

# La famille \*down

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# What is Markdown? (\*.md files)

According to **Wikipedia**,

*Markdown is a lightweight markup language with plain text formatting syntax. Its design allows it to be converted to many output formats.*

# Why Markdown?

- formatting text and documents is easy
- probably the most used lightweight markup language for numeric documents (especially technical documentations)

**But:** is sometimes a bit limited if you want to have custom outputs

# What is **R**Markdown? (\*.Rmd files)

- developed by RStudio (and especially by Yihui Xie)
- combines Markdown documents with **R** scripts (or python, C++, bash, ...) to produce dynamic (and even interactive) documents

# What is **R**Markdown? (\*.Rmd files)

- developed by RStudio (and especially by Yihui Xie)
- combines Markdown documents with **R** scripts (or python, C++, bash, ...) to produce dynamic (and even interactive) documents
- also available as **R** notebooks (similar to Jupyter notebooks)

# Basic RMarkdown documents

# What do you need? (certified exact on linux)

- **R**
- RStudio (not mandatory but highly recommended) and if you don't know how to install it on linux, please, ask your sysadmin
- **packages:** at least `knitr` but other packages (`rmarkdown`, `markdown`, ...)
- `pandoc` to obtain different output types from `*.md` files: `Rmd`  $\rightarrow$  `md`  $\rightarrow$  (with `pandoc`) HTML
- it is best to have *L<sup>A</sup>T<sub>E</sub>X* installed to render maths or obtain PDF documents

Basic demo...

# Yaml headers

```
---  
title: "A first example (RMarkdown)"  
author: "Nathalie Vialaneix"  
date: "11/8/2019"  
output: html_document  
---
```



# Yaml headers

```
---
title: "A first example (RMarkdown)"
author: "Nathalie Vialaneix"
date: "11/8/2019"
output:
  html_document:
    toc: true
    toc_float:
      collapsed: true
      number_sections: true
---
```

- 1 Main section
- 1.1 R Markdown
- 1.2 Including Plots
- 2 Section section

## 1 Main section

### 1.1 R Markdown

This is an R Markdown document. Markdown is a simple format for writing documents. For more details on using R Markdown see [http://rmarkdown.rstudio.com](#)

When you click the **Knit** button a document will be generated containing embedded R code chunks within the document. You can embed an R code chunk in a document by enclosing it in `<pre>` tags.

```
summary(cars)
```

##	speed	dist
----	-------	------

- 1 Main section
- 2 Section section

## 2 Section section

# Yaml headers

```
---  
title: "A first example (RMarkdown)"  
author: "Nathalie Vialaneix"  
date: "11/8/2019"  
output:  
  pdf_document:  
    toc: true  
  html_document:  
    toc: true  
    toc_float:  
      collapsed: true  
    number_sections: true  
---
```

# Text formatting

## Syntax

Plain text

End a line with two spaces  
to start a new paragraph.

*\*italics\** and `_italics_`

**\*\*bold\*\*** and `__bold__`

superscript<sup>2</sup>

~~strikethrough~~

[link](www.rstudio.com)

# Header 1

## Header 2

### Header 3

#### Header 4

##### Header 5

##### Header 6

endash: --

emdash: ---

ellipsis: ...

inline equation:  $A = \pi * r^2$

image: 

horizontal rule (or slide break):

\*\*\*

## Becomes

Plain text

End a line with two spaces to start a new paragraph.

*italics* and *italics*

**bold** and **bold**

superscript<sup>2</sup>

~~strikethrough~~

[link](#)

## Header 1

## Header 2

### Header 3

#### Header 4

##### Header 5

###### Header 6

endash: –

emdash: —

ellipsis: …

inline equation:  $A = \pi * r^2$

image: 

horizontal rule (or slide break):

---

# Text formatting

> block quote

```
* unordered list
* item 2
  + sub-item 1
  + sub-item 2
```

```
1. ordered list
2. item 2
  + sub-item 1
  + sub-item 2
```

Table Header	Second Header
Table Cell	Cell 2
Cell 3	Cell 4

block quote

- unordered list
- item 2
  - sub-item 1
  - sub-item 2

1. ordered list
2. item 2
  - sub-item 1
  - sub-item 2

Table Header	Second Header
Table Cell	Cell 2
Cell 3	Cell 4

# Code chunk and options

```
```{r setup, include=FALSE}  
knitr::opts_chunk$set(echo = TRUE)  
```
```

language

chunk name

chunk options

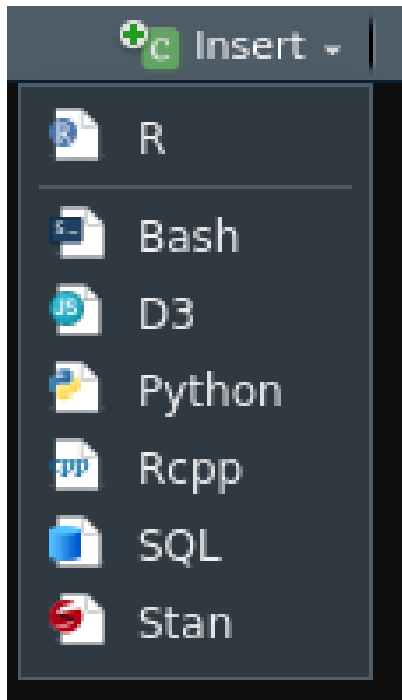
(comma separated)

Inline code can be included with

```
`r params$date`
```

# Code chunk and options

**Types of chunks:**



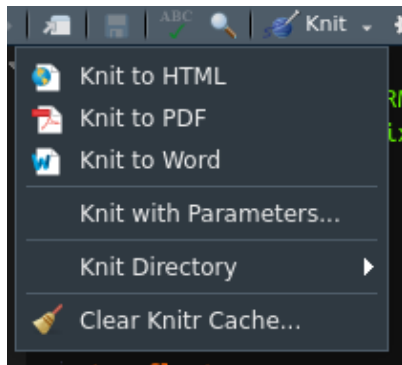
# Code chunk and options

## A few useful options:

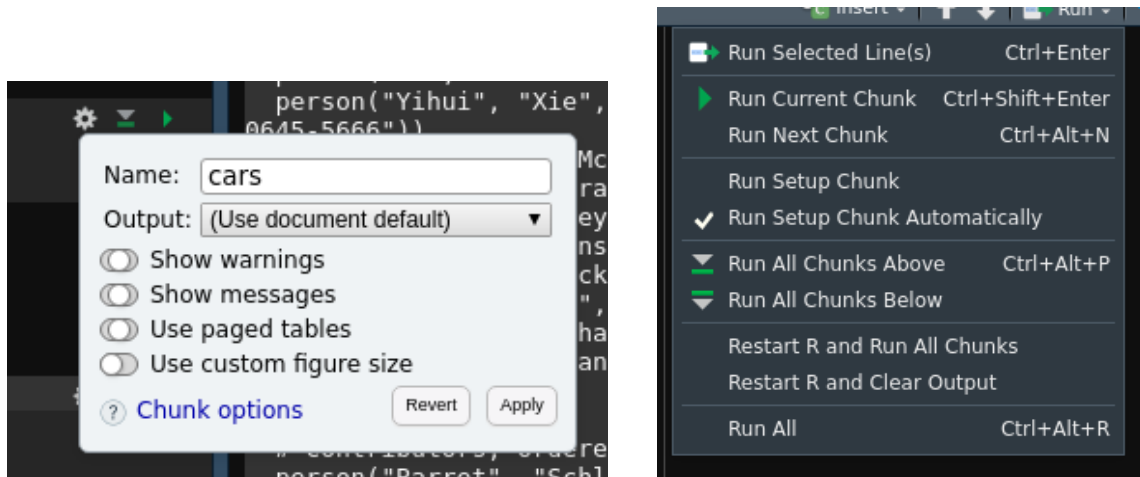
- `eval=TRUE/FALSE`: run (or not) the code in the chunk
- `include=TRUE/FALSE`: include (or not) the chunk in the final document
- `echo=TRUE/FALSE`: include (or not) the output of the code in the final document
- `results='markup'/'hide'/'asis'/'hold'`: display the output of the code normally/not/as it is (useful when combined with `xtable` for HTML outputs of tables for instance)/all in a row after the code chunk is displayed (and not one by one)
- `error/message/warning=TRUE/FALSE`: display (or not) the different types of messages obtained from the code
- `cache=TRUE/FALSE`: cache the result of the chunk
- `fig.width/height/align/cap/...`: different options on rendering of figures

# Run code and output types

## Run the whole document:



## Run interactively:





# Run code and output types

**Run the whole document externally:**

```
# render document
knitr::render("mybeautifuldoc.Rmd", output_format = "HTML",
              encoding = "UTF-8")
# extract R code from chunk
knitr::purl("mybeautifuldoc.Rmd")
```

```
## ----setup, include=FALSE-----
knitr::opts_chunk$set(echo = TRUE)

## ----cars-----
summary(cars)

## ----pressure, echo=FALSE-----
plot(pressure)
```

**Useful to run a report with computationally intensive code on a server! See:**  
[http://www.nathalieviaianeix.eu/doc/pdf/tutoR\\_cluster.pdf](http://www.nathalieviaianeix.eu/doc/pdf/tutoR_cluster.pdf)

# Run code and output types

- HTML: often light and can include interactive graphics (with `ggplotly` for instance)
  - HTML and  $LATEX$  equations can be included directly in the document
  - **But:** problems rendering equations without internet connexion, you need to copy several folders in addition to the file to make it work
  - problems partially solved with the option: `self_contained: true` (in HTML headers)
- PDF: self-contained but often heavier, needs  $LATEX$  installed
  - usually longer to knit (pandoc produces a TeX document and then  $LATEX$  is run)
  - can account for  $LATEX$  options in the headers (including bibliography)
  - can use the power of  $LATEX$  to obtain multiple version documents (student and teacher versions for instance)

(and, of course, **forget Word!**)

# Advanced options for RMarkdown documents

# Appearance and style in HTML documents

- `theme` (in header) specifies the [Bootswatch](#) theme to use
- `highlight` (in header) specifies the highlighting style to use (supports `tango`, `pygments`, `kate`, `monochrome`, `espresso`, `zenburn`, `haddock`, `breezedark` and `textmate`)

**Or:** you can use your own CSS with `css` (in header)

# *L*A<sub>T</sub>E<sub>X</sub> options in PDF documents

| Variable                                  | Description  |
|---|--|
| lang                                      | Document language code   |
| fontsize                                  | Font size (e.g., 10pt , 11pt , or 12pt )   |
| documentclass                             | LaTeX document class (e.g., <code>article</code> )                               |
| classoption                               | Options for documentclass (e.g., <code>oneside</code> )                          |
| geometry                                  | Options for geometry class (e.g., <code>margin=1in</code> )                      |
| mainfont, sansfont,<br>monofont, mathfont | Document fonts (works only with <code>xelatex</code> and <code>lualatex</code> ) |
| linkcolor, urlcolor,<br>citecolor         | Color for internal, external, and citation links                                 |

# *L*A<sub>T</sub>E<sub>X</sub> options in PDF documents

**Bibliography** is managed using:

- the citation engine (default is `pandoc-citeproc`):
  - `citation_package: natbib` (header, in `pdf_document`)
  - `citation_package: biblatex` (header, in `pdf_document`)
- the bibtex file: `bibliograph: mybib.bib` (header, in `pdf_document`)

# *L*A<sub>T</sub>E<sub>X</sub> options in PDF documents

More custom options in headers:

```
header-includes:  
  \usepackage[frenchb]{babel}  
  \graphicspath{{img/}}
```

# *L*A<sub>T</sub>E<sub>X</sub> multiple version document

```
% set this variable to 1/0 to have the teacher/student version  
\def\version{1}
```

```
\if \version1 \  
... in teacher version only  
\fi
```



# A very cool stuff: parameters!

How were useR! invoices generated (and sent)?

```
params:  
  participant: "Nathalie Vialaneix"  
  name: "INRA"  
  address1: ""  
  address2: ""  
  address3: ""  
  country: "France"  
  uid: "12345"  
  date: "2018/09/15"  
  refpaybox: NULL  
  total: "125"  
  method: "CB"
```

and then, used in the Rmd file through `params$participant`, `params$name`, ...

# A very cool stuff: parameters!

... or passed externally using render:

```
## loop over users #####
render("invoice-base.Rmd",
      params = list(participant = paste(users$FIRSTNAME[cur], users$
        name = users$"Billing.name"[cur],
        address1 = users$"Billing.address..street."[cur],
        address2 = users$"Billing.address..other."[cur],
        address3 = users$"Billing.address..state..town."[cur],
        country = users$"Billing.address..country."[cur],
        uid = users$UID[cur],
        date = gsub("-", "/", as.character(as.Date(saved
        total = users$Amount[cur],
        method = users$Payment.type[cur],
        refpaybox = users$transaction[cur]
      ),
      output_file = paste0("invoices/", file_names[cur]))

# send email
send.mail(from = "contact@user2019.fr",
          to = ...,
          attach.files = paste0("invoices/", file_names[cur]))
```

# A very cool stuff: parameters!

- used to produce automatic report on standard analyses (*e.g.*, differential analysis of RNAseq data with only two conditions)
- used to run standard analyses on multiple datasets at once
- parameters can be set interactively using the knit button
- constraints can be declared for parameters

```
year:  
  label: "Year"  
  value: 2017  
  input: slider  
  min: 2010  
  max: 2018  
  step: 1  
  sep: ""
```

# Want to know more?

- **R** Markdown [cheatsheet](#)
- **R** Markdown [reference](#)
- **R** Markdown [book](#)

# Other types of documents

# Slides

Using the same approach, you can make:

- **R** presentation (included in **R** studio) but with rather limited features

(my [old class on R](#) was made using it)

- `xaringan` slides (HTML), also developed by Yihui Xie (see Chapter 7 of the **R** Markdown book): easy to use and includes many options but if you want to obtain a custom result, you better be an HTML/CSS ninja, can be exported in PDF with `pagedown::chrome_print` (but I do not recommend it)

this presentation was made with `xaringan` using the `rladies` css

- `binb` (`binb` is not beamer) provides functionality to use themes for beamer directly in RMarkdown: if you want to obtain a custom result, you better be a *L<sup>A</sup>T<sub>E</sub>X* ninja, output PDF, long to compile (as beamer is)

(this [seminar](#) has been made using `binb`)

# Posters

[drposter](#) (example is courtesy of Pierre Neuvial)

ambroise\_etal\_SMPGD2019-poster.pdf

File Edit View Go Bookmarks Help

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## Adjacency-constrained hierarchical clustering of a band similarity matrix with application to genomics

Christophe Ambroise<sup>1</sup>, Alia Dehman<sup>2</sup>, **Pierre Neuvial**<sup>3</sup>, Guillem Rigail<sup>4</sup> and Nathalie Vialaneix<sup>5</sup>

<sup>1</sup>LaMME, Evry • <sup>2</sup>Hyphen-stat, Toulouse <sup>3</sup>Institut de Mathématiques de Toulouse/CNRS • <sup>4</sup>IPS2, CNRS/INRA <sup>5</sup>INRA MIAT •

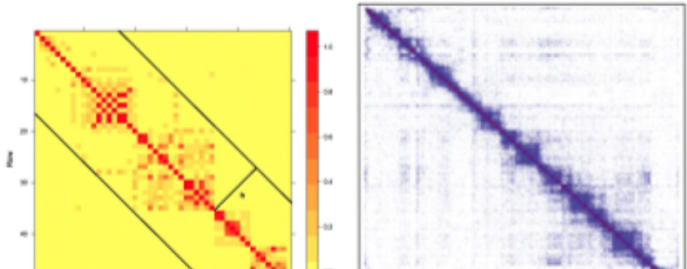
### Motivation: Regionally-structured genomic data

#### Genome-Wide Association Studies (GWAS)

- loci: SNP
- similarity: linkage disequilibrium
- regions: LD/haplotype blocks

#### Chromosome contact maps (Hi-C)

- loci: binned genome positions
- similarity: contact intensity
- regions: TAD; A/B compartments



### Key 2: Storing candidate fusions in a min-heap

#### Min heap


A partially ordered binary tree

- nodes = candidate merges
- ordering given by the linkage  $\delta$

→ next candidate fusion is the root of the heap

#### Complexity

- $O(ph)$  in space
- $O(p(h + \log(p)))$  in time



### Implementation

# Documentation for packages

pkgdown: Generate cool package documentation from your package

Example from [adjclust](#)



# Books

bookdown: generate printer ready books and ebooks from **R** Markdown

I never used it so no feedback...

# Website

`blogdown`: generate website from RMarkdown pages using [hugo](#) (python static website generator).

The [missing data reference website](#) is generated through `blogdown` and thanks to its hugo support is automatically published on netlify.

Next to come...?



coffee down... ?