"How to" in **R**

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This document present ways to perform basic operations in **R**:

- importing data
- data management
- graphical displaying
- modeling
- loops and parallel computing
- generating data through simulation

Contents

1 Packages

The following packages are necessary to run the code suggested in the document:

```r
## importing data and data management
library(data.table)

## graphical display
library(ggplot2)
library(ggthemes)
library(abind) # convert list to array

## modeling
library(car)

library(prodlim) # survival analysis
library(survival) # survival analysis

## statistical inference
library(multcomp) # adjust for multiple comparisons
library(exactci) ##  ci / p-values for proportions
library(exact2x2) ## compare proportions between groups
library(asht) ##  test on the quantile
library(BuyseTest) ## wilcoxon-test with estimated effect size
library(perm) ## permutation tests
library(quantreg) ## quantile regression
library(butils) ## partial residuals (butils::install_github("bozenne/butils"))

## diagnostics
library(gof) ## devtools::install_github("kkholst/gof")

## loops and parallel computing
library(pbapply)
library(doSNOW)
library(parallel)

## simulation
library(lava)
```

2 Import/export data

2.1 Set the working directory

The working directory is where **R** will, by default, look for files to import and export data or pictures. The current working directory can be accessed using:

```
getwd()
```

```
[1] "c:/Users/hpl802/AppData/Roaming/R"
```

It can be changed using the function `setwd()`:

```
path <- "c:/Users/hpl802/Documents/GitHub/bozenne.github.io/doc/howTo-R/"
setwd(path)
```

We can check that the working directory has indeed changed calling again `getwd()`:

```
getwd()
```

```
[1] "c:/Users/hpl802/Documents/GitHub/bozenne.github.io/doc/howTo-R"
```

2.2 See which files are present in the current directory

List all files in the current directory:

```
list.files()
```

```
 [1] "#howTo-R.org#"       "figures"             "howTo-R.aux"         "howTo-R.log"
 [5] "howTo-R.org"         "howTo-R.org_archive" "howTo-R.pdf"         "howTo-R.tex"
 [9] "howTo-R.toc"         "mydata.csv"          "mydata.txt"          "myplot.png"
[13] "Table1.docx"
```

There are many files. To list files in the current directory with a given extension, e.g. `.txt` use:

```
list.files(pattern = ".txt")
```

```
[1] "mydata.txt"
```

There is only one file with a `.txt` extension, it is called `mydata.txt`.

2.3 Check that the file we want to import exists:

Test whether the file exists:

```
file.exists("./mydata.txt")
```

```
[1] TRUE
```

2.4 Display a file before importing it

Display the first three lines of the file we want to import

```
readLines("./mydata.txt")[1:3]
```

```
[1] "Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3"
[2] "1 40 Male Yes 50 57 56 50.67 55.88 61.69"
[3] "2 38 Female No 52 57 63 50.26 55.73 60.37"
```

```
readLines("./mydata.csv")[1:3]
```

```
[1] "Id;Age;Gender;Treatment;weight_t1;weight_t2;weight_t3;size_t1;size_t2;size_t3"
[2] "1;40;Male;Yes;50;57;56;50,67;55,88;61,69"
[3] "2;38;Female;No;52;57;63;50,26;55,73;60,37"
```

2.5 Import a data from a file (.txt, .csv)

Import a file and store the dataset into a `data.frame` object:

```
dfW.data <- read.table("./mydata.txt", header = TRUE, na.strings = ".")
```

Import a file and store the dataset into a `data.table` object:

```
dtW.data <- fread("./mydata.txt", header = TRUE, na.strings = ".")
```

In both cases, the argument `na.strings` specifies which character(s) in the dataset stands for missing values. The argument `header=TRUE` indicates that the first line of the dataset contains the name of the columns of the dataset (and not the data of an observation). See `?read.table` or `?fread` for further explanations about the arguments of these functions.

Note:	`"./"`	stands for current directory, e.g. `"./mydata.txt"` abreviated in `"mydata.txt"`
	`"../"`	stands for parent directory, e.g. `"../mydata.txt"`
	`"/"`	stands for root directory, e.g. `"/mydata.txt"`

2.6 Import data from a specific format (e.g. excel files or outputs from SPSS/SAS)

There are many packages that can be used to read excel files, e.g.:

- **readxl** package (no dependency): function `read_excel`, `read_xls`, or `read_xlsx`.
- **xlsx** package: function `read.xlsx`.
- **gdata** package: function `read.xls`.
- **XLConnect** package: function `readWorksheet`.

The **foreign** package enable to read a variety for files, e.g.:

- `read.spss`: read an spss data file.
- `read.ssd`: obtain a data frame from a sas permanent dataset, via read.xport.

To load .rds files use `readRDS` and to load .rdata files use `load`.

2.7 Export data

To export a data.frame to a file one can use:

- `write.csv` to export a .csv file
- `write.table` to export a .txt file
- `readxl::read_excel` to export a .xlsx file
- `data.table::fwrite`

```
fwrite(dtW.data, file = "./mydata.csv", sep = ";", dec = ",")
fwrite(dtW.data, file = "./mydata.txt", sep = " ", dec = ".")
```

To export a single R object (can be anything) use `saveRDS`. To export several R object use `save`. To export the current workspace use `save.image`.

2.8 Export table

```
library(Publish)
myTable1 <- univariateTable(Treatment ~ Age + Gender + weight_t1, data = dtW.data)
```

Export to word:

```
library(officer)
myTable1.doc <- body_add_table(x = read_docx(),
                               value =  summary(myTable1))
print(myTable1.doc, target = "./Table1.docx")
```

```
[1] "c:/Users/hpl802/Documents/GitHub/bozenne.github.io/doc/howTo-R/Table1.docx"
```

2.9 Export graphs

The functions `pdf`, `png`, `postscript`, `svg`, `tiff` enables a graph to export to .pdf, .png, .eps, .svg, or .tiff file:

```
png("myplot.png")
plot(1:10)
dev.off()
```

```
null device
          1
```

```
file.exists("myplot.png")
```

```
[1] TRUE
```

For exporting graph generated by **ggplot2**, use `ggsave`.

3 Data management

3.1 Categorize age into groups

```
vec <- dfW.data$weight_t3
vec
```

```
 [1] 56 63 62 60 64 65 66 63 59 64 59 58 63 64 61 64 67 54 57 65 63 60 60 57 66 65 60 53 57 58 58
[32] 58 59 63 64 58 64 58 59 59 60 59 57 62 61 63 63 63 65 55 59 65 71 64 62 62 64 58 61 61 65 64
[63] 66 60 58 60 63 57 58 68 59 60 54 61 60 63 61 60 62 61 59 59 65 62 66 58 64 66 62 65 59 63 57
[94] 62 64 59 63 57 62 59 55 68
```

```
cut(vec, breaks = seq(0,100,5))
```

```
  [1] (55,60] (60,65] (60,65] (55,60] (60,65] (60,65] (65,70] (60,65] (55,60] (60,65] (55,60]
 [12] (55,60] (60,65] (60,65] (60,65] (60,65] (65,70] (50,55] (55,60] (60,65] (60,65] (55,60]
 [23] (55,60] (55,60] (65,70] (60,65] (55,60] (50,55] (55,60] (55,60] (55,60] (55,60] (55,60]
 [34] (60,65] (60,65] (55,60] (60,65] (55,60] (55,60] (55,60] (55,60] (55,60] (55,60] (60,65]
 [45] (60,65] (60,65] (60,65] (60,65] (60,65] (50,55] (55,60] (60,65] (70,75] (60,65] (60,65]
 [56] (60,65] (60,65] (55,60] (60,65] (60,65] (60,65] (60,65] (65,70] (55,60] (55,60] (55,60]
 [67] (60,65] (55,60] (55,60] (65,70] (55,60] (55,60] (50,55] (60,65] (55,60] (60,65] (60,65]
 [78] (55,60] (60,65] (60,65] (55,60] (55,60] (60,65] (60,65] (65,70] (55,60] (60,65] (65,70]
 [89] (60,65] (60,65] (55,60] (60,65] (55,60] (60,65] (60,65] (55,60] (60,65] (55,60] (60,65]
[100] (55,60] (50,55] (65,70]
20 Levels: (0,5] (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] ... (95,100]
```

3.2 Convert list to array

```
ll <- list(matrix(1,2,2),
           matrix(3,2,2),
           matrix(9,2,2))
do.call(abind, c(ll, list(along = 3)))
```

```
, , 1

     [,1] [,2]
[1,]    1    1
[2,]    1    1

, , 2

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

, , 3

     [,1] [,2]
[1,]    9    9
[2,]    9    9
```

3.3 Apply function for each element of a list

```r
ll <- list(matrix(1,2,2),
           matrix(3,2,2),
           matrix(9,2,2))
apply(do.call(abind, c(ll, list(along = 3))), 1:2, median)
```

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

4 Data management using the *data.table* package

4.1 Introduction

In **R**, data are usually stored in `data.frame` object since compared to matrices, it enables to store in a same object different types of variables (e.g. numeric, categorical, ...). Data management can be performed using the core R function, e.g. using `for` loops or the `apply`, `tapply`, `lapply` functions. However this approach will most often requires many lines of code to get the expected transformation. A faster and safer approach is to functions/packages suited to the structure of longitudinal data.

We present here how to use the *data.table* package to perform the most common operations in data management. The main benefit of using this package are:

- a concise and consistant syntax for performing the most common operations in data management.
- fast and memory efficient implementation (i.e. able to deal with dataset with millions of lines).
- share common features with the SQL terminology.

A concise summary of the features can be found at: `https://s3.amazonaws.com/assets.datacamp.com/img/blog/data+table+cheat+sheet.pdf`

Additional documentation can be found:

- in the documentation of the function `data.table`: type `?data.table` in **R**.
- on the webpage of the package: `https://github.com/Rdatatable/data.table/wiki`.
- in the vignettes of the package: `https://cran.r-project.org/web/packages/data.table/vignettes/datatable-intro.html`.

Note: the **wide format** denote a format where each line corresponds to a different individuals. Repeated measurements of the same quantity (e.g. weight) for a given individual are stored in different columns (e.g. `weight_t1`, `weight_t2`).

```
head(dtW.data)
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
2:  2  38 Female        No        52        57        63   50.26   55.73   60.37
3:  3  41   Male        No        47        54        62   46.61   50.89   56.52
4:  4  41 Female       Yes        48        55        60   45.95   53.10   59.82
5:  5  42 Female       Yes        52        56        64   52.86   58.41   63.79
6:  6  38   Male       Yes        52        59        65   49.37   57.91   64.45
```

The **long** format denote a format where the same individual may appear on different lines but a given quantity is only stored in one column. In case of repeated measurement, an additional column encodes at which repetition the measurement was obtained (e.g. `time`):

```
head(dtL.data)
```

```
   Id Gender Treatment Age time weight  size
1:  1   Male       Yes  40    1     50 50.67
2:  2 Female        No  38    1     52 50.26
3:  3   Male        No  41    1     47 46.61
4:  4 Female       Yes  41    1     48 45.95
5:  5 Female       Yes  42    1     52 52.86
6:  6   Male       Yes  38    1     52 49.37
```

4.2 Display a dataset

Using the `print` method:

```
print(dtW.data) # equivalent to just dtW.data
```

```
      Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
  1:   1  40   Male       Yes        50        57        56   50.67   55.88   61.69
  2:   2  38 Female        No        52        57        63   50.26   55.73   60.37
  3:   3  41   Male        No        47        54        62   46.61   50.89   56.52
  4:   4  41 Female       Yes        48        55        60   45.95   53.10   59.82
  5:   5  42 Female       Yes        52        56        64   52.86   58.41   63.79
 ---
 98:  98  39   Male        No        53        59        57   49.51   53.80   61.13
 99:  99  42 Female       Yes        51        57        62   47.60   56.55   59.47
100: 100  40 Female        No        53        55        59   50.06   54.90   61.89
101: 101  38 Female        No        48        58        55   49.51   54.01   62.32
102: 102  39 Female        No        52        58        68   47.35   56.08   59.49
```

To print more lines use the argument `topn`:

```
print(dtW.data, topn = 6)
```

```
      Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
  1:   1  40   Male       Yes        50        57        56   50.67   55.88   61.69
  2:   2  38 Female        No        52        57        63   50.26   55.73   60.37
  3:   3  41   Male        No        47        54        62   46.61   50.89   56.52
  4:   4  41 Female       Yes        48        55        60   45.95   53.10   59.82
  5:   5  42 Female       Yes        52        56        64   52.86   58.41   63.79
  6:   6  38   Male       Yes        52        59        65   49.37   57.91   64.45
 ---
 97:  97  39   Male        No        50        60        63   51.72   57.86   61.06
 98:  98  39   Male        No        53        59        57   49.51   53.80   61.13
 99:  99  42 Female       Yes        51        57        62   47.60   56.55   59.47
100: 100  40 Female        No        53        55        59   50.06   54.90   61.89
101: 101  38 Female        No        48        58        55   49.51   54.01   62.32
102: 102  39 Female        No        52        58        68   47.35   56.08   59.49
```

4.3 Extract row(s), i.e. all the variables relative to one or several observations

4.3.1 Extract row(s) using row numbers

Extract the third line:

```
dtW.data[3]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  3  41   Male        No        47        54        62   46.61   50.89   56.52
```

Extract line one to four:

```
dtW.data[1:4]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
2:  2  38 Female        No        52        57        63   50.26   55.73   60.37
3:  3  41   Male        No        47        54        62   46.61   50.89   56.52
4:  4  41 Female       Yes        48        55        60   45.95   53.10   59.82
```

Extract line one, three, and five:

```
dtW.data[c(1,3,5)]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
2:  3  41   Male        No        47        54        62   46.61   50.89   56.52
3:  5  42 Female       Yes        52        56        64   52.86   58.41   63.79
```

4.3.2 Extract row(s) according to conditions

Extract lines corresponding to the observations with `Id` equals to `1`:

```
dtW.data[Id == 1]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
```

Extract lines corresponding to the males:

```
newdata <- dtW.data[Gender == "Male"]
head(newdata)
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
2:  3  41   Male        No        47        54        62   46.61   50.89   56.52
3:  6  38   Male       Yes        52        59        65   49.37   57.91   64.45
4:  9  42   Male       Yes        46        52        59   49.53   52.84   60.54
5: 11  42   Male        No        55        58        59   50.03   55.09   60.94
6: 12  41   Male       Yes        50        52        58   48.66   52.73   55.86
```

Extract lines corresponding to the males whose age is inferior or equal to 38:

```
dtW.data[Gender == "Male" & Age <= 38]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  6  38   Male       Yes        52        59        65   49.37   57.91   64.45
2: 41  37   Male        No        53        55        60   47.59   53.75   57.00
3: 76  38   Male        No        53        57        63   48.10   54.82   55.29
4: 91  38   Male        No        51        55        59   52.05   57.01   59.53
```

Extract lines corresponding to observations where `Age` is inferior or equal to 37, or greater or equal to 43 :

```
dtW.data[Age <= 37 | Age >= 43]
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1: 10  43 Female       Yes        52        57        64   53.22   57.25   62.94
2: 41  37   Male        No        53        55        60   47.59   53.75   57.00
3: 45  43 Female       Yes        48        51        61   49.88   54.41   56.18
4: 73  43   Male       Yes        46        53        54   48.44   52.74   60.93
```

4.4 Extract column(s), i.e. all the observations relative to one or several variables

4.4.1 Extract column(s) using column numbers

Extract the third column:

```
dtW.data[, 3, with = FALSE]
```

```
     Gender
  1:   Male
  2: Female
  3:   Male
  4: Female
  5: Female
 ---
 98:   Male
 99: Female
100: Female
101: Female
102: Female
```

Alternatively:

```
dtW.data[[3]]
```

```
  [1] "Male"   "Female" "Male"   "Female" "Female" "Male"   "Female" "Female" "Male"   "Female"
 [11] "Male"   "Male"   "Female" "Female" "Female" "Female" "Female" "Female" "Male"   "Female"
 [21] "Male"   "Male"   "Female" "Male"   "Female" "Male"   "Male"   "Male"   "Female" "Female"
 [31] "Male"   "Male"   "Male"   "Male"   "Female" "Female" "Female" "Female" "Male"   "Male"
 [41] "Male"   "Female" "Female" "Female" "Female" "Female" "Female" "Female" "Male"   "Male"
 [51] "Female" "Male"   "Male"   "Male"   "Female" "Female" "Male"   "Male"   "Female" "Male"
 [61] "Female" "Male"   "Male"   "Male"   "Female" "Male"   "Female" "Male"   "Male"   "Male"
 [71] "Female" "Female" "Male"   "Female" "Female" "Male"   "Female" "Female" "Female" "Female"
 [81] "Male"   "Male"   "Female" "Female" "Male"   "Female" "Female" "Female" "Female" "Female"
 [91] "Male"   "Male"   "Male"   "Male"   "Male"   "Male"   "Male"   "Male"   "Female" "Female"
[101] "Female" "Female"
```

Extract column one, three, and five:

```
dtW.data[, c(1,3,5), with = FALSE]
```

```
      Id Gender weight_t1
  1:   1   Male        50
  2:   2 Female        52
  3:   3   Male        47
  4:   4 Female        48
  5:   5 Female        52
 ---
 98:  98   Male        53
 99:  99 Female        51
100: 100 Female        53
101: 101 Female        48
102: 102 Female        52
```

4.4.2 Extract column(s) using column names

Extract one column, e.g. `Id`:

```
dtW.data[, Id] # similar to dtW.data[,"Id",with=FALSE]
```

```
 [1]   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23
[24]  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40  41  42  43  44  45  46
[47]  47  48  49  50  51  52  53  54  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69
[70]  70  71  72  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90  91  92
[93]  93  94  95  96  97  98  99 100 101 102
```

Extract several columns, e.g. `Id` and `Age`:

```
dtW.data[, .(Id,Age)]
# similar to dtW.data[, c("Id","Age"), with = FALSE]
# similar to dtW.data[, .SD, .SDcols = c("Id","Age")]
```

```
      Id Age
  1:   1  40
  2:   2  38
  3:   3  41
  4:   4  41
  5:   5  42
 ---        
 98:  98  39
 99:  99  42
100: 100  40
101: 101  38
102: 102  39
```

4.5 Work with categorical variables

4.5.1 Convert a numeric/character into a factor

```
class(dtW.data[,Gender])
```

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

```
dtW.data[, Gender := as.factor(Gender)]
class(dtW.data[,Gender])
```

```
[1] "factor"
```

```
class(dtW.data[,Id])
```

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

```
dtW.data[, Id := as.factor(Id)]
class(dtW.data[,Id])
```

```
[1] "factor"
```

4.5.2 Divide a continuous variable into categories

```
dtW.data[, AgeCategory := cut(Age, breaks = c(0,38,40,42,100))]
dtW.data[,.(Age,AgeCategory)]
```

```
     Age AgeCategory
  1:  40     (38,40]
  2:  38      (0,38]
  3:  41     (40,42]
  4:  41     (40,42]
  5:  42     (40,42]
 ---
 98:  39     (38,40]
 99:  42     (40,42]
100:  40     (38,40]
101:  38      (0,38]
102:  39     (38,40]
```

Alternatively:

```
dtW.data[, AgeCategory0 := findInterval(Age, vec = c(0,38,40,42,100))]
dtW.data[,.(Age,AgeCategory0)]
```

```
     Age AgeCategory0
  1:  40            3
  2:  38            2
  3:  41            3
  4:  41            3
  5:  42            4
 ---
 98:  39            2
 99:  42            4
100:  40            3
101:  38            2
102:  39            2
```

The arguments `rightmost` and `left.open` can be used to decide what to do with the values equaling the breaks (i.e. one of the value of the argument `vec`). But it is often easier to modify `vec` such that no value equals the breaks, e.g. using `c(0,38,40,42,100)-1e12`.

4.5.3 Redefine the levels of a factor variable

```
dtW.data[,AgeCategory0 := factor(AgeCategory0,
                                 levels = 1:4,
                                 labels = c("[0-37)","[38-39)","[40-41)","[42-100)"))]
dtW.data[,.(Age,AgeCategory0,AgeCategory)]
```

```
     Age AgeCategory0 AgeCategory
  1:  40      [40-41)     (38,40]
  2:  38      [38-39)      (0,38]
  3:  41      [40-41)     (40,42]
  4:  41      [40-41)     (40,42]
  5:  42     [42-100)     (40,42]
 ---
 98:  39      [38-39)     (38,40]
 99:  42     [42-100)     (40,42]
100:  40      [40-41)     (38,40]
101:  38      [38-39)      (0,38]
102:  39      [38-39)     (38,40]
```

4.6 Extract simple features of a dataset

4.6.1 Number of rows and columns

```
dim(dtW.data)
```

```
[1] 102  12
```

The dataset has 102 rows and 7 columns.

4.6.2 Name of the columns

```
names(dtW.data)
```

```
[1] "Id"           "Age"          "Gender"       "Treatment"    "weight_t1"    "weight_t2"
[7] "weight_t3"    "size_t1"      "size_t2"      "size_t3"      "AgeCategory"  "AgeCategory0"
```

4.6.3 Type of the columns

```
str(dtW.data)
```

```
Classes 'data.table' and 'data.frame':        102 obs. of  12 variables:
 $ Id          : Factor w/ 102 levels "1","2","3","4",..: 1 2 3 4 5 6 7 8 9 10 ...
 $ Age         : num  40 38 41 41 42 38 42 40 42 43 ...
 $ Gender      : Factor w/ 2 levels "Female","Male": 2 1 2 1 1 2 1 1 2 1 ...
 $ Treatment   : chr  "Yes" "No" "No" "Yes" ...
 $ weight_t1   : num  50 52 47 48 52 52 52 51 46 52 ...
 $ weight_t2   : int  57 57 54 55 56 59 63 52 52 57 ...
 $ weight_t3   : int  56 63 62 60 64 65 66 63 59 64 ...
 $ size_t1     : num  50.7 50.3 46.6 46 52.9 ...
 $ size_t2     : num  55.9 55.7 50.9 53.1 58.4 ...
 $ size_t3     : num  61.7 60.4 56.5 59.8 63.8 ...
 $ AgeCategory : Factor w/ 4 levels "(0,38]","(38,40]",..: 2 1 3 3 3 1 3 2 3 4 ...
 $ AgeCategory0: Factor w/ 4 levels "[0-37)","[38-39)",..: 3 2 3 3 4 2 4 3 4 4 ...
 - attr(*, ".internal.selfref")=<externalptr>
 - attr(*, "index")= int
```

The column `Gender` contains a factor variable with two levels `"Yes"` and `"No"`.
The column `Id` contains integers while the columns `weight_t3` contains numeric numbers.

4.6.4 Summary statistics by column

```
summary(dtW.data)
```

```
      Id           Age            Gender       Treatment           weight_t1       weight_t2    
 1      : 1   Min.   :37.00   Female:54   Length:102         Min.   :46.00   Min.   :51.00  
 2      : 1   1st Qu.:39.00   Male  :48   Class :character   1st Qu.:49.25   1st Qu.:55.00  
 3      : 1   Median :40.00               Mode  :character   Median :51.00   Median :57.00  
 4      : 1   Mean   :40.26                                  Mean   :50.87   Mean   :56.29  
 5      : 1   3rd Qu.:41.00                                  3rd Qu.:52.00   3rd Qu.:58.00  
 6      : 1   Max.   :43.00                                  Max.   :57.00   Max.   :63.00  
 (Other):96                                                                                 
   weight_t3       size_t1         size_t2         size_t3        AgeCategory   AgeCategory0
 Min.   :53.0   Min.   :45.67   Min.   :50.89   Min.   :55.02   (0,38]  : 9   [0-37)  : 1  
 1st Qu.:59.0   1st Qu.:48.45   1st Qu.:54.17   1st Qu.:59.35   (38,40] :48   [38-39) :29  
 Median :61.0   Median :50.44   Median :55.59   Median :61.00   (40,42] :42   [40-41) :53  
 Mean   :61.2   Mean   :50.55   Mean   :55.54   Mean   :60.98   (42,100]: 3   [42-100):19  
 3rd Qu.:64.0   3rd Qu.:52.01   3rd Qu.:57.03   3rd Qu.:62.66                              
 Max.   :71.0   Max.   :59.15   Max.   :61.45   Max.   :67.06                              
```

The column `Gender` contains 48 `Male` and 54 `Female`. The median value of `Age` is 40.

4.6.5 Number of missing values

Total number

```
sum(is.na(dtW.data))
```

```
[1] 0
```

Number of missing values by variable:

```
colSums(is.na(dtW.data))
```

```
         Id          Age       Gender    Treatment    weight_t1    weight_t2    weight_t3 
          0            0            0            0            0            0            0 
    size_t1      size_t2      size_t3  AgeCategory AgeCategory0 
          0            0            0            0            0 
```

Number of missing values by observation:

```
rowSums(is.na(dtW.data))
```

```
  [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [48] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [95] 0 0 0 0 0 0 0 0
```

4.6.6 Mean value of a column

First extract the values from a column:

```
vec.tempo <- dtW.data[,Age]
```

Then compute the mean:

```
mean(vec.tempo)
```

```
[1] 40.26471
```

Alternatively:

```
dtW.data[,mean(Age)]
```

```
[1] 40.26471
```

4.6.7 Correlation between values of several columns

First extract the columns:

```
dt.tempo <- dtW.data[,.(weight_t1,weight_t2,weight_t3)]
```

Then compute the correlation:

```
cor(dt.tempo)
```

```
          weight_t1 weight_t2 weight_t3
weight_t1 1.0000000 0.1882809 0.3179175
weight_t2 0.1882809 1.0000000 0.2374259
weight_t3 0.3179175 0.2374259 1.0000000
```

Alternatively:

```
dtW.data[,cor(cbind(weight_t1,weight_t2,weight_t3))]
```

```
          weight_t1 weight_t2 weight_t3
weight_t1 1.0000000 0.1882809 0.3179175
weight_t2 0.1882809 1.0000000 0.2374259
weight_t3 0.3179175 0.2374259 1.0000000
```

4.7 Performing operations on a group of rows

4.7.1 Computing the number of observations per subgroup

Compute the number of observation per gender:

```
dtW.data[, .N, by = "Gender"]
```

```
   Gender  N
1:   Male 48
2: Female 54
```

Alternatively:

```
dtW.data[, NROW(.SD), by = "Gender"]
```

```
   Gender V1
1:   Male 48
2: Female 54
```

4.7.2 Computing the mean by subgroup

Compute the mean weight at time 1 by gender:

```
dtW.data[, mean(weight_t1), by = "Gender"]
```

```
   Gender       V1
1:   Male 50.45833
2: Female 51.24074
```

Alternative display:

```
dtW.data[, .(mean = mean(weight_t1)), by = "Gender"]
```

```
   Gender     mean
1:   Male 50.45833
2: Female 51.24074
```

Compute the mean weight at time 1 to 3 by gender:

```
dtW.data[, .(mean_t1 = mean(weight_t1),
             mean_t2 = mean(weight_t2),
             mean_t3 = mean(weight_t3)),
         by = "Gender"]
```

```
   Gender  mean_t1  mean_t2  mean_t3
1:   Male 50.45833 55.81250 60.64583
2: Female 51.24074 56.72222 61.68519
```

Compute the mean weight at time 1 to 3 by gender and treatment group:

```
dtW.data[, .(mean_t1 = mean(weight_t1),
             mean_t2 = mean(weight_t2),
             mean_t3 = mean(weight_t3)),
         by = c("Gender","Treatment")]
```

```
   Gender Treatment  mean_t1  mean_t2  mean_t3
1:   Male       Yes 50.42857 55.09524 60.23810
2: Female        No 51.65517 56.93103 61.75862
3:   Male        No 50.48148 56.37037 60.96296
4: Female       Yes 50.76000 56.48000 61.60000
```

4.7.3 Computing the correlation matrix by subgroup

We create a matrix containing the variables of interest, compute the correlation matrix and print it.

```
null.result <- dtW.data[, print(cor(cbind(weight_t1,weight_t2,weight_t3))),
                        by = "Gender"]
```

```
          weight_t1 weight_t2 weight_t3
weight_t1 1.0000000 0.2867753 0.2886667
weight_t2 0.2867753 1.0000000 0.2740567
weight_t3 0.2886667 0.2740567 1.0000000
           weight_t1  weight_t2 weight_t3
weight_t1 1.00000000 0.03214955 0.3148578
weight_t2 0.03214955 1.00000000 0.1551156
weight_t3 0.31485784 0.15511561 1.0000000
```

If we want to store the correlation matrix we need to wrap it into `.()` to keep the matrix format:

```
result <- dtW.data[, .(cor = .(cor(cbind(weight_t1,weight_t2,weight_t3)))),
                   by = "Gender"]
result[,cor]
```

```
[[1]]
          weight_t1 weight_t2 weight_t3
weight_t1 1.0000000 0.2867753 0.2886667
weight_t2 0.2867753 1.0000000 0.2740567
weight_t3 0.2886667 0.2740567 1.0000000

[[2]]
           weight_t1  weight_t2 weight_t3
weight_t1 1.00000000 0.03214955 0.3148578
weight_t2 0.03214955 1.00000000 0.1551156
weight_t3 0.31485784 0.15511561 1.0000000
```

Alternatively:

```
null.result <- dtW.data[, print(cor(.SD)),
                        .SDcols = c("weight_t1","weight_t2","weight_t3"),
                        by = "Gender"]
```

```
          weight_t1 weight_t2 weight_t3
weight_t1 1.0000000 0.2867753 0.2886667
weight_t2 0.2867753 1.0000000 0.2740567
weight_t3 0.2886667 0.2740567 1.0000000
           weight_t1  weight_t2 weight_t3
weight_t1 1.00000000 0.03214955 0.3148578
weight_t2 0.03214955 1.00000000 0.1551156
weight_t3 0.31485784 0.15511561 1.0000000
```

4.8 Sort a dataset according to one or several variables

Sort the dataset according to `Age`:

```
setkeyv(dtW.data, c("Age"))
dtW.data
```

```
     Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3 AgeCategory
  1: 41  37   Male        No        53        55        60   47.59   53.75   57.00      (0,38]
  2:  2  38 Female        No        52        57        63   50.26   55.73   60.37      (0,38]
  3:  6  38   Male       Yes        52        59        65   49.37   57.91   64.45      (0,38]
  4: 46  38 Female        No        53        57        63   49.27   61.45   66.59      (0,38]
  5: 48  38 Female        No        52        57        63   54.27   57.71   65.63      (0,38]
 ---
 98: 95  42   Male       Yes        51        55        64   51.05   56.48   60.30     (40,42]
 99: 99  42 Female       Yes        51        57        62   47.60   56.55   59.47     (40,42]
100: 10  43 Female       Yes        52        57        64   53.22   57.25   62.94    (42,100]
101: 45  43 Female       Yes        48        51        61   49.88   54.41   56.18    (42,100]
102: 73  43   Male       Yes        46        53        54   48.44   52.74   60.93    (42,100]
     AgeCategory0
  1:       [0-37)
  2:      [38-39)
  3:      [38-39)
  4:      [38-39)
  5:      [38-39)
 ---
 98:     [42-100)
 99:     [42-100)
100:     [42-100)
101:     [42-100)
102:     [42-100)
```

Sort the dataset according to `Age` and then `weight_t1`:

```
setkeyv(dtW.data, cols = c("Age","weight_t1"))
dtW.data
```

```
      Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3 AgeCategory
  1:  41  37   Male        No        53        55        60   47.59   53.75   57.00      (0,38]
  2: 101  38 Female        No        48        58        55   49.51   54.01   62.32      (0,38]
  3:  59  38 Female       Yes        49        60        61   51.08   53.77   60.75      (0,38]
  4:  91  38   Male        No        51        55        59   52.05   57.01   59.53      (0,38]
  5:   2  38 Female        No        52        57        63   50.26   55.73   60.37      (0,38]
 ---
 98:  11  42   Male        No        55        58        59   50.03   55.09   60.94     (40,42]
 99:  54  42   Male       Yes        57        60        64   58.75   57.57   63.98     (40,42]
100:  73  43   Male       Yes        46        53        54   48.44   52.74   60.93    (42,100]
101:  45  43 Female       Yes        48        51        61   49.88   54.41   56.18    (42,100]
102:  10  43 Female       Yes        52        57        64   53.22   57.25   62.94    (42,100]
     AgeCategory0
  1:       [0-37)
  2:      [38-39)
  3:      [38-39)
  4:      [38-39)
  5:      [38-39)
 ---
 98:     [42-100)
 99:     [42-100)
100:     [42-100)
101:     [42-100)
102:     [42-100)
```

4.9 Change the names of the column in a dataset

Use a small dataset

```
dt.simple <- dtW.data[,.(Age,Gender,Id,Treatment)]
head(dt.simple)
```

```
   Age Gender  Id Treatment
1:  37   Male  41        No
2:  38 Female 101        No
3:  38 Female  59       Yes
4:  38   Male  91        No
5:  38 Female   2        No
6:  38   Male   6       Yes
```

Change all names:

```
setnames(dt.simple, c("AgeXX","GenderYY","IdZZ","Treat"))
head(dt.simple)
```

```
   AgeXX GenderYY IdZZ Treat
1:    37     Male   41    No
2:    38   Female  101    No
3:    38   Female   59   Yes
4:    38     Male   91    No
5:    38   Female    2    No
6:    38     Male    6   Yes
```

Change one or several names (less memory efficient):

```
names(dt.simple)[1:2] <- c("Age","Gender")
head(dt.simple)
```

```
   Age Gender IdZZ Treat
1:  37   Male   41    No
2:  38 Female  101    No
3:  38 Female   59   Yes
4:  38   Male   91    No
5:  38 Female    2    No
6:  38   Male    6   Yes
```

4.10 Converting a dataset from the wide format to the long format

4.10.1 Univariate melt

Data in the wide format:

```
head(dtW.data)
```

```
    Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3 AgeCategory
1:  41  37   Male        No        53        55        60   47.59   53.75   57.00      (0,38]
2: 101  38 Female        No        48        58        55   49.51   54.01   62.32      (0,38]
3:  59  38 Female       Yes        49        60        61   51.08   53.77   60.75      (0,38]
4:  91  38   Male        No        51        55        59   52.05   57.01   59.53      (0,38]
5:   2  38 Female        No        52        57        63   50.26   55.73   60.37      (0,38]
6:   6  38   Male       Yes        52        59        65   49.37   57.91   64.45      (0,38]
   AgeCategory0
1:       [0-37)
2:      [38-39)
3:      [38-39)
4:      [38-39)
5:      [38-39)
6:      [38-39)
```

The convertion can be done naming explicitely the columns or using `patterns`:

```
dtL.data <- melt(dtW.data, id.vars = c("Id","Gender","Treatment","Age"),
                 measure=c("weight_t1","weight_t2","weight_t3"),
                 variable.name = "time", value.name = "weight")

dtL.data.bis <- melt(dtW.data, id.vars = c("Id","Gender","Treatment","Age"),
                     measure=patterns("weight_t"),
                     variable.name = "time", value.name = "weight")

identical(dtL.data, dtL.data.bis)
```

```
Warning message:
In melt.data.table(dtW.data, id.vars = c("Id", "Gender", "Treatment",  :
  'measure.vars' [weight_t1, weight_t2, weight_t3] are not all of the same type. By order of hierarchy, the mo
Warning message:
In melt.data.table(dtW.data, id.vars = c("Id", "Gender", "Treatment",  :
  'measure.vars' [weight_t1, weight_t2, weight_t3] are not all of the same type. By order of hierarchy, the mo
[1] TRUE
```

Arguments (see `?melt.data.table` for more details):

- `id.vars`: name of the column(s) that are kept constant over the repetitions
- `measure.vars`: name of the columns to be melted in a single one (i.e. repeated measurements).

Data in the long format:

```
head(dtL.data)
```

```
    Id Gender Treatment Age      time weight
1:  41   Male        No  37 weight_t1     53
2: 101 Female        No  38 weight_t1     48
3:  59 Female       Yes  38 weight_t1     49
4:  91   Male        No  38 weight_t1     51
5:   2 Female        No  38 weight_t1     52
6:   6   Male       Yes  38 weight_t1     52
```

Reorder the data by Id and time:

```
setkeyv(dtL.data, c("Id","time"))
head(dtL.data)
```

```
   Id Gender Treatment Age      time weight
1:  1   Male       Yes  40 weight_t1     50
2:  1   Male       Yes  40 weight_t2     57
3:  1   Male       Yes  40 weight_t3     56
4:  2 Female        No  38 weight_t1     52
5:  2 Female        No  38 weight_t2     57
6:  2 Female        No  38 weight_t3     63
```

4.10.2 Multivariate melt

Use a list of vectors each containing a vector with the columns to be melted:

```
dtL.data <- melt(dtW.data, id.vars = c("Id","Gender","Treatment","Age"),
                 measure=list(c("weight_t1","weight_t2","weight_t3"),
                              c("size_t1","size_t2","size_t3")),
                 variable.name = "time", value.name = c("weight","size"))

dtL.data.bis <- melt(dtW.data, id.vars = c("Id","Gender","Treatment","Age"),
                     measure=patterns("weight_t","size_t"),
                     variable.name = "time", value.name = c("weight","size"))

identical(dtL.data,dtL.data.bis)
```

```
[1] TRUE
```

```
dtL.data
```

```
      Id Gender Treatment Age time weight  size
  1:  41   Male        No  37    1     53 47.59
  2: 101 Female        No  38    1     48 49.51
  3:  59 Female       Yes  38    1     49 51.08
  4:  91   Male        No  38    1     51 52.05
  5:   2 Female        No  38    1     52 50.26
 ---
302:  11   Male        No  42    3     59 60.94
303:  54   Male       Yes  42    3     64 63.98
304:  73   Male       Yes  43    3     54 60.93
305:  45 Female       Yes  43    3     61 56.18
306:  10 Female       Yes  43    3     64 62.94
```

4.11 Converting a dataset from the long format to the wide format

4.11.1 Univariate

Data in the long format:

```
head(dtL.data)
```

```
    Id Gender Treatment Age time weight  size
1:  41   Male        No  37    1     53 47.59
2: 101 Female        No  38    1     48 49.51
3:  59 Female       Yes  38    1     49 51.08
4:  91   Male        No  38    1     51 52.05
5:   2 Female        No  38    1     52 50.26
6:   6   Male       Yes  38    1     52 49.37
```

The convertion can be done using a formula:

- left side: variables that do not vary
- right side: variable indexing the repetition whose values will be used to name the new columns.

```
dtW.data <- dcast(dtL.data, value.var = c("weight"),
                  formula = Id + Gender + Treatment + Age ~ time)
```

Data in the wide format:

```
setnames(dtW.data, old = c("1","2","3"), new = paste0("weight_t",1:3))
dtW.data
```

```
      Id Gender Treatment Age weight_t1 weight_t2 weight_t3
  1:   1   Male       Yes  40        50        57        56
  2:   2 Female        No  38        52        57        63
  3:   3   Male        No  41        47        54        62
  4:   4 Female       Yes  41        48        55        60
  5:   5 Female       Yes  42        52        56        64
 ---
 98:  98   Male        No  39        53        59        57
 99:  99 Female       Yes  42        51        57        62
100: 100 Female        No  40        53        55        59
101: 101 Female        No  38        48        58        55
102: 102 Female        No  39        52        58        68
```

4.11.2 Multivariate

Same as before but with several elements in the argument `value.var`. Note that the repetition index (here `time`) must be the same for both variables:

```
dtW.data <- dcast(dtL.data, value.var = c("weight","size"),
                  formula = Id + Gender + Treatment + Age ~ time)
```

Data in the wide format:

```
dtW.data
```

```
      Id Gender Treatment Age weight_1 weight_2 weight_3 size_1 size_2 size_3
  1:   1   Male       Yes  40       50       57       56  50.67  55.88  61.69
  2:   2 Female        No  38       52       57       63  50.26  55.73  60.37
  3:   3   Male        No  41       47       54       62  46.61  50.89  56.52
  4:   4 Female       Yes  41       48       55       60  45.95  53.10  59.82
  5:   5 Female       Yes  42       52       56       64  52.86  58.41  63.79
 ---
 98:  98   Male        No  39       53       59       57  49.51  53.80  61.13
 99:  99 Female       Yes  42       51       57       62  47.60  56.55  59.47
100: 100 Female        No  40       53       55       59  50.06  54.90  61.89
101: 101 Female        No  38       48       58       55  49.51  54.01  62.32
102: 102 Female        No  39       52       58       68  47.35  56.08  59.49
```

5 Graphical display

5.1 Descriptive plots

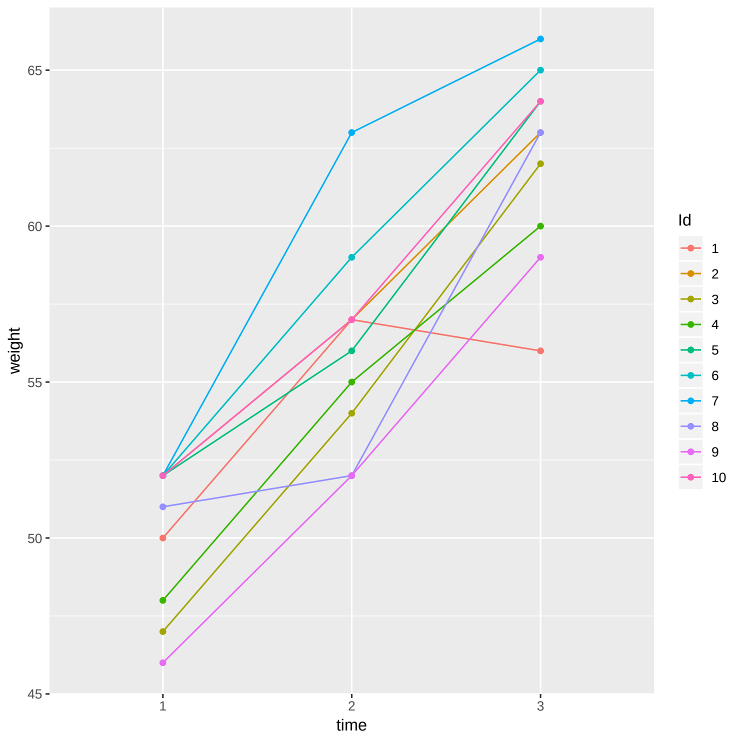
```
head(dtL.data)
```

```
   Id Gender Treatment Age time weight  size
1:  1   Male       Yes  40    1     50 50.67
2:  2 Female        No  38    1     52 50.26
3:  3   Male        No  41    1     47 46.61
4:  4 Female       Yes  41    1     48 45.95
5:  5 Female       Yes  42    1     52 52.86
6:  6   Male       Yes  38    1     52 49.37
```

5.1.1 Spaguetti plot

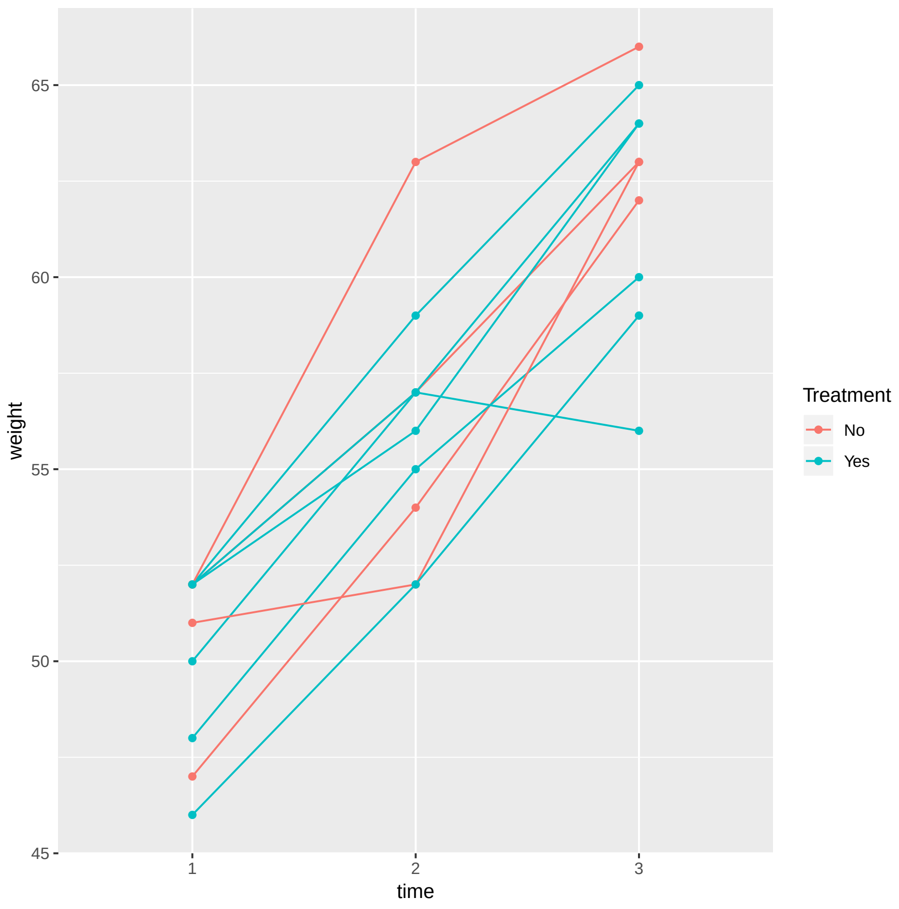
1. color by individual (first ten individuals)

```
gg.spaguetti1 <- ggplot(dtL.data[Id %in% 1:10],
                        aes(x = time, y = weight, color = Id, group = Id))
gg.spaguetti1 <- gg.spaguetti1 + geom_line() + geom_point()
gg.spaguetti1
```



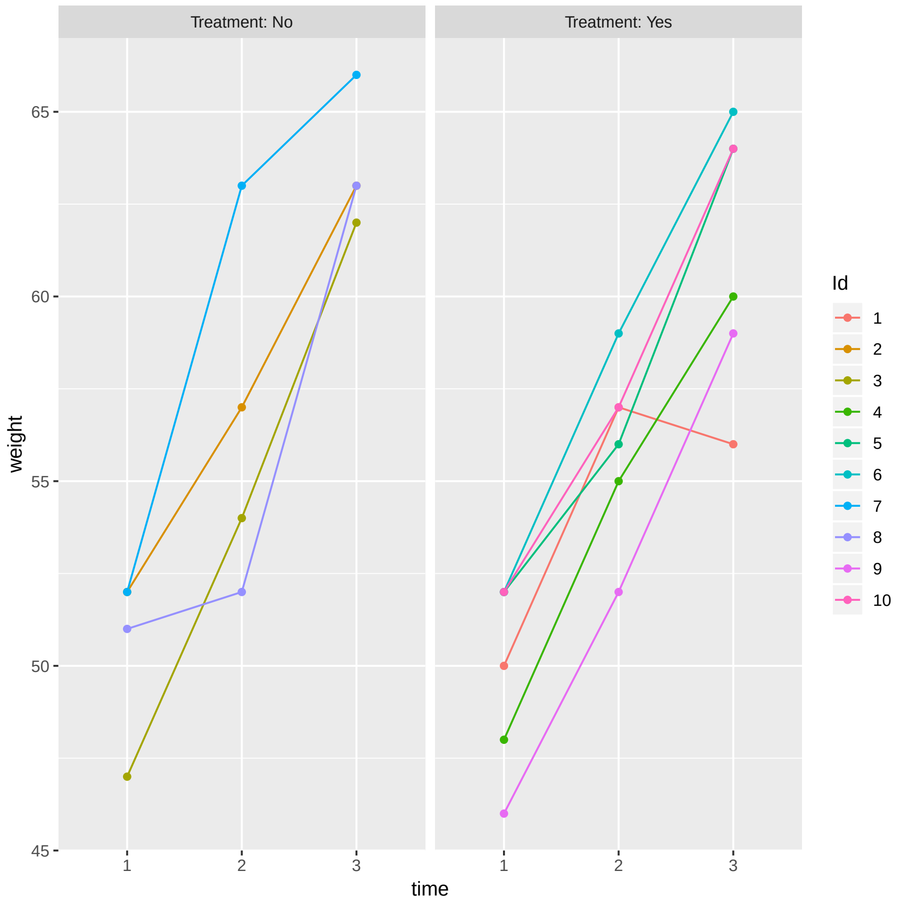
2. color by treatment group (first ten individuals)

```
gg.spaguetti2 <- ggplot(dtL.data[Id %in% 1:10],
                        aes(x = time, y = weight, color = Treatment, group = Id))
gg.spaguetti2 <- gg.spaguetti2 + geom_line() + geom_point()
gg.spaguetti2
```



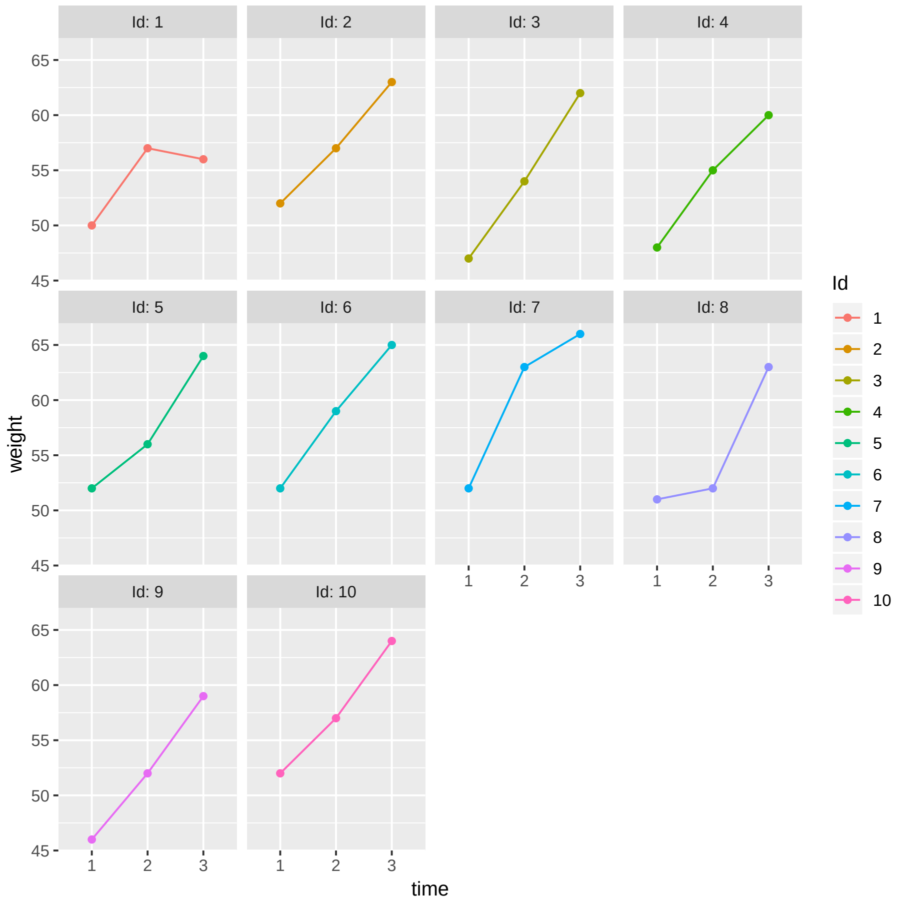
3. pannel for each treatment group (first ten individuals)

```
gg.spaguetti3 <- ggplot(dtL.data[Id %in% 1:10],
                        aes(x = time, y = weight, color = Id, group = Id))
gg.spaguetti3 <- gg.spaguetti3 + geom_line() + geom_point()
gg.spaguetti3 <- gg.spaguetti3 + facet_wrap(~ Treatment, labeller = label_both)
gg.spaguetti3
```



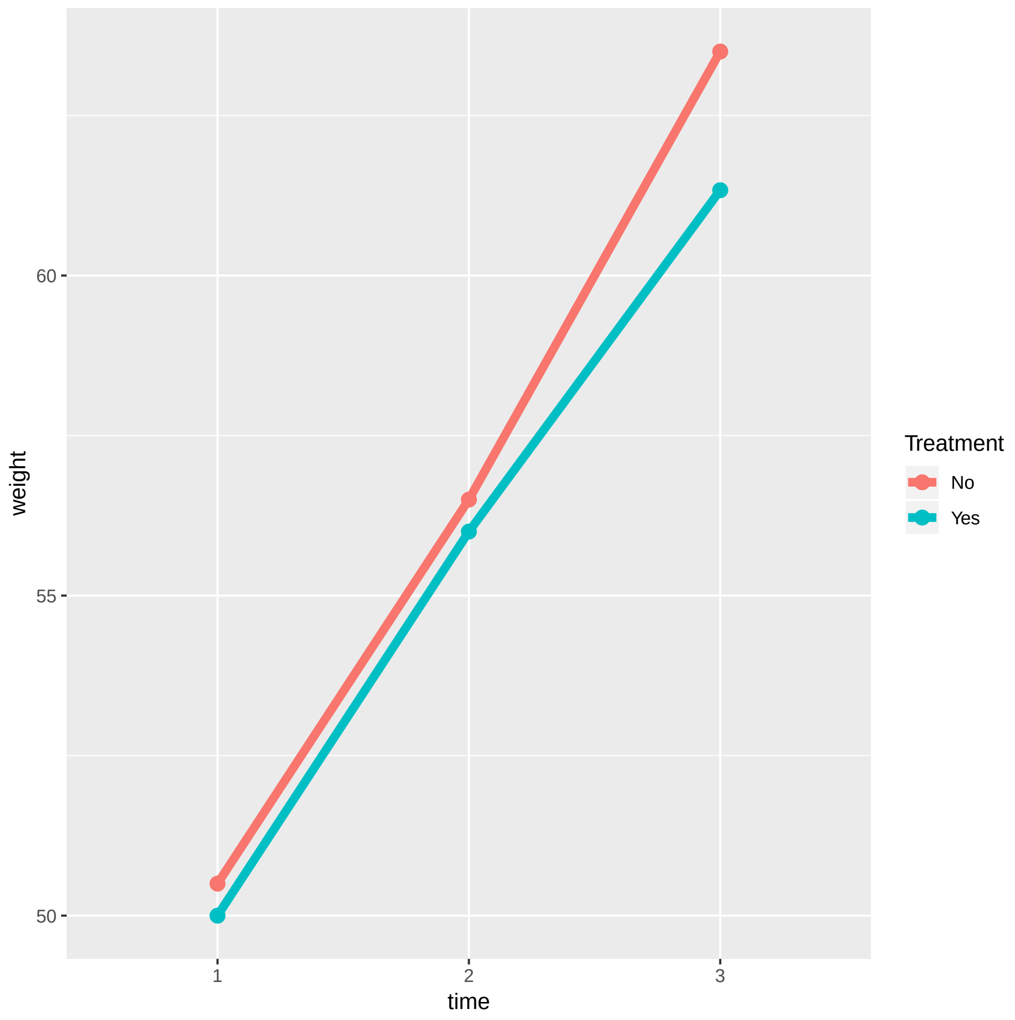
4. individual spaguetti plot (first ten individuals)

```
gg.spaguetti4 <- ggplot(dtL.data[Id %in% 1:10],
                        aes(x = time, y = weight, color = Id, group = Id))
gg.spaguetti4 <- gg.spaguetti4 + geom_line() + geom_point()
gg.spaguetti4 <- gg.spaguetti4 + facet_wrap(∼ Id, labeller = label_both)
gg.spaguetti4
```



5.1.2 Display the mean over time

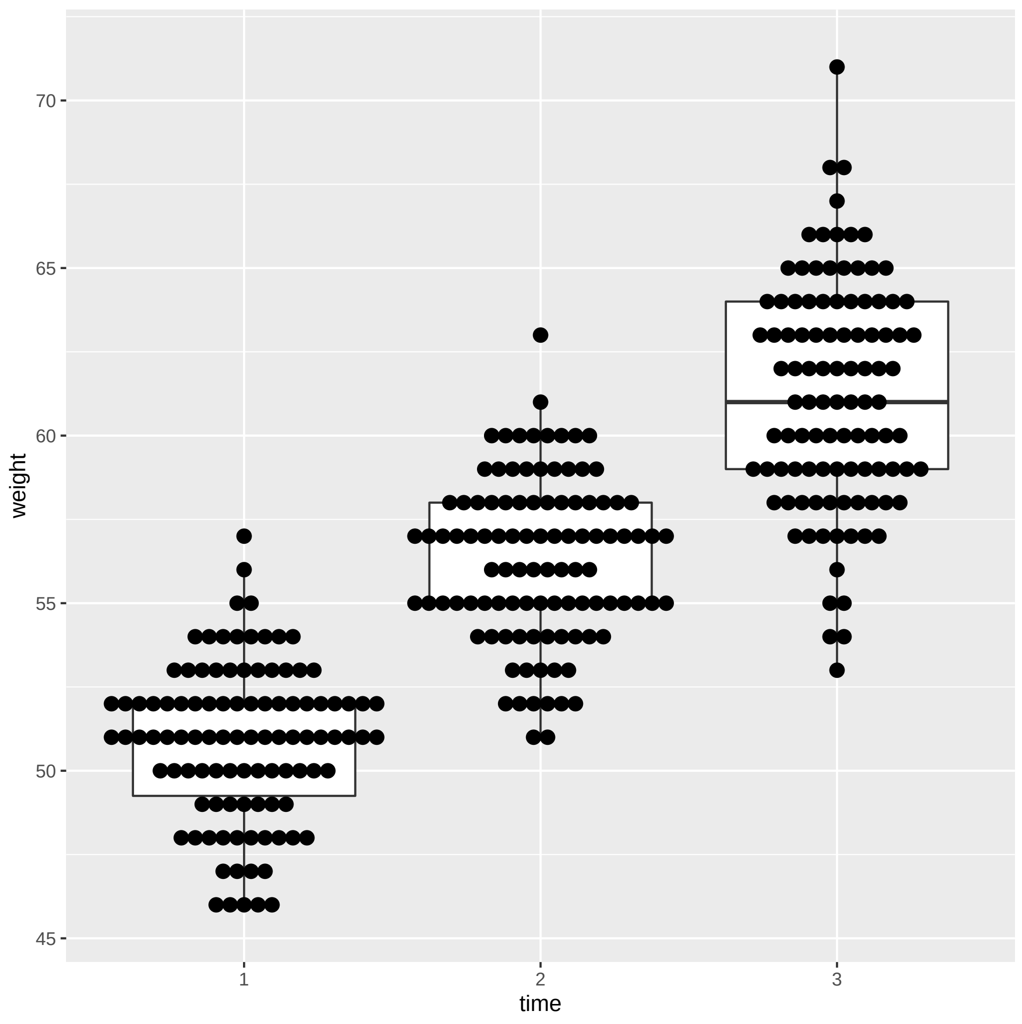
```
gg.mean <- ggplot(dtL.data[Id %in% 1:10], aes(x = time, y = weight))
gg.mean <- gg.mean + stat_summary(aes(group = Treatment, color = Treatment),
                                  geom = "line", fun.y = mean, size = 2)
gg.mean <- gg.mean + stat_summary(aes(group = Treatment, color = Treatment),
                                  geom = "point", fun.y = mean, size = 3)
```



5.1.3 Boxplot + points (non-overlapping)

```
gg.hist <- ggplot(dtL.data, aes(x = time, y = weight))
gg.hist <- gg.hist + geom_boxplot()
gg.hist <- gg.hist + geom_dotplot(binaxis = "y", stackdir = "center", dotsize = 0.5)
gg.hist
```

```
‘stat_bindot()‘ using ‘bins = 30‘. Pick better value with ‘binwidth‘.
```



5.2 Diagnostic plots

Consider the linear model:

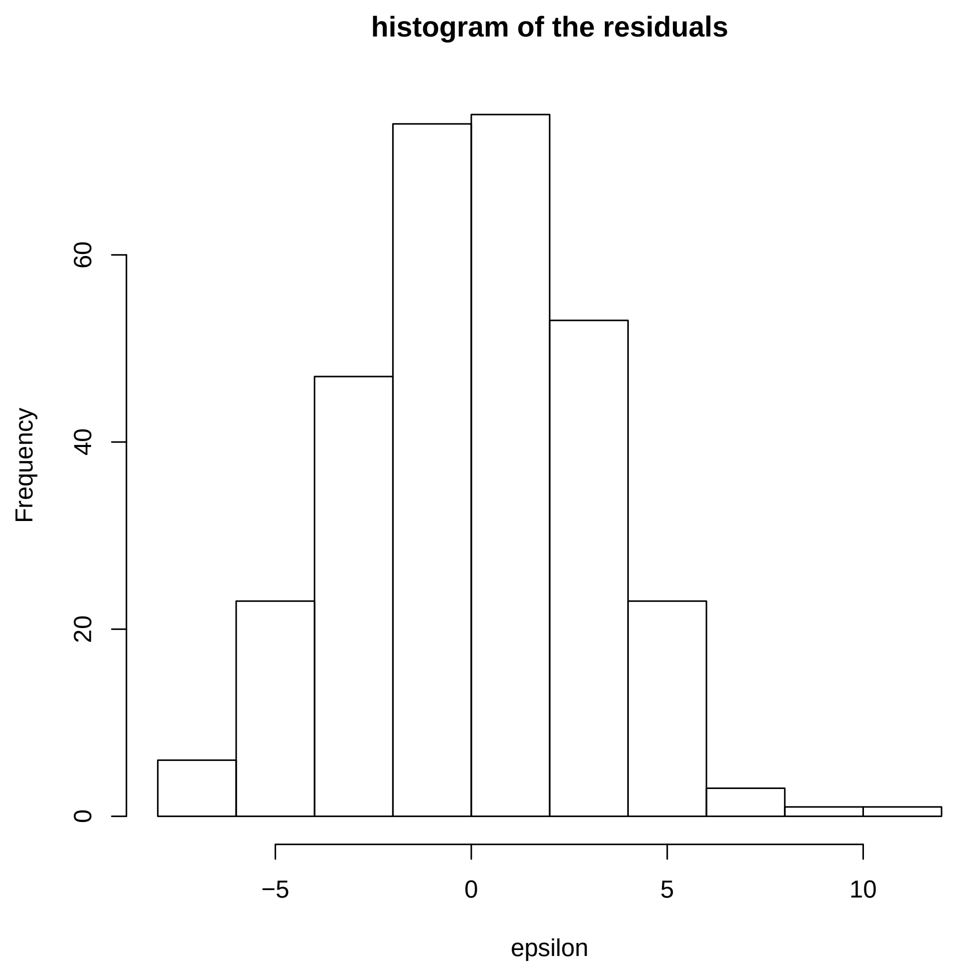
```
e.lm <- lm(weight ~ Age + Treatment + size,
            data = dtL.data)
```

5.2.1 Histogram of the residuals

Extract the residuals:

```
epsilon <- residuals(e.lm, type = "response")
```

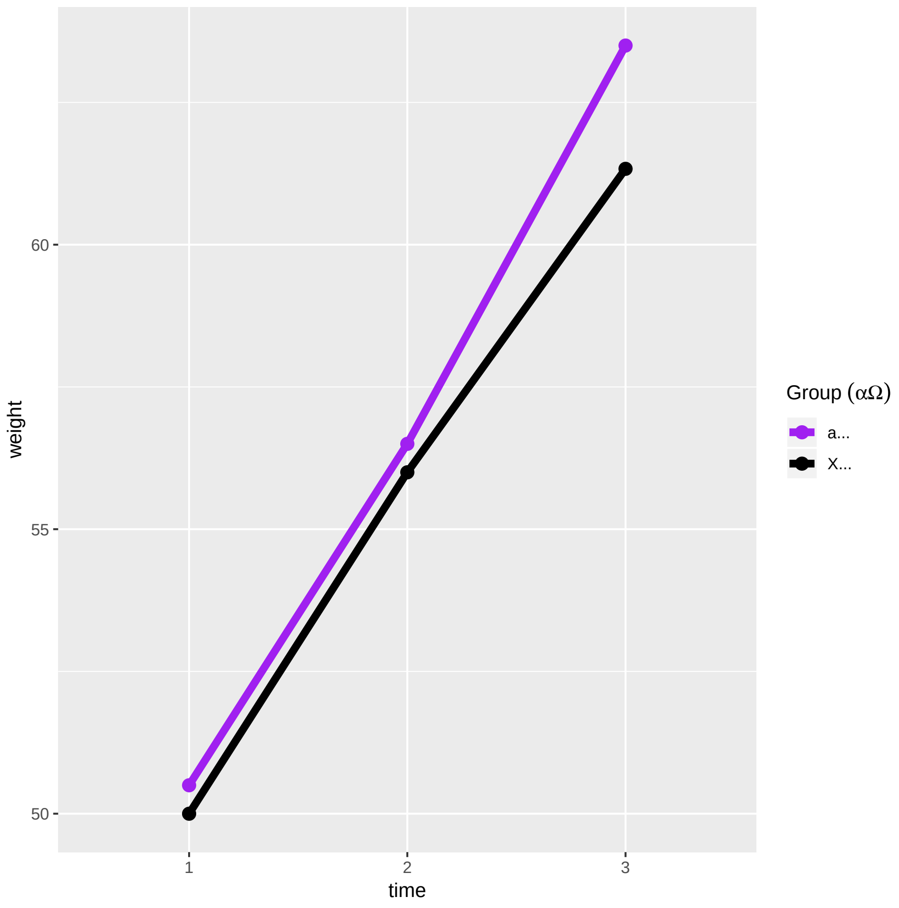
Display the histogram



5.3 Customize graphic

5.3.1 Modify the legend of a discrete scale (with greek letters)

```
gg.mean2 <- gg.mean + scale_colour_manual(name = expression("Group"~(alpha*Omega)),
                                          labels = c("\u03b1\u2090","X\u1D30"),
                                          values = c("No" = "purple",
                                                     "Yes" = "black"))
```



See also:

- https://en.wikipedia.org/wiki/List_of_Unicode_characters
- https://en.wikipedia.org/wiki/Unicode_subscripts_and_superscripts
- https://stackoverflow.com/questions/5293715/how-to-use-greek-symbols-in-ggplot2

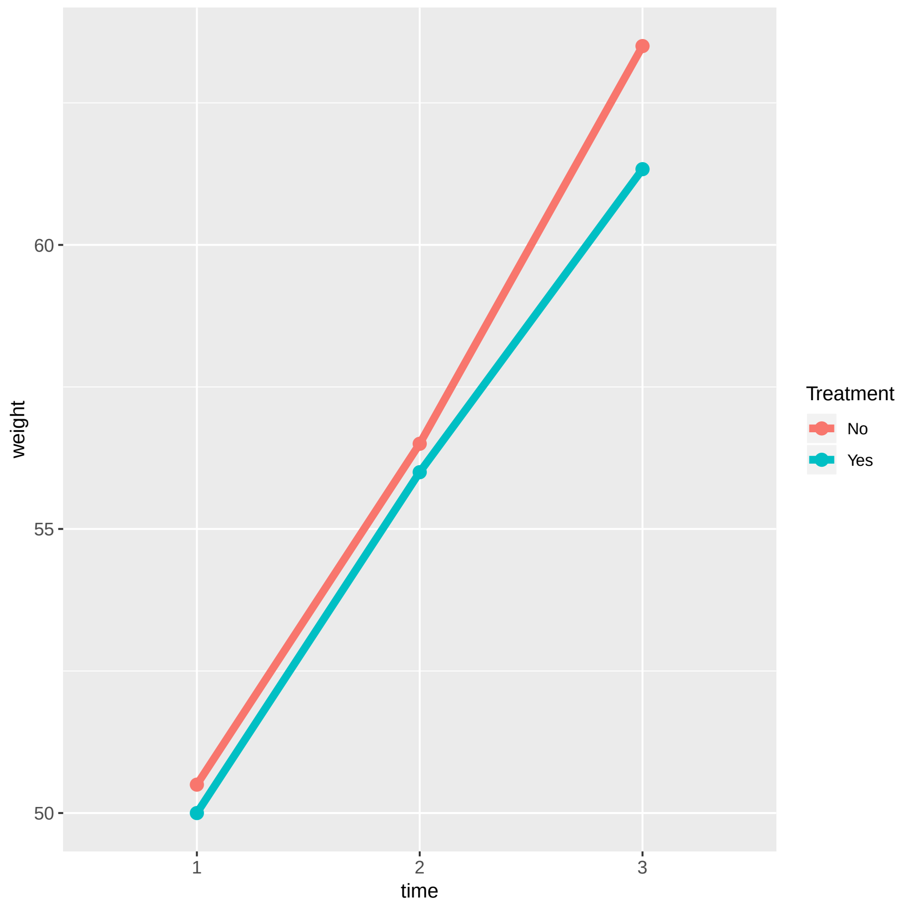
5.3.2 Change the name of the legend

```
gg.mean3 <- gg.mean2 + labs(colour="xyz")
```

5.3.3 Increase the font size

All text:

```
gg.mean3 <- gg.mean + theme(text = element_text(size=10))
```



Only x axis labels:

```
gg.mean3 <- gg.mean + theme(axis.text = element_text(size=10))
```

Only axis title:

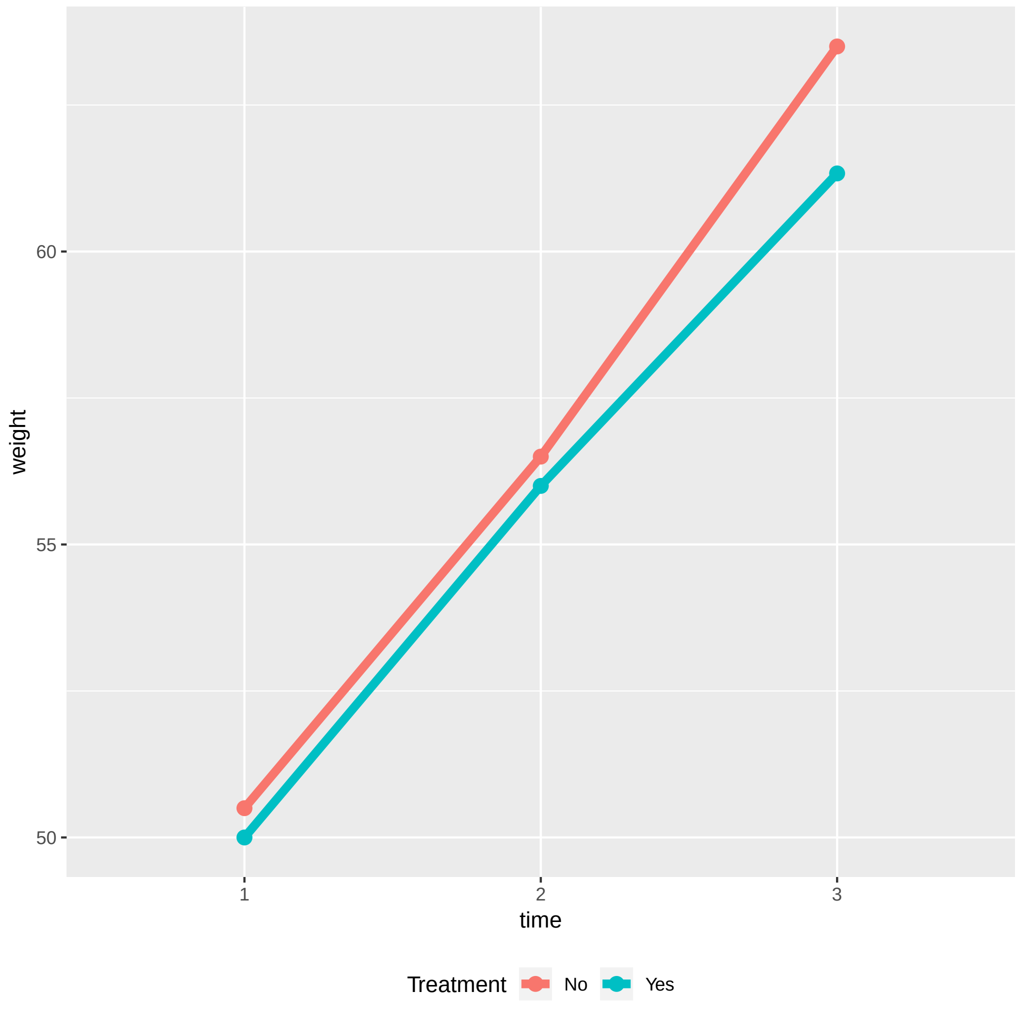
```
gg.mean3 <- gg.mean + theme(axis.title = element_text(size=10))
```

5.3.4 Increase size of the legend labels

```
gg.mean + theme(axis.title = element_text(size=10), legend.key.size = unit(3,"line"))
```

5.3.5 Put the legend at the bottom

```
gg.mean4 <- gg.mean + theme(legend.position="bottom")
```



5.3.6 Number of lines in the legend

```
gg.mean + guides(color = guide_legend(nrow = 2, byrow = TRUE))
```

5.3.7 Default ggplot color palette

```
gg_color_hue <- function(n) {
  hues = seq(15, 375, length = n + 1)
  hcl(h = hues, l = 65, c = 100)[1:n]
}
```

5.3.8 Color blind palette

```
ggthemes::colorblind_pal()(8) ## also consider scale_color_colorblind
```

```
[1] "#000000" "#E69F00" "#56B4E9" "#009E73" "#F0E442" "#0072B2" "#D55E00" "#CC79A7"
```

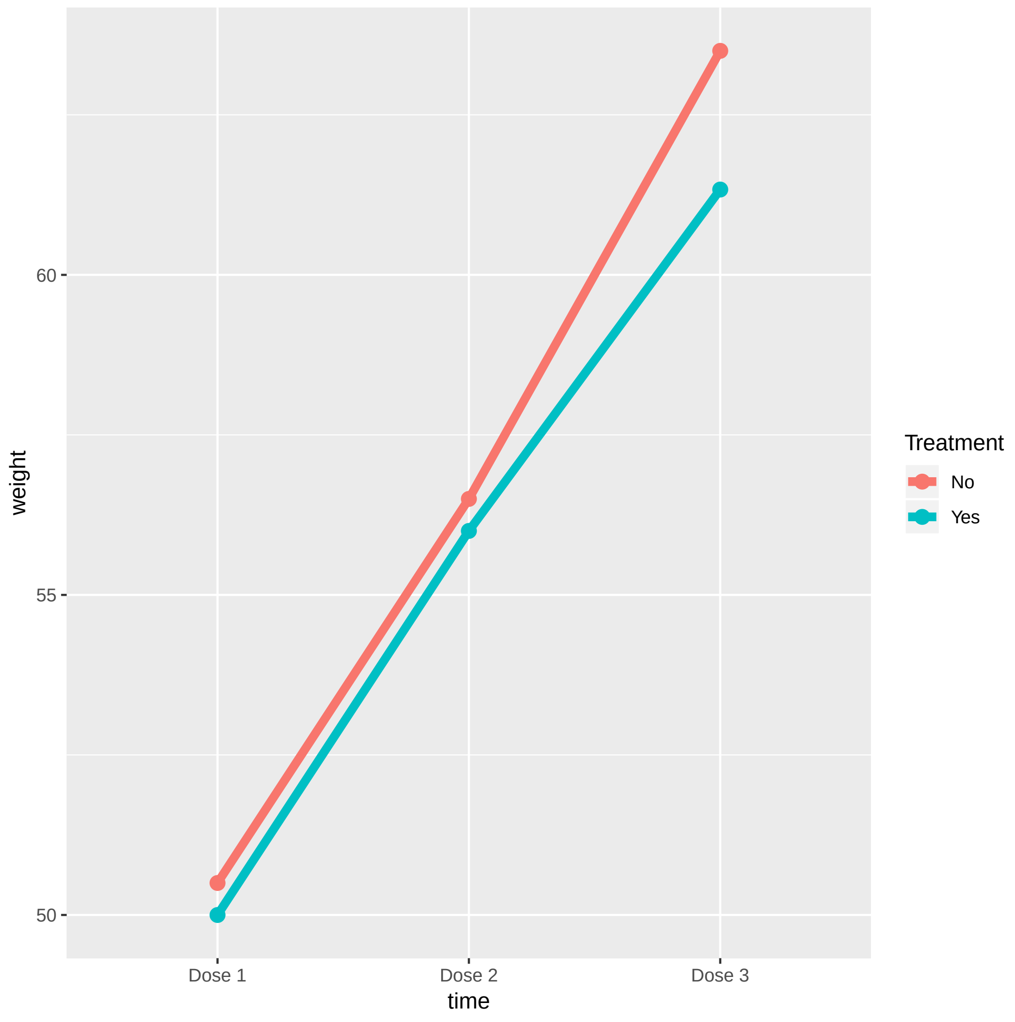
5.3.9 Rotate x-axis labels

```
theme(axis.text.x = element_text(angle = 90, hjust = 1))
```

```
List of 1
 $ axis.text.x:List of 11
  ..$ family       : NULL
  ..$ face         : NULL
  ..$ colour       : NULL
  ..$ size         : NULL
  ..$ hjust        : num 1
  ..$ vjust        : NULL
  ..$ angle        : num 90
  ..$ lineheight   : NULL
  ..$ margin       : NULL
  ..$ debug        : NULL
  ..$ inherit.blank: logi FALSE
  ..- attr(*, "class")= chr [1:2] "element_text" "element"
 - attr(*, "class")= chr [1:2] "theme" "gg"
 - attr(*, "complete")= logi FALSE
 - attr(*, "validate")= logi TRUE
```

5.3.10 Change tick mark labels

```
gg.mean5 <- gg.mean + scale_x_discrete(breaks=c("1","2","3"),
                                       labels=c("Dose 1", "Dose 2", "Dose 3"))
```

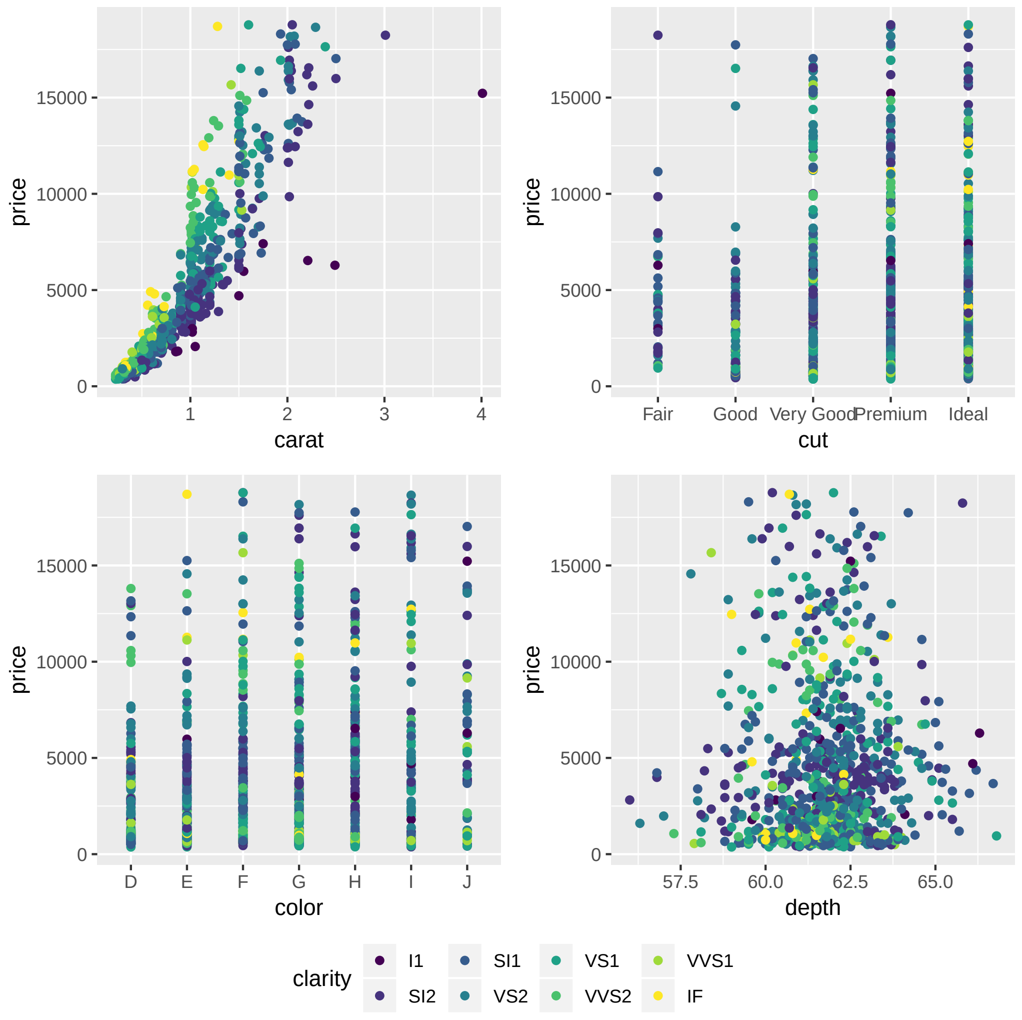


5.3.11 Combine ggplots

(from https://stackoverflow.com/questions/13649473/add-a-common-legend-for-combined-ggplots)

```
library(ggpubr)

dsamp <- diamonds[sample(nrow(diamonds), 1000), ]
p1 <- qplot(carat, price, data = dsamp, colour = clarity)
```

```
p2 <- qplot(cut, price, data = dsamp, colour = clarity)
p3 <- qplot(color, price, data = dsamp, colour = clarity)
p4 <- qplot(depth, price, data = dsamp, colour = clarity)

out <- ggarrange(p1, p2, p3, p4, ncol=2, nrow=2, common.legend = TRUE, legend="bottom")
```



5.3.12 Symbols in facet names

5.4 Path diagram

Using lava:

```
m <- lvm(Y~E+X1+X2+M,M~E,E~X2)
```

```
plot(m, plot.engine="rgraphviz")
```

Dynamic graph:

```
plot(m, plot.engine="visnetwork")
```

6 Modeling

6.1 Test proportions

```
binom.exact(c(15,4), p = 0.5) ## 15 success, 4 failures
```

```

        Exact two-sided binomial test (central method)

data:  c(15, 4)
number of successes = 15, number of trials = 19, p-value = 0.01921
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.5443469 0.9394755
sample estimates:
probability of success
             0.7894737
```

6.2 Compare proportions between groups (with fixed margins!)

Data:

```
tab <- rbind(c(8,3),
             c(5,12))
colnames(tab) <- c("worse","better")
rownames(tab) <- c("Dalteparin","Placebo")
tab <- tab[2:1,]
tab
```

```
           worse better
Placebo        5     12
Dalteparin     8      3
```

Unpaired: (fisher test)

```
fisher.exact(tab)
```

```
        Two-sided Fisher's Exact Test (usual method using minimum likelihood)

data:  tab
p-value = 0.05103
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.0272 1.0631
sample estimates:
odds ratio
  0.168551
```

Paired: (mc-nemar test)

```
mcnemar.exact(tab)
```

```
        Exact McNemar test (with central confidence intervals)

data:  tab
b = 12, c = 8, p-value = 0.5034
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.5638258 4.2303974
sample estimates:
odds ratio
       1.5
```

6.3 permutation t-test

Data:

```
set.seed(10)
X <- rlnorm(10, meanlog = 2, sdlog = 0.5)
Y <- rlnorm(10, meanlog = 1.8, sdlog = 0.5)
```

Approximation based on asymptotic result:

```
permTS(x = X, y = Y, method = "pclt")
```

```

        Permutation Test using Asymptotic Approximation

data:  X and Y
Z = -1.5476, p-value = 0.1217
alternative hypothesis: true mean X - mean Y is not equal to 0
sample estimates:
mean X - mean Y
      -1.533514
```

Approximation based on simulations:

```
permTS(x = X, y = Y, method = "exact.mc")
```

```
        Exact Permutation Test Estimated by Monte Carlo

data:  X and Y
p-value = 0.112
alternative hypothesis: true mean X - mean Y is not equal to 0
sample estimates:
mean X - mean Y
      -1.533514

p-value estimated from 999 Monte Carlo replications
99 percent confidence interval on p-value:
 0.07625212 0.15272627
```

Exact:

```
permTS(x = X, y = Y, method = "exact.ce")
```

```

        Exact Permutation Test (complete enumeration)

data:  X and Y
p-value = 0.1238
alternative hypothesis: true mean X - mean Y is not equal to 0
sample estimates:
mean X - mean Y
      -1.533514
```

6.4 Testing median

Data:

```
set.seed(10)
X <- rlnorm(100, meanlog = 2, sdlog = 0.5) - 6.5
```

Median test

```
quantileTest(X)
```

```

        Exact Test/Confidence Interval for Median

data:  X
quantile for prob = 0.5, pAG = 0.18410, pAL = 0.86437, pc = 0.36820, p-value = 0.3682
alternative hypothesis: true median is not equal to 0
95 percent confidence interval:
 -0.3701565  1.4997902
sample estimates:
   median
0.2082777
```

```
df <- data.frame(value=X)
e <- rq(value~1, tau = 0.5, data = df)
summary(e, se = "nid")
```

```
Warning message:
In rq.fit.br(x, y, tau = tau, ...) : Solution may be nonunique

Call: rq(formula = value ~ 1, tau = 0.5, data = df)

tau: [1] 0.5

Coefficients:
            Value   Std. Error t value Pr(>|t|)
(Intercept) 0.20213 0.49381    0.40932 0.68319
```

Other quantiles

```
e2 <- rq(value~1, tau = c(0.25,0.5,0.75), data = df)
summary(e2, se = "nid")
```

```
Warning messages:
1: In rq.fit.br(x, y, tau = tau, ...) : Solution may be nonunique
2: In rq.fit.br(x, y, tau = tau, ...) : Solution may be nonunique
3: In rq.fit.br(x, y, tau = tau, ...) : Solution may be nonunique

Call: rq(formula = value ~ 1, tau = c(0.25, 0.5, 0.75), data = df)
```

```
tau: [1] 0.25

Coefficients:
            Value    Std. Error t value  Pr(>|t|)
(Intercept) -1.61744  0.37283   -4.33828  0.00003

Call: rq(formula = value ~ 1, tau = c(0.25, 0.5, 0.75), data = df)

tau: [1] 0.5

Coefficients:
            Value   Std. Error t value Pr(>|t|)
(Intercept) 0.20213 0.49381    0.40932 0.68319

Call: rq(formula = value ~ 1, tau = c(0.25, 0.5, 0.75), data = df)

tau: [1] 0.75

Coefficients:
            Value   Std. Error t value Pr(>|t|)
(Intercept) 3.43848 0.68607    5.01186 0.00000
```

6.5 Testing linear hypotheses

Consider the linear model:

```
e.lm <- lm(weight ~ Age + Treatment + size,
            data = dtL.data)
summary(e.lm)$coef
```

```
                Estimate Std. Error    t value     Pr(>|t|)
(Intercept)  13.11292977 5.84498969  2.2434479 2.559263e-02
Age          -0.05479836 0.13849481 -0.3956709 6.926272e-01
TreatmentYes -0.65247721 0.36126020 -1.8061143 7.189597e-02
size          0.81718969 0.03513376 23.2593869 2.743182e-69
```

To test linear hypotheses we first need to define them using a contrast matrix:

```
name.coef <- names(coef(e.lm))
n.coef <- length(name.coef)

C <- matrix(0,nrow = 3, ncol = n.coef,
            dimnames = list (c("Age","2 Treatment","All"), name.coef))
C["Age","Age"] <- 1
C["2 Treatment","TreatmentYes"] <- 2
C["All",-1] <- 1
C
```

```
            (Intercept) Age TreatmentYes size
Age                   0   1            0    0
2 Treatment           0   0            2    0
All                   0   1            1    1
```

6.5.1 Separate Wald tests of linear hypotheses

No adjustment for multiple comparison:

```
summary(glht(e.lm, linfct = C), test = univariate())
```

```
         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Linear Hypotheses:
                 Estimate Std. Error t value Pr(>|t|)
Age == 0          -0.0548     0.1385  -0.396   0.6926
2 Treatment == 0  -1.3050     0.7225  -1.806   0.0719 .
All == 0           0.1099     0.3513   0.313   0.7546
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Univariate p values reported)
```

Adjustment using bonferroni:

```
summary(glht(e.lm, linfct = C), test = adjusted("bonferroni"))
```

```
         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Linear Hypotheses:
                 Estimate Std. Error t value Pr(>|t|)
Age == 0          -0.0548     0.1385  -0.396    1.000
2 Treatment == 0  -1.3050     0.7225  -1.806    0.216
All == 0           0.1099     0.3513   0.313    1.000
(Adjusted p values reported -- bonferroni method)
```

Adjustment using the max statistic:

```
summary(glht(e.lm, linfct = C), test = adjusted("single-step"))
```

```
         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Linear Hypotheses:
                 Estimate Std. Error t value Pr(>|t|)
Age == 0          -0.0548     0.1385  -0.396    0.916
2 Treatment == 0  -1.3050     0.7225  -1.806    0.157
All == 0           0.1099     0.3513   0.313    0.948
(Adjusted p values reported -- single-step method)
```

Alternative syntax (without contrast matrix):

```
summary(glht(e.lm,
             linfct = c("Age = 0",
                        "2*TreatmentYes = 0",
                        "Age + TreatmentYes + size = 0")),
        test = adjusted("single-step"))
```

```
         Simultaneous Tests for General Linear Hypotheses

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Linear Hypotheses:
                               Estimate Std. Error t value Pr(>|t|)
Age == 0                        -0.0548     0.1385  -0.396    0.916
2 * TreatmentYes == 0           -1.3050     0.7225  -1.806    0.157
Age + TreatmentYes + size == 0   0.1099     0.3513   0.313    0.948
(Adjusted p values reported -- single-step method)
```

6.5.2 Confidence intervals associated with linear hypotheses

With no adjustment for multiplicity:

```
confint(glht(e.lm, linfct = C), calpha = univariate_calpha())
```

```

         Simultaneous Confidence Intervals

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Quantile = 1.9679
95% confidence level


Linear Hypotheses:
                 Estimate lwr     upr
Age == 0         -0.0548  -0.3273  0.2177
2 Treatment == 0 -1.3050  -2.7268  0.1169
All == 0          0.1099  -0.5815  0.8013
```

With adjustment for multiplicity:

```
confint(glht(e.lm, linfct = C), calpha = adjusted_calpha())
```

```

         Simultaneous Confidence Intervals

Fit: lm(formula = weight ~ Age + Treatment + size, data = dtL.data)

Quantile = 2.314
95% family-wise confidence level


Linear Hypotheses:
                 Estimate lwr     upr
Age == 0         -0.0548  -0.3753  0.2657
2 Treatment == 0 -1.3050  -2.9769  0.3670
All == 0          0.1099  -0.7031  0.9229
```

6.5.3 Joint test of linear hypotheses

One can use the `Ftest()` or `Chisqtest()` to obtain a joint test:

```
summary(glht(e.lm,
             linfct = c("Age = 0",
                        "2*TreatmentYes = 0",
                        "Age + TreatmentYes + size = 0")),
        test = Ftest())
```

```
         General Linear Hypotheses

Linear Hypotheses:
                               Estimate
Age == 0                        -0.0548
2 * TreatmentYes == 0           -1.3050
Age + TreatmentYes + size == 0   0.1099

Global Test:
      F DF1 DF2    Pr(>F)
1 181.2   3 302 3.349e-67
```

The same can be obtained using the `linearHypothesis` method from the `car` package:

```
linearHypothesis(e.lm, hypothesis.matrix = C, rhs = c(0,0,0))
```

```
Linear hypothesis test

Hypothesis:
Age = 0
2 TreatmentYes = 0
Age  + TreatmentYes  + size = 0

Model 1: restricted model
Model 2: weight ~ Age + Treatment + size

  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1    305 7748.5
2    302 2767.2  3    4981.3 181.21 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6.6 Linear model

Consider the following dataset:

```
set.seed(10)
m.lvm <- lvm(Y~AgeC+Gender+Gene)
categorical(m.lvm, K = 2) <- ~Gender
categorical(m.lvm, K = 3) <- ~Gene
distribution(m.lvm, ~Age) <- uniform.lvm(20,50)
transform(m.lvm, AgeC~Age) <- function(x, ...){x-35}
transform(m.lvm, Id~Age) <- function(x, ...){1:NROW(x)}
latent(m.lvm) <- ~AgeC
d <- lava::sim(n = 1e2, m.lvm,latent=FALSE)
d$Gender <- factor(d$Gender, labels = c("Male","Female"))
d$Gene <- factor(d$Gene, labels = c("A","B","C"))
d$Y <- round(d$Y,1)
d$Age <- round(d$Age,1)
head(d)
```

```
     Y Gender Gene  Age Id
1 15.0   Male    C 48.0  1
2  9.3 Female    B 42.4  2
3  7.3   Male    C 41.7  3
4  3.8 Female    C 36.4  4
5 -6.8   Male    A 27.9  5
6 -2.4 Female    C 29.2  6
```

Imagine we would like to model the age effect on the outcome, but accounting for a possible gender and gene effect:

```
e.lm <- lm(Y~Gender+Age+Gene, data = d)
e.lm
```

```

Call:
lm(formula = Y ~ Gender + Age + Gene, data = d)

Coefficients:
 (Intercept)  GenderFemale           Age         GeneB         GeneC
    -34.2857        0.8893        0.9814        0.8337        1.8057
```

Denote for the $i-th$ patient it outcome value by Y_i (can be any real number), its gender value by $Gender_i$ (can be "Male" or "Female"), its gene value by $Gene_i$ (can be "A", "B", or "C"). Mathematically, the linear model can be written:

$$Y_i = \alpha + \beta_{Gender}\mathbb{1}_{Gender_i="Female"} + \beta_{Age}Age_i + \beta_{GeneB}\mathbb{1}_{Gene_i="B"} + \beta_{GeneC}\mathbb{1}_{Gene_i="C"} + \varepsilon_i$$

where $\boldsymbol{\beta} = (\alpha, \beta_{Gender}, \beta_{Age}, \beta_{GeneB}, \beta_{GeneC})$ is the vector of model parameters. Their value is shown just above (e.g. $\alpha = -34.2857$). Here $\mathbb{1}_.$ denotes the indicator function taking value 1 if "." is true and 0 otherwise. ε_i is the residual error, i.e. the difference between the observed value and the observed value. Consider for instance the first individual:

```
d[1,]
```

```
   Y Gender Gene Age Id
1 15   Male    C  48  1
```

its observed value is 15 and we can computed its fitted value as:

$$\begin{aligned}\hat{Y}_1 &= \alpha + \beta_{Gender} * 0 + \beta_{Age} 48 + \beta_{GeneB} * 0 + \beta_{GeneC} * 1 \\ &= -34.2857 + 0.8893 * 0 + 0.9814 * 48 + 0.8337 * 0 + 1.8057 * 1 = 14.6272\end{aligned}$$

Note that this linear model can be abreviated as:

$$Y_i = X_i \beta + \varepsilon_i$$

where $X_i = (1, \mathbb{1}_{Gender_i = "Female"}, Age_i, \mathbb{1}_{Gene_i = "B"}, \mathbb{1}_{Gene_i = "C"})$.

6.6.1 Partial residuals with respect to one variable

The partial residuals with respect to age are defined by removing the effect of all the covariates but age on the outcome:

$$\hat{\varepsilon}_i^{Age} = Y_i - (\alpha + \beta_{Gender} \mathbb{1}_{Gender_i == "Female"} + \beta_{GeneB} \mathbb{1}_{Gene_i == "B"} + \beta_{GeneC} \mathbb{1}_{Gene_i == "C"})$$

So for instance for the first individual:

$$\hat{\varepsilon}_1^{Age} = 15.0 - (-34.2857 + 0.8893 * 0 + 0.8337 * 0 + 1.8057 * 1) \quad = 15.0 - -32.48 = 47.48$$

At the dataset level, this type of partial residual is centered around the expected value of the covariate times its effect (here $0.9814 * 36.078 \approx 35$). These partial residuals can be computed using the `partialResidual` function from the butils package:

```
pRes.noI <- partialResiduals(e.lm, var = "Age", keep.intercept = FALSE)
head(pRes.noI)
```

```
      Y Gender Gene  Age Id      pFit ranef pResiduals
1: 15.0   Male    C 48.0  1 -32.48008     0   47.48008
2:  9.3 Female    B 42.4  2 -32.56265     0   41.86265
3:  7.3   Male    C 41.7  3 -32.48008     0   39.78008
4:  3.8 Female    C 36.4  4 -31.59075     0   35.39075
5: -6.8   Male    A 27.9  5 -34.28574     0   27.48574
6: -2.4 Female    C 29.2  6 -31.59075     0   29.19075
```

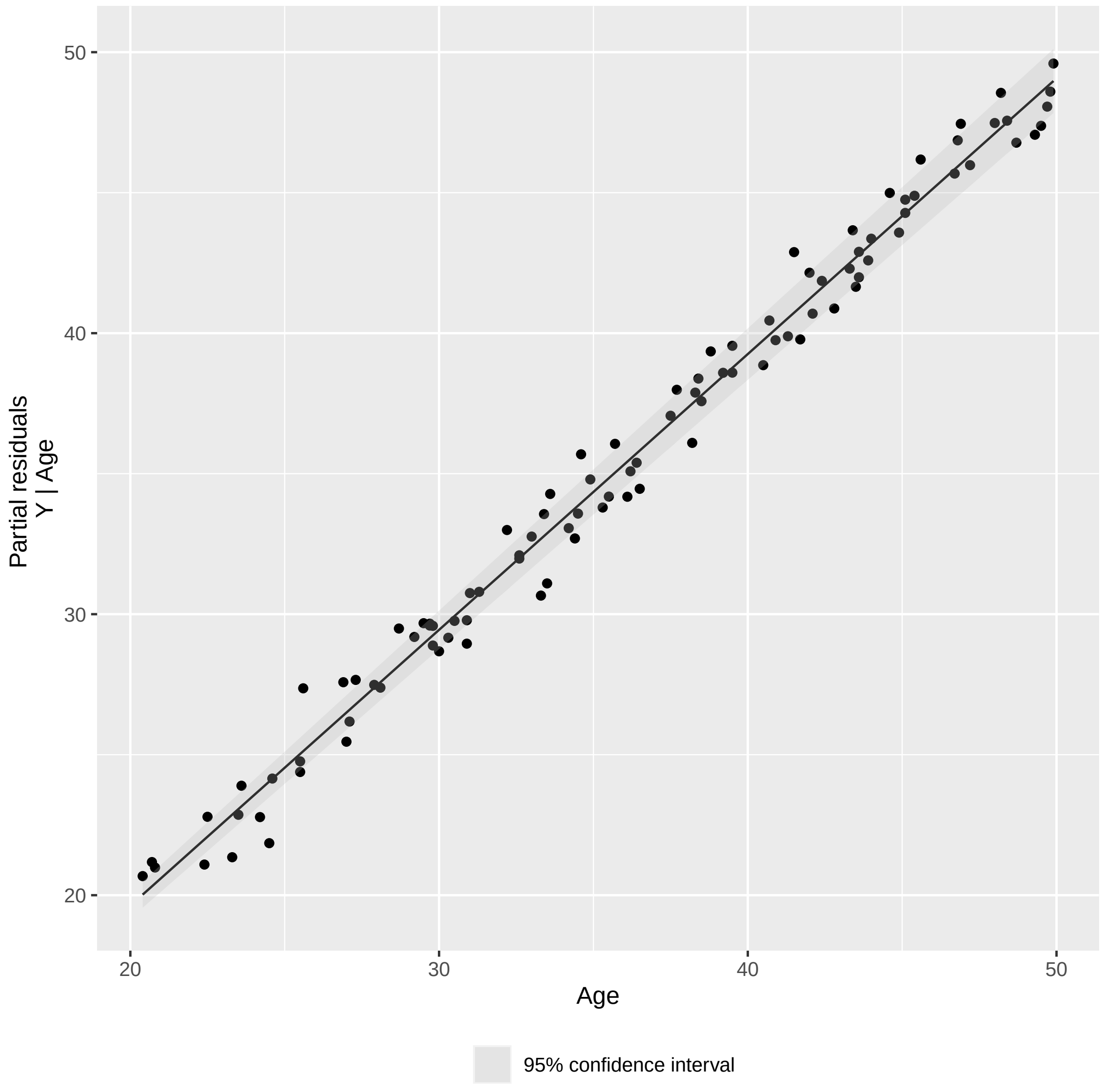
or manually:

```
keep.coef <- c("(Intercept)","GenderFemale","GeneB","GeneC")
d$Y[1] - model.matrix(e.lm)[1,keep.coef] %*% coef(e.lm)[keep.coef]
```

```
         [,1]
[1,] 47.48008
```

A graphical display can be obtained using the `autoplot` function (require the ggplot2 package):

```
autoplot(pRes.noI)
## ggsave(autoplot(pRes.noI), filename = "./figures/fig-butils-plotConf-noI.pdf")
```



- An alternative definition do not remove the intercept effect:

$$\hat{\varepsilon}_i^{Age,\alpha} = Y_i - (\beta_{Gender}\mathbb{1}_{Gender_i=="Female"} + \beta_{GeneB}\mathbb{1}_{Gene_i=="B"} + \beta_{GeneC}\mathbb{1}_{Gene_i=="C"})$$

so now the residuals are centered around the intercept plus the expected value of age times the age effect (here approximately 0). As before the partial residuals can either be obtained via the `partialResiduals` function:

```
pRes.I <- partialResiduals(e.lm, var = "Age", keep.intercept = TRUE)
head(pRes.I)
```

```
      Y Gender Gene  Age Id     pFit ranef pResiduals
1: 15.0   Male    C 48.0  1 1.805654     0  13.194346
2:  9.3 Female    B 42.4  2 1.723081     0   7.576919
3:  7.3   Male    C 41.7  3 1.805654     0   5.494346
4:  3.8 Female    C 36.4  4 2.694988     0   1.105012
5: -6.8   Male    A 27.9  5 0.000000     0  -6.800000
6: -2.4 Female    C 29.2  6 2.694988     0  -5.094988
```

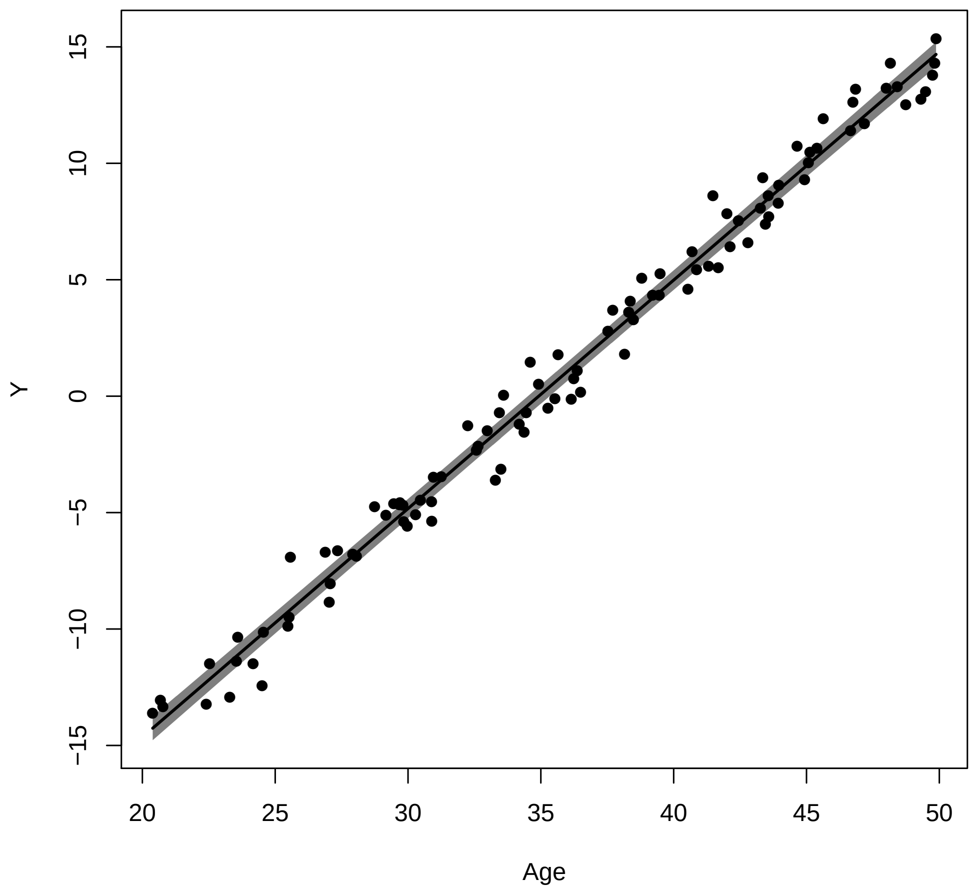
or manually:

```
keep.coef <- c("GenderFemale","GeneB","GeneC")
d$Y[1] - model.matrix(e.lm)[1,keep.coef] %*% coef(e.lm)[keep.coef]
```

```
         [,1]
[1,] 13.19435
```

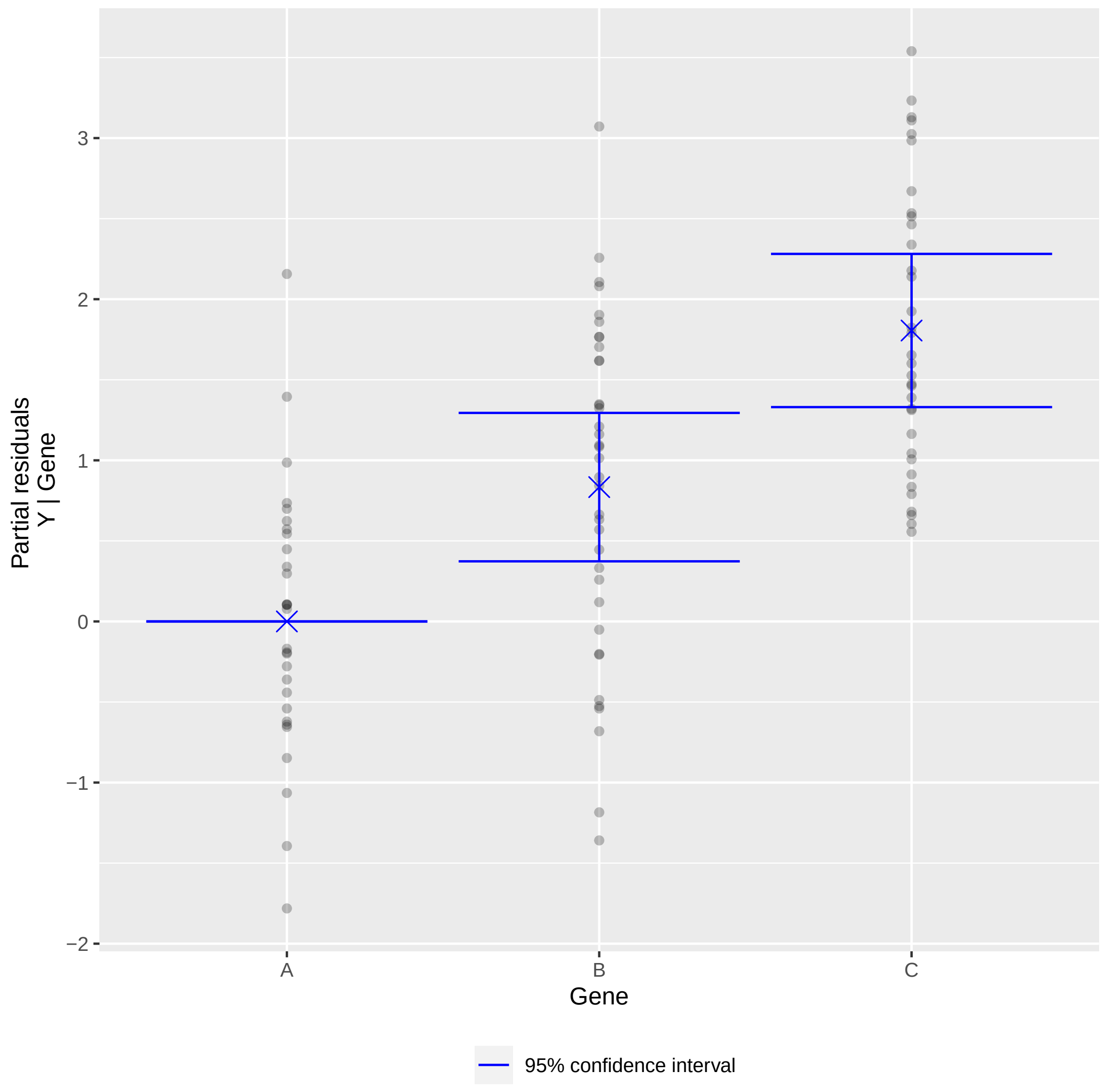
This corresponds to what the `plotConf` function is displaying (R package lava available on CRAN):

```
lava::plotConf(e.lm, var1 = "Age")
```



Note that it is also possible to display the partial residuals for a categorical variable:

```
autoplot(partialResiduals(e.lm, var = "Gene", keep.intercept = TRUE))
## ggsave(autoplot(partialResiduals(e.lm, var = "Gene")), filename = "./figures/fig-
    butils-plotConf-categorical.pdf")
```



6.6.2 Customizing a partial residual plot

The autoplot function returns the ggplot object:

```
gg <- autoplot(partialResiduals(e.lm, var = "Gene", keep.intercept = TRUE))
class(gg)
```

```
[1] "gg"     "ggplot"
```

So it can be easily customized, e.g. the text can be made bigger by doing:

```
gg + theme(text = element_text(size=25))
```

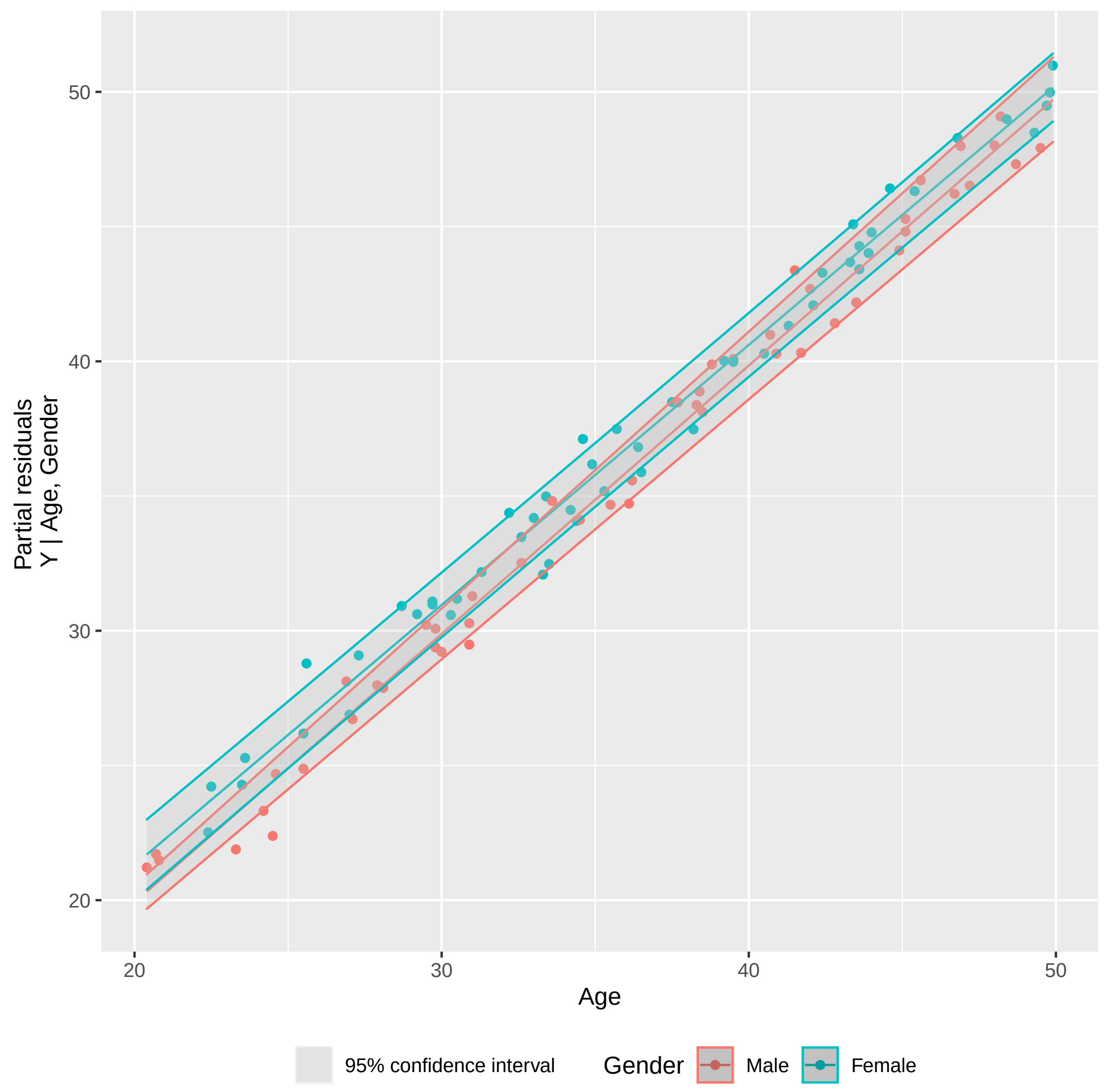
6.6.3 Partial residuals with respect to an interaction between two variables (one continuous, one categorical)

Consider now a model where the age effect can be different for males and females:

```
e.lmI <- lm(Y~Gender*Age+Gene, data = d)
```

The partial residuals can be defined in a similar way as before. Here the effect of Age and Gender (and their interaction) are not substracted from the outcome:

```
autoplot(partialResiduals(e.lmI, var = c("Age","Gender")))
## ggsave(autoplot(partialResiduals(e.lmI, var = c("Age","Gender"))), filename = "./
    figures/fig-butils-plotConf-interaction.pdf")
```



6.6.4 Assumptions made when fitting a linear model

A linear model $Y = X\beta + \varepsilon$ is a model studying the effects (β) of covariates (X) on the expected value of the outcome Y. Maximum likelihood (ML) estimation leads to unbiased estimates of β if the following assumptions are satisfied:

- **(A0)**: no unobserved confounders.
- **(A1)**: $\mathbb{E}\left[Y_i|X\right] = X_i\beta$ correct specification of the functional form of the covariates.
- **(A2)** identically distributed and **(A3)** independent residuals, which under the normality

assumption reduces to **(A2)** homoschedasticity $\mathbb{V}ar\left[Y_i|X\right] = \sigma^2$ and **(A3)** uncorrelatedness $\forall i \neq j$, $\mathbb{C}ov\left[Y_i, Y_j|X\right] = 0$.

While not needed per se, the assumption of:

- **(A4)** normally distributed residuals is often mention since (i) normality of the estimates holds exactly in finite samples (instead of asymptotically) i.e. p-value/CI are reliable even in small samples, (ii) it ensure that MLE is the best estimation procedure, (iii) checking **(A2)** and **(A3)** is simplified.

Additional assumptions are typically necessary to ensure reliable and interpretable estimates:

- **(A4-bis)** approximately symmetric and unimodal - otherwise modeling the expected value (aka the mean value) may not be very relevant.
- **(A5)** absence of outliers - otherwise the estimates may be very sensitive to the value of a few observations which is often undesirable.

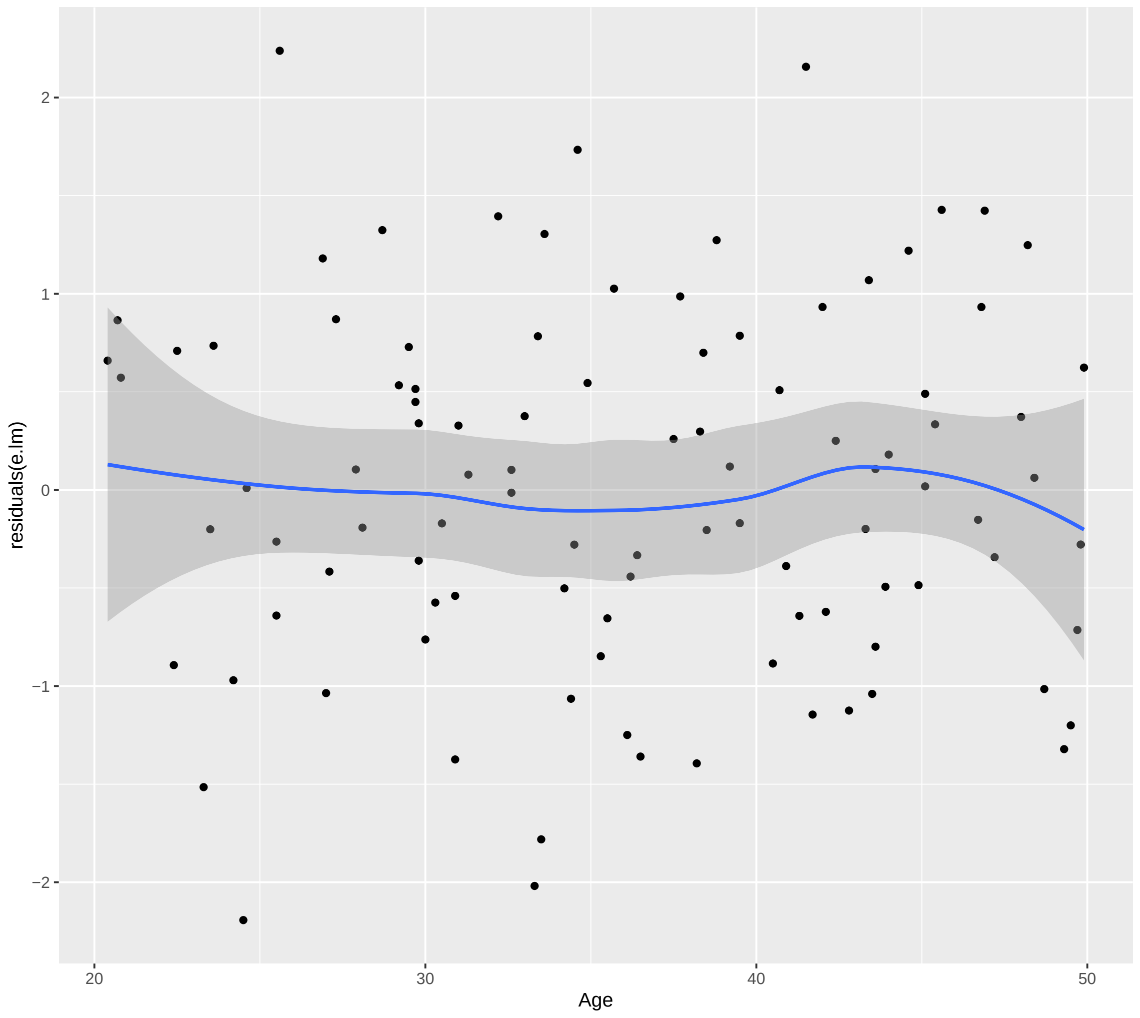
6.6.5 Checking assumptions made when fitting a linear model

(A0) is in general impossible to check.

(A1) can be (artificially) decomposed into two part:

- in absence of interaction, is the effect of the continuous variables correctly modeled. Typically it is modeled as a linear effect and the question is is there a non-linear effect. We can look at the plot of the covariate vs. the residuals and search for any trend:

```
ggplot(d, aes(x = Age, y = residuals(e.lm))) + geom_point() + geom_smooth()
## ggsave(ggplot(d, aes(x = Age, y = residuals(e.lm))) + geom_point() + geom_smooth(),
    filename = "./figures/fig-lm-diag-A2.pdf")
```



A p-value for testings the correct specification of the functional form for the covariate can be obtained using the `cumres` function from the gof package:

```
cumres(e.lm, variable = "Age")
```

```
Kolmogorov-Smirnov-test: p-value=0.816
Cramer von Mises-test: p-value=0.791
Based on 1000 realizations. Cumulated residuals ordered by Age-variable.
---
```

If a trend is found, a possible remedie is to use splines to model the non-linear relationship, e.g.

```
e.gam <- mgcv::gam(Y ∼ Gender + s(Age) + Gene, data = d)
```

- checking for interactions is hard because the number of possible

interactions grows quickly with the number of covariates. A typical test would be to compare a model with interactions to a model without interations:

```
anova(e.lm,e.lmI)
```

```
Analysis of Variance Table

Model 1: Y ~ Gender + Age + Gene
Model 2: Y ~ Gender * Age + Gene
  Res.Df    RSS Df Sum of Sq     F Pr(>F)
1     95 82.479
2     94 80.924  1    1.5548 1.806 0.1822
```

Otherwise the `cumres` function from the gof package can test the correct specification of the link function which can be used as an indirect test for interactions and a direct test for the correct specification of the functional form:

```
cumres(e.lm, variable = "predicted")
```

```
Kolmogorov-Smirnov-test: p-value=0.821
Cramer von Mises-test: p-value=0.717
Based on 1000 realizations. Cumulated residuals ordered by predicted-variable.
---
```

(A4) can be tested using an histogram of the standardized residuals:

```
hist(residuals(e.lm, type = "pearson"), freq = FALSE, breaks = 10)
curve(dnorm,-3,3,add =TRUE,col = "red")
```

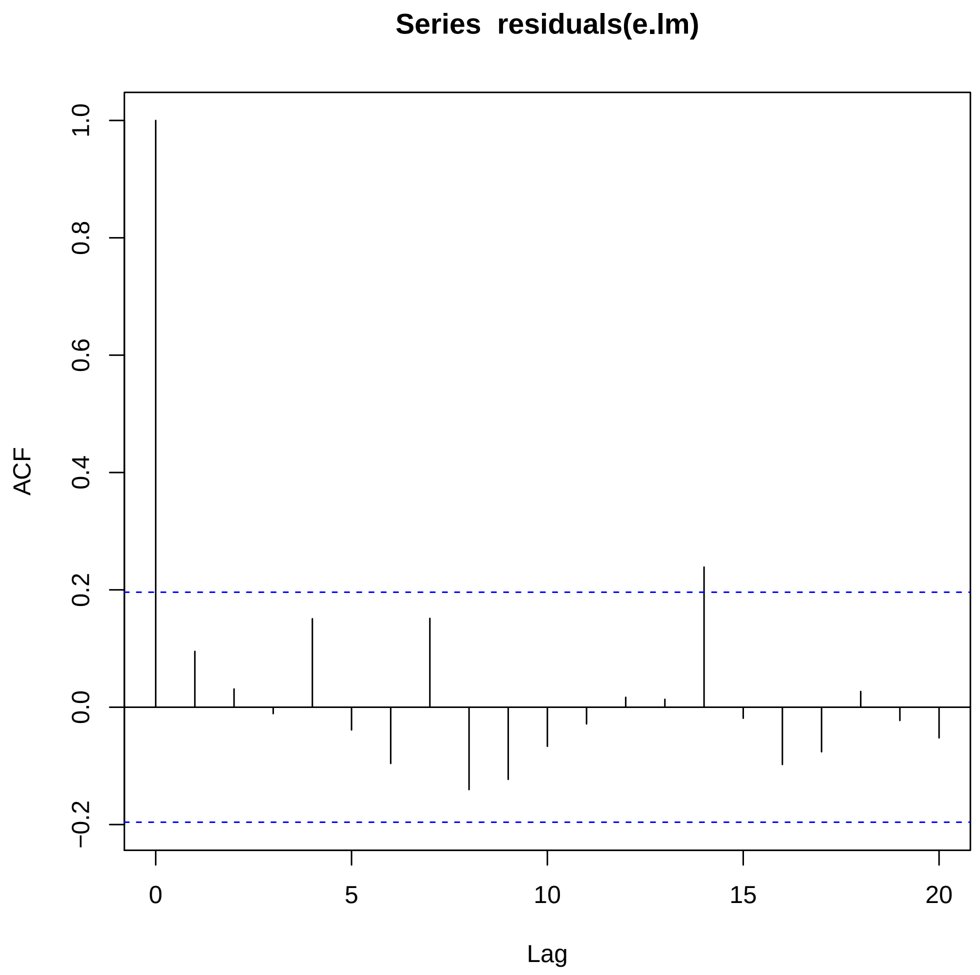
where the histogram should be close to the shape of the standard normal distribution. We could reject **(A4)** but accept **(A4-bis)** in the case where the distribution has heavy tails but is still unimodal and symmetric. While intuitive, this method is sensitive to the discretisation of the residuals values (argument break) and qq-plot is often prefered:

```
qqtest::qqtest(residuals(e.lm))
```

Here the points should follow a straight line and be within the shaded area. We could reject **(A4)** but accept **(A4-bis)** in the case where deviation to the straight line mostly arise in the tails. Statistical test (like a shapiro test) are not recommanded since they do not enable us to know whether we reject **(A4)** or **(A4bis)**. Possible

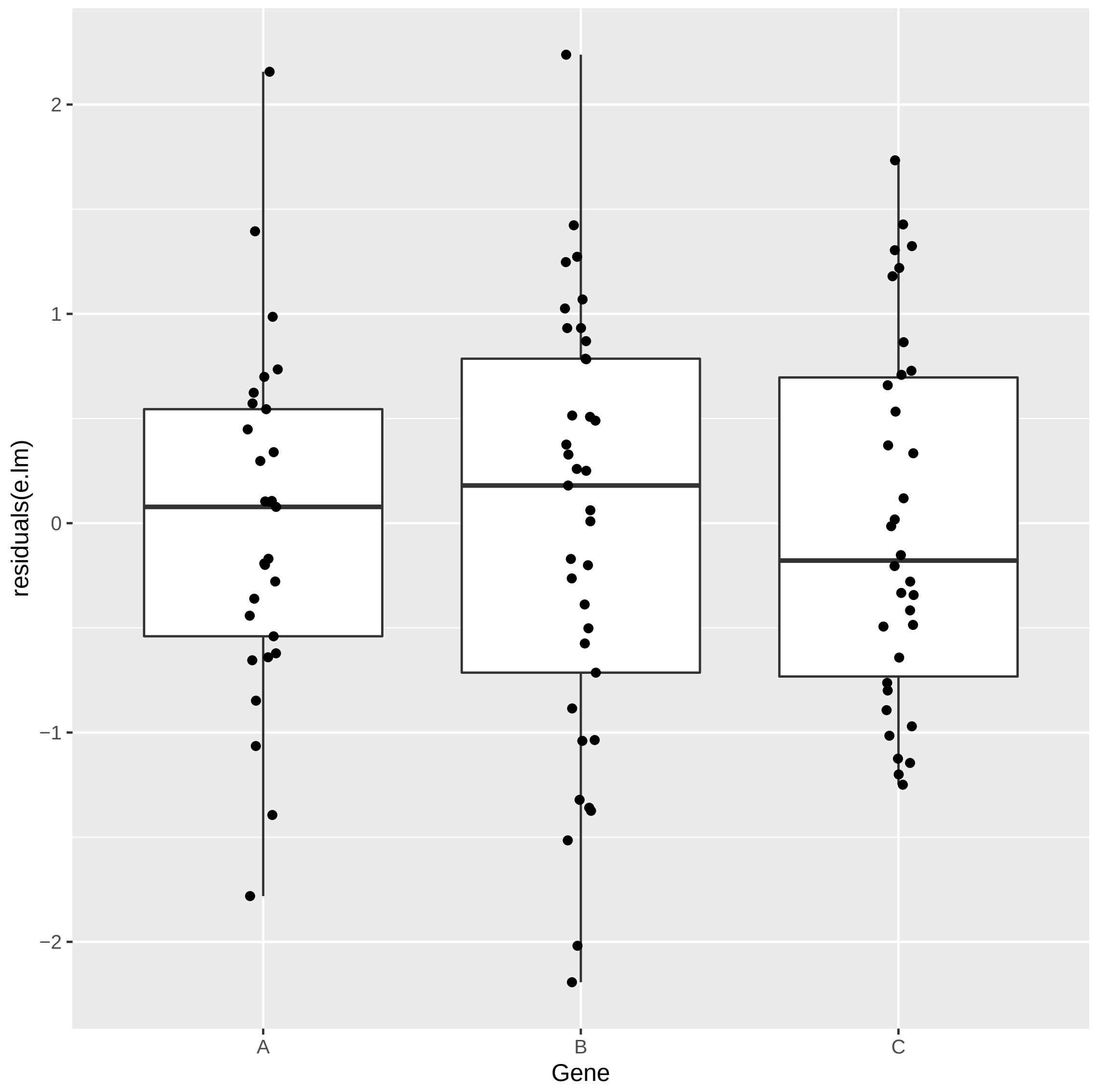
(A3) Independence is hard to check without a-priori information. But if one suspects correlation along one variable, one can use a correlagram to test the independence assumption (correlation would imply violation of A1). Let's for instance use the Id variable as a proxy for measurement time and see if observations measured in a short time interval are correlated:

```
acf(x = residuals(e.lm)) ## WARNING: assumes that the observations are ordered and
    equaly spaced in time
```



(A3) The identically distributed part implies that the variance is constant, e.g. the same for males and female or for all ages. This can be checked using a boxplot for categorical variables:

```
gg <- ggplot(d, aes(x = Gene, y = residuals(e.lm))) + geom_boxplot() + geom_jitter(
    height = 0,width = 0.05)
gg
## ggsave(gg, filename = "./figures/fig-lm-diag-A1-bin.pdf")
```



or displaying the standardized residuals along with a loess estimator of the variance:

```
gg <- ggplot(d, aes(x = Age)) + geom_point(aes(y=residuals(e.lm, type = "pearson"))) +
    geom_smooth(aes(y = residuals(e.lm, type = "pearson")^2-1))
gg
## ggsave(gg, filename = "./figures/fig-lm-diag-A1-cont.pdf")
```

```
‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```

```
plot(fitted(e.lm), sqrt(abs(residuals(e.lm, type = "pearson"))))
```

Here the variability should not depend on the covariate value (i.e. position on the x-axis).

7 Loops and parallel computations

7.1 Apply with progress bar

```
ls.res <- pbapply::pblapply(1:5, FUN = rnorm)
```

```
|                                                  | 0 % ~calculating
|++++++++++                                        | 20% ~00s
|++++++++++++++++++++                              | 40% ~00s
|++++++++++++++++++++++++++++++                    | 60% ~00s
|++++++++++++++++++++++++++++++++++++++++         | 80% ~00s
|++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 00s
```

7.2 Parallel computation

7.2.1 Detect the number of cores

```
cores <- parallel::detectCores()
cores
```

```
[1] 4
```

7.2.2 Start a cluster

```
cpus <- 2

cl <- snow::makeSOCKcluster(cpus)
doSNOW::registerDoSNOW(cl)
```

7.2.3 Get the name of each core

```
cpus.name <- unlist(parallel::clusterCall(cl = cl, function(x){
    myName <- paste(Sys.info()[['nodename']], Sys.getpid(), sep='-')
    return(myName)
}))
cpus.name
```

```
[1] "SUND31034-5800" "SUND31034-5992"
```

7.2.4 Export element to cluster

```
parallel::clusterExport(cl, varlist = "cpus.name")

parallel::clusterCall(cl = cl, function(x){
    indexCPU <- which(cpus.name == paste(Sys.info()[['nodename']], Sys.getpid(), sep='-
    '))
    indexCPU
})
```

```
[[1]]
[1] 1

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

7.2.5 Show progress bar (in console)

```
n.sim <- 20

pb <- txtProgressBar(max = n.sim, style=3)
opts <- list(progress = function(n) setTxtProgressBar(pb, n))

ls.res <- foreach::‘%dopar%‘(
                       foreach::foreach(i=1:n.sim, .options.snow=opts), {
                           Sys.sleep(0.1)
                       })
```

7.2.6 Show progress bar (external)

```
n.sim <- 20
parallel::clusterExport(cl, varlist = "n.sim")

ls.res <- foreach::‘%dopar%‘(
                       foreach::foreach(iCpus=1:cpus), {
                           pb <- tcltk::tkProgressBar(paste0("CPU ",iCpus), min = 0,
    max = n.sim, initial = 0)

                           for(iSim in 1:n.sim){
                               Sys.sleep(0.1)
                               tcltk::setTkProgressBar(pb = pb, value = iSim,
                                                       label = paste(iSim," over ",n.
    sim," iterations done") )
                           }

                           close(pb)
                       })
```

7.2.7 Stop a cluster

```
parallel::stopCluster(cl)
```

8 *lava* package

8.1 Generate repeated measurements

Model: Simulation:

```
set.seed(10)
dfW.data <- sim(m, n = 102, latent = FALSE)
```

Display simulated data:

```
head(dfW.data)
```

```
  weight_t1 Gender Treatment weight_t2 weight_t3  size_t1  size_t2  size_t3      Age Id
1  49.59633   Male       Yes  56.62904  55.58780 50.66805 55.88362 61.69410 39.54546  1
2  52.35484 Female        No  56.68563  63.21026 50.26003 55.72930 60.36953 37.70748  2
3  46.53011   Male        No  54.36636  62.05018 46.61315 50.89281 56.52237 40.80342  3
4  48.48417 Female       Yes  54.79413  59.72995 45.95248 53.09941 59.82107 40.94933  4
5  52.17022 Female       Yes  55.71550  64.21010 52.86341 58.40516 63.79082 42.06512  5
6  52.18837   Male       Yes  58.86797  64.51316 49.36853 57.90530 64.45437 37.68392  6
```

Modify simulated data

```
dtW.data <- as.data.table(dfW.data)
dtW.data[,paste0("weight_t",1:3) := lapply(.SD,round),
         .SDcols = paste0("weight_t",1:3)]
dtW.data[,paste0("size_t",1:3) := lapply(.SD,round, digit = 2),
         .SDcols = paste0("size_t",1:3)]
dtW.data[,Age := round(Age)]

setcolorder(dtW.data, c("Id","Age","Gender","Treatment",
                        paste0("weight_t",1:3),paste0("size_t",1:3)))
head(dtW.data)
```

```
   Id Age Gender Treatment weight_t1 weight_t2 weight_t3 size_t1 size_t2 size_t3
1:  1  40   Male       Yes        50        57        56   50.67   55.88   61.69
2:  2  38 Female        No        52        57        63   50.26   55.73   60.37
3:  3  41   Male        No        47        54        62   46.61   50.89   56.52
4:  4  41 Female       Yes        48        55        60   45.95   53.10   59.82
5:  5  42 Female       Yes        52        56        64   52.86   58.41   63.79
6:  6  38   Male       Yes        52        59        65   49.37   57.91   64.45
```

Export data:

```
fwrite(dtW.data, file = "./mydata.csv", sep = ";", dec = ",")
fwrite(dtW.data, file = "./mydata.txt", sep = " ", dec = ".")
```

8.2 Generate data with heteroschadasticity

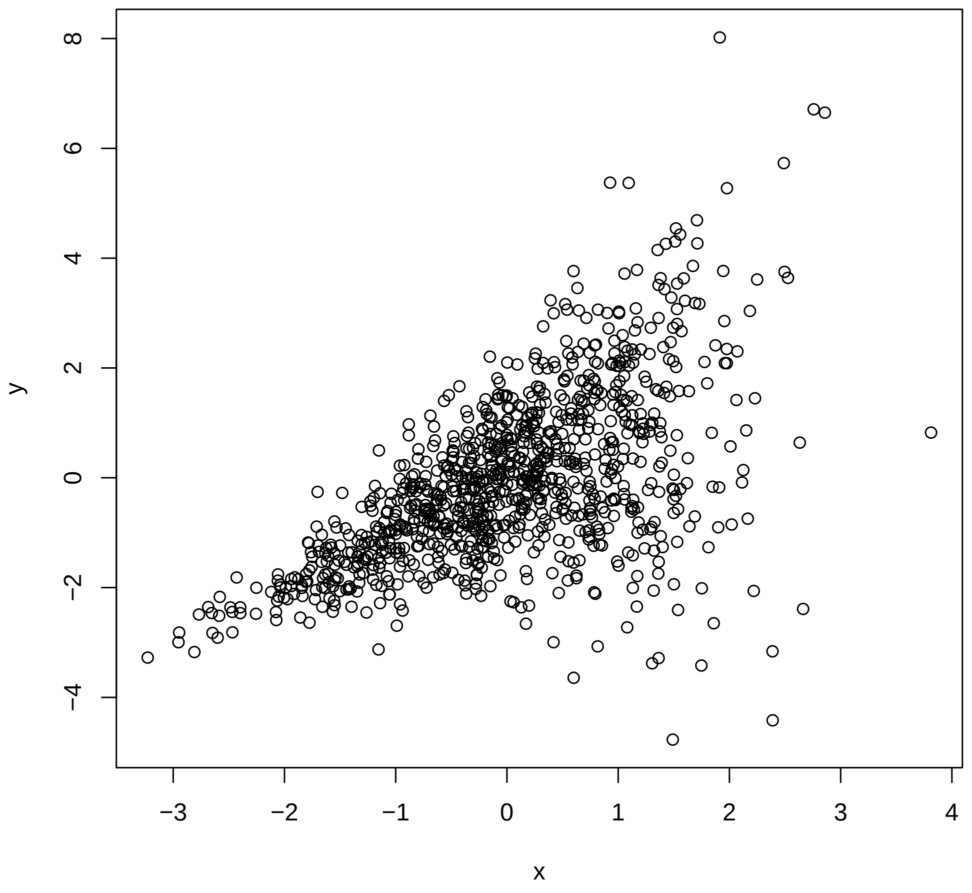
Model:

```
mSim <- lvm(y[m:v]~x)
constrain(mSim, v ~ x + a + b) <- function(x){ x[,2] + x[,3] * exp(x[,1]) }
parameter(mSim, start = c(0,1)) <- ~ a + b
```

Simulation:

```
set.seed(10)
n <- 1e3
df.tempo <- sim(mSim, n = n)
```

Display:



8.3 Generate survival time under non proportional hazard (non-PH)

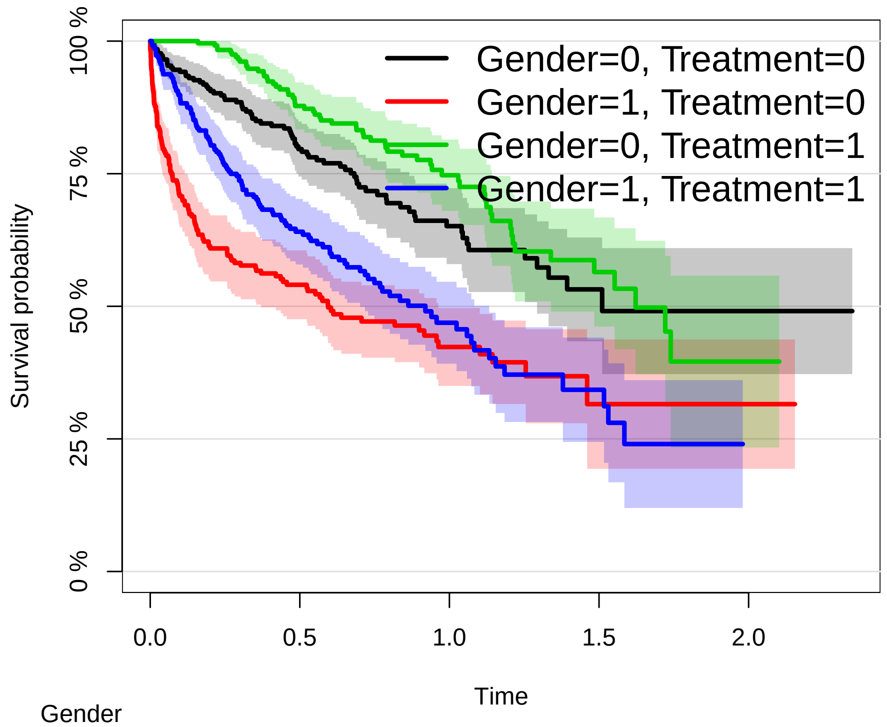
Model:

```
mSim <- lvm()
regression(mSim) <- eventtime ~ Gender + Age
regression(mSim) <- s ~ exp(0.6 * Treatment - 0.5 * Gender)
distribution(mSim,~ Treatment + Gender) <- binomial.lvm()
distribution(mSim,~cens) <- coxWeibull.lvm(scale = 1)
distribution(mSim,~eventtime) <- coxWeibull.lvm(scale = 0.3,shape =~ s)
eventTime(mSim) <- time ~ min(eventtime = 1, cens = 0)
```

Simulation:

```
set.seed(10)
n <- 1e3
df.tempo <- sim(mSim, n = n)
```

Display:



Gender											
0, Treatment:	259	216	173	107	73	45	24	10	7	2	1
1, Treatment:	236	139	99	68	43	21	8	5	1	1	0
0, Treatment:	249	234	174	128	81	49	31	14	5	0	0
1, Treatment:	256	190	120	79	46	25	12	5	1	0	0

8.4 Generate survival time with delayed treatment effect

Generative model with non-PH group effect but no Age effect:

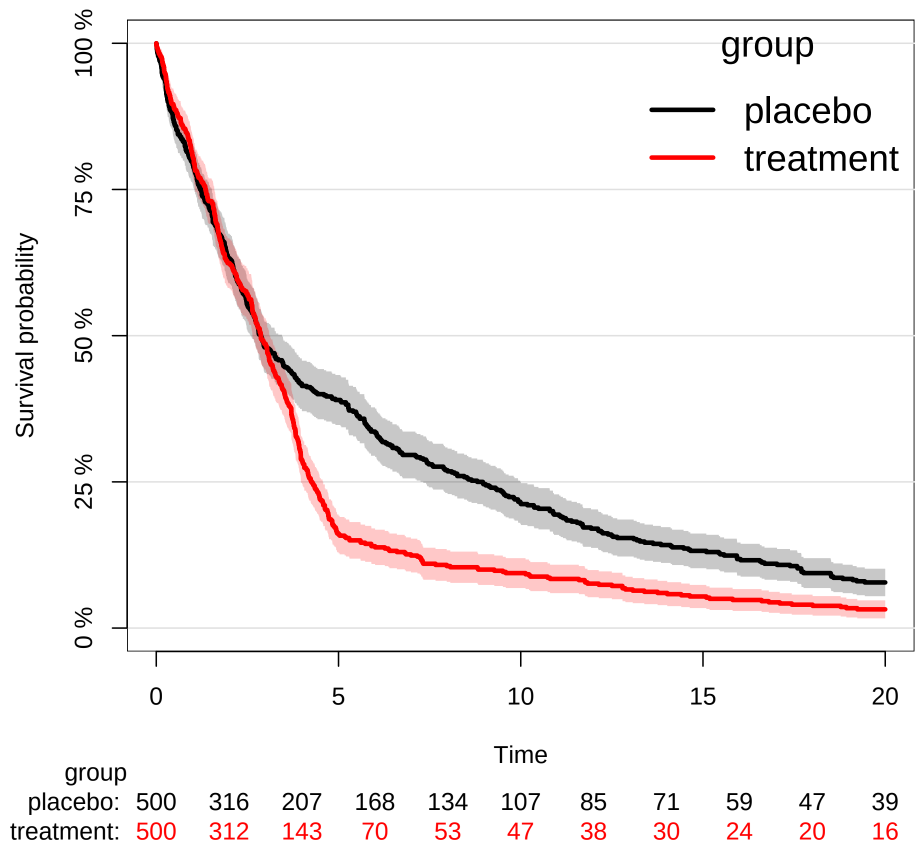
```
rates1 <- c(0.25,0.5,0.1); cuts <- c(0,3,5)
rates2 <- c(0.25,0.1,0.1); cuts <- c(0,3,5)
lasttime <- 20

m1 <- lvm(Age[50:5]~1)
m2 <- lvm(Age[50:5]~1)
distribution(m1,~eventtime) <- coxExponential.lvm(rate=rates1,timecut=cuts)
distribution(m2,~eventtime) <- coxExponential.lvm(rate=rates2,timecut=cuts)
transform(m1,status~eventtime) <- function(x){as.numeric(x[,1]<= lasttime)}
transform(m2,status~eventtime) <- function(x){as.numeric(x[,1]<= lasttime)}
transform(m1,time~eventtime) <- function(x){pmin(lasttime,x[,1])}
transform(m2,time~eventtime) <- function(x){pmin(lasttime,x[,1])}
latent(m1) <- ~eventtime
latent(m2) <- ~eventtime
```

Simulate data:

```
set.seed(12)
n <- 500
d1 <- as.data.table(sim(m1,n,latent=FALSE))
d2 <- as.data.table(sim(m2,n,latent=FALSE))
dt.data <- rbind(cbind(d1,group="treatment"),cbind(d2,group="placebo"))
dt.data
```

```
          Age status       time     group
   1: 46.68935      1  3.8755119 treatment
   2: 53.52666      1  3.2816799 treatment
   3: 47.86065      1  0.8515517 treatment
   4: 47.94281      1 10.1313180 treatment
   5: 45.53314      1  2.6198951 treatment
  ---
 996: 46.47948      1  2.1560011   placebo
 997: 52.78256      1  6.6831242   placebo
 998: 45.10627      1  6.0589065   placebo
 999: 49.24545      1 12.5248064   placebo
1000: 49.08839      1  1.9096902   placebo
```

Display survival curves by group:



group											
placebo:	500	316	207	168	134	107	85	71	59	47	39
treatment:	500	312	143	70	53	47	38	30	24	20	16

8.5 Tune optimization parameters

```
library(lava)
set.seed(10)
dd <- sim(lvm(Y~X1+X2+X3), 100)
ee <- estimate(lvm(Y~X1+X2+X3+eta), data = dd, control = list(trace = 1, iter.max =
    200))
```

```
  0:     260.69531: -0.00392152  0.00000  0.00000  0.00000  0.00000  1.89517  1.19723 0.900000
  1:     232.00124: -0.0200212 -0.0305115 0.473562 0.497905 0.592152  1.80796  1.17166 0.808180
  2:     202.02739: -0.0397653 -0.0662080 0.941194 0.998447  1.03587  1.47069  1.05604 0.430261
  3:     189.85429: -0.0476622 -0.0778219 0.942488 0.999840  1.03679  1.27746 0.902950 0.0991273
  4:     188.92755: -0.0488980 -0.0794005 0.942488 0.999840  1.03679  1.26451 0.851417 0.0150308
  5:     188.92730: -0.0489067 -0.0794116 0.942488 0.999840  1.03679  1.26448 0.850633 0.0137765
  6:     188.92730: -0.0489067 -0.0794116 0.942488 0.999840  1.03679  1.26448 0.850633 0.0137765
Warning messages:
1: In estimate.lvm(lvm(Y ~ X1 + X2 + X3 + eta), data = dd, control = list(trace = 1)) :
  Lack of convergence. Increase number of iteration or change starting values.
2: In sqrt(diag(asVar)) : NaNs produced
```

9 Miscellaneous

9.1 Profile code

```
library(lava)
m <- lvm(Y ~ X + G)
FUN <- function(n){
    d <- lava::sim(m, n = n)
    estimate(m,d)
}
profvis::profvis(FUN(n = 500))
```

#+RESULTS[*<2019-06-27 to 09:37>* a0d5077301cabedce939985d9ce7fb7eb9072578]:

9.2 Debug

To not show to many line before debug:

```
options(deparse.max.lines = 200)
```

To show at which line in the program an error occured:

```
options(error = function()revTraceback(max.lines = 5))
```

9.3 Find all function names from a package

```
r <- unclass(lsf.str(envir = asNamespace("lava"), all = T))
r[grep("coef", r)]
```

```
 [1] "coef.CrossValidated"   "coef.effects"          "coef.estimate"         "coef.estimate.list"
 [5] "coef.lvm"              "coef.lvm.mixture"      "coef.lvmfit"           "coef.multigroup"
 [9] "coef.multigroupfit"    "coef.multinomial"      "coef.ordreg"           "coef.pcor"
[13] "coef.summary.estimate" "coef.summary.lvmfit"   "coef.twostageCV"       "coef.zibreg"
[17] "describecoef"          "excoef"                "stdcoef"
```

9.4 Install development version of R

https://cran.r-project.org/bin/windows/base/rdevel.html

9.5 Install suggested packages

```r
char.package <- utils::packageDescription("butils", fields = "Suggests")
vec.package <- unlist(strsplit(gsub("[[:blank:]]", "", charPackage), split = ","))
install.packages(vec.package)
```

9.6 R version

```
sessionInfo()
```

```
R version 3.5.1 (2018-07-02)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 7 x64 (build 7601) Service Pack 1

Matrix products: default

locale:
[1] LC_COLLATE=Danish_Denmark.1252  LC_CTYPE=Danish_Denmark.1252    LC_MONETARY=Danish_Denmark.1252
[4] LC_NUMERIC=C                    LC_TIME=Danish_Denmark.1252

attached base packages:
[1] parallel  stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] ggpubr_0.2         magrittr_1.5       officer_0.3.2      Publish_2018.04.17 lava_1.6.5
 [6] doSNOW_1.0.16      snow_0.4-3         iterators_1.0.10   foreach_1.4.4      pbapply_1.3-4
[11] multcomp_1.4-8     TH.data_1.0-9      MASS_7.3-50        mvtnorm_1.0-8      survival_2.44-1.1
[16] prodlim_2018.04.18 car_3.0-2          carData_3.0-2      ggplot2_3.1.0      data.table_1.12.0

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.1        lattice_0.20-35   visNetwork_2.0.4  zoo_1.8-4         assertthat_0.2.0
 [6] digest_0.6.17     R6_2.3.0          cellranger_1.1.0  plyr_1.8.4        pillar_1.3.1
[11] rlang_0.3.1       lazyeval_0.2.1    curl_3.2          readxl_1.1.0      uuid_0.1-2
[16] Matrix_1.2-14     labeling_0.3      splines_3.5.1     stringr_1.3.1     foreign_0.8-70
[21] htmlwidgets_1.3   munsell_0.5.0     compiler_3.5.1    pkgconfig_2.0.2   base64enc_0.1-3
[26] htmltools_0.3.6   tidyselect_0.2.5  gridExtra_2.3     tibble_2.0.1      rio_0.5.10
[31] codetools_0.2-15  viridisLite_0.3.0 crayon_1.3.4      dplyr_0.7.8       withr_2.1.2
[36] grid_3.5.1        jsonlite_1.5      gtable_0.2.0      scales_1.0.0      zip_1.0.0
[41] stringi_1.2.4     ggthemes_4.0.1    bindrcpp_0.2.2    xml2_1.2.0        sandwich_2.5-0
[46] cowplot_0.9.3     openxlsx_4.1.0    tools_3.5.1       forcats_0.3.0     glue_1.3.0
[51] purrr_0.3.0       hms_0.4.2         yaml_2.2.0        abind_1.4-5       colorspace_1.3-2
[56] bindr_0.1.1       haven_1.1.2
```

9.7 CRAN check rocker

https://www.brodieg.com/2018/04/06/adventures-in-r-and-compiled-code/

docker run –rm -ti -v $(pwd):/mydir wch1/r-debug RDvalgrind -e "install.packages('/mydir/fansi$_{0.2.1.tar.gz}$')" RDvalgrind -d valgrind # and run tests

RDcsan

wget -O - https://github.com/bozenne/BuyseTest/tarball/master | tar xz