

Introduction to R

Methods to integrate multiple tables in biomedical studies to
detect biomarkers and stratify individuals

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RStudio

RStudio screen

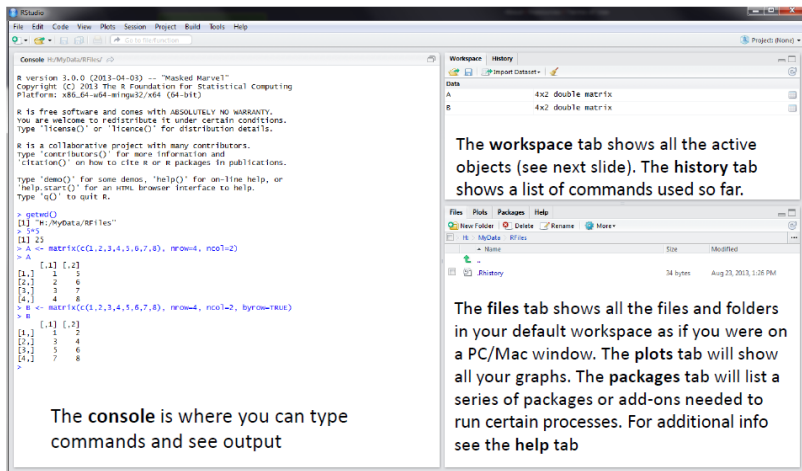
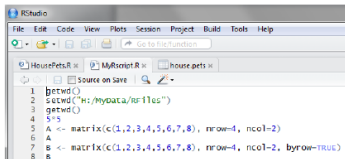


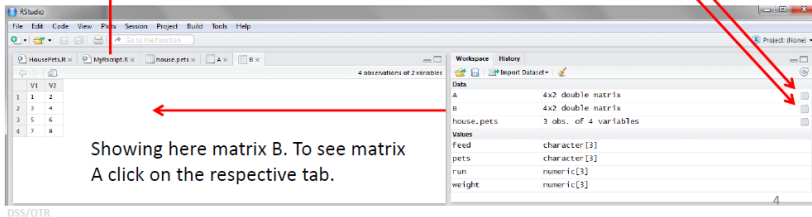
Figure 1: Rstudio screen

Workspace tab (1)

The workspace tab stores any object, value, function or anything you create during your R session. In the example below, if you click on the dotted squares you can see the data on a screen to the left.



```
1 getwd()
2 setwd("H:/mydata/Rfiles")
3 getwd()
4 5*5
5 A <- matrix(c(1,2,3,4,5,6,7,8), nrow=4, ncol=2)
6 A
7 B <- matrix(c(1,2,3,4,5,6,7,8), nrow=4, ncol=2, byrow=TRUE)
8 B
```



Showing here matrix B. To see matrix A click on the respective tab.

The screenshot shows the RStudio interface with the workspace pane on the right. The workspace pane lists objects: A (4x2 double matrix), B (4x2 double matrix), and house.pets (3 obs. of 4 variables). The environment pane on the left shows the current environment with variables V1 and V2. Red arrows indicate the workflow: one arrow points from the code editor to the workspace pane, and another points from the workspace pane to the environment pane.

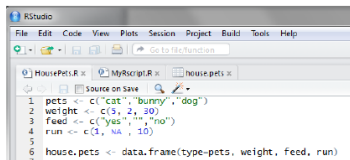
Object	Type
A	4x2 double matrix
B	4x2 double matrix
house.pets	3 obs. of 4 variables

Variable	Type
Feed	character[3]
pets	character[3]
run	numeric[3]
weight	numeric[3]

Figure 2: Workspace tab

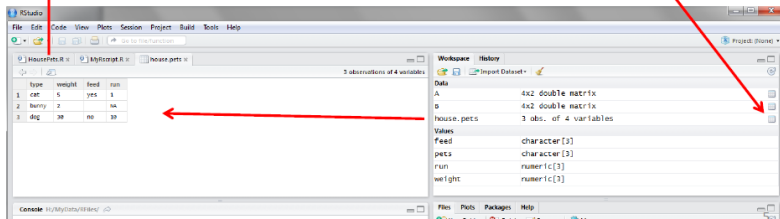
Workspace tab (2)

Here is another example on how the workspace looks like when more objects are added. Notice that the data frame `house.pets` is formed from different individual values or vectors.



```
1 pets <- c("cat","bunny","dog")
2 weight <- c(5, 2, 30)
3 feed <- c("yes","", "no")
4 run <- c(1, NA, 10)
5
6 house.pets <- data.frame(type=pets, weight, feed, run)
7
```

Click on the dotted square to look at the dataset in a spreadsheet form.



The screenshot shows the RStudio interface with the workspace tab selected. The workspace contains the following objects:

Object	Class
A	4x2 double matrix
B	4x2 double matrix
house.pets	3 obs. of 4 variables
feed	character[3]
pets	character[3]
run	numeric[3]
weight	numeric[3]

The console shows the command: `My/MyData/Rfiles/`

A red arrow points from the text "Click on the dotted square to look at the dataset in a spreadsheet form." to the dotted square next to the `house.pets` object in the workspace. Another red arrow points from the `house.pets` object to the spreadsheet view of the data frame.

	type	weight	feed	run
1	cat	5	yes	1
2	bunny	2	NA	
3	dog	30	no	10

DSS/OTR

Figure 3: Workspace tab (cont.)

History tab

The history tab keeps a record of all previous commands. It helps when testing and running processes. Here you can either **save** the whole list or you can **select** the commands you want and send them to an R script to keep track of your work.

In this example, we select all and click on the “To Source” icon, a window on the left will open with the list of commands. Make sure to save the ‘untitled1’ file as an *.R script.

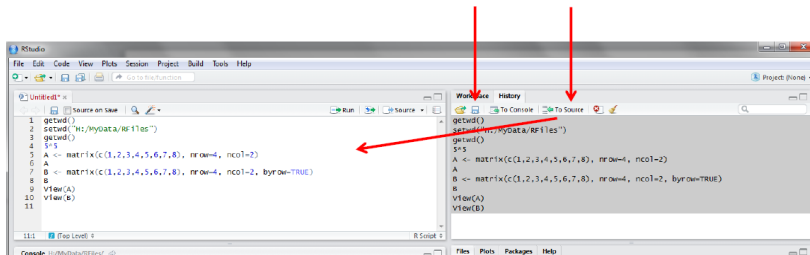


Figure 4: History tab

Getting data into R - import data

Required packages

- ▶ `foreign`: ~ import/export from SPSS, STATA, SAS,...
- ▶ `RODBC`: ~ SQL or ACCESS data bases.
- ▶ `Hmisc`: ~ SPSS, Hmisc (64bits).
- ▶ `readxl`: ~ export/import Excel files.

```
library(foreign)
library(Hmisc)
library(readxl)
```


ASCII files

- ▶ sep: column/variable separator character
- ▶ header: first row contains variable names?
- ▶ as.is: convert character to factor variables?

```
df<-read.table("data/parto2.dat", sep=";", as.is=TRUE, header=FALSE)  
head(df)
```

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11
1	1	GADI	14-JUN-2001	19-JUN-2001	26-JUL-2001	2	24	3.38	2	1	2
2	2	CAEL	15-JUN-2001	21-JUN-2001	15-FEB-2002	2	27	2.50	1	2	1
3	3	COMO	16-JUN-2001	01-JUL-2001	23-JUN-2001	1	44	3.15	2	2	1
4	4	VIMU	18-JUN-2001	23-JUN-2001	17-DEC-2001	2	25	2.74	1	1	1
5	5	PAVI	19-JUN-2001	25-JUN-2001	26-JUN-2001	1	27	3.60	2	2	1
6	6	PASA	20-JUN-2001	01-JUL-2001	27-JUN-2001	1	36	2.65	2	1	2

Excel

Use read_excel from readxl package.

```
df<-read_excel("data/mujeres.xlsx")  
class(df)
```

```
[1] "tbl_df"      "tbl"        "data.frame"
```

```
class(df) <- "data.frame"  
head(df)
```

	X__1	id	sexo	n_histo	an_diag	dondedx	dondectl	frecvisi
1	1	1	Mujer	GACA144012600	90	Ambulatorio	Ambulatorio	Cada 2-3 meses
2	3	3	Mujer	FOSA126052000	92	Ambulatorio	Ambulatorio	Cada 2-3 meses
3	5	5	Mujer	FEJI150053000	78	Hospital	Hospital	Cada 2-3 meses
4	6	6	Mujer	ORLO133102100	81	Ambulatorio	Ambulatorio	Mensual
5	7	7	Mujer	GRMA131110800	90	Ambulatorio	Ambulatorio	Cada 2-3 meses
6	16	16	Mujer	POFE121011400	71	Ambulatorio	Ambulatorio	Mensual

	tx_ab	tx_de	reflec	hbac_1	hbac_2	uso_re	uso_ok
1	ADO	ADO	Ninguno	8.57	5.95	No	<NA>
2	ADO	ADO	Ninguno	6.18	5.82	No	<NA>
3	ADO	ADO	Ninguno	8.33	6.23	No	<NA>
4	Dieta	Dieta	ACCUTREN SENSOR	5.27	10.42	Si	No
5	Dieta	ADO	Ninguno	7.40	6.81	No	<NA>
6	ADO	Insulina	Ninguno	6.90	8.33	No	<NA>

Stata

- To read Stata files (.dta), use read.dta function from foreign package

```
df <- read.dta("data/partoFin.dta",  
              convert.dates = TRUE, convert.factors = TRUE)  
head(df)
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo	tip_par
1	1	GADI	2001-06-14	2001-06-19	2001-07-26	intensivo	24	3.38	niña	instrument.
2	2	CAEL	2001-06-15	2001-06-21	2002-02-15	intensivo	27	2.50	niño	no instrum.
3	3	COMO	2001-06-16	2001-07-01	2001-06-23	estándar	44	3.15	niña	no instrum.
4	4	VIMU	2001-06-18	2001-06-23	2001-12-17	intensivo	25	2.74	niño	instrument.
5	5	PAVI	2001-06-19	2001-06-25	2001-06-26	estándar	27	3.60	niña	no instrum.
6	6	PASA	2001-06-20	2001-07-01	2001-06-27	estándar	36	2.65	niña	instrument.

	hermanos	fuma_an	fuma_de	horas_an	horas_de	naci_ca	masde12	sem_lac
1	no	si	no	6	2	sudamérica	no	6
2	si	no	no	2	2	española	si	35
3	si	no	si	3	0	española	no	1
4	si	si	si	11	6	otras	si	26
5	si	si	no	10	22	española	no	1
6	no	no	no	9	9	española	no	1

- Stata version >12 are not supported. You can use readstata13

```
library(readstata13)
```

SPSS

- ▶ To read SPSS (.sav) files, use `spss.get` function from `Hmisc` package.
- ▶ `use.value.labels`: return the label instead of codes.
- ▶ `datevars`: specify date format variables.

```
df <- spss.get("data/parto2.sav", use.value.labels=TRUE, allow="_",  
              datevars=c("dia_nac", "dia_entr", "ulti_lac"))  
head(df)
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
1	10	JUNA	2001-06-23	2001-07-02	2001-09-29	Intensivo	32	2.10	niña
2	9	BEMI	2001-06-22	2001-07-05	2001-08-31	Estándar	40	2.40	niña
3	2	CAEL	2001-06-15	2001-06-21	2002-02-15	Intensivo	27	2.50	niño
4	6	PASA	2001-06-20	2001-07-01	2001-06-27	Estándar	36	2.65	niña
5	19	TOPO	2001-07-19	2001-07-26	2001-10-11	Estándar	29	2.65	niña
6	4	VIMU	2001-06-18	2001-06-23	2001-12-17	Intensivo	25	2.74	niño

	tip_par	hermanos
1	no instrum.	no
2	no instrum.	no
3	no instrum.	si
4	instrument.	no
5	no instrum.	no
6	instrument.	si

Export data

ASCII, Excel, Stata

► ASCII file

```
write.table(df, "parto2ex.dat")
```

► Stata

```
write.dta(df, file="c:/juan/data/bd.dta"), version=7L  
save.dta13(df, file="c:/juan/data/bd.dta")
```

► Objects

Save:

```
save(df, file="c:/juan/data/bd.Rdata")) # or .rda
```

Load:

```
load("c:/juan/data/bd.Rdata")) # an object df will be in R
```

R basics

Read the data

- ▶ Read the data from a SPSS data file
- ▶ Hmisc package is required

```
library(Hmisc)
df <- spss.get("data/partoFin.sav", allow="_",
               datevars=c("dia_nac", "dia_entr", "ulti_lac"))
```

Take a look at first rows

```
head(df)
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
1	1	GADI	2001-06-14	2001-06-19	2001-07-26	Intensivo	24	3.38	niña
2	2	CAEL	2001-06-15	2001-06-21	2002-02-15	Intensivo	27	2.50	niño
3	3	COMO	2001-06-16	2001-07-01	2001-06-23	Estándar	44	3.15	niña
4	4	VIMU	2001-06-18	2001-06-23	2001-12-17	Intensivo	25	2.74	niño
5	5	PAVI	2001-06-19	2001-06-25	2001-06-26	Estándar	27	3.60	niña
6	6	PASA	2001-06-20	2001-07-01	2001-06-27	Estándar	36	2.65	niña

	tip_par	hermanos	fuma_an	fuma_de	horas_an	horas_de	naci_ca	masde12
1	instrument.	no	Si	No	6	2	Sudamérica	No
2	no instrum.	si	No	No	2	2	Española	Si
3	no instrum.	si	No	Si	3	0	Española	No
4	instrument.	si	Si	Si	11	6	Otras	Si
5	no instrum.	si	Si	No	10	22	Española	No
6	instrument.	no	No	No	9	9	Española	No

sem_lac

Explore data

- How many rows and variables

```
nrow(df)
```

```
[1] 28
```

```
ncol(df)
```

```
[1] 18
```

- View names

```
names(df)
```

```
[1] "id"      "ini"      "dia_nac"  "dia_entr" "ulti_lac" "tx"  
[7] "edad"    "peso"     "sexo"     "tip_par"  "hermanos" "fuma_an"  
[13] "fuma_de" "horas_an" "horas_de" "naci_ca"  "masde12"  "sem_lac"
```

► Summary of all variables

```
summary(df)
```

id		ini	dia_nac		dia_entr
Min.	: 1.00	ADJU : 1	Min.	:2001-06-14	Min. :2001-06-19
1st Qu.:	7.75	ANZO : 1	1st Qu.:	2001-06-20	1st Qu.:2001-07-01
Median :	14.50	BEMI : 1	Median :	2001-07-13	Median :2001-07-20
Mean :	14.50	BOPE : 1	Mean :	2001-07-06	Mean :2001-07-14
3rd Qu.:	21.25	CAEL : 1	3rd Qu.:	2001-07-20	3rd Qu.:2001-07-27
Max.	:28.00	CAGI : 1	Max.	:2001-07-25	Max. :2001-08-03

(Other) :22

ulti_lac		tx	edad		peso	sexo
Min.	:2001-06-23	Estándar :13	Min.	:17.00	Min. :2.100	niño:12
1st Qu.:	2001-08-05	Intensivo:15	1st Qu.:	24.75	1st Qu.:2.938	níña:16
Median :	2001-09-21		Median :	27.00	Median :3.260	
Mean :	2001-10-12		Mean :	29.29	Mean :3.208	
3rd Qu.:	2001-12-13		3rd Qu.:	35.00	3rd Qu.:3.470	
Max.	:2002-03-27		Max.	:44.00	Max. :4.460	

tip_par	hermanos	fuma_an	fuma_de	horas_an	horas_de
instrument.: 5	si:12	No:14	No:18	Min. : 2.000	Min. : 0.000
no instrum.:23	no:16	Si:14	Si:10	1st Qu.: 5.000	1st Qu.: 2.000
				Median : 7.000	Median : 5.500
				Mean : 7.429	Mean : 6.536
				3rd Qu.:10.000	3rd Qu.: 9.250
				Max. :12.000	Max. :23.000

naci_ca	masde12	sem_lac
Española :14	No:16	Min. : 1.00
Otras : 7	Si:12	1st Qu.: 2.75
Sudamérica: 7		Median :12.00
		Mean :13.96

Select variables

- Select a variable by its name

```
df$sexo
```

```
sexo de la criatura
```

```
[1] niña niño niña niño niña niña niño niño niña niña niño niña niña niño niño
```

```
[16] niño niño niña niña niña niña niño niño niña niña niña niño niña
```

```
Levels: niño niña
```

- Select a variable by its position

```
df[,2]
```

```
Iniciales del niño
```

```
[1] GADI CAEL COMO VIMU PAVI PASA VERI ADJU
```

```
[9] BEMI JUNA LOKO FRFU FUFU POCA LOLO BOPE
```

```
[17] ANZO MEVE TOPO PUPI ROPA LOMA CEMA CAGI
```

```
[25] GRSE GUMA PERI MAPE
```

```
28 Levels: ADJU ANZO BEMI BOPE CAEL CAGI ... VIMU
```

► Select some variables by names

```
df[,c("sexo", "peso", "edad")]
```

	sexo	peso	edad
1	niña	3.38	24
2	niño	2.50	27
3	niña	3.15	44
4	niño	2.74	25
5	niña	3.60	27
6	niña	2.65	36
7	niño	2.97	35
8	niño	3.20	23
9	niña	2.40	40
10	niña	2.10	32
11	niño	3.45	26
12	niña	3.45	29
13	niña	3.40	36
14	niño	3.05	36
15	niño	3.60	17
16	niño	3.40	40
17	niño	3.15	27
18	niña	3.32	32
19	niña	2.65	29
20	niña	4.46	21
21	niña	3.15	35
22	niño	3.70	27
23	niño	3.79	24
24	niña	3.75	18
25	niña	2.95	34
26	niña	2.90	27
27	niño	3.44	25
28	niña	3.53	24

► Select some variables by position

```
df[,c(1,3,5)]
```

	id	dia_nac	ulti_lac
1	1	2001-06-14	2001-07-26
2	2	2001-06-15	2002-02-15
3	3	2001-06-16	2001-06-23
4	4	2001-06-18	2001-12-17
5	5	2001-06-19	2001-06-26
6	6	2001-06-20	2001-06-27
7	7	2001-06-20	2001-09-12
8	8	2001-06-21	2001-09-13
9	9	2001-06-22	2001-08-31
10	10	2001-06-23	2001-09-29
11	11	2001-06-26	2001-08-21
12	12	2001-06-27	2002-03-06
13	13	2001-07-06	2001-07-13
14	14	2001-07-13	2001-11-09
15	15	2001-07-13	2001-07-20
16	16	2001-07-14	2002-01-19
17	17	2001-07-18	2001-12-05
18	18	2001-07-18	2002-03-27
19	19	2001-07-19	2001-10-11
20	20	2001-07-20	2001-10-12
21	21	2001-07-20	2001-08-17
22	22	2001-07-21	2002-03-02
23	23	2001-07-22	2001-08-12
24	24	2001-07-23	2001-07-30
25	25	2001-07-24	2001-08-07
26	26	2001-07-25	2001-12-12
27	27	2001-07-25	2002-01-16
28	28	2001-07-25	2001-11-14

Select rows

► Select a row

```
df[4,]
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
4	4	VIMU	2001-06-18	2001-06-23	2001-12-17	Intensivo	25	2.74	niño
		tip_par	hermanos	fuma_an	fuma_de	horas_an	horas_de	naci_ca	masde12
4	instrument.		si	Si	Si	11	6	Otras	Si
		sem_lac							
4		26							

► Select rows

```
df[4:10,]
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
4	4	VIMU	2001-06-18	2001-06-23	2001-12-17	Intensivo	25	2.74	niño
5	5	PAVI	2001-06-19	2001-06-25	2001-06-26	Estándar	27	3.60	niña
6	6	PASA	2001-06-20	2001-07-01	2001-06-27	Estándar	36	2.65	niña
7	7	VERI	2001-06-20	2001-06-30	2001-09-12	Intensivo	35	2.97	niño
8	8	ADJU	2001-06-21	2001-06-25	2001-09-13	Intensivo	23	3.20	niño
9	9	BEMI	2001-06-22	2001-07-05	2001-08-31	Estándar	40	2.40	niña
10	10	JUNA	2001-06-23	2001-07-02	2001-09-29	Intensivo	32	2.10	niña
		tip_par	hermanos	fuma_an	fuma_de	horas_an	horas_de	naci_ca	masde12
4	instrument.		si	Si	Si	11	6	Otras	Si
5	no instrument.		si	Si	No	10	22	Española	No
6	instrument.		no	No	No	9	9	Española	No

► Select rows by a condition, use subset

```
subset(df, sexo=="niña")
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
1	1	GADI	2001-06-14	2001-06-19	2001-07-26	Intensivo	24	3.38	niña
3	3	COMO	2001-06-16	2001-07-01	2001-06-23	Estándar	44	3.15	niña
5	5	PAVI	2001-06-19	2001-06-25	2001-06-26	Estándar	27	3.60	niña
6	6	PASA	2001-06-20	2001-07-01	2001-06-27	Estándar	36	2.65	niña
9	9	BEMI	2001-06-22	2001-07-05	2001-08-31	Estándar	40	2.40	niña
10	10	JUNA	2001-06-23	2001-07-02	2001-09-29	Intensivo	32	2.10	niña
12	12	FRFU	2001-06-27	2001-07-04	2002-03-06	Intensivo	29	3.45	niña
13	13	FUFE	2001-07-06	2001-07-17	2001-07-13	Estándar	36	3.40	niña
18	18	MEVE	2001-07-18	2001-07-27	2002-03-27	Intensivo	32	3.32	niña
19	19	TOPO	2001-07-19	2001-07-26	2001-10-11	Estándar	29	2.65	niña
20	20	PUPI	2001-07-20	2001-07-23	2001-10-12	Intensivo	21	4.46	niña
21	21	ROPA	2001-07-20	2001-07-30	2001-08-17	Estándar	35	3.15	niña
24	24	CAGI	2001-07-23	2001-07-25	2001-07-30	Intensivo	18	3.75	niña
25	25	GRSE	2001-07-24	2001-08-03	2001-08-07	Estándar	34	2.95	niña
26	26	GUMA	2001-07-25	2001-07-31	2001-12-12	Intensivo	27	2.90	niña
28	28	MAPE	2001-07-25	2001-07-30	2001-11-14	Estándar	24	3.53	niña

	tip_par	hermanos	fuma_an	fuma_de	horas_an	horas_de	naci_ca	masde12
1	instrument.	no	Si	No	6	2	Sudamérica	No
3	no instrum.	si	No	Si	3	0	Española	No
5	no instrum.	si	Si	No	10	22	Española	No
6	instrument.	no	No	No	9	9	Española	No
9	no instrum.	no	Si	Si	12	10	Española	No
10	no instrum.	no	Si	Si	7	0	Sudamérica	Si
12	no instrum.	si	Si	No	12	11	Sudamérica	Si
13	no instrum.	no	No	No	7	4	Española	No
18	no instrum.	no	Si	No	11	8	Otras	Si
19	no instrum.	no	No	Si	3	1	Española	No
20	no instrum.	no	Si	Si	7	0	Sudamérica	No

► More than one category

```
table(df$naci_ca)
```

```
Española      Otras Sudamérica  
14            7            7
```

```
subset(df, naci_ca%in%c("Española", "Otras"))
```

	id	ini	dia_nac	dia_entr	ulti_lac	tx	edad	peso	sexo
2	2	CAEL	2001-06-15	2001-06-21	2002-02-15	Intensivo	27	2.50	niño
3	3	COMO	2001-06-16	2001-07-01	2001-06-23	Estándar	44	3.15	niña
4	4	VIMU	2001-06-18	2001-06-23	2001-12-17	Intensivo	25	2.74	niño
5	5	PAVI	2001-06-19	2001-06-25	2001-06-26	Estándar	27	3.60	niña
6	6	PASA	2001-06-20	2001-07-01	2001-06-27	Estándar	36	2.65	niña
7	7	VERI	2001-06-20	2001-06-30	2001-09-12	Intensivo	35	2.97	niño
8	8	ADJU	2001-06-21	2001-06-25	2001-09-13	Intensivo	23	3.20	niño
9	9	BEMI	2001-06-22	2001-07-05	2001-08-31	Estándar	40	2.40	niña
13	13	FUFE	2001-07-06	2001-07-17	2001-07-13	Estándar	36	3.40	niña
14	14	POCA	2001-07-13	2001-07-24	2001-11-09	Intensivo	36	3.05	niño
16	16	BOPE	2001-07-14	2001-07-27	2002-01-19	Estándar	40	3.40	niño
17	17	ANZO	2001-07-18	2001-07-24	2001-12-05	Intensivo	27	3.15	niño
18	18	MEVE	2001-07-18	2001-07-27	2002-03-27	Intensivo	32	3.32	niña
19	19	TOPO	2001-07-19	2001-07-26	2001-10-11	Estándar	29	2.65	niña
21	21	ROPA	2001-07-20	2001-07-30	2001-08-17	Estándar	35	3.15	niña
22	22	LOMA	2001-07-21	2001-07-27	2002-03-02	Intensivo	27	3.70	niño
24	24	CAGI	2001-07-23	2001-07-25	2001-07-30	Intensivo	18	3.75	niña
25	25	GRSE	2001-07-24	2001-08-03	2001-08-07	Estándar	34	2.95	niña
26	26	GUMA	2001-07-25	2001-07-31	2001-12-12	Intensivo	27	2.90	niña
27	27	PERI	2001-07-25	2001-07-30	2002-01-16	Intensivo	25	3.44	niño

Descriptives

► Mean

```
mean(df$edad)
```

```
[1] 29.28571
```

► Standard deviation

```
sd(df$edad)
```

```
[1] 6.743211
```

► Median

```
median(df$edad)
```

```
[1] 27
```

► Percentiles

```
quantile(df$edad, c(0.25, 0.50, 0.75))
```

```
Edad de la madre  
25% 50% 75%  
24 27 35
```

► Pearson correlation

```
with(df, cor(peso, edad))
```

```
[1] -0.4747143
```

► Spearman correlation

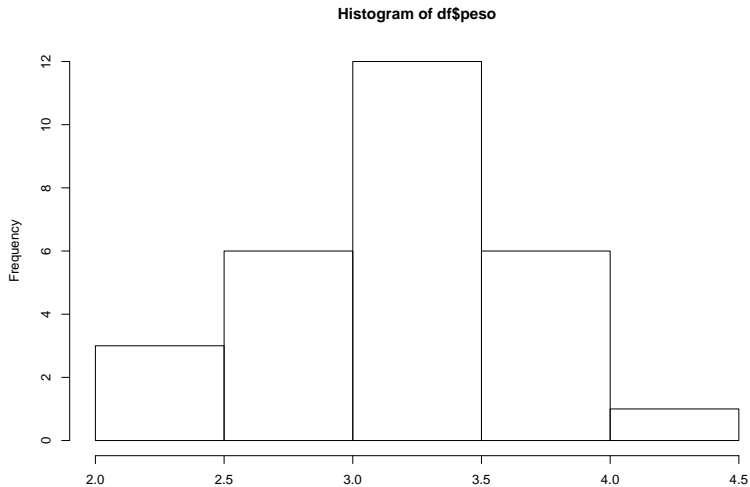
```
with(df, cor(peso, edad, method="spearman"))
```

```
[1] -0.5541522
```

Plots

► Histogram

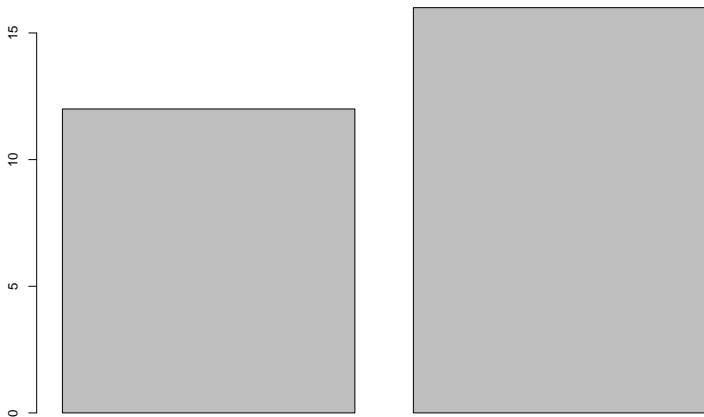
```
hist(df$peso)
```



► Barplot

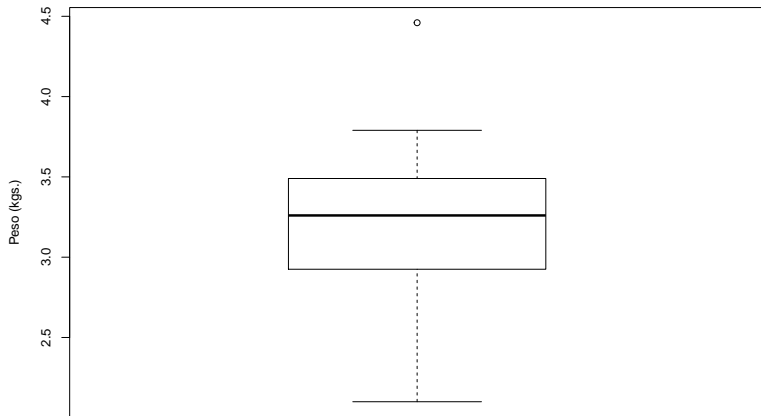
Note: The variable must be a factor or a character. If it is numeric (e.g. 0, 1) convert to a factor using `as.factor`.

```
plot(df$sexo)
```



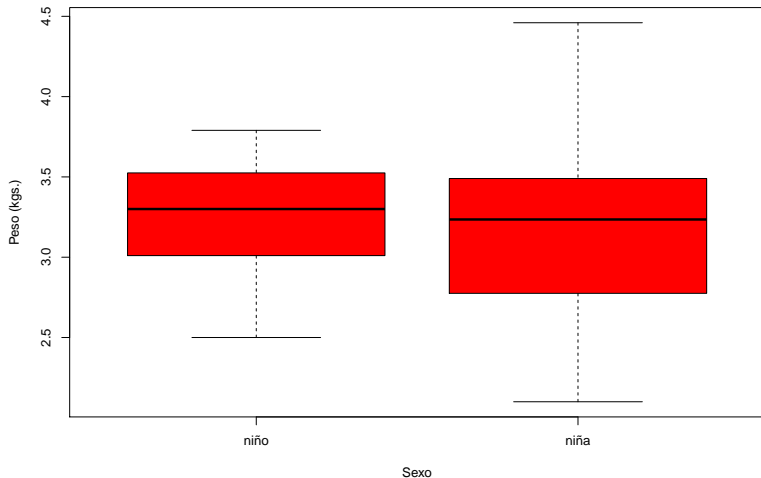
► Boxplot (I)

```
boxplot(df$peso, ylab="Peso (kgs.)")
```



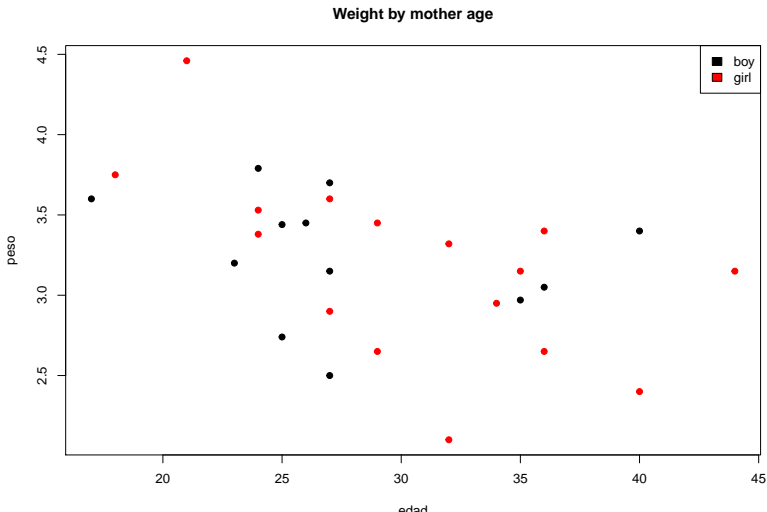
► Boxplot (II)

```
boxplot(peso ~ sexo , data=df, col="red",  
        ylab="Peso (kgs.)", xlab="Sexo")
```



► Scatterplot

```
plot(peso ~ edad, data=df, col=sexo, pch=19)  
title("Weight by mother age")  
legend("topright", c("boy", "girl"), fill=c(1,2))
```



Tests

► One sample test

```
t.test(df$peso, mu=4)
```

One Sample t-test

```
data: df$peso
t = -8.4635, df = 27, p-value = 4.471e-09
alternative hypothesis: true mean is not equal to 4
95 percent confidence interval:
 3.016260 3.400169
sample estimates:
mean of x
 3.208214
```


► Two independent sample test

```
t.test(peso ~ sexo, data=df)
```

Welch Two Sample t-test

```
data: peso by sexo
t = 0.39385, df = 25.82, p-value = 0.6969
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.3024945  0.4458278
sample estimates:
mean in group niño mean in group niña
      3.249167      3.177500
```

► Paired t-test

```
t.test(df$horas_an, df$horas_de, paired = TRUE)
```

Paired t-test

```
data: df$horas_an and df$horas_de
t = 0.88662, df = 27, p-value = 0.3831
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.173414  2.959128
sample estimates:
mean of the differences
      0.8928571
```

► Two proportions test

```
freq <- with(df, table(sexo, tip_par))  
fisher.test(freq)
```

Fisher's Exact Test for Count Data

```
data:  freq  
p-value = 1  
alternative hypothesis: true odds ratio is not equal to 1  
95 percent confidence interval:  
 0.06160374 9.21621060  
sample estimates:  
odds ratio  
 0.8710761
```

► Pearson correlation test

```
cor.test(df$peso, df$edad)
```

Pearson's product-moment correlation

```
data: df$peso and df$edad
t = -2.7502, df = 26, p-value = 0.01069
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7202342 -0.1235120
sample estimates:
      cor
-0.4747143
```

► Spearman correlation test

```
cor.test(df$peso, df$edad, method="spearman")
```

Spearman's rank correlation rho

```
data: df$peso and df$edad
S = 5678.9, p-value = 0.002215
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.5541522
```

Models

► Linear regression.

```
model <- lm(peso ~ edad, data=df)
summary(model)
```

Call:

```
lm(formula = peso ~ edad, data = df)
```

Residuals:

peso del niño

Min	1Q	Median	3Q	Max
-1.0136	-0.2515	0.0791	0.2519	0.9630

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.22882	0.38047	11.12	2.25e-11 ***
edad	-0.03485	0.01267	-2.75	0.0107 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.444 on 26 degrees of freedom

Multiple R-squared: 0.2254, Adjusted R-squared: 0.1956

F-statistic: 7.564 on 1 and 26 DF, p-value: 0.01069

- Logistic regression: predict type of treatment by mother age.

```
model <- glm(tip_par ~ edad, data=df, family="binomial")
summary(model)
```

Call:

```
glm(formula = tip_par ~ edad, family = "binomial", data = df)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.8637	0.6191	0.6251	0.6301	0.6406

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.618956	2.240114	0.723	0.470
edad	-0.003167	0.074386	-0.043	0.966

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 26.276 on 27 degrees of freedom
Residual deviance: 26.275 on 26 degrees of freedom
AIC: 30.275

Number of Fisher Scoring iterations: 4

Note: Estimate are the log-OR, or the coefficients

Scripting

Normally each execution is stored in an object and it is passed to the next core. For instance, let us assume we are interested in predicting the type of treatment by mother age only for those who received intensive treatment

```
sel <- df$tx=="Intensivo"  
sel[1:6]
```

```
[1] TRUE TRUE FALSE TRUE FALSE FALSE
```

```
df.intensive <- df[sel,]  
model.int <- glm(tip_par ~ edad, data=df.intensive,  
                 family="binomial")  
summary(model.int)
```

Call:

```
glm(formula = tip_par ~ edad, family = "binomial", data = df.intensive)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.6749	-0.4125	0.7620	0.7945	0.8857

Coefficients:

Estimate	Std. Error	z value	Pr(> z)
----------	------------	---------	----------

Dealing with multiple tables

- The simplest way of managing multiple table are lists

```
load("data/russett.Rdata")  
head(X_agric)
```

	gini	farm	rent
Argentina	86.3	98.2	3.52
Australia	92.9	99.6	3.27
Austria	74.0	97.4	2.46
Belgium	58.7	85.8	4.15
Bolivia	93.8	97.7	3.04
Brasil	83.7	98.5	2.31

```
head(X_ind)
```

	gnpr	labo
Argentina	5.92	3.22
Australia	7.10	2.64
Austria	6.28	3.47
Belgium	6.92	2.30
Bolivia	4.19	4.28
Brasil	5.57	4.11

```
head(X_polit)
```

	demostab	dictator
Argentina	0	0
Australia	1	0
Austria	0	0
Belgium	1	0
Bolivia	0	1
Brasil	0	0

```
X <- list(tab1 = X_agric, tab2 = X_ind, tab3 = X_polit)
length(X)
```

```
[1] 3
```

```
head(X[[1]])
```

	gini	farm	rent
Argentina	86.3	98.2	3.52
Australia	92.9	99.6	3.27
Austria	74.0	97.4	2.46
Belgium	58.7	85.8	4.15
Bolivia	93.8	97.7	3.04
Brasil	83.7	98.5	2.31

and more ...

- ▶ Creating functions
- ▶ Loops
- ▶ Parallel computing
- ▶ Create new packages
- ▶ Create new types of data (e.g. omic)
- ▶ ...

R facilitates data description and reproducible research

► Patients characteristics comparison

Characteristics	Cases (<i>n</i> = 416) %	Controls (<i>n</i> = 1156) %	Value of <i>p</i> ^a
Han race	97.58	96.39	0.25
Education			
None/elementary/high school	71.57	69.24	
Professional/college+	28.43	30.76	0.38
Occupation status			
Physical work	55.42	50.18	
Mental work	44.58	49.82	0.07
BMI [kg/m ²]			
Mean ± SD	23.77 ±3.60	23.21 ±2.93	0.01
≥ 24	41.71	34.93	0.05

Figure 5: Baseline comparison table of a standard case-control study

► Odds ratio estimation

Food group	Odds ratio (95% CI) for		
	Colon cancer	Rectal cancer	Colon and rectal cancers
Refined grain	1.46(1.20–1.78)	1.21(0.99–1.49)	1.32(1.12–1.56)
Whole grain	0.92(0.80–1.07)	0.86(0.72–1.02)	0.85(0.75–0.97)
Red meat	1.63(1.30–2.04)	1.50(1.20–1.88)	1.54(1.28–1.85)
Pork and processed meat	1.34(1.17–1.53)	1.18(1.02–1.37)	1.27(1.13–1.43)
Cheese	1.10(0.99–1.22)	1.07(0.94–1.21)	1.09(0.98–1.22)
Raw vegetables	0.90(0.76–1.07)	0.84(0.69–1.01)	0.85(0.74–0.98)
Cooked vegetables	0.69(0.54–0.88)	0.78(0.61–0.99)	0.69(0.57–0.83)
Citrus fruit	0.90(0.79–1.03)	0.84(0.72–0.98)	0.86(0.78–0.96)
Other fruits	0.84(0.71–0.99)	0.87(0.74–1.03)	0.85(0.75–0.96)
Alcohol	1.22(1.04–1.43)	1.38(1.16–1.63)	1.28(1.11–1.48)
Coffee	0.71(0.55–0.92)	0.79(0.62–1.00)	0.73(0.60–0.88)

*Adjusted for age, sex, education, smoking, alcohol, body mass index, physical activity and total energy intake.

##

compareGroups

compareGroups is an R package available on CRAN to create descriptive tables

It consists of three key functions:

1. `compareGroups~` generates all the calculation
2. `createTable~` creates the descriptive table obtained by `compareGroups`. You can customize it by excluding categories, 44 / 69

Example

PREDIMED project: <http://www.cat.isciii.es/ISCIIII/es/contenidos/fd-el-instituto/fd-comunicacion/fd-noticias/PREDIMED-2013.pdf>

1. Load the package and the example data existing in compareGroups package

```
library(compareGroups)
data(predimed)
# ?predimed
```

```
head(predimed)
```

	group	sex	age	smoke	bmi	waist	wth	htn	diab	hyperchol
1	Control	Male	58	Former	33.53	122	0.7530864	No	No	Yes
2	Control	Male	77	Current	31.05	119	0.7300614	Yes	Yes	No
4	MedDiet + VOO	Female	72	Former	30.86	106	0.6543210	No	Yes	No
5	MedDiet + Nuts	Male	71	Former	27.68	118	0.6941177	Yes	No	Yes
6	MedDiet + VOO	Female	79	Never	35.94	129	0.8062500	Yes	No	Yes
8	Control	Male	63	Former	41.66	143	0.8033708	Yes	Yes	Yes

	famhist	hormo	p14	toevent	event
1	No	No	10	5.374401	Yes
2	No	No	10	6.097194	No
4	Yes	No	8	5.946612	No
5	No	No	8	2.907598	Yes

2. Compute descriptives and other figures by treatment group

- ▶ Use of formula environment to select variables.
- ▶ On left hand side write the variable indicating groups (nothing indicates that descriptive analyses will be performed for the whole database).
- ▶ On the right side write all the variables you want to describe by the grouping variable

```
descr <- compareGroups(group ~ sex + age + smoke, predimed)
descr
```

```
----- Summary of results by groups of 'Intervention group'-----
```

	var	N	p.value	method	selection
1	Sex	6324	<0.001**	categorical	ALL
2	Age	6324	0.003**	continuous	normal ALL
3	Smoking	6324	0.444	categorical	ALL

```
-----
```

```
Signif. codes:  0 '***' 0.05 '*' 0.1 ' ' 1
```

- If you are interested in describing all variables use `'`

```
descr <- compareGroups(group ~ ., predimed)
descr
```

----- Summary of results by groups of 'Intervention group'-----

	var	N	p.value	method	selection
1	Sex	6324	<0.001**	categorical	ALL
2	Age	6324	0.003**	continuous normal	ALL
3	Smoking	6324	0.444	categorical	ALL
4	Body mass index	6324	<0.001**	continuous normal	ALL
5	Waist circumference	6324	0.045**	continuous normal	ALL
6	Waist-to-height ratio	6324	<0.001**	continuous normal	ALL
7	Hypertension	6324	0.249	categorical	ALL
8	Type-2 diabetes	6324	0.017**	categorical	ALL
9	Dyslipidemia	6324	0.423	categorical	ALL
10	Family history of premature CHD	6324	0.581	categorical	ALL
11	Hormone-replacement therapy	5661	0.850	categorical	ALL
12	MeDiet Adherence score	6324	<0.001**	continuous normal	ALL
13	follow-up to main event (years)	6324	<0.001**	continuous normal	ALL
14	AMI, stroke, or CV Death	6324	0.064*	categorical	ALL

Signif. codes: 0 '**' 0.05 '*' 0.1 ' ' 1

- If you are interested in describing all variables but a subset of them use '-' (this is useful when having variables such as 'id', 'hc', 'name', ...)

```
descr2 <- compareGroups(group ~ . -sex -age -event, predimed)
descr2
```

----- Summary of results by groups of 'Intervention group'-----

	var	N	p.value	method	selection
1	Smoking	6324	0.444	categorical	ALL
2	Body mass index	6324	<0.001**	continuous normal	ALL
3	Waist circumference	6324	0.045**	continuous normal	ALL
4	Waist-to-height ratio	6324	<0.001**	continuous normal	ALL
5	Hypertension	6324	0.249	categorical	ALL
6	Type-2 diabetes	6324	0.017**	categorical	ALL
7	Dyslipidemia	6324	0.423	categorical	ALL
8	Family history of premature CHD	6324	0.581	categorical	ALL
9	Hormone-replacement therapy	5661	0.850	categorical	ALL
10	MeDiet Adherence score	6324	<0.001**	continuous normal	ALL
11	follow-up to main event (years)	6324	<0.001**	continuous normal	ALL

Signif. codes: 0 '***' 0.05 '*' 0.1 ' ' 1

3. Build the descriptive table.

```
descrtable <- createTable(descr)
descrtable
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + VOO N=2182	p.overall
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001
Hypertension:				0.249
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	
Type-2 diabetes:				0.017
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)	
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	
Dyslipidemia:				0.423
No	563 (27.6%)	561 (26.7%)	622 (28.5%)	
Yes	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	
Family history of premature CHD:				0.581

Customizing results

- Hide 'No' category

```
update(descrtable, hide.no='no')
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.017
Dyslipidemia	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	0.423
Family history of premature CHD	462 (22.6%)	460 (21.9%)	507 (23.2%)	0.581
Hormone-replacement therapy	31 (1.68%)	30 (1.61%)	36 (1.84%)	0.850
MeDiet Adherence score	8.44 (1.94)	8.81 (1.90)	8.77 (1.97)	<0.001
follow-up to main event (years)	4.09 (1.74)	4.31 (1.70)	4.64 (1.60)	<0.001
AMI, stroke, or CV Death	97 (4.75%)	70 (3.33%)	85 (3.90%)	0.064

► Show number of valid data

```
update(descrtable, hide.no='no', show.n = TRUE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + VOO N=2182	p.overall	N
Sex:				<0.001	6324
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)		
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)		
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	6324
Smoking:				0.444	6324
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)		
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)		
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)		
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001	6324
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045	6324
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001	6324
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249	6324
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.017	6324
Dyslipidemia	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	0.423	6324
Family history of premature CHD	462 (22.6%)	460 (21.9%)	507 (23.2%)	0.581	6324
Hormone-replacement therapy	31 (1.68%)	30 (1.61%)	36 (1.84%)	0.850	5661
MedDiet Adherence score	8.44 (1.94)	8.81 (1.90)	8.77 (1.97)	<0.001	6324
follow-up to main event (years)	4.09 (1.74)	4.31 (1.70)	4.64 (1.60)	<0.001	6324
AMI, stroke, or CV Death	97 (4.75%)	70 (3.33%)	85 (3.90%)	0.064	6324

► Show only relative percentages

```
update(descrtable, hide.no='no', show.n = TRUE, type=1)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + VOO N=2182	p.overall	N
Sex:				<0.001	6324
Male	39.8%	46.1%	41.2%		
Female	60.2%	53.9%	58.8%		
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	6324
Smoking:				0.444	6324
Never	62.8%	60.0%	61.9%		
Current	13.2%	14.1%	13.4%		
Former	24.0%	26.0%	24.7%		
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001	6324
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045	6324
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001	6324
Hypertension	83.8%	82.8%	81.9%	0.249	6324
Type-2 diabetes	47.5%	45.2%	49.6%	0.017	6324
Dyslipidemia	72.4%	73.3%	71.5%	0.423	6324
Family history of premature CHD	22.6%	21.9%	23.2%	0.581	6324
Hormone-replacement therapy	1.68%	1.61%	1.84%	0.850	5661
MeDiet Adherence score	8.44 (1.94)	8.81 (1.90)	8.77 (1.97)	<0.001	6324
follow-up to main event (years)	4.09 (1.74)	4.31 (1.70)	4.64 (1.60)	<0.001	6324
AMI, stroke, or CV Death	4.75%	3.33%	3.90%	0.064	6324

Customizing descriptives (tests)

- By default, compareGroups report means and SD, and performs t-test or ANOVA for continuous variables.
- To report medians and quartiles and perform Kruskal-Wallis tests for continuous variable:

```
descr <- update(descr, method=2)
createTable(descr, hide.no="no")
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.0 [62.0;72.0]	66.0 [62.0;71.0]	67.0 [62.0;72.0]	0.003
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.0 [27.5;32.8]	29.5 [26.9;32.2]	29.7 [27.2;32.4]	<0.001
Waist circumference	101 [94.0;108]	100 [93.0;107]	100 [93.0;107]	0.085
Waist-to-height ratio	0.63 [0.59;0.68]	0.62 [0.58;0.66]	0.62 [0.58;0.67]	<0.001
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249

► Change number of decimals

```
update(descrtable, hide.no='no', digits=1, digits.p=5)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Sex:				0.00008
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.0 [62.0;72.0]	66.0 [62.0;71.0]	67.0 [62.0;72.0]	0.00299
Smoking:				0.44435
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.0 [27.5;32.8]	29.5 [26.9;32.2]	29.7 [27.2;32.4]	0.00002
Waist circumference	101.0 [94.0;108.0]	100.0 [93.0;107.0]	100.0 [93.0;107.0]	0.08460
Waist-to-height ratio	0.6 [0.6;0.7]	0.6 [0.6;0.7]	0.6 [0.6;0.7]	0.00019
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.24876
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.01725
Dyslipidemia	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	0.42297
Family history of premature CHD	462 (22.6%)	460 (21.9%)	507 (23.2%)	0.58131
Hormone-replacement therapy	31 (1.7%)	30 (1.6%)	36 (1.8%)	0.85009
MeDiet Adherence score	8.0 [7.0;10.0]	9.0 [8.0;10.0]	9.0 [8.0;10.0]	<0.00001
follow-up to main event (years)	4.2 [2.7;5.6]	4.7 [2.8;5.8]	5.0 [3.4;5.9]	<0.00001
AMI, stroke, or CV Death	97 (4.8%)	70 (3.3%)	85 (3.9%)	0.06386

► Perform medians and quantiles for some variables:

```
descr <- update(descr, method=c(age=2, p14=2))
createTable(descr, hide.no="no")
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.0 [62.0;72.0]	66.0 [62.0;71.0]	67.0 [62.0;72.0]	0.003
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.017
Dyslipidemia	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	0.423
Family history of premature CHD	462 (22.6%)	460 (21.9%)	507 (23.2%)	0.581
Hormone-replacement therapy	31 (1.68%)	30 (1.61%)	36 (1.84%)	0.850
MedDiet Adherence score	8.00 [7.00;10.0]	9.00 [8.00;10.0]	9.00 [8.00;10.0]	<0.001
follow-up to main event (years)	4.09 (1.74)	4.31 (1.70)	4.64 (1.60)	<0.001
AMI, stroke, or CV Death	97 (4.75%)	70 (3.33%)	85 (3.90%)	0.064

Odds Ratio

- ▶ Place the case/control variable on left hand side.
- ▶ It computes the Odds Ratio (OR) of being a case (second category). To change reference category, use `ref.y` argument from `compareGroups` function.
- ▶ Let's report the OR of being hyperchol

```
table(predimed$hyperchol)
```

No	Yes
1746	4578


```
descr <- compareGroups(hyperchol ~ ., predimed)
createTable(descr, hide.no="no", show.ratio=TRUE,
             show.p.overall=FALSE, show.p.trend = FALSE)
```

-----Summary descriptives table by 'Dyslipidemia'-----

	No N=1746	Yes N=4578	OR	p.ratio
Intervention group:				
Control	563 (32.2%)	1479 (32.3%)	Ref.	Ref.
MedDiet + Nuts	561 (32.1%)	1539 (33.6%)	1.04 [0.91;1.20]	0.536
MedDiet + VOO	622 (35.6%)	1560 (34.1%)	0.95 [0.83;1.09]	0.499
Sex:				
Male	906 (51.9%)	1773 (38.7%)	Ref.	Ref.
Female	840 (48.1%)	2805 (61.3%)	1.71 [1.53;1.91]	0.000
Age	67.6 (6.23)	66.8 (6.14)	0.98 [0.97;0.99]	<0.001
Smoking:				
Never	980 (56.1%)	2912 (63.6%)	Ref.	Ref.
Current	291 (16.7%)	567 (12.4%)	0.66 [0.56;0.77]	<0.001
Former	475 (27.2%)	1099 (24.0%)	0.78 [0.68;0.89]	<0.001
Body mass index	30.0 (3.89)	29.9 (3.79)	0.99 [0.98;1.01]	0.353
Waist circumference	101 (10.4)	100.0 (10.6)	0.99 [0.98;0.99]	<0.001
Waist-to-height ratio	0.63 (0.07)	0.63 (0.07)	0.49 [0.21;1.13]	0.096
Hypertension	1337 (76.6%)	3898 (85.1%)	1.75 [1.53;2.01]	<0.001
Type-2 diabetes	1222 (70.0%)	1780 (38.9%)	0.27 [0.24;0.31]	0.000
Family history of premature CHD	409 (23.4%)	1020 (22.3%)	0.94 [0.82;1.07]	0.331
Hormone-replacement therapy	26 (1.65%)	71 (1.74%)	1.05 [0.67;1.68]	0.844
MeDiet Adherence score	8.68 (1.90)	8.68 (1.96)	1.00 [0.97;1.03]	0.995
follow-up to main event (years)	4.59 (1.63)	4.26 (1.71)	0.89 [0.86;0.92]	<0.001
AMI, stroke, or CV Death	101 (5.78%)	151 (3.30%)	0.56 [0.43;0.72]	<0.001

Hazard Ratios

- ▶ PREDIMED is a cohort study with time-to-event outcome.
- ▶ Descriptives by cases and controls, HR taking into account time-to-event response (with possible right censoring) and p-values are easily computed

1. First, create a Surv variable

```
predimed$tevent <- with(predimed, Surv(toevent, event=="Yes"))
```

2. Then write this variable on left side of ~ in compareGroups.

Note the use of - to erase some variables.

```
descr <- compareGroups(tevent ~ .- toevent-event, predimed)
createTable(descr, hide.no="no", show.ratio=TRUE,
            show.p.overall=FALSE)
```

-----Summary descriptives table by 'tevent'-----

	No event N=6072	Event N=252	HR	p.ratio
Intervention group:				
Control	1945 (32.0%)	97 (38.5%)	Ref.	Ref.
MedDiet + Nuts	2030 (33.4%)	70 (27.8%)	0.66 [0.48;0.89]	0.008
MedDiet + VOO	2097 (34.5%)	85 (33.7%)	0.70 [0.53;0.94]	0.018
Sex:				
Male	2528 (41.6%)	151 (59.9%)	Ref.	Ref.
Female	3544 (58.4%)	101 (40.1%)	0.49 [0.38;0.63]	<0.001
Age	66.9 (6.14)	69.4 (6.65)	1.06 [1.04;1.09]	<0.001
Smoking:				
Never	3778 (62.2%)	114 (45.2%)	Ref.	Ref.
Current	809 (13.3%)	49 (19.4%)	1.96 [1.40;2.74]	<0.001

Utilities

- use `label` function from `Hmisc` package to label variables

```
label(predimed$age) <- "Age of participant"
```

- To know the original variable names (instead of labels)

```
descrtable <- createTable(compareGroups(group ~ ., predimed))  
varinfo(descrtable)
```

--- Analyzed variable names ----

	Orig varname	Shown varname
1	group	Intervention group
2	sex	Sex
3	age	Age of participant
4	smoke	Smoking
5	bmi	Body mass index
6	waist	Waist circumference
7	wth	Waist-to-height ratio
8	htn	Hypertension
9	diab	Type-2 diabetes
10	hyperchol	Dyslipidemia
11	famhist	Family history of premature CHD
12	hormo	Hormone-replacement therapy
13	p14	MeDiet Adherence score
14	toevent	follow-up to main event (years)

- To select some variables use [], indexing by names or by position

```
descrtable <- createTable(compareGroups(group ~ ., predimed))
descrtable[c('age', 'bmi')]
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age of participant	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001

```
descrtable[c(1,4)]
```

-----Summary descriptives table by 'Intervention group'-----

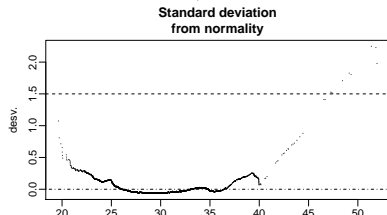
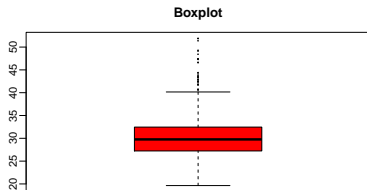
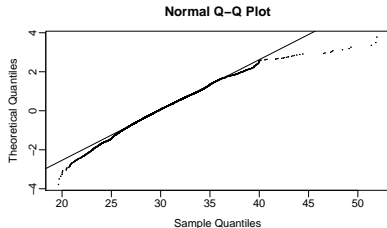
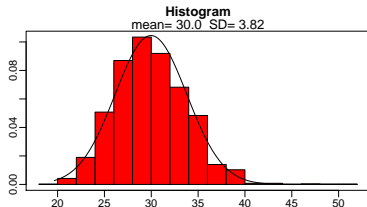
	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001

Plotting variables

► Continuous univariate

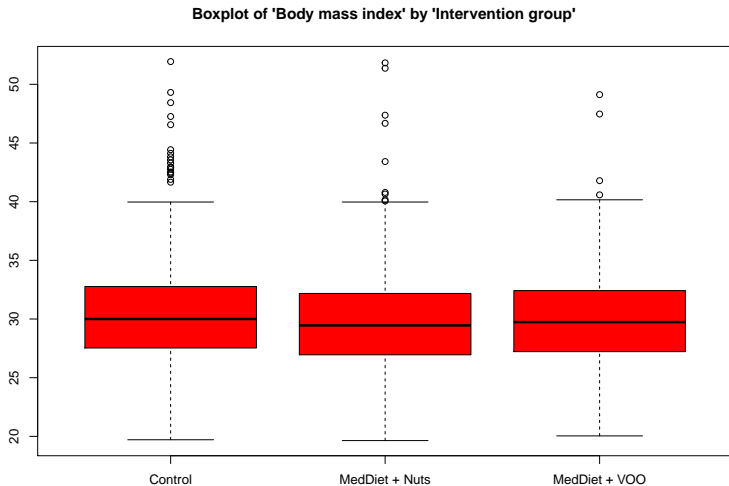
```
descr <- compareGroups(group ~ ., predimed)
plot(descr['bmi'])
```

Normality plots of 'Body mass index'



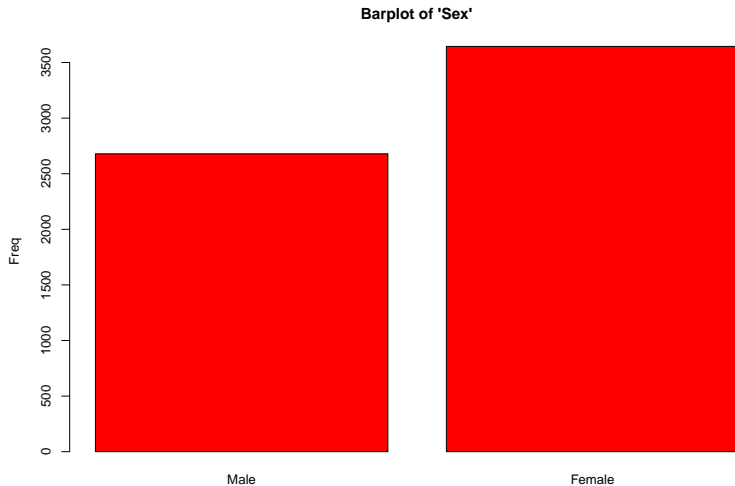
► Continuous by groups

```
plot(descr['bmi'], bivar=TRUE)
```



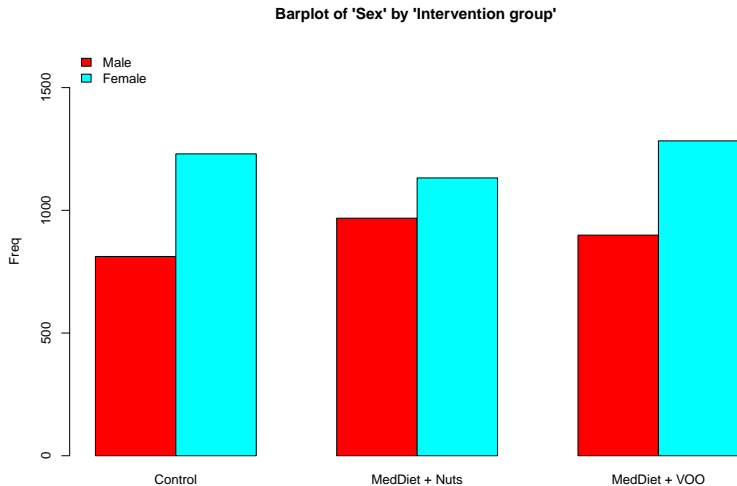
► Categorical variable

```
plot(descr['sex'])
```



► Categorical by groups

```
plot(descr['sex'], bivar=TRUE)
```



Export

```
# CSV
export2csv(descrtable, file="tabla.csv", sep=";")
# Excel
export2xls(descrtable, file="tabla.xlsx")
# Word
export2word(descrtable, file="tabla.docx")
# Latex
export2tex(descrtable, file="tabla.tex")
```

... or inside a **Rmarkdown** document chunk

```
export2md(descrtable)
```

Table 1: Summary descriptives table by groups o

	Control N=2042	MedDiet + Nuts
Sex:		
Male	812 (39.8%)	968 (46.1%)
Female	1230 (60.2%)	1132 (53.9%)
Age of participant	67.3 (6.28)	66.7 (6.02)

More

- ▶ There exists much more options
- ▶ See `?compareGroups`, `?createTable`, ...
- ▶ Visit `compareGroups` webpage
- ▶ Application made with Shiny available here

Session info

sessionInfo()

R version 3.4.1 (2017-06-30)

Platform: x86_64-w64-mingw32/x64 (64-bit)

Running under: Windows 10 x64 (build 15063)

Matrix products: default

locale:

[1] LC_COLLATE=Spanish_Spain.1252 LC_CTYPE=Spanish_Spain.1252

[3] LC_MONETARY=Spanish_Spain.1252 LC_NUMERIC=C

[5] LC_TIME=Spanish_Spain.1252

attached base packages:

[1] parallel stats graphics grDevices utils datasets methods

[8] base

other attached packages:

[1] compareGroups_3.3.1 SNPassoc_1.9-2 mvtnorm_1.0-6

[4] haplo.stats_1.7.7 xtable_1.8-2 gdata_2.18.0

[7] readxl_1.0.0 RODBC_1.3-15 foreign_0.8-69

[10] Hmisc_4.0-3 ggplot2_2.2.1 Formula_1.2-2

[13] survival_2.41-3 lattice_0.20-35

loaded via a namespace (and not attached):

[1] gtools_3.5.0 zoo_1.8-0 splines_3.4.1

[4] colorspace_1.3-2 htmltools_0.3.6 yaml_2.1.14

[7] base64enc_0.1-3 rlang_0.1.2 HardyWeinberg_1.5.8

[10] RColorBrewer_1.1-2 multcomp_1.4-7 plyr_1.8.4

[13] stringr_1.2.0 MatrixModels_0.4-1 munsell_0.4.3

[16] gtable_0.2.0 cellranger_1.1.0 htmlwidgets_0.9