"How to" in **R**

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April 14, 2020

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:

```
## 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

## 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

```
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 mol
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 mol
[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)
```

```
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 mol
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 mol
[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

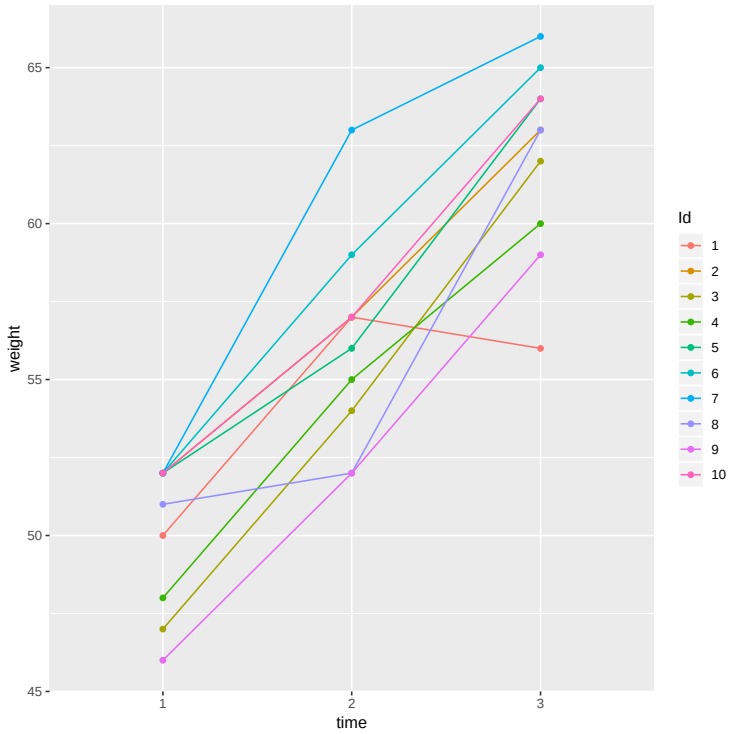
```
head(dtL.data)
```

```
   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

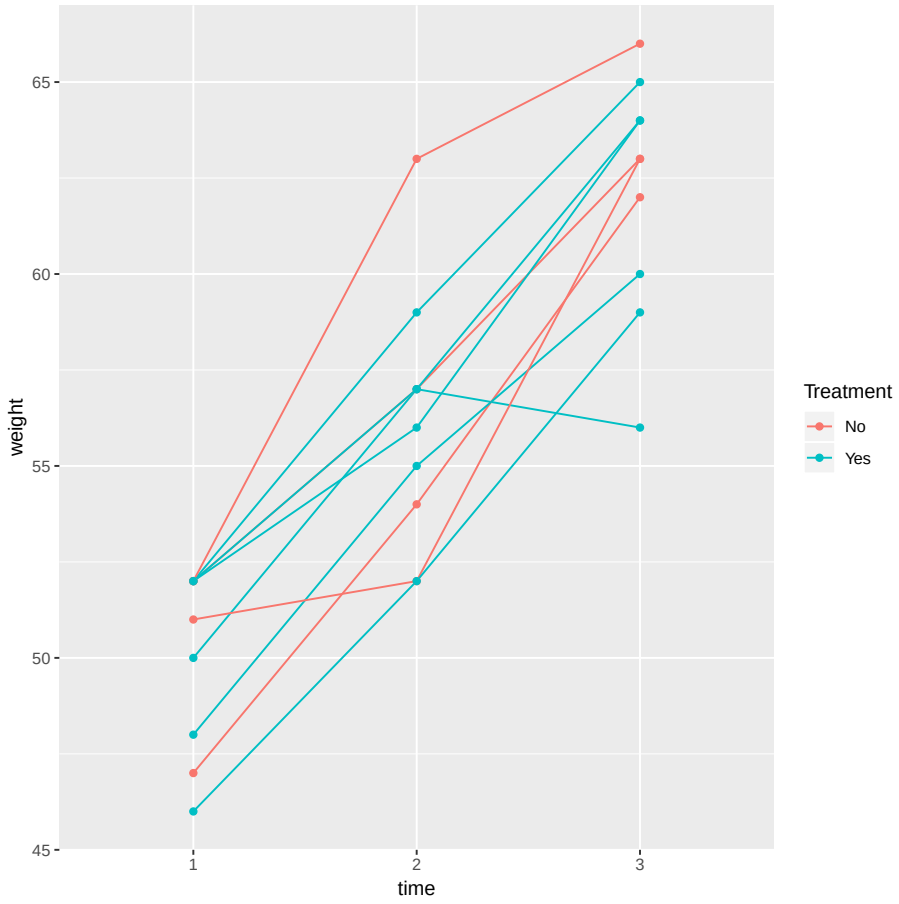
1. color by individual (first ten individuals)

```
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
```



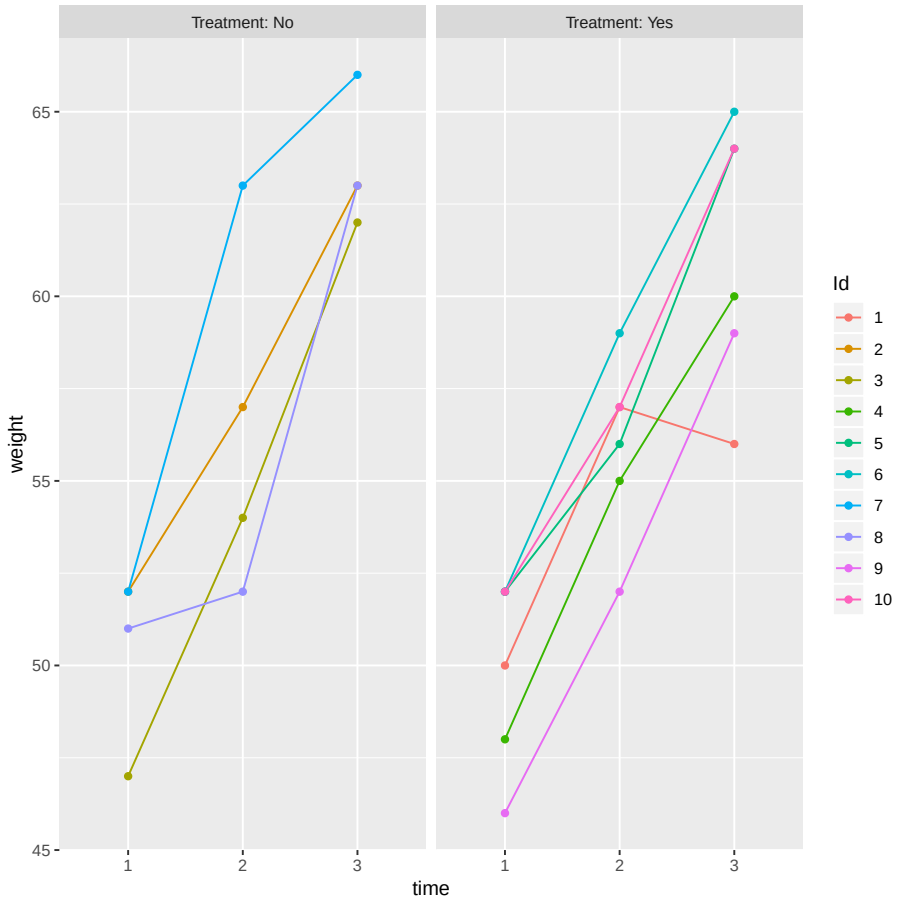
2. color by treatment group (first ten individuals)

```
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
```



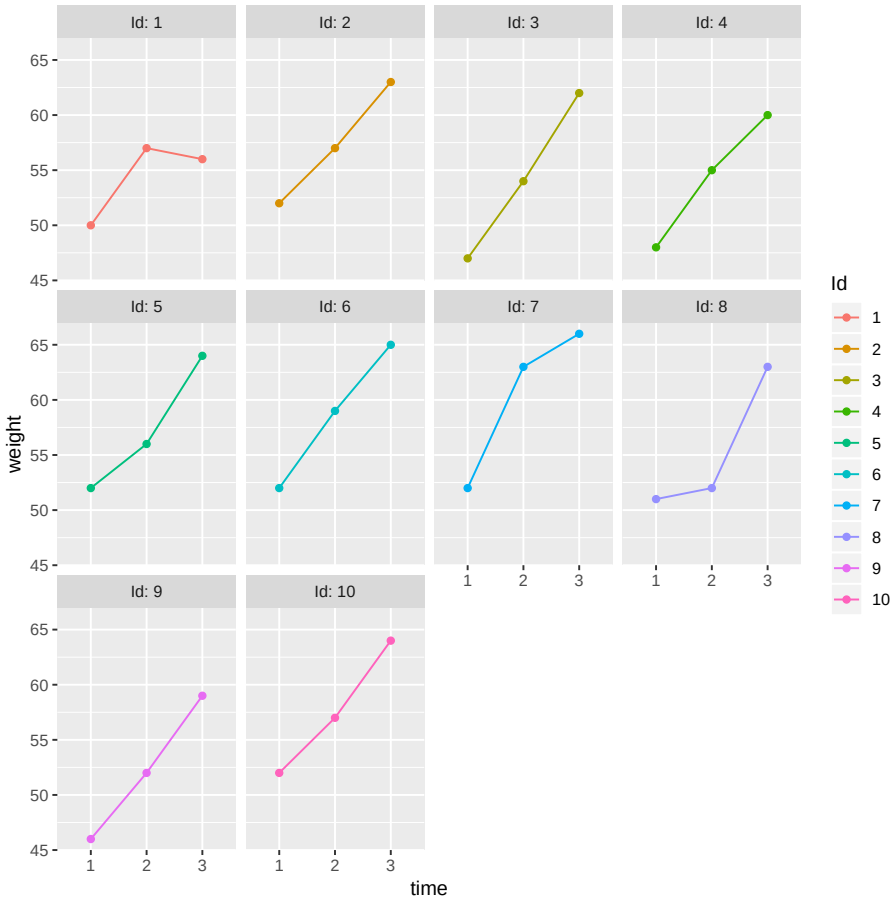
3. pannel for each treatment group (first ten individuals)

```
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
```



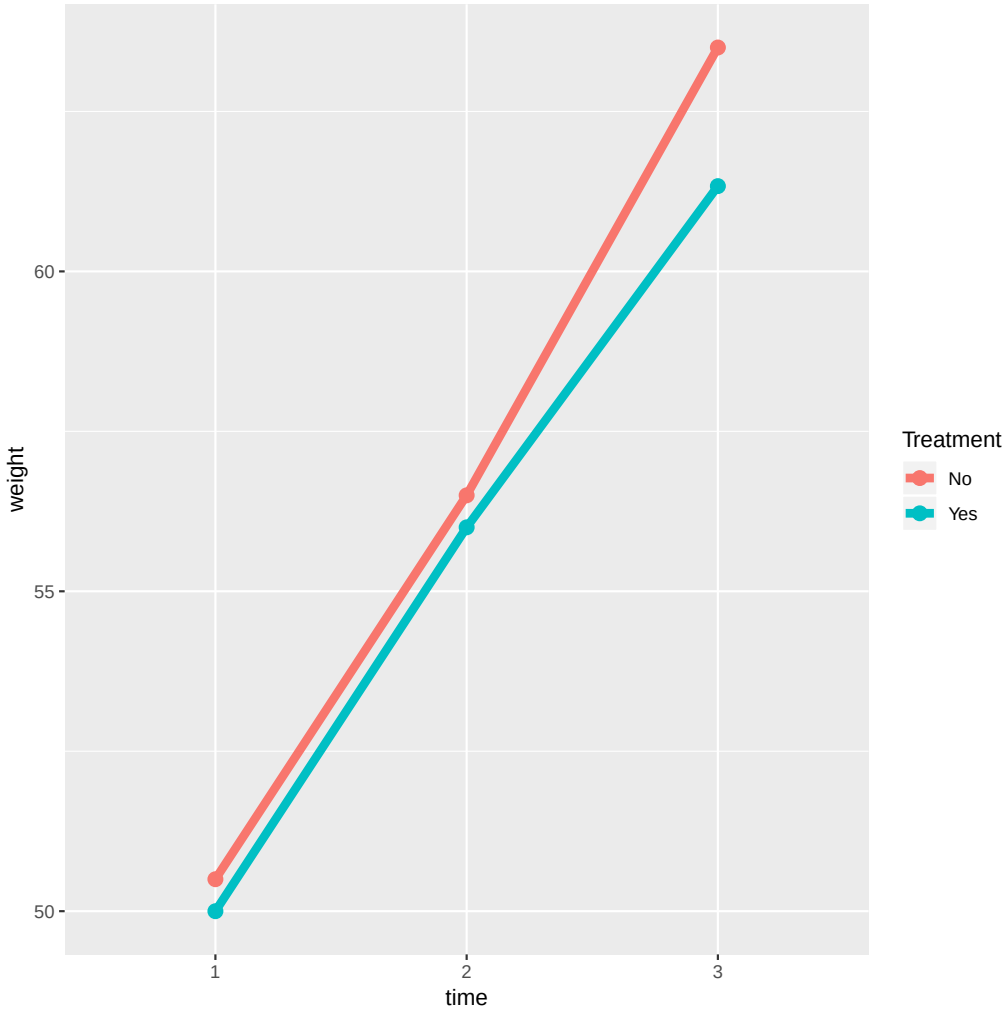
4. individual spaguetti plot (first ten individuals)

```
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

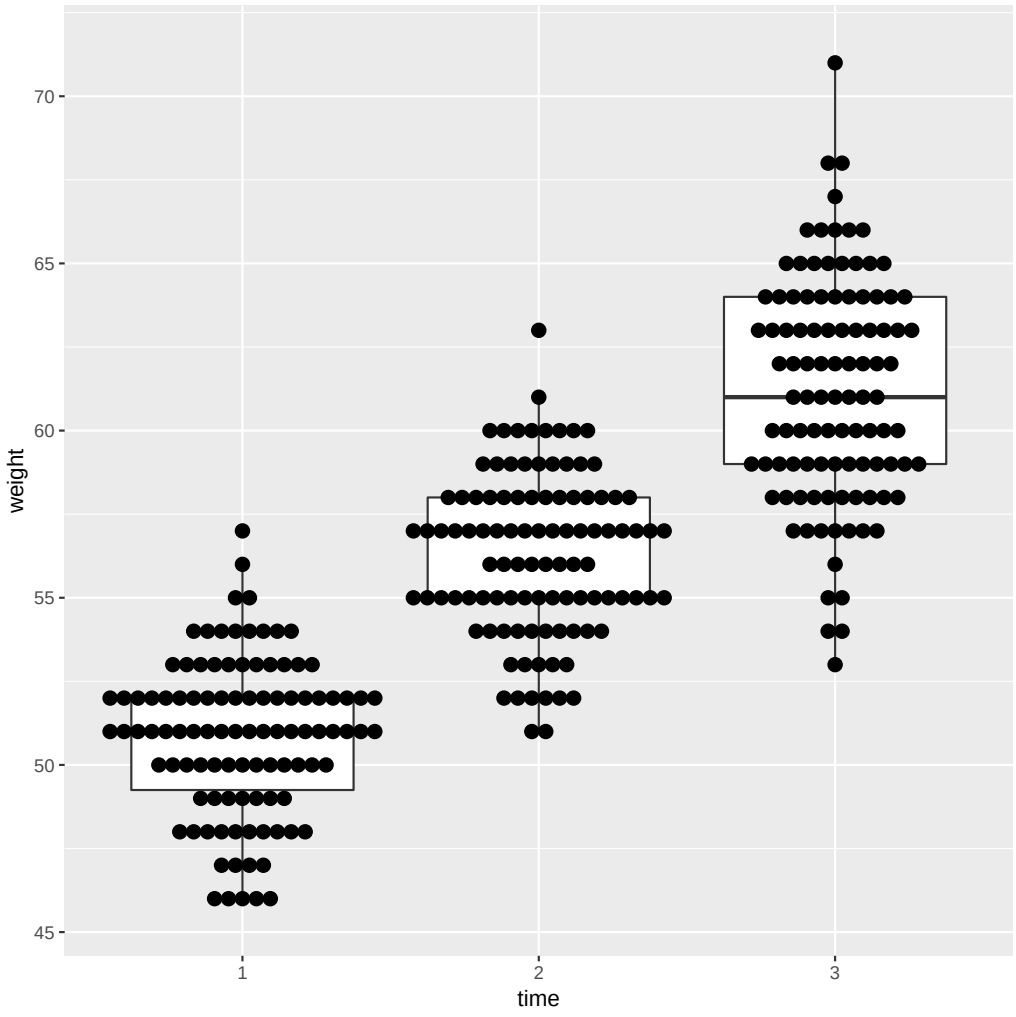
```
gg.mean <- ggplot(dtL.data[Id %in% 1:10], aes(x = time, y = weight))
gg.mean <- gg.mean + stat_summary(aes(group = Treatment, color = Treatment),
                                  geom = "line", fun.y = mean, size = 2)
gg.mean <- gg.mean + stat_summary(aes(group = Treatment, color = Treatment),
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

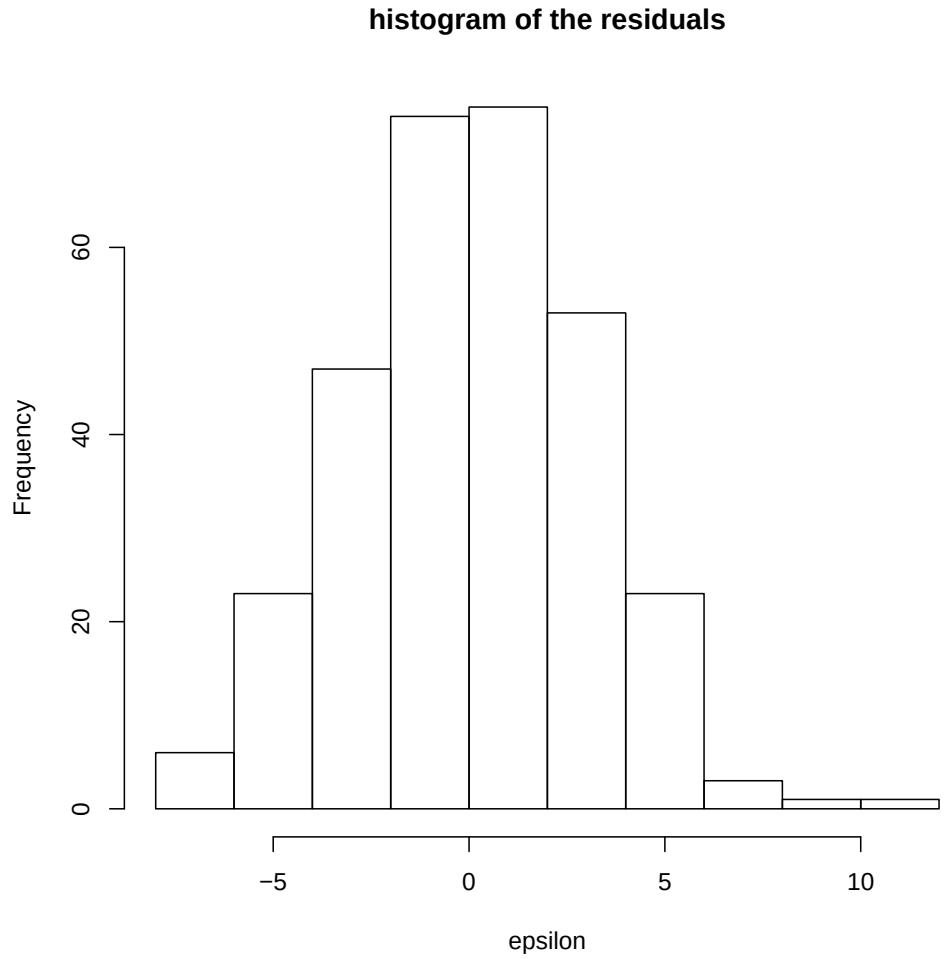
```
e.lm <- lm(weight ~ Age + Treatment + size,
           data = dtL.data)
```

5.2.1 Histogram of the residuals

Extract the residuals:

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

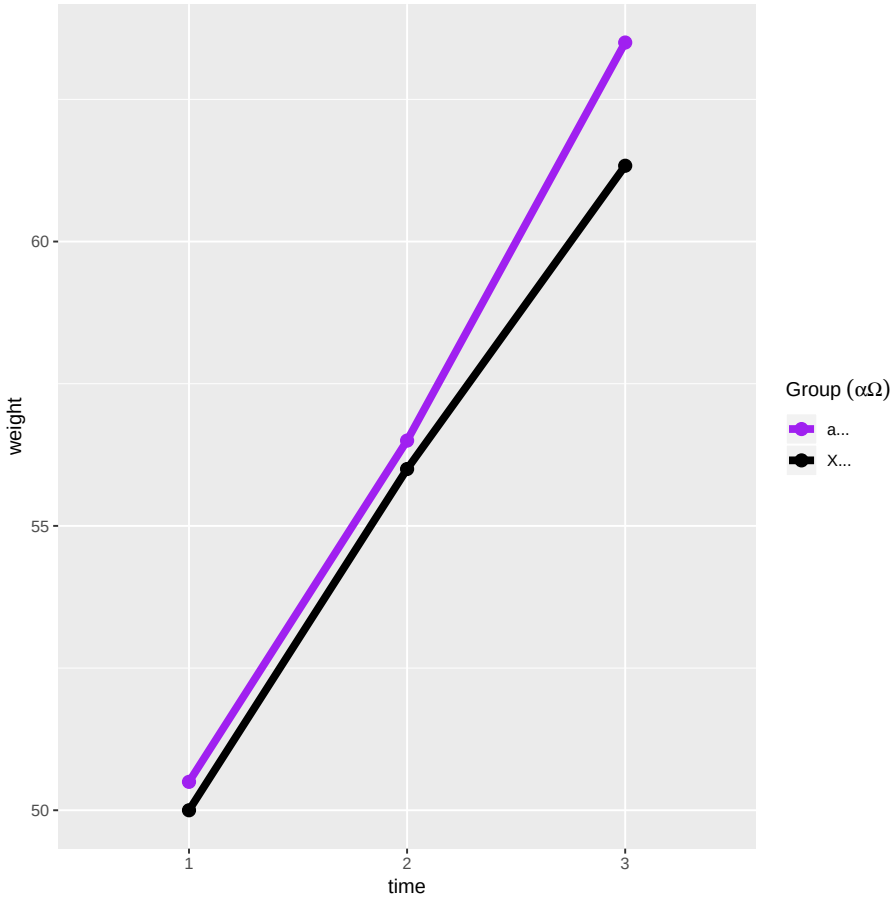
Display the histogram



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

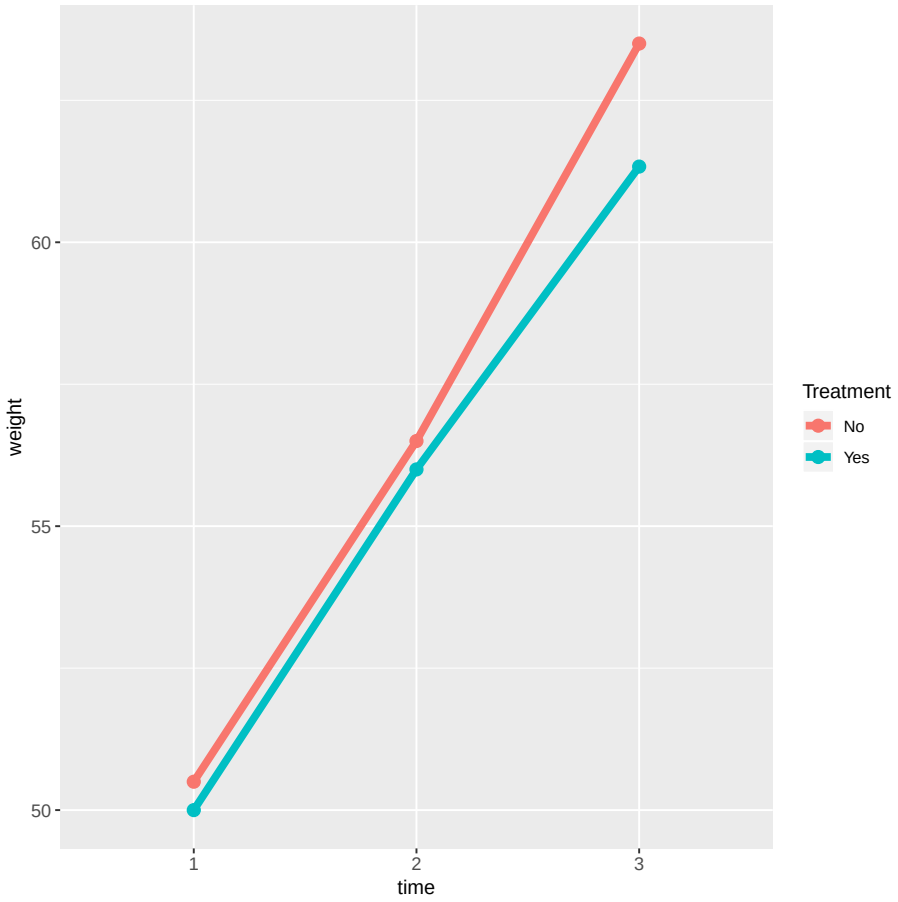
5.3.2 Change the name of the legend

```
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:

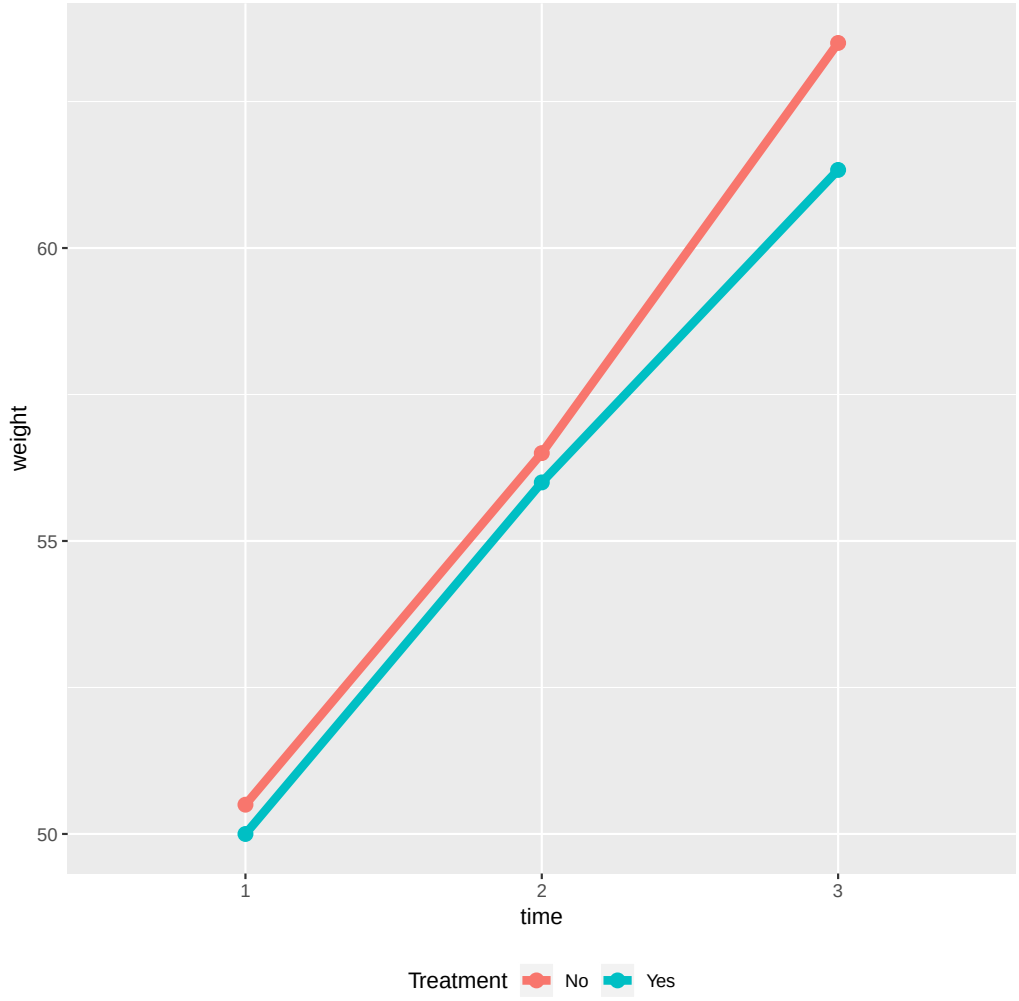
```
gg.mean3 <- gg.mean + theme(axis.text = element_text(size=10))
```

Only axis title:

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

5.3.4 Put the legend at the bottom

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



5.3.5 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]
}
```

5.3.6 Color blind palette

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

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

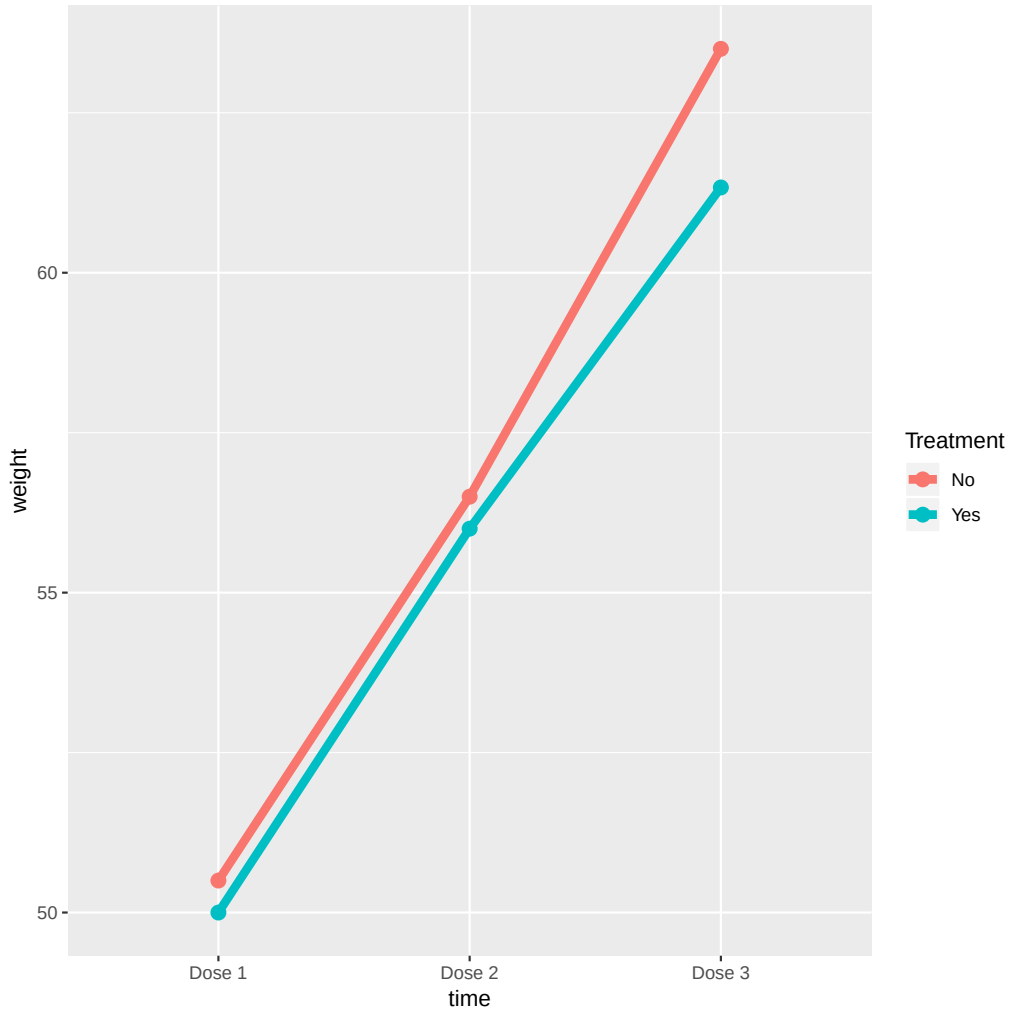
5.3.7 Rotate x-axis labels

```
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
```

5.3.8 Change tick mark labels

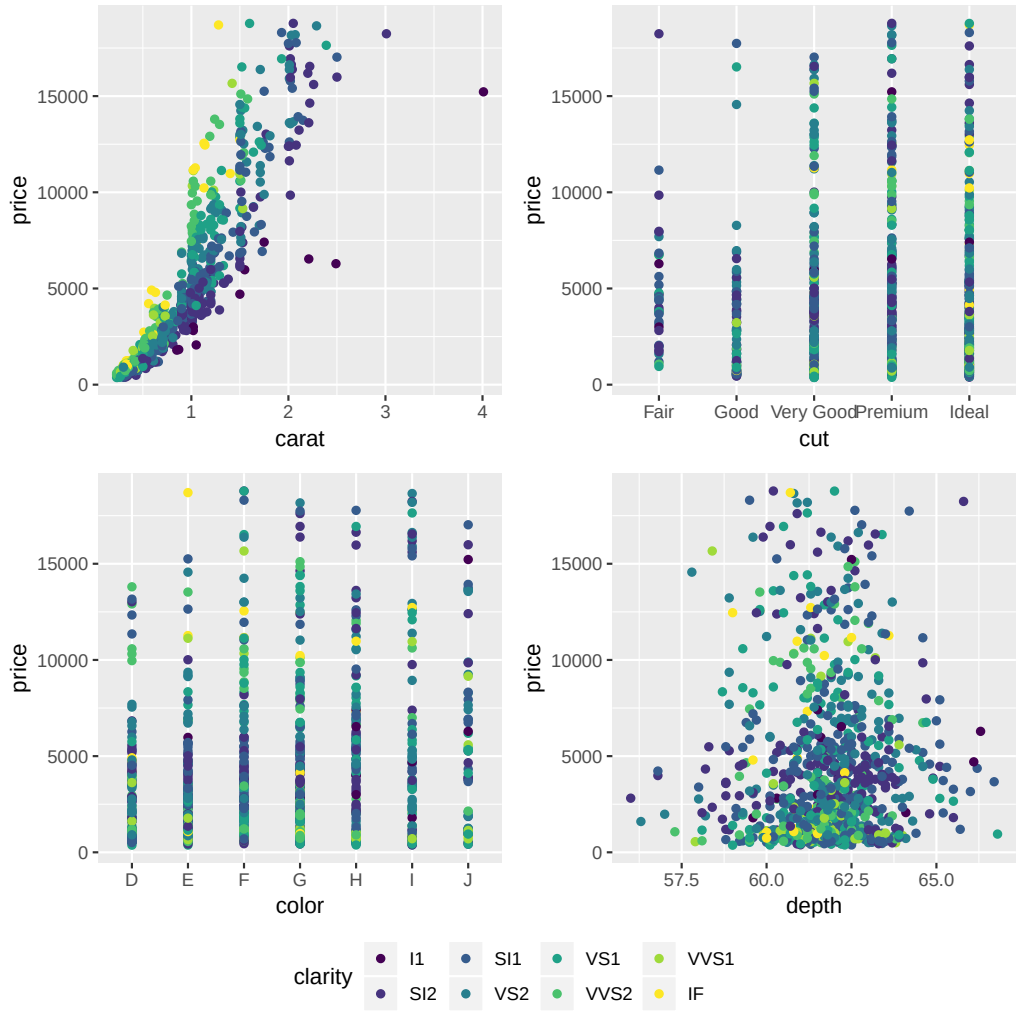
```
gg.mean5 <- gg.mean + scale_x_discrete(breaks=c("1","2","3"),
                                       labels=c("Dose 1", "Dose 2", "Dose 3"))
```



5.3.9 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")
```



5.3.10 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 (from Paul Blanche)

```
library(exact2x2)
library(Publish)
specdec <- function(x,k=0){
    format(round(x,k),nsmall=k)
}
```

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
```

Prepare output:

```
AllRes <- matrix("",nrow=4,ncol=3)
colnames(AllRes) <- c("Exact: usual Fisher","Asymptotic","Exact: central Fisher")
rownames(AllRes) <- c("Risk differrence","Relative risk","Odds ratio","p-value")
AllRes
```

```
                Exact: usual Fisher Asymptotic Exact: central Fisher
Risk differrence ""                 ""         ""
Relative risk    ""                 ""         ""
Odds ratio       ""                 ""         ""
p-value          ""                 ""         ""
```

Usual fisher test:

```
xEuF <- fisher.test(tab)
AllRes[4,1] <- specdec(xEuF$p.value,k=3)
AllRes[3,1] <- paste0(specdec(xEuF$estimate,k=3)," (",specdec(xEuF$conf.int[1],k=3),";"
    ,specdec(xEuF$conf.int[2],k=3),")")
```

Central Fisher test:

```
xEcF <- exact2x2(tab,tsmethod="central")
AllRes[4,3] <- specdec(xEcF$p.value,k=3)
AllRes[3,3] <- paste0(specdec(xEcF$estimate,k=3)," (",specdec(xEcF$conf.int[1],k=3),";"
    ,specdec(xEcF$conf.int[2],k=3),")")
```

```
ciRDEcF <- binomMeld.test(x1=tab[2,1],n1=sum(tab[2,]),
                          x2=tab[1,1],n2=sum(tab[1,]),
                          parmtype="difference")
AllRes[1,3] <- paste0(specdec(ciRDEcF$estimate,k=3)," (",specdec(ciRDEcF$conf.int[1],k
    =3),";",specdec(ciRDEcF$conf.int[2],k=3),")")

ciRREcF <- binomMeld.test(x1=tab[2,1],n1=sum(tab[2,]),
                          x2=tab[1,1],n2=sum(tab[1,]),
                          parmtype="ratio")
AllRes[2,3] <- paste0(specdec(ciRREcF$estimate,k=3)," (",specdec(ciRREcF$conf.int[1],k
    =3),";",specdec(ciRREcF$conf.int[2],k=3),")")
```

Asymptotics:

```
xA <- table2x2(tab)
AllRes[4,2] <- specdec(chisq.test(tab)$p.value,k=3)
AllRes[3,2] <- paste0(specdec(xA$or,k=3)," (",specdec(xA$or.lower,k=3),";",specdec(xA$
    or.upper,k=3),")")
AllRes[2,2] <- paste0(specdec(xA$rr,k=3)," (",specdec(xA$rr.lower,k=3),";",specdec(xA$
    rr.upper,k=3),")")
AllRes[1,2] <- paste0(specdec(xA$rd,k=3)," (",specdec(xA$rd.lower,k=3),";",specdec(xA$
    rd.upper,k=3),")")
chisq.test(tab)$expected
sum(tab[,1]/sum(tab))*sum(tab[1,])
sum(tab[,2]/sum(tab))*sum(tab[1,])
sum(tab[,1]/sum(tab))*sum(tab[2,])
sum(tab[,2]/sum(tab))*sum(tab[2,])
```

```
             worse   better
Placebo    7.892857 9.107143
Dalteparin 5.107143 5.892857
[1] 7.892857
[1] 9.107143
[1] 5.107143
[1] 5.892857
```

Comparisons

```
AllRes
```

```
                Exact: usual Fisher   Asymptotic               Exact: central Fisher
Risk differrence ""                   "-0.433 (-0.774;-0.092)" "-0.433 (-0.748;0.017)"
Relative risk    ""                   "0.404 (0.178;0.919)"    "0.404 (0.133;1.038)"
Odds ratio       "0.169 (0.020;1.072)" "0.156 (0.029;0.845)"    "0.169 (0.020;1.072)"
p-value          "0.051"               "0.063"                  "0.062"
```

6.2 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
```

6.2.1 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)
```

6.2.2 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
```

6.2.3 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
```

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

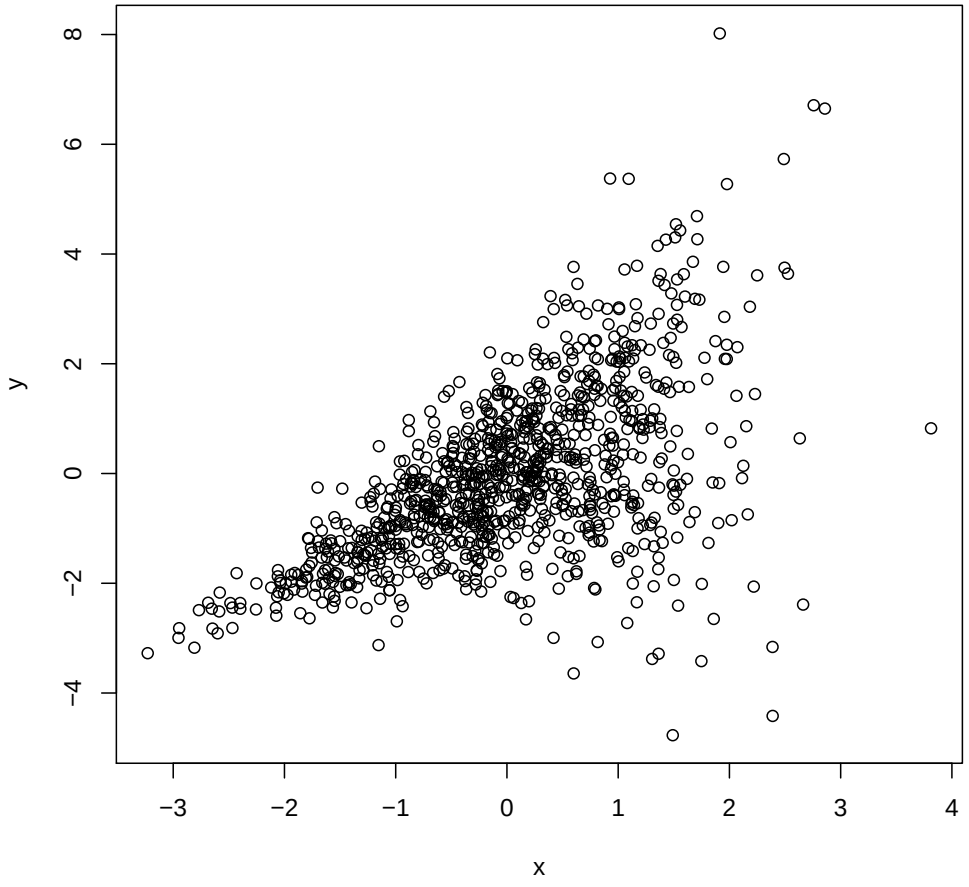
Model:

```
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)

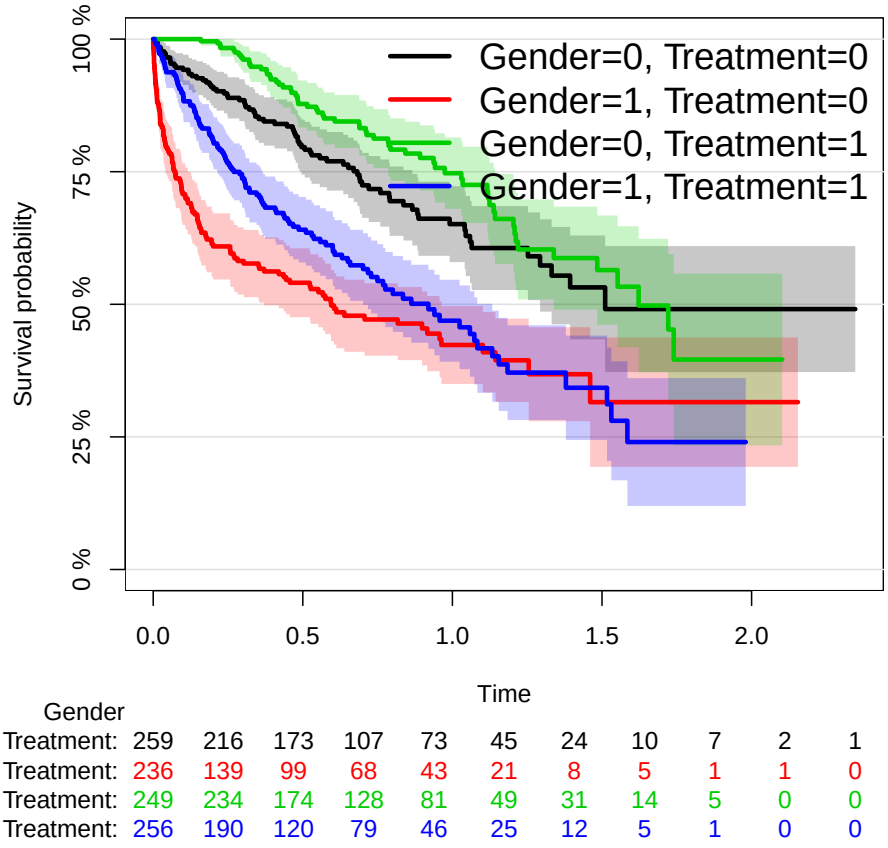
Model:

```
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:

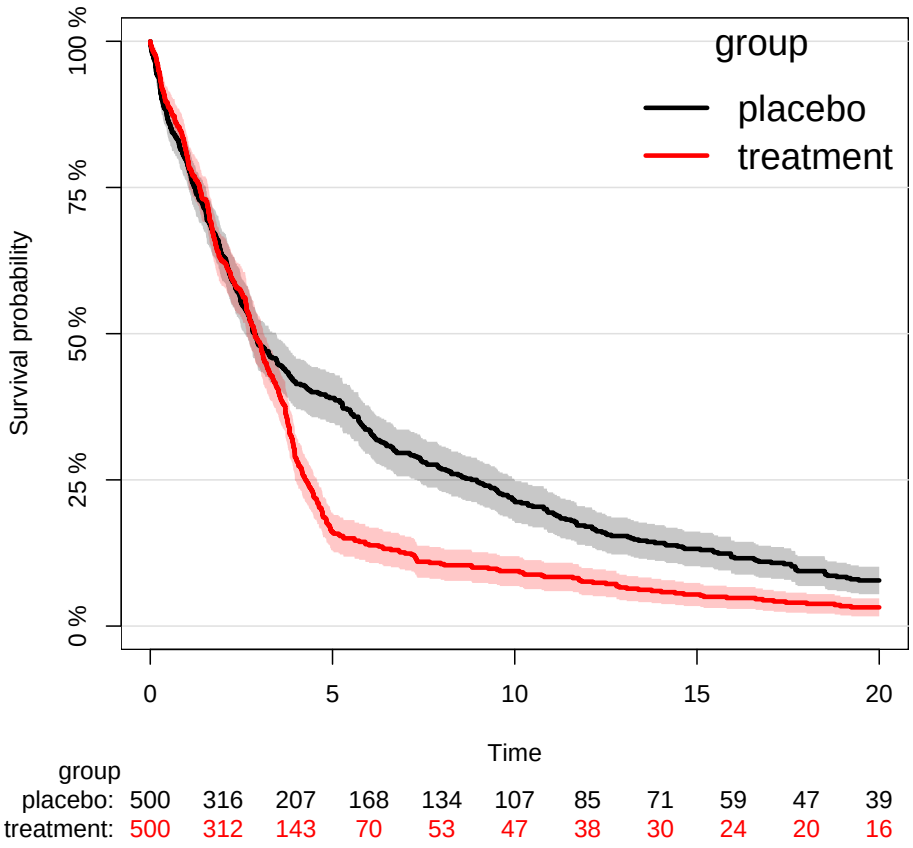
```
rates1 <- c(0.25,0.5,0.1); cuts <- c(0,3,5)
rates2 <- c(0.25,0.1,0.1); cuts <- c(0,3,5)
lasttime <- 20

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
treatment
Survival probability
100 %
75 %
50 %
25 %
0 %
0
5
10
15
20
Time
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

```
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
```