

# Introduction to R for data analysis

# - Rmarkdown -

Carl Herrmann & Carlos Ramirez IRTG Course - June 2021



# Reproducible analysis



- Reproducibility of results is important for experimental work (lab book!)
   but also for computational analysis!
- Different systems have been developed to ensure reproducibility of analysis flows
- For R based analysis, the best option is to use Rmarkdown documents
  - high levels of reproducibility
  - easy update of results
  - easy sharing of results with colleagues (html / pdf document)

## Markdown



- Markdown is a way to format plain text with a simple text editor
- Markdown documents can be converted with a renderer into
  - html
  - pdf

word

.md

pandoc

.pdf

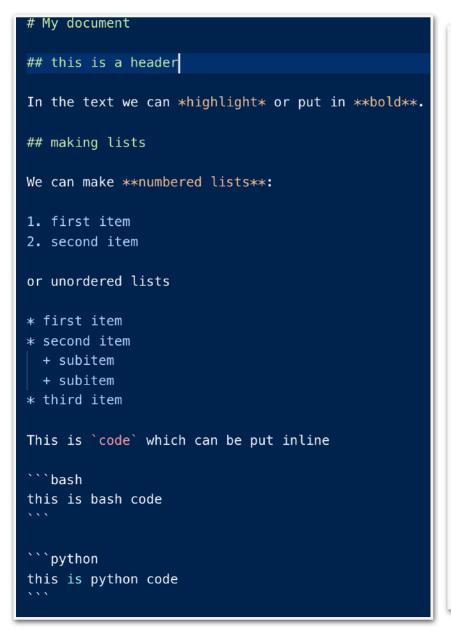
.docx

.html

# Rendering markdown



#### markdown



#### pdf

#### My document

#### this is a header

In the text we can *highlight* or put in **bold**.

#### making lists

We can make **numbered lists**:

- 1. first item
- 2. second item

or unordered lists

- first item
- second item
- subitem
- subitem
- third item

This is code which can be put inline

this is bash code

this is python code

#### html

### My document

#### this is a header

In the text we can *highlight* or put in **bold**.

#### making lists

We can make **numbered lists**:

- 1. first item
- 2. second item

or unordered lists

- first item
- second item
- subitem
- subitem
- third item

This is code which can be put inline

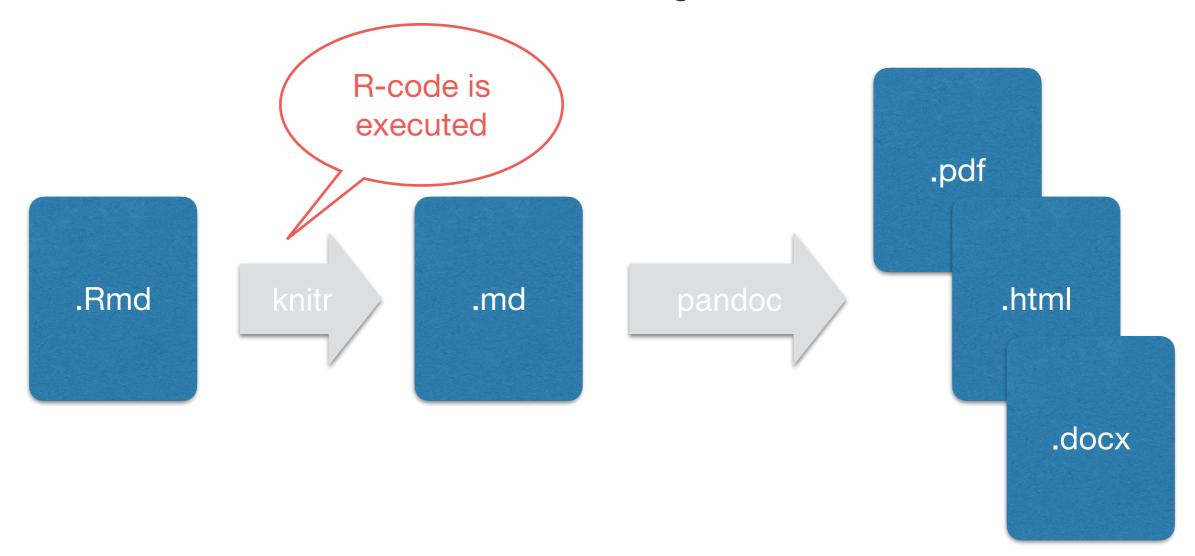
this is bash code

this is python code

## Rmarkdown

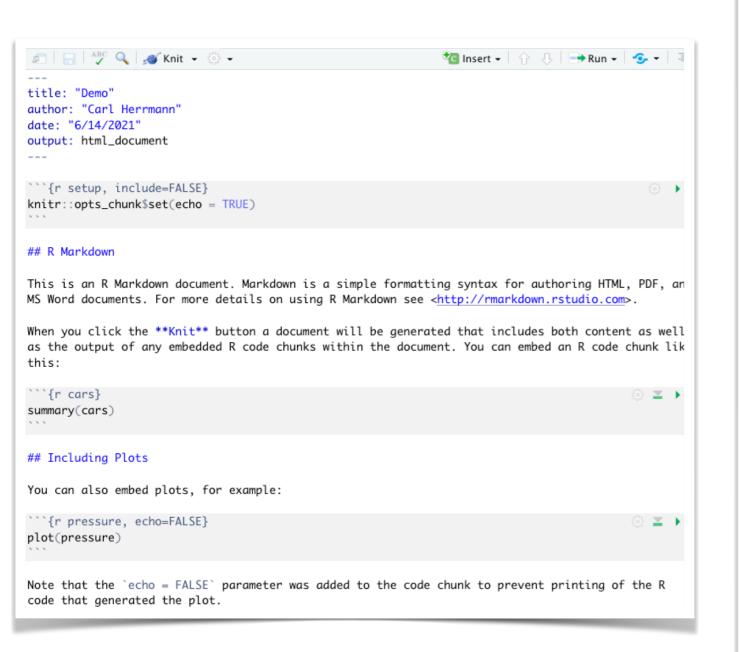


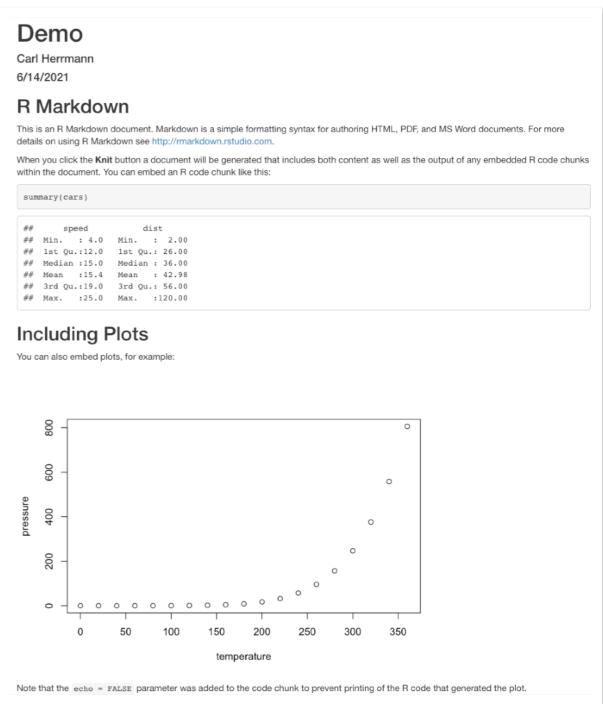
- With Rmarkdown, R-code parts can be included into the markdown document
- the R-code will be executed, the result integrated into markdown



## **Rmarkdown format**







## Rmarkdown format



```
title: "Project 01"
author: "Carl Herrmann"
date: "4/17/2019"
output:
  html_document:
    keep_md: yes
  pdf_document: default
# A Rmarkdown tutorial
This is a brief tutorial on how to use Rmarkdown to create dynamic documents
```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
knitr::opts_knit$set(root.dir='/Users/carlherrmann/Teaching/SS2019/DataAnalysis_4FS')
## Load the dataset
```{r read_data}
allDepMapData = readRDS('Data/depmap/DepMap19Q1_allData.RDS')
Now plot the distribution of the cell lines according to the tissue type
```{r plot_data}
freq = sort(table(allDepMapData$annotation$Primary.Disease))
par(las=2,mar=c(3,8,3,3));barplot(freq,horiz=TRUE, col='lightgrey')
```

header: set options

R code chunks

text in markdown

# Rmarkdown chunk options



 Display options can be set for each chunk individually, or for all chunks at the beginning of the document

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

#### valid for all chunks

- echo=TRUE : R-code is displayed in final document
- cache = TRUE : results of all chunks are cached

```
'``{r plot_data, fig.height=12, fig.width=12}
freq = sort(table(allDepMapData$annotation$Primary.Disease))
par(las=2,mar=c(3,8,3,3));barplot(freq,horiz=FALSE, col='lightgrey')
'``
```

valid for this chunks

 set height and width of output figure

## Reference



- https://rmarkdown.rstudio.com/
- https://www.rstudio.com/wp-content/uploads/2016/03/rmarkdowncheatsheet-2.0.pdf