Tarea: importación de datos en R

Análisis Exploratorio de Datos, Máster en Ciencia de Datos- UV

Daniel Lillo Plaza

2023-07-09

Índice

1	Introducción.		1

2 Apartado. Instalación de paquetes

1

1 Introducción.

El objetivo de esta tarea es realizar la importación de cinco archivos diferentes, cada uno de ellos en un formato distinto.

2 Apartado. Instalación de paquetes

Incluimos todas las librerías necesarias para la ejecucion del código en la siguiente lista. packages = c("tidyverse", "knitr", "readxl", "haven", "BiocManager", "BiocManager::install("rhdf5")")

Si la librería no está instalada se instalará y cargará, si no solo se cargará.

```
# Especificamos las librerías necesarias en esta lista

packages = c("tidyverse", "knitr", "readxl", "haven", "BiocManager")

#use this function to check if each package is on the local machine
#if a package is installed, it will be loaded
#if any are not, the missing package(s) will be installed and loaded
package.check <- lapply(packages, FUN = function(x) {
   if (!require(x, character.only = TRUE)) {
     install.packages(x, dependencies = TRUE)
     library(x, character.only = TRUE)
   }
})

if (!require("rhdf5", character.only = TRUE)) {
   BiocManager::install("rhdf5")
   library("rhdf5", character.only = TRUE)</pre>
```

```
}
#verify they are loaded
search()
 [1] ".GlobalEnv"
                            "package:rhdf5"
                                                   "package:BiocManager"
                                                                          "package:haven"
 [5] "package:readxl"
                            "package:forcats"
                                                   "package:stringr"
                                                                          "package:dplyr"
 [9] "package:purrr"
                            "package:readr"
                                                   "package:tidyr"
                                                                          "package:tibble"
[13] "package:ggplot2"
                            "package:tidyverse"
                                                   "package:knitr"
                                                                          "package:stats"
[17] "package:graphics"
                            "package:grDevices"
                                                   "package:utils"
                                                                          "package:datasets"
[21] "package:methods"
                            "Autoloads"
                                                   "package:base"
BreadBasket<-read.csv("./data/BreadBasket_DMS.csv")</pre>
save(BreadBasket, file="./data/BreadBasket.RData")
Deposito <- read.delim("./data/DFP1_11122015 124700.csv")</pre>
save(Deposito, file="./data/Deposito.RData")
ERCA - readxl::read_excel("./data/ERCA NUEVA2 20161103.xls",
    sheet = "Hoja1 - Tabla 1", col_types = c("numeric",
        "numeric", "date", "text", "date",
        "date", "numeric", "numeric", "text",
        "date", "text", "text", "text", "text",
        "text", "text", "text", "text", "text",
        "text", "numeric", "numeric", "numeric",
        "numeric", "text", "text", "text",
        "text", "text", "text", "text",
        "text", "numeric", "numeric", "skip",
        "numeric", "numeric", "numeric",
        "numeric", "numeric", "numeric",
        "numeric", "numeric", "text", "numeric", "numeric", "numeric", "text", "numeric",
        "numeric", "numeric", "numeric", "numeric",
        "numeric", "numeric", "numeric"))
save(ERCA, file="./data/ERCA.RData")
Pacientes1<- read_excel("data/subjectInfo.xlsx",
     sheet = "measurments")
Pacientes2<- read_excel("data/subjectInfo.xlsx",
     sheet = "neuropathy")
Pacientes3<- read excel("data/subjectInfo.xlsx",
     sheet = "tuning fork NSS")
Pacientes4<- read_excel("data/subjectInfo.xlsx",
     sheet = "mobility")
Pacientes5<- read_excel("data/subjectInfo.xlsx",
     sheet = "Durometer")
Pacientes<-list(Pacientes1, Pacientes2, Pacientes3, Pacientes4, Pacientes5)
save(Pacientes, file="./data/Pacientes.RData")
microRNA_Neumo <- read_sav("data/microRNAsNeumonia.sav")</pre>
save(microRNA_Neumo, file="./data/microRNA_Neumo.RData")
b<-h5dump("./data/Tensiones1.hdf5")
```

```
Tensiones<-data.frame(b["input"])
colnames(Tensiones)<-b$VarNameSelec
save(Tensiones, file="./data/Tensiones.RData")</pre>
```