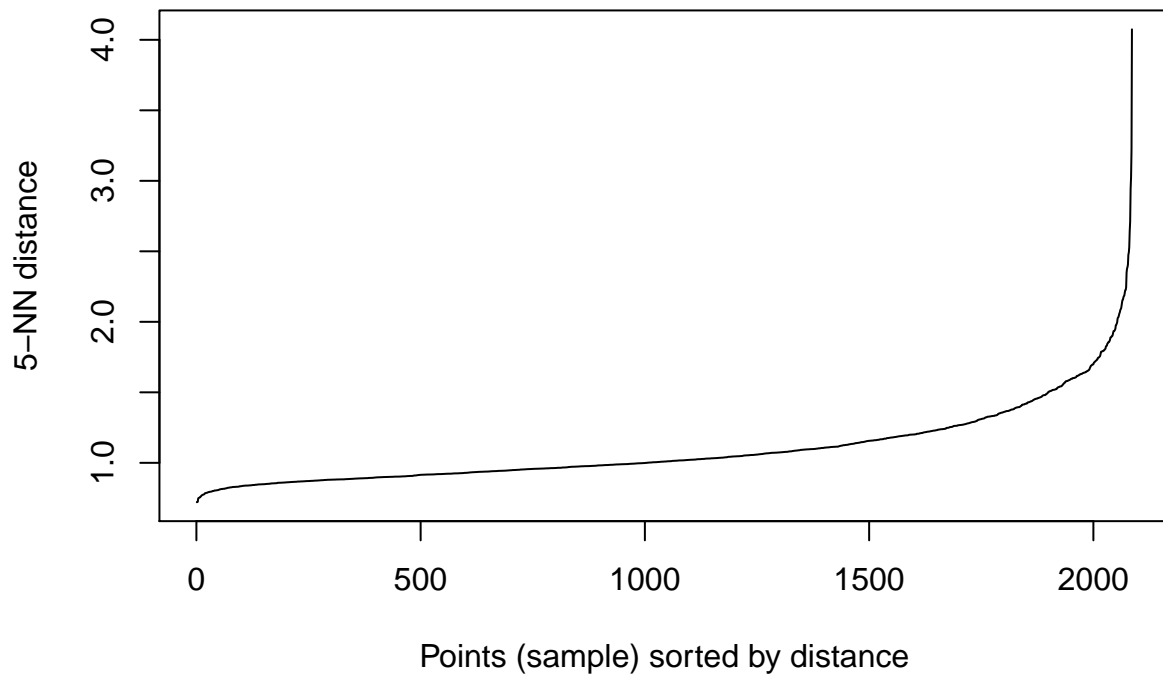
```
## DBSCAN clustering for 1000 objects.
## Parameters: eps = 0.5, minPts = 5
## The clustering contains 1 cluster(s) and 21 noise points.
##
##    0    1
## 21 979
##
## Available fields: cluster, eps, minPts
plot_desity(dbscan.glove, dissimilarity.glove, "GLOVE")
```

GLOVE



GLOVE POST

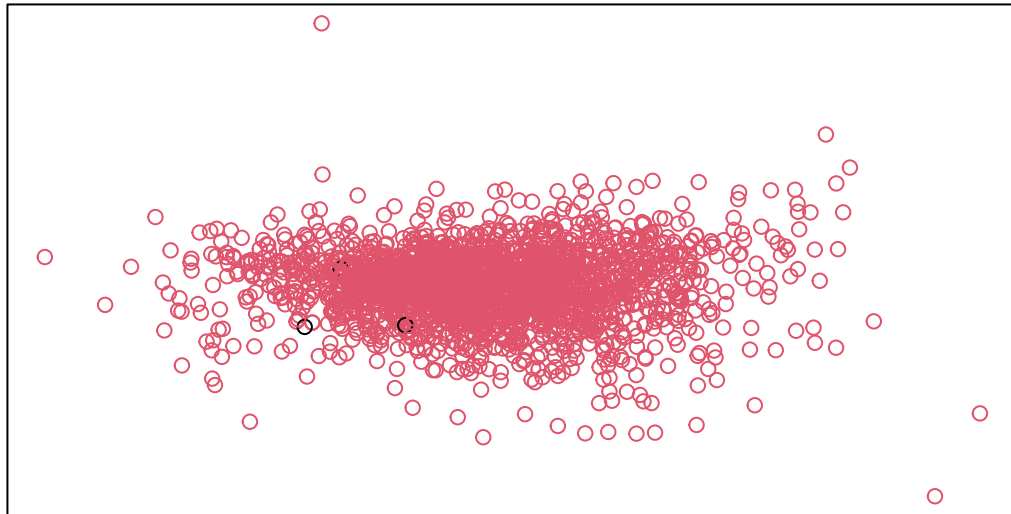
```
kNNdistplot(vectors.glove_post, k = 5)
```



```
eps = 1.5
minPts = 5
dbscan.glove_post <- dbscan(vectors.glove, eps = eps, minPts = minPts)
dbscan.glove_post
```

```
## DBSCAN clustering for 1000 objects.
## Parameters: eps = 1.5, minPts = 5
## The clustering contains 1 cluster(s) and 2 noise points.
##
##    0    1
##    2 998
##
## Available fields: cluster, eps, minPts
plot_desity(dbscan.glove_post, dissimilarity.glove_post, "GLOVE POST")
```

GLOVE POST



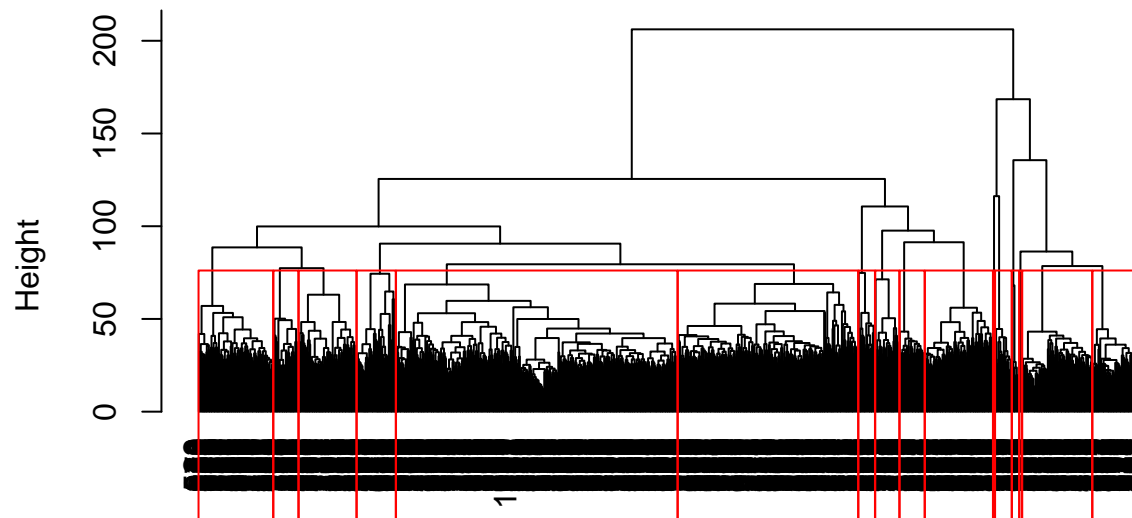
Grupowanie Hierarchiczne

```
plot_hierarchical <- function(dissimilarity, hierarchical_result, method) {  
  points <- cmdscale(dissimilarity, k = 2)  
  res.hier <- cutree(hierarchical_result, k = 16)  
  plot(points,  
        main = method,  
        col = res.hier,  
        mai = c(0, 0, 0, 0),  
        mar = c(0, 0, 0, 0),  
        xaxt = 'n', yaxt = 'n',  
        xlab = '', ylab = '')  
}
```

DTM

```
# methods = "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid"  
hc.dtm <- hclust(dissimilarity.dtm, method="ward.D2")  
plot(hc.dtm, hang = -1)  
rect.hclust(hc.dtm, k=16, border="red")
```

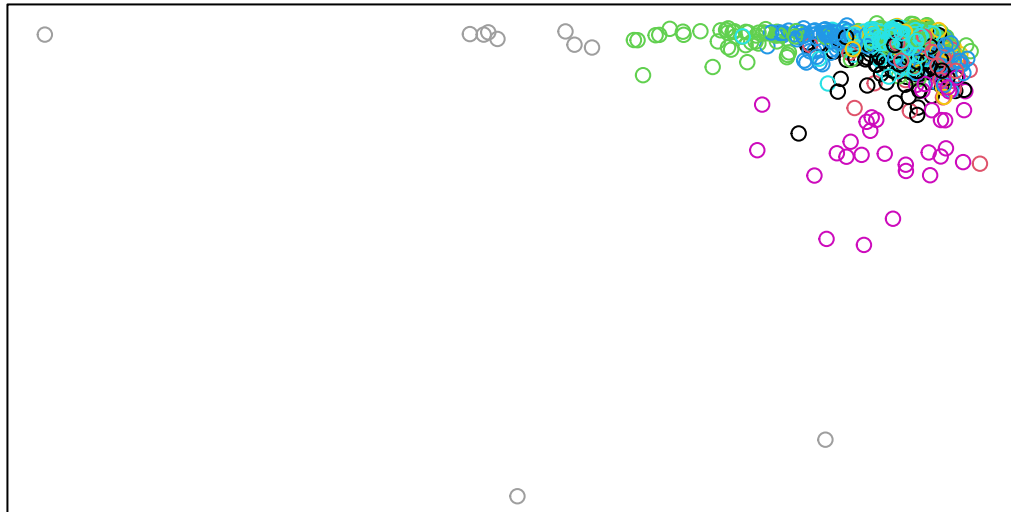
Cluster Dendrogram



```
dissimilarity.dtm  
hclust (*, "ward.D2")
```

```
plot_hierarchical(dissimilarity.dtm, hc.dtm, "DTM")
```

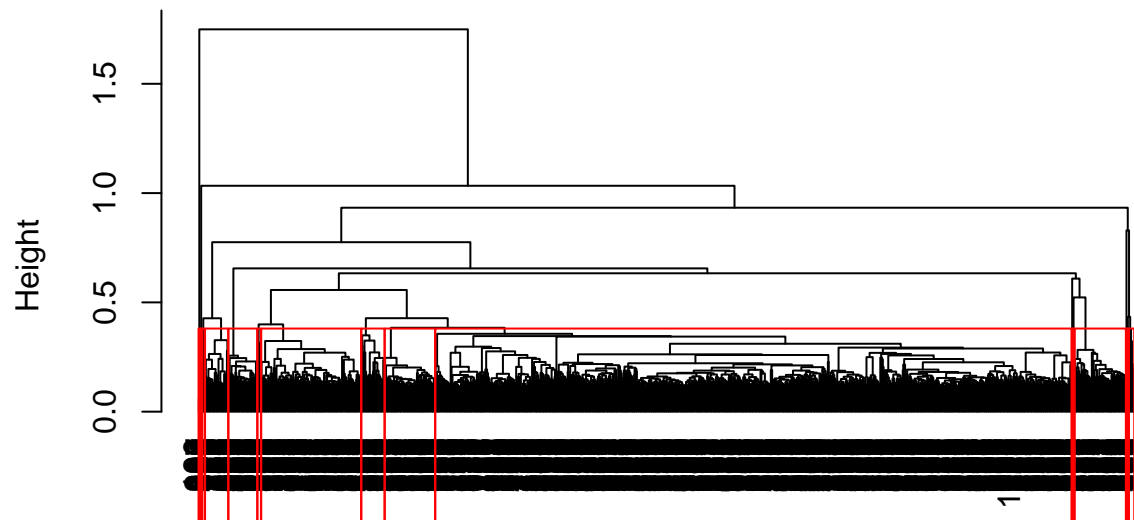
DTM



Tfidf

```
hc.tfidf <- hclust(dissimilarity.tfidf, method="ward.D2")  
plot(hc.tfidf, hang = -1)  
rect.hclust(hc.tfidf, k=16, border="red")
```


Cluster Dendrogram



dissimilarity.tfidf
hclust (*, "ward.D2")

```
plot_hierarchical(dissimilarity.tfidf, hc.tfidf, "TFIDF")
```

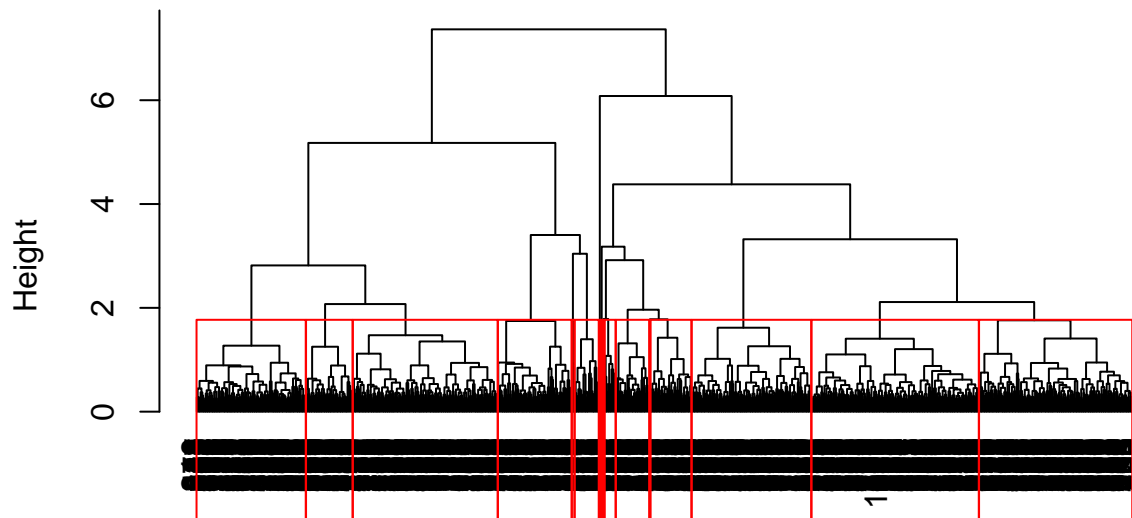
TFIDF



GLOVE

```
hc.glove <- hclust(dissimilarity.glove, method="ward.D2")  
plot(hc.glove, hang = -1)  
rect.hclust(hc.glove, k=16, border="red")
```

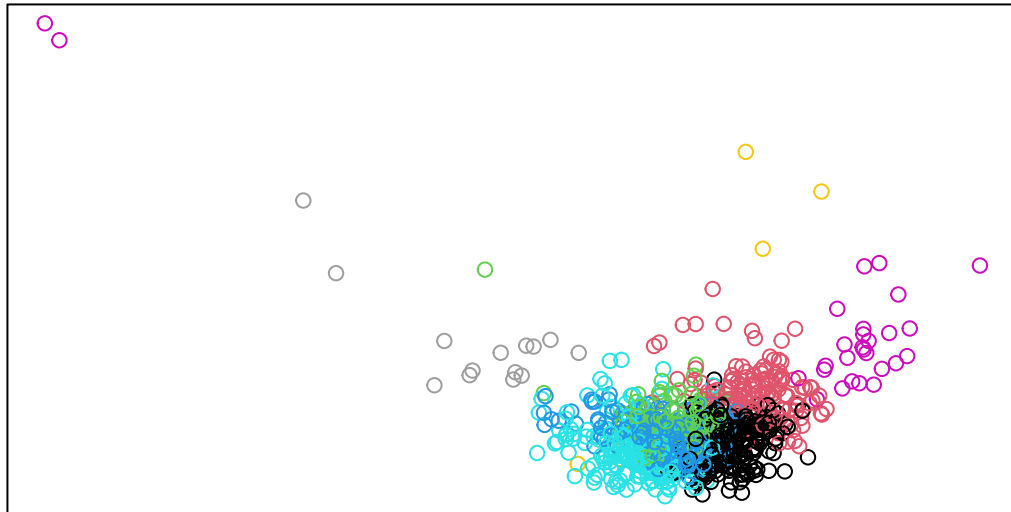
Cluster Dendrogram



```
dissimilarity.glove  
hclust (*, "ward.D2")
```

```
plot_hierarchical(dissimilarity.glove, hc.glove, "GLOVE")
```

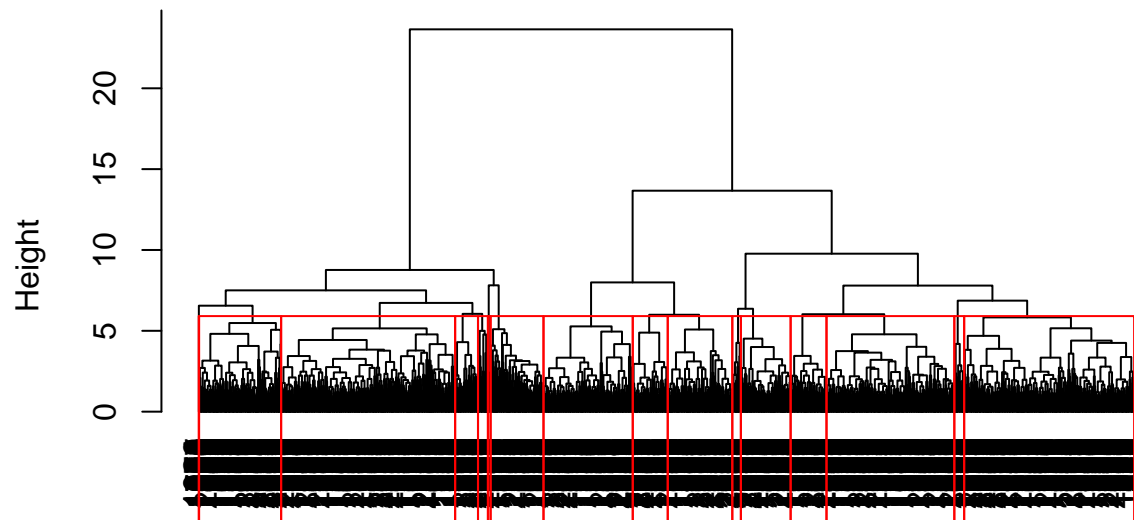
GLOVE



GLOVE Posts

```
hc.glove_post <- hclust(dissimilarity.glove_post, method="ward.D2")  
plot(hc.glove_post, hang = -1)  
rect.hclust(hc.glove_post, k=16, border="red")
```

Cluster Dendrogram



```
dissimilarity.glove_post  
hclust (*, "ward.D2")
```

```
plot_hierarchical(dissimilarity.glove_post, hc.glove_post, "GLOVE POSTS")
```

GLOVE POSTS

