stRutture di dati

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Vengono creati **c**oncatenando diverse variabili insieme

Si usa la funzione `c()`

Tutte le variaili all'interno della funzione `c()` vanno separate da una virgola

Diversi tipi di variabili $\rightarrow$ diversi tipi di vettori:

- `int`: vettori numerici (numeri interi)
- `num`: vettori numerici (numeri continui)
- `logi`: vettori logici
- `chr`: vettori character
- `factor`: vettori factor con diversi livelli

`int` & `num`

`int`: numeri interi: -3, -2, -1, 0, 1, 2, 3

```r
mesi = c(5, 6, 8, 10, 12, 16)
```

```
[1]  5  6  8 10 12 16
```

`num`: tutti i valori numerici tra $-\infty$ e $+\infty$: 1.0840991, 0.8431089, 0.494389, -0.7730161, 2.9038161, 0.9088839

```r
peso = seq(3, 11, by = 1.5)
```

```
[1]  3.0  4.5  6.0  7.5  9.0 10.5
```

logi

Valori logici possono essere veri TRUE (T) o falsi FALSE (F):

```
v_logi = c(TRUE, TRUE, FALSE, FALSE, TRUE)
```

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

Si usano per testare delle condizioni:

```
mesi > 12
```

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

chr & factor

chr: characters: a, b, c, D, E, F

```
v_chr = c(letters[1:3], LETTERS[4:6])
```

```
[1] "a" "b" "c" "D" "E" "F"
```

factor: Usa numeri o carattarri per identificare i livelli della variabile:

```
ses = factor(c(rep(c("low", "medium", "high"), each = 2)))
```

```
[1] low    low    medium medium high   high
Levels: high low medium
```

Si può cambaire l'ordine dei livelli:

```
ses1 = factor(ses, levels = c("medium", "high", "low"))
```

```
[1] low    low    medium medium high   high
Levels: medium high low
```

Creare i vettori

Concatenare le variabili con `c()`: `vec = c(1, 2, 3, 4, 5)`

Utilizzando le sequenze:

```
-5:5 # vector of 11 numbers from -5 to 5
```

```
 [1] -5 -4 -3 -2 -1  0  1  2  3  4  5
```

```
seq(-2.5, 2.5, by = 0.5) # sequence in steps of 0.5
```

```
 [1] -2.5 -2.0 -1.5 -1.0 -0.5  0.0  0.5  1.0  1.5  2.0  2.5
```

Ripetendo gli elementi:

```
rep(1:3, 4)
```

```
 [1] 1 2 3 1 2 3 1 2 3 1 2 3
```

Creare i vettori II

```r
rep(c("condA", "condB"), each = 3)
```

```
[1] "condA" "condA" "condA" "condB" "condB" "condB"
```

```r
rep(c("on", "off"), c(3, 2))
```

```
[1] "on"  "on"  "on"  "off" "off"
```

```r
paste0("item", 1:4)
```

```
[1] "item1" "item2" "item3" "item4"
```

Non mischiate i vettori! a meno che non lo vogliate davvero

$\texttt{int} + \texttt{num} \rightarrow \texttt{num}$

$\texttt{int/num} + \texttt{logi} \rightarrow \texttt{int/num}$

$\texttt{int/num} + \texttt{factor} \rightarrow \texttt{int/num}$

$\texttt{int/num} + \texttt{chr} \rightarrow \texttt{chr}$

$\texttt{chr} + \texttt{logi} \rightarrow \texttt{chr}$

Vettori e operazioni

I vettori possono essere sommati/divisi/moltiplicati tra di loro o anche per un numero singolo

```
a = c(1:8) # vettore di lunghezza 8
a
```

```
[1] 1 2 3 4 5 6 7 8
```

```
b = c(4:1) # vettore di lunghezza 4
b
```

```
[1] 4 3 2 1
```

```
a - b # il vettore b è "riciclato" sul vettore a
```

```
[1] -3 -1  1  3  1  3  5  7
```

Se i vettori non hanno la stessa lunghezza (o uno non è un multiplo dell'altro) ottenete un warning

Vettori e operazioni II

Applicando una funzione a un vettore → viene applicata a **tutti** gli elementi del vettore

```
sqrt(a)
```

```
[1] 1.000000 1.414214 1.732051 2.000000 2.236068 2.449490 2.6
```

La stessa operazione si può applicare a ogni singolo elemento del vettore

```
(a - mean(a))^2 # squared deviation
```

```
[1] 12.25  6.25  2.25  0.25  0.25  2.25  6.25 12.25
```

Indicizzare i vettori

Come si va a “raggiungere” un particolare elemento all’interno del vettore?

```
nomi = c("Pasquale", "Egidio", "Debora", "Luca", "Andrea")
```

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

Indicizzare i vettori

Come si va a “raggiungere” un particolare elemento all’interno del vettore?

```
nomi = c("Pasquale", "Egidio", "Debora", "Luca", "Andrea")
```

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

```
nome_vettore[indice]
```

Indicizzare i vettori II

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

Indicizzare i vettori II

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

`nomi[1]` $\rightarrow$

Indicizzare i vettori II

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

`nomi[1]` $\rightarrow$ Pasquale

`nomi[3]` $\rightarrow$

Indicizzare i vettori II

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

`nomi[1]` $\rightarrow$ Pasquale

`nomi[3]` $\rightarrow$ Debora

`nomi[seq(2, 5, by = 2)]` $\rightarrow$

Indicizzare i vettori II

Pasquale	Egidio	Debora	Luca	Andrea
1	2	3	4	5

`nomi[1]` → Pasquale

`nomi[3]` → Debora

`nomi[seq(2, 5, by = 2)]` → Egidio, Luca

Indicizzare i vettori: Esempi

```
peso
```

```
[1]  3.0  4.5  6.0  7.5  9.0 10.5
```

```
peso[2]        # secondo elemento del vettore peso
```

```
[1] 4.5
```

```
(peso[6] = 15.2) # sostituisce il sesto elemento del v. peso
```

```
[1] 15.2
```

```
peso[seq(1, 6, by = 2)] # elementi 1, 3, 5
```

```
[1] 3 6 9
```

```
peso[2:6]      # dal 2 al 6 elemento di peso
```

```
[1]  4.5  6.0  7.5  9.0 15.2
```

```
peso[-2]      # vettore peso senza il secondo elemento
```

Indicizzare i vettori usando la logica

```
peso[peso > 7] # valori in peso maggiori di 7
```

```
[1]  7.5  9.0 15.2
```

```
peso[peso >= 4.5 & peso < 8] # valori tra 4.5 e 8
```

```
[1] 4.5 6.0 7.5
```

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Un vettore che ci ha creduto abbastanza

Quel che basta per vincere una seconda dimensione

`matrix(data, nrow, ncol, byrow = TRUE)`

Crea una matrice 3×4 e la assegna all'oggetto `A`:

```
A = matrix(1:12, nrow=3, ncol = 4, byrow = FALSE)
A
```

```
     [,1] [,2] [,3] [,4]
[1,]    1    4    7   10
[2,]    2    5    8   11
[3,]    3    6    9   12
```

WARNING: i dati all'interno della matrice devono essere tutti dello stesso tipo

Etichette

```
rownames(A) = c(paste("riga", 1:nrow(A), sep = "_"))

colnames(A) = c(paste("colonna", 1:ncol(A), sep = "_"))

A
```

```
        colonna_1 colonna_2 colonna_3 colonna_4
riga_1          1         4         7        10
riga_2          2         5         8        11
riga_3          3         6         9        12
```

Trasposta della matrice:

```
A
```

```
        colonna_1 colonna_2 colonna_3 colonna_4
riga_1          1         4         7        10
riga_2          2         5         8        11
riga_3          3         6         9        12
```

```
t(A)
```

```
          riga_1 riga_2 riga_3
colonna_1      1      2      3
colonna_2      4      5      6
colonna_3      7      8      9
colonna_4     10     11     12
```

Creare le matrici (ancora)

Le matrici si possono anche creare concatenando vettori colonna:

```r
cbind(a1 = 1:4, a2 = 5:8, a3 = 9:12)
```

```
     a1 a2 a3
[1,]  1  5  9
[2,]  2  6 10
[3,]  3  7 11
[4,]  4  8 12
```

o vettori riga:

```r
rbind(a1 = 1:4, a2 = 5:8, a3 = 9:12)
```

```
   [,1] [,2] [,3] [,4]
a1    1    2    3    4
a2    5    6    7    8
a3    9   10   11   12
```

Indicizzare le matrici

Abbiamo due dimensioni:

	[,1]	[,2]	[,3]
[1,]	$1,1$	$1,2$	$1,3$
[2,]	$2,1$	$2,2$	$2,3$
[3,]	$3,1$	$3,2$	$3,3$

```
my_matrix[righe, colonne]
```

Indicizzare le matrici: In pratica

```
A
```

```
      colonna_1 colonna_2 colonna_3 colonna_4
riga_1         1         4         7        10
riga_2         2         5         8        11
riga_3         3         6         9        12
```

`A[1, ]` $\rightarrow$

`A[2, ]` $\rightarrow$

`A[2, 3]` $\rightarrow$

Indicizzare le matrici: In pratica

```
A
```

```
       colonna_1 colonna_2 colonna_3 colonna_4
riga_1         1         4         7        10
riga_2         2         5         8        11
riga_3         3         6         9        12
```

`A[1, ]` $\rightarrow$ 1, 4, 7, 10

`A[2, ]` $\rightarrow$

`A[2, 3]` $\rightarrow$

Indicizzare le matrici: In pratica

```
A
```

```
        colonna_1 colonna_2 colonna_3 colonna_4
riga_1          1         4         7        10
riga_2          2         5         8        11
riga_3          3         6         9        12
```

`A[1, ]` $\rightarrow$ 1, 4, 7, 10

`A[2, ]` $\rightarrow$ 2, 5, 8, 11

`A[2, 3]` $\rightarrow$

Indicizzare le matrici: In pratica

```
A
```

```
        colonna_1 colonna_2 colonna_3 colonna_4
riga_1          1         4         7        10
riga_2          2         5         8        11
riga_3          3         6         9        12
```

`A[1, ]` $\rightarrow$ 1, 4, 7, 10

`A[2, ]` $\rightarrow$ 2, 5, 8, 11

`A[2, 3]` $\rightarrow$ 8

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Una matrice che ci ha creduto davvero

Davvero troppo

```
array(data, c(nrow, ncol, ntab))
```

Avendo 3 argomenti oltre i dati `nrow, ncol, ntab`, la loro indicizzazione prevede l'utilizzo di due virgole per accedere ai singoli argomenti:
`nome_array[righe, colonne, tab]`

Un array

```
my_array = array(1:20, c(2, 5, 3)) # 2 x 5 x 3 array
my_array
```

```
, , 1

     [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    5    7    9
[2,]    2    4    6    8   10

, , 2

     [,1] [,2] [,3] [,4] [,5]
[1,]   11   13   15   17   19
[2,]   12   14   16   18   20

, , 3

     [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    5    7    9
[2,]    2    4    6    8   10
```

Indicizzare l’array

```
my_array[1, , ]
```

```
my_array[, 2, ]
```

```
my_array[, , 3]
```

Indicizzare l'array

```
my_array[1, , ]
```

```
     [,1] [,2] [,3]
[1,]    1   11    1
[2,]    3   13    3
[3,]    5   15    5
[4,]    7   17    7
[5,]    9   19    9
```

```
my_array[, 2, ]
```

```
my_array[, , 3]
```

Indicizzare l’array

```
my_array[1, , ]
```

```
     [,1] [,2] [,3]
[1,]    1   11    1
[2,]    3   13    3
[3,]    5   15    5
[4,]    7   17    7
[5,]    9   19    9
```

```
my_array[, 2, ]
```

```
     [,1] [,2] [,3]
[1,]    3   13    3
[2,]    4   14    4
```

```
my_array[, , 3]
```

Indicizzare l'array

```
my_array[1, , ]
```

```
     [,1] [,2] [,3]
[1,]    1   11    1
[2,]    3   13    3
[3,]    5   15    5
[4,]    7   17    7
[5,]    9   19    9
```

```
my_array[, 2, ]
```

```
     [,1] [,2] [,3]
[1,]    3   13    3
[2,]    4   14    4
```

```
my_array[, , 3]
```

```
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    3    5    7    9
[2,]    2    4    6    8   10
```

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Un array con più senso

Sono dei contenitori per diversi tipi di oggetti (e.g., vettori, data frames, altre liste, matrici, array ecc.)

Ai loro elementi possono essere assegnati dei nomi:

```
my_list = list(w = peso, m = mesi, s = ses1, a = A)
names(my_list)
```

```
[1] "w" "m" "s" "a"
```

```
str(my_list)
```

```
List of 4
 $ w: num [1:6] 3 4.5 6 7.5 9 15.2
 $ m: num [1:6] 5 6 8 10 12 16
 $ s: Factor w/ 3 levels "medium","high",..: 3 3 1 1 2 2
 $ a: int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:3] "riga_1" "riga_2" "riga_3"
  .. ..$ : chr [1:4] "colonna_1" "colonna_2" "colonna_3" "colonna_4
```

Indicizzare le liste

Gli elementi della lista possono essere indicizzati con $ (se la lista ha dei nomi):

```
my_list$m # vettore dei mesi
```

```
[1]  5  6  8 10 12 16
```

oppure con `[[]]`:

Nome dell'elemento

```
my_list[["m"]]
```

```
[1]  5  6  8 10 12 16
```

Posizione dell'elemento:

```
my_list[[2]]
```

```
[1]  5  6  8 10 12 16
```

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Una lista più ordinata

I data frames sono delle liste di vettori di uguale lunghezza

I diversi vettori possono contenere informazioni di diverse natura

I data frame più comuni sono i data frame in versione wide (i.e., *soggetti* $\times$ *variabili*) $\rightarrow$ `nrow(data)` $=$ numero di soggetti:

```
id = paste0("sbj", 1:6)
babies = data.frame(id, mesi, peso)
```

```
babies
```

```
    id mesi peso
1 sbj1    5  3.0
2 sbj2    6  4.5
3 sbj3    8  6.0
4 sbj4   10  7.5
5 sbj5   12  9.0
6 sbj6   16 15.2
```

Indicizzare i data frame

Vale tutto quello visto per le matrici:

Prima riga del data frame babies
`babies[1, ]`

Prima colonna del data frame babies
`babies[, 1]`

In più:

```
babies$mesi # colonna mesi di babies

babies$mesi[2] # secondo elemento del vettore colonna

babies[, "id"] # column id

babies[2, ] # second row of babies (obs on baby 2)
```

Logic applies:

```
babies[babies$peso > 7, ] # filtra per tutte le righe con pes
```

Working with data frames II

```
dim(babies) # data frame con 6 righe e 3 colonne
```

```
[1] 6 3
```

```
names(babies) # = colnames(babies)
```

```
[1] "id"   "mesi" "peso"
```

```
View(babies) # open data viewer
```

Questi comandi possono essere usati anche su altri oggetti `R`

Working with data frames III

```
str(babies) # show details on babies
```

```
'data.frame':   6 obs. of  3 variables:
 $ id  : chr  "sbj1" "sbj2" "sbj3" "sbj4" ...
 $ mesi: num  5 6 8 10 12 16
 $ peso: num  3 4.5 6 7.5 9 15.2
```

```
summary(babies) # descriptive statistics
```

```
      id                  mesi            peso       
 Length:6           Min.   : 5.0   Min.   : 3.000  
 Class :character   1st Qu.: 6.5   1st Qu.: 4.875  
 Mode  :character   Median : 9.0   Median : 6.750  
                    Mean   : 9.5   Mean   : 7.533  
                    3rd Qu.:11.5   3rd Qu.: 8.625  
                    Max.   :16.0   Max.   :15.200  
```

Sorting

order():

```
babies[order(babies$peso), ] # sort by increasing peso
```

```
    id mesi peso
1 sbj1    5  3.0
2 sbj2    6  4.5
3 sbj3    8  6.0
4 sbj4   10  7.5
5 sbj5   12  9.0
6 sbj6   16 15.2
```

```
babies[order(babies$peso,    # sort by decreasing peso
             decreasing = T), ]
```

Multiple arguments in order:

```
babies[order(babies$peso, babies$mesi, decreasing = TRUE), ]
```

Aggregating

Aggregate a response variable according to grouping variable(s) (e.g., averaging per experimental conditions):

```r
# Single response variable, single grouping variable
aggregate(y ~ x, data = data, FUN, ...)

# Multiple response variables, multiple grouping variables
aggregate(cbind(y1, y2) ~ x1 + x2, data = data, FUN, ...)
```

Aggregating: Example

```
ToothGrowth # Vitamin C and tooth growth (Guinea Pigs)
```

```
    len supp dose
1   4.2   VC  0.5
2  11.5   VC  0.5
3   7.3   VC  0.5
....
```

```
aggregate(len ~ supp + dose, data = ToothGrowth, mean)
```

```
  supp dose   len
1   OJ  0.5 13.23
2   VC  0.5  7.98
3   OJ  1.0 22.70
4   VC  1.0 16.77
5   OJ  2.0 26.06
6   VC  2.0 26.14
```

Reshaping: Long to wide

Data can be organized in wide format (i.e., one line for each statistical unit) or in long format (i.e., one line for each observation).

```
Indometh # Long format
```

```
   Subject time conc
1        1 0.25 1.50
2        1 0.50 0.94
3        1 0.75 0.78
4        1 1.00 0.48
5        1 1.25 0.37
6        1 2.00 0.19
....
```

Long to wide

```r
# From long to wide
df.w <- reshape(Indometh, v.names = "conc", timevar = "time",
    idvar = "Subject", direction = "wide")
```

```
   Subject conc.0.25 conc.0.5 conc.0.75 conc.1 conc.1.25 conc.2 con
1        1      1.50     0.94      0.78   0.48      0.37   0.19   0
12       2      2.03     1.63      0.71   0.70      0.64   0.36   0
23       3      2.72     1.49      1.16   0.80      0.80   0.39   0
34       4      1.85     1.39      1.02   0.89      0.59   0.40   0
45       5      2.05     1.04      0.81   0.39      0.30   0.23   0
56       6      2.31     1.44      1.03   0.84      0.64   0.42   0
   conc.5 conc.6 conc.8
....
```

Reshaping: Wide to long

```
# From wide to long
df.l <- reshape(df.w, varying = list(2:12), v.names = "conc",
    idvar = "Subject", direction = "long", times = c(0.25, 0.5,
        0.75, 1, 1.25, 2, 3, 4, 5, 6, 8))
```

```
       Subject time conc
1.0.25       1 0.25 1.50
2.0.25       2 0.25 2.03
3.0.25       3 0.25 2.72
....
```

```
df.l[order(df.l$Subject), ] # reorder by subject
```

```
       Subject time conc
1.0.25       1 0.25 1.50
1.0.5        1 0.50 0.94
1.0.75       1 0.75 0.78
....
```

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Reading tabular txt files:

ASCII text files in tabular or spread sheet form (one line per observation, one column per variable) are read using `read.table()`

```
data = read.table("C:/RcouRse/file.txt", header = TRUE)
```

`data` is a data frame where the original numerical variables are converted in numeric vectors and character variables are converted in factors (not always).

Arguments:

- `header`: variable names in the first line? `TRUE/FALSE`
- `sep`: which separator between the columns (e.g., comma, `\t`)
- `dec`: `1.2` or `1,2`?

Reading other files

```
data = read.csv("C:/RcouRse/file.csv",
                header = TRUE, sep = ";",
                dec = ",")
```

From SPSS (file `.sav`):

```
install.packages("foreign")
library(foreign)
data = read.spss("data.sav", to.data.frame = TRUE)
```

Combine data frames

If they have the same number of columns/rows

```
all_data = rbind(data, data1, data2) # same columns
all_data = cbind(data, data1, data2) # same rows
```

If they have different rows/columns but they share at least one characteristic (e.g., `ID`):

```
all_data = merge(data1, data2,
                 by = "ID")
```

If there are different IDs in the two datasets $\rightarrow$ added in new rows

`all_data` contains all columns in `data1` and `data2`. The columns of the IDs in `data1` but not in `data2` (and vice versa) will be filled with `NA`s accordingly

Export data

Writing text (or csv) file:

```
write.table(data, # what you want to write
            file = "mydata.txt", # its name + extension
            header = TRUE, # first row with col names?
            sep = "\t",  # column separator
            ....) # other arguments
```

R environment (again):

```
save(dat, file = "exp1_data.rda") # save something specific
save(file = "the_earth.rda")      # save the environment
load("the_earth.rda")             # load it back
```

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Be ready to make mistakes (a lot of mistakes)

Coding is ~~hard~~ art

Eyes on the prize, but take your time (and the necessary steps) to get there

Remember: You're not alone $\rightarrow$ `stackoverflow` (or Google in general) is your best friend

ifelse()

Conditional execution:

Easy: `ifelse(test, if true, if false)`

```
ifelse(peso > 7, "big boy", "small boy")
```

```
[1] "small boy" "small boy" "small boy" "big boy"   "big boy"
```

Pros
- Super easy to use
- Can embed multiple `ifelse()` cycles

Cons
- It works fine until you have simple tests

if () {} else {}

If you have only one condition:

```
if (test_1) {
  command_1
} else {
  command_2
}
```

if () {} else {}

Multiple conditions:

```
if (test_1) {
  command_1
} else if (test_2) {
  command_2
} else {
  command_3
}
```

`test_1` (and `test_2`, if you have it) **must** evaluate in either `TRUE` or `FALSE`

```
if(!is.na(x)) y <- x^2 else stop("x is missing")
```

Loops

`for()` and `while()`

Repeat a command over and over again:

```r
# Don't do this at home
x <- rnorm(10)
y <- numeric(10)   # create an empty container
for(i in seq_along(x)) {
y[i] <- x[i] - mean(x)
}
```

The best solution would have been:

```r
y = x - mean(x)
```

Avoiding loops

Don't loop, `apply()`!

`apply()`

```
X <- matrix(rnorm(20),
            nrow = 5, ncol = 4)
apply(X, 2, max) # maximum for each column
```

```
[1] 1.4203744 1.0716663 2.3329026 0.9084482
```

Avoiding loops

Don't loop, `apply()`!

`apply()`

```
X <- matrix(rnorm(20),
            nrow = 5, ncol = 4)
apply(X, 2, max) # maximum for each column
```

```
[1] 1.4203744 1.0716663 2.3329026 0.9084482
```

`for()`

```
y = NULL
for (i in 1:ncol(X)) {
  y[i] = max(X[, i])
}
```

Avoiding loops

Group-wise calculations: `tapply()`

`tapply()` (`t` for table) may be used to do group-wise calculations on vectors. Frequently it is employed to calculate group-wise means.

```
with(ToothGrowth,
     tapply(len, list(supp, dose), mean))
```

```
     0.5     1     2
OJ 13.23 22.70 26.06
VC  7.98 16.77 26.14
```

(You could have done it with `aggregate()`)

Writing functions

Compute Cohen's *d*:

```
dcohen = function(group1, group2) { # Arguments
  mean_1 = mean(group1) ; mean_2 = mean(group2)
  var_1 = var(group1) ; var_2 = var(group2) # body
  d = (mean_1 - mean_2)/sqrt(((var_1 + var_2)/2) )
  return(d) # results
}
```

Use it:

```
dcohen(data$placebo, data$drug)
```

Named arguments

Take this function:

```
fun1 <- function(data, data.frame, graph, limit) { ... }
```

It can be called as:

```
fun1(d, df, TRUE, 20)
fun1(d, df, graph=TRUE, limit=20)
fun1(data=d, limit=20, graph=TRUE, data.frame=df)
```

Positional matching and keyword matching (as in built-in functions)

Defaults

Arguments can be given default values → the arguments can be omitted!

```
fun1 <- function(data, data.frame, graph=TRUE,
                 limit=20) { ... }
```

It can be called as

```
ans <- fun1(d, df)
```

which is now equivalent to the three cases above, but:

```
ans <- fun1(d, df, limit=10)
```

which changes one of the defaults.

Methods and classes

The return value of a function may have a specified `class` $\rightarrow$ determines how it will be treated by other functions.

For example, many classes have tailored `print` methods.

```
methods(print)
```

```
  [1] print.acf*
  [2] print.AES*
  [3] print.all_vars*
  [4] print.anova*
  [5] print.any_vars*
  [6] print.aov*
  [7] print.aovlist*
....
```

Define a print method!

. . . as another function:

```
print.cohen <- function(obj){
  cat("\nMy Cohen's d\n\n")
  cat("Effect size: ", obj$d, "\n")
  invisible(obj) # return the object
}
```

We have to change our dcohen function a bit:

```
dcohen = function(group1, group2) { # Arguments
  ...
  dvalue = list(d = d)
  class(dvalue) = "cohend"
  return(dvalue) # results
}
```

Example

Compute the Cohen's *d* between a test group and a control group:

```r
set.seed(082022) # results equal for everyone
data <- data.frame(drug = rnorm(6, 10),
                   placebo = rnorm(6, 2))
my_d = dcohen(data$drug, data$placebo)
print.cohen(my_d)
```

```
My Cohen's d

Effect size:  6.900794
```

Debugging

Use the `traceback()` function:

```
foo <- function(x) { print(1); bar(2) }
bar <- function(x) { x + a.variable.which.does.not.exist }
```

Call `foo()` and...

```
foo() #
[1] 1
Error: object 'a.variable.which.does.not.exist' not found
```

Use `traceback()`:

```
traceback() # find out where the error occurred
2: bar(2)
1: foo()
```

Note: `traceback()` appears as default

Table of Contents

- Traditional graphics
- Grid graphics & `ggplot2`

For both:

- High level functions $\rightarrow$ actually produce the plot
- Low level functions $\rightarrow$ make it looks better =)

Export graphics file

```
postscript()  # vector graphics
pdf()

png()            # bitmap graphics
tiff()
jpeg()
bmp()
```

Remember to run off the graphic device once you've saved the graph:

```
dev.off()
```

(You can do it also manually)

Traditional graphics I

High level functions

```
plot()          # scatter plot, specialized plot methods
boxplot()
hist()          # histogram
qqnorm()        # quantile-quantile plot
barplot()
pie()           # pie chart
pairs()         # scatter plot matrix
persp()         # 3d plot
contour()       # contour plot
coplot()        # conditional plot
interaction.plot()
```

`demo(graphics)` for a guided tour of base graphics!

Traditional graphics II

Low level functions

```
points()        # add points
lines()         # add lines
rect()
polygon()
abline()        # add line with intercept a, slope b
arrows()
text()          # add text in plotting region
mtext()         # add text in margins region
axis()          # customize axes
box()           # box around plot
legend()
```

Plot layout

Each plot is composed of two regions:

- The plotting regions (contains the actual plot)
- The margins region (contain axes and labels)

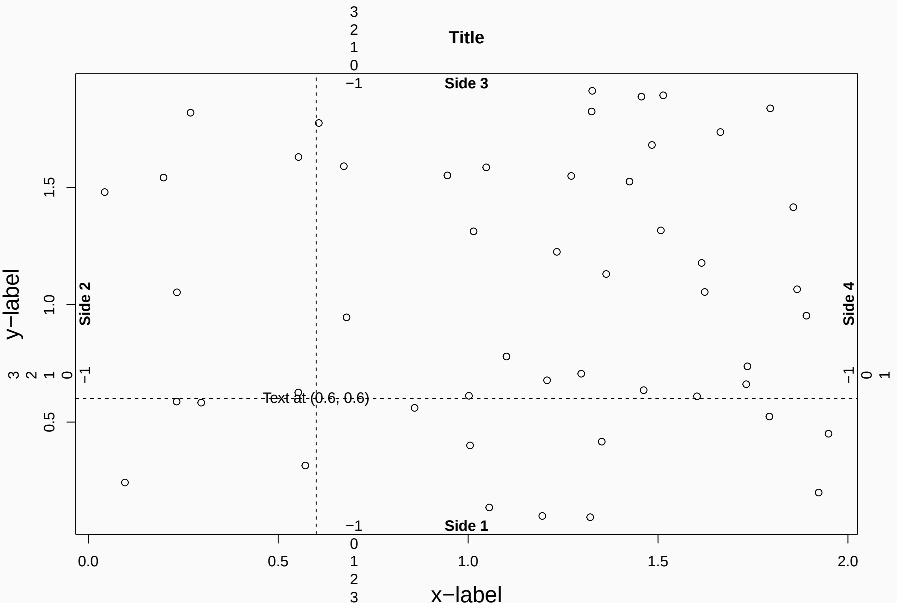
A scatter plot:

```
x <- runif(50, 0, 2) # 50 uniform random numbers
y <- runif(50, 0, 2)
plot(x, y, main="Title",
     sub="Subtitle", xlab="x-label",
     ylab="y-label") # produce plotting window
```

Now add some text:

```
text(0.6, 0.6, "Text at (0.6, 0.6)")
abline(h=.6, v=.6, lty=2) # horizont. and vertic.
                          # lines
```

Margins region



Rome wasn't built in a day and neither your graph

Display the interaction between the two factors of a two-factorial experiment:

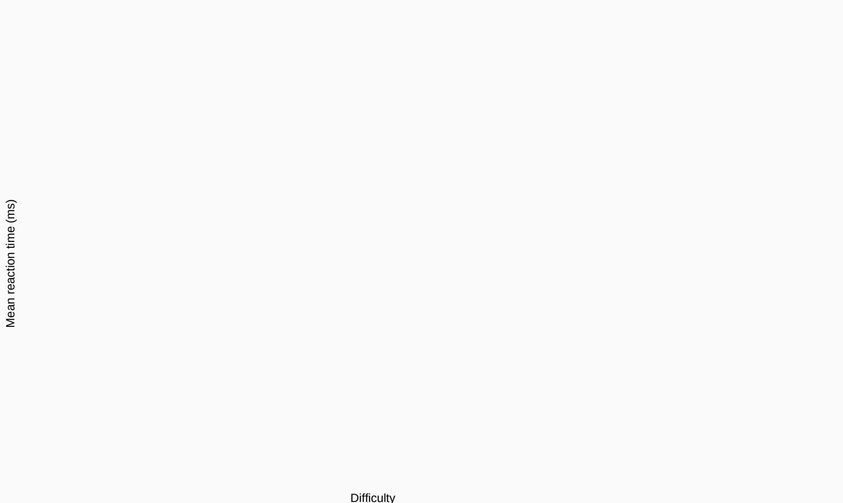
```
dat <- read.table(header=TRUE, text="
A B rt
a1 b1 825
a1 b2 792
a1 b3 840
a2 b1 997
a2 b2 902
a2 b3 786
")
```

Force `A` and `B` to be `factor`:

```
dat[,1:2] = lapply(dat[,1:2], as.factor)
```

First: The plot

```r
plot(rt ~ as.numeric(B), dat, type="n", axes=FALSE,
     xlim=c(.8, 3.2), ylim=c(750, 1000),
     xlab="Difficulty", ylab="Mean reaction time (ms)")
```



Populate the content

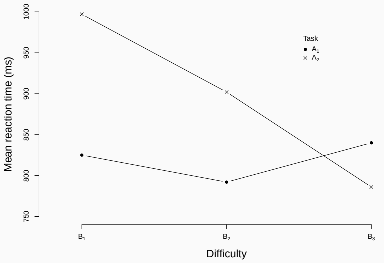
Plot the data points separately for each level of factor `A`.

```
points(rt ~ as.numeric(B), dat[dat$A=="a1",],
       type="b", pch=16)
points(rt ~ as.numeric(B), dat[dat$A=="a2",],
       type="b", pch=4)
```

Add axes and a legend.

```
axis(side=1, at=1:3, expression(B[1], B[2], B[3]))
axis(side=2)
legend(2.5, 975, expression(A[1], A[2]), pch=c(16, 4),
       bty="n", title="Task")
```

Final result



- Error bars may be added using the `arrows()` function.
- Via `par()` many graphical parameters may be set (see `?par`), for example `par(mgp=c(2, .7, 0))` reduces the distance between labels and axes

Graphical parameters I

```
adj # justification of text
bty # box type for legend
cex # size of text or data symbols (multiplier)
col # color, see colors()
las # rotation of text in margins
lty # line type (solid, dashed, dotted, ...)
lwd # line width
mpg # placement of axis ticks and tick labels
pch # data symbol type
tck # length of axis ticks
type # type of plot (points, lines, both, none)
```

Graphical parameters II

par()

```
mai # size of figure margins (inches)
mar # size of figure margins (lines of text)
mfrow # number of sub-figures on a page:
      # par(mfrow=c(1, 2)) creates two sub-figures
oma # size of outer margins (lines of text)
omi # size of outer margins (inches)
pty # aspect ratio of plot region (square, maximal)
```

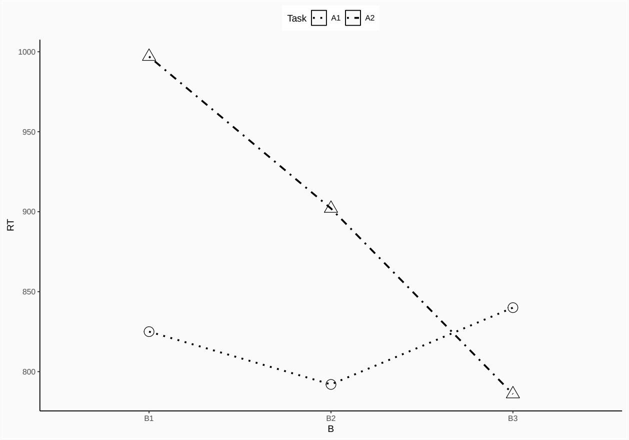
ggplot2

ggplot2 (Grammar of Graphics plot, Wickman, 2016) is one of the best packages for plotting raw data and results:

```
install.packages("ggplot2") ; library(ggplot2)
```

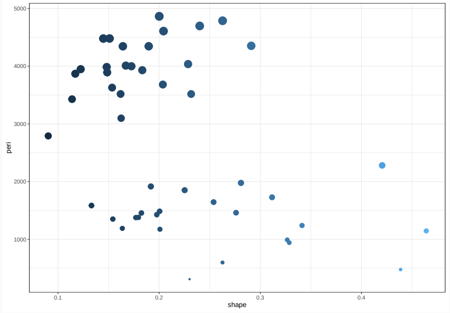
The code for the previous plot:

```
ggplot(dat, aes(x = B, y = rt, group = A)) +
  geom_point(pch=dat$A, size = 5) +
  geom_line(aes(linetype=A), size=1)  + theme_classic() +
  ylab("RT") +  scale_linetype_manual("Task", values =c(3,4),
                                   labels = c("A1", "A2")) +
  scale_x_discrete(labels = c("B1", "B2", "B3")) +
  theme(legend.position="top",
        panel.background =  element_rect(fill = "#FAFAFA",
                                         colour = "#FAFAFA"),
        plot.background = element_rect(fill = "#FAFAFA"),
        legend.key = element_rect(fill = "#FAFAFA"))
```


Task
A1
A2
1000
950
900
850
800
RT
B1
B2
B3
B

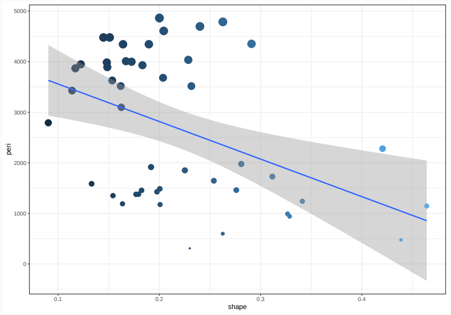
Raw data

```
ggplot(rock,
       aes(y=peri,x=shape, color =shape,
           size = peri)) + geom_point() +
  theme_bw() + theme(legend.position = "none")
```

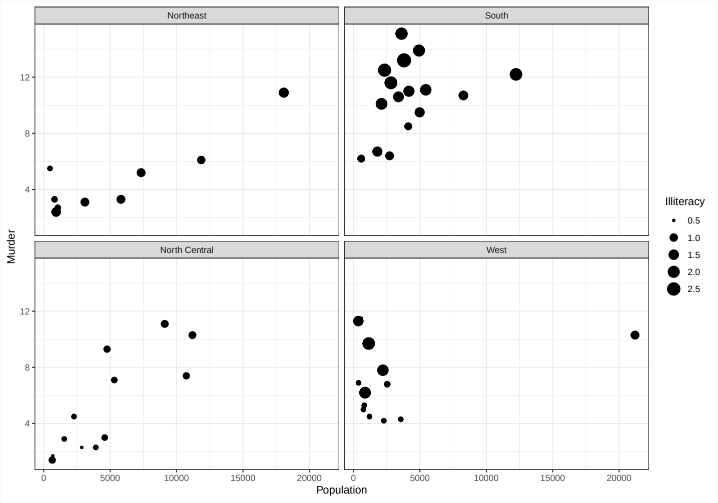


Linear model

```
ggplot(rock,
       aes(y=peri,x=shape, color =shape,
           size = peri)) + geom_point() +
  theme_bw() + theme(legend.position = "none") +
  geom_smooth(method="lm")
```



Multi Panel


Northeast
South
North Central
West
Murder
Population
4
8
12
0
5000
10000
15000
20000
Illiteracy
0.5
1.0
1.5
2.0
2.5

Multi panel code

```
states = data.frame(state.x77, state.name = state.name,
                    state.region = state.region)

ggplot(states,
       aes(x = Population, y = Murder,
           size = Illiteracy)) + geom_point() +
  facet_wrap(~state.region) + theme_bw()
```

Different plots in the same panel

use grid.arrange() function from the gridExtra package:

```
install.packages("grideExtra") ; library(gridExtra)
```

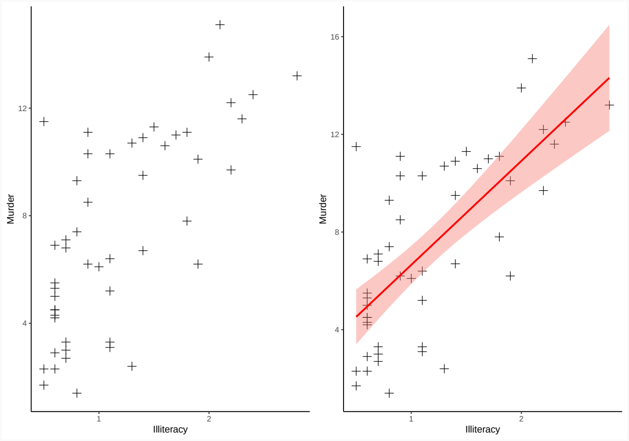
```
murder_raw = ggplot(states,  # raw data
                    aes(x = Illiteracy, y = Murder)) +
           .....

murder_lm = ggplot(states,  # lm
                    aes(x = Illiteracy, y = Murder)) +
           .....
```

Combine the plots together:

```
grid.arrange(murder_raw, murder_lm,
             nrow=1) # plots forced to be the same row
```

Combine the plots together



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The `stats` package (built-in package in `R`) contains function for statistical calculations and random number generator

see `library(help=stats)`

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Nominal data:

- `binom.test()`: exact test of a simple null hypothesis about the probability of success in a Bernoulli experiment
- `chisq.test()`: contingency table χ^2 tests

Metric response variable:

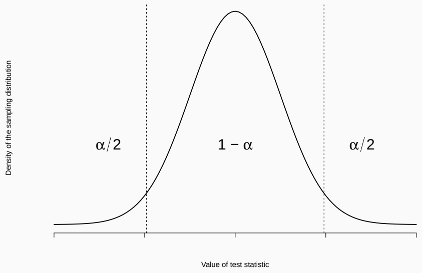
- `cor.test()`: association between paired samples
- `t.test()`: one- and two-sample t tests (also for paired data)
- `var.test()`: F for testing the homogeneity of variances

What is the *p*-value?

p-value:

> *conditional probability of obtaining a test stastic that is at least as extreme as the one observed, given that the null hyphothesis is true*

If $p < \alpha$ (i.e., the probability of rejecting the null hypothesis when it is true) $\rightarrow$ the null hypothesis is rejected



Binomial test

Observations X_i **must** be independent

Hypotheses:

1. $H_0\colon\ p = p_0 \quad H_1\colon\ p \neq p_0$
2. $H_0\colon\ p = p_0 \quad H_1\colon\ p < p_0$
3. $H_0\colon\ p = p_0 \quad H_1\colon\ p > p_0$

Test statistic:

$$T = \sum_{i=1}^{n} X_i, \quad T \sim \mathcal{B}(n, p_0)$$

In R:

```
binom.test(5, 10, p = 0.25)
```

χ^2 test

Independence of observations

Hypothesis:

- H_0: $P(X_{ij} = k) = p_k$ for all $i = 1, \ldots, r$ and $j = 1, \ldots, c$
- H_0: $P(X_{ij} = k) \neq P(X_{i'j} = k)$ for *at least* one $i \in \{1, \ldots, r\}$ and $j \in \{1, \ldots, c\}$

Test statistic:

$$\chi^2 = \sum_{i=1}^{n} \frac{(x_{ij} - \hat{x}_{ij})^2}{\hat{x}_{ij}}, \; \chi^2 \sim \chi^2(r-1)(c-1)$$

In R:

```r
tab <- xtabs(~ education + induced, infert)
chisq.test(tab)
```

Correlation test

Hypothesis:

- H_0: $\rho_{XY} = 0$, H_1: $\rho_{xy} \neq 0$
- H_0: $\rho_{XY} = 0$, H_1: $\rho_{xy} < 0$
- H_0: $\rho_{XY} = 0$, H_1: $\rho_{xy} > 0$

Test statistic:

$$T = \frac{r_{xy}}{\sqrt{1 - r_{xy}^2}} \sqrt{n-2}, \;\; T \sim t(n-2)$$

In R:

```r
cor.test(~ speed + dist, cars,
         alternative = "two.sided")
```

Two (indepdent) sample t test

Independent samples from normally distributions where σ^2 are unknown but homogeneous

- H_0: $\mu_{x_1-x_2} = 0$, H_1: $\mu_{x_1-x_2} \neq 0$
- H_0: $\mu_{x_1-x_2} = 0$, H_1: $\mu_{x_1-x_2} < 0$
- H_0: $\mu_{x_1-x_2} = 0$, H_1: $\mu_{x_1-x_2} > 0$

Test statistic:

$$T = \frac{\bar{x_1} - \bar{x_2}}{\sigma_{\bar{x_1}-\bar{y_2}}},\ \ T \sim t(n_1 + n_2 - 2)$$

R function:

```
t.test(len ~ supp, data = ToothGrowth,
       var.equal = TRUE)
```

Two (depedent) sample t test

Observations on the same sample

Hypothesis:

- H_0: $\mu_D = 0$, H_1: $\mu_D \neq 0$
- H_0: $\mu_D = 0$, H_1: $\mu_D < 0$
- H_0: $\mu_D = 0$, H_1: $\mu_D > 0$

Test statistic:

$$T = \frac{d}{\sigma_d}, \quad T \sim t(m-1)$$

R function:

```
with(sleep,
     t.test(extra[group == 1],
            extra[group == 2], paired = TRUE))
```

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Formulae

Statistical models are represented by formulae which are extremely close to the actual statistical notation:

in `R`	Model
`y ~ 1 + x`	$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$
`y ~ x`	(same but short)
`y ~ 0 + x`	$y_i = \beta_1 x_i + \varepsilon_i$
`y ~ x_A * x_B`	$y_i = \beta_0 + \beta_1 x_i + \beta_2 x_j + (\beta_1 \beta_2) x_{ij} + \varepsilon_{ij}$

Linear models

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + \varepsilon$$

In R:

```
lm(y ~ x1 + x2 + ... + xk, data)
```

Extractor functions I

```
coef()    # Extract the regression coefficients
summary() # Print a comprehensive summary of the results of
          # the regression analysis
anova()   # Compare nested models and produce an analysis
resid()   # Extract the (matrix of) residuals
plot()    # Produce four plots, showing residuals, fitted
          # values and some diagnostics
model.matrix()
          # Return the design matrix
```

Extractor functions II

```
vcov()    # Return the variance-covariance matrix of the
          # main parameters of a fitted model object
predict() # A new data frame must be supplied having the
          # same variables specified with the same labels
          # as the original. The value is a vector or
          # matrix of predicted values corresponding to
          # the determining variable values in data frame
step()    # Select a suitable model by adding or dropping
          # terms and preserving hierarchies. The model
          # with the smallest value of AIC (Akaike's
          # Information Criterion) discovered in the
          # stepwise search is returned
```

Generalized linear models

$$g(\mu) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + \varepsilon$$

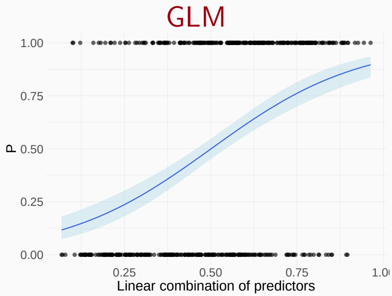
$g()$ is the link functions that connects the mean to the linear combination of predictors.

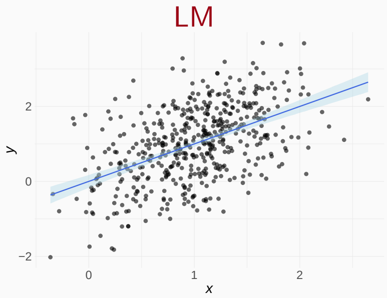
A GLM is composed of three elements: The response distribution, the link function, and the linear combination of predictors

In `R`:

```
glm(y ~ x1 + x2 + ... + xk, family(link), data)
```

LM vs GLM


GLM
1.00
0.75
0.50
0.25
0.00
P
0.25
0.50
0.75
1.00
Linear combination of predictors


LM
2
0
−2
y
0
1
2
x

Families

A special link function to each response variable. In R some different link functions are available by default:

```
## Family name       Link functions
binomial            logit, probit, log, cloglog
gaussian            identity, log, inverse
Gamma               identity, inverse, log
inverse.gaussian    1/mu^2, identity, inverse, log
poisson             log, identity, sqrt
quasi               logit, probit, cloglog, identity, inverse,
                    log, 1/mu^2, sqrt
```

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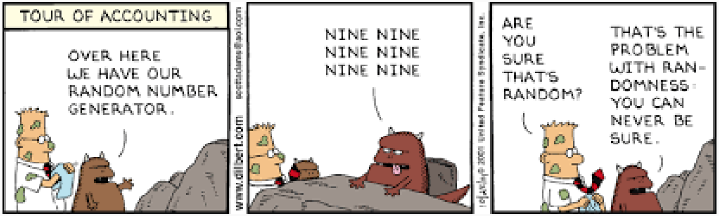
Random numbers generation

Use a random monster:


TOUR OF ACCOUNTING
OVER HERE WE HAVE OUR RANDOM NUMBER GENERATOR.
NINE NINE NINE NINE NINE NINE
ARE YOU SURE THAT'S RANDOM?
THAT'S THE PROBLEM WITH RANDOMNESS: YOU CAN NEVER BE SURE.
www.dilbert.com
scottadams@aol.com
© 2001 United Feature Syndicate, Inc.

but its better with R

Random numbers drawn from a statistical distribution → the distribution name (see `??Distributions` for an exhaustive list of distribution) prefixed by `r` (random)

```
rnorm(10, mean = 0, sd = 1) # draw 10 numbers from a
                            # normal distr.
rt(10, df = 20)             # draw 10 numbers from a
                            # t distr. with 20df
```

Sampling (with or without replacement) from a vector:

```
sample(1:5, size = 10, replace = T)
```

```
 [1] 5 1 1 2 5 4 4 1 2 5
```

Make the simulations replicable by *seeding* them:

```
set.seed(999)
rpois(4, 5)
```

Bootstrap by resampling

- Compute the sample statistics on multiple bootstrap samples Bs drawn with replacement from the original data
- Assess the variability of the statistics via the distribution of the bootstrap replicates (i.e., the statics computed on the bootstrap samples)

Bootstrap confidence intervals

Percentile intervals are the $1 - \alpha$ confidence intervals for the sample statistics with limits given by the quantiles of the bootstrap distribution

In R

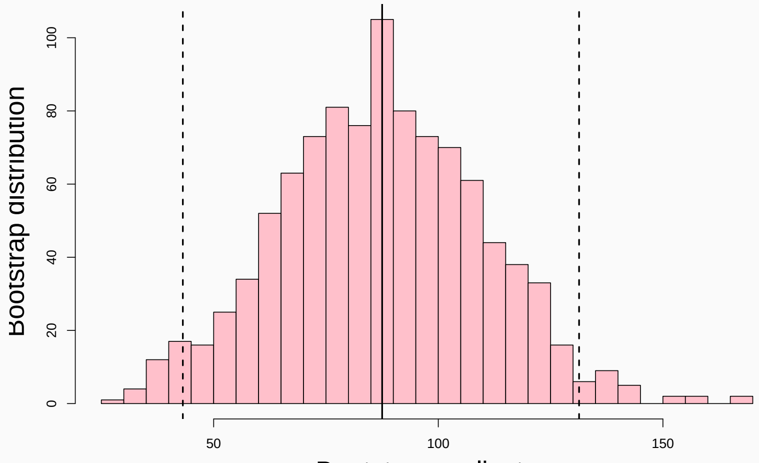
```r
# example taken from Prof. Wickelmaier
mouse <- data.frame(
   grp = rep(c("trt", "ctl"), c(7, 9)),
   surv = c(94, 197, 16, 38, 99, 141, 23, # trt
            52, 104, 146, 10, 50, 31, 40, 27, 46) # ctl
   )
mean(mouse$surv[mouse$grp == "trt"]) #
```

```
[1] 86.85714
```

```r
## Resampling
sam1 <- numeric(1000) # 1000 bootstrap replicates
for(i in seq_along(sam1)){
 trt <- sample(mouse$surv[mouse$grp == "trt"], 7, replace=T)
 sam1[i] <- mean(trt)
}
```

```
quantile(sam1, c(.025, .975))
```

```
    2.5%     97.5%
 43.14286 131.33929
```



Parametric bootstrap

For the likelihood ratio test:

- Fit a general (M_1) and a restricted model (M_0) to the original data x. Compute the original likelihood ratio s(x) between M_1 and M_0
- Simulate B bootstrap samples based on the stochastic part of the restricted model: These are observations for which H_0 is true
- For each sample, fit M_1 and M_0 and compute the bootstrap replicate of the likelihood ratio between them
- Assess the significance of the original likelihood ratio via the sampling distribution of bootstrap replicates

```
## Model fit to original data
lm0 <- lm(surv ~ 1, mouse)  # H0: no difference between gr
lm1 <- lm(surv ~ grp, mouse) # H1: group effect
anova(lm0, lm1)             # original likelihood ratio
```

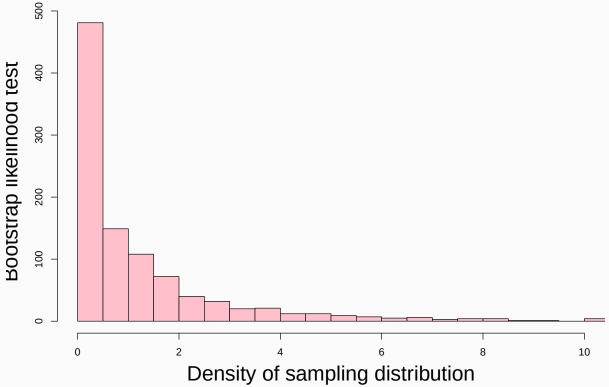
```
[1] 1.257516
```

```
 ## Parametric bootstrap
sim1 <- numeric(1000)
for(i in seq_along(sim1)){
  surv0 <- simulate(lm0)$sim_1  # simulate from null model
  m0 <- lm(surv0 ~ 1, mouse)    # fit null model
  m1 <- lm(surv0 ~ grp, mouse)  # fit alternative model
  sim1[i] <- anova(m0, m1)$F[2] # bootstrap likeli. ratio
  }
```

The bootstrap $p - value$ is the proportion of bootstrap replicates that exceed the original likelihood ratio:

```
mean(sim1 >
anova(lm0, lm1)$F[2])
```

```
[1] 0.304
```



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