


"How to" in

Brice Ozenne

October 29, 2018

This document present ways to perform basic operations in .

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

Contents

1	Packages	4
2	Import/export data	5
2.1	Set the working directory	5
2.2	See which files are present in the current directory	6
2.3	Check that the file we want to import exists:	7
2.4	Display a file before importing it	8
2.5	Import a data from a file (.txt, .csv)	9
2.6	Import data from a specific format (e.g. excel files or outputs from SPSS/SAS) . . .	10
2.7	Export data	11
2.8	Export table	12
2.9	Export graphs	13
3	Data management	14
3.1	Categorize age into groups	14
4	Data management using the <i>data.table</i> package	15
4.1	Introduction	15
4.2	Display a dataset	17
4.3	Extract row(s), i.e. all the variables relative to one or several observations	18
4.3.1	Extract row(s) using row numbers	18
4.3.2	Extract row(s) according to conditions	18
4.4	Extract column(s), i.e. all the observations relative to one or several variables	20
4.4.1	Extract column(s) using column numbers	20
4.4.2	Extract column(s) using column names	21
4.5	Work with categorical variables	22
4.5.1	Convert a numeric/character into a factor	22
4.5.2	Divide a continuous variable into categories	22
4.5.3	Redefine the levels of a factor variable	23
4.6	Extract simple features of a dataset	24
4.6.1	Number of rows and columns	24
4.6.2	Name of the columns	24
4.6.3	Type of the columns	24
4.6.4	Summary statistics by column	24
4.6.5	Number of missing values	25
4.6.6	Mean value of a column	25
4.6.7	Correlation between values of several columns	26
4.7	Performing operations on a group of rows	27
4.7.1	Computing the number of observations per subgroup	27
4.7.2	Computing the mean by subgroup	27
4.7.3	Computing the correlation matrix by subgroup	28
4.8	Sort a dataset according to one or several variables	30
4.9	Change the names of the column in a dataset	32
4.10	Converting a dataset from the wide format to the long format	33

4.10.1	Univariate melt	33
4.10.2	Multivariate melt	35
4.11	Converting a dataset from the long format to the wide format	36
4.11.1	Univariate	36
4.11.2	Multivariate	37
5	Graphical display	38
5.1	Descriptive plots	38
5.1.1	Spaguetti plot	38
5.1.2	Display the mean over time	42
5.2	Diagnostic plots	43
5.2.1	Histogram of the residuals	43
5.3	Customize graphic	44
5.3.1	Modify the legend of a discrete scale	44
5.3.2	Increase the font size	44
5.3.3	Put the legend at the bottom	45
5.3.4	Default ggplot color palette	46
5.3.5	Color blind palette	46
5.3.6	Rotate x-axis labels	46
5.3.7	Change tick mark labels	46
5.4	Path diagram	48
6	Modeling	49
6.1	Testing linear hypotheses	49
6.1.1	Separate Wald tests of linear hypotheses	49
6.1.2	Confidence intervals associated with linear hypotheses	51
6.1.3	Joint test of linear hypotheses	51
7	Loops and parallel computations	53
7.1	Apply with progress bar	53
7.2	Parallel computation	54
7.2.1	Detect the number of cores	54
7.2.2	Start a cluster	54
7.2.3	Get the name of each core	54
7.2.4	Export element to cluster	54
7.2.5	Show progress bar (in console)	55
7.2.6	Show progress bar (external)	55
7.2.7	Stop a cluster	55
8	Generate data using the <i>lava</i> package	56
8.1	Generate repeated measurements	56
8.2	Generate data with heteroschadasticity	57
8.3	Generate survival time under non proportional hazard (non-PH)	58
8.4	Generate survival time with delayed treatment effect	60

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)

## 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  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/Teaching/repeated measurements 2017/Doc/howTo/"  
setwd(path)
```

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

```
getwd()
```

```
[1] "c:/Users/hpl802/Documents/Teaching/repeated measurements 2017/Doc/howTo"
```

2.2 See which files are present in the current directory

List all files in the current directory:

```
list.files()
```

```
[1] "#howTo.org#"      "figures"          "howTo.org"        "howTo.org.~1~"
[5] "howTo.org.~2~"    "howTo.org.~3~"    "howTo.org.~4~"    "howTo.org.~5~"
[9] "howTo.org.~6~"    "howTo.org.~7~"    "howTo.org_archive" "howTo.pdf"
[13] "howTo.soc"        "howTo.tex"        "howTo.tex.~1~"    "howTo.tex.~100~"
[17] "howTo.tex.~101~"  "howTo.tex.~102~"  "howTo.tex.~103~"  "howTo.tex.~104~"
[21] "howTo.tex.~105~"  "howTo.tex.~106~"  "howTo.tex.~2~"     "howTo.tex.~3~"
[25] "howTo.tex.~4~"    "howTo.tex.~5~"    "howTo.tex.~6~"     "howTo.tex.~98~"
[29] "howTo.tex.~99~"   "mydata.csv"        "mydata.txt"        "myplot.png"
```

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. <code>"./mydata.txt"</code> abbreviated in <code>"mydata.txt"</code>
"../"	stands for parent directory, e.g. <code>"../mydata.txt"</code>
"/"	stands for root directory, e.g. <code>"/mydata.txt"</code>

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.:

- **xlsx** package: function `read.xlsx`.
- **gdata** package: function `read.xls`.

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
- `xlsx::write.xlsx` 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/Teaching/repeated measurements 2017/Doc/howTo/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]
```

4 Data management using the *data.table* package

4.1 Introduction


In , 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 .
- 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         : int   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   : int   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)
```


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

Total number

[1] 0

Number of missing values by variable:

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:

[illegible]

First extract the values from a column:

25

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

```

```
[[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

```

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 conversion can be done naming explicitly 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)
```

```
[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 conversion 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

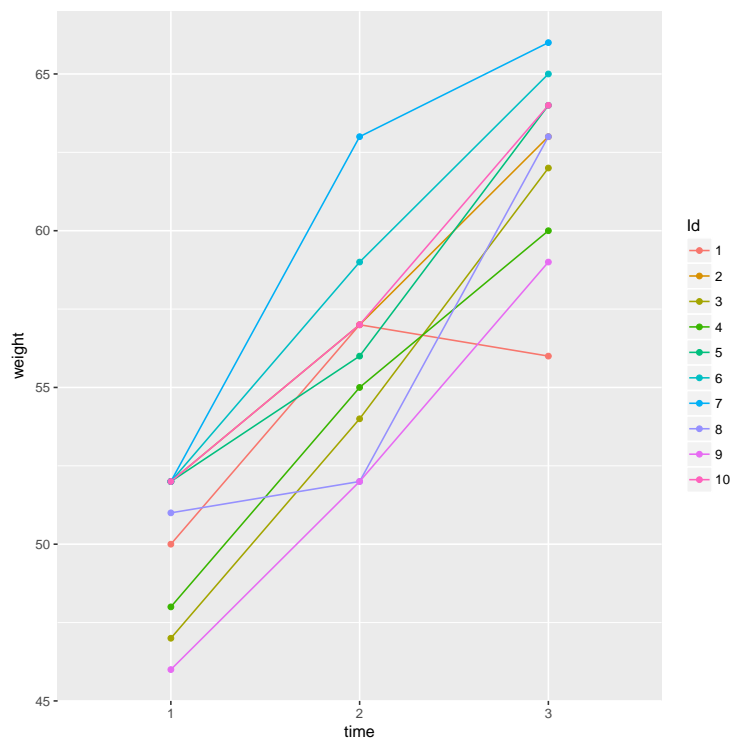
```
head(dtL.data)
```

	Id	Gender	Treatment	Age	time	weight	size
1:	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

5.1.1 Spagueti plot

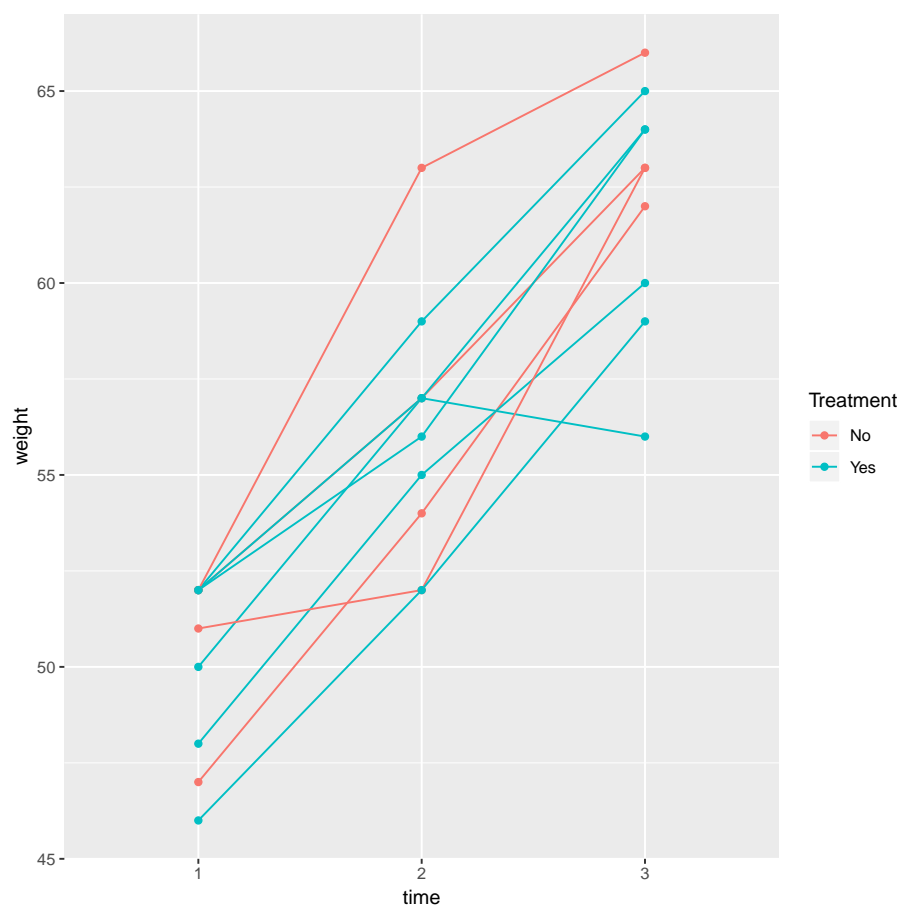
1. color by individual (first ten individuals)

```
gg.spagueti1 <- ggplot(dtL.data[Id %in% 1:10],  
                        aes(x = time, y = weight, color = Id, group = Id))  
gg.spagueti1 <- gg.spagueti1 + geom_line() + geom_point()  
gg.spagueti1
```



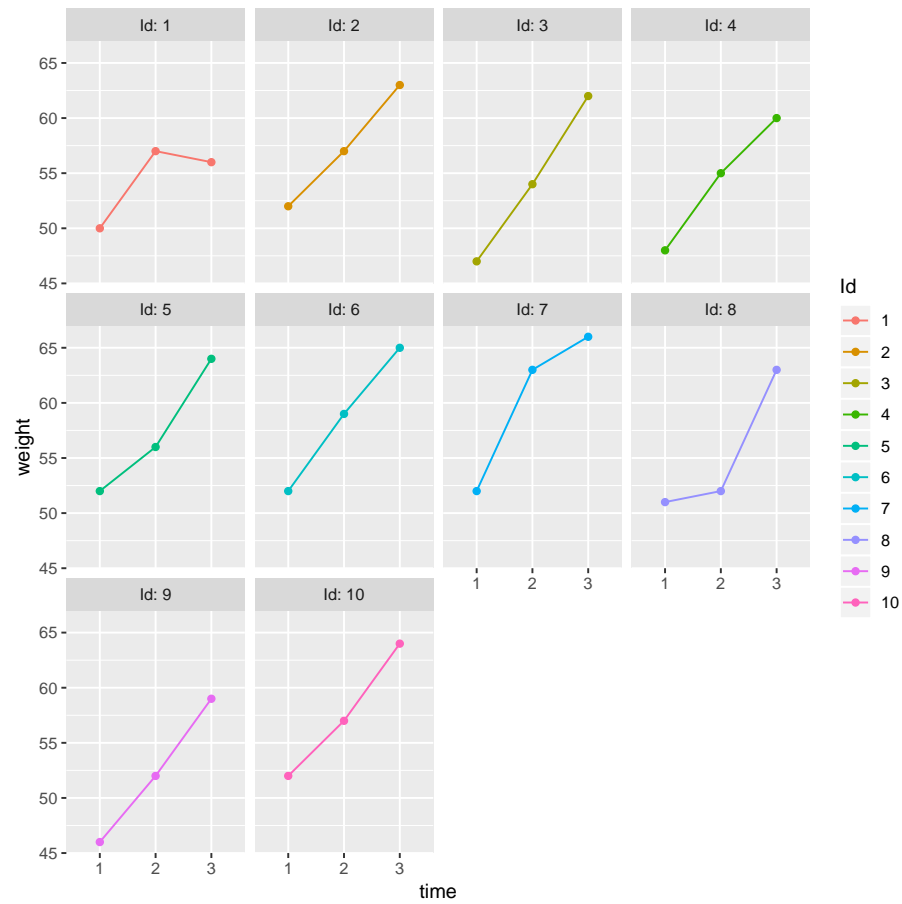
2. color by treatment group (first ten individuals)

```
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
```



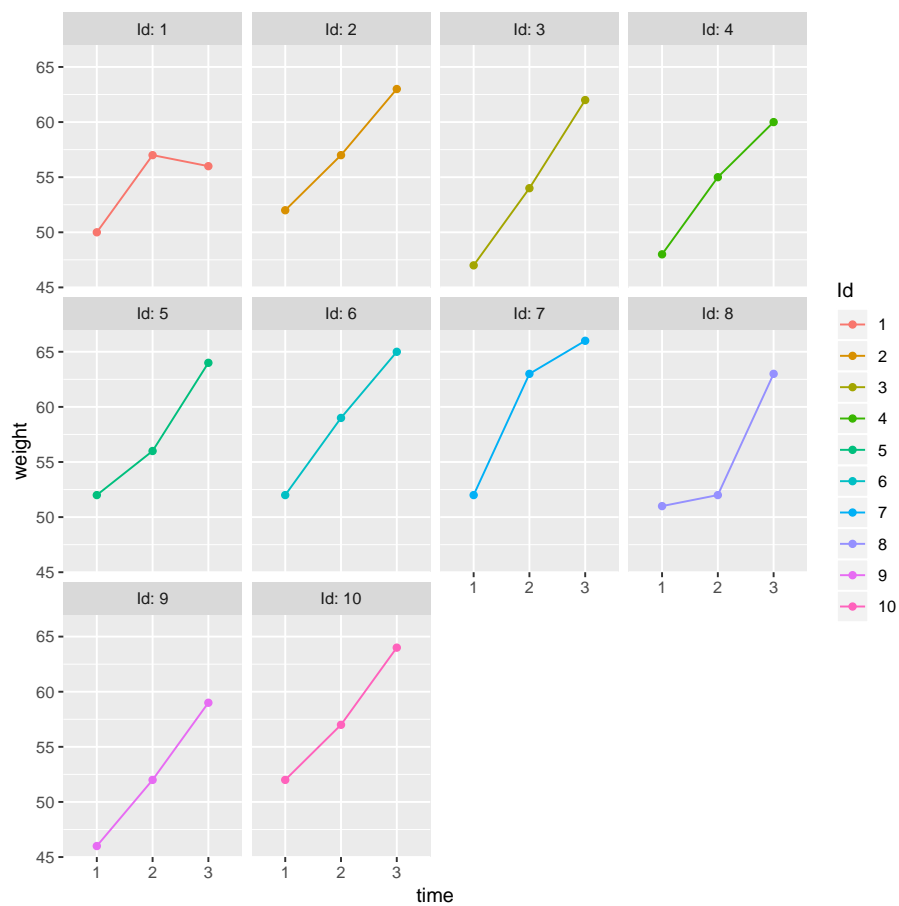
3. pannel for each treatment group (first ten individuals)

```
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
```



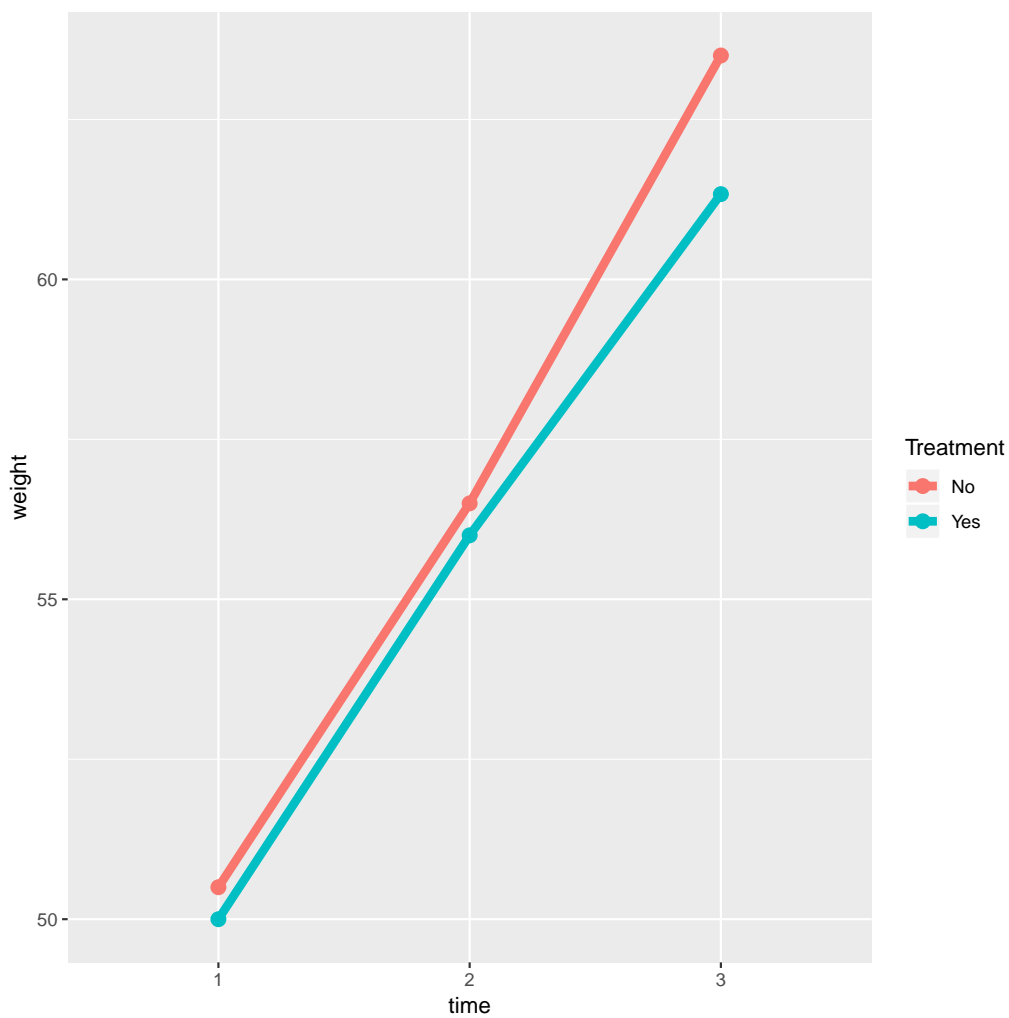
4. individual spaghetti plot (first ten individuals)

```
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)
```



5.2 Diagnostic plots

Consider the linear model:

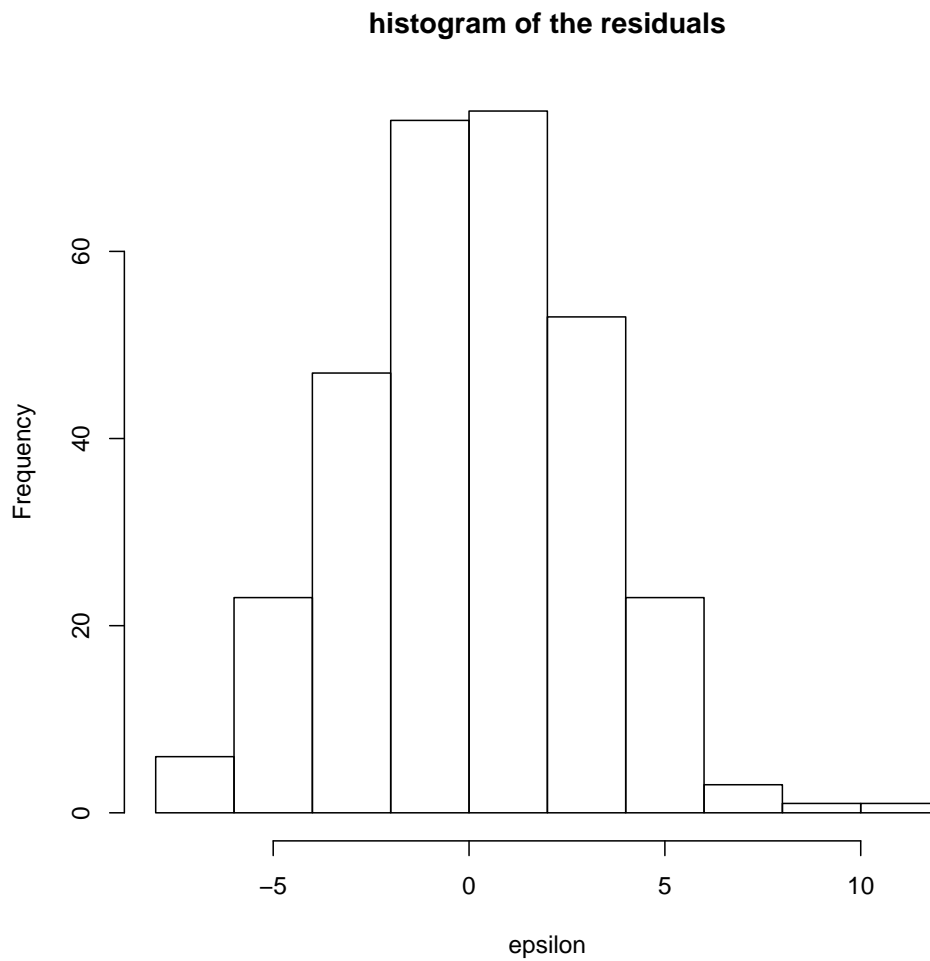
```
e.lm <- lm(weight ~ Age + Treatment + size,  
            data = dtL.data)
```

5.2.1 Histogram of the residuals

Extract the residuals:

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

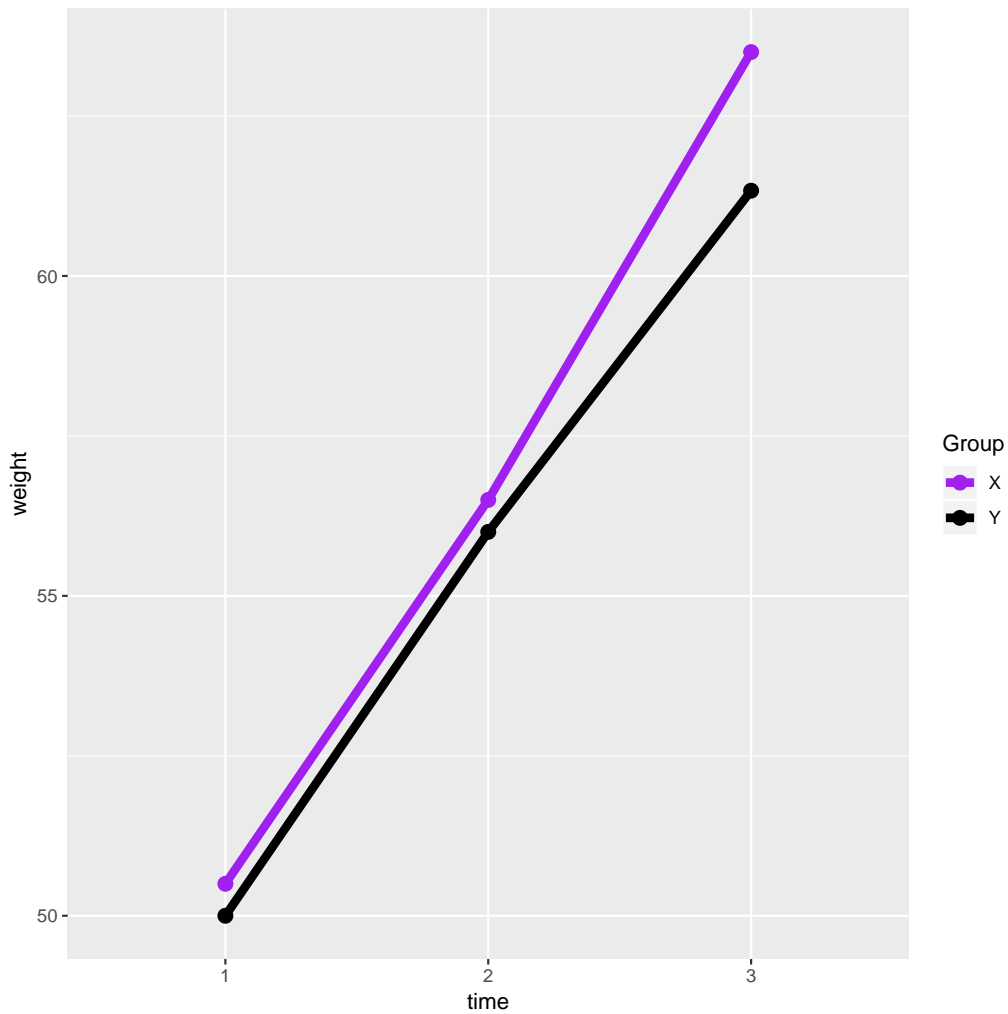
Display the histogram



5.3 Customize graphic

5.3.1 Modify the legend of a discrete scale

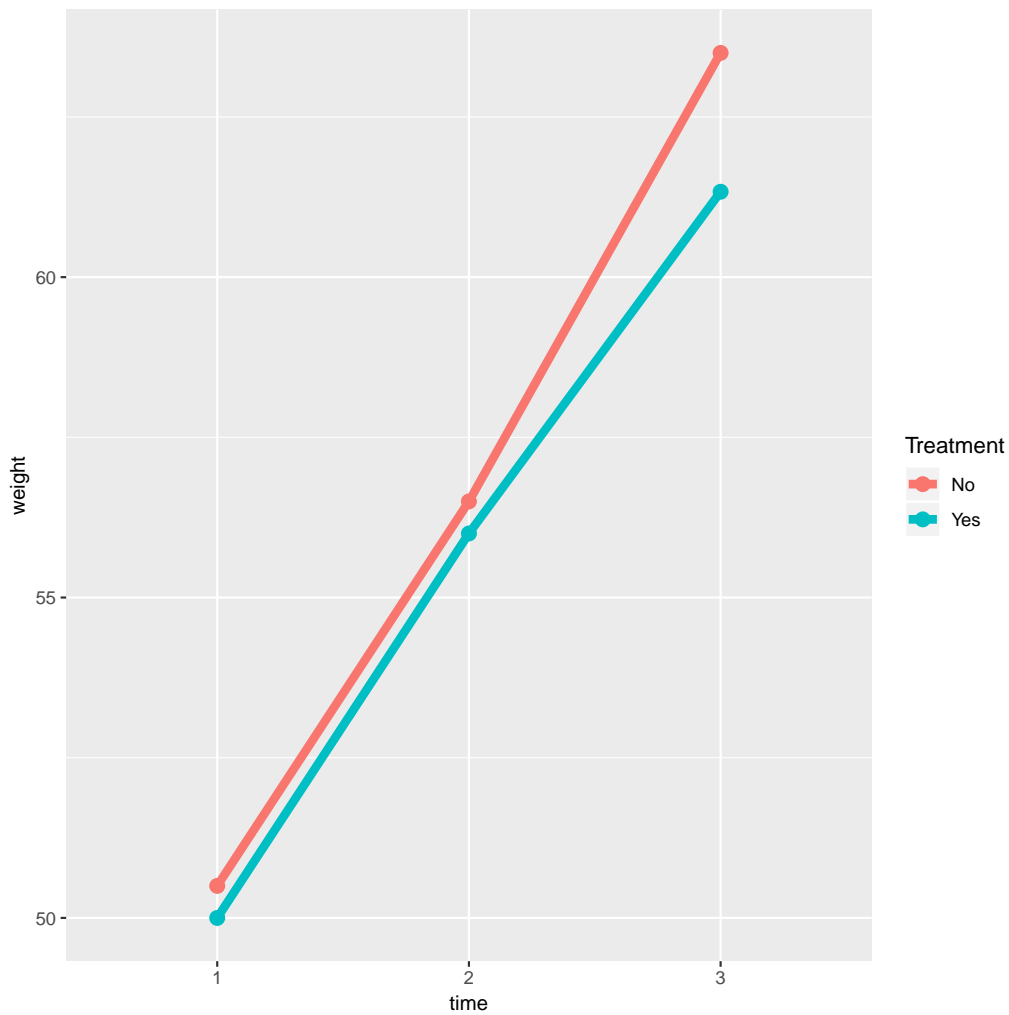
```
gg.mean2 <- gg.mean + scale_colour_manual(name = "Group",  
                                           labels = c("X", "Y"),  
                                           values = c("No" = "purple",  
                                                       "Yes" = "black"))
```



5.3.2 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))
```

5.3.3 Put the legend at the bottom

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

5.3.4 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]  
}
```

5.3.5 Color blind palette

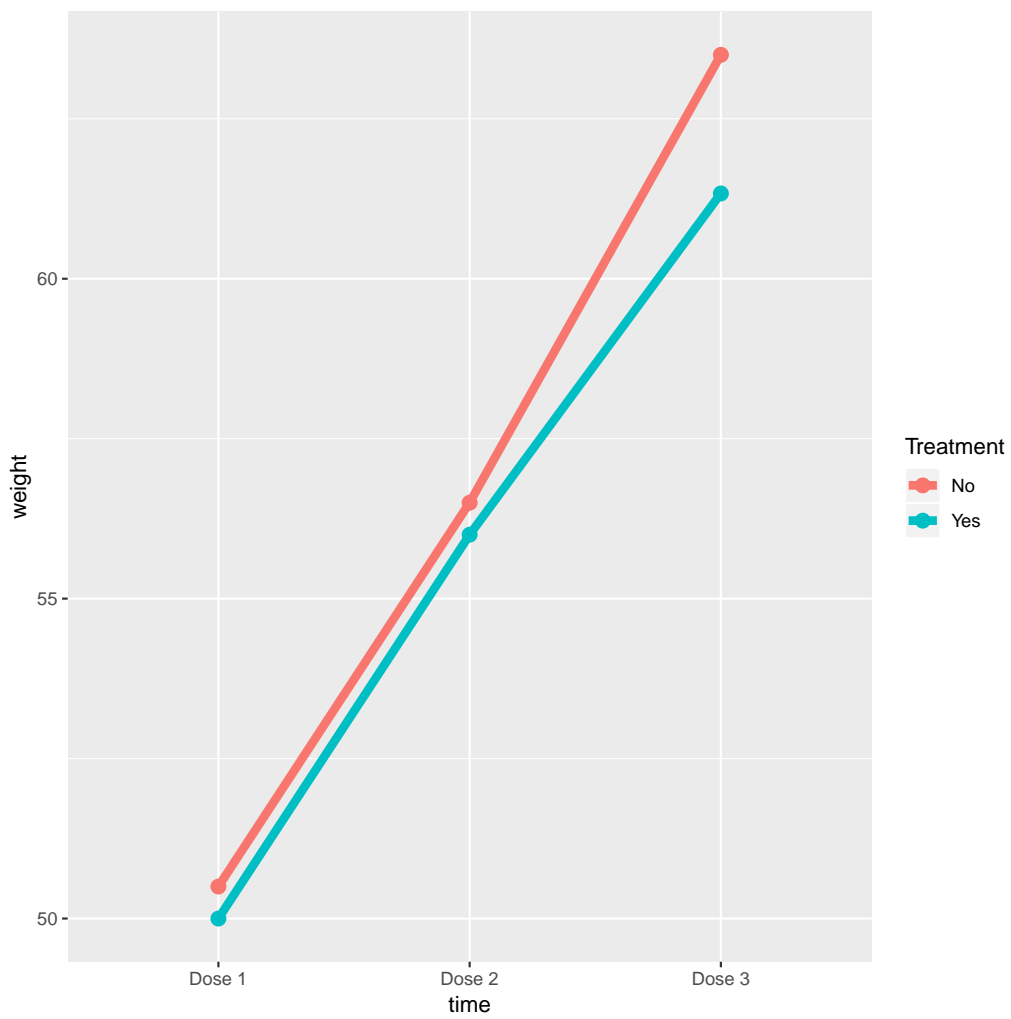
```
ggthemes::colorblind_pal()(10)
```

5.3.6 Rotate x-axis labels

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

5.3.7 Change tick mark labels

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

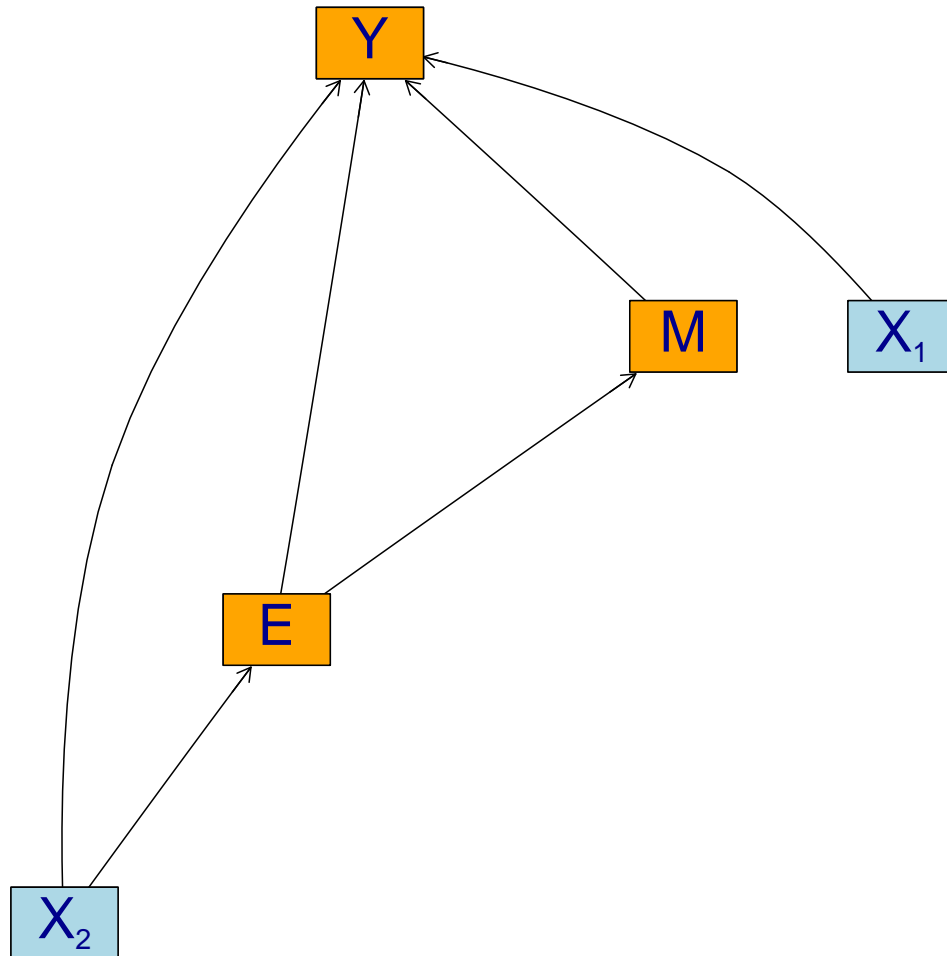


5.4 Path diagram

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 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) 13.1129277  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
```

6.1.1 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	0.156
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)

6.1.2 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 = 2.3128  
95% family-wise confidence level
```

Linear Hypotheses:

	Estimate	lwr	upr
Age == 0	-0.0548	-0.3751	0.2655
2 Treatment == 0	-1.3050	-2.9760	0.3661
All == 0	0.1099	-0.7027	0.9225

6.1.3 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] "SUND31034-8096" "SUND31034-1476"
```

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 Generate data using the *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)]

setcolororder(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

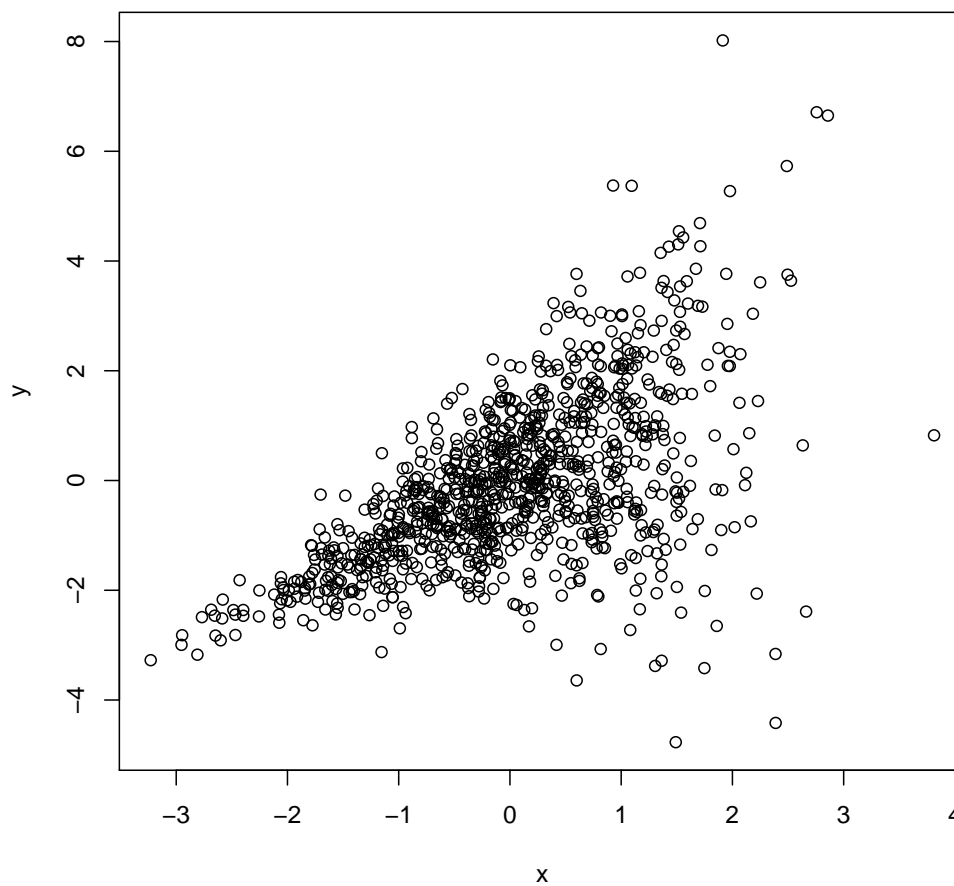
Model:

```
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)

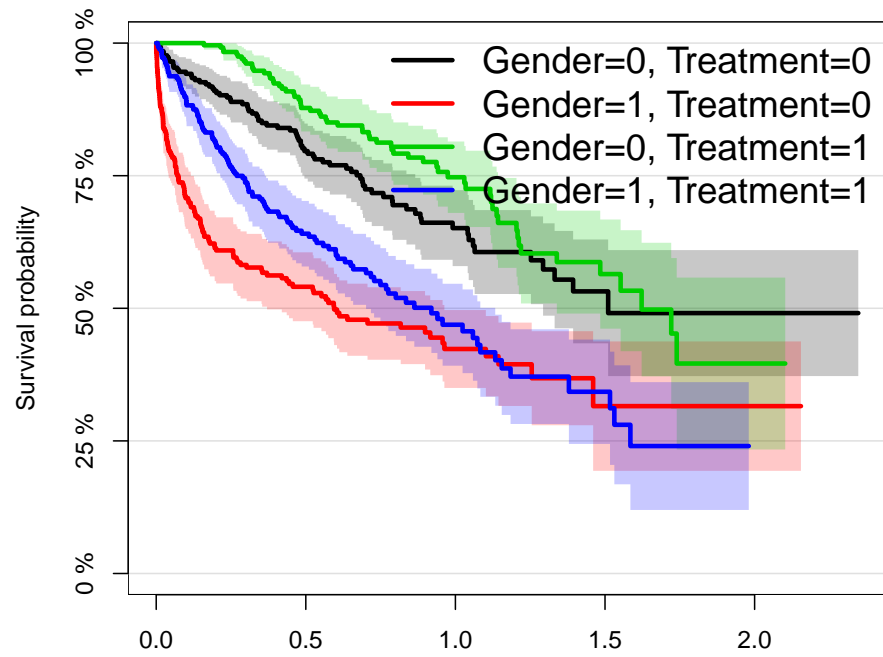
Model:

```
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					Time						
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:

