

Reproducible Research in R

How to do the same thing more than once

Andreas Brandmaier

University of Leipzig | 2024-09-23

Please ask questions anytime



Reproducible Research

=

same data + same analysis

=

same results

Why should we work reproducibly?

Why should we work reproducibly?

Many good reasons like

- Transparency
- Trustworthiness
- Replication

Transparency and accessibility are central scientific values, and open, reproducible projects will increase the efficiency and veracity of knowledge accumulation (Bar-Anan and Nosek, 2012).

Your closest collaborator is you six months ago, but you don't reply to emails.

From Karl Broman's lecture on reproducibility, paraphrasing Mark Holden

What should be reproducible?

Everything

(Almost) Everything

Statistical Data Analysis

- Replication attempt of articles in journal *Cognition* (Hardwicke, Mathur, MacDonald, Nilsonne, Banks, Kidwell, Hofelich Mohr, Clayton, Yoon, Henry Tessler, and others, 2018)
- Out of 35 published articles with open code and data, the results of 22 articles could be reproduced,
- Further assistance from the original authors was required in 11 cases
- For 13 articles, at least one outcome could not be reproduced—even with the original authors' assistance.

Statistical Data Analysis

- in 62 registered reports only 41 had data available, and 37 had analysis scripts available (Obels, Lakens, Coles, Gottfried, and Green, 2020).
- The authors could execute only 31 of the scripts without error
- They reproduced the results of only 21 articles (within a reasonable time).
- Lesson: Just because it's open data/code, it's not necessarily useful

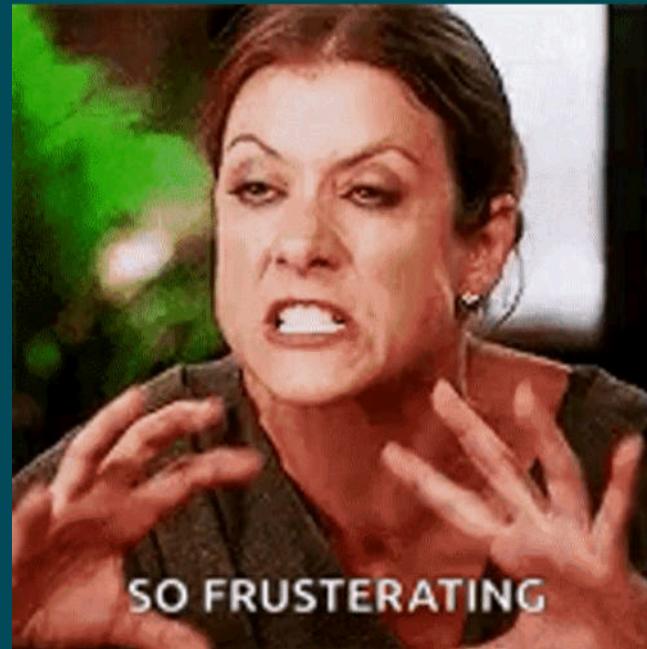
Power Analysis

Reproducibility of power analyses (Thibault, Zavalis, Malički, and Pedder, 2024):

- 2% reproduced
- (likely) 28% reproduced with additional assumptions
- 75% not reported transparently enough to assess reproducibility (e.g., unclear whether power analysis matches later statistical analysis)

**Me: Reproducible research is
conceptually very simple**

Also me:



in practice

KAPWING

Meme by Aaron Peikert

Also reproducible research:



KAPWING

Rule 1: Make it portable & keep your stuff together!

Always avoid absolute file paths. (e.g., `setwd()`)

Probably (*not*) a good idea to add this to your user-wide `.Rprofile` (`usethis::edit_r_profile()`):

```
setwd <- function(...) { stop("Bad boy!")}
```

```
setwd("C:/Users/brandmaier/SOEP")
```

| Error in `setwd()`: Bad boy!

Use projects and here

Use RStudio and *R projects* instead

The command **here** retrieves files relative to project root

```
here("data/soep.csv")
```

```
## [1] "C:/Users/andreas.brandmaier/LokaleDokumente/GitHub/reproducibility_workshop/data/soep.csv"
```

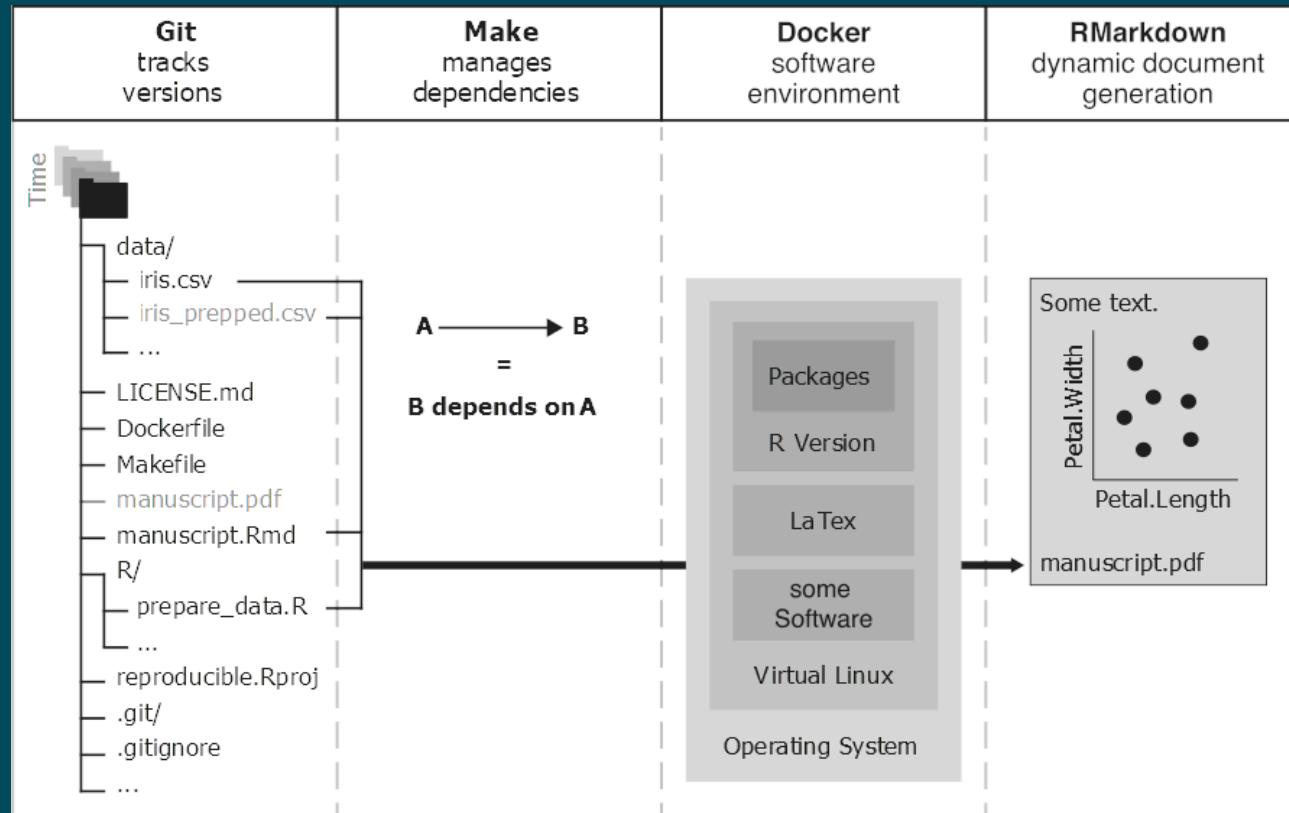
Project should be self-contained

Sources of Failure to Reproduce Results

1. **Multiple versions of scripts/data** (e.g., dataset has changed over, i.e., was further cleaned or extended)
2. **Multiple scripts** in a pipeline; unclear which scripts should be executed in which order
3. **Copy&paste errors** (e.g., inconsistency between reported result and reproduced result)
4. Broken **software dependencies** (e.g., analysis broken after update, missing package, just comes out differently on a different computer)



Four Elements of Reproducibility



from Peikert and Brandmaier (2020)

Version Control

Okay everyone, now listen carefully.
I don't want to end up with 4 different versions of this!



Problem: Multiple versions of scripts/data

Version control

manuscript_revised.docx

manuscript_revised_final.docx

manuscript_revised_final_commentsAB.docx

manuscript_revised_final_commentsAB_final.docx

Version control in a nutshell

Version 1 → Version 2 → Version 3 → Current

+

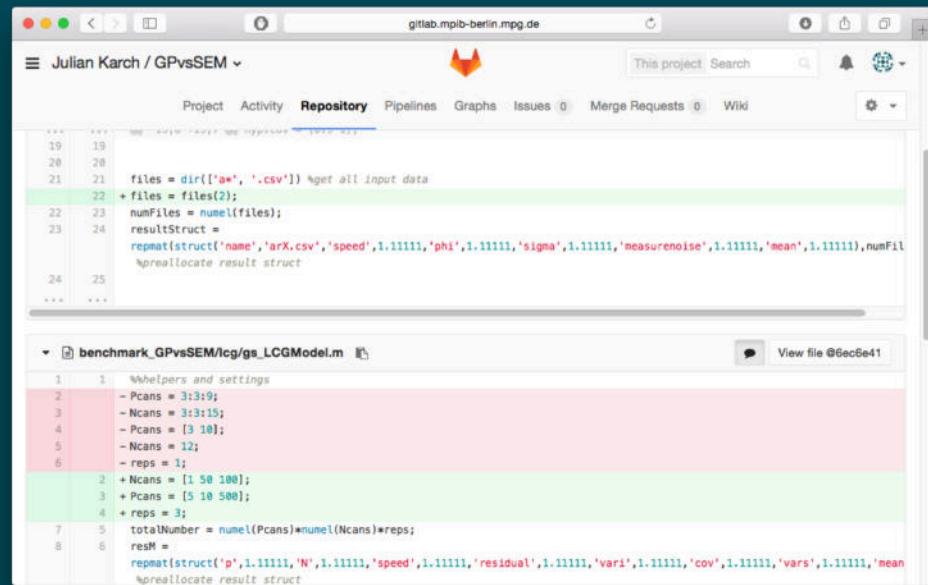
Time travel

+

Change detection

Version Control

- Version control systems (VCS) such as `git` record changes to a set of files over time; restore specific versions later.
- VCS guarantee that code and data are exactly the same version as used for publication.
- Allows collaboration and track-changes



The screenshot shows a GitLab project interface for 'Julian Karch / GPvsSEM'. The 'Repository' tab is selected. A code diff is displayed between two commits. The top commit (green background) contains lines 19 through 25 of a MATLAB script. Lines 22 and 23 have '+' signs added before them, indicating new code. The bottom commit (pink background) contains lines 1 through 8 of the same script, also with '+' signs added to lines 2, 3, 4, and 5, indicating changes made to the helper variables.

```
19: %get all input data
20: files = dir(['a*', '.csv']);
21: %get all input data
22: + files = files(2);
23: numFiles = numel(files);
24: resultStruct =
25: repmat(struct('name','arX.csv','speed',1.11111,'phi',1.11111,'sigma',1.11111,'measurenoise',1.11111,'mean',1.11111),numFil
...
1: %helpers and settings
2: - Pcams = 3:3:9;
3: - Ncams = 3:3:15;
4: - Pcams = [3 10];
5: - Ncams = 12;
6: - reps = 1;
7: + Ncams = [1 50 100];
8: + Pcams = [5 10 500];
9: + reps = 3;
10: totaNumber = numel(Pcams)*numel(Ncams)*reps;
11: resh =
12: repmat(struct('p',1.11111,'N',1.11111,'speed',1.11111,'residual',1.11111,'vari',1.11111,'cov',1.11111,'vars',1.11111,'mean
...
%preallocate result struct
```

Collaborative editing

- Multiple authors can **commit** changes to their local repositories and **push** (synchronize) with a central repository (automated merge of non-conflicting changes)
- Authors can work on separate branches, which can be merged later (e.g., **pull request** with mandatory **review**)
- Authors can **fork** (clone) the entire repository
- Added value in some systems (issues, project management, ...)

[Edit](#)

v0.2.0-submission



Releases on github.com

[Compare ▾](#)

This is the release to the third version of the preprint and resubmission.

Assets 4

	manuscript.pdf	562 KB
	reproducible-research.tar.gz	1.06 GB
	Source code (zip)	
	Source code (tar.gz)	

[Edit](#)

v0.1.1-submission

-o d840bf1

[Compare ▾](#)

Submission

R aaronpeikert released this on 12 Nov 2019 · 134 commits to master since this release

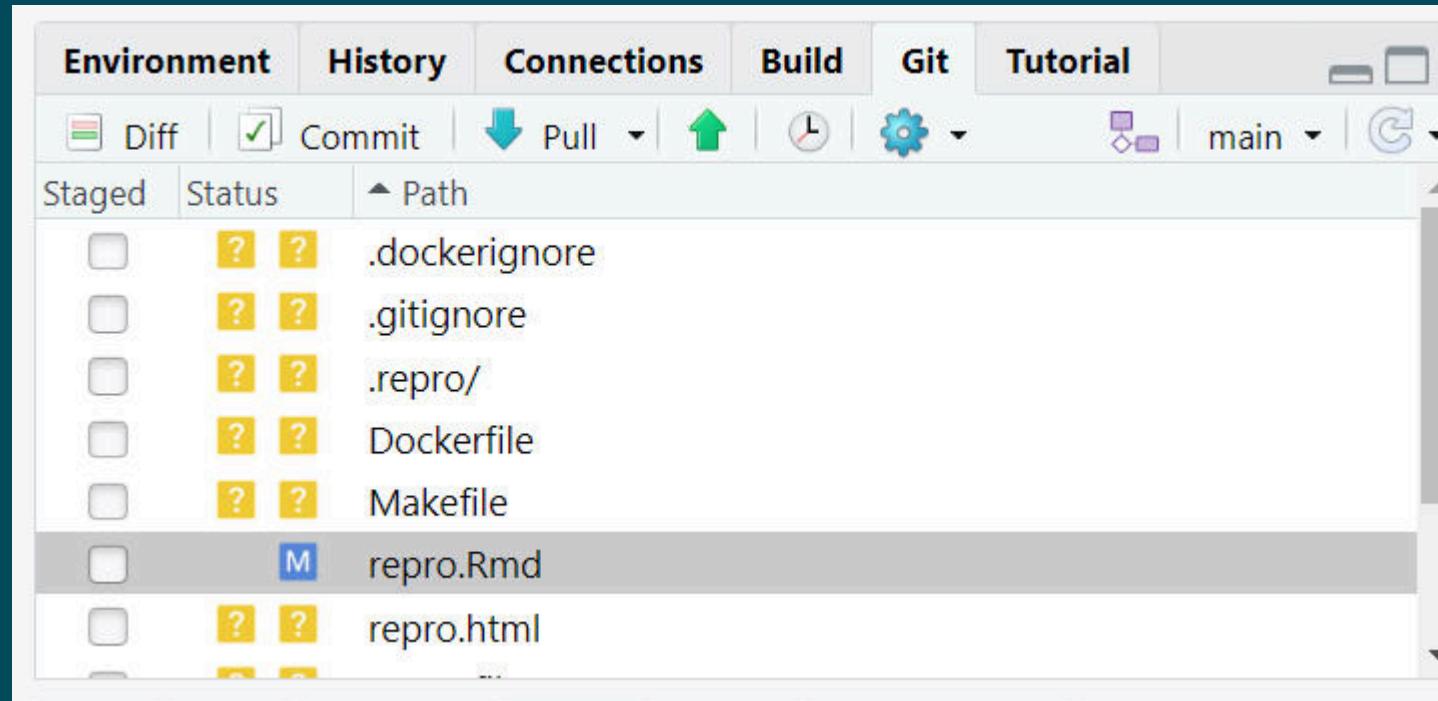
This is the release to the second version of the preprint and submission.

Assets 4

Long-Term Storage

- GitHub has no long-term guarantees for the availability of its service
- even though they do [LOCKSS](#) (for Lots Of Copies Keeps Stuff Safe, e.g., the Arctic World Archive)
- Mirror snapshots with meta-data and DOI to other providers (e.g., Zenodo, FigShare, [OSF via plugin](#))
- This helps making the repository (F)indable (as in FAIR)

In RStudio

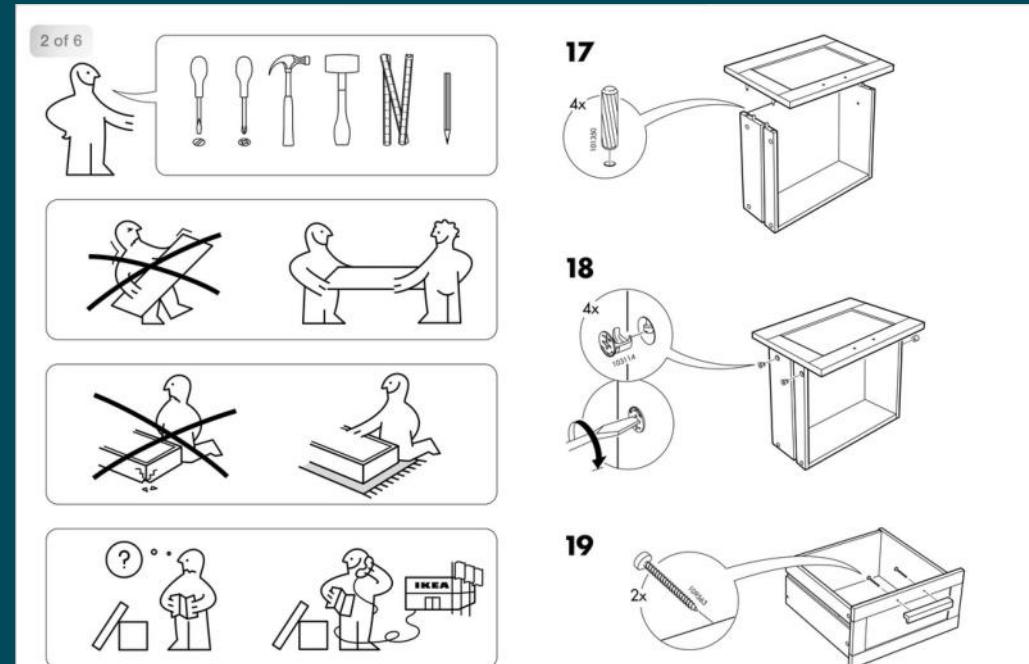


Dependency Management



Problem

Once someone found our files...
which of those files are executable
and in which order are they to be
executed?



What's cooking?

Arrabbiata sauce, or sugo all'arrabbiata in Italian, is a spicy **sauce** for **pasta** made from **garlic**, **tomatoes**, and dried red **chili** peppers cooked in olive oil.

"Arrabbiata sauce" from Wikipedia under CC BY-SA 3.0, emphasis added

1. Bring 6 quarts of **water** to a boil in a large pot, and add 3 tablespoons **kosher salt**.
2. Meanwhile, put 4 tablespoons **olive oil** in a large sauté pan over medium heat, [...]

Source: cooking.nytimes.com

Solution: GNU Make

A Makefile

- contains a number of recipes
- Each recipe contains its ingredients (=dependencies) and commands to create the product
- There is a default recipe (defined entry point)
- By convention, there is an „all“ recipe to create everything
- Recipes can depend on other recipes and/or files



Example Makefile

Makefile Schema

```
recipe name: ingredients  
instructions
```

An example Makefile

```
all: manuscript.pdf  
  
manuscript.pdf: data/iris_preppepd.csv manuscript.Rmd  
    Rscript -e 'rmarkdown::render("manuscript.Rmd")'  
  
data/iris_preppepd.csv: R/preprocess_data.R data/iris.csv  
    Rscript -e 'source("R/preprocess_data.R")'
```

Key features

Missing ingredients will be generated,
e.g., if the cleaned data is missing, the raw data is first cleaned.

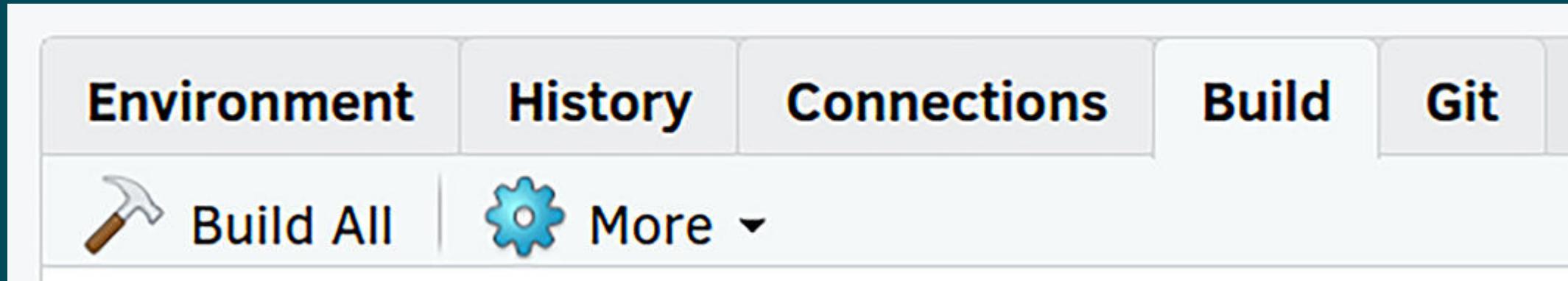
Newer ingredients trigger updates,
e.g., new data leads to recreation of the whole manuscript.

Always the same "button" that triggers reproduction,
e.g., regardless of programming language, file format, and intermediate steps.

Why Make

- A single, well-defined entry point for your analysis (default target): `make`
- Management of all external dependencies in one file via (dependend) targets, such as
 - Installing extra software
 - Starting external programs (such as pre-processing pipelines)
 - Downloading data from external repositories

Make in RStudio



Trigger default make using **build all**

Native R alternative?

Alternative: build automation using the `targets` package Landau (2021)

- using `tar_target(y, f(x))` instead of `y <- f(x)`
- then `tar_make()` builds/updates all targets
- like in Make, things are built only if they changed
- built-in visualization of dependency graph

Containerization



Problem: Broken *software dependencies*
('dependency hell')

Docker

A Docker container is like a shareable virtual machine that runs identically on any computer (Linux, macOS, Windows)

- You can either provide a short **recipe** how to create a container (few kilobytes) or
- the entire **container** (few gigabytes)

Docker Recipes

Recipes are instructions how to create a container from publicly available sources, e.g.,

- Rocker project (Boettiger & Eddelbuettel, 2017), with pre-configured Debian images including R/Rstudio
- Microsoft R Application Network (MRAN) providing CRAN snapshots in their „time machine“ (out of service now!)

```
FROM rocker/verse:3.6.1
ARG BUILD_DATE=2019-11-11
RUN install2.r --error --skipinstalled here lavaan
WORKDIR /home/rstudio
```

Docker Recipes

Recipes are instructions how to create a container from publicly available sources, e.g.,

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```
FROM rocker/verse:3.6.1
ARG BUILD_DATE=2019-11-11
RUN install2.r --error --skipinstalled here lavaan
WORKDIR /home/rstudio
```

Run in Docker

Example of how to run R in a docker image from the terminal interactively (--it) and without saving its state (--rm)

```
# start an interactive R session in the  
# container named 'reproducible-research'  
docker run --rm -it reproducible-research R
```

more info in (Peikert and Brandmaier, 2021)

The *maybe good enough* way: `renv`

- The collection of installed packages is a *library* in R
- The R package `renv` (Ushey & Wickham, 2024) separates system library from *project-specific local libraries* in R
- Key concept: *isolation* of your project's dependencies from your system and other projects (different projects can use different package versions)

Components

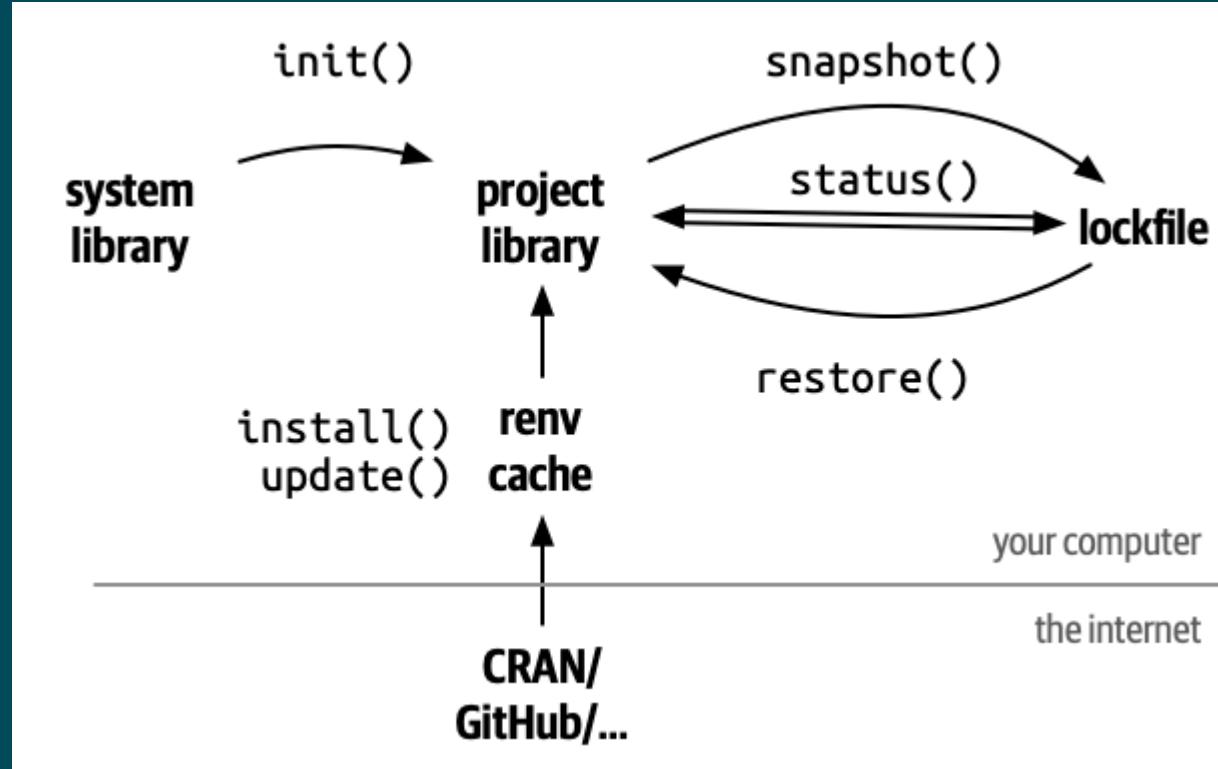
- The project library, `renv/library`, is a library that contains all packages currently used by your project
- the `renv.lock` file, which contains meta data about the local library (**share** this with collaborators)
- A project R profile `.Rprofile`, which is loaded once a project is loaded (remember `setwd()`)

Commands

- Create a private R library with `renv::init()` (the project will now always rely on the local library)
- Update a library with `renv::snapshot()` (e.g. when updating packages to a newer version)
- Restore a library with `renv::restore()`

cf. the WORCS approach by (Van Lissa, Brandmaier, Brinkman, Lamprecht, Peikert, Struiksma, and Vreede, 2021)

Overview



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

But is this really enough?

The case of pseudo random numbers

- Pseudo random numbers are important in modern statistics, e.g. permutation tests, bootstrapping, random forests but also for reproducible allocation of participants to experimental conditions
- PRN generators can be thought of as long lists of numbers that repeat only after a very long time (efficiently represented as a mathematical function); the list is determined by a starting condition (**seed**)
- For reproducibility, we need to fix that initial **seed** (ideally by another random process)

Examples of Non-Reproducible Code in R

Here are some examples of non-reproducible code that cannot be captured easily from within a given R environment

1. Bugfix in random number generator in R between R 3.5 and R 3.6

```
set.seed(1234);  
sample(1:10, 5)
```

```
2 6 5 8 9 (R3.5)
```

```
10 6 5 4 1 (R3.6.1)
```

Examples of Non-Reproducible Code in R

Confidence intervals (95%) of a simple regression coefficient estimate (with identical random seed):

```
[1] "R version 3.5.0 (2018-04-23)"  
2.5 % 97.5 %  
0.0097 0.3842
```

```
[1] "R version 3.6.1 (2019-07-05)"  
2.5 % 97.5 %  
-0.0005 0.3748
```

Note that the results are not reproduced but replicated.

Examples of Non-Reproducible Code in R

2. Locale-dependent behavior (e.g., English vs Lithuania):

```
sort(state.abb)

[1] "AK" "AL" "AR" "AZ" "CA" "CO" "CT" "DE" "FL" "GA" "HI" "IA"
[13] "ID" "IL" "IN" "KY" "KS" "LA" "MA" "MD" "ME" "MI" "MN" "MO"
[25] "MS" "MT" "NC" "ND" "NE" "NH" "NY" "NJ" "NM" "NV" "OH" "OK"
[37] "OR" "PA" "RI" "SC" "SD" "TN" "TX" "UT" "VA" "VT" "WA" "WI"
[49] "WY" "WV"
```

3. Defaults change over time

- Loading data has different defaults from R 4.0+
- `read.csv()` now has `stringsAsFactors = FALSE`
- Earlier strings were converted to factors automatically (with levels sorted by local language) => non-reproducibility

```
c("0", "1", "A", "B", "a", "b")
```

```
## [1] "0" "1" "A" "B" "a" "b"
```

sorted to 01aAbB in German, 01AaBb in Norwegian, 01ABab in Korean

**There is a need for reproducible
computational environments**

Containers

Docker containers

- guarantee identical execution of its contents across platforms (and time) including cloud computing (such as github actions)
- can run interactively: R/Rstudio can run in the container (i.e., there is no need to ever run the analysis in your local computing environment, see Peikert and Brandmaier (2021))
- Analyses can be run in different containers (simulating different package versions) to find out what downstream updates broke your code / your results

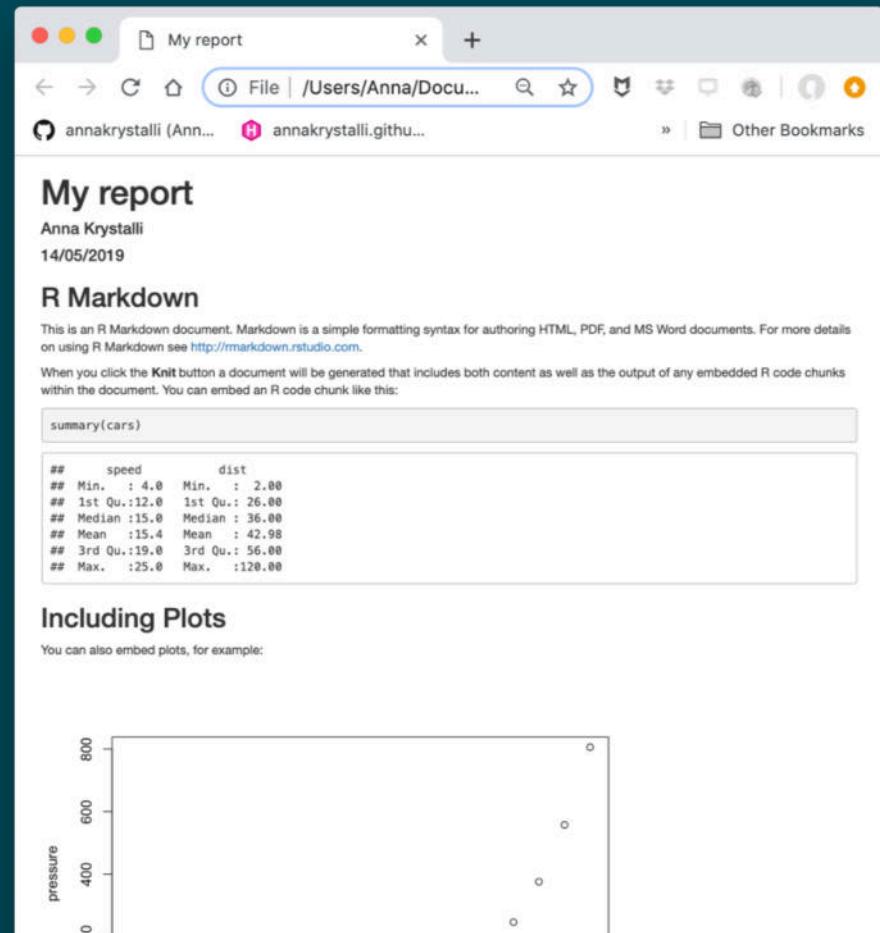


Dynamic Document Generation

Problem: Oh these darn copy&paste errors!

R Markdown Example

```
my-report.Rmd x
Knit Insert Run
1* ---
2 title: "My report"
3 author: "Anna Krystalli"
4 date: "14/05/2019"
5 output: html_document
6 ---
7
8 *{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ...
11
12 ## R Markdown
13
14 This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.
15
16 When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:
17
18 *{r cars}
19 summary(cars)
20 ...
21
22 ## Including Plots
23
24 You can also embed plots, for example:
25
26 *{r pressure, echo=FALSE}
27 plot(pressure)
28 ...
29
30 Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.
31
```



Number reporting (APA style) with papaja

```
+ 111  
112     ### APA-style numbers  
113  
114  
115     The observed values were  
116     `r printnum(1)`,  
117     `r printnum(0.0001)` , and  
118     `r printnum(0.2)`.  
119  
120     The p values were  
121     `r printp(1)`,  
122     `r printp(0.0001)` , and  
123     `r printp(0.2)`.  
124  
125     ````  
126
```

APA-style numbers. The observed values were 1.00, 0.00, and 0.20.

The p values were $> .999$, $< .001$, and .200.

Reporting statistics with papaja

```
138
139  ```{r result="asis"}
140  oasis$ID <- 1:nrow(oasis)
141  aresult <- afex::aov_ez(data=oasis, dv="nWBV", between =
142  .           c("Gender","CDRc"), id = "ID")
143
144  apaa <- apa_print(aresult)
145  ```
146
147  Results were analyzed using a two-factor ANOVA. We found no
148  significant effect of gender (`r apaa$full_result$Gender`)
149  but a significant effect of diagnosis (`r
150  apaa$full_result$CDRc`).
1
1  The interaction was not significant (`r
1  apaa$full_result$Gender_CDRc`).
```

Results were analyzed using a two-factor ANOVA. We found no significant effect of gender ($F(1, 122) = 1.21, MSE = 0.00, p = .273, \hat{\eta}_G^2 = .010$) but a significant effect of diagnosis ($F(1, 122) = 32.11, MSE = 0.00, p < .001, \hat{\eta}_G^2 = .208$). The interaction was not significant ($F(1, 122) = 0.04, MSE = 0.00, p = .835, \hat{\eta}_G^2 = .000$).

APA Table

```
mod1 <-
  " musicG =~ X1+X2+X3+X4+X5+X7+X8+X9+X10+X11+X12+X13 "

model1.fit <- cfa(mod1,data = model.dat)
fitMeasures(model1.fit,c("CFI","RMSEA","BIC"))

##      cfi      rmsea      bic
##  0.882    0.165  1439.369

sl<- standardizedSolution(model1.fit)
knitr::kable(sl,digits = 2,caption = "Standardized Estimates")
```

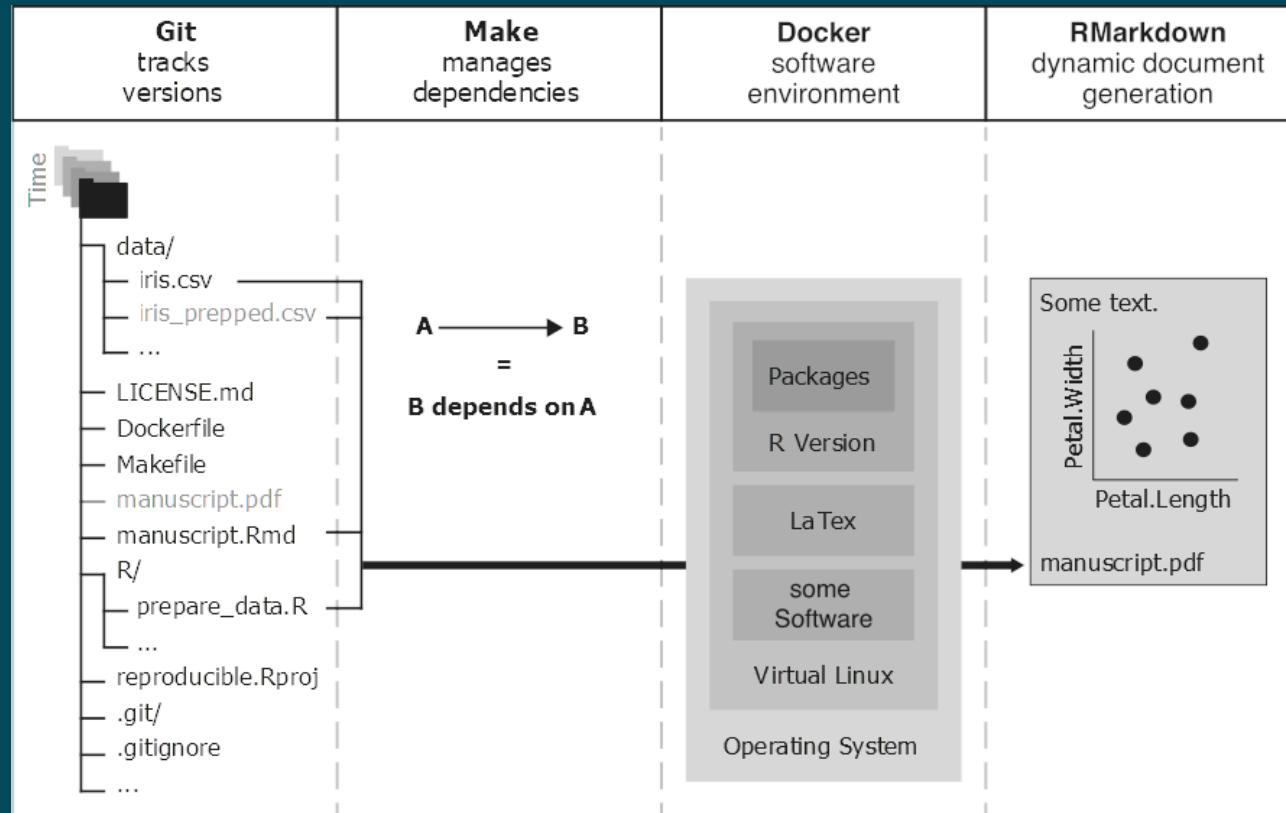
Table 1: Standardized Estimates

lhs	op	rhs	est.std	se	z	pvalue	ci.lower	ci.upper
musicG	=~	X1	0.89	0.03	29.27	0	0.83	0.95
musicG	=~	X2	0.90	0.03	33.27	0	0.85	0.95
musicG	=~	X3	0.76	0.06	13.60	0	0.65	0.87
musicG	=~	X4	0.81	0.05	17.61	0	0.72	0.90
musicG	=~	X5	0.88	0.03	27.11	0	0.81	0.94

Thank you, statcheck, we'll take it from here

The repro package

Four Elements of Reproducibility



from Peikert and Brandmaier (2020)

YAML header (repro)

`repro` extends the YAML header of `R Markdown` to track dependencies on code (internal scripts and external packages) and data files.

...and takes care of preparing your project for `git`, `Make`, and `Docker`

YAML header (R Markdown)

A standard YAML header:

```
---
```

```
title: My worst academic fails
author: Andreas Brandmaier
date: 2020-11-17
output: html_document
```

```
---
```

Example

```
---
```

```
title: My worst academic fails
author: Andreas Brandmaier
date: 2020-11-17
repro:
  packages:
    - usethis
    - fs
    - aaronpeikert/repro@d09def75df
  scripts:
    - R/clean.R
  data:
    mycars: data/mtcars.csv
output: html_document
---
```

System setup with repro

Load the package:

```
library(repro)
```

Run some checks:

```
check_git()
```

```
## ✓ Git is installed, don't worry.
```

```
check_make()
```

```
## ✗ Make is not installed.  
## i We recommend Chocolatey for Windows users.  
## ✗ Chocolatey is not installed.  
## • To install it, follow directions on:  
##   'https://chocolatey.org/docs/installation'
```

Project setup with `repro`

- Use `repro::automate()` to make an existing RMarkdown analysis reproducible
- creates a Dockerfile & Makefile based on every RMarkdown in the project folder
- use `automate_load_packages()` to load all packages in your script, `automate_load_data()` for data, and `automate_load_scripts()` to attach external scripts

Under the hood

```
cat("✓ Setting active project to 'C:/Users/andreas.brandmaier/LokaleDokumente/GitHub/reproducibility_workshop'
✓ Directory `repro` created!
✓ Writing '.repro/Dockerfile_base'
✓ Writing '.repro/Dockerfile_packages'
✓ Writing '.repro/Dockerfile_manual'
✓ Writing 'Dockerfile'
✓ Writing '.repro/Makefile_Rmds'
✓ Writing '.repro/Makefile_Docker'
✓ Writing '.dockerignore'
• Modify '.dockerignore'
✓ Writing 'Makefile'
• Modify 'Makefile'
• Maybe you want to add:
'repro.html'
to the 'Makefile'-target 'all'.")

## 
## ✓ Setting active project to 'C:/Users/andreas.brandmaier/LokaleDokumente/GitHub/reproducibility_workshop'
## ✓ Directory `repro` created!
```

Docker

```
1 # Generated by repro: do not edit by hand
2 # Please edit Dockerfiles in .repro/
3 FROM rocker/verse:4.2.2
4 WORKDIR /home/rstudio
5 RUN apt-get update -y && apt-get install -y rsync
6 RUN tlmgr install collection-latexrecommended
7 RUN install2.r --error --skipinstalled \
8   here \
9   patchwork \
10  qrcode \
11  showtext \
12  stargazer \
13  svglite \
14  tidyverse \
15  xaringantheme
16 RUN installGithub.r \
17  aaronpeikert/repro@fc7e884
```

Reproduction

To reproduce a project completely:

```
library(repro)  
reproduce()
```

What could possibly go wrong?



Problems

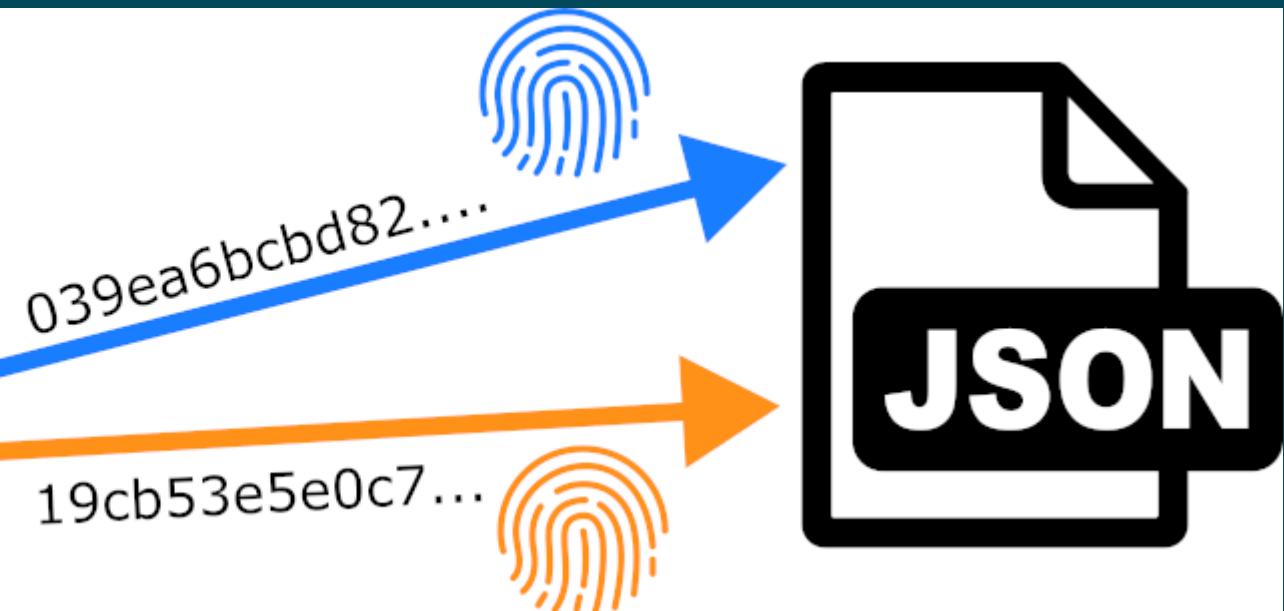
- Docker not available (e.g., no admin rights, unsupported computing platform)
- After upgrading to new R, new package versions, new computer, how do we know whether results still reproduce?

Solution

reproducibleRchunks are just like regular R Markdown chunks but verify reproducibility of computations

reproducibleRchunks

```
14  
15 - ## Some Computation  
16  
17 Here is a computation:  
18  
19 - ```{reproducibleR addition}  
20 my_sum <- x + 1  
21 -```  
22
```



Reproduction reports

Here is a computation:

```
my_sum <- x + 1
```

Code Chunk Reproduction Report

Creating reproduction file This seems to be the first run of the R Markdown file including reproducible chunks. Storing reproducibility information for variables:

- my_sum

Reproduction reports (Success)

Here is a computation:

```
my_sum <- x + 1
```

Code Chunk Reproduction Report

- my_sum: REPRODUCTION SUCCESSFUL

Reproduction reports (Failed)

Here is a computation:

```
my_sum <- x + 1
```

Code Chunk Reproduction Report

- **X** my_sum: **REPRODUCTION FAILED** Fingerprints are not identical.

How does it work?

```
set.seed(42)
numbers <- sample(1:10, 5)
```

becomes a serialized JSON file (whose changes are trackable via *git*):

```
{
  "type": "integer",
  "attributes": {},
  "value": [1, 5, 10, 8, 2]
}
```

but really, we store a hash fingerprint for privacy and space reasons

What are valid variables?

All of the following variables (**x** of class *integer*, **y** of class *character*, **z** of class *lm*, and **lst** of class *list*) are valid examples for the automated reproducibility checks:

```
x <- 1:10
y <- "qr"
z <- lm(x~1, method=y)
lst <- list(x, y, z)
```

What should be reproducible?

(Almost) Everything

Some things we do not care about

Time information such as:

- current time or date
- run time of a model
- time elapsed for a given computation

Other information that changes between sessions (should be avoided anyhow):

- user names
- local paths

Extract only necessary bits from a model and verify them

The `broom` package has a generic function `tidy` with model-specific functions (e.g., `lm`, `anova`, `factanal`, `glm`, `lavaan`, `gam`,...) to extract all relevant parameter estimates:

```
x <- rnorm(10)
y <- rnorm(10)
broom::tidy(lm(y~x))
```

```
## # A tibble: 2 × 5
##   term      estimate std.error statistic p.value
##   <chr>      <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)  0.568     0.204     2.79    0.0237
## 2 x           0.487     0.205     2.38    0.0448
```

Reproducibility + Preregistration

Outlook: PAC

- preregistration currently entail a lot of work because we need two write two manuscripts (prereg + final ms)
- preregistrations still suffer from ambiguities of written language, omissions, underdefined processes
- With reproducible pipelines, we could move towards Preregistration as Code (PAC)

Outlook: PAC

Advantages

- Write your manuscript once with everything but the discussion
- Generate all tables and figures based on simulated data
- Once real data is collected, replace data, reproduce manuscript
- Deviate from original plan if necessary, summarize, also: all changes are *transparently* documented in git
- Write discussion, done.

How would this look in practice?

Example online here ("gender differences in Machiavellianism") (Peikert, Van Lissa, and Brandmaier, 2021) including power analysis

![<https://github.com/aaronpeikert/repro-tutorial/blob/main/preregistration.Rmd>]

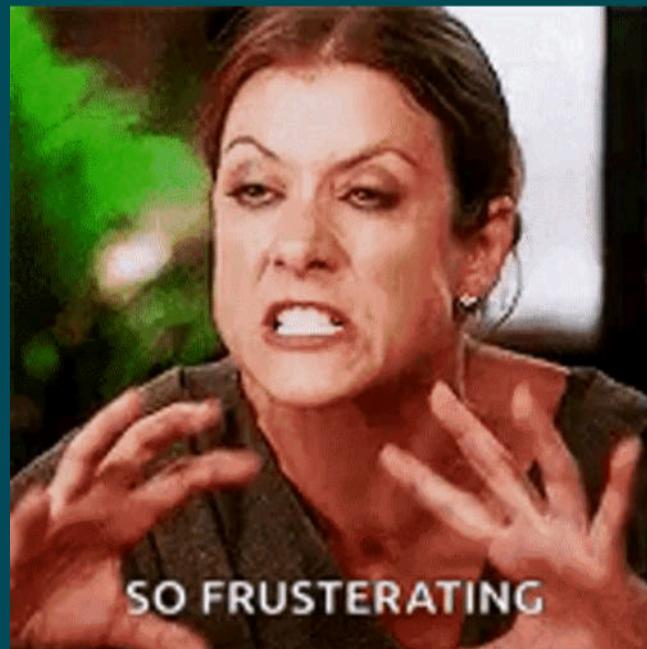
Modifications we had to make after the simulated PAC:

- recoding gender from (1,2) to (male, female)
- removal of NA values was missing
- half of the items of Machiavellianism are reverse-coded

Take-home message

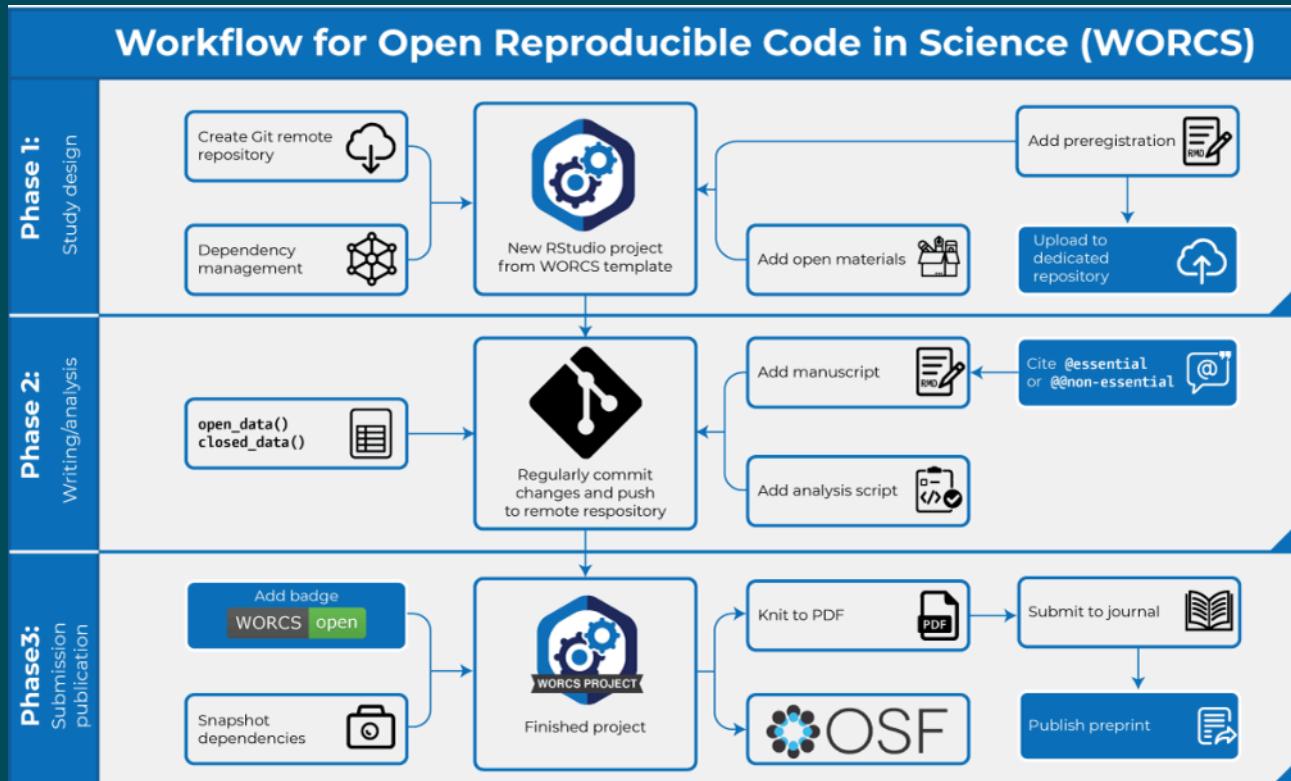
Me: Reproducible research is conceptually very simple

Also me:



in practice

Where to start



(Van Lissa, Brandmaier, Brinkman et al., 2021)

Where to start

Link to this talk:



Thank you!

Many thanks to the team: **Aaron Peikert, Caspar van Lissa**

If you want to engage:

- Ask us a question via a [github issue](#)
- Follow [@brandmaier](#) on twitter or [@brandmaier.bsky.social](#)
- Read our papers on the topic (see refs)
- Contribute to our [repro](#) repository on GitHub or [reproducibleRchunks](#)

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