codigo

November 25, 2020

[1]:
```
#install.packages(c('tidyverse', 'tidytext", 'dplyr', 'ggplot2',␣
 ↪'wordcloud','rjson', 'quanteda', 'feather', 'cld2', 'ggplot2', 'plotly',␣
 ↪'scales', 'cowplot', 'tau', 'stopwords', 'tm', 'textstem', 'pbapply',␣
 ↪'text2vec', 'rlist', 'dbscan'))

library(rjson); library(tidyverse); library(quanteda); library(feather);␣
 ↪library(cld2); library(ggplot2); library(plotly); library(scales);␣
 ↪library(cowplot); library(tau); library(stopwords); library(tm);␣
 ↪library(textstem); library(pbapply); library(text2vec); library(rlist);␣
 ↪library(wordcloud); library(dbscan)
```

```
Warning message:
"package 'tidyverse' was built under R version 3.6.3"
-- Attaching packages --------------------------------------- tidyverse
1.3.0 --

v ggplot2 3.3.2     v purrr   0.3.4
v tibble  3.0.3     v dplyr   1.0.2
v tidyr   1.1.2     v stringr 1.4.0
v readr   1.3.1     v forcats 0.5.0

Warning message:
"package 'ggplot2' was built under R version 3.6.3"
Warning message:
"package 'tibble' was built under R version 3.6.3"
Warning message:
"package 'tidyr' was built under R version 3.6.3"
Warning message:
"package 'purrr' was built under R version 3.6.3"
Warning message:
"package 'dplyr' was built under R version 3.6.3"
Warning message:
"package 'forcats' was built under R version 3.6.3"
-- Conflicts ------------------------------------------
tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

```
Warning message:
"package 'quanteda' was built under R version 3.6.3"
Package version: 2.1.2

Parallel computing: 2 of 16 threads used.

See https://quanteda.io for tutorials and examples.


Attaching package: 'quanteda'


The following object is masked from 'jupyter:irkernel':

    View


The following object is masked from 'package:utils':

    View


Warning message:
"package 'feather' was built under R version 3.6.3"
Warning message:
"package 'cld2' was built under R version 3.6.3"
Warning message:
"package 'plotly' was built under R version 3.6.3"

Attaching package: 'plotly'


The following object is masked from 'package:ggplot2':

    last_plot


The following object is masked from 'package:stats':

    filter


The following object is masked from 'package:graphics':

    layout
```

```
Warning message:
"package 'scales' was built under R version 3.6.3"

Attaching package: 'scales'


The following object is masked from 'package:purrr':

    discard


The following object is masked from 'package:readr':

    col_factor


Warning message:
"package 'cowplot' was built under R version 3.6.3"
Warning message:
"package 'tau' was built under R version 3.6.3"

Attaching package: 'tau'


The following object is masked from 'package:readr':

    tokenize


Warning message:
"package 'stopwords' was built under R version 3.6.3"
Warning message:
"package 'tm' was built under R version 3.6.3"
Loading required package: NLP


Attaching package: 'NLP'


The following objects are masked from 'package:quanteda':

    meta, meta<-


The following object is masked from 'package:ggplot2':

    annotate
```

```
Attaching package: 'tm'


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

    stopwords


The following objects are masked from 'package:quanteda':

    as.DocumentTermMatrix, stopwords


Warning message:
"package 'textstem' was built under R version 3.6.3"
Loading required package: koRpus.lang.en

Warning message:
"package 'koRpus.lang.en' was built under R version 3.6.3"
Loading required package: koRpus

Loading required package: sylly

For information on available language packages for 'koRpus', run

  available.koRpus.lang()

and see ?install.koRpus.lang()



Attaching package: 'koRpus'


The following object is masked from 'package:tm':

    readTagged


The following object is masked from 'package:tau':

    tokenize


The following objects are masked from 'package:quanteda':
```

```
    tokens, types


The following object is masked from 'package:readr':

    tokenize


Warning message:
"package 'pbapply' was built under R version 3.6.3"
Warning message:
"package 'text2vec' was built under R version 3.6.3"
Warning message:
"package 'rlist' was built under R version 3.6.3"
Warning message:
"package 'wordcloud' was built under R version 3.6.3"
Loading required package: RColorBrewer

Warning message:
"package 'dbscan' was built under R version 3.6.3"
```

CODIGO PARA CARGAR METADATA Y VER SU ESTRUCTURA

[2]:
```
# Cargamos los datos del archivo "metadata.csv"
# stringAsFactors evita que las cadenas de texto se conviertan en factores
# na.strings indica qué consideramos valores nulos. En este caso celdas vacías y␣
 ↪"NA"
metadata_df <- read.csv("D:/COVID/metadata.csv", stringsAsFactors = FALSE, na.
 ↪strings = c("", "NA"))

# str() permite ver la estructura del archivo: número de filas, columnas y␣
 ↪muestra el primero objeto almacenado
str(metadata_df)
```

```
'data.frame':   253454 obs. of  19 variables:
 $ cord_uid        : chr  "ug7v899j" "02tnwd4m" "ejv2xln0" "2b73a28n" ...
 $ sha             : chr  "d1aafb70c066a2068b02786f8929fd9c900897fb"
"6b0567729c2143a66d737eb0a2f63f2dce2e5a7d"
"06ced00a5fc04215949aa72528f2eeaae1d58927"
"348055649b6b8cf2b9a376498df9bf41f7123605" ...
 $ source_x        : chr  "PMC" "PMC" "PMC" "PMC" ...
 $ title           : chr  "Clinical features of culture-proven Mycoplasma
pneumoniae infections at King Abdulaziz University Hospital, Jed"| __truncated__
"Nitric oxide: a pro-inflammatory mediator in lung disease?" "Surfactant
protein-D and pulmonary host defense" "Role of endothelin-1 in lung disease" ...
 $ doi             : chr  "10.1186/1471-2334-1-6" "10.1186/rr14" "10.1186/rr19"
"10.1186/rr44" ...
 $ pmcid           : chr  "PMC35282" "PMC59543" "PMC59549" "PMC59574" ...
```

```
 $ pubmed_id       : chr  "11472636" "11667967" "11667972" "11686871" ...
 $ license         : chr  "no-cc" "no-cc" "no-cc" "no-cc" ...
 $ abstract        : chr  "OBJECTIVE: This retrospective chart review describes
the epidemiology and clinical features of 40 patients with"| __truncated__
"Inflammatory diseases of the respiratory tract are commonly associated with
elevated production of nitric oxide"| __truncated__ "Surfactant protein-D (SP-D)
participates in the innate response to inhaled microorganisms and organic
antigens,"| __truncated__ "Endothelin-1 (ET-1) is a 21 amino acid peptide with
diverse biological activity that has been implicated in num"| __truncated__ ...
 $ publish_time    : chr  "2001-07-04" "2000-08-15" "2000-08-25" "2001-02-22"
...
 $ authors         : chr  "Madani, Tariq A; Al-Ghamdi, Aisha A" "Vliet, Albert
van der; Eiserich, Jason P; Cross, Carroll E" "Crouch, Erika C" "Fagan, Karen A;
McMurtry, Ivan F; Rodman, David M" ...
 $ journal         : chr  "BMC Infect Dis" "Respir Res" "Respir Res" "Respir
Res" ...
 $ mag_id          : logi  NA NA NA NA NA NA ...
 $ who_covidence_id: chr  NA NA NA NA ...
 $ arxiv_id        : chr  NA NA NA NA ...
 $ pdf_json_files  : chr
"document_parses/pdf_json/d1aafb70c066a2068b02786f8929fd9c900897fb.json"
"document_parses/pdf_json/6b0567729c2143a66d737eb0a2f63f2dce2e5a7d.json"
"document_parses/pdf_json/06ced00a5fc04215949aa72528f2eeaae1d58927.json"
"document_parses/pdf_json/348055649b6b8cf2b9a376498df9bf41f7123605.json" ...
 $ pmc_json_files  : chr  "document_parses/pmc_json/PMC35282.xml.json"
"document_parses/pmc_json/PMC59543.xml.json"
"document_parses/pmc_json/PMC59549.xml.json"
"document_parses/pmc_json/PMC59574.xml.json" ...
 $ url             : chr  "https://www.ncbi.nlm.nih.gov/pmc/articles/PMC35282/"
"https://www.ncbi.nlm.nih.gov/pmc/articles/PMC59543/"
"https://www.ncbi.nlm.nih.gov/pmc/articles/PMC59549/"
"https://www.ncbi.nlm.nih.gov/pmc/articles/PMC59574/" ...
 $ s2_id           : int  NA NA NA NA NA NA NA NA NA NA ...
```

FUNCIÓN PARA EXTRAER INFORMACIÓN

[6]:
```r
# Función de ayuda  para extraer información de JSON
leer_json <- function(json){
  # Obtenemos el identificador del texto
  paper_id <- json$paper_id
  # Obtenemos sus autores
  authors <- json$metadata$authors
  author_list <- list()
  # Separamos cada autor
  for (author in authors) {
      name <- paste0(author$first," ", author$last, ";")
      author_list <- paste0(author_list, as.character(name))
  }
```

```
  # Obtenemos el título del artículo
  title_text <- json$metadata$title
  # Obtenemos todo el abstract o resumen
  abstract_text <- ''
  for (each_abstract in json$abstract) {
      abstract_text <- paste(abstract_text, each_abstract$text)
  }
  # Obtenemos el cuerpo del artículo
  body_text <- ''
  for (each_body in json$body_text) {
      body_text <- paste(body_text, each_body$text)
  }

  # Devolvemos el resultado en forma de Data Frame
  return(tibble(paper_id, author_list, title_text, abstract_text, body_text))
}
```

DIRECTORIO DE LOS ARCHIVOS

[4]:
```
# Identificamos la carpeta que contiene los JSON
directorio <- 'D:/COVID/document_parses/pdf_json/'
#Cogemos todos los archivos del directorio
archivos <- list.files(directorio)
# Mostramos el número de archivos
length(archivos)
```

106137

PROCESAMIENTO DE LOS ARHIVOS (covid_df.csv)

30 minutos

[7]:
```
# Inicializamos el contenido del artíuculo en formato lista
articulos <- list()
# Inicializamos el índice de artículos
indice <- 0

# Iteramos cada uno de los archivos
for (archivo in archivos) {
  # Actualizamos el puntero
  indice <- indice + 1
  # Breve comprobación para mostrar el estado de carga
  if (indice %% (length(archivos) %/% 10) == 0) {
    cat("Artículos procesados:  ", indice, " de ", length(archivos), "\n")
  }

  # Modificamos el camino o PATH hacia el archivo actual
  ruta_archivo <- paste0(directorio, '/', archivo)
  # Convertimos el archivo JSON a objeto de R para poder tratarlo
```

```
 json <- fromJSON(file = ruta_archivo)
 # Aplicamos la función para extraer la informaciópn del archivo
 contenido <- leer_json(json)

 # Comprobamos si el formato del archivo es el correcto
 if(length(contenido$paper_id) > 0){
   # Si se ha obtenido información del archivo
   # Buscamos el artículo en el archivo "metadata.csv"
   meta <- metadata_df[which(metadata_df$sha == contenido$paper_id), ]
   # Si no hay información en metadata.csv o el cuerpo del artículo está vacío␣
↪saltamos el artículo
   if (length(meta) > 0 | length(contenido$body_text) <= 0) {
     # Si no se encuentra autor en el JSON buscamos en metadata
     if (length(contenido$author_list) <= 0) {
       authors <- metadata_df$authors
       author_list <- list()
       # Separamos cada autor
       for (author in authors) {
           name <- paste0(author$first," ", author$last, ";")
           author_list <- paste0(author_list, as.character(name))
       }
       # Sustituimos los autores
       contenido$author_list <- author_list
     }

     # Si no se encuentra el título en el JSON lo buscamos en metadata
     if (contenido$title_text == '') {
       contenido$title_text <- 'NoIncluido'
     }

     # Si no se encuentra el abstract lo dejamos como 'No incluido'
     if (nchar(contenido$abstract_text) <= 0) {
       contenido$abstract_text <- 'NoIncluido'
     }

     # Añadimos la revista de publicación
     if (length(meta$journal) > 0) {
       contenido$journal <- meta$journal[1]
     }
     else {
       contenido$journal <- 'NoIncluido'
     }
     # Añadimos el DOI
     if (length(meta$doi) > 0) {
       contenido$doi <- meta$doi[1]
     }
     else {
```

```
        contenido$doi <- 'NoIncluido'
      }

      # Incluimos el contenido al conjunto de artículos
      articulos[[indice]] <- contenido
    }
  }
}

# Enlazamos todas las filas generadas en un único Data Frame
covid_df <- bind_rows(articulos)
```

```
Artículos procesados:   10613  de  106137
Artículos procesados:   21226  de  106137
Artículos procesados:   31839  de  106137
Artículos procesados:   42452  de  106137
Artículos procesados:   53065  de  106137
Artículos procesados:   63678  de  106137
Artículos procesados:   74291  de  106137
Artículos procesados:   84904  de  106137
Artículos procesados:   95517  de  106137
Artículos procesados:   106130  de  106137
```

[1]:
```
covid_df <- read.csv("D:/COVID/covid_df.csv", stringsAsFactors = FALSE, na.
 ↪strings = c("", "NA"))
```

[10]:
```
# Observamos la primera fila del nuevo Data Frame menos el cuerpo
as.list(covid_df[1, -5])
# Comprobamos el número de artículos existentes
nrow(covid_df)
```

$paper_id '0001418189999fea7f7cbe3e82703d71c85a6fe5'

$author_list 'E Cornelissen;H Dewerchin;E Hamme;H Nauwynck;'

$title_text 'Absence of surface expression of feline infectious peritonitis virus (FIPV) antigens on infected cells isolated from cats with FIP'

$abstract_text ' Feline infectious peritonitis virus (FIPV) positive cells are present in pyogranulomas and exudates from cats with FIP. These cells belong mainly to the monocyte/macrophage lineage. How these cells survive in immune cats is not known. In this study, FIPV positive cells were isolated from pyogranulomas and exudates of 12 naturally FIPV-infected cats and the presence of two immunologic targets, viral antigens and MHC I, on their surface was determined. The majority of the infected cells were confirmed to be cells from the monocyte/macrophage lineage. No surface expression of viral antigens was detected on FIPV positive cells. MHC I molecules were present on all the FIPV positive cells. After cultivation of the isolated infected cells, 52 AE 10% of the infected cells re-expressed viral antigens on the plasma membrane. In conclusion, it can be stated that in FIP cats, FIPV replicates in cells of the monocyte/macrophage lineage without carrying viral antigens in

their plasma membrane, which could allow them to escape from antibody-dependent cell lysis. #'

$journal 'Veterinary Microbiology'

$doi '10.1016/j.vetmic.2006.11.026'

95980

¡¡¡¡CONTADOR DE PALABRAS!!!! (/covid_df_feather_palabras) 1 minutos

[17]:
```
# Contamos el número de palabras para el abstracto ...
covid_df$words_abstract <- apply(covid_df['abstract_text'], 2, function(s)␣
 ↪str_count(s, '\\w+'))
# ... y el cuerpo del texto
covid_df$words_body <- apply(covid_df['body_text'], 2, function(s) str_count(s,␣
 ↪'\\w+'))
# Mostramos el número de palabras de los primeros textos
head(covid_df[,c('title_text', 'words_abstract', 'words_body')])
```

A tibble: 6 × 3

title_text <chr>
Absence of surface expression of feline infectious peritonitis virus (FIPV) antigens on infected cel
Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) by Mass Spectrom
Title: Rethinking high-risk groups in COVID-19
ScienceDirect ScienceDirect Effect of Nanomaterial Shape on Fabrication of Conformal Circuits
Plasma inflammatory cytokines and chemokines in severe acute respiratory syndrome
Journal Pre-proofs The Fire This Time: The Stress of Racism, Inflammation and COVID-19

¡¡¡¡DUPLICADOS!!! (covid_df_feather_duplicados) 5 segundos

[18]:
```
# Comprobamos cuantos objetos tienen el mismo cuerpo
duplicados <- duplicated(covid_df$body_text)
# Mostramos la información obtenida
summary(duplicados)
# Obtenemos los 5 primeros objetos detectados como duplicados
head(which(duplicados==TRUE))
```

```
   Mode   FALSE    TRUE
logical   94519    1461
```

1. 2176 2. 2590 3. 3334 4. 4426 5. 5000 6. 5018

[20]:
```
# Mostramos los seis primeros duplicados
covid_df[c(2176,2590,3334,4426,5000,5018),'title_text']
```

A tibble: 6 × 1

title_text <chr>
Remdesivir in Treatment of COVID-19: A Systematic Benefit-Risk Assessment
Autoantibodies in Patients with Rheumatoid Arthritis
Initial High Viral Load Is Associated with Prolonged Shedding of Human Rhinovirus in Allogene
Autoantibodies in Patients with Rheumatoid Arthritis
Extracellular superoxide dismutase, a molecular transducer of health benefits of exercise
COVID-19 pneumonia: different respiratory treatments for different phenotypes?

¡¡¡¡MOSTRAR DUPLICADOS!!!!

[21]:
```
length(which(covid_df$title_text=='Autoantibodies in Patients with Rheumatoid␣
 ↪Arthritis'))
length(which(covid_df$title_text=='Remdesivir in Treatment of COVID-19: A␣
 ↪Systematic Benefit-Risk Assessment'))
length(which(covid_df$title_text=='Initial High Viral Load Is Associated with␣
 ↪Prolonged Shedding of Human Rhinovirus in Allogeneic Hematopoietic Cell␣
 ↪Transplant Recipients'))
length(which(covid_df$title_text=='Extracellular superoxide dismutase, a␣
 ↪molecular transducer of health benefits of exercise'))
length(which(covid_df$title_text=='COVID-19 pneumonia: different respiratory␣
 ↪treatments for different phenotypes?'))
```

69

2

2

2

2

¡¡¡¡ELIMINAR DUPLICADOS!!!!

[22]:
```
# Eliminamos duplicados
covid_df <- covid_df[!duplicated(covid_df$body_text),]
nrow(covid_df)
```

94519

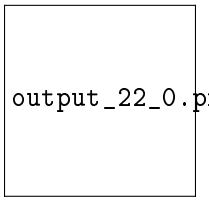
¡¡¡¡DETECCION LENGUAJE!!!! (covid_df_feather_idioma.csv)

[23]:
```
# Añadimos una nueva columna con el idioma de cada texto
covid_df$language <- apply(covid_df['body_text'], 2, function(s)␣
 ↪detect_language(substring(s, 1,  2000)))
# Información
summary(covid_df$language)
```

```
  body_text
en     :92213
de     :  842
```

```
es      :  658
fr      :  517
nl      :  130
(Other):   87
NA's    :   72
```

[24]:
```
# Creación de matriz con los datos
idiomas <- matrix(c(842, 92212, 658, 517, 130, 71, 88), ncol = 7, byrow = TRUE)
colnames(idiomas) <- (c('Alemán','Inglés', 'Español', 'Francés', 'Holandés',␣
 ↪'Otros', 'NA'))
# Generación de gráfico
barplot(idiomas, main = 'Distribución de idiomas', xlab = 'Idiomas', ylab =␣
 ↪'Número de artículos', col = '#69b3a2', axes = FALSE)
usr <- par("usr")
par(usr=c(usr[1:2], 0, 100000))
axis(2, at=seq(0, 100000,25000))
```



¡¡¡¡FILTRADO DE INGLES!!!! (covid_df_feather_ingles.csv)

[27]:
```
# Nos quedamos únicamente con textos en inglés
covid_df <- covid_df[which(covid_df$language=='en'),]
# Mostramos el número de artículos restantes
nrow(covid_df)
```

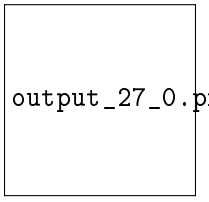
92213

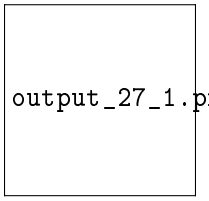
¡¡¡¡INFORMACION PALABRAS!!!!

[28]:
```
# Información sobre el número de palabras
summary(covid_df[,c('words_abstract','words_body')])
```

```
words_abstract.abstract_text words_body.body_text
Min.   :   1.000             Min.   :     1.00
1st Qu.:   1.000             1st Qu.:  1658.00
Median : 162.000             Median :  3119.00
Mean   : 174.521             Mean   :  4022.11
3rd Qu.: 249.000             3rd Qu.:  4834.00
Max.   :7922.000             Max.   :293299.00
```

[29]:
```
# Generación del grafo para el resumen con histograma y densidad
palabras_abstract <- ggplot(covid_df, aes(x=words_abstract)) +␣
 ↪geom_histogram(aes(y=..density..), alpha=.3, fill="cyan", bins=80) +␣
 ↪geom_density( colour="blue") + theme_classic() + ggtitle('Distribución del␣
 ↪número de palabras en el resumen') +  xlab('Número de palabras del resumen') +␣
 ↪ylab('Densidad')
# Misma operación para el cuerpo del texto
palabras_cuerpo <- ggplot(covid_df, aes(x=words_body)) + geom_histogram(aes(y=..
 ↪density..), alpha=.3, fill="cyan", bins=80) + geom_density( colour="blue") +␣
 ↪theme_classic() + scale_x_continuous(labels = comma) + ggtitle('Distribución␣
 ↪del número de palabras en el cuerpo')  +  xlab('Número de palabras del␣
 ↪cuerpo') + ylab('Densidad')
# Mostramos los gráficos
palabras_abstract
palabras_cuerpo
```





¡¡¡¡MAS INFORMACION PALABRAS!!!!

[34]:
```
# Cinco primeros artículos con menos de diez palabras en el abstracto
covid_df[head(which(covid_df$words_abstract < 10 & covid_df$abstract_text !=␣
 ↪'NoIncluido')), c('title_text', 'abstract_text', 'words_abstract')]
```

A tibble: 6 × 3

title_text <chr>
Loss of IKK subunits limits NF-<U+03BA>B signaling in reovirus infected cells 4 5
Title: Piloting Forensic Tele-Mental Health Evaluations of Asylum Seekers
NoIncluido
A Cluster-Randomized Trial of Hydroxychloroquine as Prevention of Covid-19 Transmission and
Early View Sleep apnoea management in Europe during the COVID-19 pandemic: data from the
Initial characterisation of ELISA assays and the immune response of the clinically correlated SAR

[36]:
```
# Y menos de diez palabras en el cuerpo
covid_df[head(which(covid_df$words_body < 10)), c('title_text', 'body_text','␣
↪'words_body')]
```

A tibble: 6 × 3

title_text <chr>
Severe SARS-CoV-2 infection in humans is defined by a shift in the serum lipidome resulting in d
Journal Pre-proof How to optimize the management of gestational trophoblastic disease during t
NoIncluido
Journal Pre-proof Are healthcare workers during the COVID-19 pandemic at risk of psychosis? F
Der Chirurg Journal Club
Journal Pre-proof THORACIC SURGERY FOR MALIGNANCY AND EMERGENCY IRRESPECT

¡¡¡¡ELIMINACION DE PALABRAS!!!!

[37]:
```
# Cargamos la lista del paquete stopwords
p_vacias <- stopwords::stopwords("en",source = "stopwords-iso")
# Añadimos más palabrasa
p_propias <- c('doi', 'preprint', 'copyright', 'org', 'https', 'et', 'al',␣
↪'author', 'figure', 'table',
   'rights', 'reserved', 'permission', 'use', 'used', 'using', 'biorxiv',␣
↪'medrxiv', 'license', 'fig', 'fig.', 'al.', 'Elsevier', 'PMC', 'CZI',
   '-PRON-', 'usually')
# Y las juntamos
p_vacias <- append(p_vacias, p_propias)
# Eliminamos cualquier posible duplicado
p_vacias <- unique(p_vacias)
# Vemos información al respecto
length(p_vacias)
sample(p_vacias, 10)
```

1317

1. 'trying' 2. 'grouping' 3. 'resulting' 4. 'ge' 5. 'following' 6. 'sy' 7. 'primarily' 8. 'kw' 9. 'one\'s' 10. 'arent'

[38]:
```
# Almacenamos el primer resumen para comparar
resumen <- covid_df$abstract_text[1]
# Conversión del resumen a minúsculas
covid_df$abstract_text <- apply(covid_df['abstract_text'], 2, function(s)␣
↪tolower(s))
# Eliminación de signos de puntuación
covid_df$abstract_text <- apply(covid_df['abstract_text'], 2, function(s)␣
↪removePunctuation(s, preserve_intra_word_contractions = TRUE,␣
↪preserve_intra_word_dashes = TRUE))
# Eliminación de palabras vacías
covid_df$abstract_text <- apply(covid_df['abstract_text'], 2, function(s)␣
↪remove_stopwords(s, p_vacias, lines = TRUE))
# Añadimos nueva columna con número de palabras actuales
```

```
covid_df$new_word_abstract <- apply(covid_df['abstract_text'], 2, function(s)␣
 ↪str_count(s, '\\w+'))
```

[ ]:
```
# Repetimos la operación con el cuerpo
# Conversión del cuerpo a minúsculas
covid_df$body_text <- apply(covid_df['body_text'], 2, function(s) tolower(s))
# Eliminación de signos de puntuación
covid_df$body_text <- apply(covid_df['body_text'], 2, function(s)␣
 ↪removePunctuation(s))
# Eliminación de palabras vacías
covid_df$body_text <- apply(covid_df['body_text'], 2, function(s)␣
 ↪remove_stopwords(s, p_vacias, lines = TRUE))
# Añadimos nueva columna con número de palabras actuales
covid_df$new_word_body <- apply(covid_df['body_text'], 2, function(s)␣
 ↪str_count(s, '\\w+'))
```

[41]:
```
# Comparamos el resumen original con el actual
substring(resumen, 1, 100)
substring(covid_df[1,'abstract_text'], 1, 100)
```

' Feline infectious peritonitis virus (FIPV) positive cells are present in pyogranulomas and exudates'

' feline infectious peritonitis virus fipv positive cells pyogranulomas exudates cats fip cell'

[43]:
```
#cargo covid_df_feather_stopwords.csv porque no he hecho lo anterior
covid_df <- read_feather("D:/COVID/covid_df_feather_stopwords.csv")
```

¡¡¡¡COMPARAMOS NUMERO DE PALABRAS!!!!

[45]:
```
# Creamos dos nuevas columnas con la resta de palabras originales y actuales
covid_df$abstract_comparative <- covid_df$words_abstract -␣
 ↪covid_df$new_word_abstract
covid_df$body_comparative <- covid_df$words_body - covid_df$new_word_body
# Mostramos un resumen de la información
summary(covid_df[c('new_word_abstract', 'new_word_body', 'abstract_comparative',␣
 ↪'body_comparative')])
# Calculamos el total de palabras iniciales
inicial_resumen <- sum(covid_df$words_abstract)
inicial_cuerpo <- sum(covid_df$words_body)
inicial <- inicial_resumen + inicial_cuerpo
# Calculamos el total de palabras finales
final_resumen <- sum(covid_df$new_word_abstract)
final_cuerpo <- sum(covid_df$new_word_body)
final <- final_resumen + final_cuerpo
# Calculamos las palabras eliminadas
quitadas_resumen <- sum(covid_df$abstract_comparative)
quitadas_cuerpo <- sum(covid_df$body_comparative)
```

```
quitadas <- quitadas_resumen + quitadas_cuerpo
# Mostramos los datos
datos <- matrix(c(inicial_resumen, inicial_cuerpo, inicial, final_resumen,␣
 ↪final_cuerpo, final, quitadas_resumen, quitadas_cuerpo, quitadas), nrow = 3,␣
 ↪dimnames = list(c("Resumen", "Cuerpo", "Total"), c("Inicial", "Final",␣
 ↪"Eliminadas")))
datos
```

```
 new_word_abstract new_word_body    abstract_comparative body_comparative
 Min.   :   0.00   Min.   :     1   Min.   :   0.00      Min.   :     0
 1st Qu.:   1.00   1st Qu.:   848   1st Qu.:   0.00      1st Qu.:   798
 Median :  88.00   Median :  1590   Median :  73.00      Median :  1504
 Mean   :  95.74   Mean   :  2085   Mean   :  79.24      Mean   :  1945
 3rd Qu.: 136.00   3rd Qu.:  2495   3rd Qu.: 111.00      3rd Qu.:  2343
 Max.   :4696.00   Max.   :162073   Max.   :5126.00      Max.   :131565
```

A matrix: 3 × 3 of type int

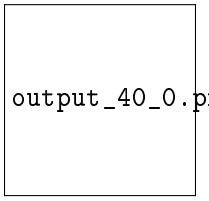
	Inicial	Final	Eliminadas
Resumen	16134914	8828313	7306601
Cuerpo	371628162	192247004	179381158
Total	387763076	201075317	186687759

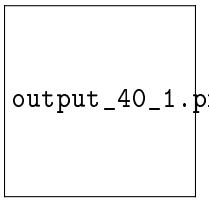
¡¡¡¡GRAFICOS PARA LAS PALABRAS!!!!

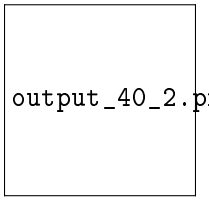
[46]:
```
# Generación del grafo para el resumen con histograma y densidad
nuevas_palabras_abstract <- ggplot(covid_df, aes(x=new_word_abstract)) +␣
 ↪geom_histogram(aes(y=..density..), alpha=.3, fill="cyan", bins=80) +␣
 ↪geom_density( colour="blue") + theme_classic() + ggtitle('Distribución del␣
 ↪número de palabras en el resumen') + xlab('Número actual de palabras del␣
 ↪resumen') + ylab('Densidad')
# Misma operación para el cuerpo del texto
nuevas_palabras_cuerpo <- ggplot(covid_df, aes(x=new_word_body)) +␣
 ↪geom_histogram(aes(y=..density..), alpha=.3, fill="cyan", bins=80) +␣
 ↪geom_density( colour="blue") + theme_classic() + scale_x_continuous(labels =␣
 ↪comma) + ggtitle('Distribución del número de palabras en el cuerpo') +␣
 ↪xlab('Número actual de palabras del cuerpo') + ylab('Densidad')
# Generamos grafo para ver cuantas palabras se han quitado
comparacion_abstract<-ggplot(covid_df, aes(x=abstract_comparative)) +␣
 ↪geom_histogram(aes(y=..density..), alpha=.3, fill="red", bins=80) +␣
 ↪geom_density( colour="red") + theme_classic() + ggtitle('Palabras eliminadas␣
 ↪del resumen') +  xlab('Número de palabras retiradas del resumen') +␣
 ↪ylab('Densidad') + geom_vline(aes(xintercept= mean(abstract_comparative)),␣
 ↪linetype="dashed")
# Misma operaciópn para el cuerpo del texto
```

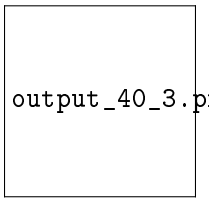
```
comparacion_cuerpo <- ggplot(covid_df, aes(x=body_comparative)) +␣
 ↪geom_histogram(aes(y=..density..), alpha=.3, fill="red", bins=80) +␣
 ↪geom_density( colour="red") + theme_classic() + scale_x_continuous(labels =␣
 ↪comma) + ggtitle('Palabras eliminadas del resumen') + xlab('Número de palabras␣
 ↪retiradas del cuerpo') + ylab('Densidad') + geom_vline(aes(xintercept=␣
 ↪mean(body_comparative)), linetype="dashed")

# Mostramos los gráficos
nuevas_palabras_abstract
nuevas_palabras_cuerpo
comparacion_abstract
comparacion_cuerpo
```









¡¡¡¡TOKENIZACION!!!!

[54]:
```
# Tokenizamos tanto abstracto como texto completo
covid_df['abstract_text'] <- apply(covid_df['abstract_text'], 2, function(s)␣
 ↪word_tokenizer(s, xptr = TRUE, pos_keep = character('-')))
covid_df['body_text'] <- apply(covid_df['body_text'], 2, function(s)␣
 ↪word_tokenizer (s, xptr = TRUE))

# Mostramos los primeros cinco términos de los resúmenes y el cuerpo
covid_df$abstract_text[[1]][1:10]
covid_df$body_text[[1]][1:10]
```

1. 'feline' 2. 'infectious' 3. 'peritonitis' 4. 'virus' 5. 'fipv' 6. 'positive' 7. 'cells' 8. 'pyogranulomas' 9. 'exudates' 10. 'cats'

1. 'feline' 2. 'infectious' 3. 'peritonitis' 4. 'fip' 5. 'fatal' 6. 'chronic' 7. 'disease' 8. 'cats' 9. 'caused' 10. 'coronavirus'

¡¡¡¡LEMATIZACION!!!!

[50]:
```
# Haciendo "apply <- lapply" conseguimos una paralelización del trabajo gracias␣
 ↪a la lista que genera la tokenización de los textos
system.time(covid_df['abstract_text'] <- apply(covid_df['abstract_text'], 2,␣
 ↪function(s) lapply(s, function(t) lemmatize_words(t))))
system.time(covid_df['body_text'] <- apply(covid_df['body_text'], 2, function(s)␣
 ↪lapply(s, function(t) lemmatize_words(t))))
```

!!MOSTRAR LEMATIZACION!!

[52]:
```
# Mostramos los primeros cinco términos de los resúmenes y el cuerpo
covid_df$abstract_text[[1]][1:10]
covid_df$body_text[[1]][1:10]
```

1. 'feline' 2. 'infectious' 3. 'peritonitis' 4. 'virus' 5. 'fipv' 6. 'positive' 7. 'cell' 8. 'pyogranulomas' 9. 'exudate' 10. 'cat'

1. 'feline' 2. 'infectious' 3. 'peritonitis' 4. 'fip' 5. 'fatal' 6. 'chronic' 7. 'disease' 8. 'cat' 9. 'cause' 10. 'coronavirus'

[55]:
```
covid_df$abstract_text <- list.load("D:/COVID/lemas_abs.RData")
covid_df$body_text <- list.load("D:/COVID/lemas_body.RData")
```

[ ]:
```

```