

INTRODUCTION TO R

UEB – VHIR

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- 1. Some data types in R**
- 2. Getting data into R**
- 3. Access to data**
- 4. Plots with R**
- 5. Install packages**
- 6. Help!!**

- 1. Some data types in R**
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1. Some data types in R

- R store information in different types of objects.
- The most common are:
 1. **Variables**: A variable is a name for a value. We can create a new variable by assigning a value to it, using `<-`

```
width <- 5
```

```
width
```

```
## [1] 5
```


1. Some data types in R

2. Vectors: a collection of numbers or characters:

```
myvec <- c(10,20,30,40,50)
```

```
myvec
```

```
## [1] 10 20 30 40 50
```

```
myvec + 1
```

```
## [1] 11 21 31 41 51
```

```
myvec + myvec
```

```
## [1] 20 40 60 80 100
```

```
food <- c("eggs", "beans", "bacon", "sausage")
```

1. Some data types in R

3. **Dataframe**: is a table or a two-dimensional array-like structure in which each column contains values of one variable and each row contains one set of values from each column :

`iris`

Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
setosa	5.1	3.5	1.4	0.2
setosa	4.9	3.0	1.4	0.2
setosa	4.7	3.2	1.3	0.2
versicolor	7.0	3.2	4.7	1.4
versicolor	6.4	3.2	4.5	1.5
versicolor	6.9	3.1	4.9	1.5
versicolor	5.5	2.3	4.0	1.3
virginica	6.3	3.3	6.0	2.5
virginica	5.8	2.7	5.1	1.9
virginica	7.1	3.0	5.9	2.1
virginica	6.3	2.9	5.6	1.8
virginica	6.5	3.0	5.8	2.2

1. Some data types in R

4. List: is a generic vector containing other objects

```
n <- c(2, 3, 5)
s <- c("aa", "bb", "cc", "dd", "ee")
b <- c(TRUE, FALSE, TRUE, FALSE, FALSE)
x <- list(n, s, b, 3)  # x contains copies of n, s, b
```

```
x[2]
```

```
[[1]]
```

```
[1] "aa" "bb" "cc" "dd" "ee"
```

5. Matrix: is a collection of data elements arranged in a two-dimensional rectangular layout:

```
A <- matrix(c(2, 4, 3, 1, 5, 7), nrow=2, ncol=3, byrow = TRUE)
```

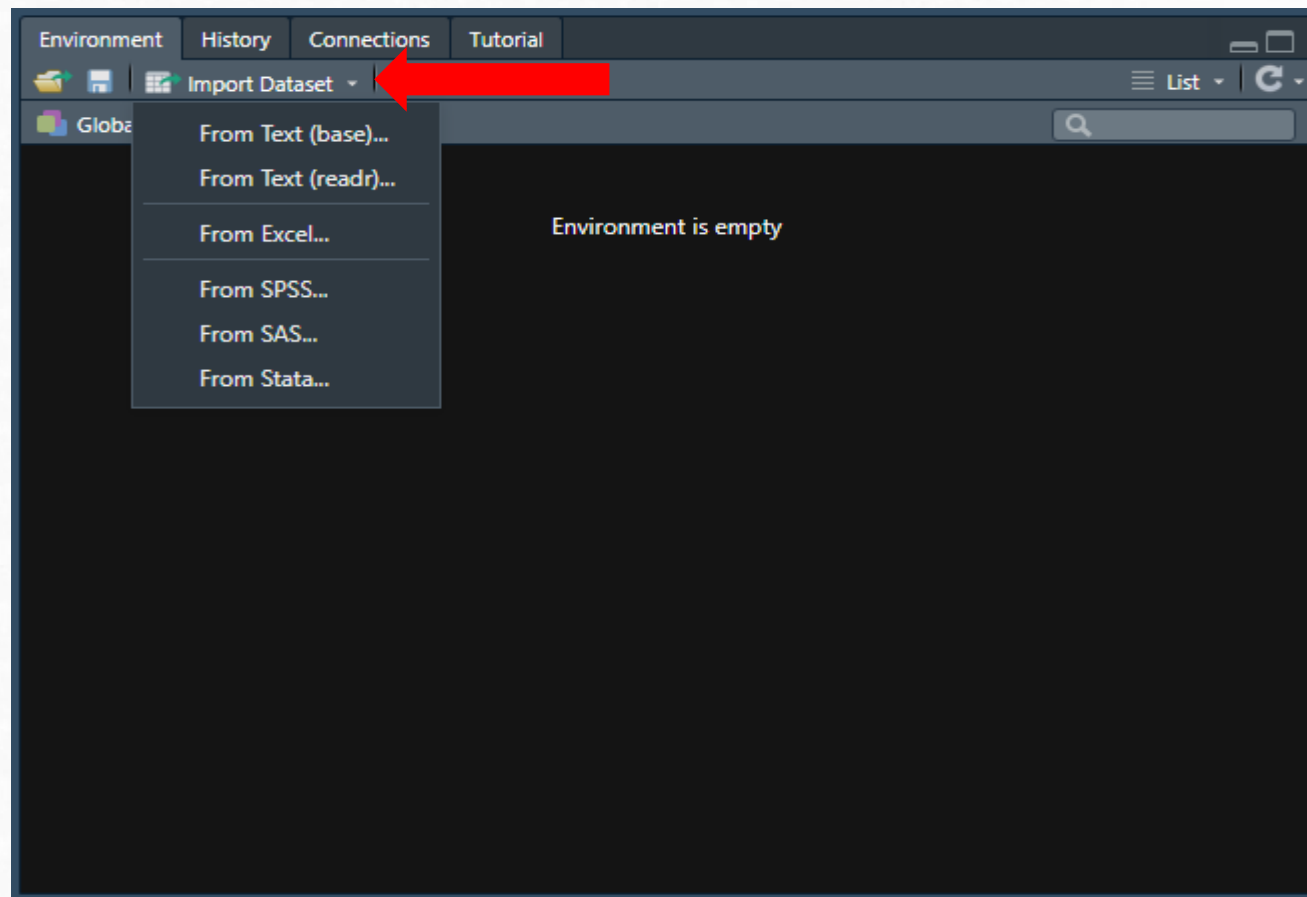
```
A
```

```
[,1] [,2] [,3]
[1,]  2   4   3
[2,]  1   5   7
```

- 1. Some data types in R**
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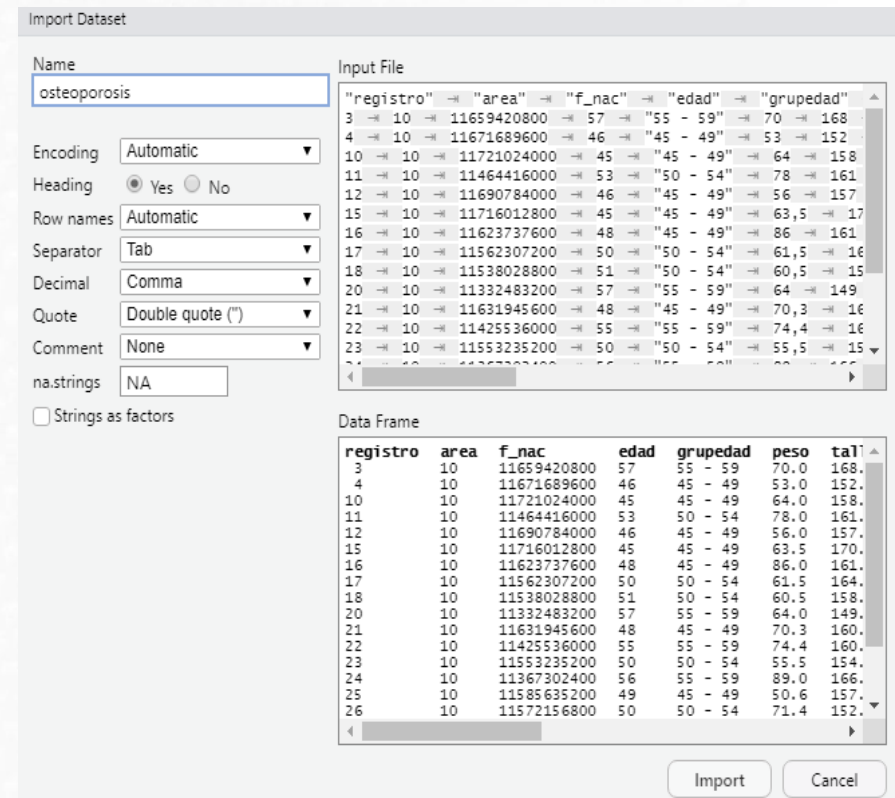
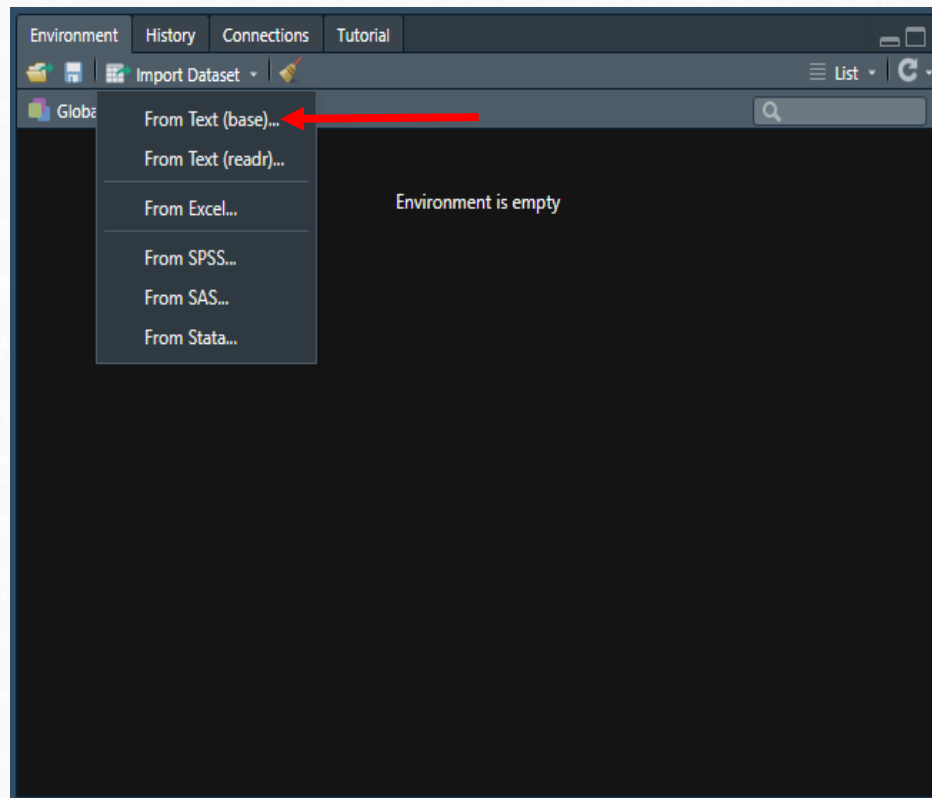
2. Getting data into R

- The easiest way to get data into R is to click on the “Import Datasets” button.



2. Getting data into R

- The easiest way to get data into R is to click on the “Import Datasets” button.



2. Getting data into R

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
1	3	10	11659420800	57	55 - 59	70.0	168.0	24.80	69	OSTEOPENIA	12	99	NO	NO MENOPAUSIA/NO CONSTA	SECUNDARIOS
2	4	10	11671689600	46	45 - 49	53.0	152.0	22.94	73	OSTEOPENIA	13	99	NO	NO MENOPAUSIA/NO CONSTA	SECUNDARIOS
3	10	10	11721024000	45	45 - 49	64.0	158.0	25.64	81	NORMAL	14	99	NO	NO MENOPAUSIA/NO CONSTA	PRIMARIOS
4	11	10	11464416000	53	50 - 54	78.0	161.0	30.09	58	OSTEOPENIA	10	50	SI	NATURAL	PRIMARIOS
5	12	10	11690784000	46	45 - 49	56.0	157.0	22.72	89	NORMAL	13	99	NO	NO MENOPAUSIA/NO CONSTA	PRIMARIOS
6	15	10	11716012800	45	45 - 49	63.5	170.0	21.97	76	NORMAL	14	99	NO	NO MENOPAUSIA/NO CONSTA	SECUNDARIOS
7	16	10	11623737600	48	45 - 49	86.0	161.0	33.18	87	NORMAL	11	99	NO	NO MENOPAUSIA/NO CONSTA	PRIMARIOS
8	17	10	11562307200	50	50 - 54	61.5	164.0	22.87	74	NORMAL	10	99	NO	NO MENOPAUSIA/NO CONSTA	PRIMARIOS
9	18	10	11538028800	51	50 - 54	60.5	158.0	24.23	58	OSTEOPENIA	14	99	NO	NO MENOPAUSIA/NO CONSTA	SECUNDARIOS
10	20	10	11332483200	57	55 - 59	64.0	149.0	28.83	61	OSTEOPENIA	13	50	SI	AMBAS	PRIMARIOS
11	21	10	11631945600	48	45 - 49	70.3	160.0	27.46	67	OSTEOPENIA	12	48	SI	OVARECTOMIA	SECUNDARIOS
12	22	10	11425536000	55	55 - 59	74.4	160.0	29.06	68	OSTEOPENIA	14	50	SI	NATURAL	PRIMARIOS
13	23	10	11553235200	50	50 - 54	55.5	154.5	23.25	73	OSTEOPENIA	11	48	SI	NATURAL	PRIMARIOS
14	24	10	11367302400	56	55 - 59	89.0	166.0	32.30	61	OSTEOPENIA	14	47	SI	NATURAL	PRIMARIOS
15	25	10	11585635200	49	45 - 49	50.6	157.0	20.53	68	OSTEOPENIA	14	40	SI	NATURAL	PRIMARIOS
16	26	10	11572156800	50	50 - 54	71.4	152.0	30.90	74	NORMAL	14	48	SI	AMBAS	PRIMARIOS
17	27	10	11590992000	49	45 - 49	78.0	157.0	31.64	62	OSTEOPENIA	12	46	SI	NATURAL	PRIMARIOS
18	28	10	11293516800	58	55 - 59	72.0	162.0	27.43	65	OSTEOPENIA	11	54	SI	NATURAL	PRIMARIOS
19	29	10	11215238400	61	60 - 64	68.0	155.5	28.12	65	OSTEOPENIA	14	50	SI	NATURAL	PRIMARIOS

What type of data is?

2. Getting data into R

With R instructions:

```
osteoporosis2 <- read.csv2("osteoporosis.csv", sep = "\t", dec = ",", header = TRUE)
```



check the folder you are working on!

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3. Access to data

- Once you have loaded the data, it is necessary to check it
- Different ways to do it
 - **head(*name of dataframe*)**: to see the first rows of a dataframe
 - **tail(*name of dataframe*)**: to see the last rows of a dataframe
 - **str(name of dataframe)**: to check the structure of the dataframe and their variables
 - **summary(name of dataframe)**: Little summary of the variables of the dataframe

3. Access to data

```
head(osteoporosis)
```

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
1	3	10	11659420800	57	55 - 59	70.0	168	24.80	69	OSTEOPENIA	12	99	NO NO MENOPAUSIA/NO CONSTA	SECUNDARIOS	
2	4	10	11671689600	46	45 - 49	53.0	152	22.94	73	OSTEOPENIA	13	99	NO NO MENOPAUSIA/NO CONSTA	SECUNDARIOS	
3	10	10	11721024000	45	45 - 49	64.0	158	25.64	81	NORMAL	14	99	NO NO MENOPAUSIA/NO CONSTA	PRIMARIOS	
4	11	10	11464416000	53	50 - 54	78.0	161	30.09	58	OSTEOPENIA	10	50	SI NATURAL	PRIMARIOS	
5	12	10	11690784000	46	45 - 49	56.0	157	22.72	89	NORMAL	13	99	NO NO MENOPAUSIA/NO CONSTA	PRIMARIOS	
6	15	10	11716012800	45	45 - 49	63.5	170	21.97	76	NORMAL	14	99	NO NO MENOPAUSIA/NO CONSTA	SECUNDARIOS	

```
tail(osteoporosis)
```

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
995	1028	11	11190182400	63	60 - 64	71	161	27.39	57	OSTEOPENIA	14	48	SI NATURAL	PRIMARIOS	
996	1029	11	11287036800	60	60 - 64	64	158	25.64	69	OSTEOPENIA	10	40	SI AMBAS	SUPERIORES	
997	1030	11	11066371200	67	65 - 69	68	157	27.59	75	NORMAL	11	55	SI NATURAL	PRIMARIOS SIN FINALIZAR	
998	1031	11	11289196800	59	55 - 59	72	153	30.76	67	OSTEOPENIA	12	56	SI NATURAL	PRIMARIOS	
999	1032	11	11137219200	64	60 - 64	80	152	34.63	55	OSTEOPENIA	14	50	SI NATURAL	PRIMARIOS	
1000	1033	11	11213164800	62	60 - 64	67	161	25.85	65	OSTEOPENIA	13	54	SI NATURAL	SECUNDARIOS	

3. Access to data

```
str(osteoporosis)
'data.frame':   1000 obs. of  15 variables:
 $ registro: int  3 4 10 11 12 15 16 17 18 20 ...
 $ area    : int  10 10 10 10 10 10 10 10 10 10 ...
 $ f_nac   : chr  "11659420800" "11671689600" "11721024000" "11464416000" ...
 $ edad    : int  57 46 45 53 46 45 48 50 51 57 ...
 $ grupedad: chr  "55 - 59" "45 - 49" "45 - 49" "50 - 54" ...
 $ peso     : num  70 53 64 78 56 63.5 86 61.5 60.5 64 ...
 $ talla    : num  168 152 158 161 157 170 161 164 158 149 ...
 $ imc      : num  24.8 22.9 25.6 30.1 22.7 ...
 $ bua      : int  69 73 81 58 89 76 87 74 58 61 ...
 $ clasific: chr  "OSTEOPENIA" "OSTEOPENIA" "NORMAL" "OSTEOPENIA" ...
 $ menarqui: int  12 13 14 10 13 14 11 10 14 13 ...
 $ edad_men: int  99 99 99 50 99 99 99 99 99 50 ...
 $ menop    : chr  "NO" "NO" "NO" "SI" ...
 $ tipo_men: chr  "NO MENOPAUSIA/NO CONSTA" "NO MENOPAUSIA/NO CONSTA" "NO MENOPAUSIA/NO
CONSTA" "NATURAL" ...
 $ nivel_ed: chr  "SECUNDARIOS" "SECUNDARIOS" "PRIMARIOS" "PRIMARIOS" ...
```


3. Access to data

```
summary(osteoporosis)
```

registro	area	f_nac	edad	grupedad	peso	talla	imc
Min. : 3.0	Min. :10.00	Length:1000	Min. :45.00	Length:1000	Min. : 44.00	Min. :138.0	Min. :17.21
1st Qu.: 280.8	1st Qu.:10.00	Class :character	1st Qu.:48.00	Class :character	1st Qu.: 60.50	1st Qu.:153.0	1st Qu.:24.80
Median : 531.5	Median :11.00	Mode :character	Median :52.00	Mode :character	Median : 68.00	Median :157.0	Median :27.51
Mean : 529.9	Mean :11.58		Mean :53.42		Mean : 69.12	Mean :156.9	Mean :28.11
3rd Qu.: 781.2	3rd Qu.:13.00		3rd Qu.:58.00		3rd Qu.: 75.00	3rd Qu.:161.0	3rd Qu.:30.82
Max. :1033.0	Max. :13.00		Max. :69.00		Max. :123.50	Max. :180.0	Max. :48.39

bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
Min. : 11.0	Length:1000	Min. : 8.00	Min. :24.00	Length:1000	Length:1000	Length:1000
1st Qu.: 62.0	Class :character	1st Qu.:12.00	1st Qu.:46.00	Class :character	Class :character	Class :character
Median : 72.0	Mode :character	Median :13.00	Median :51.00	Mode :character	Mode :character	Mode :character
Mean : 73.3		Mean :12.71	Mean :63.04			
3rd Qu.: 84.0		3rd Qu.:14.00	3rd Qu.:99.00			
Max. :136.0		Max. :17.00	Max. :99.00			

3. Access to data

```
nrow(osteoporosis)
```

```
[1] 1000
```

```
ncol(osteoporosis)
```

```
[1] 15
```

```
colnames(osteoporosis)
```

```
[1] "registro" "area"      "f_nac"      "edad"      "grupedad" "peso"      "talla"      "imc"  
"bua"      "clasific" "menarqui" "edad_men" "menop"  
[14] "tipo_men" "nivel_ed"
```

3. Access to data

- Sometimes you are not interested in working with all the variables of cases of the dataset
- There are different ways to select them:

```
#select the first 3 rows and columns  
osteoporosis[1:3, 1:3]
```

	registro	area	f_nac
1	3	10	11659420800
2	4	10	11671689600
3	10	10	11721024000

3. Access to data

```
#select the different rows and columns  
osteoporosis[c(31:36, 115, 950), c(2, 4:6,13:15)]
```

	area	edad	grupedad	peso	menop	tipo_men	nivel_ed
31	10	67	65 - 69	60.0	SI	NATURAL	PRIMARIOS
32	10	50	50 - 54	70.0	SI	NATURAL	PRIMARIOS
33	10	56	55 - 59	68.0	SI	NATURAL	PRIMARIOS
34	10	67	65 - 69	63.0	SI	NATURAL	PRIMARIOS
35	10	58	55 - 59	64.0	SI	NATURAL	PRIMARIOS
36	10	57	55 - 59	75.0	SI	NATURAL	SIN ESTUDIOS
115	10	45	45 - 49	57.0	NO NO MENOPAUSIA/NO	CONSTA	SECUNDARIOS
950	11	62	60 - 64	75.5	SI	NATURAL	PRIMARIOS

```
#select all the rows and by variable name and save the dataset with another name  
osteoporosis2 <- osteoporosis[, c("edad", "grupedad", "tipo_men", "nivel_ed")]  
head(osteoporosis2)
```

	edad	grupedad	tipo_men	nivel_ed
1	57	55 - 59 NO MENOPAUSIA/NO	CONSTA	SECUNDARIOS
2	46	45 - 49 NO MENOPAUSIA/NO	CONSTA	SECUNDARIOS
3	45	45 - 49 NO MENOPAUSIA/NO	CONSTA	PRIMARIOS
4	53	50 - 54	NATURAL	PRIMARIOS
5	46	45 - 49 NO MENOPAUSIA/NO	CONSTA	PRIMARIOS
6	45	45 - 49 NO MENOPAUSIA/NO	CONSTA	SECUNDARIOS

3. Access to data

- It is also possible to select some rows depending on logic expressions:

```
#select patients older than 60 years
osteoporosis3 <- osteoporosis[which(osteoporosis$edad > 60), ]
head(osteoporosis3)
```

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
19	29	10	11215238400	61	60 - 64	68.0	155.5	28.12	65	OSTEOPENIA	14	50	SI	NATURAL	PRIMARIOS
23	34	10	10992758400	68	65 - 69	66.5	145.0	31.63	57	OSTEOPENIA	13	50	SI	NATURAL	PRIMARIOS SIN FINALIZAR
24	35	10	10909382400	69	65 - 69	70.0	168.0	24.80	48	OSTEOPOROSIS	13	45	SI	NATURAL	PRIMARIOS
27	38	10	11043907200	66	65 - 69	67.0	144.0	32.31	79	NORMAL	12	56	SI	NATURAL	PRIMARIOS
28	39	10	10948089600	69	65 - 69	70.5	148.5	31.97	40	OSTEOPOROSIS	11	43	SI	NATURAL	SIN ESTUDIOS
29	40	10	11051251200	66	65 - 69	66.5	147.0	30.77	48	OSTEOPOROSIS	13	40	SI	NATURAL	PRIMARIOS

```
osteoporosis4 <- subset(osteoporosis, edad > 60)
head(osteoporosis4)
```

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqui	edad_men	menop	tipo_men	nivel_ed
19	29	10	11215238400	61	60 - 64	68.0	155.5	28.12	65	OSTEOPENIA	14	50	SI	NATURAL	PRIMARIOS
23	34	10	10992758400	68	65 - 69	66.5	145.0	31.63	57	OSTEOPENIA	13	50	SI	NATURAL	PRIMARIOS SIN FINALIZAR
24	35	10	10909382400	69	65 - 69	70.0	168.0	24.80	48	OSTEOPOROSIS	13	45	SI	NATURAL	PRIMARIOS
27	38	10	11043907200	66	65 - 69	67.0	144.0	32.31	79	NORMAL	12	56	SI	NATURAL	PRIMARIOS
28	39	10	10948089600	69	65 - 69	70.5	148.5	31.97	40	OSTEOPOROSIS	11	43	SI	NATURAL	SIN ESTUDIOS
29	40	10	11051251200	66	65 - 69	66.5	147.0	30.77	48	OSTEOPOROSIS	13	40	SI	NATURAL	PRIMARIOS

3. Access to data

- We can combine different logic expressions

```
osteoporosis4 <- subset(osteoporosis, edad > 60 & nivel_ed == "PRIMARIOS")  
head(osteoporosis4)
```

	registro	area	f_nac	edad	grupedad	peso	talla	imc	bua	clasific	menarqu	edad_men	menop	tipo_men	nivel_ed
19	29	10	11215238400	61	60 - 64	68.0	155.5	28.12	65	OSTEOPENIA	14	50	SI	NATURAL	PRIMARIOS
24	35	10	10909382400	69	65 - 69	70.0	168.0	24.80	48	OSTEOPOROSIS	13	45	SI	NATURAL	PRIMARIOS
27	38	10	11043907200	66	65 - 69	67.0	144.0	32.31	79	NORMAL	12	56	SI	NATURAL	PRIMARIOS
29	40	10	11051251200	66	65 - 69	66.5	147.0	30.77	48	OSTEOPOROSIS	13	40	SI	NATURAL	PRIMARIOS
31	45	10	11029651200	67	65 - 69	60.0	147.0	27.77	49	OSTEOPENIA	13	53	SI	NATURAL	PRIMARIOS
34	48	10	11034489600	67	65 - 69	63.0	157.0	25.56	66	OSTEOPENIA	13	50	SI	NATURAL	PRIMARIOS

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4. Plots with R

- R is a powerful tool to plot your data
- Hadley Wickam (2009) introduced a modern (and perhaps easier) way to plot your data
- Extensions to ggplot2
 - GGally, ggrepel, ...

Hadley Wickam book

<http://moderngraphics11.pbworks.com/f/ggplot2-Book09hWickham.pdf>

<https://ggplot2-book.org/>

STHDA (Statistical tools for high-throughput data analysis)

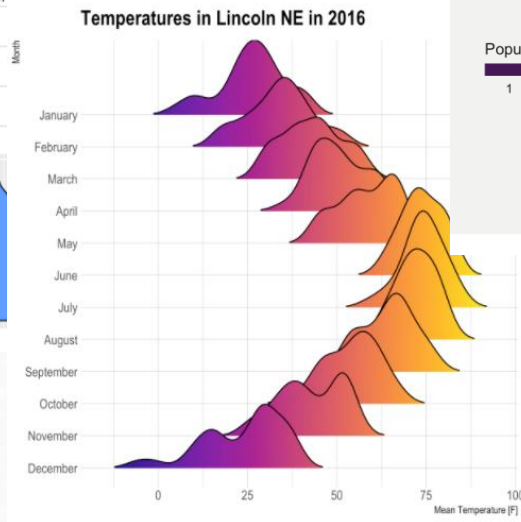
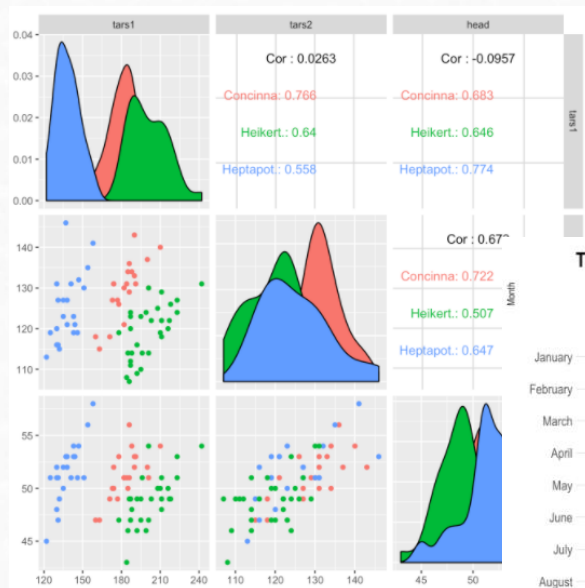
<http://www.sthda.com/english/wiki/ggplot2-essentials>

R Colors

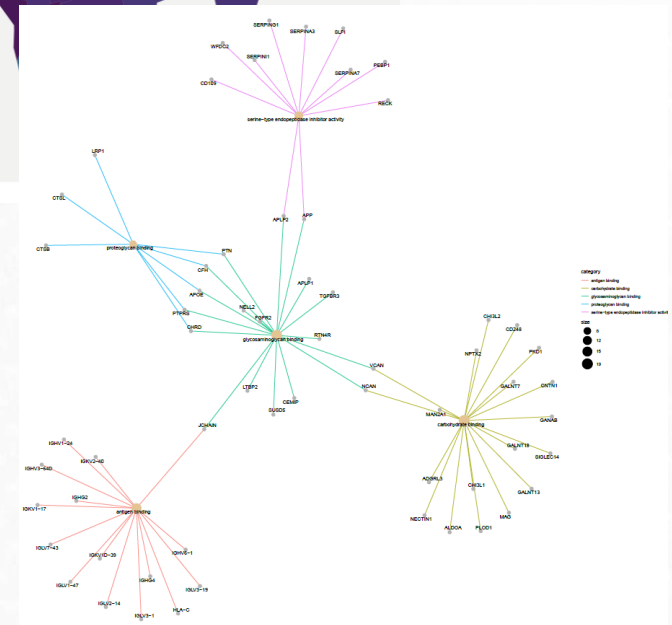
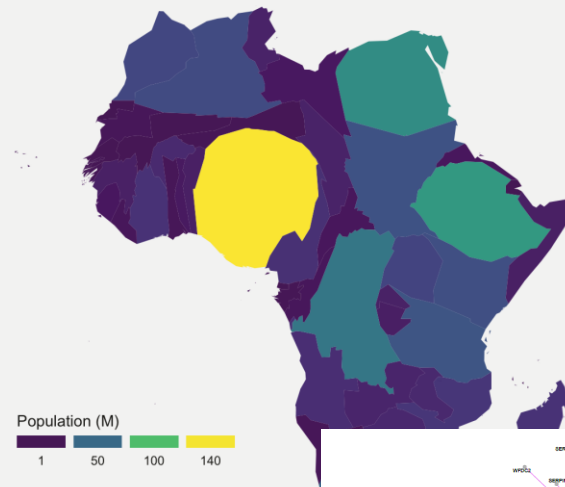
<http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf>

4. Plots with R

<https://www.r-graph-gallery.com/>



Africa 2005 Population



4. Plots with R

```
library(ggplot2) #Remember to install the packages before call it
```

```
ggplot(osteoporosis, aes(x = peso, y = imc)) +  
  geom_point()
```

4. Plots with R

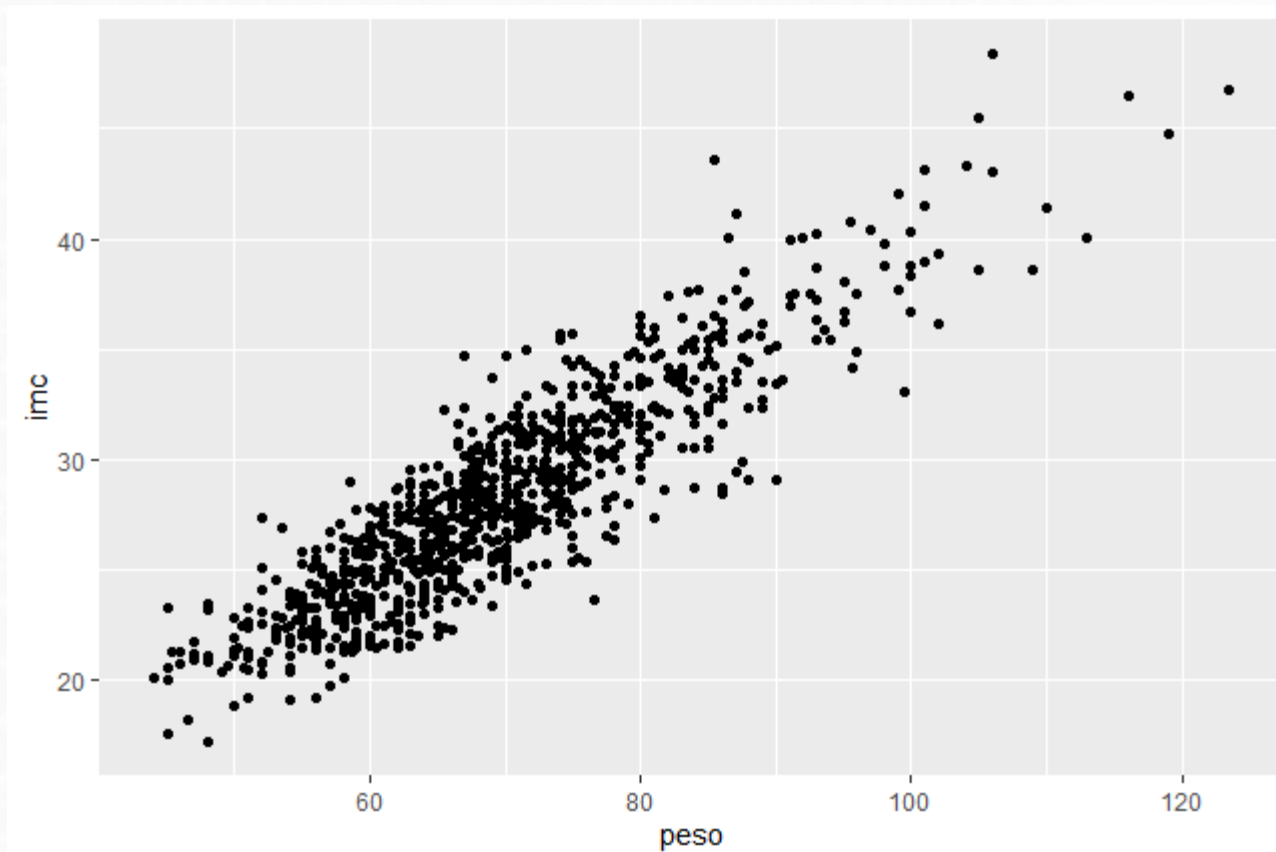
```
library(ggplot2) #Remember to install the packages before call it
```

```
ggplot(osteoporosis, aes(x = peso, y = imc)) +  
  geom_point()
```

4. Plots with R

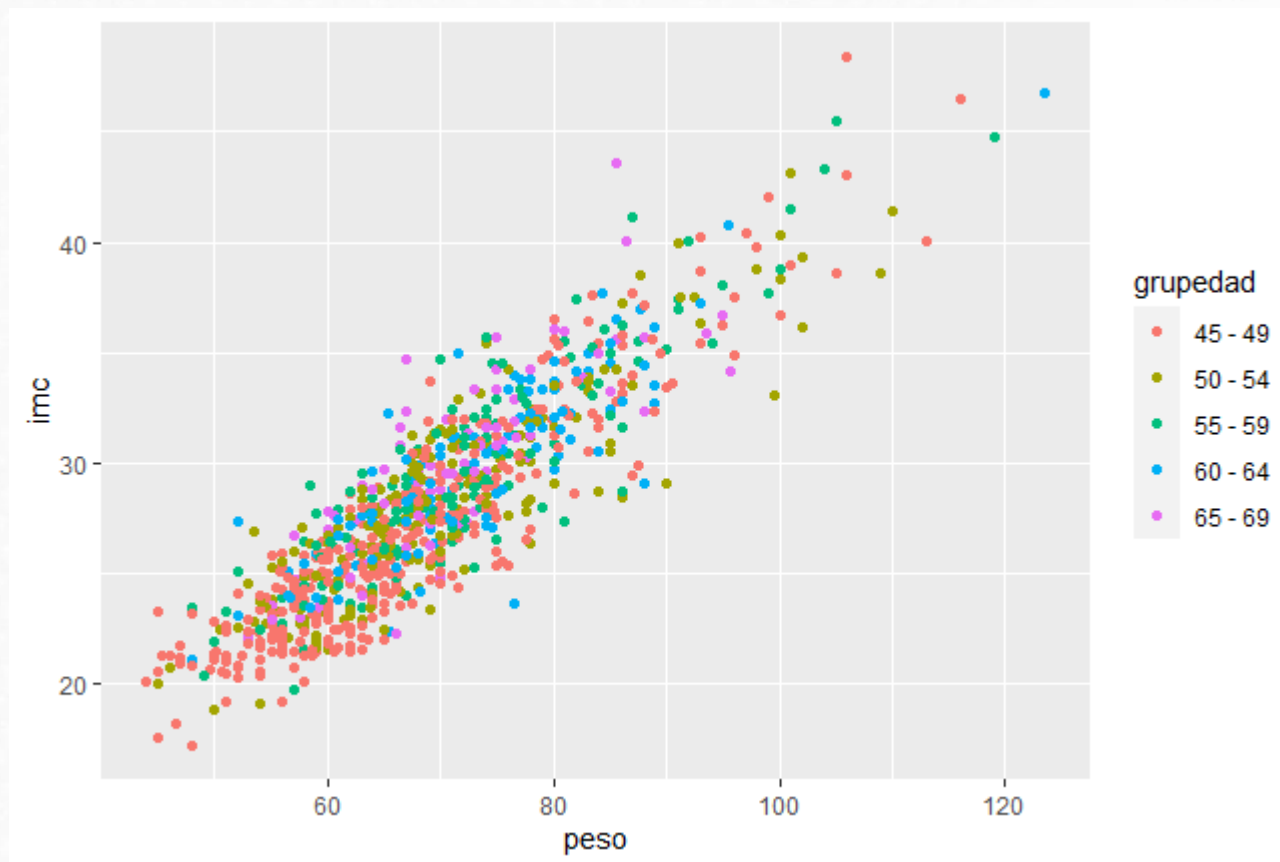
```
library(ggplot2) #Remember to install the packages before call it
```

```
ggplot(osteoporosis, aes(x = peso, y = imc)) +  
  geom_point()
```



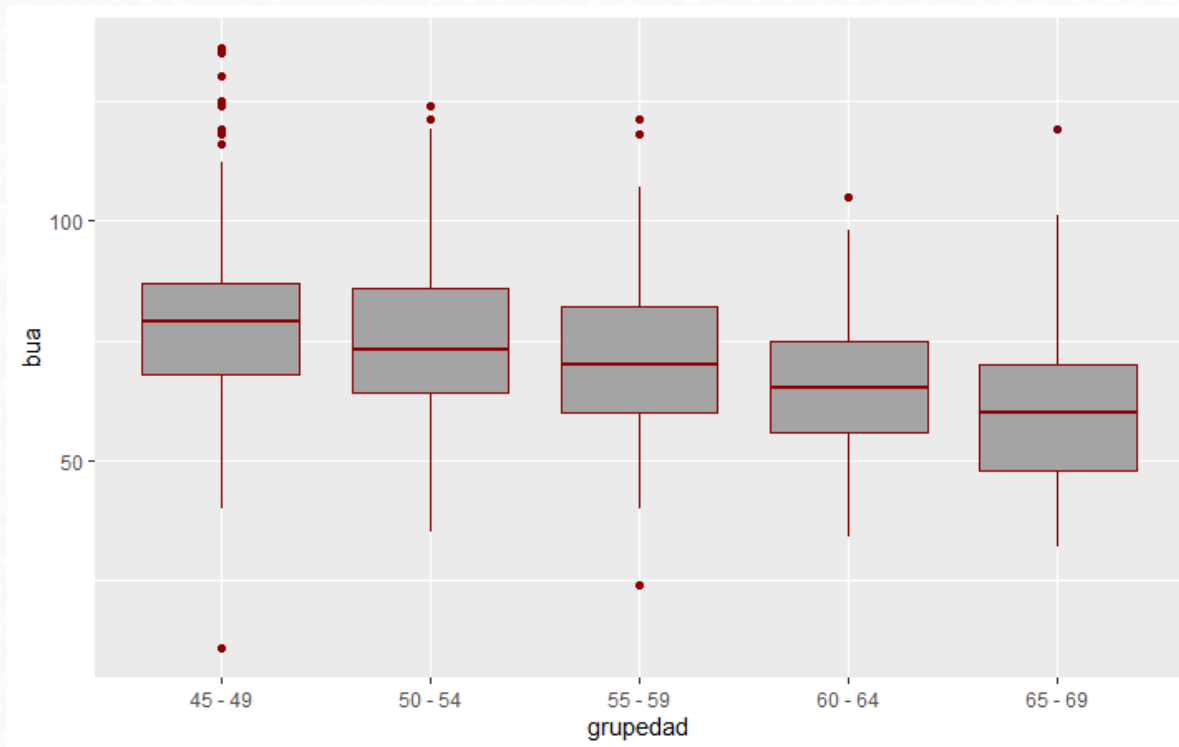
4. Plots with R

```
ggplot(osteoporosis, aes(x = peso, y = imc, color = grupedad)) +  
  geom_point()
```



4. Plots with R

```
bp <- ggplot(osteoporosis, aes(x = grupedad, y = bua)) +  
  geom_boxplot(fill='#A4A4A4', color="darkred")
```



4. Plots with R

```
bp + geom_jitter(shape = 16, position = position_jitter(0.2)) +  
  labs(x = "Age Group", y = "Women", title = "Osteo disease classified by age group")
```



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5. Install packages

- Packages are extensions of the basic R functions
- It is necessary to install once in each computer when needed
- Call it each time you want to use it
- Two ways to install the packages:
 - `install.packages("name of the package")`

5. Install packages

The screenshot shows the R Studio interface. On the left, the 'Install Packages' dialog box is open, with a red circle highlighting its content. The dialog has the following fields and options:

- Install from:** A dropdown menu set to 'Repository (CRAN)' with a help icon and the text '? Configuring Repositories'.
- Packages (separate multiple with space or comma):** An empty text input field.
- Install to Library:** A dropdown menu set to 'C:/Users/rgonz/Documents/R/win-library/4.0 [Default]'.
- ☒ **Install dependencies**
- Buttons:** 'Install' and 'Cancel' at the bottom right.

On the right, the 'Packages' pane is visible, also with a red circle highlighting the 'Install' button. The pane shows a table of installed and available packages:

Name	Description	Version
User Library		
<input type="checkbox"/> abind	Combine Multidimensional Arrays	1.4-5
<input type="checkbox"/> acepack	ACE and AVAS for Selecting Multiple Regression Transformations	1.4.1
<input type="checkbox"/> ActivePathways	[Failed to read package metadata]	[Unknown]
<input type="checkbox"/> ade4	Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	1.7-15
<input type="checkbox"/> anaStatsUEB	Statistical analysis function, Statistics and Bioinformatics Unit (UEB, VHIR)	0.0.0.9000
<input type="checkbox"/> annotate	Annotation for microarrays	1.66.0
<input type="checkbox"/> AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.50.3
<input type="checkbox"/> arsenal	An Arsenal of 'R' Functions for Large-Scale Statistical Summaries	3.5.0
<input type="checkbox"/> askpass	Safe Password Entry for R, Git, and SSH	1.1
<input type="checkbox"/> assertthat	Easy Pre and Post Assertions	0.2.1
<input type="checkbox"/> backports	Reimplementations of Functions Introduced Since R-3.0.0	1.1.10
<input type="checkbox"/> base64enc	Tools for base64 encoding	0.1-3

5. Install packages

- If package are hosted in Bioconductor repository:

```
if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")
```

```
BiocManager::install("airway")
```

5. Install packages

Bioconductor

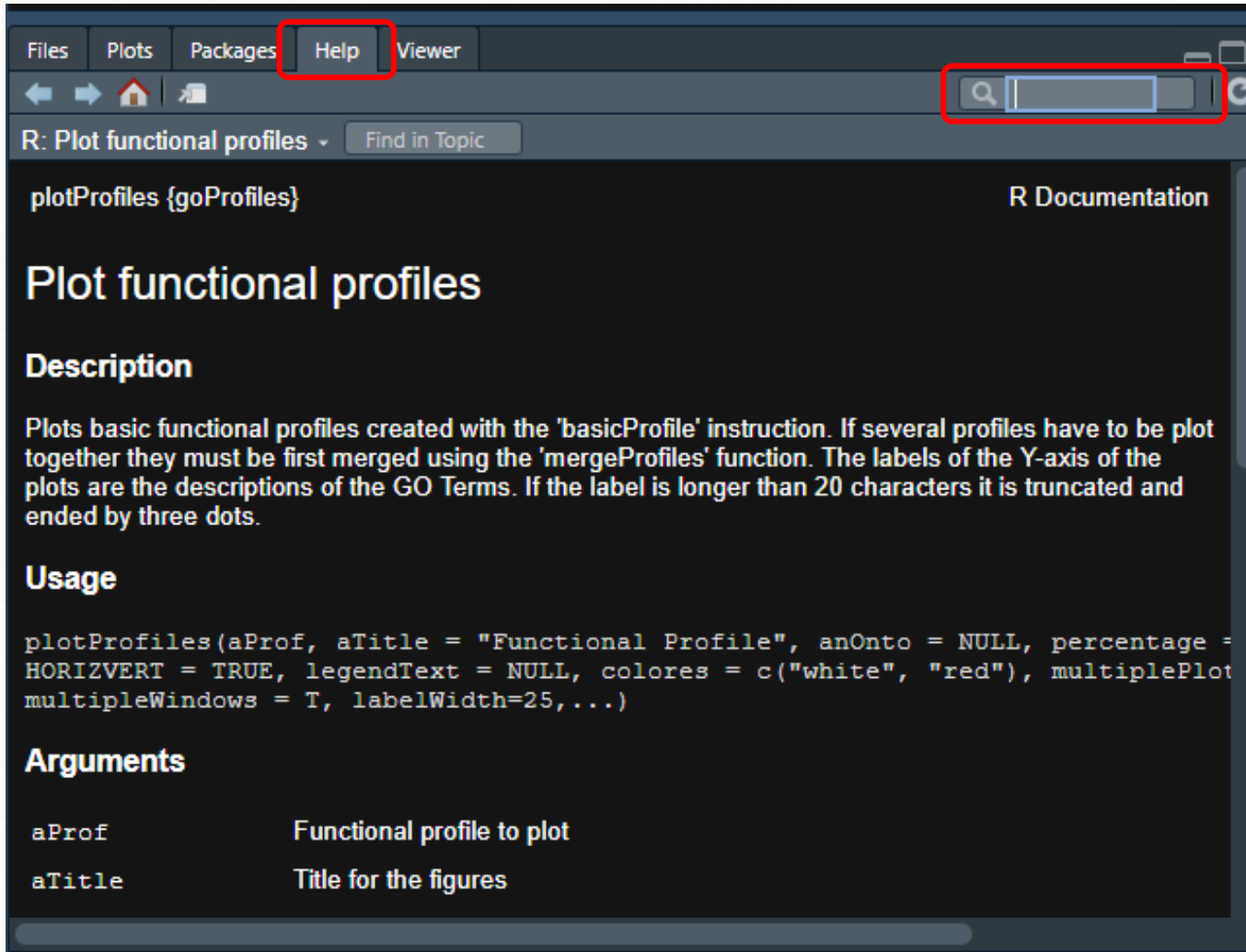
airway
Rsamtools
GenomicFeatures
GenomicAlignments
BiocParallel
DESeq2
apeglm
genefilter
AnnotationDbi
org.Hs.eg.db
Gviz
ReportingTools
sva
RUVSeq
AnnotationHub
clusterProfiler
ReactomePA
topGO
GOstats
pasilla
IHW

Cran R

magrittr
dplyr
ggplot2
pheatmap
RColorBrewer
ggbeeswarm

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6. Help!!



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R: Plot functional profiles

plotProfiles {goProfiles} R Documentation

Plot functional profiles

Description

Plots basic functional profiles created with the 'basicProfile' instruction. If several profiles have to be plot together they must be first merged using the 'mergeProfiles' function. The labels of the Y-axis of the plots are the descriptions of the GO Terms. If the label is longer than 20 characters it is truncated and ended by three dots.

Usage

```
plotProfiles(aProf, aTitle = "Functional Profile", anOnto = NULL, percentage =  
HORIZVERT = TRUE, legendText = NULL, colores = c("white", "red"), multiplePlot  
multipleWindows = T, labelWidth=25,...)
```

Arguments

aProf	Functional profile to plot
aTitle	Title for the figures