Generating dynamic reports using R Markdown in RStudio

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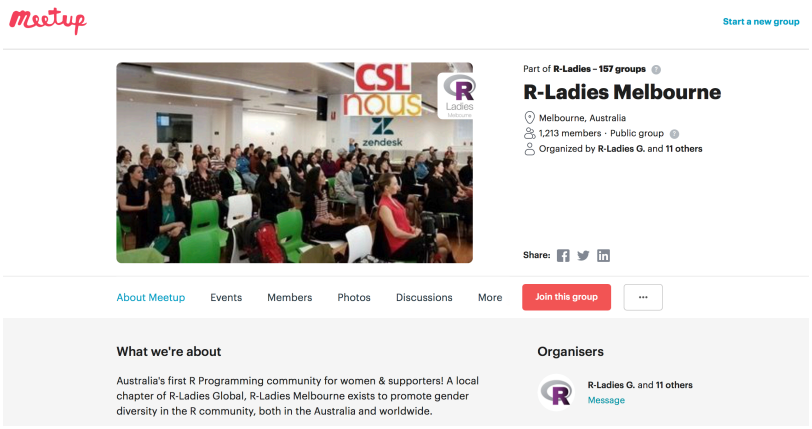
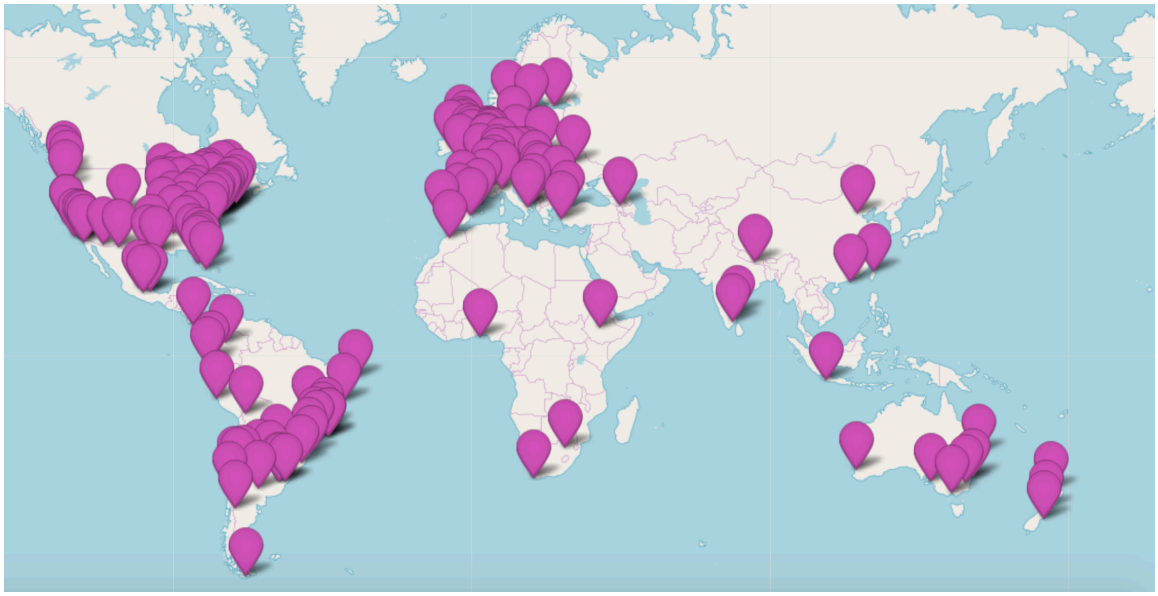
About me and R

- Background in Molecular Genetics (BSc and MSc)
- PhD in Computational Cancer Biology
- Self teaching R through on-line courses and forums
- Co-founder of R-Ladies Melbourne in Sep 2016
- President of R-Ladies Melbourne Inc.



https://www.meetup.com/en-AU/rladies-melbourne/

R-Ladies



https://blog.revolutionanalytics.com/2018/12/women-and-r.html

Motivation

Imagine a project ...

You are given:

- Gene expression data for some cancer samples
- A gene experssion signature

You are asked to:

- Find out which samples are more concordant with that signature?
- Communicate the analyses with your colleagues

How I used to do these without R Markdown

I would have:

- a folder with several analysis **scripts**
- a folder with several **figures**
- a folder with several **tables** (e.g. .csv, txt, tsv, etc)
- a **notebook** storing all the notes (rationale of the analyses, methodology, interpretation and descriptions)
- a folder of **papers** that have relevant figures and information.
- **It was always pretty hectic to *communicate* all these information with colleagues, *reproduce* all the results, and *share* my analyses.**

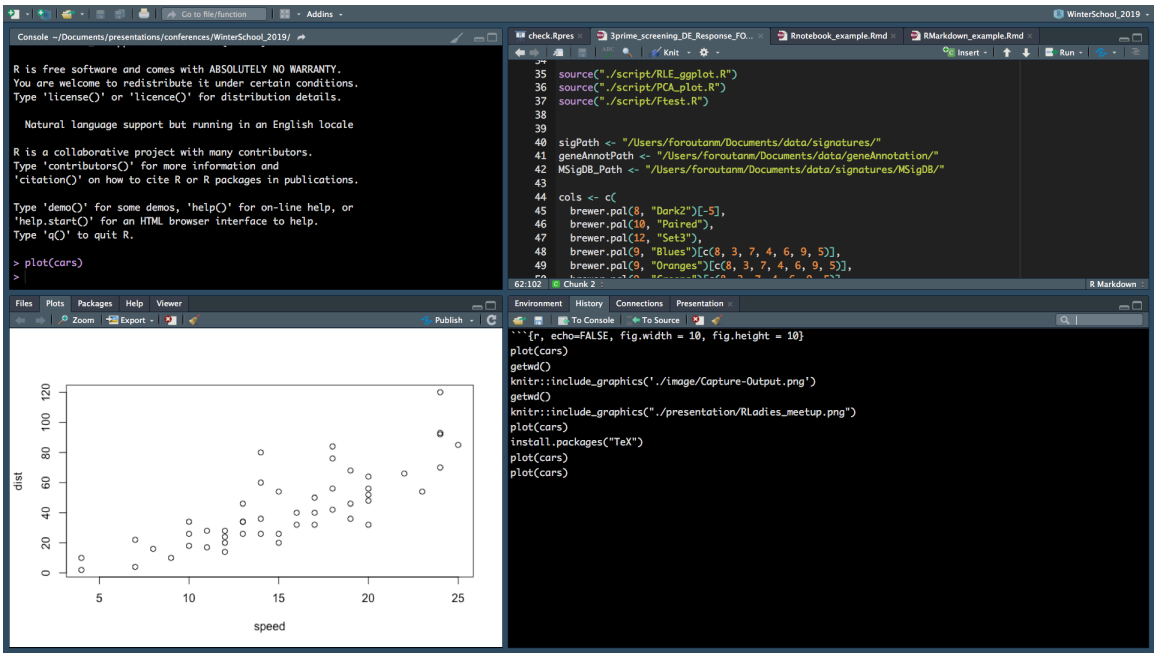
R Markdown was a game changer!

R Markdown is an authoring framework provided by RStudio, which can keep all steps of the analyses together:

- Codes (save and execute)
- Figures and tables
- Methodology, interprations, and descriptions of the analyses
- Link to papers, and images from papers
- **It is now much eaier to *communicate* all these information with colleagues, *reproduce* all the results, and *share* my analyses.**
- **Several output formats, and possibilities for static and dynamic (interactive) reports.**

RStudio

RStudio is an integrated development environment (IDE) for R which includes a console, syntax-highlighting editor, and tools for plotting, history, debugging, etc. Rstudio help you to interact with R more readily.



Things you can do using RStudio

- Write, save and run codes
- Generate interactive web application
- Generate high quality reports and documents
- Making presentation slides
- Version control (Git/Github)
- Many more
- **RStudio website**
- **Introduction to R and RStudio**
- **RStudio cheatsheet**

Online courses

Data Science Specialisation by JHU on Coursera

R Markdown and knitr

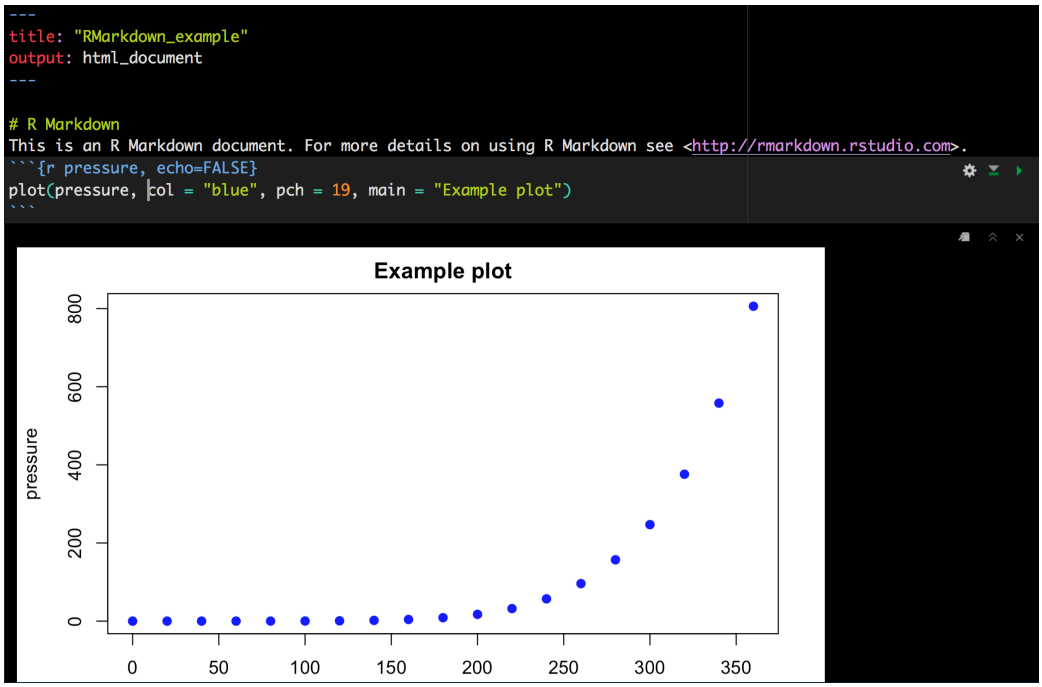
R Markdown (.Rmd) combines **R codes** (.R) and **documentatiuon language** (.md) using **knitr**.

knitr ...

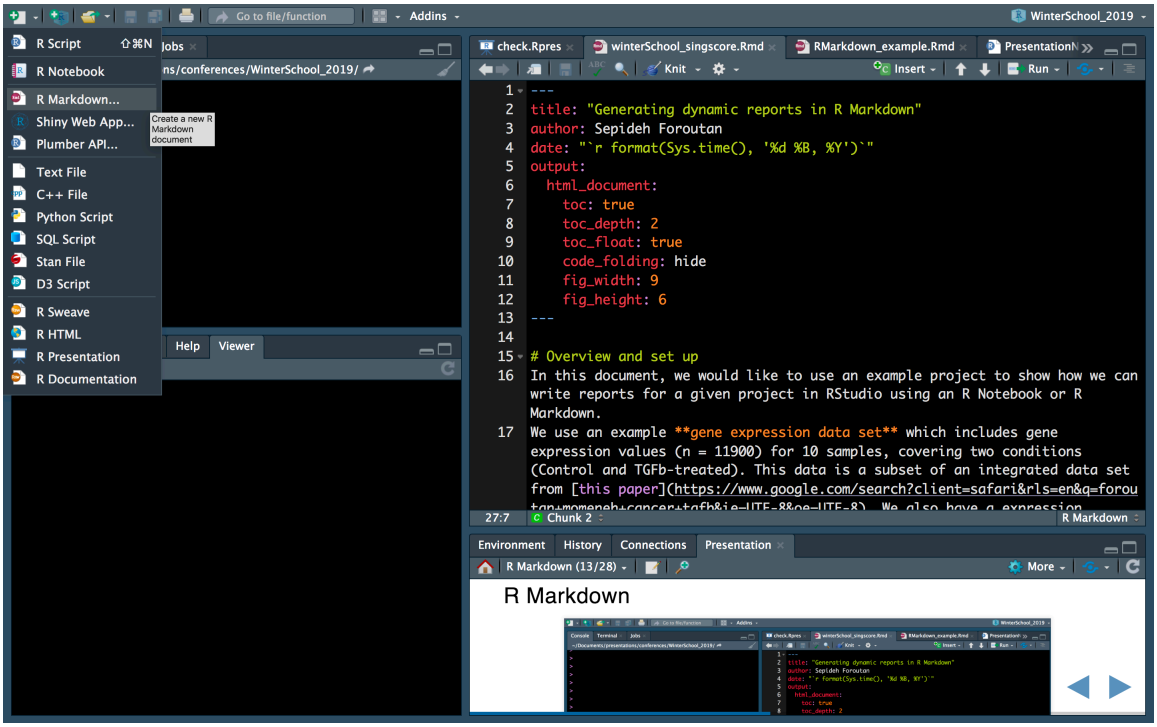
- inspired by Sweave
- is an R package which works as an engine for dynamic report generation in R.
- helps us to integrate R codes into other documents (e.g. Markdown, LaTeX, HTML, etc).
- can generate HTML, PDF or Word documents.
- supports other languages, such as Python, Perl, C++, Shell scripts, etc.
- enables reproducible research

R Markdown main sections

YAML header, Markdown text, and code chunks (with outputs).



Open a new R Markdown



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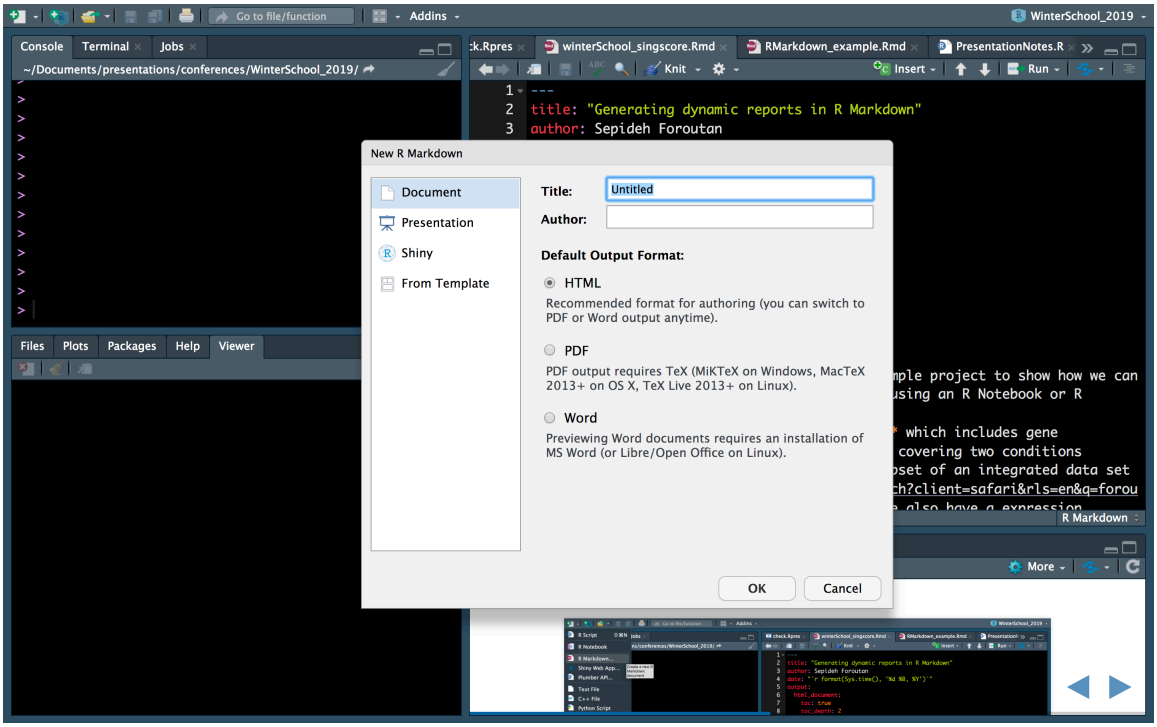
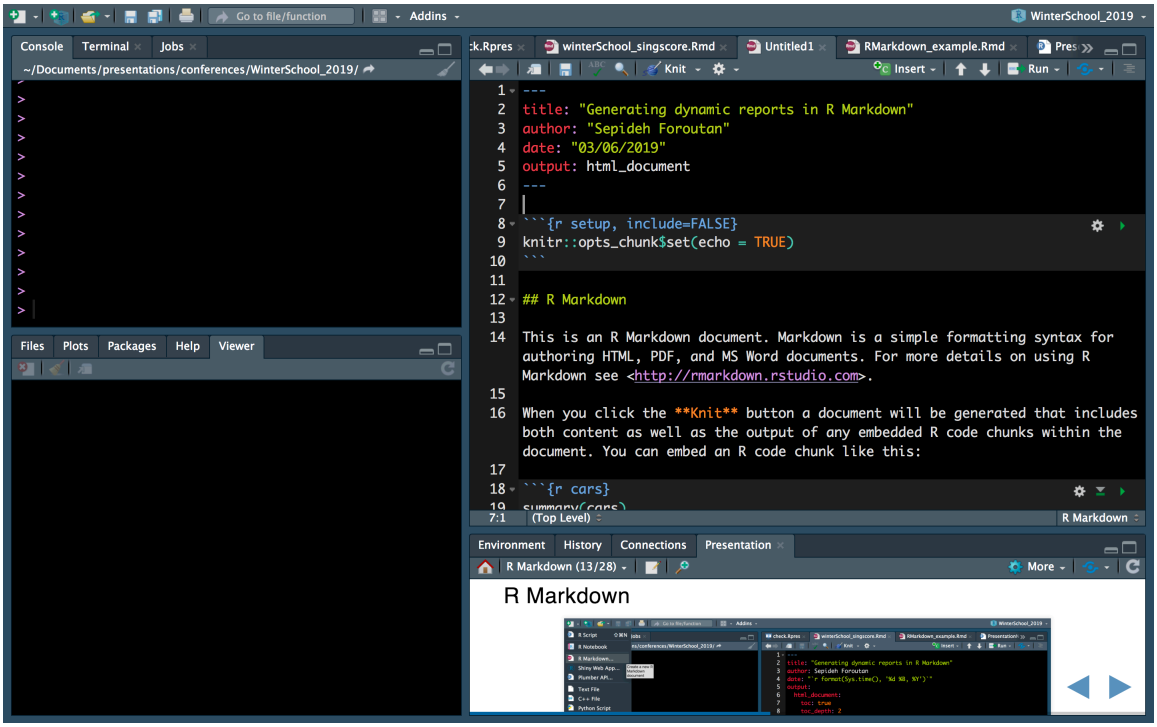
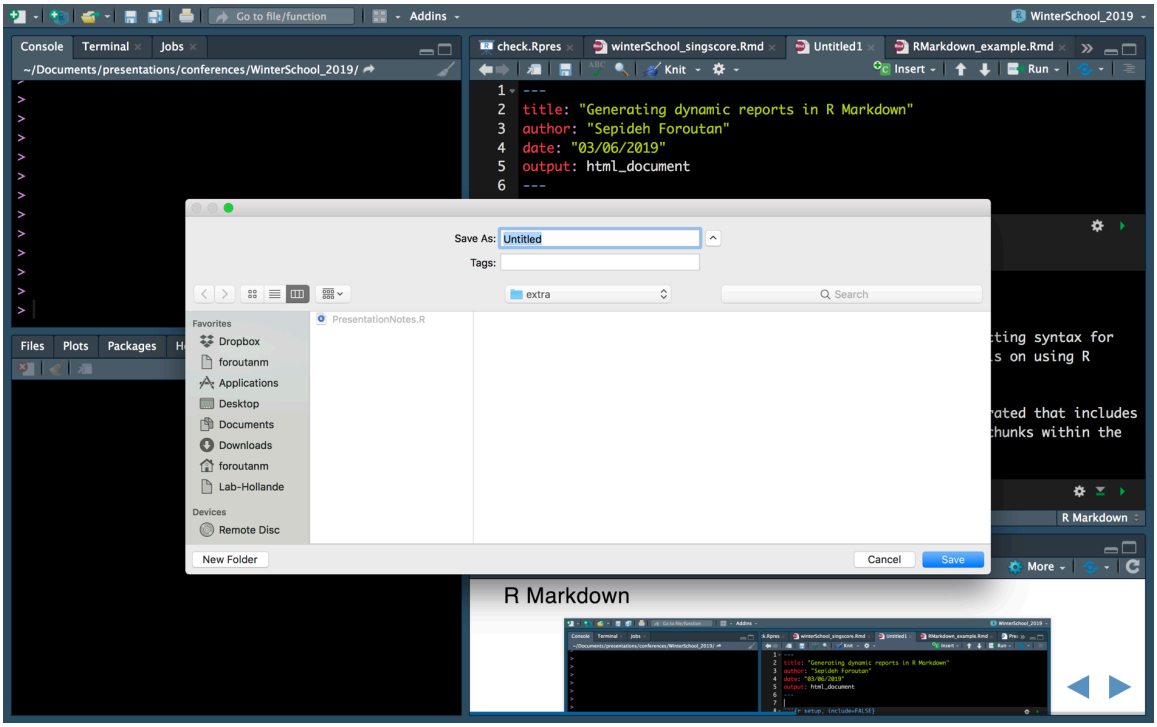


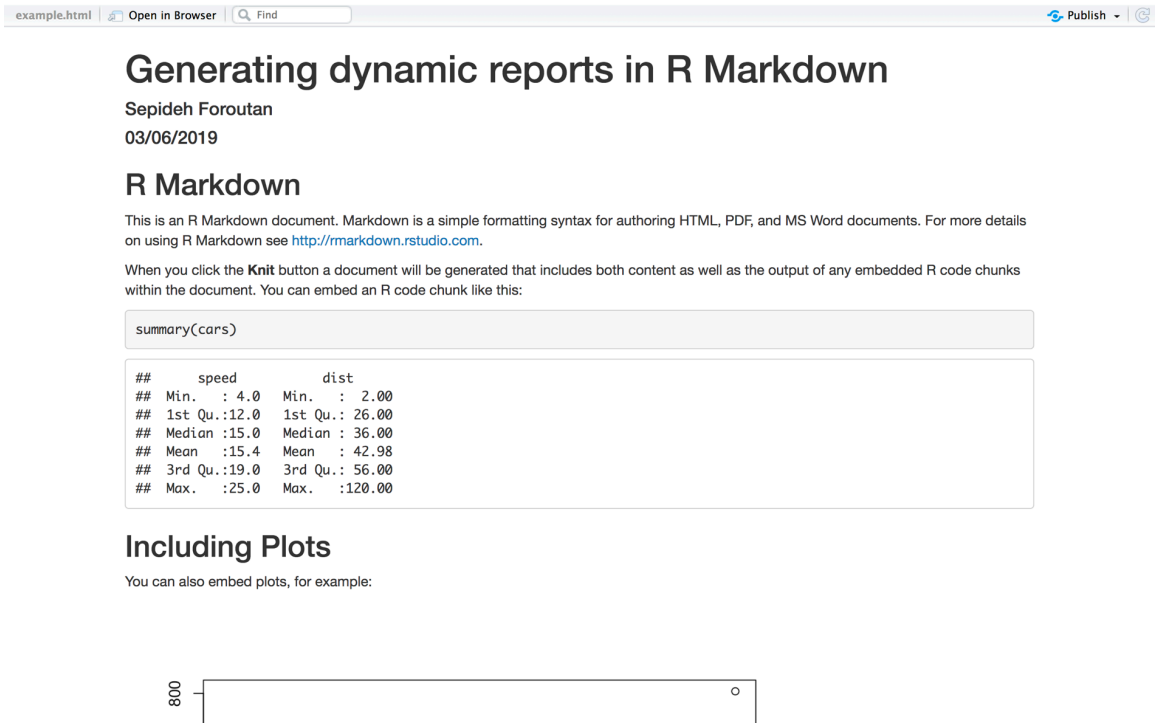
Open a new R Markdown



Open a new R Markdown



Open a new R Markdown



R Notebook

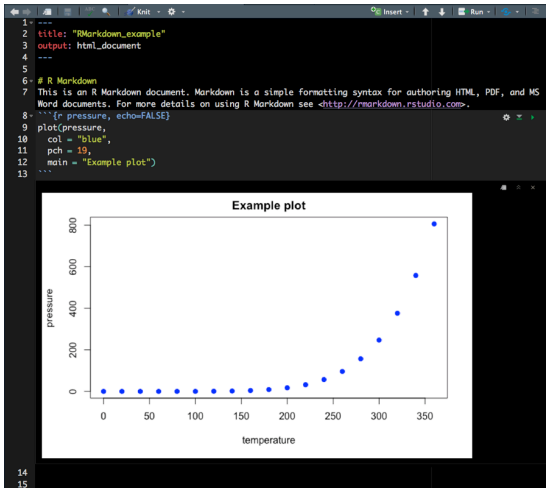
An **R Notebook** is an R Markdown document with chunks that can be executed independently and interactively, with output visible immediately beneath the input.

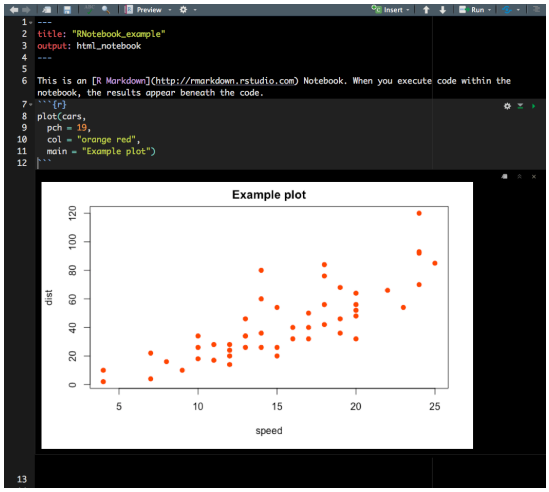
- **R Markdown** (knitr botton): executes and evaluates all code in one go. It can be very time-consuming when we have heavy processing
- **R Notebook** (preview botton): has caching behaviour; it evaluates a code chunk and save it.

"The immediacy of notebook mode makes it a good choice while authoring the R Markdown document and iterating on code. When you are ready to publish the document, you can share the notebook directly, or render it to a publication format with the Knit button."

R Markdown and R Notebook

- R Markdown
  - **knit** botton
  - output: **html_document**
- R Notebook
  - **preview** botton
  - output: **html_notebook**





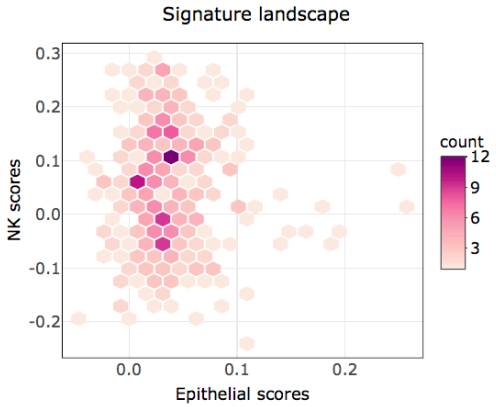
How does it look when we knit?

3 Explore the scores

3.1 Landscape plots

We would like to plot landscape of NK scores versus epithelial scores; to do this, we use the `plotScoreLandscape` function from `singscore` package.

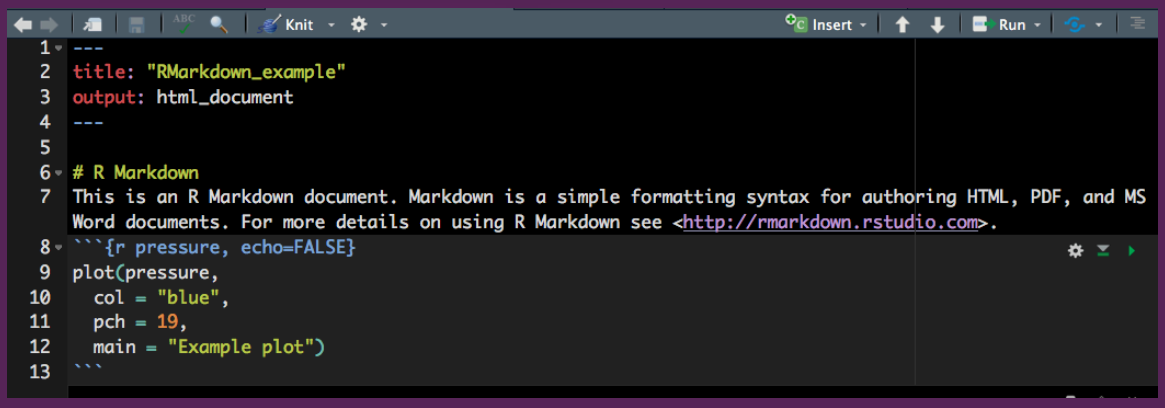
```
plotScoreLandscape(scoredf1 = epiScore_tcga,
                   scoredf2 = nkScore_tcga,
                   scorenames = c("Epithelial scores", "NK scores"),
                   textSize = 1,
                   isInteractive = T,
                   hexMin = 100)
```



https://github.com/DavisLaboratory/NK_scoring/

Creating the document

- Modify YAML header
- Structure and format the text
- Insert and modify code chuncks
- Generate interactive tables
- Generate interactive figures



YAML header

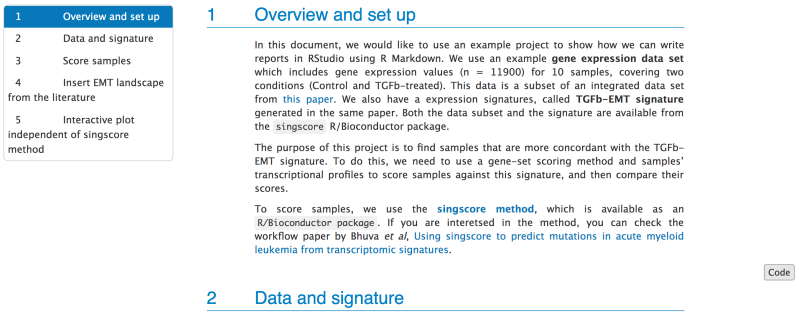
"YAML (YAML Ain't Markup Language) is a human-friendly data serialization standard for all programming languages."

YAML header allows us to modify the output of the domunent; YAML section can evaluate R expressions. By modifying the YAML header, we can add/change:

- Output format
- Table of content (toc)
- Tabbed sections
- Global figure options (width and height)
- Custom CSS
- a lot more

YAML header

```yaml
---
title: "Generating dynamic reports in R Markdown - an example using singscore"
author: Sepideh Foroutan
date: "`r format(Sys.time(), '%d %B, %Y')`"
output:
  BiocStyle::html_document:
    toc: true
    toc_depth: 2
    toc_float: true
    fig_caption: true
    number_sections: true
    code_folding: hide
    fig_width: 9
    fig_height: 6
params:
  output_dir: "./reports"
---
```



1 Overview and set up
2 Data and set up
3 Score samples
4 Insert EMT landscape from the literature
5 Interactive plot independent of singscore method

1 Overview and set up

In this document, we would like to use an example project to show how we can write reports in RStudio using R Markdown. We use an example **gene expression data set** which includes gene expression values (n = 11900) for 10 samples, covering two conditions (Control and TGFb-treated). This data is a subset of an integrated data set from this paper. We also have a expression signatures, called **TGFb-EMT signature** generated in the same paper. Both the data subset and the signature are available from the `singscore` R/Bioconductor package.

The purpose of this project is to find samples that are more concordant with the TGFb-EMT signature. To do this, we need to use a gene-set scoring method and samples' transcriptional profiles to score samples against this signature, and then compare their scores.

To score samples, we use the **singscore method**, which is available as an `R/Bioconductor package`. If you are interetsed in the method, you can check the workflow paper by Bhuva *et al*, Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures.

Code

2 Data and signature

YAML header

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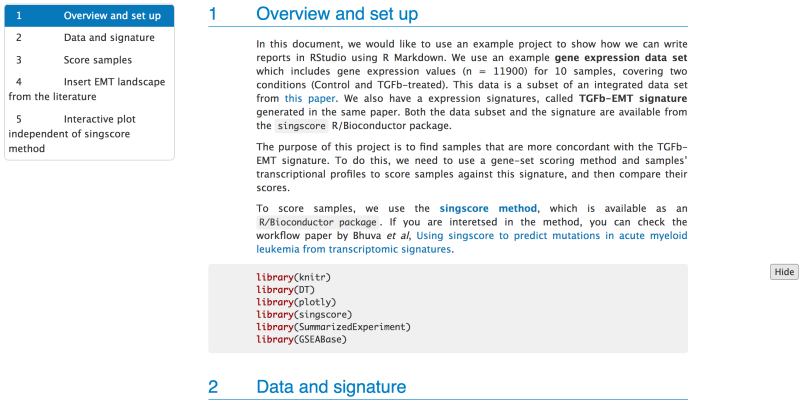
    toc_depth: 2
    toc_float: true
    fig_caption: true
    number_sections: true
    code_folding: hide
    fig_width: 9
    fig_height: 6
params:
  output_dir: "./reports"
---
```



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1 Overview and set up

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Hide

```r
library(knitr)
library(DT)
library(plotly)
library(singscore)
library(SummarizedExperiment)
library(GSEABase)
```

2 Data and signature

Structure and modify the text

- Headings and sub-headings are generated using **#**:

```
# Heading 1
```

Heading 1

```
## Heading 2
```

Heading 2

- Italic texts are generated using :

```
*This is italic!*
```

This is italic!

- Bold texts are generated using :

```
**This is bold!**
```

This is bold!

Structure and modify the text

- Add hyperlinks using `[your_text](your_url)`; for example:

`[R Markdown documnetation](https://rmarkdown.rstudio.com)` will make R Markdown documnetation clickable, which opens up the corresponding webpage for the documentation.

- Use **single backticks** as wrappers to change the font to make the code, package names, etc different from other plain texts.
- Add bullet points using **minus** and **plus** signs as well as tab.

For example:

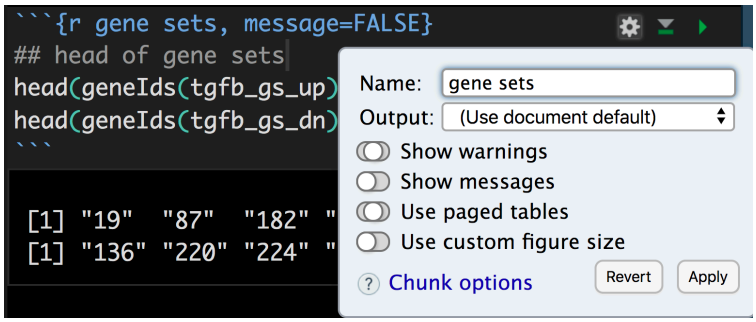
```
- First point

Tab + class A

Tab + class B

- Second point
```

Will result in:

- First point
  - class A
  - class B
- Second point

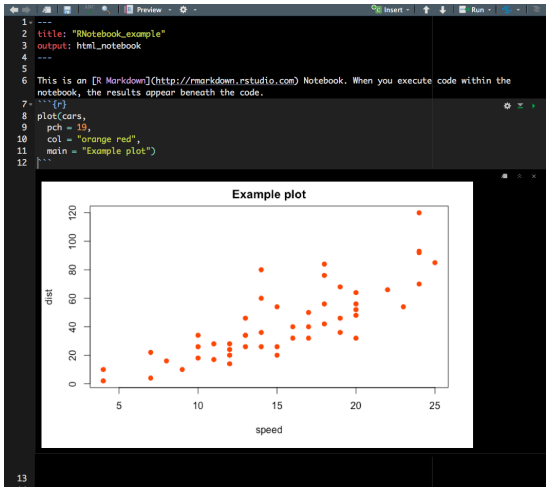
Code chunks

````
```{r gene sets, message = FALSE}
## head of gene sets
head(geneIds(tgfb_gs_up))
head(geneIds(tgfb_gs_dn))
```
````



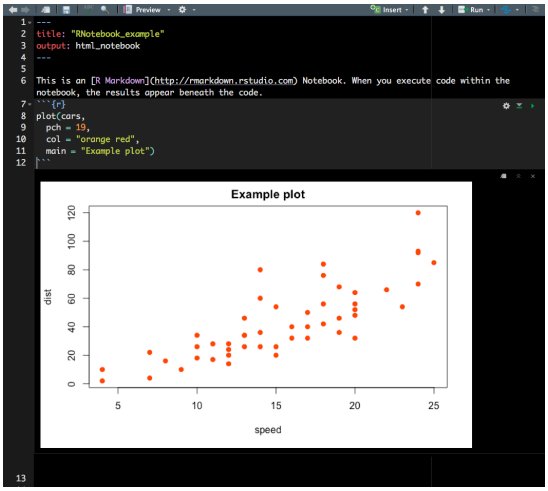

````
```{r set-up}
knitr::opts_chunk$set(warning = FALSE, message = FALSE)
```
````

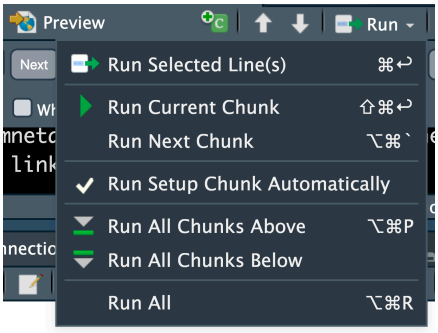
Insert/run code chunks



- In Mac: Command + Option + i
- In Windows: Ctrl + Alt + i

Insert/run code chunks





Interactive tables using DT package

- Interface to the DataTable javascript library
- Very easy-to-use: `datatable(df)`
- filtering, paging, sorting, formatting the tables, etc.
- DT documentation

```
library(DT)
library(reshape2)
data("tips")

datatable(tips, filter = 'top', options = list(pageLength = 12)) %>%  ## Bold some numbers:
  formatStyle('total_bill',
    fontWeight = styleInterval(18, c('normal', 'bold'))) %>%  ## show colour bar
  formatStyle('tip',
    background = styleColorBar(tips$tip, 'mediumpurple'),
    backgroundSize = '100% 95%'
    # backgroundRepeat = 'no-repeat',
    # backgroundPosition = 'centre'
    ) %>%  ## transform values
  formatStyle('sex',
    transform = 'rotateX(-45deg) rotateY(-30deg) rotateZ(-50deg)',
    backgroundColor = styleEqual(unique(tips$sex), c('lightblue', 'lightseagreen'))) %>%  ## colour value/backgrou
nd
  formatStyle('size',
    color = styleInterval(c(2, 4), c('blue', 'black', 'red')),
    backgroundColor = styleInterval(c(2, 4), c('white', 'gray', 'gray50')))
```

Show 12 entries Search:

	total_bill	tip	sex	smoker	day	time	size
	All	All	All	All	All	All	All
1	16.99	1.01	Female	No	Sun	Dinner	2
2	10.34	1.66	Male	No	Sun	Dinner	3
3	**21.01**	3.5	Male	No	Sun	Dinner	3
4	**23.68**	3.31	Male	No	Sun	Dinner	2
5	**24.59**	3.61	Female	No	Sun	Dinner	4
6	**25.29**	4.71	Male	No	Sun	Dinner	4
7	8.77	2	Male	No	Sun	Dinner	2
8	**26.88**	3.12	Male	No	Sun	Dinner	4
9	15.04	1.96	Male	No	Sun	Dinner	2
10	14.78	3.23	Male	No	Sun	Dinner	2
11	10.27	1.71	Male	No	Sun	Dinner	2
12	**35.26**	5	Female	No	Sun	Dinner	4

Showing 1 to 12 of 244 entries Previous 1 2 3 4 5 … 21 Next

Interactive plots using plotly package

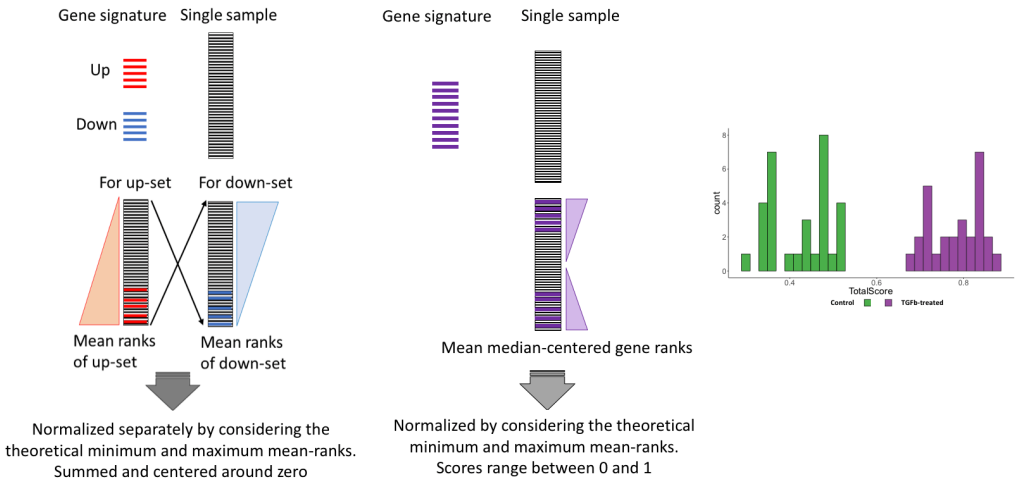
- Plotly can generate 2D and 3D plots, as well as animations
- It is possible to zoom, pan, label, and toggle between items in the legend
- Save static image functionality
- Configurable tooltips
- Very easy-to-use with **ggplot**: `ggplotly(ggplot_object)`
- Plotly documentation

Back to our theoritical project...

Use samples' gene expression data and a gene set scoring method to score samples against gene sets and identify those that are more concordant with a given signature.

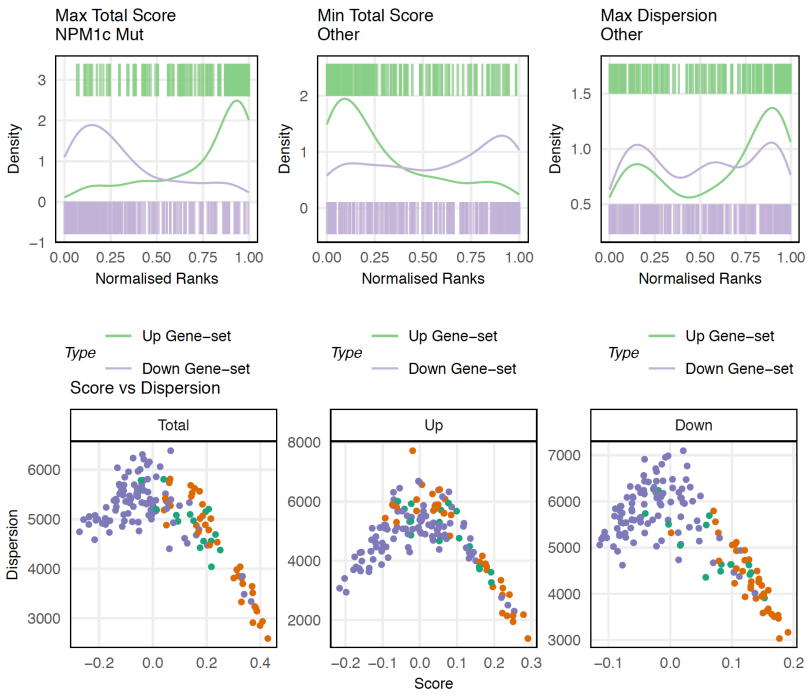
- Rank-based method
- Single-sample approach
- R/Bioconductor package
- Interactive plots

The singscore method



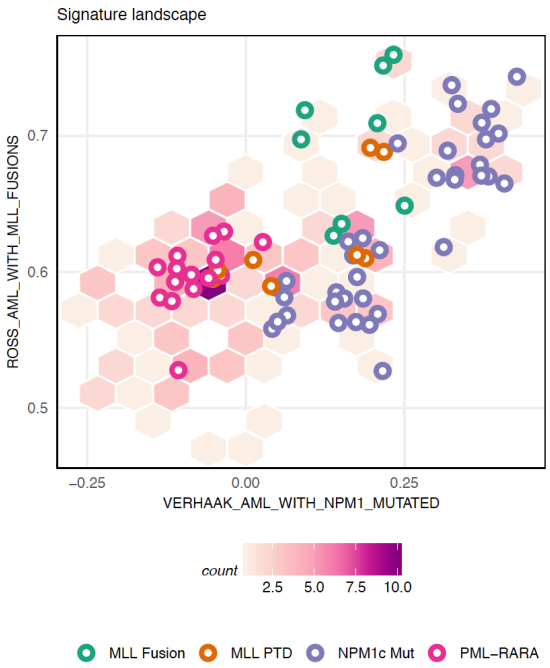
Single sample scoring of molecular phenotypes. Foroutan M, Bhuva D, et al. *BMC Bioinformatics*

Visualisations by `singscore`



Using singscore to predict mutations in AML from transcriptomic signatures. Bhuva D. et al. *f1000 research*.

Visualisations by `singscore`



Using singscore to predict mutations in AML from transcriptomic signatures. Bhuva D. et al. *f1000 research*.

Let's look at our R Markdown report

Generating dynamic reports in R Markdown - an example using singscore

Resources I used for this presentation

- **RStudio website**
- **R Markdown documentation**
- **R Notebook documentation**

- **Baby one more time - Reproducibility in R and when to pull in the big guns** by *Lavinia Gordon*

- **RLadies presentation Ninja** by *Alison Presmanes Hill*

- **Making slides in R Markdown** by *Alison Hill*

Thank you!