Lesson 9: Read and write files in R

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Contents

Wellcome & Disclaimer

This site contains the materials for the *Coding tools for Biochemistry & Molecular Biology* (Herramientas de Programación para Bioquímica y Biología Molecular) course of fall 2022 in the Bachelor's Degree in Biochemistry @UAM. This materials are the basis for GitHub-pages-based website that can be accessed here. Detailed academic information about the course contents, dates and assessment only can be found at the UAM Moodle site.

Data input & output in R

As you already know, launching R starts an interactive session with input from the keyboard and output to the screen. If you are using small datasets, you can directly define and introduce your data in the Console, as you did in the examples before. Additionally, you can define your objects and introduce your data interactively with the functions `scan()`and `readline()` as in the following examples. Regarding the output, you can just call the object by its name or use the function `print()`, which displays on the screen the contents of its argument object.

```
vector <- scan(n = 4)
vector2 <- scan()
str <- readline()
vector
```

```
## [1]  4  5 67  3
```

```
print(vector2)
```

```
## [1]  4 57  8
```

```
print(str)
```

```
## [1] "hola clase"
```

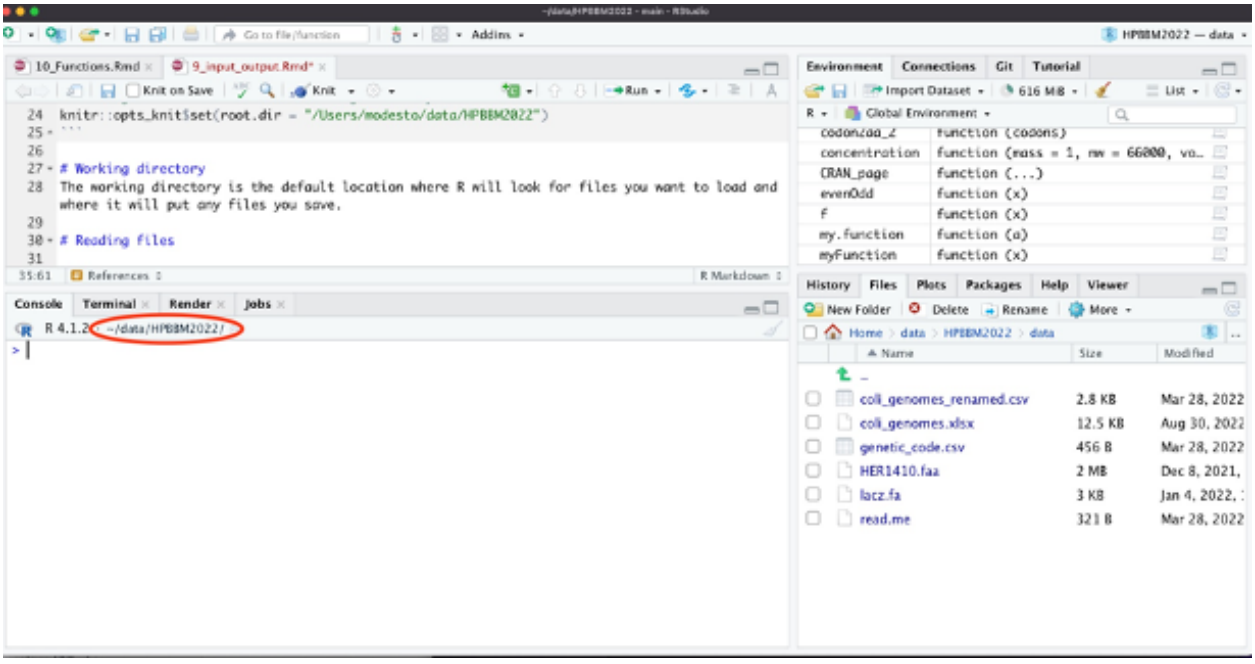
```
edit(str)
```

```
## [1] "Hola clase"
```

Although, seldom used, you can also edit the contents of your objects using the function `edit()`. This function can be used to edit different objects, including vectors, strings, matrices or dataframes. MacOS users need to install XQuartz X11 tool.

Working directory

More often, you can process commands from a script file (a file containing R statements) and also import data from text files, databases (MySQL) or other proprietary formats, such as Excel or GraphPad Prism. We will focus on text files by the moment, as importing files in specific formats requires dedicated external packages. By default, R will read/write in the *working directory (wd)*, which is indicated in your Console panel.



Note that the abbreviation '~' stands for your home directory (for me `/Users/modesto` or `/home/modesto` on MacOS or Linux, respectively).

The functions `getwd()` and `setwd()` allow you to check and change the *wd*. As this is a Markdown document, that `setwd()` within an R chunk only changes the working directory **for that particular chunk**. Remember

that you can write `?getwd()` or `?setwd()` for help.

```
getwd()
```

```
## [1] "/Users/modesto/data/HPBBM2022"
```

```
setwd("/Users/modesto")
getwd()
```

```
## [1] "/Users/modesto"
```

```
setwd("/Users/modsto/data/HPBBM2022")
```

```
## Error in setwd("/Users/modsto/data/HPBBM2022"): no es posible cambiar el directorio de trabajo
```

```
setwd("/Users/modesto/data/HPBBM2022")
getwd()
```

```
## [1] "/Users/modesto/data/HPBBM2022"
```

In RStudio, the *default working directory* can be set from the "tools" and "global options" menu. Also, you can change the *wd* for your session in the menu **Session > Set Working Directory** and change it to that of source file (for instant your R script), the project or the selected directory in the files panel.

Reading/writing data in R

The most common way to read your data in R is importing it as a table, using the function `read.table()`. Note that the resultant object will become a *Dataframe*, even when all the entries got to be numeric. A followup call towards `as.matrix()` will turn it into in a matrix.

In the following example we read a file called *small_matrix.csv*, located in the folder data. If we attempt to make some matrix calculations, R will force the dataframe to a matrix when possible, but it will return an Error for many matrix-specific operations or functions unless, we transform the dataframe into a matrix.

```
sm <- read.table("data/small_matrix.csv", sep = ",")
sm
```

```
##   V1 V2 V3
## 1  2  7 19
## 2 22 10 80
## 3 18  3 13
## 4 25  6 16
```

```
is.matrix(sm)
```

```
## [1] FALSE
```

```
t(sm)
```

```
##    [,1] [,2] [,3] [,4]
## V1    2   22   18   25
## V2    7   10    3    6
## V3   19   80   13   16
```

```
sm * 3
```

```
##   V1 V2  V3
## 1  6 21  57
## 2 66 30 240
## 3 54  9  39
## 4 75 18  48
```

```
diag(sm)
```

```
## Error in diag(sm): 'list' object cannot be coerced to type 'double'
```

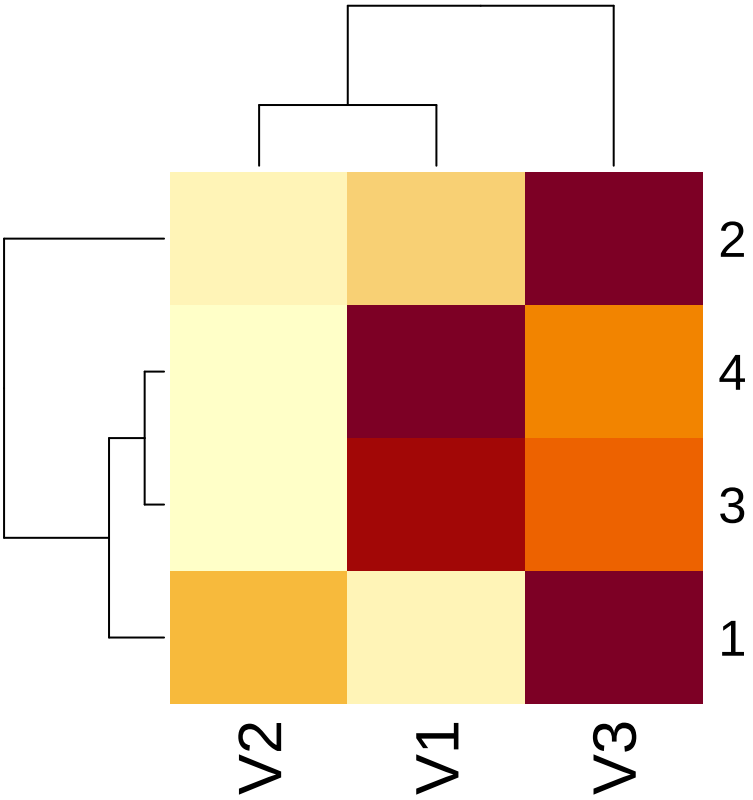
```
diag(as.matrix(sm))
```

```
## [1]  2 10 13
```

```
heatmap(sm)
```

```
## Error in heatmap(sm): 'x' must be a numeric matrix
```

```
heatmap(as.matrix(sm))
```



You can write any data object(s) as binary data file or as text files.

```
write(vector2, file = "data/vector2.txt")
write.table(sm, "data/sm.csv")
write.table(sm, "data/sm2.csv", row.names = FALSE, col.names = FALSE,
    sep = ";")

save(vector, vector2, file = "data/vector2.Rdata")
save.image(file = "data/myEnvironment.RData")
```

Data files in RData format can be open from the *Environment* tab or with the `load()` function

```
sm_bis <- load("data/vector2.Rdata")
sm_bis
```

```
## [1] "vector"  "vector2"
```

Basic Data Management in R

Now we are going to import and explore an example dataset, containing metadata from an Illumina sequencing project of pathogenic *E. coli* strains (Flament-Simon et al. 2020, https://doi.org/10.1038/s41598-020-69356-6). However, for didactic purposes, the original data have been simplified and manipulated and the attached datasets do not fully correspond to the actual data.

Explore a dataframe

As you can see in the R help, the function `read.table()` has several default options as FALSE, like `header=FALSE`. When you have a spreadsheet export file, i.e. having a table where the fields are divided by commas in place of spaces, you can use `read.csv()` in place of read.table(). For Spaniards, there is also `read.csv2()`, which uses a comma for the decimal point and a semicolon for the separator. The latter functions are wrappers of `read.table()` with custom default options.

```
# Note differences between read.table(), read.csv() and
# read.csv2()
coli_genomes <- read.table(file = "data/coli_genomes.csv")
```

```
## Error in scan(file = file, what = what, sep = sep, quote = quote, dec = dec, : line 2 did not have 1
```

```
head(coli_genomes)
```

```
##    Strain    Biosample Year  Source Phylogroup Serotype Clonotype Sequence.Type VF Plasmids kmer
## 1 LREC237 SAMN14278613   NA   Human          D  ONT:H28  CH23-331         ST524 18        3  117
## 2 LREC239 SAMN14278614 2010   Human          C O153:H19    CH4-25          ST88 14        3  117
## 3 LREC240 SAMN14278615 2008   Human         B1  O76:H30   CH29-38         ST156 10        2   89
## 4 LREC241 SAMN14278616   NA   Human          A  O78:H11   CH11-41          ST48  5        3  117
## 5 LREC242 SAMN14278617 2011 Porcine          A  ONT:HNM    CH7-54         ST746  5        9   89
## 6 LREC243 SAMN14278618 2007 Porcine          A   O9:H37    CH7-31        ST3011  7        3   93
##   Contigs    N50 longest.contig..bp. Assembly_length contigs1kb average_contig
## 1     223 272287              662555         5341632         74       23953.51
## 2     159 323172              760527         5415613         57       34060.46
## 3     114 270767              738861         4875343         47       42766.17
## 4     212 112160              285056         5167401        101       24374.53
## 5     320  45936              128053         4858138        212       15181.68
## 6     158 106897              369508         4638334         93       29356.54
```

```
coli_genomes <- read.table(file = "data/coli_genomes.csv", sep = ";",
    dec = ".", header = TRUE)
head(coli_genomes)
```

```
##    Strain    Biosample Year.of.isolation   Source Phylogroup Serotype Clonotype Sequence.Type VF
## 1 LREC237 SAMN14278613               NA   Human          D  ONT:H28  CH23-331         ST524 18
## 2 LREC239 SAMN14278614             2010   Human          C O153:H19    CH4-25          ST88 14
## 3 LREC240 SAMN14278615             2008   Human         B1  O76:H30   CH29-38         ST156 10
## 4 LREC241 SAMN14278616               NA    Human          A  O78:H11   CH11-41          ST48  5
## 5 LREC242 SAMN14278617             2011 Porcine          A  ONT:HNM    CH7-54         ST746  5
## 6 LREC243 SAMN14278618             2007 Porcine          A   O9:H37    CH7-31        ST3011  7
##   No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 1            3  117     223 272287              662555            5341632            74
## 2            3  117     159 323172              760527            5415613            57
## 3            2   89     114 270767              738861            4875343            47
## 4            3  117     212 112160              285056            5167401           101
## 5            9   89     320  45936              128053            4858138           212
## 6            3   93     158 106897              369508            4638334            93
```

```
coli_genomes <- read.csv(file = "data/coli_genomes.csv")
head(coli_genomes)
```

```
##   Strain.Biosample.Year.of.isolation.Source.Phylogroup.Serotype.Clonotype.Sequence.Type.VF.No..Plasmi
## 1                                                                                    LREC237;SAMN14278613
## 2                                                                                    LREC239;SAMN14278614
## 3                                                                                   LREC240;SAMN14278615;1
## 4                                                                                       LREC241;SAMN14278
## 5                                                                                    LREC242;SAMN14278617
## 6                                                                                    LREC243;SAMN14278618
```

```
coli_genomes <- read.csv(file = "data/coli_genomes.csv", sep = ";")
head(coli_genomes)
```

```
##    Strain    Biosample Year.of.isolation   Source Phylogroup Serotype Clonotype Sequence.Type VF
## 1 LREC237 SAMN14278613               NA    Human           D  ONT:H28  CH23-331         ST524 18
## 2 LREC239 SAMN14278614             2010    Human           C O153:H19    CH4-25          ST88 14
## 3 LREC240 SAMN14278615             2008    Human          B1  O76:H30   CH29-38         ST156 10
## 4 LREC241 SAMN14278616               NA     Human           A  O78:H11   CH11-41          ST48  5
## 5 LREC242 SAMN14278617             2011 Porcine           A  ONT:HNM    CH7-54         ST746  5
## 6 LREC243 SAMN14278618             2007 Porcine           A   O9:H37    CH7-31        ST3011  7
##   No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 1            3  117     223 272287              662555            5341632            74
## 2            3  117     159 323172              760527            5415613            57
## 3            2   89     114 270767              738861            4875343            47
## 4            3  117     212 112160              285056            5167401           101
## 5            9   89     320  45936              128053            4858138           212
## 6            3   93     158 106897              369508            4638334            93
```

```
coli_genomes <- read.csv2(file = "data/coli_genomes.csv")
head(coli_genomes)
```

```
##    Strain    Biosample Year.of.isolation   Source Phylogroup Serotype Clonotype Sequence.Type VF
## 1 LREC237 SAMN14278613               NA    Human           D  ONT:H28  CH23-331         ST524 18
## 2 LREC239 SAMN14278614             2010    Human           C O153:H19    CH4-25          ST88 14
## 3 LREC240 SAMN14278615             2008    Human          B1  O76:H30   CH29-38         ST156 10
## 4 LREC241 SAMN14278616               NA     Human           A  O78:H11   CH11-41          ST48  5
## 5 LREC242 SAMN14278617             2011 Porcine           A  ONT:HNM    CH7-54         ST746  5
## 6 LREC243 SAMN14278618             2007 Porcine           A   O9:H37    CH7-31        ST3011  7
##   No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 1            3  117     223 272287              662555            5341632            74
## 2            3  117     159 323172              760527            5415613            57
## 3            2   89     114 270767              738861            4875343            47
## 4            3  117     212 112160              285056            5167401           101
## 5            9   89     320  45936              128053            4858138           212
## 6            3   93     158 106897              369508            4638334            93
```

```
# read some data
head(coli_genomes)
```

```
##    Strain    Biosample Year.of.isolation   Source Phylogroup Serotype Clonotype Sequence.Type VF
## 1 LREC237 SAMN14278613               NA    Human           D  ONT:H28  CH23-331         ST524 18
## 2 LREC239 SAMN14278614             2010    Human           C O153:H19    CH4-25          ST88 14
## 3 LREC240 SAMN14278615             2008    Human          B1  O76:H30   CH29-38         ST156 10
## 4 LREC241 SAMN14278616               NA     Human           A  O78:H11   CH11-41          ST48  5
## 5 LREC242 SAMN14278617             2011 Porcine           A  ONT:HNM    CH7-54         ST746  5
```

```
## 6 LREC243 SAMN14278618              2007 Porcine           A   O9:H37    CH7-31        ST3011  7
##   No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 1            3  117     223 272287              662555            5341632            74
## 2            3  117     159 323172              760527            5415613            57
## 3            2   89     114 270767              738861            4875343            47
## 4            3  117     212 112160              285056            5167401           101
## 5            9   89     320  45936              128053            4858138           212
## 6            3   93     158 106897              369508            4638334            93
```

```
tail(coli_genomes, n = 2)
```

```
##     Strain    Biosample Year.of.isolation Source Phylogroup Serotype Clonotype Sequence.Type VF
## 24 LREC261 SAMN14278636              2016 Human           A  O98:H26   CH27-23        ST8233  2
## 25 LREC262 SAMN14278637              2012 Human          B1  O66:H10    CH4-32        ST1049  4
##    No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 24            4   89     114 187945              537848            4821342            53
## 25            2  113      94 325747              822206            4839344            32
```

```
coli_genomes[1, ]
```

```
##    Strain    Biosample Year.of.isolation Source Phylogroup Serotype Clonotype Sequence.Type VF
## 1 LREC237 SAMN14278613               NA Human           D  ONT:H28  CH23-331         ST524 18
##   No..Plasmids kmer Contigs    N50 longest.contig..bp. total.assembled.bp contigs...1kb
## 1            3  117     223 272287              662555            5341632            74
```

```
coli_genomes[, 1]
```

```
##  [1] "LREC237" "LREC239" "LREC240" "LREC241" "LREC242" "LREC243" "LREC244" "LREC245" "LREC246"
## [10] "LREC247" "LREC248" "LREC249" "LREC250" "LREC251" "LREC252" "LREC253" "LREC254" "LREC255"
## [19] "LREC256" "LREC257" "LREC258" "LREC259" "LREC260" "LREC261" "LREC262"
```

```
coli_genomes[1:6, 2:4]
```

```
##      Biosample Year.of.isolation   Source
## 1 SAMN14278613               NA   Human
## 2 SAMN14278614             2010   Human
## 3 SAMN14278615             2008   Human
## 4 SAMN14278616               NA    Human
## 5 SAMN14278617             2011 Porcine
## 6 SAMN14278618             2007 Porcine
```

```
# explore the dataframe structure
dim(coli_genomes)
```

```
## [1] 25 16
```

```
length(coli_genomes)
```

```
## [1] 16
```

```
ncol(coli_genomes)
```

```
## [1] 16
```

```
nrow(coli_genomes)
```

```
## [1] 25
```

```
# dataframe estructure in one line
str(coli_genomes)
```

```
## 'data.frame':    25 obs. of  16 variables:
##  $ Strain             : chr  "LREC237" "LREC239" "LREC240" "LREC241" ...
##  $ Biosample          : chr  "SAMN14278613" "SAMN14278614" "SAMN14278615" "SAMN14278616" ...
##  $ Year.of.isolation  : int  NA 2010 2008 NA 2011 2007 2006 2006 2010 2013 ...
##  $ Source             : chr  "Human " "Human " "Human " "Human" ...
##  $ Phylogroup         : chr  "D" "C" "B1" "A" ...
##  $ Serotype           : chr  "ONT:H28" "O153:H19" "O76:H30" "O78:H11" ...
##  $ Clonotype          : chr  "CH23-331" "CH4-25" "CH29-38" "CH11-41" ...
##  $ Sequence.Type      : chr  "ST524" "ST88" "ST156" "ST48" ...
##  $ VF                 : int  18 14 10 5 5 7 4 2 10 22 ...
##  $ No..Plasmids       : int  3 3 2 3 9 3 7 7 1 4 ...
##  $ kmer               : int  117 117 89 117 89 93 115 115 113 113 ...
##  $ Contigs            : int  223 159 114 212 320 158 277 203 131 215 ...
##  $ N50                : int  272287 323172 270767 112160 45936 106897 89185 94368 326769 248158 ...
##  $ longest.contig..bp.: int  662555 760527 738861 285056 128053 369508 281444 280268 451887 504233 .
##  $ total.assembled.bp : int  5341632 5415613 4875343 5167401 4858138 4638334 5406295 4796593 5173794
##  $ contigs...1kb      : int  74 57 47 101 212 93 155 114 56 76 ...
```

```
# type of data in each variable
typeof(coli_genomes$Strain)
```

```
## [1] "character"
```

```
typeof(coli_genomes[, 2])
```

```
## [1] "character"
```

```
typeof(coli_genomes[, 9])
```

```
## [1] "integer"
```

```
# col and row names
names(coli_genomes)
```

```
##  [1] "Strain"              "Biosample"           "Year.of.isolation"   "Source"
##  [5] "Phylogroup"          "Serotype"            "Clonotype"           "Sequence.Type"
##  [9] "VF"                  "No..Plasmids"        "kmer"                "Contigs"
## [13] "N50"                 "longest.contig..bp." "total.assembled.bp"  "contigs...1kb"
```

```
colnames(coli_genomes)
```

```
##  [1] "Strain"              "Biosample"           "Year.of.isolation"   "Source"
##  [5] "Phylogroup"          "Serotype"            "Clonotype"           "Sequence.Type"
##  [9] "VF"                  "No..Plasmids"        "kmer"                "Contigs"
## [13] "N50"                 "longest.contig..bp." "total.assembled.bp"  "contigs...1kb"
```

```
rownames(coli_genomes)
```

```
##  [1] "1"  "2"  "3"  "4"  "5"  "6"  "7"  "8"  "9"  "10" "11" "12" "13" "14" "15" "16" "17" "18" "19"
## [20] "20" "21" "22" "23" "24" "25"
```

```
names(coli_genomes[3]) <- "Year"
names(coli_genomes)[3] <- "Year"
colnames(coli_genomes[3]) <- "Year"
```

Some of the columns include 'chr' data that may be actually a categorical variable, so we can code them as **factor**. Using the expression *as.factor()* you can check whether the data would correspond to a text or a categorical variable.

```
coli_genomes$Source <- as.factor(coli_genomes$Source)
coli_genomes$Phylogroup <- as.factor(coli_genomes$Phylogroup)

str(coli_genomes)  #dataframe estructure updated
```

```
## 'data.frame':    25 obs. of  16 variables:
##  $ Strain             : chr  "LREC237" "LREC239" "LREC240" "LREC241" ...
##  $ Biosample          : chr  "SAMN14278613" "SAMN14278614" "SAMN14278615" "SAMN14278616" ...
##  $ Year               : int  NA 2010 2008 NA 2011 2007 2006 2006 2010 2013 ...
##  $ Source             : Factor w/ 4 levels "Avian ","Human",..: 3 3 3 2 4 4 4 4 4 3 ...
##  $ Phylogroup         : Factor w/ 4 levels "A","B1","C","D": 4 3 2 1 1 1 1 1 3 4 ...
##  $ Serotype           : chr  "ONT:H28" "O153:H19" "O76:H30" "O78:H11" ...
##  $ Clonotype          : chr  "CH23-331" "CH4-25" "CH29-38" "CH11-41" ...
##  $ Sequence.Type      : chr  "ST524" "ST88" "ST156" "ST48" ...
##  $ VF                 : int  18 14 10 5 5 7 4 2 10 22 ...
##  $ No..Plasmids       : int  3 3 2 3 9 3 7 7 1 4 ...
##  $ kmer               : int  117 117 89 117 89 93 115 115 113 113 ...
##  $ Contigs            : int  223 159 114 212 320 158 277 203 131 215 ...
##  $ N50                : int  272287 323172 270767 112160 45936 106897 89185 94368 326769 248158 ...
##  $ longest.contig..bp.: int  662555 760527 738861 285056 128053 369508 281444 280268 451887 504233 .
##  $ total.assembled.bp : int  5341632 5415613 4875343 5167401 4858138 4638334 5406295 4796593 5173794
##  $ contigs...1kb      : int  74 57 47 101 212 93 155 114 56 76 ...
```

How many levels are there in *Source*?? It is not uncommon to see some mistake in our data, usually made when the data were recorded, for example a space may have been inserted before a data value. By default this white space will be kept in the R environment, such that 'Human' will be recognized as a different value than 'Human'. In order to avoid this type of error, we can use the *strip.white* argument.

```
unique(coli_genomes$Source)
```

```
## [1] Human    Human    Porcine  Avian
## Levels: Avian  Human Human  Porcine
```

```
table(coli_genomes$Source)
```

```
##
##   Avian     Human   Human  Porcine
##       3         1        16        5
```

```
coli_genomes <- read.csv2(file = "data/coli_genomes.csv", strip.white = TRUE)
coli_genomes$Source <- as.factor(coli_genomes$Source)
coli_genomes$Phylogroup <- as.factor(coli_genomes$Phylogroup)

unique(coli_genomes$Source)
```

```
## [1] Human   Porcine Avian
## Levels: Avian Human Porcine
```

We can also rename some variables to use more easy names.

```
names(coli_genomes)  #see all variable names
```

```
##  [1] "Strain"             "Biosample"          "Year.of.isolation"   "Source"
##  [5] "Phylogroup"         "Serotype"           "Clonotype"           "Sequence.Type"
##  [9] "VF"                 "No..Plasmids"       "kmer"                "Contigs"
## [13] "N50"                "longest.contig..bp." "total.assembled.bp"  "contigs...1kb"
```

```
# rename variables
names(coli_genomes)[3] <- "Year"
names(coli_genomes)[10] <- "Plasmids"
names(coli_genomes)[15] <- "Assembly_length"
names(coli_genomes)[16] <- "contigs1kb"
# check
names(coli_genomes)
```

```
##  [1] "Strain"             "Biosample"          "Year"               "Source"
##  [5] "Phylogroup"         "Serotype"           "Clonotype"          "Sequence.Type"
##  [9] "VF"                 "Plasmids"           "kmer"               "Contigs"
## [13] "N50"                "longest.contig..bp." "Assembly_length"    "contigs1kb"
```

Change and add variables

We are going to simplify our dataframe by dropping variables:

```
coli_genomes <- coli_genomes[-c(9:11), ]
# this can be also used to remove rows
coli_genomes[, -1]
```

```
##       Biosample Year  Source Phylogroup Serotype  Clonotype Sequence.Type VF Plasmids kmer Contigs
## 1  SAMN14278613   NA   Human          D  ONT:H28   CH23-331          ST524 18        3  117     223
## 2  SAMN14278614 2010   Human          C O153:H19     CH4-25           ST88 14        3  117     159
## 3  SAMN14278615 2008   Human         B1  O76:H30    CH29-38          ST156 10        2   89     114
## 4  SAMN14278616   NA   Human          A  O78:H11    CH11-41           ST48  5        3  117     212
## 5  SAMN14278617 2011 Porcine          A  ONT:HNM     CH7-54          ST746  5        9   89     320
## 6  SAMN14278618 2007 Porcine          A   O9:H37     CH7-31         ST3011  7        3   93     158
## 7  SAMN14278619 2006 Porcine          A   O2:H32    CH11-23           ST10  4        7  115     277
## 8  SAMN14278620 2006 Porcine          A  ONT:H45    C11-398        ST10888  2        7  115     203
## 12 SAMN14278624 2013   Human          D O145:H28   CH23-331           ST32 22        1  115     376
## 13 SAMN14278625 2013   Human          D O145:H28   CH23-331          ST137 22        3  111     205
## 14 SAMN14278626 2013   Human          D O145:H28   CH23-331           ST32 20        1  113     206
## 15 SAMN14278627 2013   Human          A  ONT:H37     C11-54           ST48  1        0  113     140
## 16 SAMN14278628 2013   Avian          A  ONT:H19    CH94-23          ST347  2        0  117     134
## 17 SAMN14278629 2011   Avian         B1 O142:H30     C41-35          ST359  9        4  113     102
## 18 SAMN14278630 2005   Avian          C  O78:H19     CH4-27           ST88 11        4  113     108
## 19 SAMN14278631 2012   Human          C   O8:H19     CH4-54           ST88 14        2  113     108
## 20 SAMN14278632 2012   Human          C   O9:H19     CH4-27           ST88 14        4   91     224
## 21 SAMN14278633 2012   Human          A    O9:H4     CH7-34           ST46  8        4   85     204
## 22 SAMN14278634 2015   Human          C   O9:H19 CH4like-27        ST10890 13        3  113     171
## 23 SAMN14278635 2012   Human          A  ONT:H33    CH11-54           ST10  2        5  117     120
## 24 SAMN14278636 2016   Human          A  O98:H26    CH27-23         ST8233  2        4   89     114
## 25 SAMN14278637 2012   Human         B1  O66:H10     CH4-32         ST1049  4        2  113      94
##       N50 longest.contig..bp. Assembly_length contigs1kb
## 1  272287              662555         5341632         74
## 2  323172              760527         5415613         57
## 3  270767              738861         4875343         47
## 4  112160              285056         5167401        101
## 5   45936              128053         4858138        212
## 6  106897              369508         4638334         93
## 7   89185              281444         5406295        155
## 8   94368              280268         4796593        114
## 12 200150              424527         5389075        131
## 13 281589              617142         5340478         78
```

```
## 14 182651              412836         5276782         95
## 15 105396              272304         4507328         78
## 16 110661              497785         4664768         77
## 17 240847              460510         4992565         42
## 18 405376             1190696         5196698         38
## 19 281822             1140163         5252065         43
## 20 140521              284241         5085107        110
## 21  86565              300086         4915667        121
## 22 326962              749412         5200701         77
## 23 228491              576949         4881205         48
## 24 187945              537848         4821342         53
## 25 325747              822206         4839344         32
```

We know the 'Assembly length' and the number of 'Contigs', but we would like to represent the average contig length.

```
coli_genomes$average_contig <- coli_genomes$Assembly_length/coli_genomes$Contigs
```

Dealing with *NAs*

It is very easy to calculate statistics of one variable. Imagine we want to know the average year of sample isolation.

```
mean(coli_genomes$Year.of.isolation)
```

```
## Warning in mean.default(coli_genomes$Year.of.isolation): argument is not numeric or logical:
## returning NA
```

```
## [1] NA
```

Yes, that error means that there are some NA values and mean cannot be calculated. We can check that and omit the NAs.

```
# check if there is any NA
is.na(coli_genomes)
```

```
##    Strain Biosample  Year Source Phylogroup Serotype Clonotype Sequence.Type    VF Plasmids  kmer
## 1   FALSE     FALSE  TRUE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 2   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 3   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 4   FALSE     FALSE  TRUE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 5   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 6   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 7   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 8   FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 12  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 13  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 14  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 15  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 16  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 17  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 18  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 19  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 20  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 21  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 22  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 23  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
```

```
## 24  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
## 25  FALSE     FALSE FALSE  FALSE      FALSE    FALSE     FALSE         FALSE FALSE    FALSE FALSE
##    Contigs   N50 longest.contig..bp. Assembly_length contigs1kb average_contig
## 1    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 2    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 3    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 4    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 5    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 6    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 7    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 8    FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 12   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 13   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 14   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 15   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 16   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 17   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 18   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 19   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 20   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 21   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 22   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 23   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 24   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
## 25   FALSE FALSE               FALSE           FALSE      FALSE          FALSE
```

```
# na.rm=TRUE will omit the NAs for this function
mean(coli_genomes$Year.of.isolation, na.rm = TRUE)
```

```
## Warning in mean.default(coli_genomes$Year.of.isolation, na.rm = TRUE): argument is not numeric or
## logical: returning NA
```

```
## [1] NA
```

What if we want to remove observations with an NA from a dataset?

```
coli_genomes2 <- na.omit(coli_genomes)
```

Finally, we are going to save our new dataset for future examples.

```
write.csv2(coli_genomes, "data/coli_genomes_renamed.csv", row.names = FALSE)
```

References

- *An introduction to R*, https://intro2r.com/work-d.html
- *R programming for data science,* https://bookdown.org/rdpeng/rprogdatascience/
- Using RStudio projects, https://support.rstudio.com/hc/en-us/articles/200526207
- Importar y exportar datos en R, https://rsanchezs.gitbooks.io/rprogramming/content/chapter3/index.html
- *R in action.* Robert I. Kabacoff. March 2022 ISBN 9781617296055
- R para análisis científicos reproducibles. Sofware Carpentry Foundation. https://swcarpentry.github.io/r-novice-gapminder-es/

Short exercises

1. Try the input/output examples from *Techvidvan* website https://techvidvan.com/tutorials/r-input-and-output-functions/
2. Load the file *colis3.csv* as *colis* and explore the dataset structure.
3. Calculate the mean of numerical variables: isolation date (*Year*), antimicrobial resistance genes (*AMR*), virulence factors (*VF*), CRISPR cassesttes (*CRISPR*), integron cassettes (*Integron*) and sequencing date (*seqs*) in those strains? Note. For the *seqs* variable you will need to use the function `as.Date()`.
4. Save the tables *coli_genomes_renamed* and *colis* in a single *Rdata* file.
5. Add the values of the exercise 3 as a last row in the table. Note. For the *seqs* variable you will need to use the function `format.Date()` (or just `format()`)

Session Info

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Monterey 12.5.1
##
## Matrix products: default
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
##
## locale:
## [1] es_ES.UTF-8/es_ES.UTF-8/es_ES.UTF-8/C/es_ES.UTF-8/es_ES.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] formatR_1.12  knitr_1.40    ggplot2_3.3.6 xlsx_0.6.5
##
## loaded via a namespace (and not attached):
##  [1] highr_0.9        pillar_1.8.1     compiler_4.2.2   bslib_0.4.0      jquerylib_0.1.4
##  [6] tools_4.2.2      digest_0.6.30    jsonlite_1.8.3   evaluate_0.17    lifecycle_1.0.3
## [11] tibble_3.1.8     gtable_0.3.1     pkgconfig_2.0.3  rlang_1.0.6      cli_3.4.1
## [16] rstudioapi_0.14  yaml_2.3.6       xfun_0.34        fastmap_1.1.0    rJava_1.0-6
## [21] stringr_1.4.1    withr_2.5.0      dplyr_1.0.10     sass_0.4.2       generics_0.1.3
## [26] xlsxjars_0.6.1   vctrs_0.5.0      grid_4.2.2       tidyselect_1.2.0 glue_1.6.2
## [31] R6_2.5.1         fansi_1.0.3      rmarkdown_2.17   farver_2.1.1     magrittr_2.0.3
## [36] scales_1.2.1     htmltools_0.5.3  colorspace_2.0-3 labeling_0.4.2   utf8_1.2.2
## [41] stringi_1.7.8    munsell_0.5.0    cachem_1.0.6
```

Course home