

Juli Nagel | RG Psychology and  
Neurobiology of Sleep and  
Memory



Zentralinstitut für  
Seelische Gesundheit

# Reproducible Research

Trifels Summer School, 27.09.2022



# What is reproducible research?



|          |           | Data         |               |
|----------|-----------|--------------|---------------|
|          |           | Same         | Different     |
| Analysis | Same      | Reproducible | Replicable    |
|          | Different | Robust       | Generalisable |




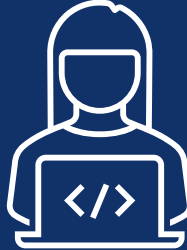


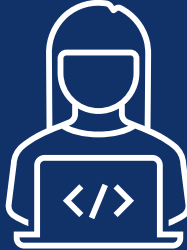

Definition: The Turing Way

# Reproducibility vs. replicability

National Academies of Sciences Engineering (Chapter 3, p.4)



Zentralinstitut für  
Seelische Gesundheit

|    | reproducibility   | replicability   |
|----|---|---|
| B1 |  same data +<br>code   |  collect new<br>data   |
| B2 |  collect new<br>data   |  same data +<br>code   |
| A  |   |   |

# Reproducibility vs. replicability

National Academies of Sciences Engineering (Chapter 3, p.4)



Zentralinstitut für  
Seelische Gesundheit

|           |      |      |
|-----------|------|------|
| <b>B1</b> | code | data |
| <b>B2</b> |      | code |
| <b>A</b>  |      |      |

signal processing, scientific computing, econometry, epidemiology, clinical studies, internal medicine, (neuro)physiology, computational biology, biomedical research, statistics

microbiology, immunology (FASEB), computer science (ACM)

political science, economics

# What is reproducibility?

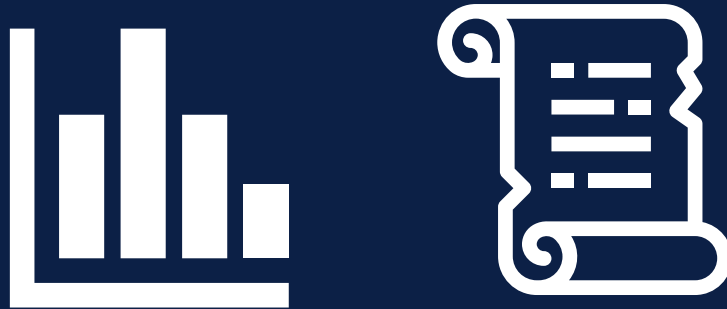
National Academies of Sciences Engineering



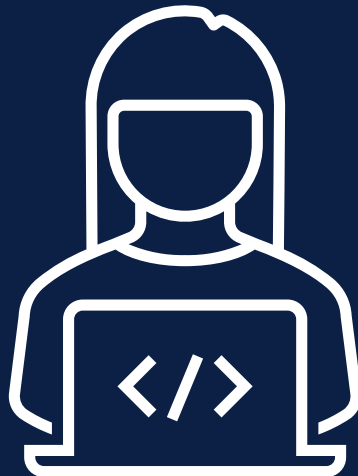
Zentralinstitut für  
Seelische Gesundheit

“Computational scientists generally use the term reproducibility to answer just the first question—that is, reproducible research is research that is **capable of being checked** because the data, code, and methods of analysis are available to other researchers. The term reproducibility can also be used in the context of the second question: research is reproducible if another researcher **actually uses the available data and code** and obtains the same results. The difference between the first and the second questions is one of action by another researcher; the first refers to the availability of the data, code, and methods of analysis, while the second refers to the act of recomputing the results using the available data, code, and methods of analysis.”

# What is reproducibility?



Data and code are  
available



Someone actually  
uses them

---

Same data, same analysis  
– why should it be hard to  
get the same results?!

---





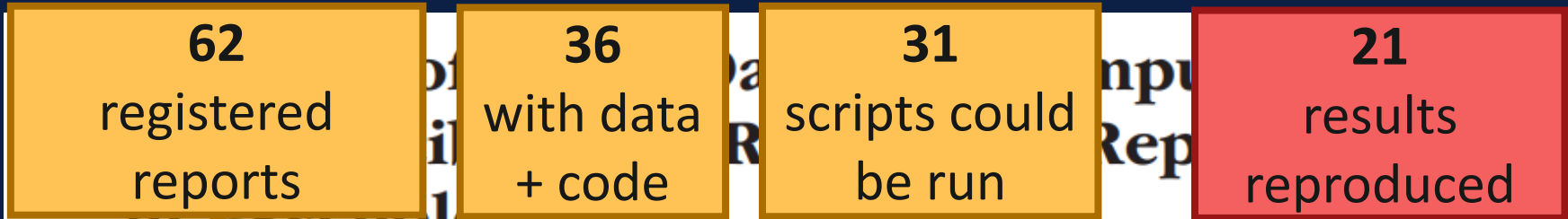
## Analysis of Open Data and Computational Reproducibility in Registered Reports in Psychology

### Abstract

Ongoing technological developments have made it easier than ever before for scientists to share their data, materials, and analysis code. Sharing data and analysis code makes it easier for other researchers to reuse or check published research. However, these benefits will emerge only if researchers can reproduce the analyses reported in published articles and if data are annotated well enough so that it is clear what all variable and value labels mean. Because most researchers are not trained in computational reproducibility, it is important to evaluate current practices to identify those that can be improved. We examined data and code sharing for Registered Reports published in the psychological literature from 2014 to 2018 and attempted to independently computationally reproduce the main results in each article. Of the 62 articles that met our inclusion criteria, 41 had data available, and 37 had analysis scripts available. Both data and code for 36 of the articles were shared. We could run the scripts for 31 analyses, and we reproduced the main results for 21 articles. Although the percentage of articles for which both data and code were shared (36 out of 62, or 58%) and the percentage of articles for which main results could be computationally reproduced (21 out of 36, or 58%) were relatively high compared with the percentages found in other studies, there is clear room for improvement. We provide practical recommendations based on our observations and cite examples of good research practices in the studies whose main results we reproduced.

Obels et al., 2022





## Abstract

Ongoing technological developments have made it easier than ever before for scientists to share their data, materials, and analysis code. Sharing data and analysis code makes it easier for other researchers to reuse or check published research. However, these benefits will emerge only if researchers can reproduce the analyses reported in published articles and if data are annotated well enough so that it is clear what all variable and value labels mean. Because most researchers are not trained in computational reproducibility, it is important to evaluate current practices to identify those that can be improved. We examined data and code sharing for Registered Reports published in the psychological literature from 2014 to 2018 and attempted to independently computationally reproduce the main results in each article. Of the 62 articles that met our inclusion criteria, 41 had data available, and 37 had analysis scripts available. Both data and code for 36 of the articles were shared. We could run the scripts for 31 analyses, and we reproduced the main results for 21 articles. Although the percentage of articles for which both data and code were shared (36 out of 62, or 58%) and the percentage of articles for which main results could be computationally reproduced (21 out of 36, or 58%) were relatively high compared with the percentages found in other studies, there is clear room for improvement. We provide practical recommendations based on our observations and cite examples of good research practices in the studies whose main results we reproduced.

Obels et al., 2022

## Is Economics Research Replicable? Sixty Published Papers from Thirteen Journals Say “Usually Not”

Andrew C. Chang\* and Phillip Li†

September 4, 2015

[Chang & Li \(2015\)](#)



# But why?

---

# Step 1: Access data and code

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

|                                      |  |                   |                                |
|--------------------------------------|--|-------------------|--------------------------------|
| <b>39</b><br>data + code<br>required | <b>28</b><br>data + code<br>not required |                   |                                |
| <b>-4</b>                            | <b>-2</b>                                | proprietary data  |                                |
| <b>-6</b>                            | <b>-15</b>                               | missing data/code | After emailing<br>the authors! |

## Step 2: Run the code

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

For the papers for which we are able to obtain data and code replication files, we attempt to replicate the key results of the paper using only the instructions provided in the author readme files. If the readme files are insufficient or if the replication files are incomplete (or both) and the paper is subject to a replication policy, then we email the corresponding author (if no corresponding author, then the first author) for either clarification or to request the missing files. If we do not receive a response within a week, then we query the second author, and so on, until all authors on the paper had been contacted.<sup>11</sup>

**Try to run code with instructions only first.  
If necessary, ask authors for help.**

## Step 2: Run the code

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

| <b>39</b><br>data + code<br>required | <b>28</b><br>data + code<br>not required |                   |                                |
|--------------------------------------|--|-------------------|--------------------------------|
| <b>-4</b>                            | <b>-2</b>                                | proprietary data  |                                |
| <b>-6</b>                            | <b>-15</b>                               | missing data/code | After emailing<br>the authors! |
| <b>-1</b>                            | <b>-1</b>                                | missing software  |                                |

## Step 2: Run the code

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

One dimension where we are unable to follow the authors exactly is the software version they use. To execute the replications, we make use of the following software version-operating system combinations: Dynare 4.3 and 4.4.2 (Windows), EViews 6 and 7 (Windows), EViews 8 (Linux), Gauss 9.0.2 (Linux), Fortran f90 (Linux), Matlab R2008a and R2012a and R2013a (Windows), Matlab R2010a and R2012a (Linux), OX 6.30 (Windows), Oxmetrics 6.30 (Windows), Stata 11.0 and 13.1 (Windows), Stata 13.0 (Windows and Linux), R 2.15.1 and 3.0.1 and 3.0.2 and 3.0.3 and 3.1.0 (Linux), and RATS 7.10 (Linux).<sup>15</sup> When available in the readme, we attempt to run the software version-operating system combination specified by the authors. When the replication files fail to execute on a given software version-operating system combination, the author readme did not specify a particular software version-operating system combination, and it appeared that the data and code were complete, we email the authors to find out which combination they use.





[← Back to product pricing](#)

## Configure your IBM product

IBM SPSS Statistics

Subscription

### Subscription details

Choose subscription term

Subscription Term: 12 months auto-renewal

1 month

12 months

### Plan options

[Reset](#)

Unit price: \$1,188.00 USD per authorized user

Enter the number of authorized users

1 - +

+ \$1,188.00 USD

... prevents people who don't have access from running your code.



[← Back to product pricing](#)

## Subscription details

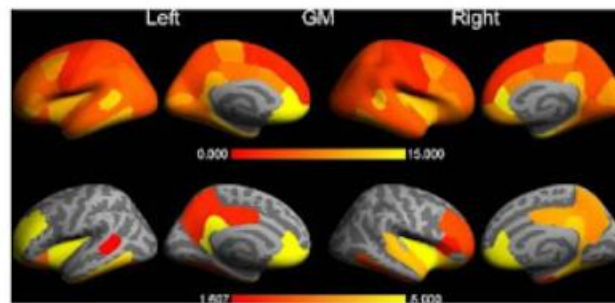
|                     | Base | Standard | Professional |
|---------------------|------|----------|--------------|
| Statistics base     | ✓    | ✓        | ✓            |
| Data preparation    | ✓    | ✓        | ✓            |
| Bootstrapping       | ✓    | ✓        | ✓            |
| Advanced statistics |      | ✓        | ✓            |
| Regression          |      | ✓        | ✓            |
| Custom tables       |      | ✓        | ✓            |
| Missing values      |      |          | ✓            |

Thursday, 14 June 2012

## Brains are Different on Macs

**Update** - A number of articles linking to this post are wrongly stating that FreeSurfer is medical software used to diagnose diseases or measure the size of brain tumors. It's not. It is purely for research purposes as [the software license states](#), "*The Software has been designed for research purposes only and has not been reviewed or approved by the Food and Drug Administration or by any other agency. CLINICAL APPLICATIONS ARE NEITHER RECOMMENDED NOR ADVISED.*"

Last month, [neuroscientists were warned](#) about potential biases in SPM8, a popular software tool for analysis of fMRI data.



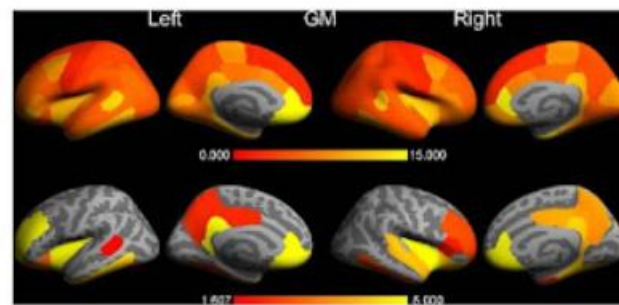
This your brain on FreeSurfer version  
4.3.1 vs version 5.0.0

<http://neuroskeptic.blogspot.com/2012/06/brains-are-different-on-macs.html>

Thursday, 14 June 2012

## Brains are Different on Macs

How much of a difference it made varied by brain location. The differences were 5-15% with version changes. For Mac vs PC and Mac OS updates it was less bad, 2-5% mostly, but in the worst regions - the parahippocampal and entorhinal cortex - it was still almost 15% different. Why those regions are so variable is unclear.



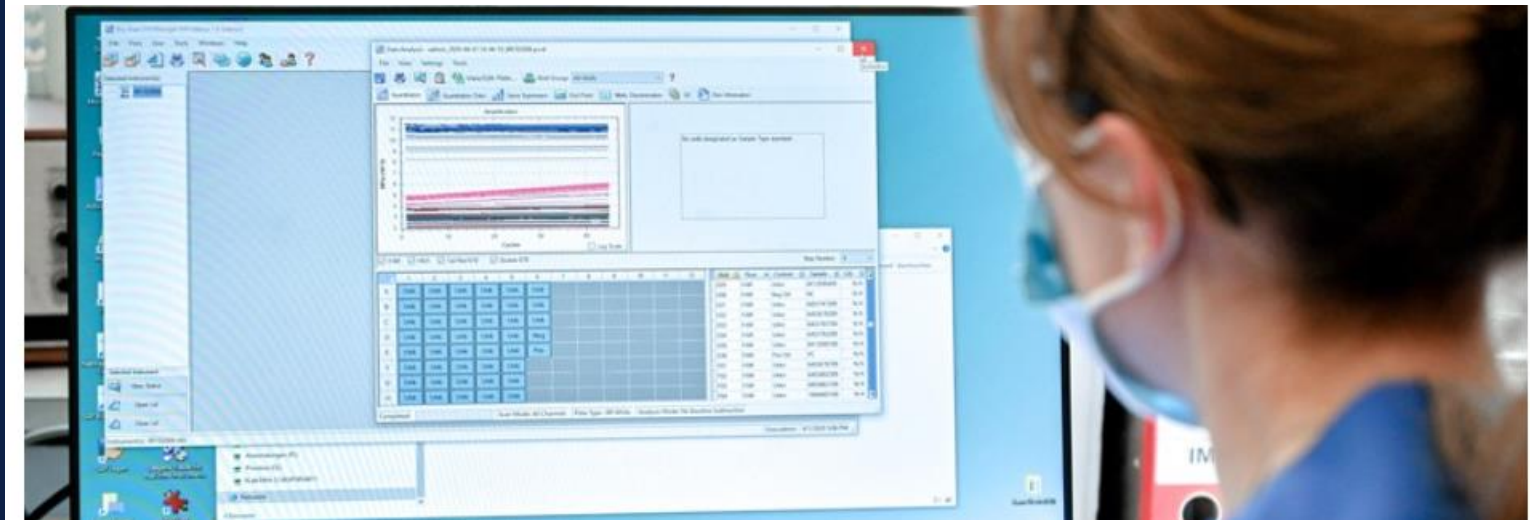
This your brain on FreeSurfer version  
4.3.1 vs version 5.0.0

<http://neuroskeptic.blogspot.com/2012/06/brains-are-different-on-macs.html>

NEWS | 13 August 2021 | Correction [25 August 2021](#)

# Autocorrect errors in Excel still creating genomics headache

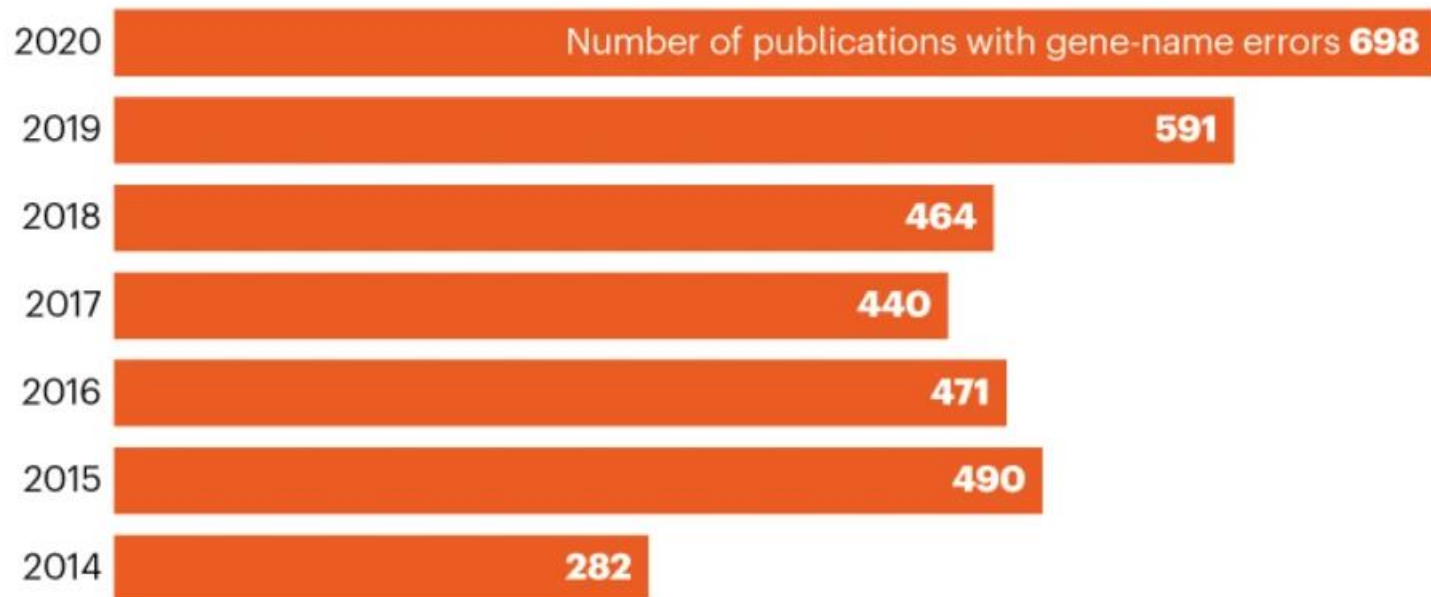
**Despite geneticists being warned about spreadsheet problems, 30% of published papers contain mangled gene names in supplementary data.**



<https://www.nature.com/articles/d41586-021-02211-4>

## A GROWING PROBLEM

A 2016 analysis found that 20% of papers featuring gene names had errors created by spreadsheet autocorrect functions, but a bigger survey now finds the proportion is up to 30%. Since 2014, the number of papers with errors has increased significantly.



## Step 2: Run the code

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

| <b>39</b><br>data + code<br>required | <b>28</b><br>data + code<br>not required |                     |                                |
|--------------------------------------|--|---------------------|--------------------------------|
| <b>-4</b>                            | <b>-2</b>                                | proprietary data    |                                |
| <b>-6</b>                            | <b>-15</b>                               | missing data/code   | After emailing<br>the authors! |
| <b>-1</b>                            | <b>-1</b>                                | missing software    |                                |
| <b>-5</b>                            | <b>-4</b>                                | incorrect data/code |                                |



## Step 3: Same results?

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

### A (deliberately) lenient definition of “same”.

We define a successful replication as when the authors or journal provide data and code files that allow us to qualitatively reproduce the key results of the paper. For example, if the paper estimates a fiscal multiplier for GDP of 2.0, then any multiplier greater than 1.0 would produce the same qualitative result (i.e., there is a positive multiplier effect and

Unfortunately, the authors don't distinguish between “different results” and “code execution failed”.

# Final count

Chang & Li (2015)



Zentralinstitut für  
Seelische Gesundheit

| <b>39</b><br>data + code<br>required | <b>28</b><br>data + code<br>not required |                     |                                |
|--------------------------------------|--|---------------------|--------------------------------|
| <b>-4</b>                            | <b>-2</b>                                | proprietary data    |                                |
| <b>-6</b>                            | <b>-15</b>                               | missing data/code   | After emailing<br>the authors! |
| <b>-1</b>                            | <b>-1</b>                                | missing software    |                                |
| <b>-5</b>                            | <b>-4</b>                                | incorrect data/code |                                |
| <b>23 (58.97%)</b><br>reproduced     | <b>6 (21.43%)</b><br>reproduced          |                     |                                |

**“But it works on my machine.”**

**Assumption: Most researchers publish code that  
works – for them.**

(Or at least it did at some point).



# Solutions?

---



- Here are a few things that can improve reproducibility (by no means a complete list).
- They may be more or less relevant for you, depending on your field.
- Depending on your background, some tools might take a while to master.
- Some things cost quite some time, at least initially.
- You don't have to implement everything!



# Make data and code available

---



- Make sure you have permission to share the data.
- Beware: Even anonymous data might be used to identify people.
- Especially tricky: genetical data, imaging (e.g. brain) data, medical data, small (rare) samples
- That's a whole different topic we won't talk about here!



- Sometimes, journals allow/want you to upload data and code.
- Sometimes, you find data/code on personal/institute websites.
- Better: Data repositories
  - Offers a DOI?
  - Independent/safe?
  - If relevant storage in Germany/the EU?
- E.g.: OSF, ZPID (psychology)





---

Will help others to work with your  
data and code – including your  
future self.

- **How were the data collected?**
  - Which task, how were the data recorded, which sample, where, by whom, part of which paper ... ?
- **Codebook**
  - Which variables?
  - What are valid values? (e.g. age in years; “How happy are you” on a scale from 1 (“not at all”) to 10 (“very”))
  - How are missing values coded?

# Good: In a table - human and machine readable

\*hs1.sav [] - PASW Statistics Data Editor

File Edit View Data Transform Analyze Graphs Utilities Add-ons Window Help

|    | Name    | Type    | Width | Decimals | Label                                    | Values              | Missing | Columns | Align | Measure |
|----|---------|---------|-------|----------|--|---------------------|---------|---------|-------|---------|
| 1  | id      | Numeric | 9     | 2        |  | None                | None    | 8       | Right | Scale   |
| 2  | female  | Numeric | 9     | 2        | The gender of the student.               | {.00, male}...      | None    | 8       | Right | Nominal |
| 3  | race    | Numeric | 12    | 2        |  | {1.00, hispanic}... | None    | 8       | Right | Nominal |
| 4  | ses     | Numeric | 9     | 2        |  | {1.00, low}...      | None    | 8       | Right | Nominal |
| 5  | schtyp  | Numeric | 9     | 2        | The type of school the student attended. | {1.00, public}...   | None    | 8       | Right | Nominal |
| 6  | prgtype | String  | 8     | 0        |  | None                | None    | 8       | Left  | Nominal |
| 7  | read    | Numeric | 9     | 2        | reading score                            | None                | None    | 8       | Right | Scale   |
| 8  | write   | Numeric | 9     | 2        | writing score                            | None                | None    | 8       | Right | Scale   |
| 9  | math    | Numeric | 9     | 2        | math score                               | None                | None    | 8       | Right | Scale   |
| 10 | science | Numeric | 9     | 2        | science score                            | None                | None    | 8       | Right | Scale   |
| 11 | socst   | Numeric | 9     | 2        | social studies score                     | None                | None    | 8       | Right | Nominal |

<https://stats.oarc.ucla.edu/spss/faq/how-can-spss-help-me-document-my-data/>

- Best use a “lightweight” file format (.csv or .txt)
- Here is a very thorough guide: [Horstmann et al. \(2020\)](#)

**Table 2.** Example on how to provide information about response options of Rating Scale Items

| Response list        | Coded response | Label                     | Translation       |
|----------------------|----------------|---------------------------|-------------------|
| response_list_bfi    | 1              | Stimme überhaupt nicht zu | Disagree strongly |
|                      | 2              | Stimme eher nicht zu      | Disagree a little |
|                      | 3              | Teils, teils              | Neutral           |
|                      | 4              | Stimme eher zu            | Agree a little    |
|                      | 5              | Stimme voll und ganz zu   | Agree strongly    |
| response_list_gender | 1              | Männlich                  | Male              |
|                      | 2              | Weiblich                  | Female            |
|                      | 3              | Divers                    | Non-binary        |
|                      | 4              | Keine Angabe              | Prefer not to say |

*Note.* response\_list = the name of the list, which can then be referenced in each item that makes use of this scale; coded response = the numerical value in the data frame that corresponds to the “label”; translation = an English translation of the label.



- Descriptive column names.
  - Bad: item1, column12, sumscore, test
  - Good: bdi1, bdi\_sumscore, age\_category
  - Don't use spaces or “weird” characters
- Clear, consistent labels, e.g.
  - E.g. 0 = no, 1 = yes for entire data set
- Maybe: Provide a raw and a “clean” version of your data set

# Making data meaningful: guidelines for good quality open data

Andrea S. Towse, David A. Ellis & John N. Towse

To cite this article: Andrea S. Towse, David A. Ellis & John N. Towse (2021) Making data meaningful: guidelines for good quality open data, *The Journal of Social Psychology*, 161:4, 395-402, DOI: [10.1080/00224545.2021.1938811](https://doi.org/10.1080/00224545.2021.1938811)

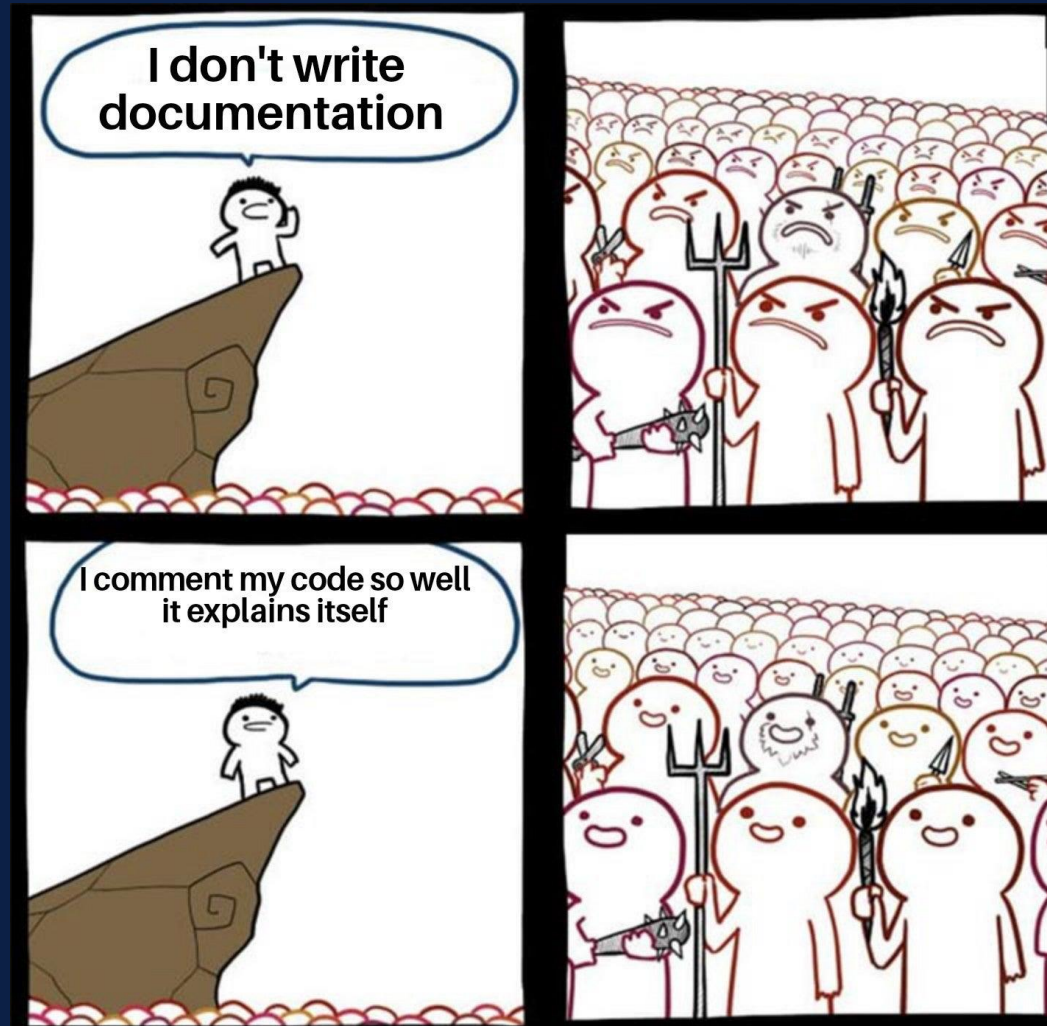
[Towse et al. \(2021\)](#)



- Report which versions you used (operating system, software and packages!)
- Provide a README file how the code should be handled, e.g. in which order the files need to be run.
- Write comments in your code to explain what's happening



# “Good code is self-documenting”



[Reddit](#)

“Good code is self-documenting”



Zentralinstitut für  
Seelische Gesundheit

# “GOOD CODE DOCUMENTS ITSELF” AND OTHER HILARIOUS JOKES YOU SHOULDN’T TELL YOURSELF

by: **Sven Gregori**

 **156 Comments**



March 5, 2019

[article link](#)



**Alex Naka**

@gottapatchemall

Looking at some old code and was initially puzzled by a variable named 'feet'

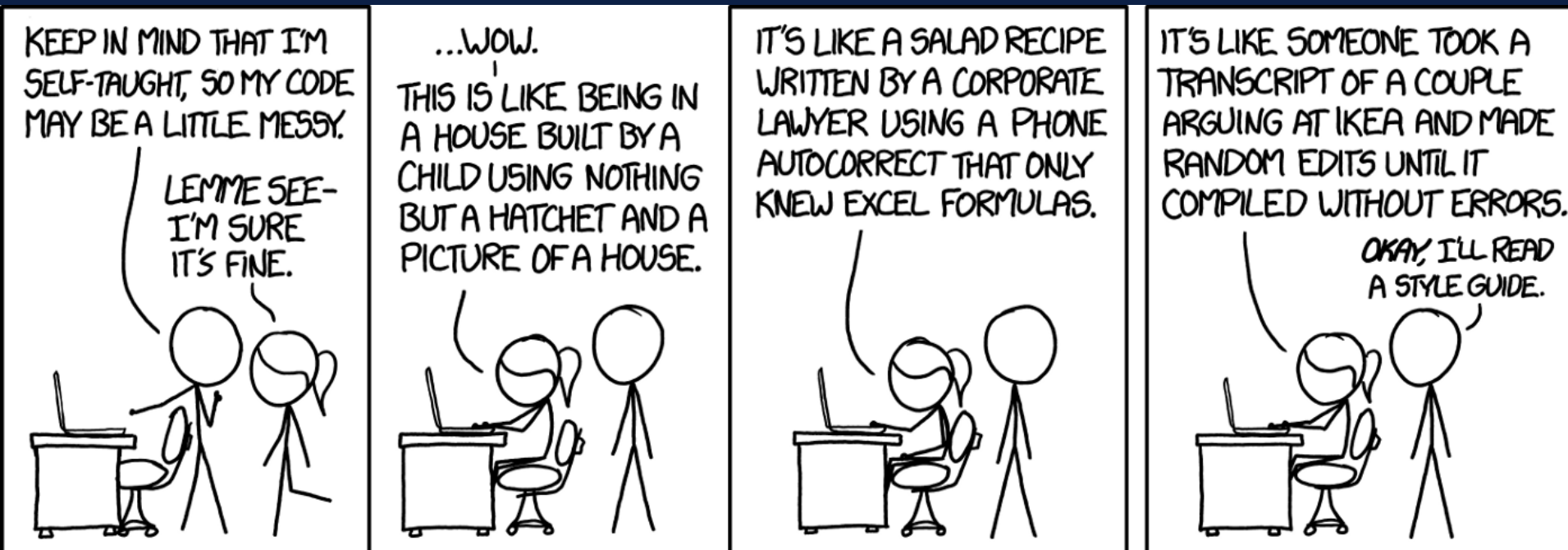
I have now worked out that this was at one point called 'legend\_handles', which then became 'leg\_hands', which then became 'feet'

sometimes I truly hate my past self

[Twitter](#)

- Use descriptive variable names, e.g. `min_age`, `ttest_rt_gender`, `alpha_level`

- Write comments (balance between helpful explanations and “wall of text”)
- Organise your code: Divide different parts into different scripts, draw repetitive elements into functions, use headings etc.



[Explain xkcd](#)

- Familiarise yourself with style guides



- SPSS syntax/Excel functions is fine!
- Reduce the amount of manual interaction with the data.
- But maybe you'll enjoy coding?

**“But it works on my machine.”**

**Be mindful of the things that are unique to your  
computer.**

```
1  
2  
3 data <-  
4   read.csv("C:/Users/julit/Documents/r_stuff/schedule_drm_batches/configs/drm_config_2022-11-12-14-37.csv")  
5  
6
```

Only exists on  
my computer!

Find the data in the folder  
“config” that lies in the same  
folder as my analysis script.

```
1  
2  
3 data <- read.csv("./configs/drm_config_2022-11-12-14-37.csv")  
4  
5
```



**If possible, switch to free software.**





**Test you analysis on a colleague's computer.**



# More advanced stuff

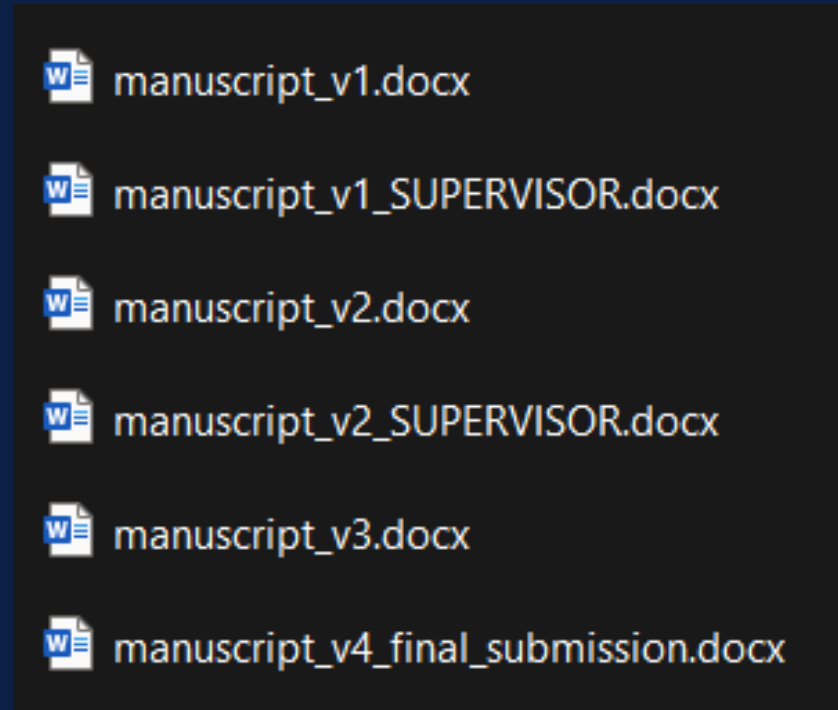
---



# Version Control

---

- Keep track of what changed in your code.
- If necessary, go back to a previous version.





git

[Get git here](#)



GitHub

[visit GitHub](#)

Projects organised  
in repositories



**Juli Nagel**  
einGlasRotwein

PhD on a quest through sleep and  
memory (and bad at both). Typo tyrant.  
Talk R to me.

Edit profile

34 followers · 56 following

Central Institute of Mental Health  
Mannheim

Overview Repositories 37 Projects Packages Stars 45

Pinned

advent\_of\_code\_2021 Public  
Solving the advent of code puzzles in R.  
R ☆ 3

r\_workshop\_pug Public  
Materials for the PUG R introductory workshop.  
HTML ☆ 1 🍷 29

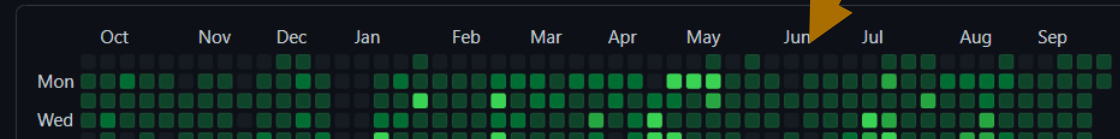
MOSM\_talk Public  
TeX ☆ 4 🍷 2

sitp Public

bits-and-pieces Public  
for sharing little pieces of code  
HTML ☆ 9 🍷 2

Nice record of how much  
code you've contributed

2,090 contributions in the last year





Different branches for “parallel versions” of your code

Keep track of all changes (“commits”) you’ve made

The screenshot shows a GitHub repository page for 'einGlasRotwein / advent\_of\_code\_2021'. The repository is public and has 1 branch (main) and 0 tags. The commit history shows a list of files and their commit messages:

| File                    | Commit Message          | Time Ago      |
|-------------------------|-------------------------|---------------|
| README_files/figure-gfm | added origami to readme | 10 months ago |
| inputs                  | stuck at day 16 part 2  | 9 months ago  |
| .gitignore              | Initial commit          | 10 months ago |
| README.Rmd              | added origami to readme | 10 months ago |
| README.md               |                         | 10 months ago |
| day01.R                 |                         | 10 months ago |
| day02.R                 |                         | 10 months ago |
| day03.R                 |                         | 10 months ago |
| day04.R                 |                         | 10 months ago |
| day05.R                 | added vent plot         | 10 months ago |

Annotations on the screenshot:

- A yellow box highlights the '48 commits' link in the commit history.
- A yellow box highlights the file list on the left side of the repository page.
- A yellow box highlights the '48 commits' link in the commit history.

A list of all the files your project contains.

# Version Control GitHub

ID of your commit – you can always go back or refer to a previous commit!

The screenshot shows a GitHub commit history page for the 'main' branch. The commits are grouped by date: Dec 23, 2021; Dec 22, 2021; and Dec 17, 2021. Each commit entry includes a description, the author's name (einGlasRotwein), the commit date, a copy icon, the commit ID, and a navigation icon. Two yellow callout boxes are overlaid on the image. The first box, at the top, points to the commit ID 'c98db95' and contains the text 'ID of your commit – you can always go back or refer to a previous commit!'. The second box, in the middle, points to the commit description 'deleted old comment' and contains the text 'Description of what you've changed and when.'.

main

Commits on Dec 23, 2021

- deleted old comment  
einGlasRotwein committed on Dec 23, 2021
- forgot to push functions for day 16  
einGlasRotwein committed on Dec 23, 2021
- completed day 17  
einGlasRotwein committed on Dec 23, 2021

Commits on Dec 22, 2021

- stuck at day 16 part 2  
einGlasRotwein committed on Dec 22, 2021
- solved part 1 day 17  
einGlasRotwein committed on Dec 22, 2021

Commits on Dec 17, 2021

- completed day 15  
einGlasRotwein committed on Dec 17, 2021



# Version Control GitHub

ID of your commit – you can always go back or refer to a previous commit!

How many files changed, how much was added/deleted.

deleted old comment

main

einGlasRotwein committed on Dec 23, 2021

Showing 1 changed file with 0 additions and 1 deletion.

1 parent dd88d50 commit c98db95af8ad4e6ebbf10c69ea60570712756509

Split Unified

```
@@ -83,7 +83,6 @@ for (i in 1:nrow(positions)) {
83   highest_y <- NA
84   y_cap <- 100
85
86 - # TO DO: CHANGE! DON'T STOP AT FIRST VALID VALUE, BUT COUNT VALID VALUES!
87   # Move until a valid position is found or y_cap is reached
88   while(y < y_cap) {
89     highest_y <- c(highest_y, move_probe(x, y, xmin, xmax, ymin, ymax))
```

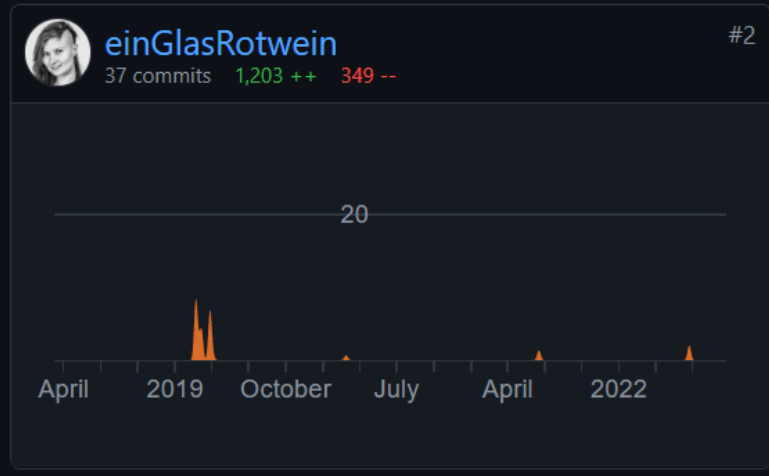
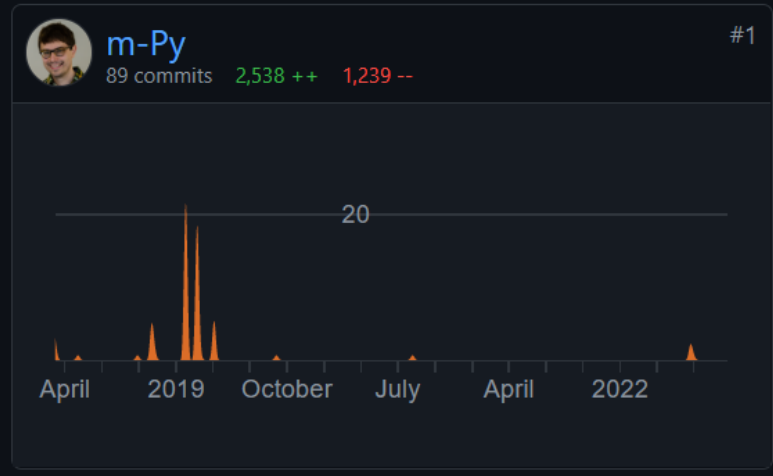
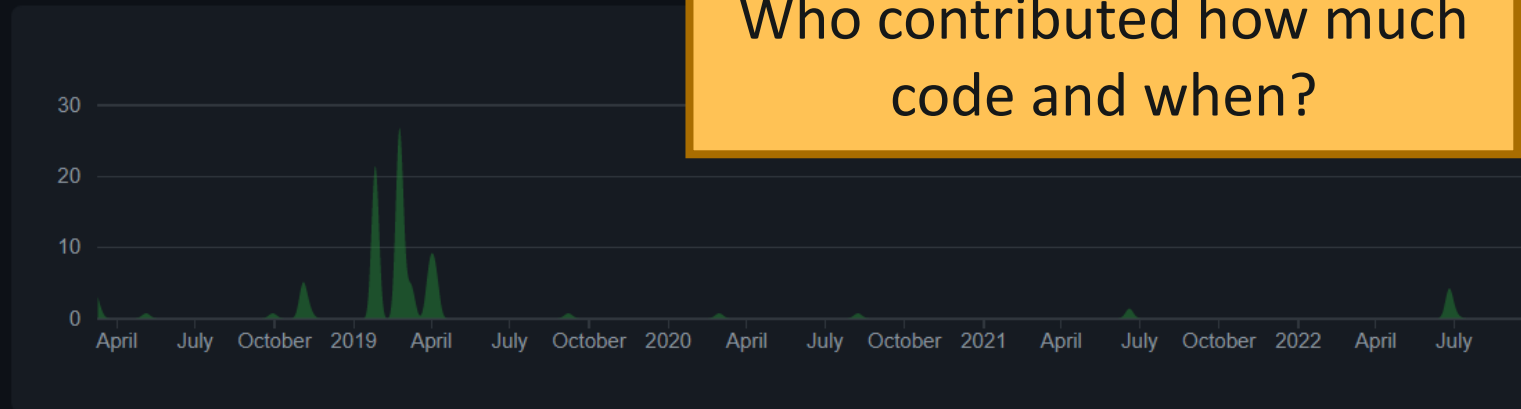
Highlights which lines of code have been added/deleted. (Here: only one line deleted.)

Mar 11, 2018 – Sep 26, 2022

Contributions: Commits ▾

Contributions to master, excluding merge commits and bot accounts

Who contributed how much code and when?





Work on the code in your own repository/branch and then ask for your changes to be implemented in the main repository/branch.

Merge pull request #19 from einGlasRotwein/master  
Replace effsize with effectsize

master (#19)

m-Py committed on Jul 4 Verified 2 parents 2d1a27e + b7515af commit 693ddd5c74b0257ace1bf0a9d61b6488aa9e7f9e

Showing 4 changed files with 37 additions and 30 deletions.

| DESCRIPTION                |                         |
|----------------------------|-------------------------|
| @@ -22,8 +22,8 @@ Depends: |                         |
| 22 R (>= 3.0.0)            | 22 R (>= 3.0.0)         |
| 23 Suggests:               | 23 Suggests:            |
| 24 afex,                   | 24 afex,                |
| 25 - effsize,              | 25 + effectsize,        |
| 26 spgs                    | 26 spgs                 |
| 27 Encoding: UTF-8         | 27 Encoding: UTF-8      |
| 28 LazyLoad: yes           | 28 LazyLoad: yes        |
| 29 - RoxygenNote: 7.1.2    | 29 + RoxygenNote: 7.2.0 |

Highlights what has been changed/deleted in your version.

# Version Control - Collaboration GitHub



Zentralinstitut für  
Seelische Gesundheit

quarto-dev / quarto-cli Public

Watch 21 Fork 99

Code Issues 396 Pull requests 6 Discussions Actions Security Insights

Filters is:issue is:open Labels 28 Milestones 5 New issue

396 Open 997 Closed Author Label Projects Milestones Assignee Sort

- Mermaid diagrams in reveal JS don't render after 2nd slide **bug**  
#2607 opened 13 hours ago by d-chambers 4 tasks done
- DOCX not rendering Latex **bug**  
#2602 opened yesterday by emstruong 4 tasks done
- PDF output does not respect Latex Line Breaks **bug**  
#2601 opened yesterday by emstruong 4 tasks done
- Several Bugs Report for the .pdf format output + doubts **bug**  
#2596 opened 2 days ago by Nicholas-R-Sheriff 4 of 5 tasks
- Conditional content does not work with latex macros **bug**  
#2580 opened 3 days ago by lcnhb Future
- Website listings - filter by category  
#2577 opened 3 days ago by kmsiello v1.3

Report bugs or request features in the “issues” section of a repository.



# Containers

---

Your code  
(scripts etc.)

packages

In whatever version  
you used (e.g. ggplot2  
3.2.1)

Software

In whatever version  
you used (e.g. R 3.6.1)



[@agenlaku from unsplash](#)

# Code Containers

## E.g. CodeOcean



Zentralinstitut für  
Seelische Gesundheit

Published MOSM\_talk (Juli Tkotz)

Capsule File Help [Sign up or login to edit and run](#) [Edit Capsule](#)

Files

- Core Files
- metadata 1.42 KB
- environment 1.98 KB
- code 2.21 MB
  - .Rproj.user 15.71 KB
  - .Rhistory 0 B
  - 00reproducible\_manuscript... 2.19 MB
  - 00reproducible\_manuscripts... 6.8 KB
  - capsule.Rproj 205 B
  - LICENSE 1.04 KB
  - README.md 1.18 KB
  - run.sh 127 B
- data Manage Datasets 6.45 MB
  - pics 2.13 MB
  - codebook.txt 4.64 KB
  - LICENSE 6.4 KB
  - nerd.csv 4.31 MB
  - rep\_manuscripts.bib 1.04 KB
  - .gitignore 40 B
- Results 2.19 MB
  - results
- Other Files 205 B
  - files

View Raw

## Reproducible Manuscripts - Mannheim Open Science Meetup

Primer on **reproducible manuscripts**, held at the Mannheim Open Science Meetup on 27th March 2020.

### Mannheim Open Science Meetup

The Mannheim Open Science Meetup is a grassroots initiative that brings together Mannheim-based academics from diverse backgrounds with a shared interest in transparent, reliable research. Scholars from all scientific disciplines are welcome, both experts and Open Science novices. Find them on [Twitter](#) or look at the slides from previous meetings at the [OSF](#).

### Reproducible Manuscripts

Reliable research involves sharing your analyses and your manuscript in a way that others can reproduce it. But how can you achieve that? I will showcase how to write up reproducible manuscripts with R Markdown. Sounds complicated and like a lot of work? Don't worry: We will also discuss how it will save you time and effort when writing your manuscript and how you can implement things like collaborative writing and citation management.

### Recording of the Talk

You can find a recording of the talk on the [OSF](#) some days after the Meetup.

Reproducible Run  
or launch a cloud workstation

Timeline

- May 28, 2020  
Published Version 2.0  
[Currently viewing](#)
- Author ran May 28, 2020 00:00:14  
Published Result
  - 00reproducible\_man... 2.19 MB
  - output 9.19 KB
- Juli Tkotz committed May 28, 2020  
Version 2.0
- May 26, 2020  
Published Version 1.0  
[Switch to this version](#)
- Author ran May 26, 2020 00:00:08  
Published Result
- Juli Tkotz committed May 26, 2020  
Version 1.0

<https://codeocean.com/capsule/0399419/tree/v2>

# Code Containers E.g. CodeOcean



Files in your  
capsule.

README to describe  
your capsule.

Run the code  
capsule online.

Keep track of  
different versions.

You can add a  
license if you want.

Output of the  
latest version.

<https://codeocean.com/capsule/0399419/tree/v2>



## Environment

### R (3.6.0 (deprecated))


R is a language and environment for statistical computing and graphics  
Ubuntu 18.04 R

Software used

## Additional Packages ?


Customize the selected environment with any other packages you need. You can also use these package managers to install other package managers, such as for different languages. Packages will be installed when you run. [Learn more.](#)

### Package Managers


apt-get  ▾

### Packages


lmodern 2.004.5-3   pandoc 1.19.2.4-dfsg-1build4   pandoc-citeproc 1.17.0-1  
rstudio-server 1.2.5033   wget 1.19.4-1ubuntu2.2   + Add

Bioconductor  ▾

+ Add

R (CRAN)  ▾

binb 0.0.5   dplyr 0.8.5   effsize 0.8.0   ggplot2 3.3.0   knitr 1.28   rmarkdown 2.1  
tinytex 0.23   + Add

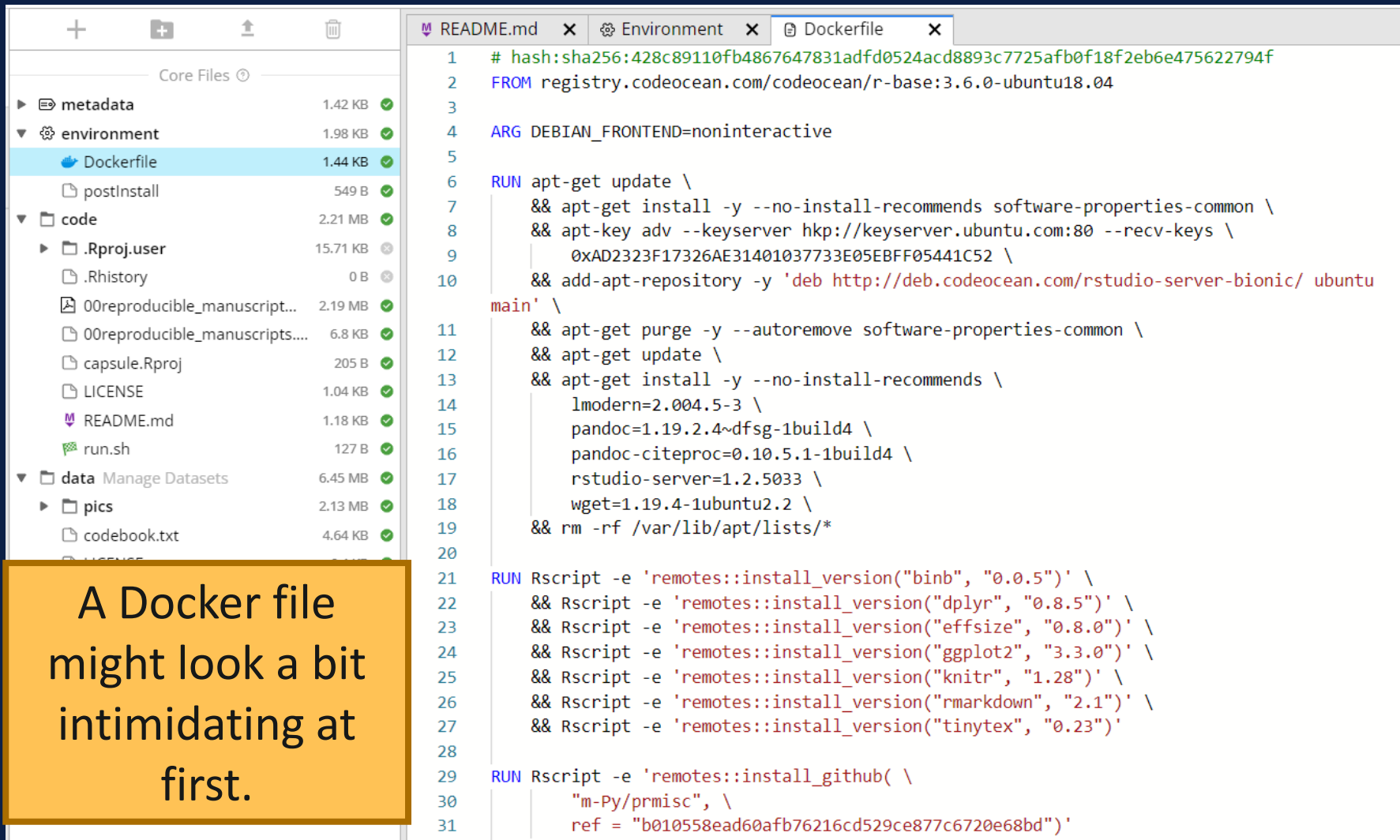
R (GitHub)  ▾

m-Py/prmisc b010558ead60afb76216cd529ce877c6720e68bd   + Add

Packages for data  
analysis and  
creating the slides  
of my presentation

- Runs entirely online.
- A bit clunky to use.
- You need to pay for more computational time.
- Probably not suitable if you thoroughly want to look at the code.

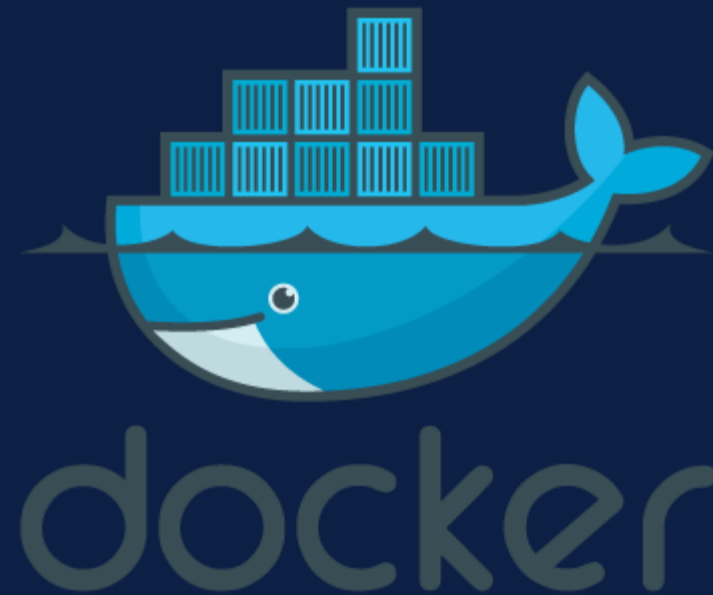
# Code Containers under the hood: Docker



A Docker file might look a bit intimidating at first.

```
1 # hash:sha256:428c89110fb4867647831adfd0524acd8893c7725afb0f18f2eb6e475622794f
2 FROM registry.codeocean.com/codeocean/r-base:3.6.0-ubuntu18.04
3
4 ARG DEBIAN_FRONTEND=noninteractive
5
6 RUN apt-get update \
7     && apt-get install -y --no-install-recommends software-properties-common \
8     && apt-key adv --keyserver hkp://keyserver.ubuntu.com:80 --recv-keys \
9     | 0xAD2323F17326AE31401037733E05EBFF05441C52 \
10    && add-apt-repository -y 'deb http://deb.codeocean.com/rstudio-server-bionic/ ubuntu
main' \
11    && apt-get purge -y --autoremove software-properties-common \
12    && apt-get update \
13    && apt-get install -y --no-install-recommends \
14    | modern=2.004.5-3 \
15    | pandoc=1.19.2.4~dfsg-1build4 \
16    | pandoc-citeproc=0.10.5.1-1build4 \
17    | rstudio-server=1.2.5033 \
18    | wget=1.19.4-1ubuntu2.2 \
19    && rm -rf /var/lib/apt/lists/*
20
21 RUN Rscript -e 'remotes::install_version("binb", "0.0.5")' \
22     && Rscript -e 'remotes::install_version("dplyr", "0.8.5")' \
23     && Rscript -e 'remotes::install_version("effsize", "0.8.0")' \
24     && Rscript -e 'remotes::install_version("ggplot2", "3.3.0")' \
25     && Rscript -e 'remotes::install_version("knitr", "1.28")' \
26     && Rscript -e 'remotes::install_version("rmarkdown", "2.1")' \
27     && Rscript -e 'remotes::install_version("tinytex", "0.23")'
28
29 RUN Rscript -e 'remotes::install_github( \
30     "m-Py/prmisc", \
31     ref = "b010558ead60afb76216cd529ce877c6720e68bd")'
```

- Widely used for containerisation.
- Let's you run different operating systems with different software versions on your computer.
- Different pre-configured “images” are available.
- <https://www.docker.com/>
- [Tutorial for beginners for R](#)
- Learning curve might be steep!



More lightweight  
e.g. renv



Zentralinstitut für  
Seelische Gesundheit

- Local environment for R
- Stores the packages you used in your project (the versions you've used)

<https://rstudio.github.io/renv/articles/renv.html>

A screenshot of the renv 0.15.5 documentation page. The page has a white background with a light blue header. The header contains the text "renv 0.15.5" on the left and navigation links "Get started", "Reference", "Articles", and "Changelog" on the right. The main content area features the title "Introduction to renv" in a large, bold, black font. Below the title, the author's name "Kevin Ushey" and the date "2022-07-07" are displayed. At the bottom left, the source is listed as "Source: vignettes/renv.Rmd". On the right side of the page, there is a hexagonal logo with a green border, containing a stylized plant and the word "renv" in a white box at the bottom.

```
03_wordpair_plots.R x 01_analysis_wordpairs.R x 02_control_analyses.R x 00_README.txt x
Source on Save Run
1
2 # This script was written in R version 4.2.0 (2022-04-22 ucrt).
3
4 # For reproducibility, the package renv can be used to create a local library
5 # that contains the packages needed to run this analysis script, in the version
6 # that was used when this script was written.
7
8 # If you opened the entire R project and want to use renv (see README
9 # option 2), uncomment and run:
10
11 # renv::restore()
12
13 # If you don't want to use renv, these are the packages used in this script
14 # (and their dependencies).
15 # Uncomment and run to install.
16
17 # if(!require(tidyverse, quietly = TRUE)) install.packages("tidyverse")
18 # if(!require(ggpubr, quietly = TRUE)) install.packages("ggpubr")
19 # if(!require(rstatix, quietly = TRUE)) install.packages("rstatix")
20
21 library(tidyverse)
22 library(ggpubr)
23 # library(rstatix) # not loaded, because cohens_d() would be overwritten
24
25 # Plot customisation
26 custom_theme <-
27   theme(
28     legend.position = "top",
11:2 (Top Level) R Script
```

```
Console Terminal Background Jobs
R 4.2.1 · C:/Users/julit/Nextcloud2/asfestani_data_code/
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

* Project 'C:/Users/julit/Nextcloud2/asfestani_data_code' loaded. [renv 0.15.4]
Registered S3 method overwritten by 'parameters':
  method          from
format.parameters_distribution datawizard
Registered S3 methods overwritten by 'effectsize':
  method          from
standardize.Surv  datawizard
standardize.bcp1m datawizard
standardize.c1m2  datawizard
standardize.default datawizard
standardize.mediate datawizard
standardize.wbgee datawizard
standardize.wbm   datawizard
```

Environment History Connections Tuto

Import Dataset 522 M

R Global Environment

Files Plots Packages Help Viewer

New Folder New Blank File

C:/Users/julit/Nextcloud2/asfes

Name

- ..
- .Rhistory
- .Rprofile
- 00\_README.txt
- 01\_analysis\_wordpairs.R
- 02\_control\_analyses.R
- 03\_wordpair\_plots.R
- asfestani\_codebook.txt
- asfestani\_data\_code.Rproj
- asfestani\_data\_set.csv
- renv
- renv.lock

```
1  
2 # This script was written in R version 4.2.0 (2022-04-22 ucrt).  
3  
4 # For reproducibility, the package renv can be used to create a local library  
5 # that contains the packages needed to run this analysis script, in the version  
6 # that was used when this script was written.  
7  
8 # If you opened the entire R project and (option 1) you want to use the local library (option  
9 # option 2), uncomment and run:  
10  
11 # renv::restore()  
12  
13 # If you don't want to use renv, these lines can be commented out.  
14 # (and their dependencies).  
15 # Uncomment and run to install.  
16  
17 # if(!require(tidyverse, quietly = TRUE)) install.packages("tidyverse")  
18 # if(!require(ggpubr, quietly = TRUE)) install.packages("ggpubr")  
19 # if(!require(rstatix, quietly = TRUE)) install.packages("rstatix")  
20  
21 library(tidyverse)  
22 library(ggpubr)  
23 # library(rstatix) # not loaded, because cohens_d() would be overwritten  
24  
25 # Plot customisation  
26 custom_theme <-  
27   theme(  
28     legend.position = "top",
```

Others can recreate my package library by running `renv::restore()`

Lets me know a local package library has been loaded using `renv`.

renv folder with all the relevant files/information about my local library.

```
11:2 (Top Level) :-  
  
Console Terminal Background Jobs ×  
R 4.2.1 · C:/Users/julit/Nextcloud2/asfestani_data_code/ ↗  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
* Project 'C:/Users/julit/Nextcloud2/asfestani_data_code' loaded. [renv 0.15.4]  
Registered S3 method overwritten by 'parameters':  
  method from  
  format.parameters_distribution datawizard  
Registered S3 methods overwritten by 'effectsizer':  
  method from  
  standardize.Surv datawizard  
  standardize.bcplm datawizard  
  standardize.clm2 datawizard  
  standardize.default datawizard  
  standardize.mediate datawizard  
  standardize.wbgee datawizard  
  standardize.wbm datawizard
```

- asfestani\_data\_code.Rproj
- asfestani\_data\_set.csv
- renv
- renv.lock



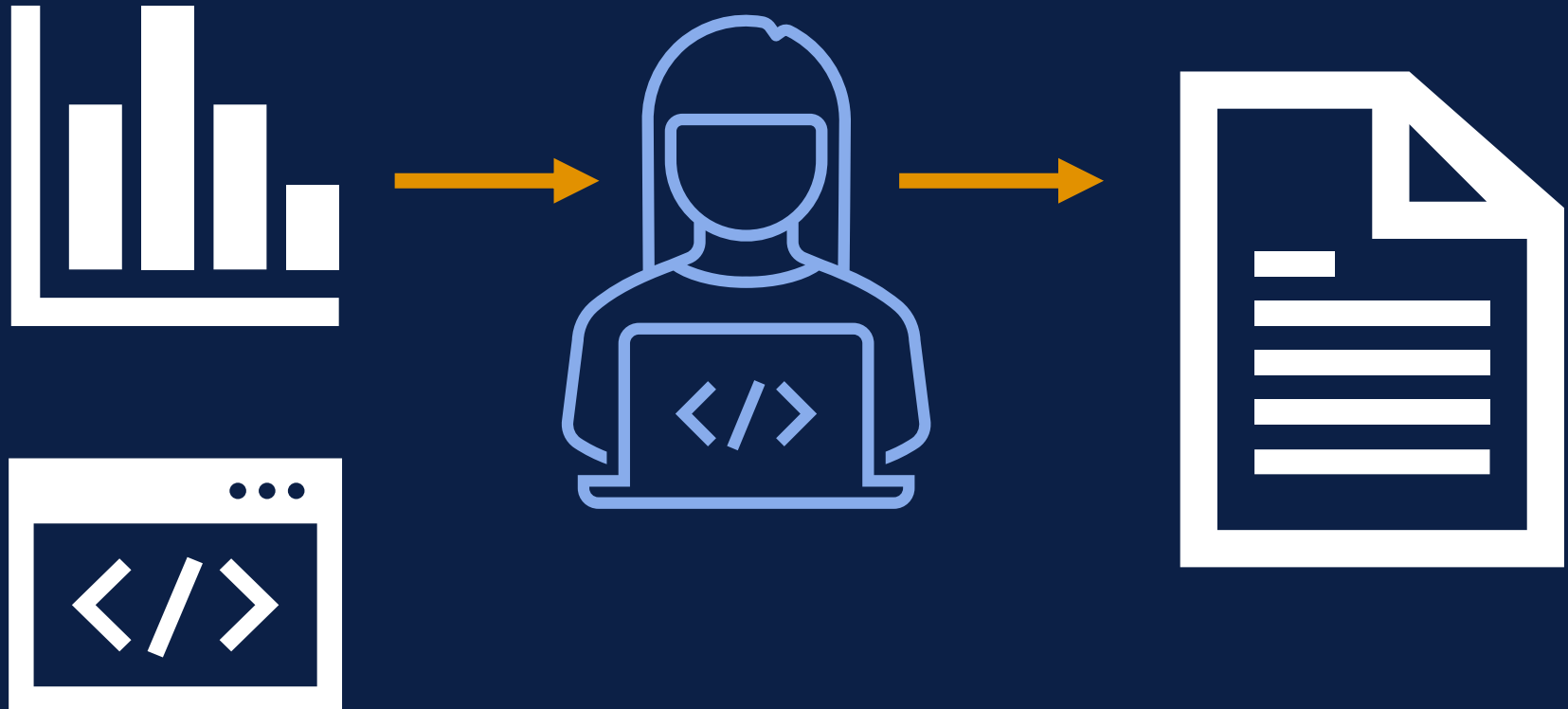
- Problem: Steep learning curve
- Most solutions put a least some burden on the recipient of your code





# Reproducible manuscripts

---



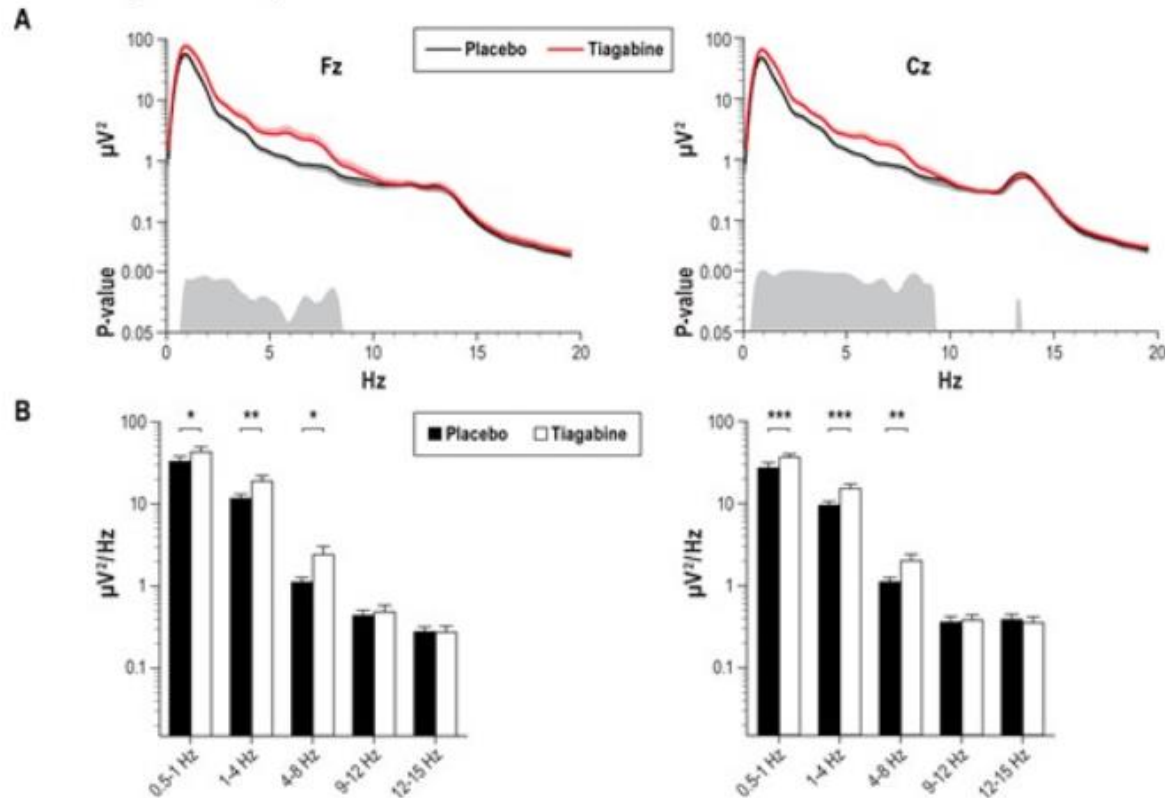


For the sequence finger tapping task, the overnight gain expressed by the difference of correctly tapped sequences at recall minus performance at learning was significantly reduced by tiagabine (tiagabine: 2.50 [0.5] Placebo: 5.03 [1.17],  $F_{1,11} = 5.58$ ,  $P \leq 0.05$ , Figure 1C). At learning, the number of correctly tapped sequences did not differ significantly between the treatment conditions (tiagabine: 18.19 [1.56], placebo: 16.83 [1.13],  $t_{11} = -1.54$ ,  $P = 0.15$ ). Also, tapping on the control sequence did not reveal any difference between the tiagabine and placebo conditions ( $t_{11} = 0.47$  and  $P = 0.65$ ). Error rates were variable, and there was a trend toward error rates reducing more across sleep in the placebo condition, i.e., participants made fewer errors in the placebo condition (mean reduction in error rate tiagabine: -1.01% [1.25], placebo: -4.47% [3.25],  $t_{11} = 1.91$ ,  $P = 0.08$ ).

Feld et al. (2013), *Sleep*

Figure 2

Power during NonREM sleep



Feld et al. (2013), *Sleep*

**Table 1** Sleep parameters and control measures

| Measure           | Minutes        |                |    |
|-------------------|----------------|----------------|----|
|                   | Placebo        | Tiagabine      |    |
| Wakefulness       | 20.41 (4.98)   | 14.90 (2.53)   | ns |
| Stage 1           | 37.50 (4.86)   | 19.31 (5.41)   | ** |
| Stage 2           | 240.05 (11.44) | 236.68 (16.89) | ns |
| SWS               | 63.68 (5.91)   | 98.95 (11.91)  | ** |
| REM               | 77.55 (4.44)   | 55.86 (9.62)   | *  |
| Movement time     | 4.18 (0.84)    | 3.27 (0.54)    | ns |
| Total sleep time  | 443.45 (12.57) | 429.00 (26.50) | ns |
| Sleep latency     | 24.91 (12.46)  | 24.09 (4.94)   | ns |
| SWS latency       | 23.82 (4.27)   | 16.68 (2.34)   | †  |
| REM sleep latency | 115.50 (10.23) | 136.27 (35.33) | ns |

Feld et al. (2013), *Sleep*

```
1 ---
2 title: "Quarto Example"
3 format: html
4 editor: visual
5 ---
6
7 |
8
```

## Quarto Example

### This is a headline

---

Here is some example text. Let's write some more stuff. This is another example.

### Here comes another headline

---

And here is some additional text.

```
16
17 ▾ ## Stuff about flowers
18
19 The iris species "Setosa" has rather small petals (width M = `r
round(mean(iris$Petal.Width[iris$Species == "setosa"]), 2)`), SD = `r
round(sd(iris$Petal.Width[iris$Species == "setosa"]), 2)`), while those of the species
"Versicolor" are larger (width M = `r round(mean(iris$Petal.Width[iris$Species ==
"versicolor"]), 2)`), SD = `r round(sd(iris$Petal.Width[iris$Species == "versicolor"]), 2)`).
20
```

## Stuff about flowers

The iris species "Setosa" has rather small petals (width  $M = 0.25$ ,  $SD = 0.11$ ), while those of the species "Versicolor" are larger (width  $M = 1.33$ ,  $SD = 0.2$ ).



# Reproducible manuscripts

## Examples

Function that prints a t-test from the R package [prmisc](#)

```
```{r}
iris_ttest <-
  t.test(
    iris$Petal.Length[iris$Species == "setosa"],
    iris$Petal.Length[iris$Species == "versicolor"]
  )

iris_cohens_d <-
  cohens_d(
    iris$Petal.Length[iris$Species == "setosa"],
    iris$Petal.Length[iris$Species == "versicolor"]
  )
```
```

That's a pretty big difference ``r print_ttest(iris_ttest, iris_cohens_d)``.

## Stuff about flowers

The iris species "Setosa" has rather small petals (width  $M = 0.25$ ,  $SD = 0.11$ ), while those of the species "Versicolor" are larger (width  $M = 1.33$ ,  $SD = 0.2$ ).

That's a pretty big difference  $t(62.14) = -39.49$ ,  $p < .001$ ,  $d = -7.90$ .

```
### A table about flowers
```

```
```{r}
iris %>%
  group_by(Species) %>%
  summarise(
    across(
      Sepal.Length:Petal.Width,
      ~paste0(force_decimals(mean(.), 2), " (" , force_decimals(mean(.), 2), ")")
    )
  ) %>%
  kable() %>%
  kable_styling("striped")
```
```

Styling tables with  
[kableExtra](#)

### A table about flowers

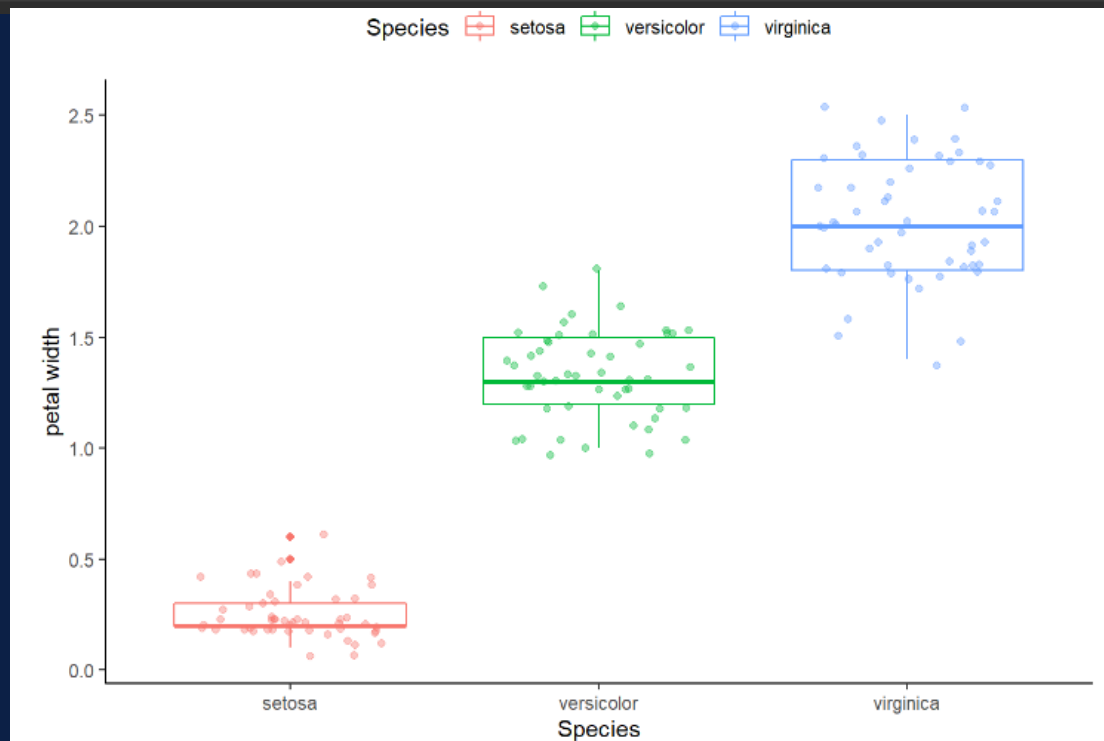
| Species    | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|------------|--------------|-------------|--------------|-------------|
| setosa     | 5.01 (5.01)  | 3.43 (3.43) | 1.46 (1.46)  | 0.25 (0.25) |
| versicolor | 5.94 (5.94)  | 2.77 (2.77) | 4.26 (4.26)  | 1.33 (1.33) |
| virginica  | 6.59 (6.59)  | 2.97 (2.97) | 5.55 (5.55)  | 2.03 (2.03) |

# Reproducible manuscripts

## Examples



```
```{r}
iris %>%
  ggplot(aes(x = Species, y = Petal.Width, colour = Species)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = .3), alpha = .4) +
  theme_classic() +
  labs(y = "petal width") +
  theme(legend.position = "top")
```
```



# Quarto Example

## This is a headline

---

Here is some example text. Let's write some more stuff. This is another example.

## Here comes another headline

---

And here is some additional text.

## Stuff about flowers

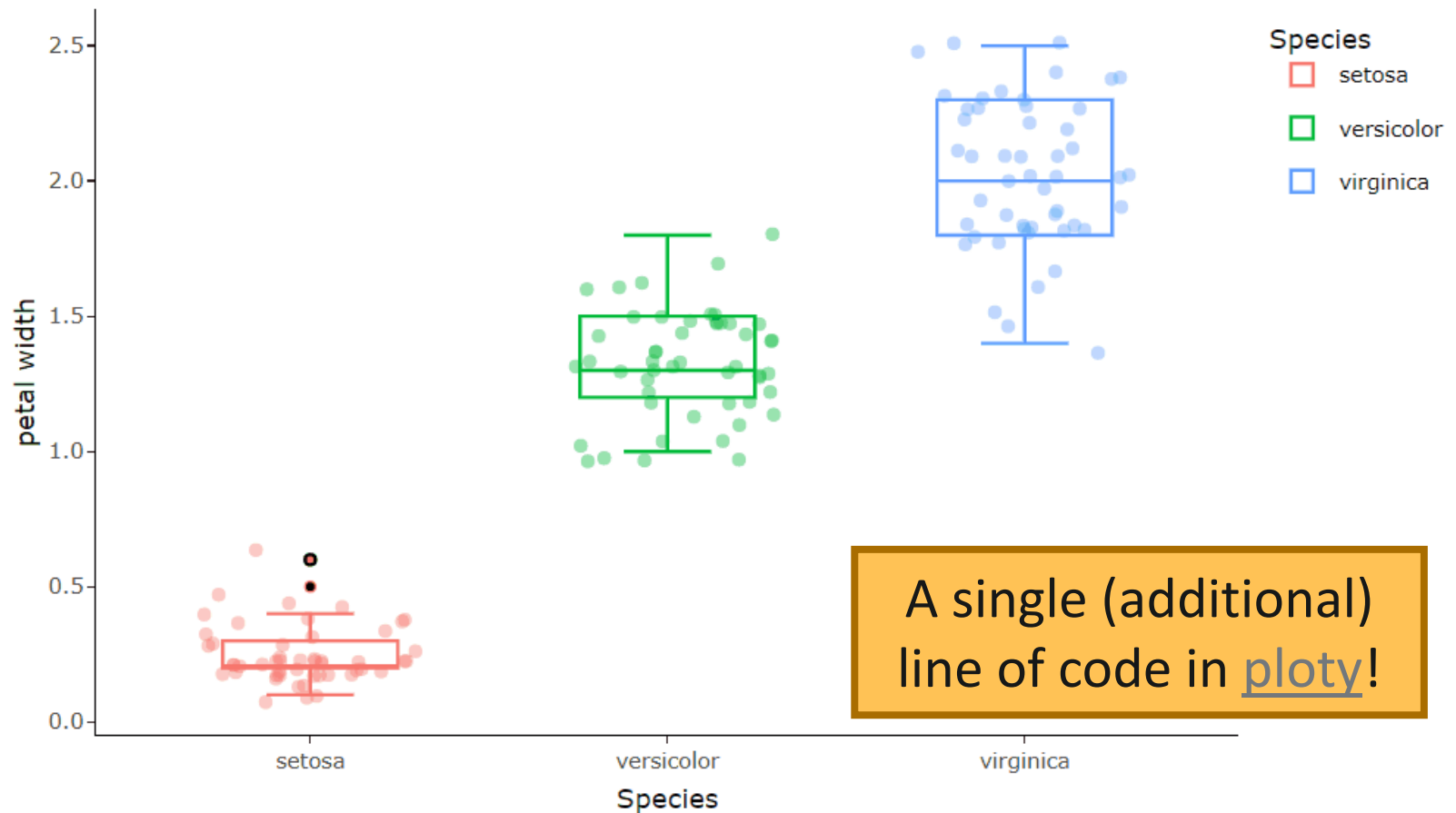
---

The iris species "Setosa" has rather small petals (width  $M = 0.25$ ,  $SD = 0.11$ ), while those of the species "Versicolor" are larger (width  $M = 1.33$ ,  $SD = 0.2$ ).

That's a pretty big difference  $t(62.14) = -39.49$ ,  $p < .001$ ,  $d = -7.90$ .

## A table about flowers

### An interactive plot about flowers



# Reproducible manuscripts

## Examples



The screenshot displays the Quarto editor interface. The main editor shows the following R code:

```
iris %>%  
  ggplot(aes(x = Species, y = Petal.width, colour = Species)) +  
  geom_boxplot() +  
  geom_point(position = position_jitter(width = .3), alpha = .4) +  
  theme_classic() +  
  labs(y = "petal width") +  
  theme(legend.position = "top")  
iris_plot
```

Below the code, the rendered output is shown, including a headline, a plot, and a table. The plot is titled "An interactive plot about flowers".

The right sidebar shows a file explorer with the following files:

- ..
- .gitignore
- .Rhistory
- adcock\_payment.R
- bib\_files
- cairo\_test.html
- cairo\_test.pdf
- cairo\_test.Rmd
- cairo\_test2\_files
- cairo\_test2.pdf
- cairo\_test2.Rmd
- cairo\_test2.tex
- calculate\_prolific\_payment.R
- check\_mid.R
- commit\_tree.R
- confidence\_intervals.csv
- csv\_metadata.R
- dirty\_data\_set.R
- dirty\_data.csv
- distribute\_stimuli.R
- examples\_marsxp.R
- exploratory\_confirmatory.R
- false\_memory\_power\_idk.R
- fremt\_calculations\_functions.R
- fremt\_calculations.R
- generate\_sql\_table.R
- ggplots\_kplus.R

The bottom console shows the R terminal output for the code execution:

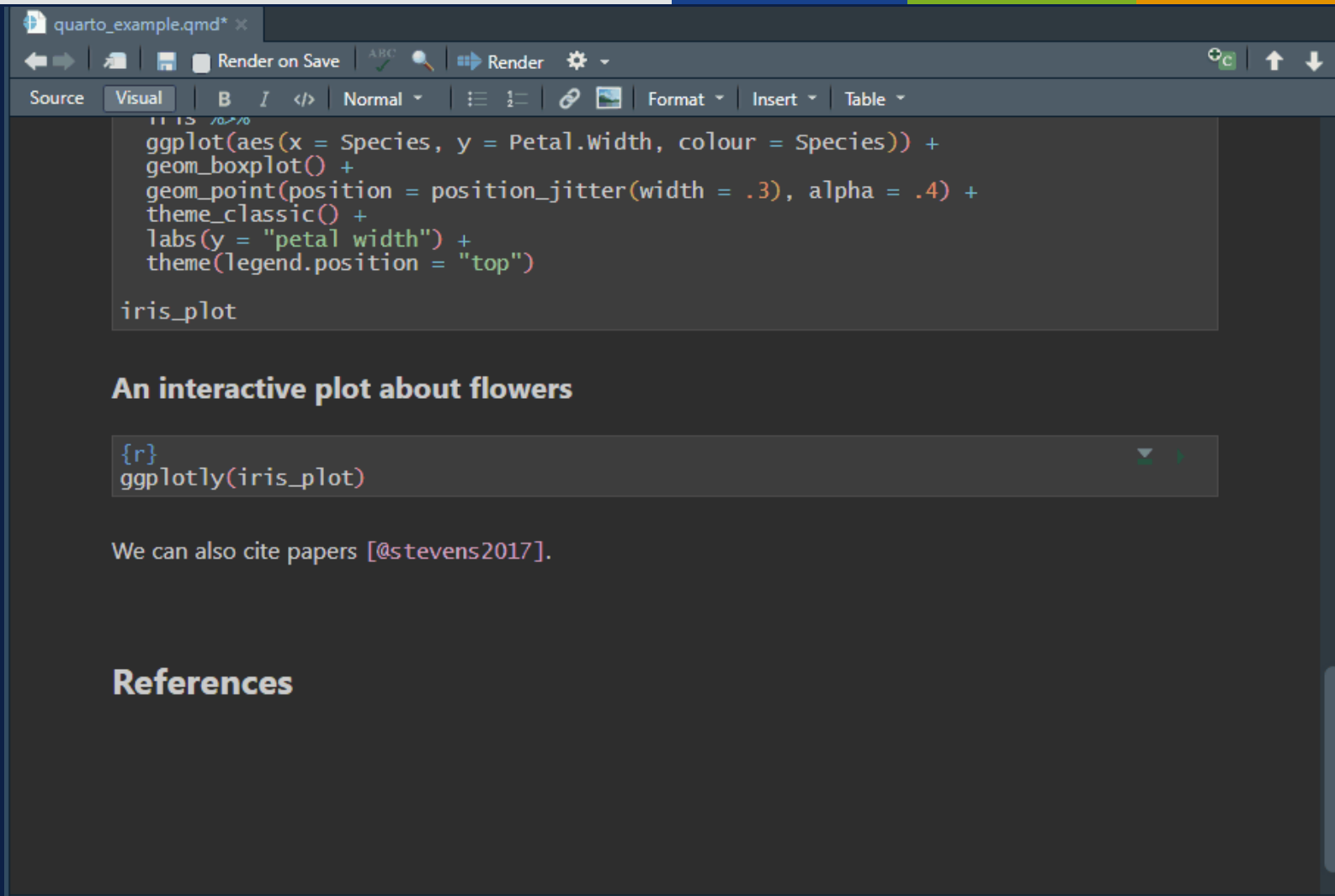
```
R 4.2.1 ~/_r_stuff/Julie-goes-PhD/  
The downloaded binary packages are in  
  C:\Users\julit\AppData\Local\Temp\RtmpaupZOY\downloaded_packages  
> iris_plot <-  
+   iris %>%  
+   ggplot(aes(x = Species, y = Petal.width, colour = Species)) +  
+   geom_boxplot() +  
+   geom_point(position = position_jitter(width = .3), alpha = .4) +
```



We can also cite papers (Stevens 2017).

### References

Stevens, Jeffrey R. 2017. "Replicability and Reproducibility in Comparative Psychology." *Frontiers in Psychology* 8 (May). <https://doi.org/10.3389/fpsyg.2017.00862>.



The screenshot shows a Quarto editor window with the following content:

```
quarto_example.qmd* x
Render on Save
Render
Source Visual B I </> Normal Format Insert Table
ggplot(aes(x = Species, y = Petal.Width, colour = Species)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = .3), alpha = .4) +
  theme_classic() +
  labs(y = "petal width") +
  theme(legend.position = "top")

iris_plot
```

### An interactive plot about flowers

```
{r}
ggplotly(iris_plot)
```

We can also cite papers [[@stevens2017](#)].

### References



## Articles & Reports

Write a single markdown file and create output in a variety of formats.

### HTML for web publishing

Interactivity

You can also add interactive plots. For example:

```
library(ggplot2)
dymaps(loszsp) %>%
  dyRangeSelector(dateMinIndex = c("1920-01-01", "1920-01-01"))
```

Figure 2: New Haven Temperatures

### PDF for high quality print

**Your Logo**

## The SocioEconomic Aspects of Stock Assessments

Recommendations for Increasing Assessment Accuracy and Improving Management Advice

Jane Doe<sup>1,2</sup>, Eva Nováková<sup>3</sup>, Matti Meikäläinen<sup>4\*</sup> and Ashok Kumar<sup>2,5</sup>

1. Minnesota Department of Natural Resources, 500 Lafayette Road Saint Paul, MN 55155
2. University of Minnesota, Department of Mathematics
3. Czech University of Life Sciences, Dražbovská 666, Věžeňovice, Czechia
4. University of Jyväskylä, Department of Biological and Environmental Sciences, Kytimiesentie 79, 98120, KEMILJÄRVI, Finland
5. ...

### MS Word for Office workflows

```
import numpy as np
import matplotlib.pyplot as plt

r = np.arange(0, 2, 0.01)
theta = 2 * np.pi * r
fig, ax = plt.subplots(subplot_kw={'projection': 'polar'})
ax.plot(theta, r)
ax.set_ticks([0.5, 1, 1.5, 2])
ax.grid(True)
plt.show()
```

Figure 1: A line plot on a polar axis

- Quarto supports multiple languages, e.g. Python, R, Julia, and Observable.
- Loads of different output formats with the same code (html, pdf, presentations etc.).

This is an executable code view. [See the original article.](#)

▶ RUN DOCUMENT

🔗 SOURCE



## Replication Study: Transcriptional amplification in tumor cells with elevated c-Myc



L Michelle Lewis, Meredith C Edwards, Zachary R Meyers, C Conover Talbot, Haiping Hao, David Blum, Reproducibility Project: Cancer Biology, Elizabeth Iorns, Rachel Tsui, Alexandria Denis, Nicole Perfito, Timothy M Errington

University of Georgia, Bioexpression and Fermentation Facility, Georgia, United States; Johns Hopkins University, Deep Sequencing and Microarray Core Facility, Maryland, United States; Science Exchange, Palo Alto, United States; Center for Open Science, Charlottesville, United States

Jan 9, 2018

## Induction of c-Myc in P493-6 cells and impact on total RNA levels.

P493-6 cells were grown in the presence of tetracycline (Tet) for 72 hr and switched into Tet-free growth medium to induce c-Myc expression. Cells were cultured in two separate lots of serum. **(B)** Quantification of total RNA levels (ng of total RNA per 1,000 cells) for cells at 0, 1, and 24 hr after release from Tet. Means reported and error bars represent s.e.m. from 3 independent biological repeats. For serum lot one, one-way ANOVA on total RNA levels of all groups;  $F(2, 6) = 1.25$ ,  $p = .353$ . Planned contrast between 0 hr and 24 hr;  $t(6) = 1.02$ ,  $p = .347$  with a priori alpha level = .05. For serum lot two, one-way ANOVA on total RNA levels of all groups;  $F(2, 6) = 21.87$ ,  $p = .00176$ . Planned contrast between 0 hr and 24 hr;  $t(6) = 5.03$ ,  $p = .0024$  with a priori alpha level = .05. Additional details for this experiment can be found at <https://osf.io/tfd57/>.

## Total RNA levels following c-Myc overexpression

We sought to independently replicate whether increased levels of c-Myc resulted in increased absolute levels of RNA. This experiment is similar to what was reported in Figure 3E of (Lin et al. 2012) and used the same extraction method for total RNA quantification.





---

# HOWEVER ...

---

- Especially when rendering PDFs (likely using a Latex engine), you run into all sort of error messages that are sometimes very frustrating to debug.



The screenshot shows a collaborative writing interface. At the top, a file named '01\_example\_introduction.Rmd' is open. The main area displays a diff view of text. Line 15: 'Fusce posuere, magna sed pulvinar ultricies, purus lectus malesuada libero, sit'. Line 16: 'Fusce est.'. Line 17: 'Vivamus a tellus.'. Line 18: '- Pellentesque habitant morbi tristique \*test\* senectus et netus et malesuada fames ac turpis egestas. Proin pharetra nonummy pede.' The diff shows a change from a red background (deletion) to a green background (addition). The addition is '+ Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Proin pharetra nonummy pede.' Below the diff view is a comment box with a 'Write' tab selected. The comment text is 'I deleted this!'. The comment box also contains a toolbar with icons for bold, italic, link, and other text formatting options. At the bottom of the comment box are 'Cancel' and 'Add single comment' buttons.

There is no real equivalent of the “track changes” in Word that many people use. We use GitHub as a substitute, but that requires that all people involved know how to use reproducible manuscripts and GitHub ...



# Downsides?

---



---

# Discussion: Do we need reproducibility? (Or rather: Is it worth the effort?)

---

Thank you. Stay reproducible.

[juliane.nagel@zi-mannheim.de](mailto:juliane.nagel@zi-mannheim.de)

