

Project 1

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1 Preamble

This document was generated from a text file in the org format. See org-mode in the free software Emacs. For non-Emacs user, pandoc is the solution.

Note however, that Emacs is much preferred because, contrary to it, pandoc can't execute code while processing an org file to PDF or HTML. Moreover, Emacs and org-mode are not language-specific, e.g. not restricted to R or Python (see examples below).

Example of an equation written in L^AT_EX (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

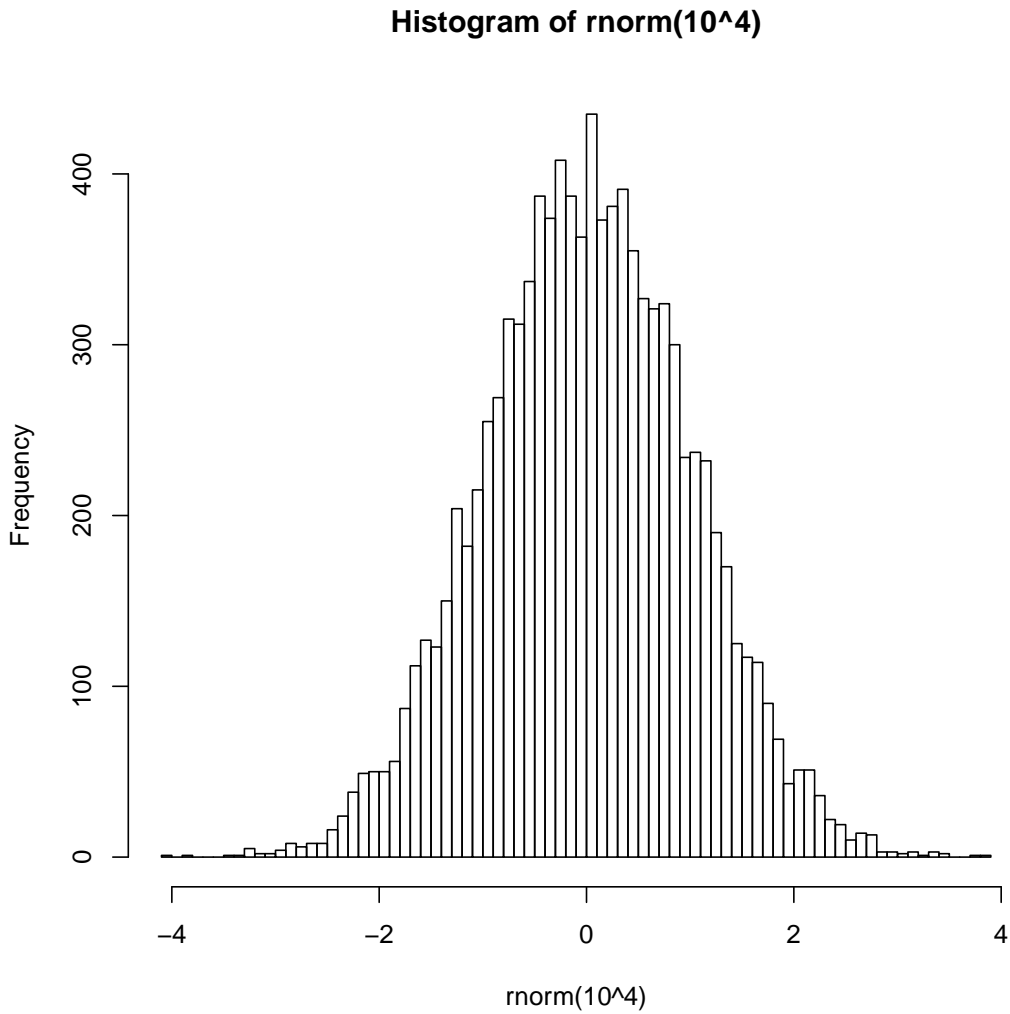
Example of **bold**, *italics*, underlined, `verbatim`, ~~code~~, ~~strike-through~~.

Example of a table:

header1	header2
a	1
b	2

Example of an included plot from R:

```
hist(rnorm(10^4), breaks="FD")
```



Example of an executed command from Python:

```
print "%i + %i = %i" % (2, 2, 4)
```

2 + 2 = 4

Example of an executed command from Bash:

```
echo "Hello World!"
```

Hello World!

2 Overview

This document contains the documentation for project 1. 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 bin results
```

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

```
cd ..; tar -czvf project2.tar.gz \  
--exclude=project2/data/data_extern \  
--exclude="*~" --exclude=".*" project2
```

3 Data

Just as an example:

```
cd data/  
wget ftp://ftp.ensemblgenomes.org/pub/plants/release-24/fasta/vitis_vinifera/  
dna/Vitis_vinifera.IGGP_12x.24.dna.genome.fa.gz
```

4 Results

```
cd results/
```