01-PRactice

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Import csv

```
data = read.csv("data/benessere.csv",
                header = TRUE,
                sep =",", dec = ".")
head(data)
```

```
  benessere stipendio genere
1         5 1461.0983      m
2         7 1132.3637      f
3         7 1675.9004      m
4         2  328.9587      f
5         6 1370.0146      m
6         5  954.3540      f
```

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Data set is in wide format

- Sum across columns $\rightarrow$ sum scores of the respondents
  rowSums() (rowMean() for computing the mean)

- Sum across rows (righe) $\rightarrow$ sum scores of the items
  colSums() (colMean() for computing the mean)

Well-being

```
library(readxl)
benessere = read_xlsx("data/datiBenessere.xlsx")

head(benessere,2)
```

```
# A tibble: 2 x 19
     ID   età genere  frat item1 item2 item3 item4 item5   au1   au2   au3
  <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1     1    16      1     0     1     2     4     3     4     5     4     5
2     2    21      1     1     2     2     3     4     3     5     4     5
# i 6 more variables: au5 <dbl>, au6 <dbl>, au7 <dbl>, au8 <dbl>, au9 <dbl
#   au10 <dbl>
```

`rowSums()` :

Well-being continue

```
rowSums(benessere)
```

```
  [1]  65  79  88  74  75  83  78  79  85  87  80  88  83  84  92 1
 [19]  79  83 112 105  98  86  94  94 120 108  98 100 107 111 113 1
 [37] 100 108 107 126 126 116 116 110 117 117 106 111 122 123 129 1
 [55] 121 120 121 148 141 129 130 128 132 148 145 152 136 137 138 1
 [73] 140 140 143 151 148 158 156 143 149 157 165 162 159 170 163 1
 [91] 149 168 173 176 162 171 174 169 176 172 175 175 172 182 191 1
[109] 178 190 189 186 184 174 187 189 190 187 199 192 191 194 199 1
[127] 207 214 208 213 214 205 205 207 227 212 213 208 209 209 216 2
[145] 208 216 215 219 222 210
```

Is it meaningful. . . .?

Conditioning according to variable labels

They must present a regular expression (common root):

```
colnames(benessere)
```

```
[1] "ID" "età" "genere" "frat" "item1" "item2"
"item3" "item4"
[9] "item5" "au1" "au2" "au3" "au4" "au5" "au6"
"au7"
[17] "au8" "au9" "au10"
```

Columns with `item` → well-being items

Columns with `au` → self-esteem items

grep()e grepl(): functions for filtering data according to a regular expression (regex)

```
grep("regex", vector)
```

Same functioning, different results

```
(my_vector = colnames(benessere))
```

```
 [1] "ID"      "età"     "genere"  "frat"    "item1"   "item2"   "item3"   "item4
 [9] "item5"   "au1"     "au2"     "au3"     "au4"     "au5"     "au6"     "au7"
[17] "au8"     "au9"     "au10"
```

grep()

```
grep("au", my_vector)
```

```
 [1] 10 11 12 13 14 15 16 17 18 19
```

grepl()

```
grepl("au", my_vector)
```

```
 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TR
[13]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Compute sum scores

rowSums() conditioned on specific columns:

```
cat(rowSums(benessere[, grep("item",
                             colnames(benessere))])[1:15], "...")
```

```
14 14 13 13 17 10 16 16 9 13 14 16 17 12 9 ...
```

Assign to a new column (new variable)

```
benessere$score_ben = rowSums(benessere[, grep("item", colnames(benessere)
```

summary()

```
babies <- read.table("data/babies.tab")
summary(babies$peso)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  5.411   7.809   9.429   9.970  11.268  17.343
```

data set

```
summary(babies)
```

```
      id               genere               peso            altezza
 Length:10          Length:10          Min.   : 5.411   Min.   :46.80
 Class :character   Class :character   1st Qu.: 7.809   1st Qu.:62.90
 Mode  :character   Mode  :character   Median : 9.429   Median :78.73
                                       Mean   : 9.970   Mean   :74.88
                                       3rd Qu.:11.268   3rd Qu.:84.98
                                       Max.   :17.343   Max.   :99.22
```

table()

```
table(babies$genere)
```

```
f m
6 4
```

Contingency tables

```
benessere = read.csv("data/benessere.csv", header = T)
# new dichotomous variable to identify the well-being level
# as high or low
benessere$new_benessere = with(benessere,
                               ifelse(benessere > mean(benessere),
                                      "low",
                                      "high"))
with(benessere, table(new_benessere, genere))
```

```
             genere
new_benessere  f  m
         high 32 28
         low  22 18
```

table() and percentages

Single variable

```
(table(babies$genere)/nrow(babies))*100
```

```
 f  m
60 40
```

Multiple variables

```
my_perc = with(benessere, table(new_benessere, genere))
(my_perc = cbind(my_perc, rowSums(my_perc)))
```

```
      f  m
high 32 28 60
low  22 18 40
```

```
# ta-dan!
my_perc/my_perc[,3]
```

```
             f         m
high 0.5333333 0.4666667 1
low  0.5500000 0.4500000 1
```

Aggregating

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

```
# one depenent variable (y) and 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: Examples

```
benessere = read.csv("data/benessereScores.csv",
                     header = T, sep =",")
head(benessere, 3)
```

```
  ID età genere frat item1 item2 item3 item4 item5 au1 au2 au3 au4 au5 au6
1  1  16      1    0     1     2     4     3     4   5   4   5   2   3   3
2  2  21      1    1     2     2     3     4     3   5   4   5   2   4   4
3  3  28      2    4     2     3     5     1     2   4   4   4   4   4   4
  au8 au9 au10 score_ben score_au
1   4   2    4        14       33
2   5   1    5        14       40
3   4   2    4        13       38
```

Compute the mean of the self esteem according to gender

```
aggregate(score_au ~ genere, data = benessere, mean)
```

```
  genere score_au
1      1 33.08750
2      2 32.62857
```

Compute the mean according of self esteem and well being according to gender

```
aggregate(cbind(score_ben, score_au) ~ genere,
          data = benessere, mean)
```

```
  genere score_ben score_au
1      1  14.46250 33.08750
2      2  14.41429 32.62857
```

Your turn!

- Recode `frat` and assign it to a new var into the data frame (`siblings`: > 0 siblings → no > > 1+ sibilings → yes
- Compute the mean of `score_ben` according to `siblings`
- Compute the mean of `score_ben` and `score_au` according to `sibilings`and gender (assign it to the object `mean_dep`)
- Compute the standard deviation of `score_ben` and `score_au` according to `sibilings`and gender (assign it to the object `sd_dep`)
- merge `mean_dep` and `sd_dep` and assign the resulting object to `descr`

WARNING!

When using merge the column names must be different

Result

```
descr
```

```
  siblings genere mean_score_ben mean_score_au sd_score_ben sd_score_au
1       no      1       13.90909      33.27273     3.250042    4.452734
2       no      2       14.51852      32.11111     3.309315    3.004270
3      yes      1       14.67241      33.01724     3.347625    3.743961
4      yes      2       14.34884      32.95349     3.228472    4.396717
```

Solution

```
benessere$siblings = ifelse(benessere$frat == 0, "no", "yes")

mean_dep = aggregate(cbind(score_ben, score_au) ~ siblings + genere,
                     data = benessere,
                     mean)
colnames(mean_dep)[3:4] = paste("mean",
                                colnames(mean_dep)[3:4],
                                sep = "_")
sd_dep = aggregate(cbind(score_ben, score_au) ~ siblings + genere,
                     data = benessere,
                   sd)
colnames(sd_dep)[3:4] = paste("sd", colnames(sd_dep)[3:4],
                              sep =  "_")

descr = merge(mean_dep, sd_dep)
```

tidyverse()

```
install.packages("tidyverse")
library(tidyverse)
```

tidyverse()

```r
install.packages("tidyverse")
library(tidyverse)
```

%>% (Pipe)

Use the combo `shift + ctrl + M`

Logic:

```
object %>%
  grouping %>%
  function
```

Descriptive statistics

```
benessere %>%  # object
  group_by(siblings, genere) %>%  # groupings
  summarise(m_benessere = mean(score_ben),  # functions
            sd_benessere = sd(score_ben),
            m_au = mean(score_au),
            sd_au = sd(score_au))
```

```
# A tibble: 4 x 6
# Groups:   siblings [2]
  siblings genere m_benessere sd_benessere  m_au sd_au
  <chr>     <int>       <dbl>        <dbl> <dbl> <dbl>
1 no            1        13.9         3.25  33.3  4.45
2 no            2        14.5         3.31  32.1  3.00
3 yes           1        14.7         3.35  33.0  3.74
4 yes           2        14.3         3.23  33.0  4.40
```

Your turn!

- Compute minimum, maximum, median of `score_au` and `score_ben` with `tidyverse`
- Import the `babies` data set and compute the descriptive stats of `weight` and `height` with `tidyverse`

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 $=$)

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)

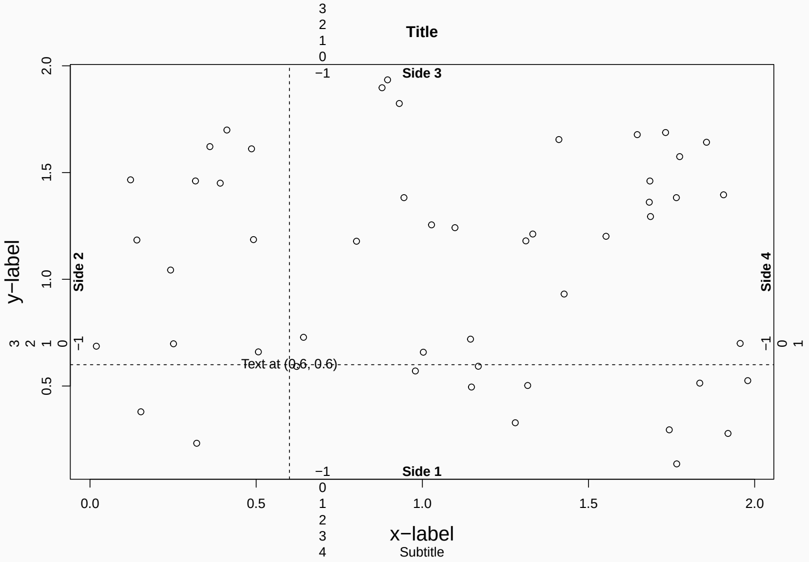
A scatter plot:

```
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

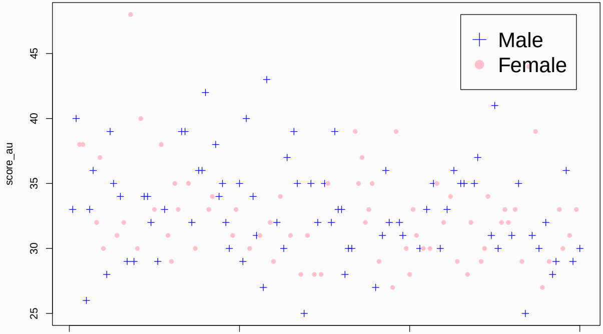


plot()

```
plot(x) # one variable
plot(x, y) # scatter plot
plot(y ~ x) # scatter plot (unless X is categorical)
```

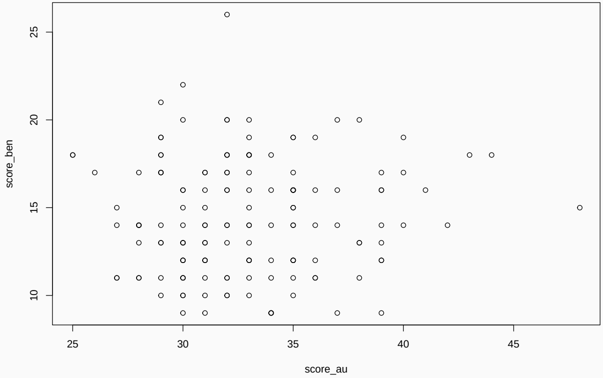
Example: `plot(x)`

```
with(benessere,
     plot(score_au,
          col = ifelse(genere == 1, "blue", "pink"),
          pch = ifelse(genere == 1, 3, 16)))
legend(x = 115, y = 48,
       c("Male", "Female"), pch = c(3, 16),
       col =c("blue", "pink"), cex = 2)
```



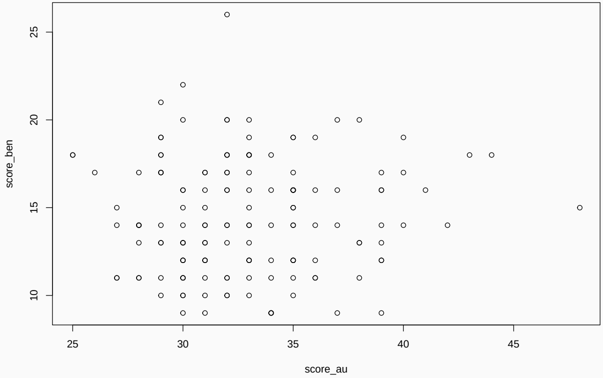
Example: `plot(x, y)`

```r
with(benessere,
     plot(score_au, score_ben))
```



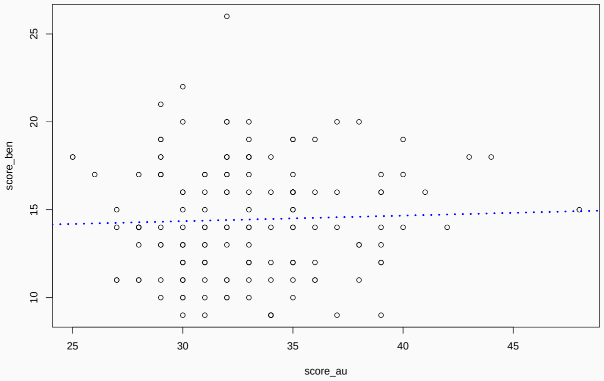
Example: `plot(y ~ x)`

```r
with(benessere,
     plot(score_ben ~ score_au))
```



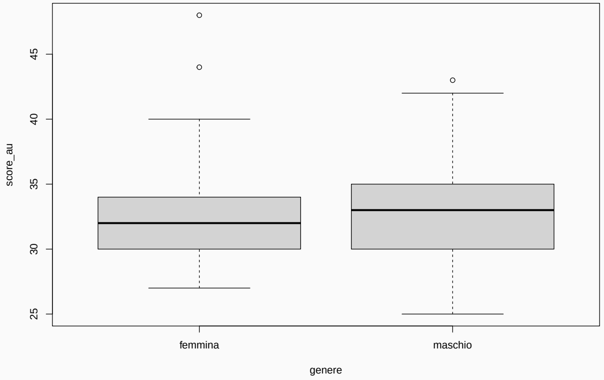
Example: `plot(y ~ x)` with regression line

```r
with(benessere,
     plot(score_ben ~ score_au))
abline(lm(score_ben ~ score_au, data = benessere),
          col = "blue", lty = 3, lwd = 3)
```



Example: `plot(y ~ x)` (x categorical)

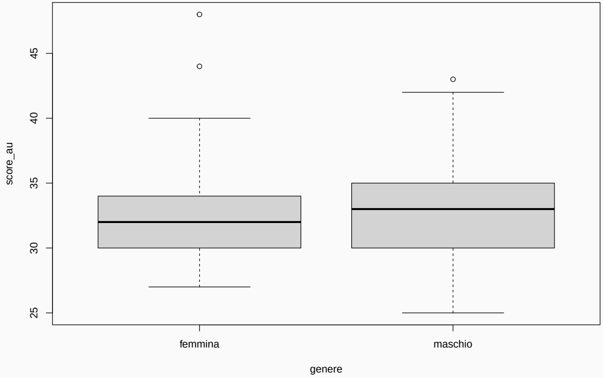
```
benessere$genere <- factor(ifelse(benessere$genere == 1,
                                  "maschio", "femmina"))
plot(score_au ~ genere, data = benessere)
```



Warning!

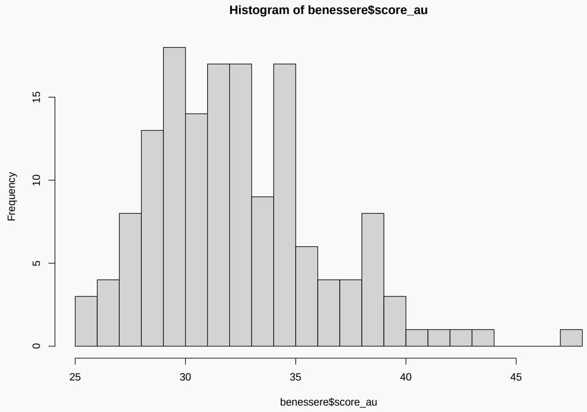
`plot(y ~ x)` with x categorical is equivalent to `boxplot(y ~ x)`

```
boxplot(score_au ~ genere, data = benessere)
```



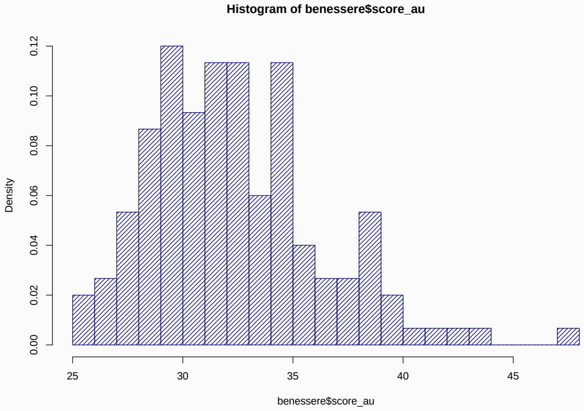
hist(): Frequency

```r
hist(benessere$score_au, breaks = 20)
```



hist(): Density

```
hist(benessere$score_au, density=20, breaks=20,
     prob=TRUE, col = "darkblue")
```

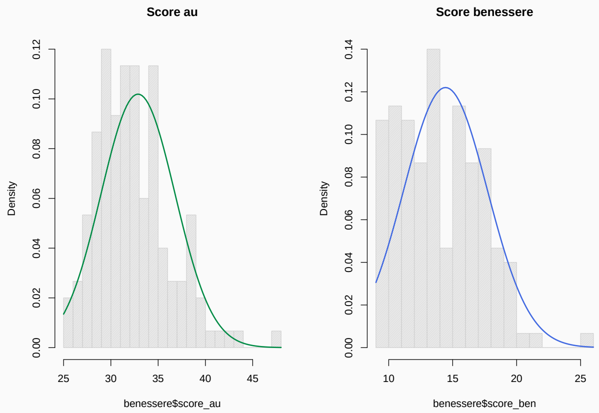


Modify the layout

Create the panels

```
par(mfrow=c(nrows, ncolumns)) # panels filled by rows
par(mfcol=c(nrows, ncolumns)) # panels filled by columns
```

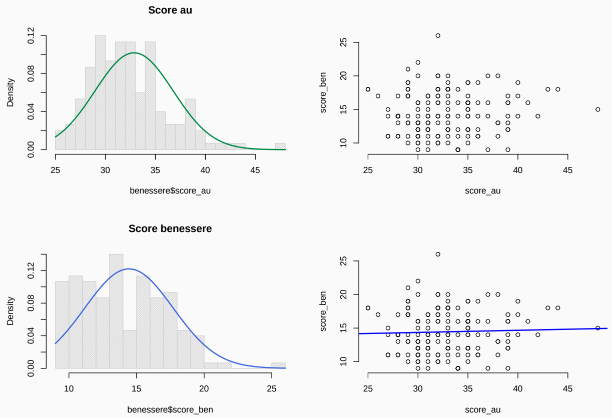
Multi plot: Rows



Multi plot: Rows

```
par(mfrow=c(1, 2))

hist(benessere$score_au,density=50, breaks=20, prob=TRUE,
     main = "Score au")
curve(dnorm(x, mean=mean(benessere$score_au),
            sd=sd(benessere$score_au)),
      col="springgreen4", lwd=2, add=TRUE, yaxt="n")

hist(benessere$score_ben,density=50, breaks=20, prob=TRUE,
     main = "Score benessere")
curve(dnorm(x, mean=mean(benessere$score_ben),
            sd=sd(benessere$score_ben)),
      col="royalblue", lwd=2, add=TRUE, yaxt="n")
```

Multiplot columns



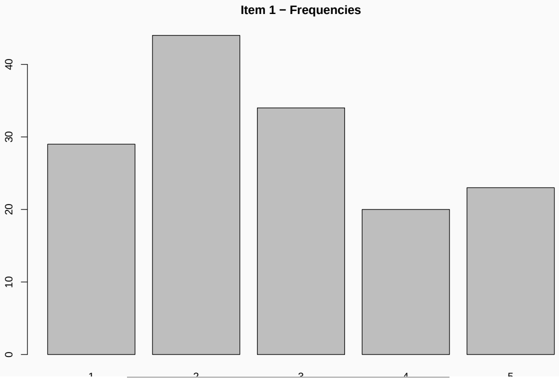
Multi plot Columns

```
par(mfcol= c(2,2))
hist(benessere$score_au,density=50, breaks=20, prob=TRUE,
     main = "Score au")
curve(dnorm(x, mean=mean(benessere$score_au),
            sd=sd(benessere$score_au)),
      col="springgreen4", lwd=2, add=TRUE, yaxt="n")

hist(benessere$score_ben,density=50, breaks=20, prob=TRUE,
     main = "Score benessere")
curve(dnorm(x, mean=mean(benessere$score_ben),
            sd=sd(benessere$score_ben)),
      col="royalblue", lwd=2, add=TRUE, yaxt="n")

with(benessere,
     plot(score_au, score_ben, frame = FALSE))


with(benessere,
     plot(score_au, score_ben, frame = FALSE))
abline(lm(score_ben ~ score_au, data = benessere), col = "blue", lwd = 2)
```

barplot(): Absolute frequency

Discrete variables

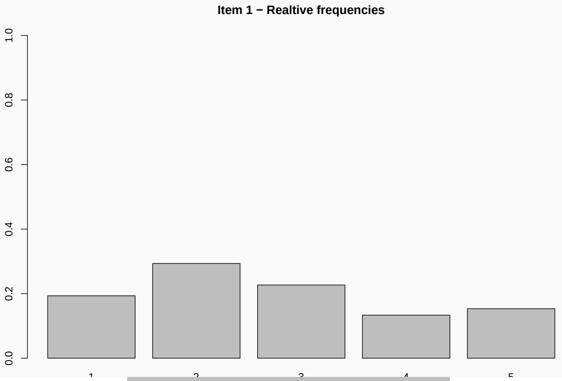
```
freq_item1 = table(benessere$item1)
barplot(freq_item1,
        main = "Item 1 - Frequencies")
```



barplot(): Relative frequency

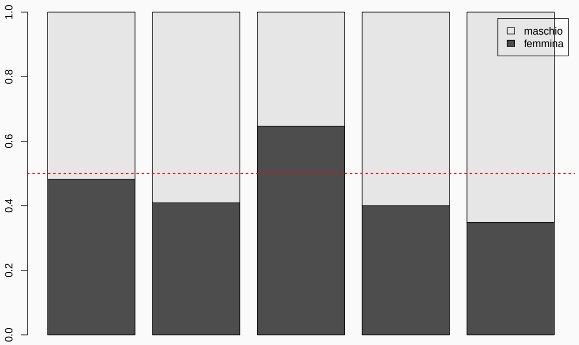
First step: Frequency tables

```
perc_item1 = freq_item1/sum(freq_item1)
barplot(perc_item1, ylim = c(0, 1),
        main = "Item 1 - Realtive frequencies")
```

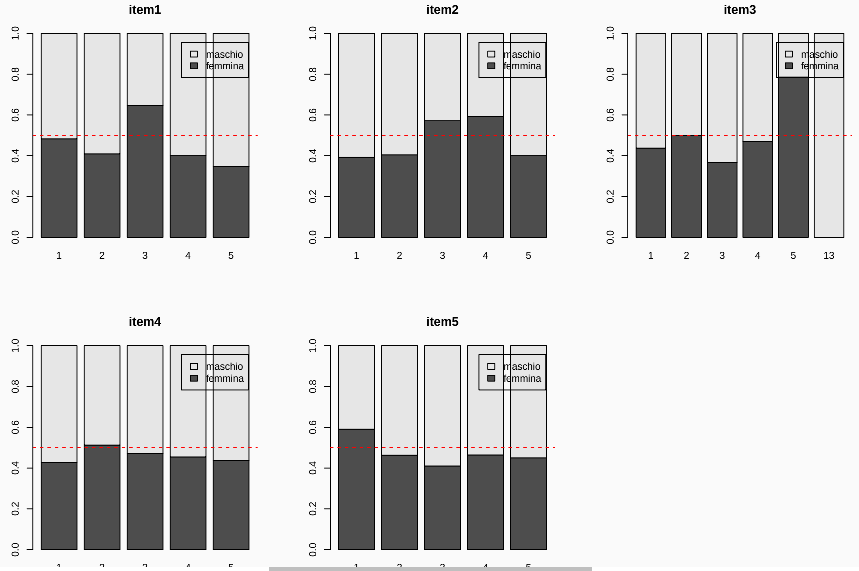


barplot() with multiple variables

```
perc_item1_gender = table(benessere$genere, benessere$item1)
perc_item1_gender[1,] = perc_item1_gender[1,]/table(benessere$item1)
perc_item1_gender[2,] = perc_item1_gender[2,]/table(benessere$item1)

barplot(perc_item1_gender, ylim=c(0,1),
        legend = rownames(perc_item1_gender))
abline(h = .5, lty = 2, col = "red")
```



Multi plot: Example



Multi plot: Example

```
item_ben = benessere[, grep("item", colnames(benessere))]

par(mfrow = c(2, round(ncol(item_ben)/2  + 0.2)))
temp = NULL
for (i in 1:ncol(item_ben)) {
  temp = table(benessere$genere, item_ben[,i])
  for (j in 1:nrow(temp)) {
    temp[j,] = temp[j,]/table(item_ben[,i])
  }
barplot(temp, ylim=c(0,1), legend = rownames(temp),
        main = colnames(item_ben)[i])
abline(h = .5, lty = 2, col = "red")
}
```

interaction.plot()

Intearction between x and y given a categorical variable z

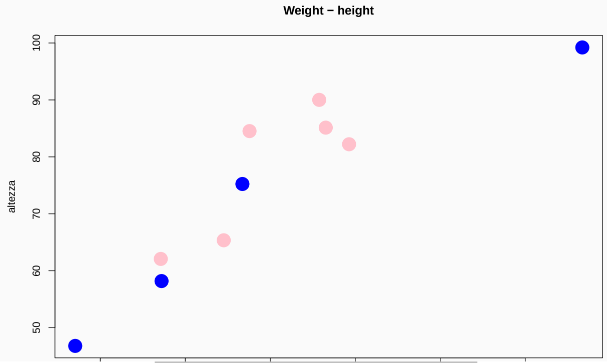
```
interaction.plot(x, z, y)
```

interaction.plot()

Intearction between *x* and *y* given a categorical variable *z*

```
interaction.plot(x, z, y)
```

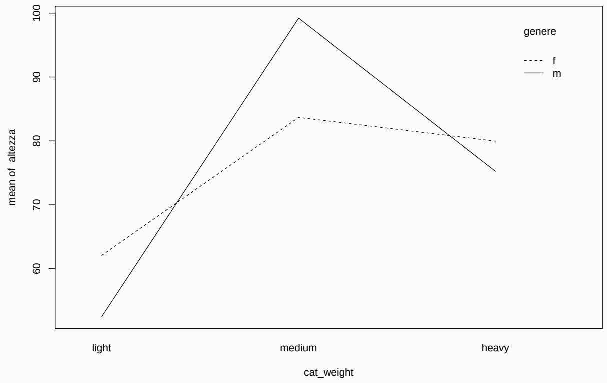
Does the relationship between height and weight change according to gender?



```
babies$cat_weight = with(babies,
                         ifelse(
                           peso <= quantile(babies$peso)[2],
                           "light", ifelse(peso > quantile(babies$peso)[2]
                                    peso > quantile(babies$peso)[4], "medi
                                    "heavy")))
babies$cat_weight = factor(babies$cat_weight,
                           levels = c("light", "medium", "heavy"))


babies
```

```
       id genere      peso  altezza cat_weight
1    baby1      f  7.424646 62.07722      light
2    baby2      m  7.442727 58.18877      light
3    baby3      f  9.512598 84.52737      heavy
4    baby4      f 11.306349 85.13573     medium
....
```

```
with(babies,
     interaction.plot(cat_weight, genere, altezza))
```



ggplot2

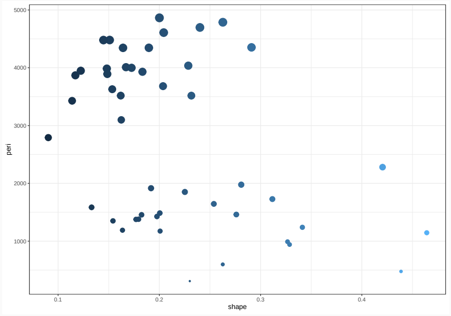
ggplot2 (Grammar of Graphics plot, Wickman, 2016) is one of the best packages for plotting raw data and results:

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

```
ggplot(data,
       ars(x = var.x,
           y = var.y,
           col = var.color, # factor or character
           fill =  var.filling, # factor or character
           shape =  var.shape, # actor or character
           size = var.size,  # numeric
           ...)) + geom_graph.type() + ...
```

Raw data

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



Some new data

```
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
")
```

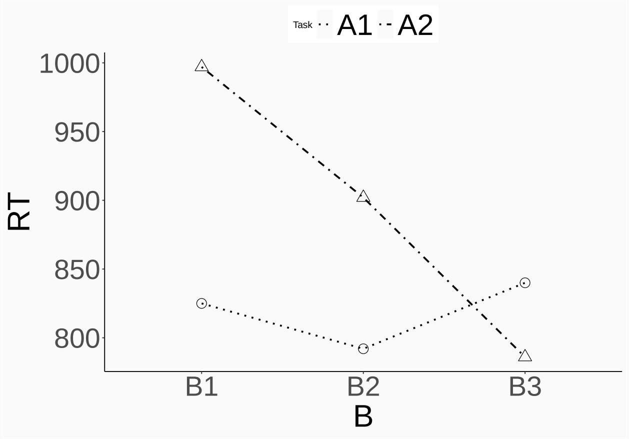
Force `A` and `B` to be `factor`:

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

The code for the interaction plot

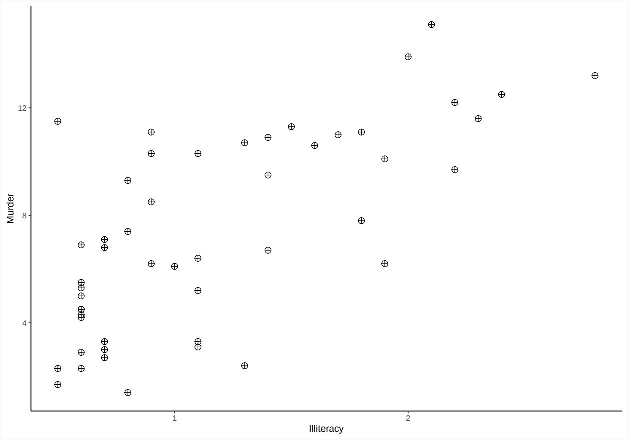
```r
ggplot(dat, aes(x = B, y = rt, group = A)) +
  geom_point(pch=dat$A, size = 5) +
  geom_line(aes(linetype=A), size=1)  + theme_classic() +
  ylab("RT") +  scale_linetype_manual("Task", values =c(3,4),
                                    labels = c("A1", "A2")) +
  scale_x_discrete(labels = c("B1", "B2", "B3"))
```

The result



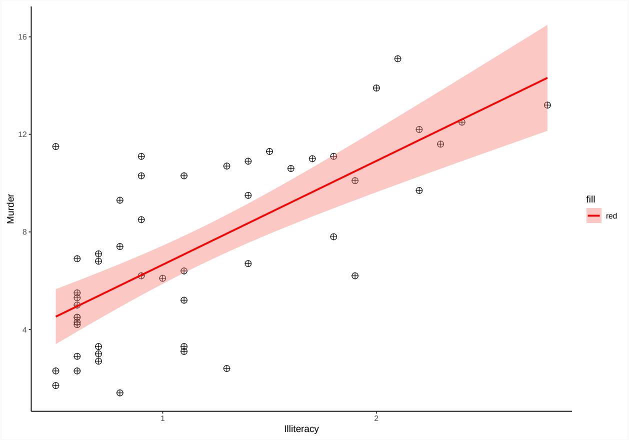
Scatter plot

```
states = data.frame(state.x77)
ggplot(states,  # raw data
               aes(x = Illiteracy, y = Murder)) +
  geom_point(size =3, pch=10) + theme_classic()
```



Linear model

```
ggplot(states,  # raw data
               aes(x = Illiteracy, y = Murder)) +
  geom_point(size =3, pch=10) + theme_classic() +
  geom_smooth(method="lm", color="red", aes(fill="red"))
```



Different plots in the same panel

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

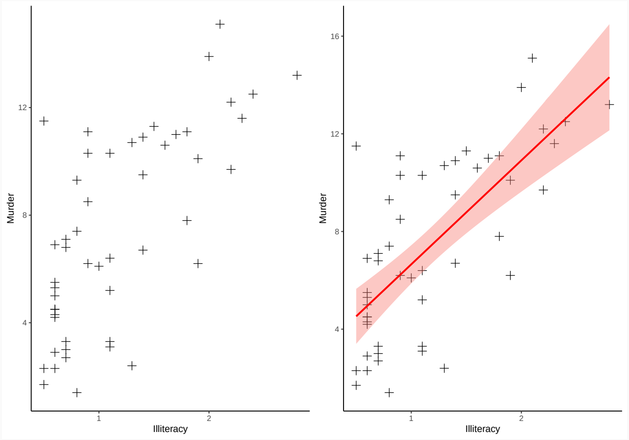
```
install.packages("gridExtra") ; library(gridExtra)
```

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

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

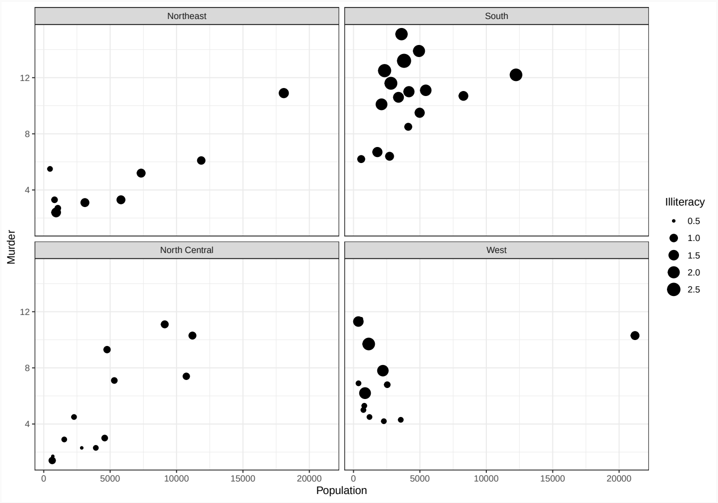
Combine the plots together:

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

Combine the plots together



Multi Panel (automatic)



Multi panel (automatic)

```
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()
```

boxplot() e violinplot()

Data need to be in long format:

```
    id condition mean_time
1 sbj1         A  3.477760
2 sbj1         B  1.748681
3 sbj2         A  2.405326
4 sbj2         B  2.915242
5 sbj3         A  3.294477
6 sbj3         B  2.763332
```

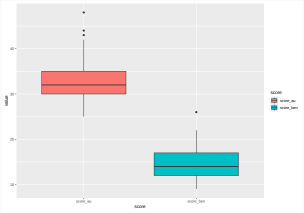
```
small = benessere[, c("ID", "score_au", "score_ben")]
score_long  = reshape(small,
        idvar = "ID",
        times =names(small)[-1],
        timevar = "score", v.names = "value",
        varying = list(names(small)[-1]),
        direction = "long")
head(score_long)
```

```
            ID    score value
1.score_au  1 score_au    33
2.score_au  2 score_au    40
3.score_au  3 score_au    38
4.score_au  4 score_au    38
5.score_au  5 score_au    26
6.score_au  6 score_au    33
```

boxplot vs violinplot

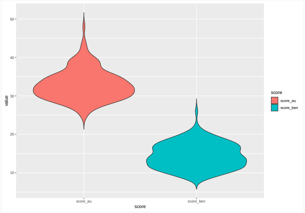
Boxplot

```
ggplot(score_long,
       aes(x = score, y = value,
           fill = score)) +
  geom_boxplot()
```

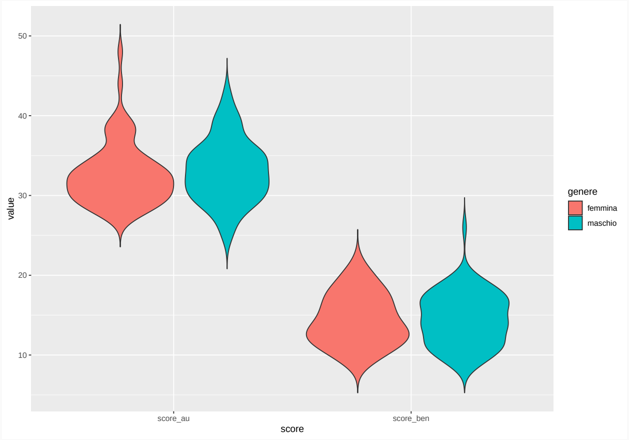


Violinplot

```
ggplot(score_long,
       aes(x = score, y = value,
           fill = score)) +
  geom_violin(trim = FALSE)
```



```
score_long = merge(score_long, benessere[, c("ID", "genere")])

ggplot(score_long,
       aes(x = score, y = value,
           fill = genere)) + geom_violin(trim = FALSE)
```



barplot and histogram

`geom_hist()`: histogram (continuous variables)

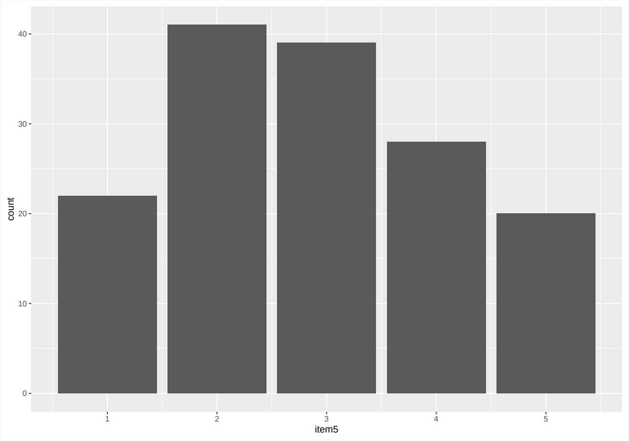
`geom_bar()`: bar plot

Arguments:

- `geom_bar(stat = "count")`: automatically counts the frequencies for each category, **does not need a y variable**
- `geom_bar(stat = "identity")`: plots a value associated to each category **does need a y variable**

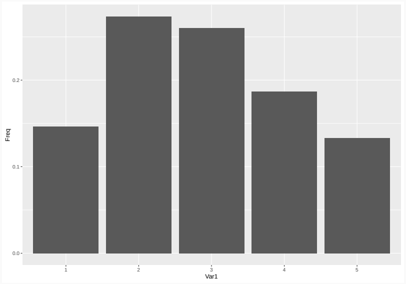
geom_bar(stat = "count"):

```
ggplot(benessere,
       aes(x = item5)) + geom_bar(stat = "count")
```



geom_bar(stat = "identity")

```r
item_5 = data.frame(table(benessere$item5)/nrow(benessere))
ggplot(item_5,
       aes(x = Var1, y = Freq)) + geom_bar(stat = "identity")
```



All together

Long format

```
new_item = benessere[, c(grep("ID", colnames(benessere)),
                        grep("item", colnames(benessere)))]
new_item = reshape(new_item,
        idvar = "ID",
        times =names(new_item)[-1],
        timevar = "item", v.names = "value",
        varying = list(names(new_item)[-1]),
        direction = "long")
new_item
```

```
           ID  item value
1.item1     1 item1     1
2.item1     2 item1     2
3.item1     3 item1     2
4.item1     4 item1     3
5.item1     5 item1     4
....
```

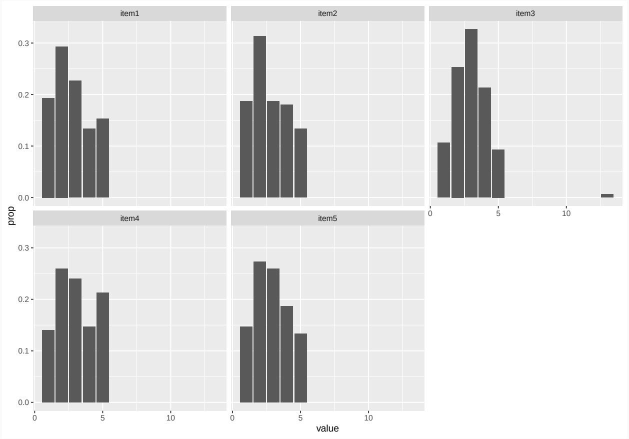
Compute the proportion

```
proporzione = new_item %>%
  group_by(item, value) %>%
  summarise(prop = n()/nrow(benessere))
proporzione
```

```
# A tibble: 26 x 3
# Groups:   item [5]
   item  value  prop
   <chr> <int> <dbl>
 1 item1     1 0.193
 2 item1     2 0.293
....
```

The plot

```
ggplot(proporzione,
       aes(x = value, y = prop)) +
  geom_bar(stat = "identity") +
  facet_wrap(~item)
```



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Automatically

```
pdf("nome_grafico.pdf")
png("nome_grafico.png")
tiff("nome_grafico.tiff")
jpeg("nome_grafico.jpeg")
bmp("nome_grafico.bmp")
```

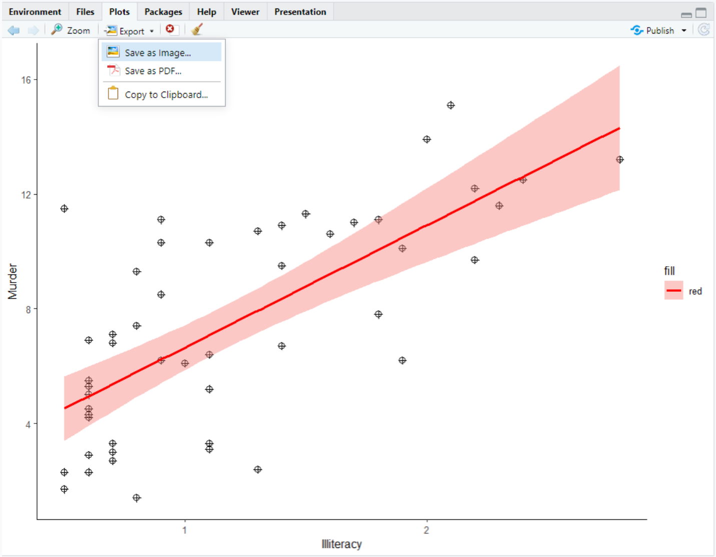
Remember to turn off the graphical device

```
dev.off()
```

Example

```
pdf("il_mio_violin.pdf")
ggplot(score_long,
       aes(x = score, y = value,
           fill = score)) + geom_violin(trim = FALSE)
dev.off()
```

Manually


Environment
Files
Plots
Packages
Help
Viewer
Presentation
Zoom
Export
Publish
Save as Image...
Save as PDF...
Copy to Clipboard...
16
12
8
4
Murder
1
2
Illiteracy
fill
red

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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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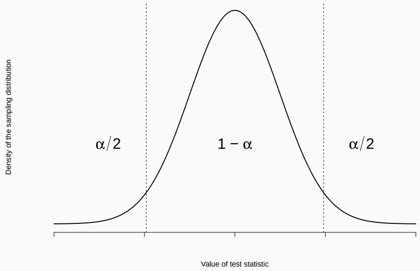
- `chisq.test()`: contingency table χ^2 tests
- `cor.test()`: association between paired samples
- `t.test()`: one- and two-sample *t* tests (also for paired data)
- `lm(y ~ x1 + x2 + x3 ...)`: fit a linear model
- `glm(y ~ x1 + x2 + x3 ...)`: fit a generalize linear model

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 hypothesis is true*

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



χ^2 test

Independence of observations

Hypothesis:

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

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:

```
tab <- xtabs(~ education + induced, infert)
tab
```

```

          induced
education   0  1  2
  0-5yrs    4  2  6
  6-11yrs  78 27 15
  12+ yrs  61 39 16
```

```
chisq.test(tab)
```

```


    Pearson's Chi-squared test

data:  tab
X-squared = 16.531, df = 4, p-value = 0.002384
```

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")
```

```

	Pearson's product-moment correlation

data:  speed and dist
t = 9.464, df = 48, p-value = 1.49e-12
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.6816422 0.8862036
sample estimates:
      cor 
0.8068949 
```

Correlation matrix

```
cor(benessere[, grep("item", colnames(benessere))])
```

```
            item1       item2      item3       item4       item5
item1  1.00000000  0.07820461 0.11579134 -0.05894317 -0.18117877
item2  0.07820461  1.00000000 0.24890831  0.21963611 -0.07757221
item3  0.11579134  0.24890831 1.00000000  0.04977145  0.03830005
item4 -0.05894317  0.21963611 0.04977145  1.00000000  0.05751880
item5 -0.18117877 -0.07757221 0.03830005  0.05751880  1.00000000
```

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:

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

In R:

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

```

    Welch Two Sample t-test

data:  len by supp
t = 1.9153, df = 55.309, p-value = 0.06063
alternative hypothesis: true difference in means between grou
95 percent confidence interval:
 -0.1710156  7.5710156
sample estimates:
mean in group OJ mean in group VC
        20.66333         16.96333
```

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:

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

In R function:

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

```

    Paired t-test

data:  extra[group == 1] and extra[group == 2]
t = -4.0621, df = 9, p-value = 0.002833
alternative hypothesis: true mean difference is not equal to
95 percent confidence interval:
 -2.4598858 -0.7001142
sample estimates:
mean difference
          -1.58
```

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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

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

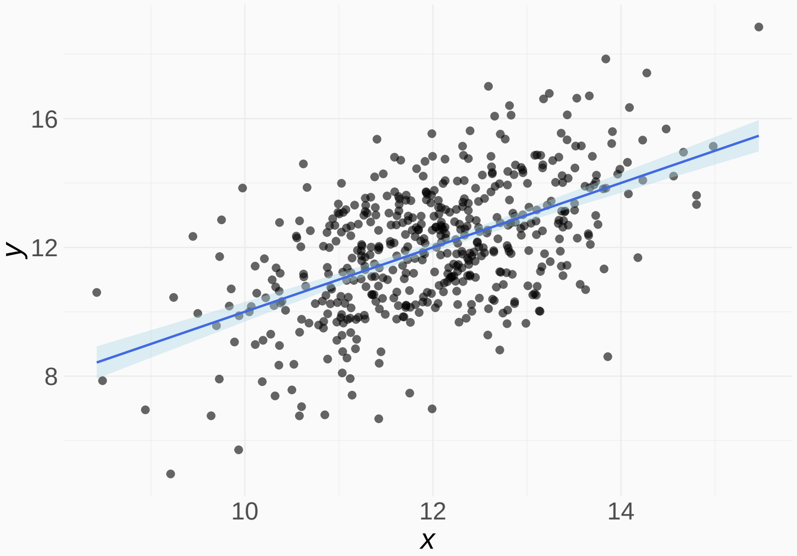
$g()$ is the link functions that connects the mean to the linear combination of predictors.

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: data



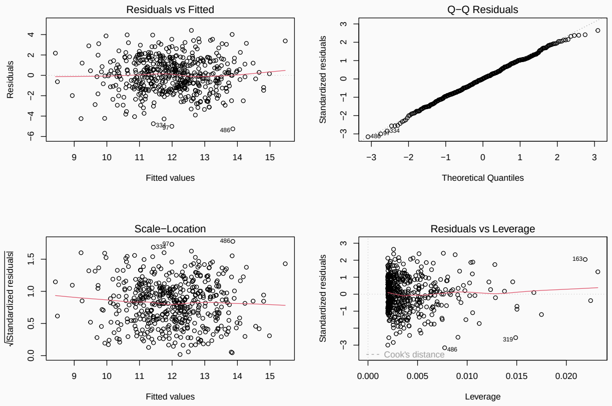
LM: Model

```r
model = lm(y ~ x, data = data)
summary(model)
```

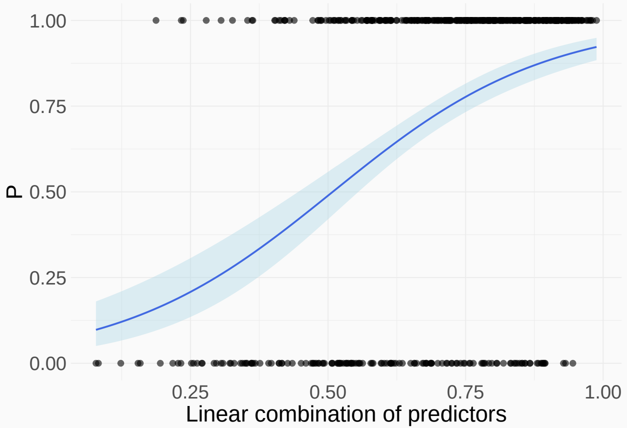
```

Call:
lm(formula = y ~ x, data = data)

Residuals:
    Min      1Q  Median      3Q     Max 
-5.2559 -1.1314  0.0162  1.1889  4.4123 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 10.90000    0.10580   103.0   <2e-16 ***
x            0.55000    0.03742    14.7   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.672 on 498 degrees of freedom
Multiple R-squared:  0.3025,	Adjusted R-squared:  0.3011 
F-statistic:   216 on 1 and 498 DF,  p-value: < 2.2e-16
```

Diagnostic

```r
par(mfrow = c(2,2))
plot(model)
```



GLM: Data


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

GLM: Model

```
model_bin <- glm(z ~x, data = data, family = "binomial")
summary(model_bin)
```

```
Call:
glm(formula = z ~ x, family = "binomial", data = data)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.04795    0.14021  -0.342    0.732
x            0.53713    0.06486   8.281   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 612.55  on 499  degrees of freedom
Residual deviance: 521.91  on 498  degrees of freedom
AIC: 525.91

Number of Fisher Scoring iterations: 4
```

Interpreting the parameters

```
# the coefficients are on the log-odds scale
my_coef = coef(model_bin)
# this function yields the probabilty values
binomial()$linkinv(my_coef)
```

```
(Intercept)           x
  0.4880139   0.6311456
```

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
```