Reproducible papers in the life sciences using R

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Introduction

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- However, R is rarely used in the life sciences as a default method to create papers
- Why?

Reasons

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- "R is just for Stats"
- "There is a learning curve"
- **"I can't create figures for publication"**

The Problem

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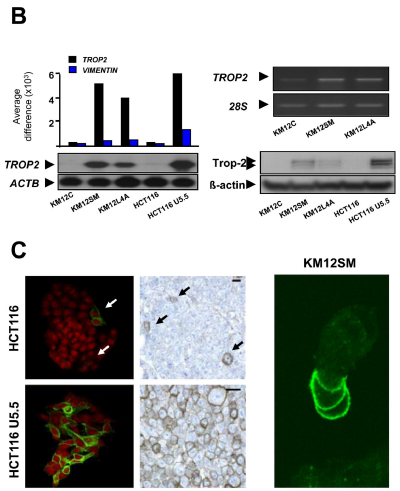
  - Images from cells/tissues
  - Figures that summarize data
  - Figures that present statistical analyses (with "p-values")

The Problem

Figure 1: A typical figure



Guerra et al. *Neoplasia* **2021**

- Can figures like this be created using 'RMarkdown'?

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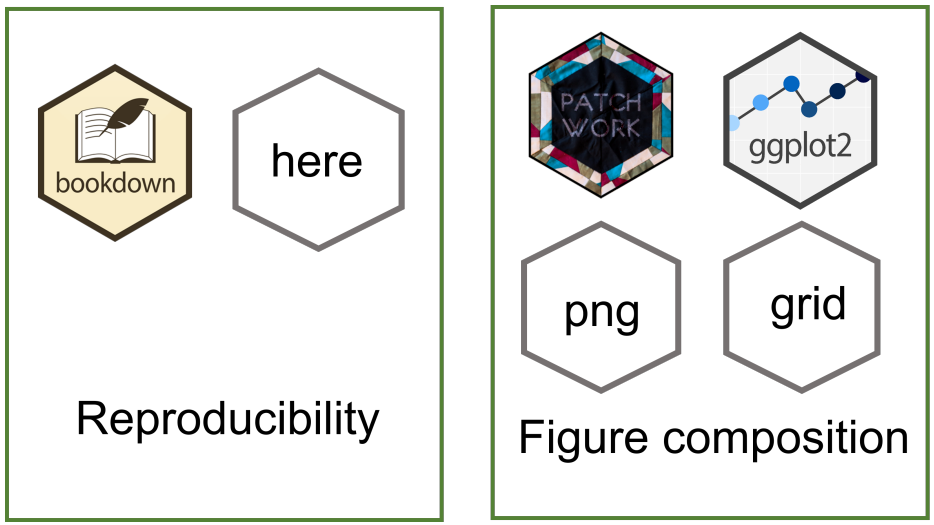
The Solution

- Yes, we can create figures like this using R!

Figure 2: The packages



The Solution

- Yes, we can create figures like this using R!
- We will need to use a combination of packages to achieve this

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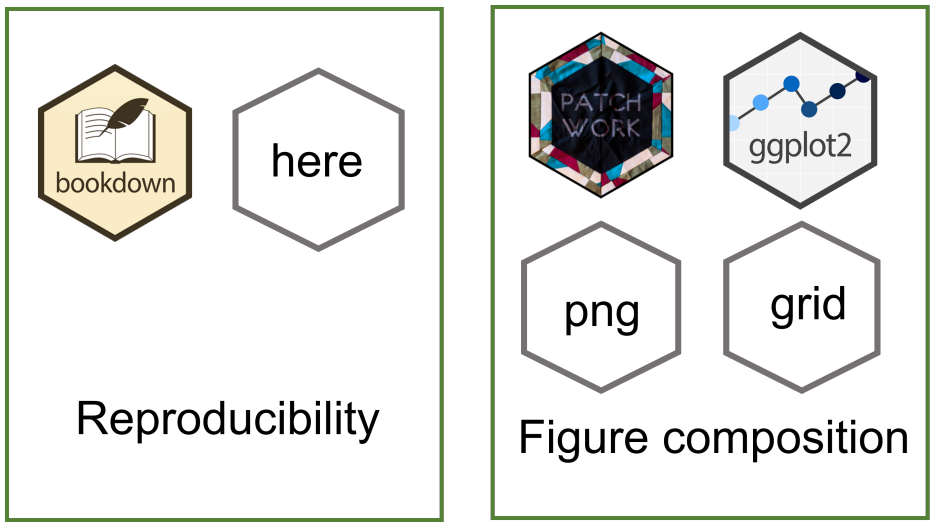

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  - Each section of the paper: (Materials and Methods, Results, etc.) is in a separate `Rmd` file
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- here allows to easily call scripts within the document (we will look at this later)

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  - Have written your paper sections (Methods, Results, etc) each section is in a `Rmd` file
  - Have some images
  - Have some data that needs to be analyzed
  - Want to create a composite figure of images/data analysis
  - **For the sake of time, I will focus on the image composition/data analysis part**

Project Organization

- How to organize the files:

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```
Project
├── Data
│   └── csv files
├── Code
│   └── R Script(s)
├── Figures
│   └── PNGs (or other image files)
└── Manuscript
    └── Rmd files (Sections)
```

A Handy Script: Images

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  - Reading the images is achieved by `grid` and `png`
  - ggplot2 creates the plot of our analysis
  - patchwork allows us to assemble everything

A Handy Script: Images

- How do we read a PNG image?

```
cells<-rasterGrob(readPNG(here("figures",
                               "cells.png"),
                          native=TRUE))
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```

- We use here to call the PNG file located in the "figures" directory.

A Handy Script: Data Analysis

```
# for regression

formula<-y~x

# create a plot of the data and the regression
a1<-ggplot(data=data,
           aes(x=weight,y=body_fat,fill=Group,color=Group)
           )+
    geom_point(show.legend=FALSE,shape=21,colour='black',size=5,
               alpha=0.7)+
    geom_smooth(method="lm",formula=formula, se=T)+
    stat_poly_eq(use_label(c("R2","p.value")),
                 formula = formula, size = 3)
```

- Try ggpmisc

A Handy Script: Layout

- Provide a layout for the figure https://patchwork.data-imaginist.com/articles/guides/layout.html

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```
layout<-"
AAAABBBB
AAAABBBB
AAAABBBB
AAAABBBB
CCCCDDDD
CCCCDDDD
CCCCEEEE
CCCCEEEE
"
```

A Handy Script: Assemble!

- Use `wrap_elements` and patchwork

```
image_a<-wrap_elements(
    panel=cells
)+
    wrap_elements(
        panel=molecule
    )+
    wrap_elements(
        panel=jellyfish
    )+
    ylab("jellyfish")+
    a1+
    a2+
    plot_layout(design=layout)
```

Conclusion

- We can use R to create reproducible papers and complex figures

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- We can use R to create reproducible papers and complex figures
- There **is** a learning curve, but once you learn you won't go back to W**d!

Acknowlegdments

- Nasri Lab @Université de Montréal

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