web_scrapping_EMA

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1 Data Scrapping form the European Medicines Agency (EMA)

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1.2 0. Load required dependencies

[3]:
```
# libraries
library(RSelenium)
library(stringr)

# self-made package
source("EMA_webScrapping.R")
```

1.3 1. Set parameters

[ ]:
```
# start automated navigator
initRSelenium()

# Navigate to a list of all drugs
url = "https://www.ema.europa.eu/medicines/
 ↪field_ema_web_categories%253Aname_field/Human/ema_group_types/ema_medicine"
remDr$navigate(url)

# Define pages to look through
page <- "https://www.ema.europa.eu/en/medicines/
 ↪field_ema_web_categories%253Aname_field/Human/ema_group_types/ema_medicine?
 ↪page=" #link to navigate through each page of the list.
n <- as.character(round(1495/25)-1) #no. of pages to navigate, as.character()␣
 ↪to allow pasting with the 'page' string.
```

1.4 2. Download information from each drug

[ ]:
```
# Obtain each drug's link
drug_links = getURLs(page,n)

# Use drug links to retrieve information from EMA's webpage for each drug
# (Slow)
drugsDB = getDrugInfo(drug_links)
```

1.5 3. Save information in spreadsheet

[ ]:
```
# reshape dataframe and fill when features available
drug_df = processTable(drugsDB)

# save
file_name = "drug_df_EMA.csv"
#saveTable(drug_df,file_name)
```

1.6 4. Exploratory Data Analysis

[87]:
```
# load
drug_df = read.table('drug_df_EMA.csv',sep=',',header=T,stringsAsFactors = F)
```

[24]:
```
# Number of registered drugs
paste('Total EMA registered drugs:',nrow(drug_df))

# Fields names
"Table fields:"
print(colnames(drug_df))
```

'Total EMA registered drugs: 1272'

'Table fields:'

```
 [1] "Name"
 [2] "Agency.product.number"
 [3] "Active.substance"
 [4] "International.non.proprietary.name..INN..or.common.name"
 [5] "Therapeutic.area..MeSH."
 [6] "Anatomical.therapeutic.chemical..ATC..code"
 [7] "Generic"
 [8] "Marketing.authorisation.holder"
 [9] "Revision"
[10]
"Date.of.issue.of.marketing.authorisation.valid.throughout.the.European.Union"
```

```
[11] "Contact.address"
[12] "Additional.monitoring"
[13] "Orphan"
[14] "Conditional.approval"
[15] "Biosimilar"
[16] "Marketing.autorisation.applicant"
[17] "Date.of.opinion"
[18] "Exceptional.circumstances"
[19] "Date.of.refusal.of.marketing.authorisation"
[20] "Countries"
```

1.6.1 4.1. What are the most common therapeutic areas?

[53]:
```r
# list drugs and their therapeutic area MeSH

# split mesh terms
list_mesh <- lapply(drug_df$Therapeutic.area..MeSH.,split="\n",strsplit)

# add drug names
attributes(list_mesh)$names <- drug_df$Name

# compute total diversity
paste('Diversity in therapeutic areas:',length(unique(list_mesh)))

# compute frequency table of MeSH terms
tab_mesh = table(unlist(list_mesh))
tab_mesh = tab_mesh/length(tab_mesh)

'Top 10:'
sort(tab_mesh,decreasing = T)[1:10]

'Last 10:'
sort(tab_mesh,decreasing = F)[1:10]
```

'Diversity in therapeutic areas: 509'

'Top 10:'

```
     Diabetes Mellitus, Type 2                 HIV Infections
                    0.15839243                     0.14420804
                  Immunization                   Hypertension
                    0.12056738                     0.10401891
              Breast Neoplasms          Myocardial Infarction
                    0.09929078                     0.09456265
Carcinoma, Non-Small-Cell Lung          Arthritis, Rheumatoid
                    0.09219858                     0.08510638
                        Cancer              Diabetes Mellitus
                    0.08274232                     0.06855792
```

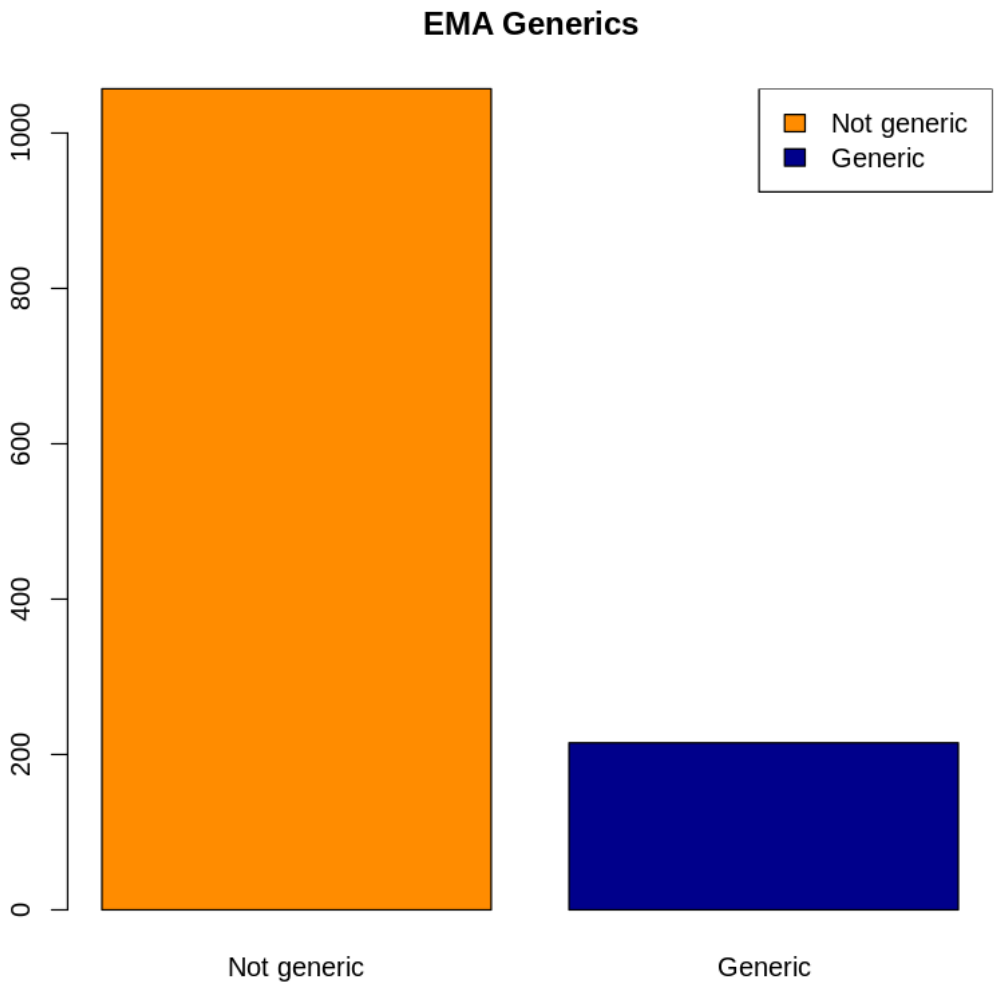
'Last 10:'

```
                Acromegaly                    Adenoma
                0.002364066                0.002364066
Adenomatous Polyposis Coli    Adrenal Cortex Neoplasms
                0.002364066                0.002364066
     Adrenal Insufficiency   Alcohol-Related Disorders
                0.002364066                0.002364066
        alpha-Mannosidosis       Amyloidosis, Familial
                0.002364066                0.002364066
   Anemia, Iron-Deficiency         Anemia, Sickle Cell
                0.002364066                0.002364066
```

1.6.2 4.2. How many drugs are generics?

[79]:
```
# list drugs and whether they are generic or not
list_gene = drug_df['Generic']!=''
names(list_gene) = drug_df['Name']

# visualize
barplot(table(list_gene), main = 'EMA␣
↪Generics',col=c('darkorange','darkblue'),names.arg = c('Not␣
↪generic','Generic'))
legend('topright',legend = c('Not generic','Generic'),fill =␣
↪c('darkorange','darkblue'))
```



drug_df$Marketing.authorisation.holder

drug_df$Revision

drug_df$Contact.address

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drug_df$Countries

drug_df$Exceptional.circumstances

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