Project "light"

authors (individual or team names)

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Abstract

This document is part of project "light". This project is part of a presentation which teaches the fundamentals of reproducible research, using the free software R.

Contents

1 Preamble

This document was generated from a text file in the Rmd format, especially useful with the free software R (use a recent-enough version).

For an Rmd file to be successfully exported to HTML and PDF, read this page.

Concretely, open R and type:

```
library(rmarkdown)
render("file.Rmd", "all")
```

Any Rmd file is best edited with RStudio, or Emacs with ESS, markdown and polymode.

Example of an equation written in LaTeX (free, online book): $y_i \sim \mathcal{N}(\mu, \sigma^2)$

Example of an unordered list:

- μ
- σ

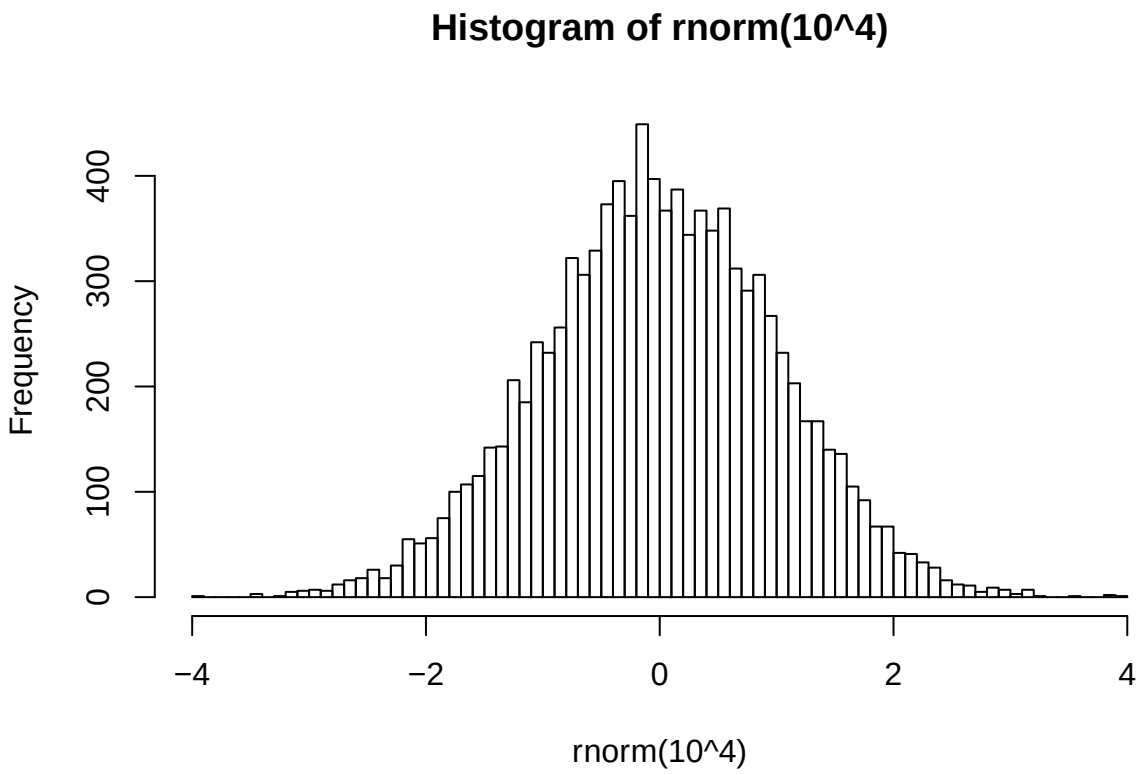
Example of an ordered list:

1. μ
2. σ

Example of **bold** and *italics*.

Example of a plot from R (setting the seed for reproducibility):

```
set.seed(1859)
hist(rnorm(10^4), breaks="FD")
```



Example of a table from R:

```
knitr::kable(mtcars[1:5,])
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2

2 Overview

This document is part of project "light". This project is part of a presentation which teaches the fundamentals of reproducible research.

The project directory is organized as advised by Noble (PLoS Computational Biology, 2009).

On any Unix-like system, it is easily done with the following commands:

```
touch AUTHORS COPYING README; mkdir -p doc data src results
```

On any Unix-like system, it can also be easily compressed and transferred:

```
cd ..; tar -czvf project-light.tar.gz \
--exclude="*~" --exclude=".*" project-light
```

This project involves the following persons:

- Firstname Lastname (specify contributions following R guidelines)
- ...

Importantly, before anything else, one must specify all paths relatively to the root of the project:

```
project.name <- "project-light"
project.dir <- ""
if(Sys.info()["user"] == "tflutre"){
  project.dir <- "~/src/tuto-reproducible-research/project-light"
} else if(Sys.info()["user"] == "<collaborator1>"){
  project.dir <- "C:/Documents/tuto-reproducible-research/project-light"
}
stopifnot(file.exists(project.dir))
data.dir <- paste0(project.dir, "/data")
stopifnot(file.exists(data.dir))
src.dir <- paste0(project.dir, "/src")
stopifnot(file.exists(src.dir))
## source(paste0(src.dir, "/utils_project-light.R"))
```

This document will also require external packages to be available, for instance:

```
## suppressPackageStartupMessages(library(MASS))
```

This R chunk is used to assess how much time it takes to execute the R code in this document until the end:

```
t0 <- proc.time()
```

3 Load (or simulate) some data

...

4 Explore the data

...

5 Write the model

...

6 Perform inference

...

7 Check assumptions and improve the model

...

8 Appendix

```
t1 <- proc.time(); t1 - t0
```

```
##    user  system elapsed
##   0.008   0.000   0.008
```

```
print(sessionInfo(), locale=FALSE)
```

```
## R version 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/openblas-base/libblas.so.3
## LAPACK: /usr/lib/libopenblasp-r0.2.18.so
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  base
##
## other attached packages:
## [1] knitr_1.20    rmarkdown_1.9
##
## loaded via a namespace (and not attached):
##  [1] compiler_3.4.4  backports_1.1.2 magrittr_1.5    rprojroot_1.3-2
##  [5] tools_3.4.4     htmltools_0.3.6 yaml_2.1.19     Rcpp_0.12.17
##  [9] stringi_1.2.2   highr_0.6       methods_3.4.4   stringr_1.3.1
## [13] digest_0.6.15   evaluate_0.10.1
```