A tutorial by Yan Holtz, Florian Rohart & Baptiste Couvy-Duchesne

Introduction to R Markdown

Or how to boost reproducibility in your research projects

bit.ly/2SxJFlV

Brisbane, Australia, December 2018

What

“ An R Markdown (.Rmd) file is a record of your research. It contains the **code** that a scientist needs to reproduce your work along with the **narration** that a reader needs to understand your work. “

Why

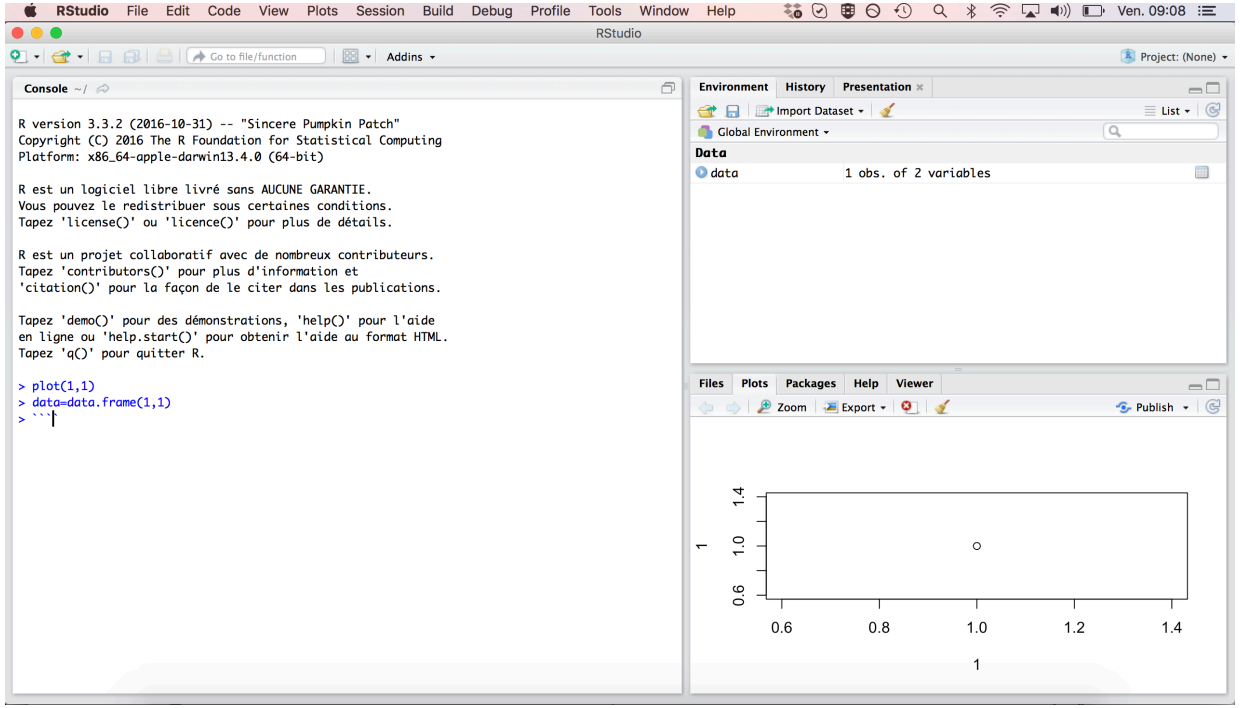
- Efficiency
- Reproducibility
- Interactivity
- Automation
- Notebook

And much more..

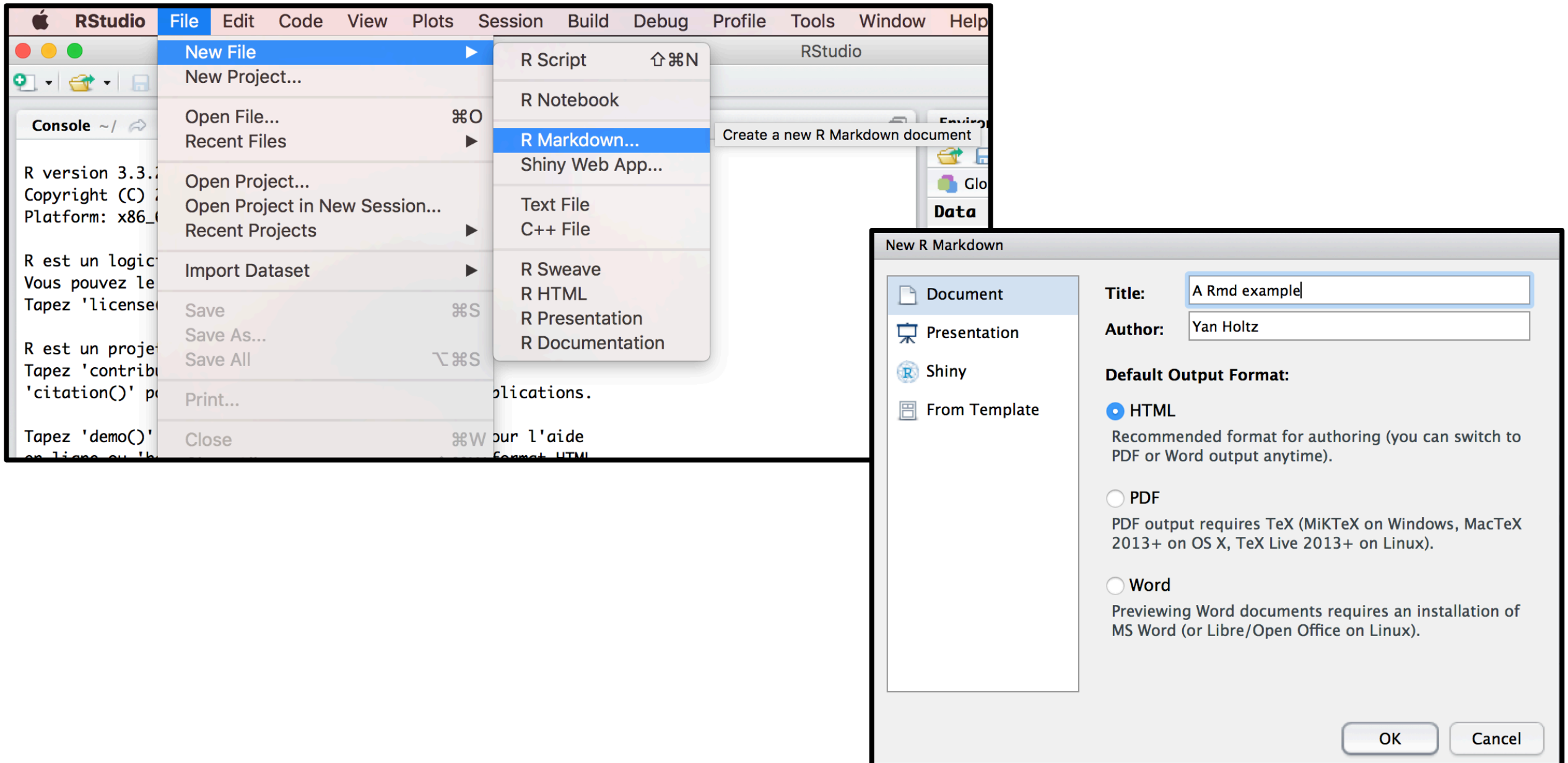
Most Basic Document

1 - Open R studio:

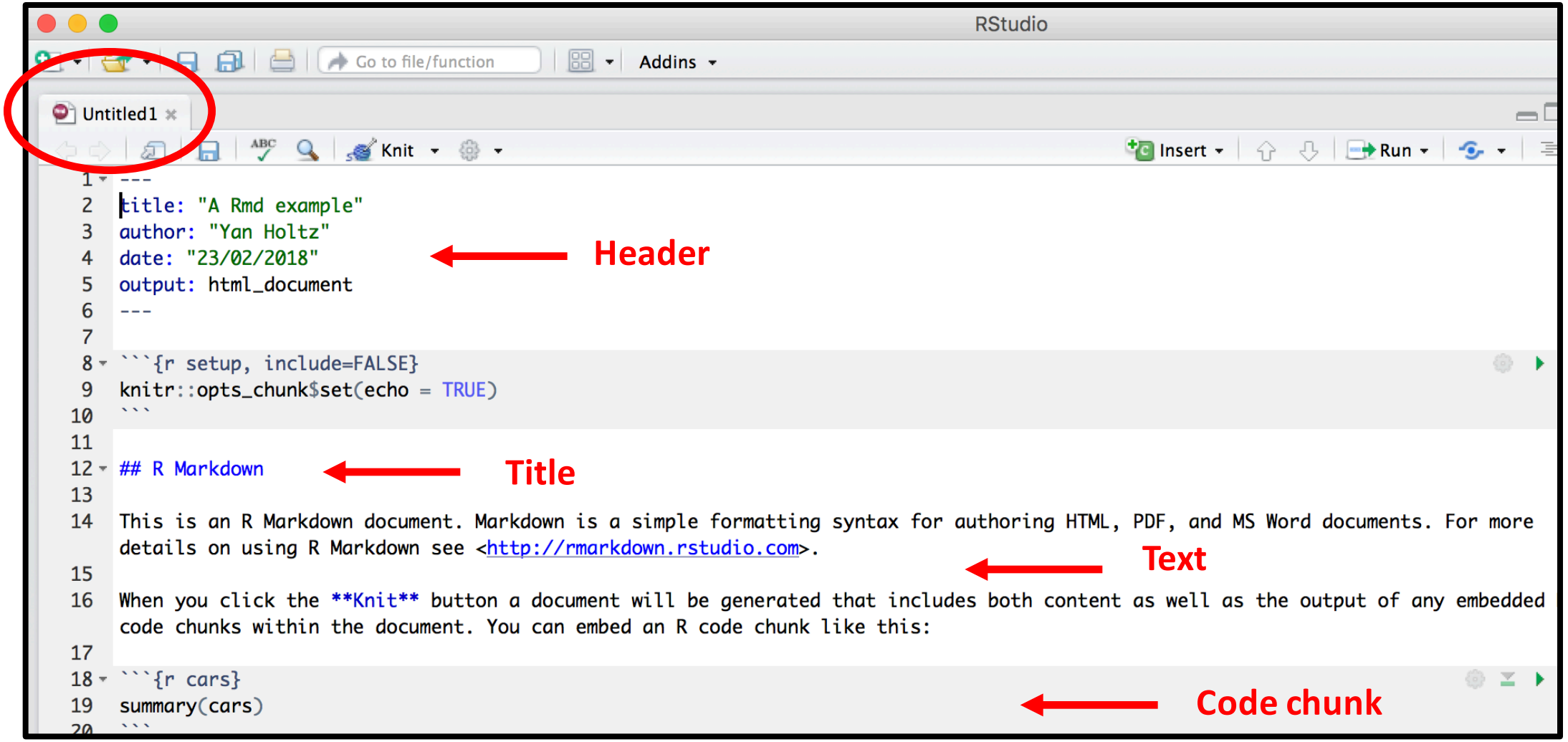
- User Friendly environment
- Auto completion
- Run a line of code with Cmd + Enter



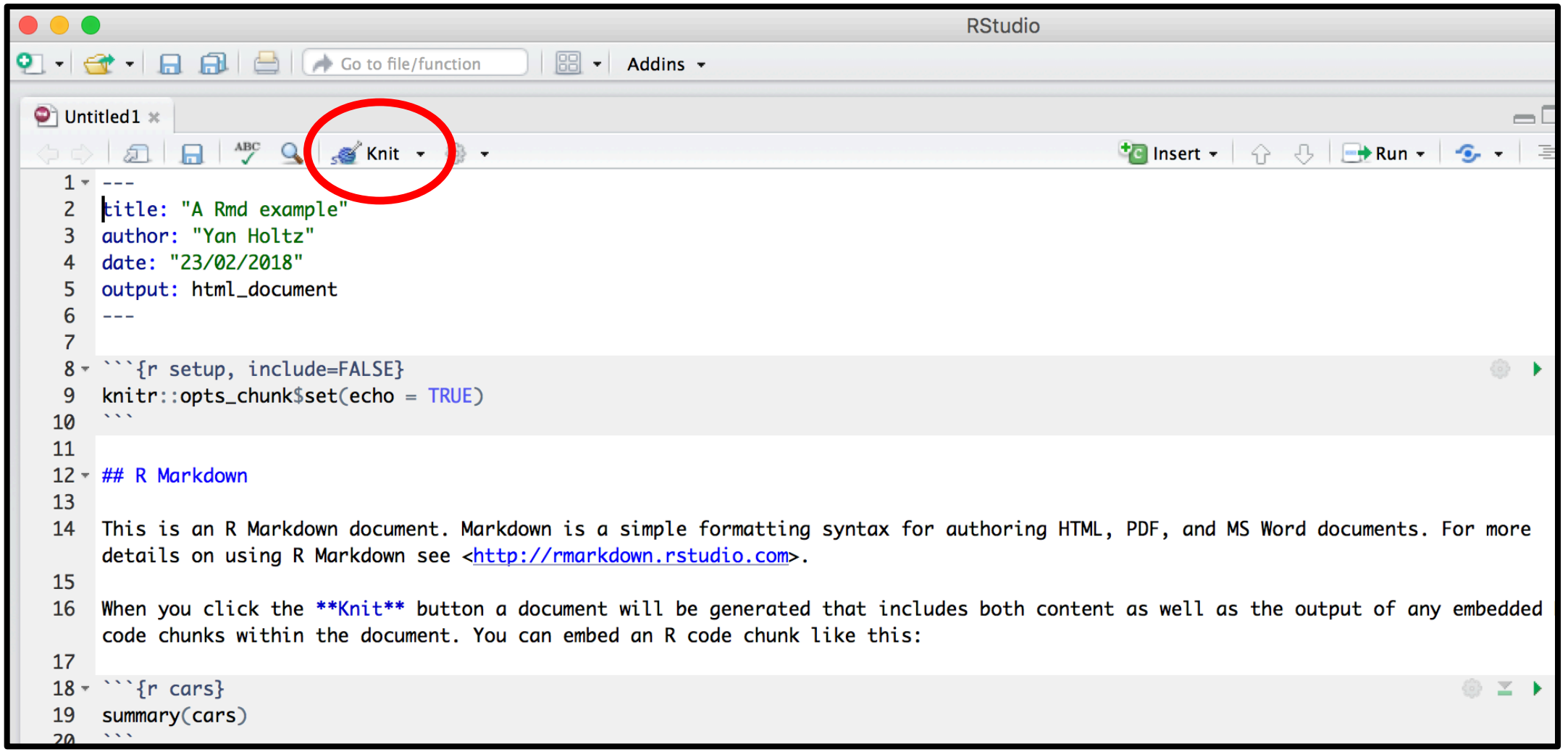
2 - Open a .Rmd file:



Anatomy of a .Rmd file:

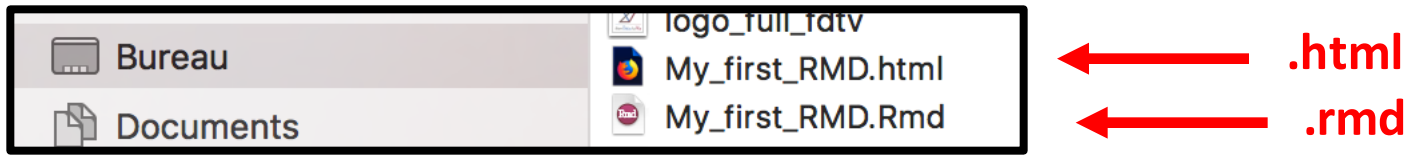


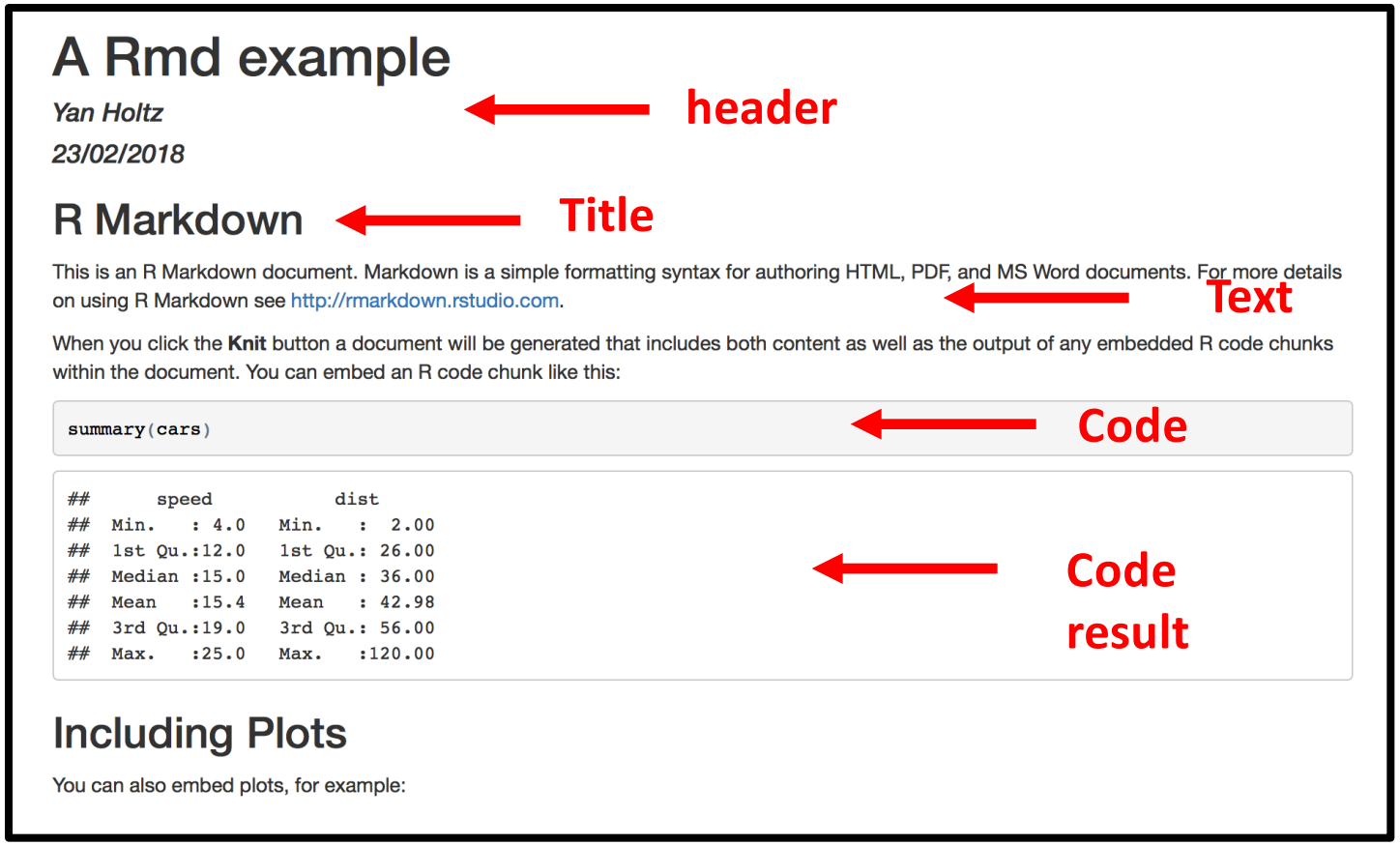
3 - Knit the .Rmd file:



4 - .HTML output is ready

- Have a look to your current directory
- Open the .html in a browser





Customize text

Customize the text

R Markdown cheat sheet

bit.ly/1SuNTo9

syntax

```
Plain text
End a line with two spaces to start a new paragraph.
*italics* and _italics_
**bold** and __bold__
superscript^2^
~~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: ![](path/to/smallorb.png)

horizontal rule (or slide break):

***

> block quote

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

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

becomes

Plain text
End a line with two spaces to start a new paragraph.
italics and *italics*
bold and **bold**
superscript^2
~~strikethrough~~
link

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Code chunks option

Anatomy of a Code chunk:

Code chunk options:

option	default	effect
eval	TRUE	Whether to evaluate the code and include its results
echo	TRUE	Whether to display code along with its results
warning	TRUE	Whether to display warnings
error	FALSE	Whether to display errors
message	TRUE	Whether to display messages
tidy	FALSE	Whether to reformat code in a tidy way when displaying it
results	"markup"	"markup", "asis", "hold", or "hide"
cache	FALSE	Whether to cache results for future renders
comment	"##"	Comment character to preface results with
fig.width	7	Width in inches for plots created in chunk
fig.height	7	Height in inches for plots created in chunk

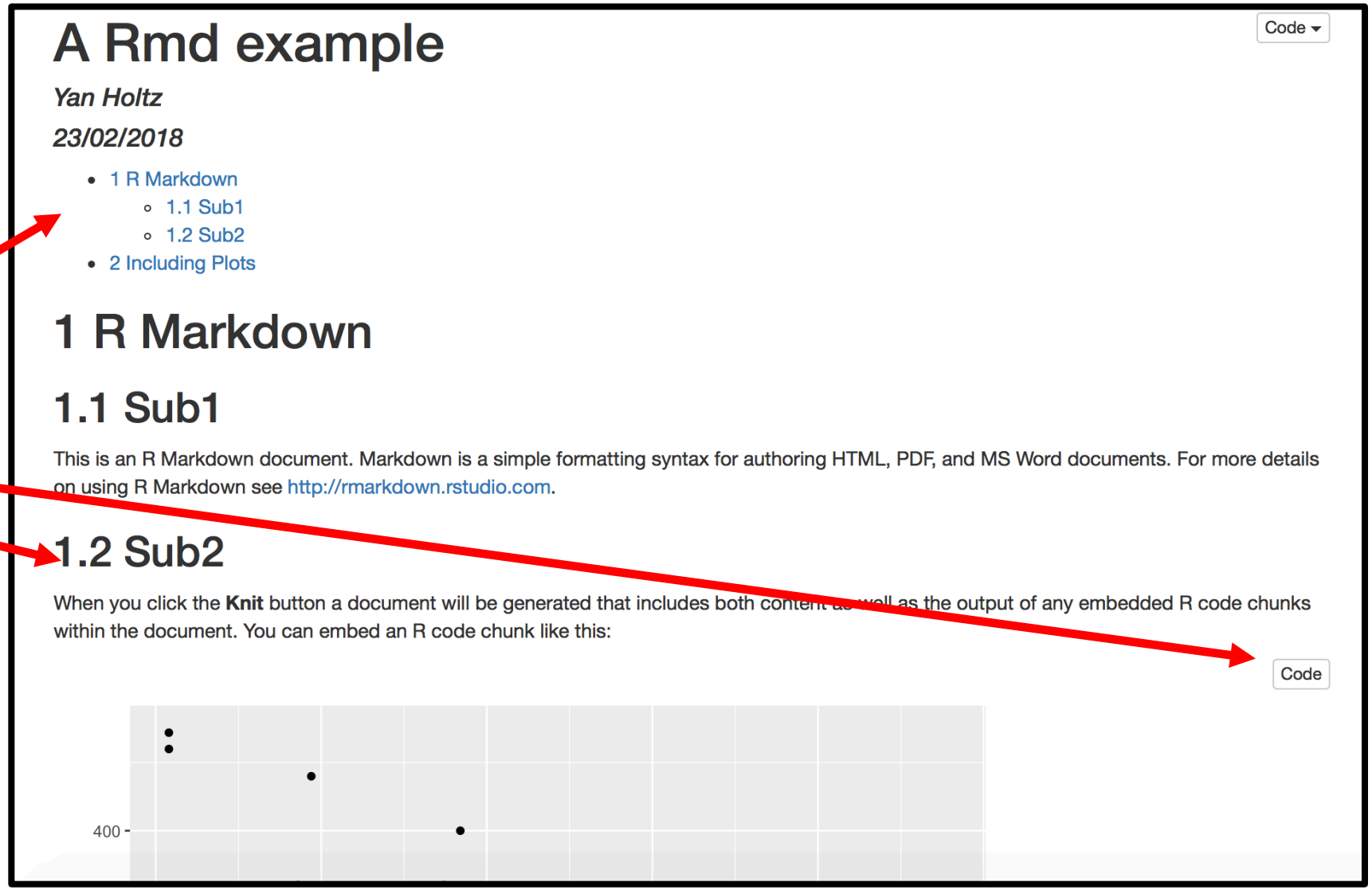
Do not always run the whole document

→ R Markdown document is a Notebook !!

Header

Anatomy of the header:

```
---
title: "A Rmd example"
author: "Yan Holtz"
date: "23/02/2018"
output:
  html_document:
    toc: TRUE
    code_folding: "hide"
    number_sections: TRUE
---
```



Going further

Insert a table: the DT library

```
```{r}
library(DT)
datatable(mtcars, rownames = FALSE, filter="top", options = list(pageLength = 5, scrollX=T) )
```
```

Data frame

Show 5 entries

Search:

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear
6	160	110	3.9	2.875			1	4	4
6	258	110	3.08	3.215			0	3	1
8	360	175	3.15	3.44	17.02	0	0	3	2
6	225	105	2.76	3.46	20.22	1	0	3	1
8	360	245	3.21	3.57	15.84	0	0	3	4

2.751 5.424

Showing 1 to 5 of 23 entries (filtered from 32 total entries)

Previous 1 2 3 4 5 Next

Use Interactive charts

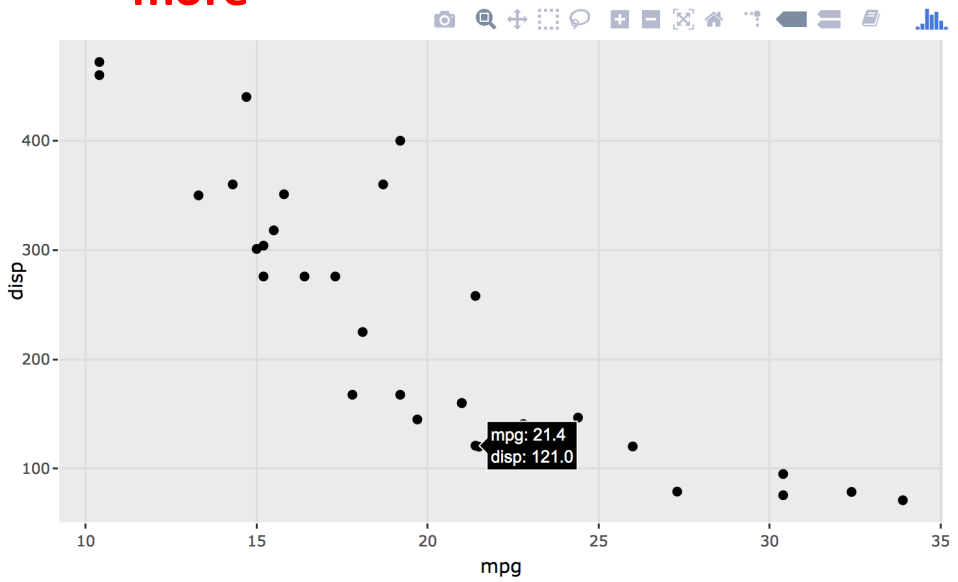
```{r, warning=FALSE, message=FALSE}
# Load a library
library(ggplot2)
library(plotly)

# make a static plot with ggplot2
p <- mtcars %>%
  ggplot( aes(x=mpg, y=disp)) +
    geom_point()

# turn it interactive with plotly
ggplotly(p)
```

Plotly library

Basic ggplot2 graphic

Ggplotly turn the plot interactive

Result: zoom / hover / export .. And more

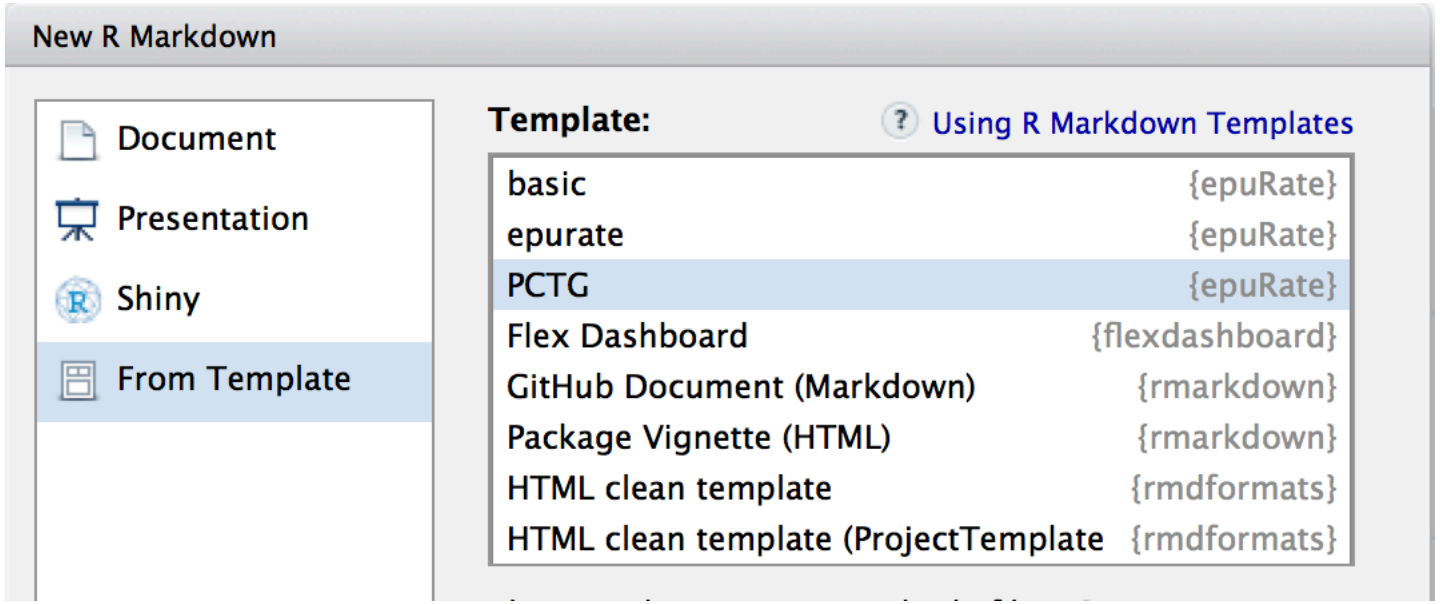


http://www.htmlwidgets.org

Use a template

- The PCTG template: www.github.com/holtzy/epuRate

-
```
library(devtools)
install_github("holtzy/epuRate")
library(epuRate)
```

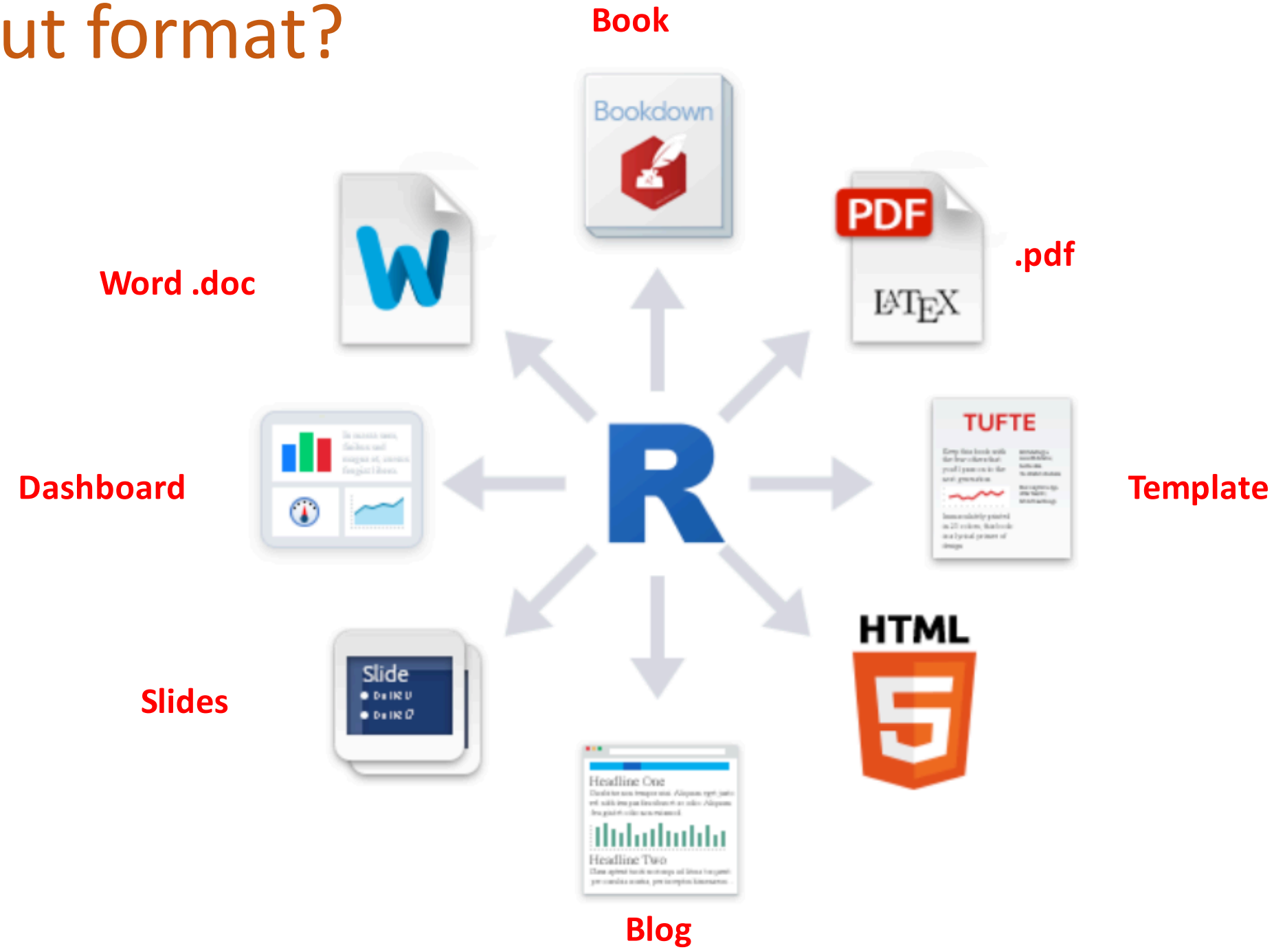
- 

Pimp my .Rmd

- holtzy.github.io/Pimp-my-rmd/
- Everything is possible
- Use CSS and HTML code
- Add header and footer
- More

Sharing

Output format?



Share your analysis

- Mail with colleagues, supervisor
- Publication as a supplementary material
- Github: www.github.com
- Website

Example

An example: my bioinfo pipeline:

- Interaction with clusters
- One unique folder
- Several .rmd wrapped in a website
- Shared online

Thanks

Slides: bit.ly/2SxJFlV

Cheat Sheet: bit.ly/2AZySd9

Pimp my rmd: bit.ly/2QDX7Hz

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 www.yan-holtz.com

 @R_Graph_Gallery

 github.com/holtzy