

# Reproducible Workflows for Better Science and Efficient Collaboration

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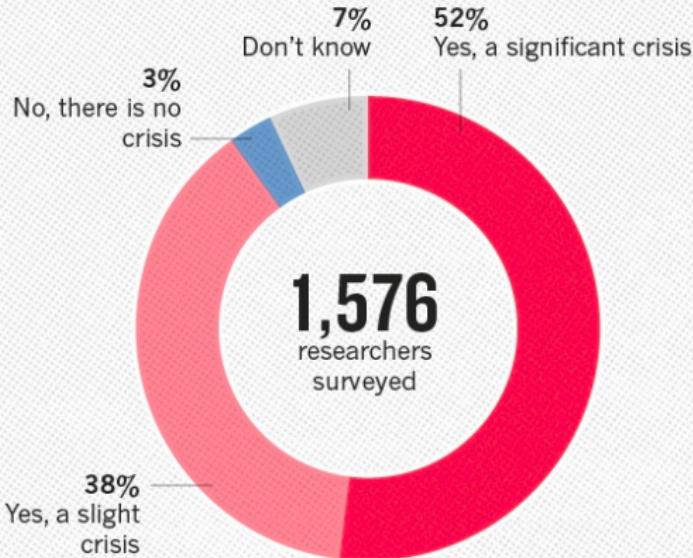
Francisco Rodriguez-Sanchez

<https://frodriguezsanchez.net>

# The Reproducibility Crisis/Revolution

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## IS THERE A REPRODUCIBILITY CRISIS?



©nature

Baker 2016

≡ EL PAÍS

Materia  
III

## La ciencia vive una epidemia de estudios inservibles

Científicos de EE UU, Reino Unido y Holanda denuncian que la investigación está perdiendo parte de su credibilidad

El País

NEWS | 09 December 2021

## Half of top cancer studies fail high-profile reproducibility effort

- Goal: Replicate 193 experiments from 53 papers

[Errington et al 2021](#)

NEWS | 09 December 2021

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[Errington et al 2021](#)

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NEWS | 09 December 2021

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NEWS | 09 December 2021

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[Errington et al 2021](#)

NEWS | 09 December 2021

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- 1/3 authors didn't respond or help

[Errington et al 2021](#)



Sylvain Deville ❄️💡  
@DevilleSy

...

Trying to reproduce the results of a paper using only what's in the Methods section



Most scientific articles

are NOT reproducible

Reproducibility

*crisis*

REVOLUTION

## What is reproducibility?

---

# Reproducibility vs Replicability

		Data	
		Same	Different
Analysis	Same	Reproducible	Replicable
	Different	Robust	Generalisable

[The Turing Way](#)

We can't guarantee that  
our results are **REPLICABLE**.

But at least  
they should be **REPRODUCIBLE**.

Most scientific articles

**are NOT reproducible**

## The prevalence of statistical reporting errors in psychology (1985–2013)

Michèle B. Nuijten<sup>1</sup> · Chris H. J. Haggerink<sup>1</sup> · Marcel A. L. M. van Assen<sup>1</sup> ·  
Sacha Epskamp<sup>2</sup> · Jelte M. Wicherts<sup>1</sup>

### WHAT STATCHICK LOOKS FOR

This computer algorithm scans papers for statistical tests, uses reported results to recompute the  $P$  value and flags up inconsistencies.

#### Type of test

The  $t$ -test assesses differences between two groups.

#### Test statistic

Compares observed values with those expected under the null hypothesis.

$$t(37) = 4.93, P < 0.01$$

#### Degrees of freedom

Accounts for size of sample.

#### $P$ value

The likelihood of observing differences as extreme, or more so, if the null hypothesis is true.

## **The prevalence of statistical reporting errors in psychology (1985–2013)**

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1/2 articles: **inconsistencies** in p-values

1/8 articles: **grossly inconsistent** p-values

(affecting conclusions -> significance)

In ecology

**< 20% articles are reproducible**

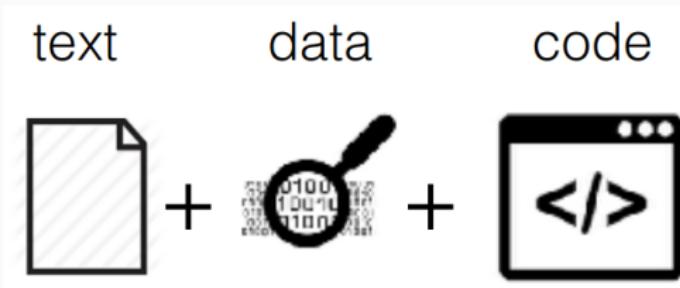
[Culina et al 2020](#)

# We can't even reproduce our own work

## Data/Code lost or unusable

qualitative_data.csv	04/07/2016 15:50
cleandata.xlsx	25/06/2015 01:14
cleandata_YC.xlsx	30/06/2015 16:22
COORDENADAS PACO_20-05-2016 CON REVIEWS.xlsx	20/05/2016 16:23
COORDENADAS PACO_20-05-2016 CON REVIEWS_FRS.xlsx	27/05/2016 19:41
COORDENADAS_papel195(Girella_elevata).xlsx	08/06/2016 13:09
coordenadas_raw_2016-06-08.xlsx	09/06/2016 15:53
coordenadas_raw_2016-06-08_old.xlsx	08/06/2016 16:00
coordenadas_raw_2016-06-21.xlsx	21/06/2016 16:12
coords_2015-09-09_modif.xlsx	05/11/2015 15:23
coords_2015-10-11_modif_YC.xlsx	17/11/2015 13:37
coords_2015-10-11_modif_YC_PACO.xlsx	17/11/2015 17:06
coords_2015-10-18_modif_YC.xlsx	18/11/2015 17:24
coords_2015-12-26_modif_YC.xlsx	30/03/2016 19:38
coords_2016-04-02.xlsx	06/04/2016 17:46
coords_2016-04-02_YC.xlsx	06/04/2016 18:03
coords_2016-04-08_YC.xlsx	11/04/2016 13:51
dataset_y_coords_09_09_15.xlsx	23/09/2015 17:18
Datos metaanalisis_18-04-2016.xlsx	19/04/2016 16:24
FINAL METAANALYSIS_14-6-2016_WITH REVIEWS.xlsx	21/06/2016 16:15
FINAL METAANALYSIS_16-6-2016_WITH REVIEWS.xlsx	21/06/2016 16:13
FINAL METAANALYSIS_2016-04-27_WITH REVIEWS.xlsx	25/05/2016 18:05
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FINAL METAANALYSIS_2016-04-29_EXCLUDING REVIEWS.xlsx	08/06/2016 13:06
FINAL VOTECOUNTING_1-7-2016.xlsx	04/07/2016 15:46
fitnessdata_2016-06-22.xlsx	22/06/2016 21:00
IFs for Bastien_19-3-2016_YC.xlsx	28/03/2016 19:26
Metaanalysis final_01-05-2015 with coordinates.xlsx	18/05/2015 19:20
Metaanalysis final_22-05-2015 coords.xlsx	24/06/2015 15:50
Metaanalysis final_25-06-2015.xlsx	30/06/2015 16:55
Metaanalysis y coords revisadas_06-08-2015_AH_JE.xlsx	23/09/2015 12:57

## What's a reproducible manuscript?



DATA + CODE

- analysis fully **traceable**
- results can be **regenerated**

A scientific article is **advertising**, not scholarship.

The actual scholarship is the **full software environment, code and data**, that produced the result.

Claerbout & Karrenbach 1992

text

data

code



+



+



Are we sharing the data?

PERSPECTIVE

## Public Data Archiving in Ecology and Evolution: How Well Are We Doing?

Dominique G. Roche<sup>1,2\*</sup>, Loeske E. B. Kruuk<sup>1,3</sup>, Robert Lanfear<sup>1,4</sup>, Sandra A. Binning<sup>1,2</sup>

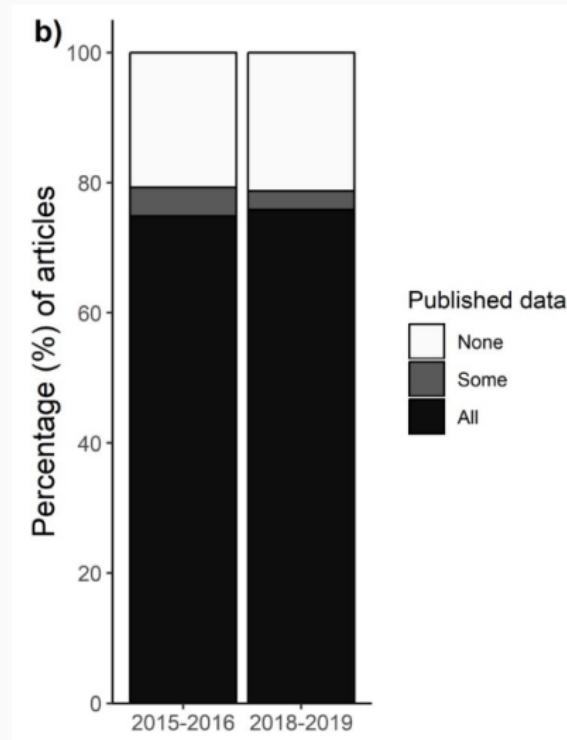
**1** Division of Evolution, Ecology and Genetics, Research School of Biology, The Australian National University, Canberra, Australian Capital Territory, Australia, **2** Éco-Éthologie, Institut de Biologie, Université de Neuchâtel, Neuchâtel, Switzerland, **3** Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom, **4** Department of Biological Sciences, Macquarie University, Sydney, Australia

\* [dominique.roche@mail.mcgill.ca](mailto:dominique.roche@mail.mcgill.ca)

### Abstract

Policies that mandate public data archiving (PDA) successfully increase accessibility to data underlying scientific publications. However, is the data quality sufficient to allow reuse and reanalysis? We surveyed 100 datasets associated with nonmolecular studies in journals that commonly publish ecological and evolutionary research and have a strong PDA policy. Out of these datasets, **56% were incomplete, and 64% were archived in a way that partially or entirely prevented reuse**. We suggest that cultural shifts facilitating clearer benefits to authors are necessary to achieve high-quality PDA and highlight key guidelines to help authors increase their data's reuse potential and compliance with journal data policies.

# Are we sharing data?



Are we sharing data?

Quickly getting better

## Scientific Life

Early Career  
Researchers Embrace  
Data Sharing

Hamish A. Campbell,<sup>1,\*</sup>  
Mariana A. Micheli-Campbell,<sup>1</sup>  
and Vinay Udyawer<sup>2</sup>

[Campbell et al. 2019](#)

Are we sharing the code?

## Code exists but rarely shared

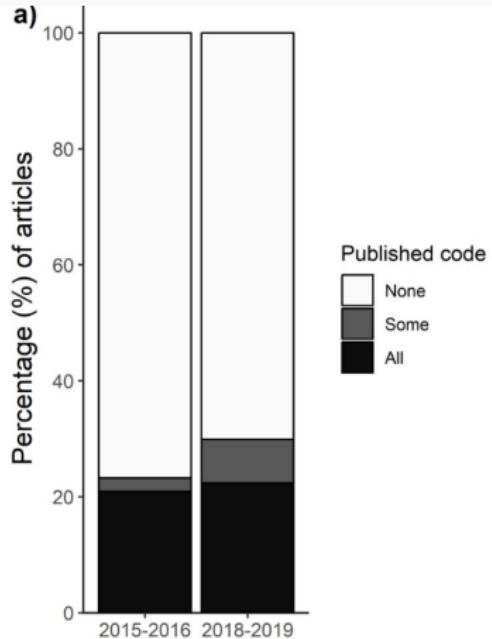


Fig 1. Code-sharing is at its infancy in ecology, where

WHY?

# Poor incentives



O'Dea et al 2021

Doing reproducible research can be costly

# The Costs of Reproducibility

Russell A. Poldrack<sup>1,\*</sup>

<sup>1</sup>Department of Psychology, Stanford University, Stanford, CA, USA

\*Correspondence: [poldrack@stanford.edu](mailto:poldrack@stanford.edu)

<https://doi.org/10.1016/j.neuron.2018.11.030>

PERSPECTIVE

## Open science challenges, benefits and tips in early career and beyond

Christopher Allen<sup>1,\*</sup>, David M. A. Mehler<sup>1,2,\*</sup>

Must value diverse contributions to reproducible research

## Credit data generators for data reuse

To promote effective sharing, we must create an enduring link between the people who generate data and its future uses, urge **Heather H. Pierce** and colleagues.

[Pierce et al 2019](#)

## Publish your computer code: it is good enough

*Freely provided working code – whatever its quality – improves programming and enables others to engage with your research, says **Nick Barnes**.*

Barnes 2010

- Improve training
- Code review, preprints...
- Avoid shaming -> constructive critique
- Ugly code better than no code

## Why doing reproducible research?

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Reproducibility: good for you, good  
for everyone

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## Automation (good code) saves time

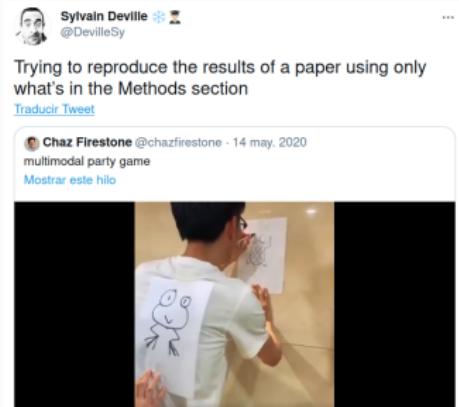


**Trevor Branch**  
@TrevorABranch

...

My rule of thumb: every analysis you do on a dataset will have to be redone 10–15 times before publication. Plan accordingly. [#Rstats](#)

# Code = fully traceable, reproducible analysis



## Code advantages:

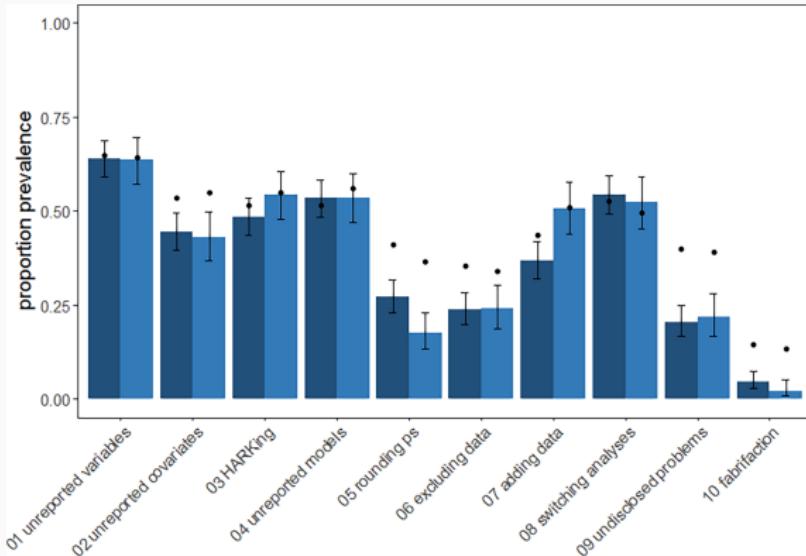
- Easier writing
- Easier, deeper review
- Reusable

# Transparency prevents bad practices

RESEARCH ARTICLE

## Questionable research practices in ecology and evolution

Hannah Fraser<sup>1\*</sup>, Tim Parker<sup>2</sup>, Shinichi Nakagawa<sup>3</sup>, Ashley Barnett<sup>1</sup>, Fiona Fidler<sup>1,4</sup>



p-hacking, HARKing, data fabrication...

DOI:10.1063/PT.6.1.20180822a

22 Aug 2018 in **Research & Technology**

## **The war over supercooled water**

How a hidden coding error fueled a seven-year dispute between two of condensed matter's top theorists.

**Ashley G. Smart**

Over the next seven years, the perplexing discrepancy would ignite a bitter conflict, with junior scientists caught in the crossfire. At stake were not only the reputations of the two groups but also a peculiar theory that sought to explain some of water's deepest and most enduring mysteries. Earlier this year, the dispute was finally settled. And as it turns out, the entire ordeal was the result of botched code.

# Transparency brings better science



Alexey Shiklomanov  
@ashiklom711

...

I'm co-author on a study currently published only as a publicly available discussion paper. My code was on GitHub.

A colleague read the paper, thought the results looked weird, checked my code, found a bug and emailed me about it.

This is how science should work. [#openscience](#)

## Many journals (and funders) value/require reproducibility

As a condition for publication in ESA journals, all underlying data and statistical code pertinent to the results presented in the publication must be made available in a permanent, publicly accessible data archive or repository, with rare exceptions (see



## Many journals value reproducibility

'Papers with exemplary **data and code archiving**

are **more valuable** for future research and [...]

will be given **higher priority** for publication'

*(Molecular Ecology)*

Many journals require reproducibility

EDITORIAL

ECOLOGY LETTERS  WILEY

## **From raw data to publication: Introducing data editing at Ecology Letters**

‘We require the **data and code** for reproducing statistical results and generating figures and tables’

‘This material will need to be supplied at the **time of submission**’

# Higher impact: cites, reuse, reputation

RESEARCH ARTICLE

## The citation advantage of linking publications to research data

Giovanni Colavizza<sup>1,2</sup>, Iain Hrynaszkiewicz<sup>3,4</sup>, Isla Staden<sup>1,5</sup>, Kirstie Whitaker<sup>1,6</sup>, Barbara McGillivray<sup>1,6\*</sup>

Colavizza et al 2020

ACADEMIC PRACTICE IN ECOLOGY AND EVOLUTION

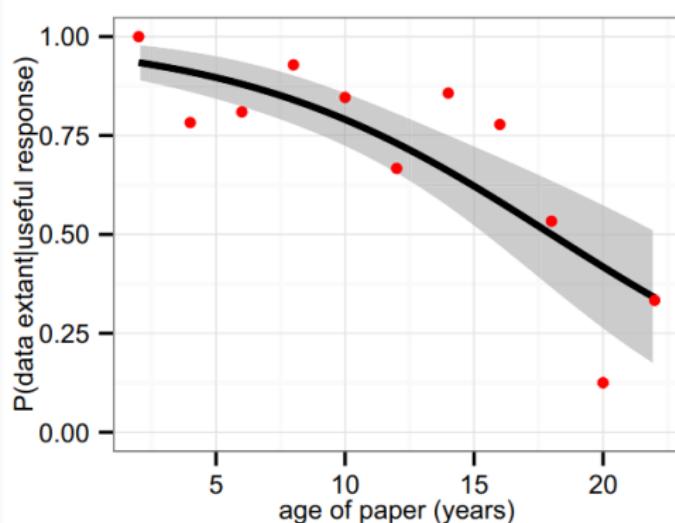
Ecology and Evolution  WILEY

Code sharing in ecology and evolution increases citation rates but remains uncommon  

Maitner et al 2024

Let's stop losing data & code

**The Availability of Research Data Declines Rapidly with Article Age**



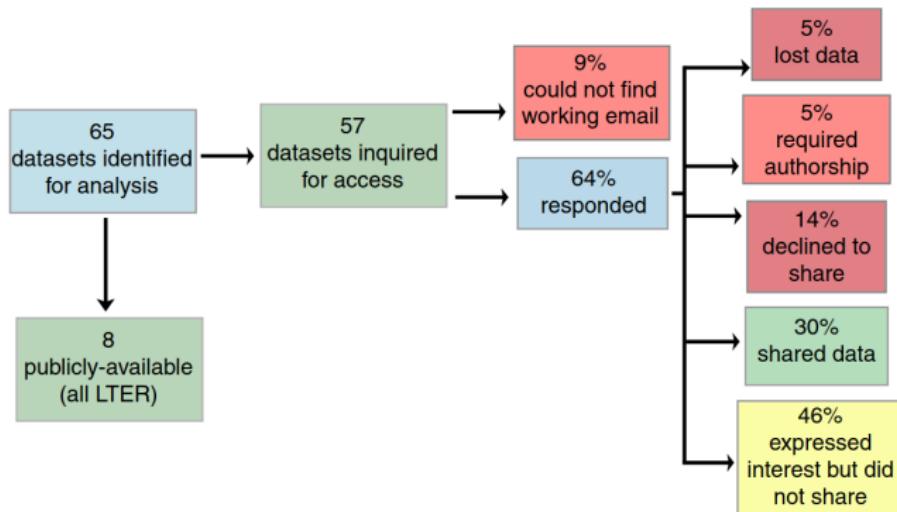
Vines et al 2014

# Open data & code enable synthesis

## REVIEW

### Advances in global change research require open science by individual researchers

ELIZABETH M. WOLKOVICH<sup>\*†</sup>, JAMES REGETZ<sup>‡</sup> and MARY I. O'CONNOR<sup>†</sup>



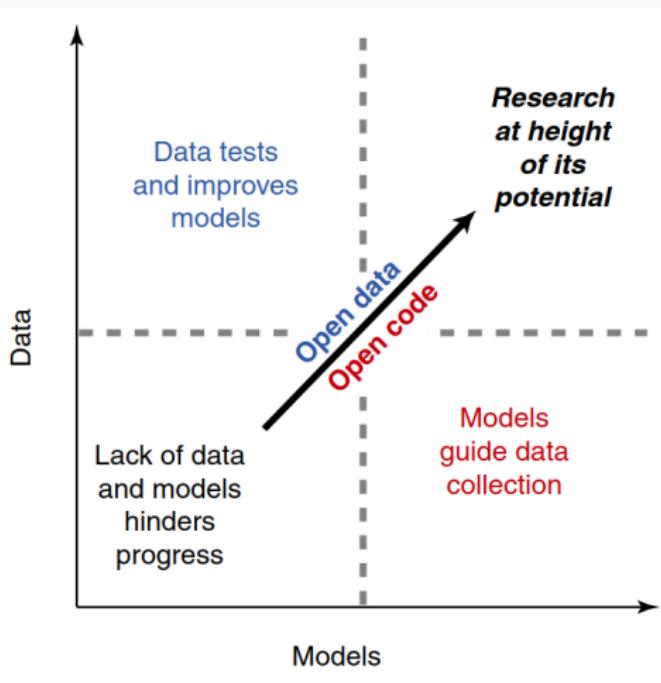
Wolkovich et al 2012

# Open data & code enable synthesis

## REVIEW

Advances in global change research require open science by individual researchers

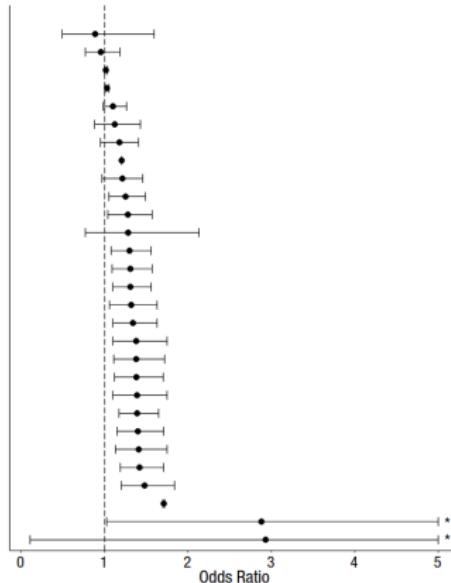
ELIZABETH M. WOLKOVICH\*,†, JAMES REGETZ‡ and MARY I. O'CONNOR†



# Same data -> different results

Do soccer referees give more red cards to dark-skin players?

Team	Analytic Approach	Odds Ratio
12	Zero-Inflated Poisson Regression	0.89
17	Bayesian Logistic Regression	0.96
15	Hierarchical Log-Linear Modeling	1.02
10	Multilevel Regression and Logistic Regression	1.03
18	Hierarchical Bayes Model	1.10
31	Logistic Regression	1.12
1	OLS Regression With Robust Standard Errors, Logistic Regression	1.18
4	Spearman Correlation	1.21
14	WLS Regression With Clustered Standard Errors	1.21
11	Multiple Linear Regression	1.25
30	Clustered Robust Binomial Logistic Regression	1.28
6	Linear Probability Model	1.28
26	Hierarchical Generalized Linear Modeling With Poisson Sampling	1.30
3	Multilevel Logistic Regression Using Bayesian Inference	1.31
23	Mixed-Model Logistic Regression	1.31
16	Hierarchical Poisson Regression	1.32
2	Linear Probability Model, Logistic Regression	1.34
5	Generalized Linear Mixed Models	1.38
24	Multilevel Logistic Regression	1.38
28	Mixed-Effects Logistic Regression	1.38
32	Generalized Linear Models for Binary Data	1.39
8	Negative Binomial Regression With a Log Link	1.39
20	Cross-Classified Multilevel Negative Binomial Model	1.40
13	Poisson Multilevel Modeling	1.41
25	Multilevel Logistic Binomial Regression	1.42
9	Generalized Linear Mixed-Effects Models With a Logit Link	1.48
7	Dirichlet-Process Bayesian Clustering	1.71
21	Tobit Regression	2.88
27	Poisson Regression	2.93



29 teams: 2/3 found significant effect

73 teams testing the same hypothesis with the same data

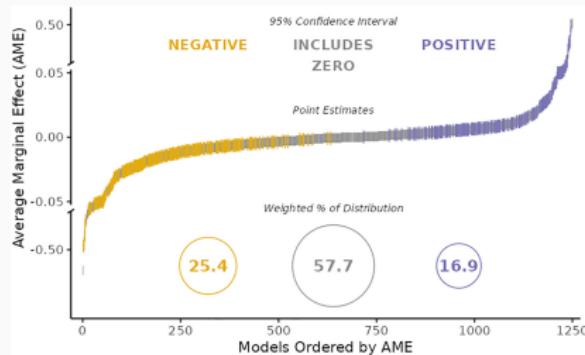
PNAS

RESEARCH ARTICLE

SOCIAL SCIENCES

OPEN ACCESS

Observing many researchers using the same data and hypothesis reveals a hidden universe of uncertainty

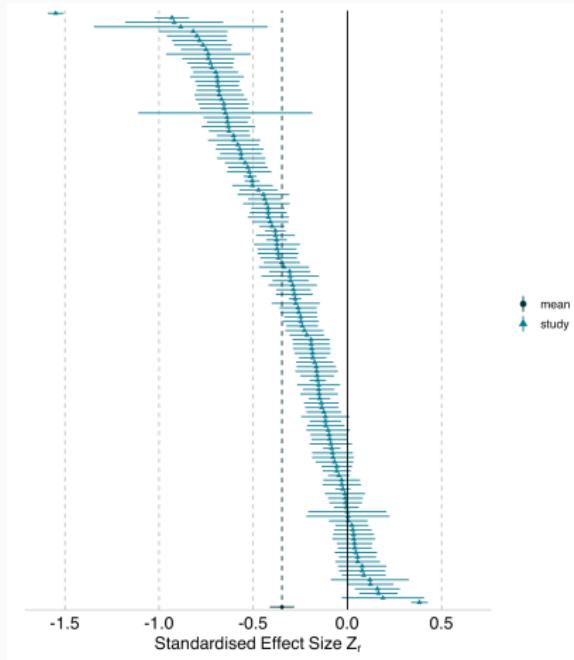


'This reveals a **universe of uncertainty** that remains hidden when considering a single study in isolation'

'These results call for greater **epistemic humility** and **clarity** in reporting scientific findings'

132 teams asking same question with same data

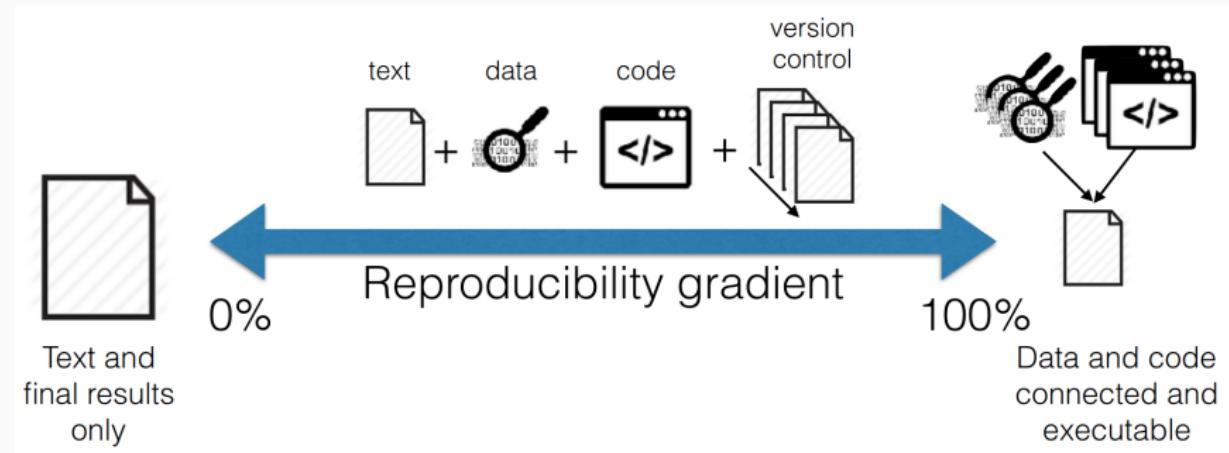
How does sibling competition affect nestling growth in blue tits?



## How to do reproducible research

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# Reproducibility is a gradient



Rodríguez-Sánchez et al. 2016 (modif. Peng 2011)

## Basic reproducibility

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## Basic reproducibility

- **MANUSCRIPT** (Text + Tables + Figures)
- **DATA** in permanent archive (see [Tierney & Ram 2020](#))
- **CODE** in permanent archive (see [Eglen et al 2016](#))

*Permanent archive:*

- Zenodo, Dryad, OSF, Figshare, Data Paper...
- NOT GitHub, website...

## How to share data

- **Open** format (csv, txt)
- **README** (who, what, when, where, why, how)
- **Describe variables**
- **Licence** (CC0, CC-BY, ODbL)
- **Citation** (DOI)
- **Metadata** standardised (JSON, XML)

Tierney & Ram 2020

## Document your data

```
library('dataspice')
create_spice()    # create CSV templates for metadata

edit_creators()  # open Shiny apps to edit the CSVs
prep_access()
edit_access()
prep_attributes()
edit_attributes()
edit_biblio()

write_spice()    # write machine-readable metadata

build_site()    # build human-readable metadata report
```

## How to share code

- Scripts: plain text (.R)
- Permanent archive (eg. Zenodo) with DOI (citable)
- Licence
- README
- Computational environment (session info)

Eglen et al 2016

# sessionInfo records OS & used packages

```
## R version 4.4.2 (2024-10-31)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 20.04.6 LTS
##
## Matrix products: default
## BLAS:    /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK:  /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3;  LAPACK version 3.9.0
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=es_ES.UTF-8      LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=es_ES.UTF-8    LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=es_ES.UTF-8      LC_NAME=C
##  [9] LC_ADDRESS=C              LC_TELEPHONE=C
## [11] LC_MEASUREMENT=es_ES.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Europe/Madrid
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats      graphics   grDevices  utils      datasets   methods    base
##
## other attached packages:
## [1] knitr_1.49
##
## loaded via a namespace (and not attached):
## [1] compiler_4.4.2   fastmap_1.2.0    cli_3.6.3      htmltools_0.5.8.1
## [5] tools_4.4.2     rstudioapi_0.17.1  yaml_2.3.10    codetools_0.2-20
## [9] rmarkdown_2.29    binb_0.0.7      xfun_0.50     digest_0.6.37
## [13] grid_4.4.2      gridExtra_2.3.3  lifecycle_0.2.10  pillar_1.9.1
## [17] purrr_0.3.4     readr_2.1.2     vctrs_0.6.0     generics_0.1.3
## [21] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [25] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [29] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [33] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [37] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [41] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [45] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [49] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [53] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [57] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [61] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [65] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [69] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [73] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [77] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [81] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [85] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [89] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
## [93] stringr_1.5.0    dplyr_1.1.0     forcats_0.5.1  readxl_1.1.0
## [97] readr_2.1.2     vctrs_0.6.0     generics_0.1.3  purrr_0.3.4
```

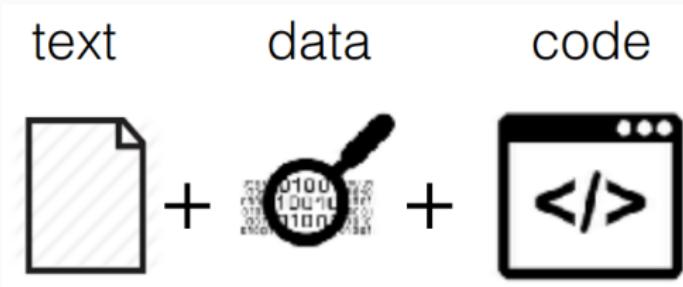
`renv` also records packages used

```
renv::snapshot()
```

creates `renv.lockfile` recording dependencies.

Can use `renv::restore()` to restore packages later or in different computer.

## Basic reproducibility

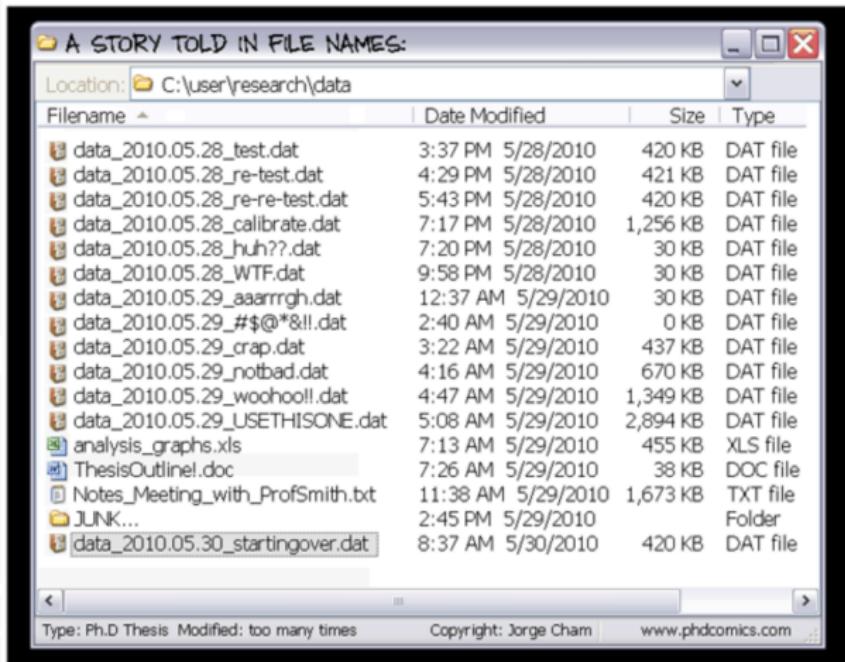


DATA + CODE

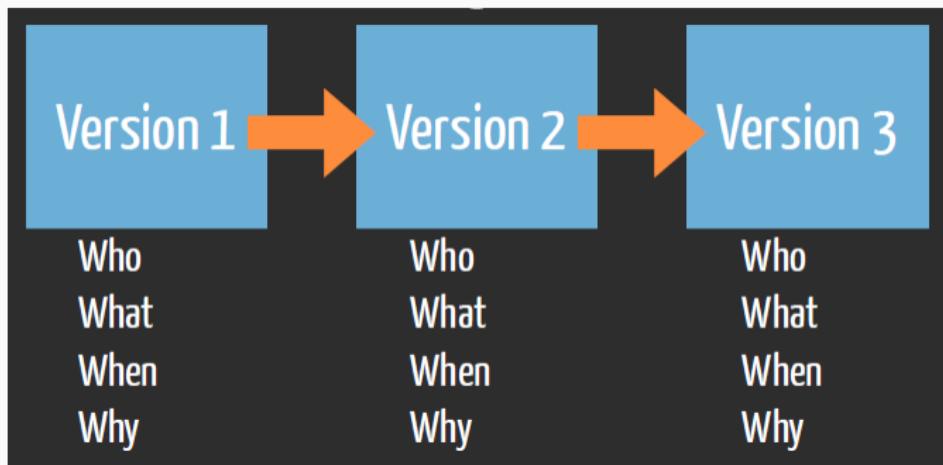
- analysis fully **traceable**
- results can be **regenerated**

## Version control

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# Version control with git

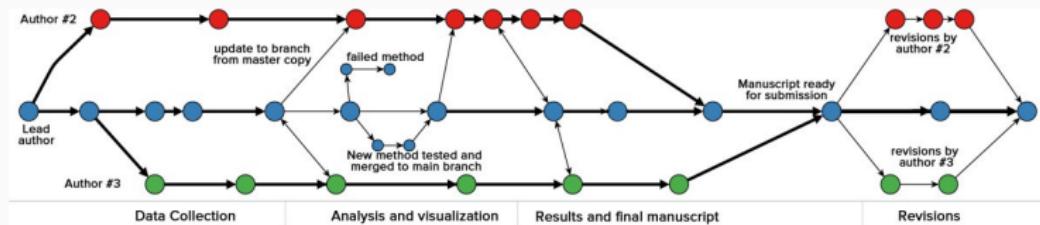


R. Fitzjohn

# Much to learn from software engineering

Git can facilitate greater reproducibility and increased transparency in science

Karthik Ram



Ram 2013

# Automatic checks with Continuous Integration

Reproducibility of computational workflows is automated using continuous analysis

Brett K Beaulieu-Jones<sup>1</sup> & Casey S Greene<sup>2</sup>

Pakillo / Carex.bipolar  

Current	Branches	Build History	Pull Requests	More options	☰
 master 	add two more articles to pkgdown	 #7 passed  1c006ff	 3 min 22 sec  a day ago		
 master 	added leaflet occurrence maps to appear as a	 #6 passed  57f5374	 5 min 23 sec  a day ago		
 master 	build site with pkgdown	 #5 passed  6108a7a	 17 min 35 sec  a day ago		
 master 	still trying to fix error with sf in travis (via rmat)	 #4 failed  2c922d4	 16 min 58 sec  2 days ago		
 master 	adding more sf dependencies to travis	 #3 errored  5a60b49	 13 min 59 sec  2 days ago		
 master 	trying to fix error with rgdal on travis	 #2 errored  076af29	 14 min 15 sec  2 days ago		
 master 	add travis	 #1 errored  4bce6e8	 18 min 54 sec  3 days ago		

## Structuring projects

---

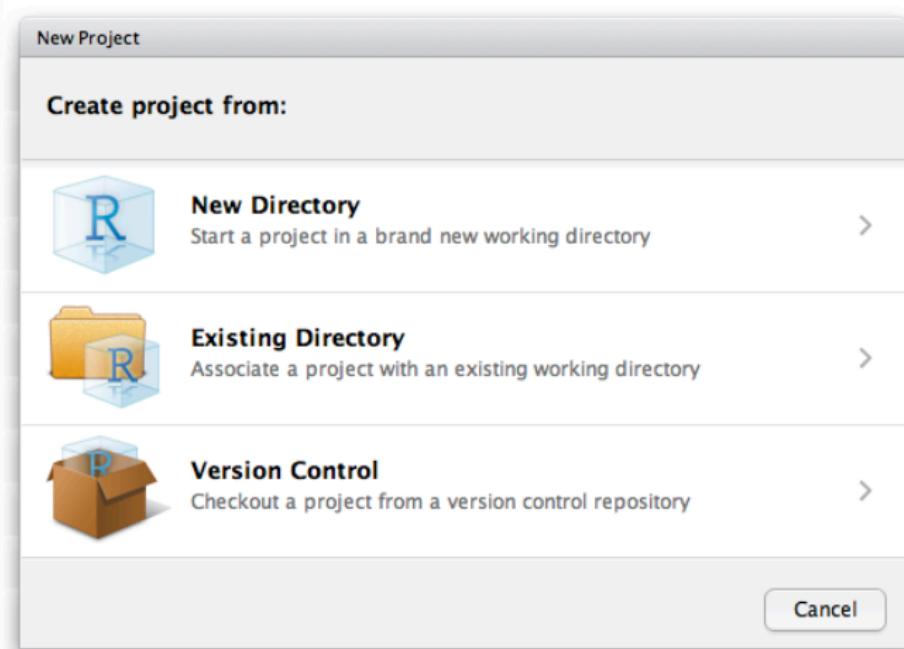
## One Project = One Folder

```
myproject
|
|- data
|
|- code
|
|- output (figures etc)
|
|- manuscript
```

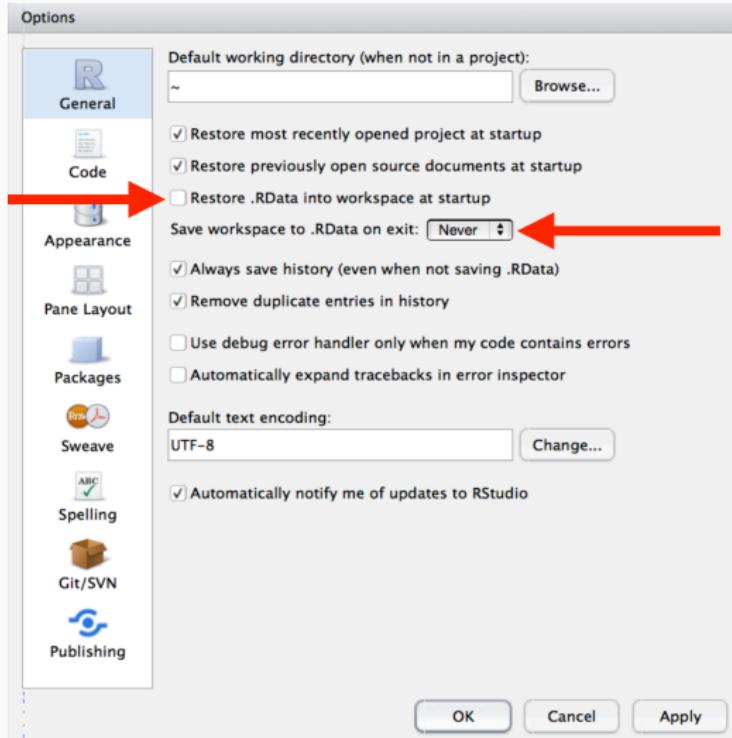
## Project-Oriented Workflow: advantages

- Self-contained
- Easy to navigate (file paths)
- Easy to share

# Rstudio projects



# Avoid saving workspace



<https://rstats.wtf>

# Use `here` for file paths



```
setwd('C:/Users/PACO/myproject')
```

```
mydata <- read.csv('data/mydata.csv')
```



```
library('here')
```

```
mydata <- here('data', 'mydata.csv')
```

## fertile package: real-time feedback on reproducibility

```
library('fertile')  
  
setwd("C:/Users/FRS")
```

*Error: setwd() is likely to break reproducibility. Use here::here() instead.*

<https://github.com/baumer-lab/fertile>

## Structuring projects: guidelines

---

## Guidelines for structuring projects

- All files in **same directory**

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Guidelines for structuring projects

- All files in **same directory**
- **Raw data** separate from **clean data**

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

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- All files in **same directory**
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- **Modular code** (functions)

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Guidelines for structuring projects

- All files in **same directory**
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- **Output disposable & separate** from code

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Guidelines for structuring projects

- All files in **same directory**
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- **Output disposable & separate** from code
- **makefile** runs analyses in **appropriate order**

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Guidelines for structuring projects

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- **Software dependencies** under control

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

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- All files in **same directory**
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- **Output disposable & separate** from code
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- **Software dependencies** under control
- **README**

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Guidelines for structuring projects

- All files in **same directory**
- **Raw data** separate from **clean data**
- **Modular code** (functions)
- **Output disposable & separate** from code
- **makefile** runs analyses in **appropriate order**
- **Software dependencies** under control
- **README**
- **License**

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

## Project organisation example

- data
  - data-raw
  - data-clean
- code
- output (figures etc)
- manuscript
- README
- License
- Makefile

- What
- Who
- How
- Licence
- Citation
- etc

**README.md**

## pandanusisotopes

 [Launch Binder](#)

This repository contains the data and code for our paper:

Florin, A. et al. (2020). *Palaeoprecipitation data from Madjedbebe, northern Australia: A novel proxy from ancient pandanus*.

### How to cite

Please cite this compendium as:

Marwick, B., A. Florin et al., (2020). *Compendium of R code and data for Palaeoprecipitation data from Madjedbebe, northern Australia: A novel proxy from ancient pandanus*. Accessed 16 Oct 2020. Online at <https://doi.org/xxx/xxx>

### How to download

You can download the compendium as a zip from this URL: <https://github.com/benmarwick/pandanusisotopes/archive/master.zip>

### Licenses

**Text and figures :** [CC-BY-4.0](#)

**Code :** See the [DESCRIPTION](#) file

**Data :** [CC-0](#) attribution requested in reuse

## Document your data

```
library("dataspice")
create_spice()    # create CSV templates for metadata

edit_creators()  # open Shiny apps to edit the CSVs
prep_access()
edit_access()
prep_attributes()
edit_attributes()
edit_biblio()

write_spice()    # write machine-readable metadata

build_site()    # build human-readable metadata report
```

Write modular code

Break up scripts

```
prepare_data.R
```

```
run_analysis.R
```

```
make_figures.R
```

(and `makefile` will run them in the right order)

makefile runs code in appropriate order

makefile.R

```
source("prepare_data.R")  
  
source("run_analysis.R")  
  
source("make_figures.R")
```

## Don't Repeat Yourself (DRY)

```
dataset %>%  
  filter(species == "Laurus nobilis") %>%  
  ggplot() +  
  geom_point(aes(x, y))  
  
dataset %>%  
  filter(species == "Laurus azorica") %>%  
  ggplot() +  
  geom_point(aes(x, y))
```

# Don't Repeat Yourself

Write functions (documented + tested)

```
plot_species <- function(sp, data) {  
  data %>%  
    filter(species == sp) %>%  
    ggplot() +  
    geom_point(aes(x, y))  
}
```

# Don't Repeat Yourself

Use functions

```
plot_species(sp = "Laurus nobilis", dataset)
```

```
plot_species(sp = "Laurus azorica", dataset)
```

# Don't Repeat Yourself

Use for loops

```
for (i in species) {  
  plot_species(sp = i, dataset)  
}
```

## Don't Repeat Yourself

Good ol' `lapply`

```
lapply(species, plot_species, data = dataset)
```

## Don't Repeat Yourself

```
library("purrr")  
  
map(species, plot_species, data = dataset)
```

## Comment your code

Why rather than What

```
## Response is not linear, so fit gam rather than lm  
  
model.height <- gam(height ~ s(diameter), data = trees)
```

## Use meaningful names for objects

```
m1 <- lm(height ~ diameter, data = trees)  
m2 <- gam(height ~ s(diameter), data = trees)
```

## Use meaningful names for objects

```
m1 <- lm(height ~ diameter, data = trees)  
m2 <- gam(height ~ s(diameter), data = trees)
```

```
model.linear <- lm(height ~ diameter, data = trees)  
model.gam <- gam(height ~ s(diameter), data = trees)
```

## Project templates

---

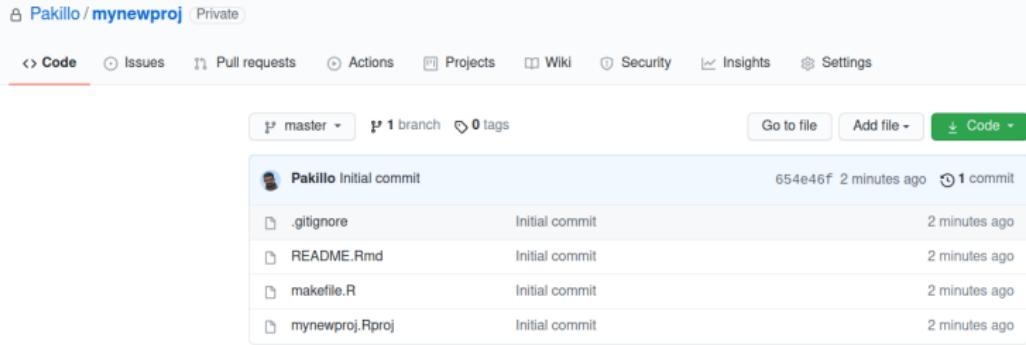
# Automatic project creation with template

```
library('template')  
  
new_project("mynewproj",  
            package = FALSE)
```

	analyses
	data
	data-raw
	manuscript
	R
	.Rproj.user
	makefile.R
	mynewproj.Rproj
	README.Rmd
	.gitignore

## template: New projects also on GitHub

```
new_project("mynewproj",  
           package = FALSE,  
           github = TRUE)
```



A screenshot of a GitHub repository page for 'Pakillo / mynewproj'. The repository is private. The 'Code' tab is selected. At the top, it shows 'master' branch, '1 branch', '0 tags', and a commit history. The commit history shows an 'Initial commit' by 'Pakillo' with commit hash '654e46f' and timestamp '2 minutes ago'. The commit details list four files: '.gitignore', 'README.Rmd', 'makefile.R', and 'mynewproj.Rproj', all with 'Initial commit' status and '2 minutes ago' timestamp.

File	Commit	Timestamp
.gitignore	Initial commit	2 minutes ago
README.Rmd	Initial commit	2 minutes ago
makefile.R	Initial commit	2 minutes ago
mynewproj.Rproj	Initial commit	2 minutes ago

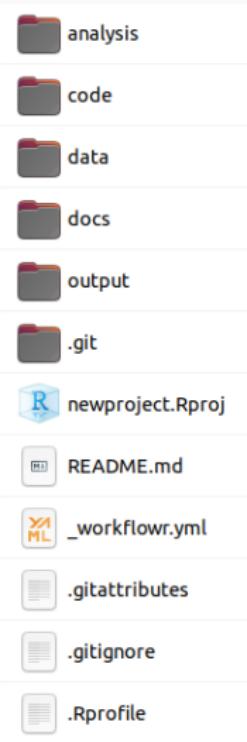


## workflowr: reproducible projects with website

---

## wflow\_start creates project scaffolding

```
library('workflowr')  
  
wflow_start("newproject")
```



## wflow\_open starts new analysis

```
wflow_open("analysis/first-analysis.Rmd")
```

```
---
```

```
title: "first-analysis"
author: "Pakillo"
date: "2021-06-15"
output: workflowr::wflow_html
editor_options:
  chunk_output_type: console
---
```

```
|
```

```
## Introduction
```

```
```{r}
data(iris)
plot(iris)
```
```

# wflow\_build runs analyses and generates website

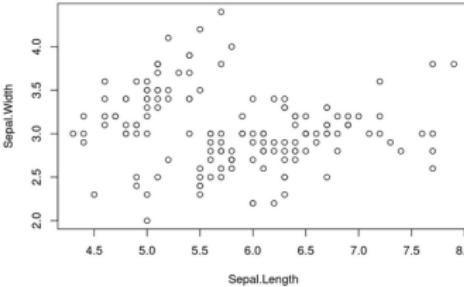
## wflow\_build()

newproject Home About License

Introduction first-analysis  
Pakillo  
2021-06-15  
workflow ✓

Introduction

```
data(iris)  
plot(iris[, 1:2])
```



A scatter plot showing the relationship between Sepal.Length (x-axis, ranging from 4.5 to 8.0) and Sepal.Width (y-axis, ranging from 2.0 to 4.0). The data points are open circles, representing the first two columns of the Iris dataset. The plot shows a clear positive correlation, with Sepal.Length generally increasing as Sepal.Width increases.

Past versions of unnamed-chunk-1-1.png

Session information

wflow\_publish commits changes & updates everything

```
wflow_publish(c("analysis/first-analysis.Rmd",
  "analysis/index.Rmd",
  "analysis/about.Rmd",
  "analysis/license.Rmd"),
  message = "Publish initial analyses")
```

## Connect with GitHub/GitLab and deploy website

```
wflow_use_github("Pakillo")
```

```
wflow_git_push()
```

## Research compendia: projects as packages

---

## Projects as packages

- Standard structure

[Rodríguez-Sánchez et al. 2016](#), [Marwick et al 2018](#), but see [McBain 2020](#)

## Projects as packages

- Standard structure
- Promotes modular code, documented and tested

[Rodríguez-Sánchez et al. 2016](#), [Marwick et al 2018](#), but see [McBain 2020](#)

## Projects as packages

- Standard structure
- Promotes modular code, documented and tested
- Easy to share and run

[Rodríguez-Sánchez et al. 2016](#), [Marwick et al 2018](#), but see [McBain 2020](#)

## Projects as packages

- Standard structure
- Promotes modular code, documented and tested
- Easy to share and run
- Automatic checks (Continuous Integration)

[Rodríguez-Sánchez et al. 2016](#), [Marwick et al 2018](#), but see [McBain 2020](#)

## Projects as packages

- Standard structure
- Promotes modular code, documented and tested
- Easy to share and run
- Automatic checks (Continuous Integration)
- Automatic code review (**good practice**)

Rodríguez-Sánchez et al. 2016, Marwick et al 2018, but see [McBain 2020](#)

## Projects as packages

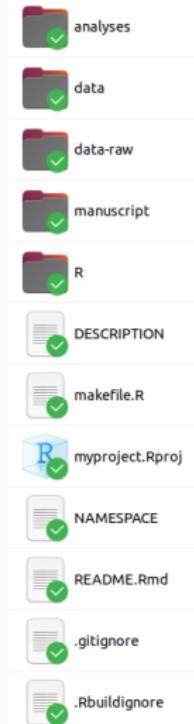
- Standard structure
- Promotes modular code, documented and tested
- Easy to share and run
- Automatic checks (Continuous Integration)
- Automatic code review ([goodpractice](#))
- Easily create website with `pkgdown`

[Rodríguez-Sánchez et al. 2016](#), [Marwick et al 2018](#), but see [McBain 2020](#)

# Creating package structure with template

```
library('template')
```

```
new_project('myproject',  
           package = TRUE)
```



rrtools

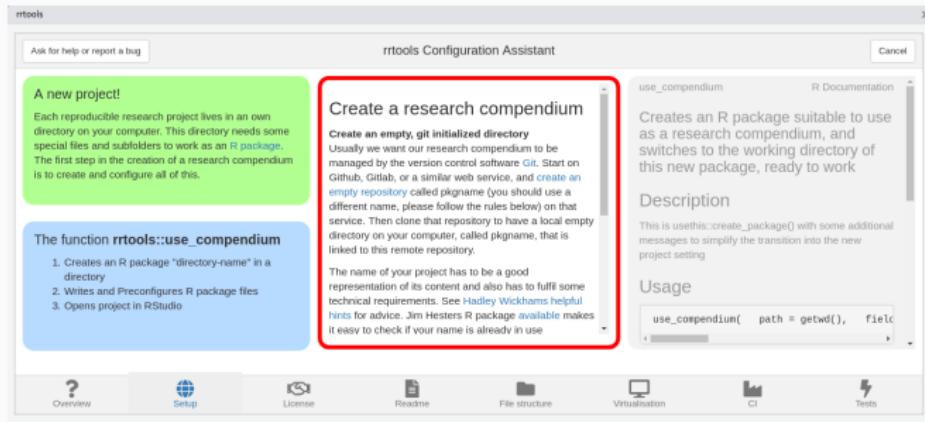
---

# rrtools creates research compendia

```
library('rrtools')

use_compendium('~/myproject/')
```

Rstudio addin: <https://github.com/nevrome/rrtools.addin>



## rrtools: project structure

```
- README
- LICENSE
- DESCRIPTION
- renv/
- Dockerfile
- analysis/
|
|- paper/
  |- paper.qmd
  |- references.bib
|
|- figures/
|
|- data/
  |- raw_data/
  |- derived_data/
```



rcompendium

---

## rcompendium creates new project with all scaffolding

```
library('rcompendium')  
  
new_compendium()
```

- R package structure
- GitHub repository
- Automatic testing & website update

# Continuous Integration (GitHub Actions, GitLab CI...)

Automatic testing with every commit!

| Pakillo / Carex.bipolar |          |  |                             |                             |
|-------------------------|----------|--|-----------------------------|-----------------------------|
| Current                 | Branches | Build History  | Pull Requests               |                             |
| ✓ master                | Pakillo  | add two more articles to pkgdown                       | → #7 passed<br>→ 1c006ff ↗  | 3 min 22 sec<br>a day ago   |
| ✓ master                | Pakillo  | added leaflet occurrence maps to appear as a           | → #6 passed<br>→ 57f5374 ↗  | 5 min 23 sec<br>a day ago   |
| ✓ master                | Pakillo  | build site with pkgdown                                | → #5 passed<br>→ 6108a7a ↗  | 17 min 35 sec<br>a day ago  |
| ✗ master                | Pakillo  | still trying to fix error with sf in travis (via rnat) | → #4 failed<br>→ 2c922d4 ↗  | 16 min 58 sec<br>2 days ago |
| ✗ master                | Pakillo  | adding more sf dependencies to travis                  | → #3 errored<br>→ 5a60b49 ↗ | 13 min 59 sec<br>2 days ago |
| ✗ master                | Pakillo  | trying to fix error with rgdal on travis               | → #2 errored<br>→ 076af29 ↗ | 14 min 15 sec<br>2 days ago |
| ✗ master                | Pakillo  | add travis   | → #1 errored<br>→ 4bce6e8 ↗ | 18 min 54 sec<br>3 days ago |

## Minimalistic compendium

<https://github.com/cboettig/compendium>

- DESCRIPTION (dependencies)
- Manuscript (Rmd)
- GitHub Actions

## Data management

---

# Data management

See

<https://dataoneorg.github.io/Education/bestpractices/>

- 1. [Planification](#) (e.g. [DMPTool](#))
- 2. Collection
- 3. [Metadata description](#) ([dataspice](#), [EML](#), [Data Packages](#), [DataPackageR](#))
- 4. [Quality control](#) (e.g. [assertr](#), [validate](#), [pointblank](#))
- 5. [Storage](#)

## Document your data

```
library('dataspice')

create_spice()    # create CSV templates for metadata

edit_creators()  # open Shiny apps to edit the CSVs
prep_access()
edit_access()
prep_attributes()
edit_attributes()
edit_biblio()

write_spice()    # write machine-readable metadata

build_site()    # build human-readable metadata report
```

<https://docs.ropensci.org/dataspice/>

## Check data before analysis

```
library('assertr')

dataset %>%
  assert(within_bounds(0, 0.20), fruit.weight) %>%
  assert(in_set('black', 'red'), colour)
```

Check out also [pointblank](#)

## *Editorial expression of concern*

IN THE 3 June issue, *Science* published the Report “Environmentally relevant concentrations of microplastic particles influence larval fish ecology” by Oona M. Lönnstedt and Peter Eklöv (1). The authors have notified *Science* of the theft of the computer on which the raw data for the paper were stored. These data were not backed up on any other device nor deposited in an appropriate repository. *Science* is publishing this Editorial Expression of Concern to alert our readers to the fact that no further data can be made available, beyond those already presented in the paper and its supplement, to enable readers to understand, assess, reproduce, or extend the conclusions of the paper.

*Jeremy Berg*  
Editor in Chief

# Storage

Use the **cloud**: safe, persistent, easy to share

- Open Science Framework
- GitHub
- Dropbox
- Figshare, Zenodo, etc
- See all data repositories in [www.re3data.org](http://www.re3data.org)

## Tidy data

---

# Tidy data

| country     | year | cases  | population |
|-------------|------|--------|------------|
| Afghanistan | 1999 | 745    | 1537071    |
| Afghanistan | 2000 | 2666   | 2059360    |
| Brazil      | 1999 | 37737  | 17206362   |
| Brazil      | 2000 | 80488  | 174504898  |
| China       | 1999 | 212258 | 1272015272 |
| China       | 2000 | 213766 | 128012583  |

variables

| country     | year | cases  | population |
|-------------|------|--------|------------|
| Afghanistan | 1999 | 745    | 1537071    |
| Afghanistan | 2000 | 2666   | 2059360    |
| Brazil      | 1999 | 37737  | 17206362   |
| Brazil      | 2000 | 80488  | 174504898  |
| China       | 1999 | 212258 | 1272015272 |
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observations

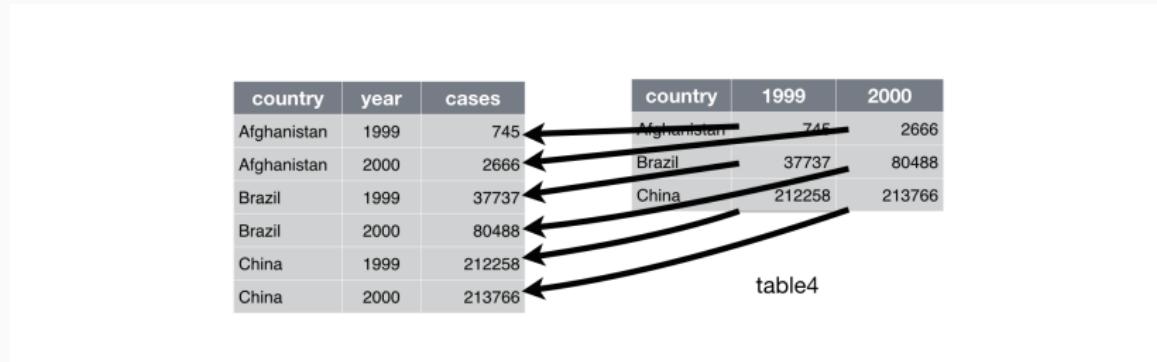
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values

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| country     | 1999   | 2000   |
|-------------|--------|--------|
| Afghanistan | 745    | 2666   |
| Brazil      | 37737  | 80488  |
| China       | 212258 | 213766 |

table4



COMMENT

Open Access



## Gene name errors are widespread in the scientific literature

Mark Ziemann<sup>1</sup>, Yotam Eren<sup>1,2</sup> and Assam El-Osta<sup>1,3\*</sup>

### Abstract

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

frequently reused. Our aim here is to raise awareness of the problem.

We downloaded and screened supplementary files from 18 journals published between 2005 and 2015 using a suite of shell scripts. Excel files (.xls and .xlsx suffixes) were converted to tabular separated files (tsv) with ssconvert (v1.12.9). Each sheet within the Excel file was converted to a separate tsv file. Each column of data in the tsv file was screened for the presence of gene sym-

### A. Hallmarks of well managed tabular data

|   |   |   |   |  |
|---|---|---|---|--|
| 1 Computer friendly   | 2 Descriptive headers   | 3 Atomized  | 4 Quality controlled  | 9 Data dictionary  |
|  |  |  |  |  |
| 10 Non-proprietary format   |   |   |   |  |
|   |   |   |   | sample_id: unique identifier for each sample<br>loc: collection site<br>habitat: collection habitat<br>temp: air temperature during collection (Celsius)<br>date: collection date<br>species: scientific name of specimen<br>length_mm: specimen length in millimeters |
|   |   |   |   | 8 Analysis saved in separate file  |
|   |   |   |   | 7 Read only copy   |
|   |   |   | 5 Defined null value  | 6 Date consistent  |

### B. Hallmarks of poorly managed tabular data

|   |   |  |   |                             |
|---|---|--|---|-----------------------------|
| 1 Colors as data  | 2 Headers not machine readable  | 3 Multiple data points per cell  | 4 Unvalidated data  | 9 Metadata in column header |
|  |  |  |  |                             |
| 10 Proprietary format   |   |  |   |                             |
|   |   |  |   | 8 Analysis in the same file |
|   |   |  | 5 Undefined null value  | 6 Date inconsistent         |
|   |   |  |   | 7 Edited raw data           |

## Spreadsheet good practices

- Put **variables** in **columns** (things you are measuring: height, weight, sex)

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- Input dates as **year, month, day** in separate columns. Or **YYYY-MM-DD** as text.

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- **Don't touch raw data.** Do all data manipulation through code.

# Spreadsheet good practices

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- Export data as plain text (txt, csv).

# Spreadsheet good practices

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- Use **Data validation** in Excel (or GForms) to constrain data entry to accepted values.
- Don't combine multiple pieces of information in one cell.
- **Don't touch raw data.** Do all data manipulation through code.
- Export data as plain text (txt, csv).
- <http://www.datacarpentry.org/spreadsheet-ecology-lesson/>

# Spreadsheet good practices

- Put **variables** in **columns** (things you are measuring: height, weight, sex)
- Each **observation** in one **row** (e.g. individuals).
- Avoid spaces, numbers, and **special characters** in column names.
- Always **write zero values**, to distinguish from blank/missing data.
- Use blank/empty cells, or NA, for missing data.
- Input dates as **year, month, day** in separate columns. Or YYYY-MM-DD as text.
- Use **Data validation** in Excel (or GForms) to constrain data entry to accepted values.
- Don't combine multiple pieces of information in one cell.
- **Don't touch raw data.** Do all data manipulation through code.
- Export data as plain text (txt, csv).
- <http://www.datacarpentry.org/spreadsheet-ecology-lesson/>
- <http://kbroman.org/dataorg/>

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- <http://kbroman.org/dataorg/>
- Broman & Woo: [Data organization in spreadsheets](#)

## Common spreadsheet errors

---

## More than one variable per column

| Date collected | Plot | Species-Sex | Weight |
|----------------|------|-------------|--------|
| 1/9/78         | 1    | DM-M        | 40     |
| 1/9/78         | 1    | DM-F        | 36     |
| 1/9/78         | 1    | DS-F        | 135    |
| 1/20/78        | 1    | DM-F        | 39     |
| 1/20/78        | 2    | DM-M        | 43     |
| 1/20/78        | 2    | DS-F        | 144    |
| 3/13/78        | 2    | DM-F        | 51     |
| 3/13/78        | 2    | DM-F        | 44     |
| 3/13/78        | 2    | DS-F        | 146    |

| Date collected | Plot | Species | Sex | Weight |
|----------------|------|---------|-----|--------|
| 1/9/78         | 1    | DM      | M   | 40     |
| 1/9/78         | 1    | DM      | F   | 36     |
| 1/9/78         | 1    | DS      | F   | 135    |
| 1/20/78        | 1    | DM      | F   | 39     |
| 1/20/78        | 2    | DM      | M   | 43     |
| 1/20/78        | 2    | DS      | F   | 144    |
| 3/13/78        | 2    | DM      | F   | 51     |
| 3/13/78        | 2    | DM      | F   | 44     |
| 3/13/78        | 2    | DS      | F   | 146    |

Source: Data Carpentry

# Multiple tables

|    | A                     | B       | C    | D    | E           | F       | G   | H     | I                     | J       | K    | L           | M      | N       | O    | P        | Q                     | R       | S    | T            | U      | V       | W     | X         | Y                     | Z    | AA   | AB          | AC     | AD      | AE      | AF     | AI     |  |  |
|----|-----------------------|---------|------|------|-------------|---------|-----|-------|-----------------------|---------|------|-------------|--------|---------|------|----------|-----------------------|---------|------|--------------|--------|---------|-------|-----------|-----------------------|------|------|-------------|--------|---------|---------|--------|--------|--|--|
| 1  |                       |         |      |      |             |         |     |       |                       |         |      |             |        |         |      |          |                       |         |      |              |        |         |       |           |                       |      |      |             |        |         |         |        |        |  |  |
| 2  | lake site May 29 2012 |         |      |      | 29-May      |         |     |       | lake site Jun 12 2012 |         |      |             | 12-Jun |         |      |          | lake site Jun 19 2012 |         |      |              | 19-Jun |         |       |           | Lake site Jun 26 2012 |      |      |             | 26-Jun |         |         |        |        |  |  |
| 3  |                       |         |      |      | avr         | SEM     |     |       | plot                  | bug1    | bug2 |             | avr    | SEM     |      |          | plot                  | bug1    | bug2 | gene<br>(al) | avr    | SEM     |       |           | plot                  | bug1 | bug2 | gener<br>al | avr    | SEM     |         |        |        |  |  |
| 4  | 1                     | T1      | 1    | 1    | 2           | T1      | 2.6 | 0.51  | 1                     | T1      | 6    | 85          | 91     | T1      | 30.4 | 15.47126 | 1                     | T1      | 17   | 80           | 97     | avr     | SEM   |           |                       | 1    | T1   | 52          | 191    | 243     | avr     | SEM    |        |  |  |
| 5  | 2                     | T1      | 1    | 2    | 3           | T2      | 0.2 | 0.2   | 2                     | T1      | 8    | 13          | 21     | T2      | 0.2  | 0.2      | 2                     | T1      | 44   | 136          | 180    | T1      | 77.8  | 30.384865 | 2                     | T1   | 50   | 270         | 320    | T1      | 141.6   | 60.313 |        |  |  |
| 6  | 3                     | T1      | 1    | 3    | 4           | control | 0.2 | 0.2   | 3                     | T1      | 12   | 0           | 11     | control | 0.6  | 0.6      | 3                     | T1      | 18   | 0            | 18     | T2      | 1.8   | 1.5620499 | 3                     | T1   | 6    | 0           | 6      | T2      | 0.2     | 0.2    |        |  |  |
| 7  | 4                     | T1      | 1    | 0    | 1           |         |     |       | 4                     | T1      | 0    | 6           | 6      |         |      |          | 4                     | T1      | 0    | 14           | 14     | control | 0.4   | 0.244949  | 4                     | T1   | 0    | 39          | 39     |         | control | 0      | 0      |  |  |
| 8  | 5                     | T1      | 0    | 3    | 3           |         |     |       | 5                     | T1      | 5    | 20          | 23     |         |      |          | 5                     | T1      | 10   | 70           | 80     |         |       | 5         | T1                    | 4    | 96   | 100         |        |         |         |        |        |  |  |
| 9  | 6                     | T2      | 1    | 0    | 1           |         |     |       | 6                     | T2      | 0    | 0           | 0      |         |      |          | 6                     | T2      | 1    | 7            | 8      |         |       | 6         | T2                    | 0    | 1    | 1           |        |         |         |        |        |  |  |
| 10 | 7                     | T2      | 0    | 0    | 0           |         |     |       | 7                     | T2      | 0    | 0           | 0      |         |      |          | 7                     | T2      | 0    | 1            | 1      |         |       | 7         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 11 | 8                     | T2      | 0    | 0    | 0           |         |     |       | 8                     | T2      | 1    | 0           | 1      |         |      |          | 8                     | T2      | 0    | 0            | 0      |         |       | 8         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 12 | 9                     | T2      | 0    | 0    | 0           |         |     |       | 9                     | T2      | 0    | 0           | 0      |         |      |          | 9                     | T2      | 0    | 0            | 0      |         |       | 9         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 13 | 10                    | T2      | 0    | 0    | 0           |         |     |       | 10                    | T2      | 0    | 0           | 0      |         |      |          | 10                    | T2      | 0    | 0            | 0      |         |       | 10        | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 14 | 11                    | control | 0    | 0    | 0           |         |     |       | 11                    | control | 0    | 0           | 0      |         |      |          | 11                    | control | 0    | 0            | 0      |         |       | 11        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 15 | 12                    | control | 0    | 0    | 0           |         |     |       | 12                    | control | 0    | 0           | 0      |         |      |          | 12                    | control | 0    | 0            | 0      |         |       | 12        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 16 | 13                    | control | 0    | 0    | 0           |         |     |       | 13                    | control | 0    | 0           | 0      |         |      |          | 13                    | control | 0    | 0            | 0      |         |       | 13        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 17 | 14                    | control | 0    | 0    | 0           |         |     |       | 14                    | control | 0    | 0           | 0      |         |      |          | 14                    | control | 0    | 1            | 1      |         |       | 14        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 18 | 15                    | control | 1    | 0    | 1           |         |     |       | 15                    | control | 0    | 3           | 3      |         |      |          | 15                    | control | 0    | 1            | 1      |         |       | 15        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 19 |                       |         |      |      |             |         |     |       |                       |         |      |             |        |         |      |          |                       |         |      |              |        |         |       |           |                       |      |      |             |        |         |         |        |        |  |  |
| 20 |                       |         |      |      |             |         |     |       |                       |         |      |             |        |         |      |          |                       |         |      |              |        |         |       |           |                       |      |      |             |        |         |         |        |        |  |  |
| 21 | Barn site May 29 2012 |         |      |      | 29-May      |         |     |       | Barn site Jun 12 2012 |         |      |             | 12-Jun |         |      |          | Barn site Jun 19 2012 |         |      |              | 19-Jun |         |       |           | Barn Site Jun 26 2012 |      |      |             | 26-Jun |         |         |        |        |  |  |
| 22 |                       | plot    | bug1 | bug2 | gen<br>eral |         |     |       | plot                  | bug1    | bug2 | gen<br>(al) |        |         |      |          | plot                  | bug1    | bug2 | gene<br>(al) |        |         |       |           | plot                  | bug1 | bug2 | gener<br>al | avr    | SEM     |         |        |        |  |  |
| 23 | 1                     | T1      | 3    | 3    | 6           |         |     |       | 1                     | T1      | 21   | 0           | 21     |         |      |          | 1                     | T1      | 5    | 0            | 5      |         |       |           |                       | 1    | T1   | 0           | 0      | 0       |         |        |        |  |  |
| 24 | 2                     | T1      | 1    | 4    | 5           |         |     |       | 2                     | T1      | 36   | 74          | 110    |         |      |          | 2                     | T1      | 65   | 502          | 567    |         |       |           |                       | 2    | T1   | 44          | 2057   | 2101    | T1      | 431.8  | 417.33 |  |  |
| 25 | 3                     | T1      | 0    | 0    | 0           | T1      | 2.4 | 1.288 | 3                     | T1      | 18   | 0           | 13     | T1      | 30.6 | 20.10124 | 3                     | T1      | 10   | 7            | 17     | T1      | 119.4 | 111.92882 | 3                     | T1   | 12   | 20          | 32     | T2      | 0.4     | 0.4    |        |  |  |
| 26 | 4                     | T1      | 0    | 0    | 0           | T2      | 0.4 | 0.245 | 4                     | T1      | 7    | 0           | 7      | T2      | 5    | 0.774597 | 4                     | T1      | 0    | 6            | 6      | T2      | 5     | 1908902   | 4                     | T1   | 0    | 16          | 16     | control | 1.2     | 0.5831 |        |  |  |
| 27 | 5                     | T1      | 0    | 1    | 1           | control | 1   | 0.316 | 5                     | T1      | 2    | 0           | 2      | control | 2.2  | 1.714643 | 5                     | T1      | 0    | 2            | 2      | control | 2.8   | 0.969536  | 5                     | T1   | 0    | 10          | 10     |         |         |        |        |  |  |
| 28 | 6                     | T2      | 0    | 0    | 0           |         |     |       | 6                     | T2      | 1    | 0           | 1      |         |      |          | 6                     | T2      | 0    | 8            | 8      |         |       | 6         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 29 | 7                     | T2      | 0    | 0    | 0           |         |     |       | 7                     | T2      | 0    | 4           | 4      |         |      |          | 7                     | T2      | 0    | 12           | 12     |         |       | 7         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 30 | 8                     | T2      | 0    | 1    | 1           |         |     |       | 8                     | T2      | 0    | 0           | 0      |         |      |          | 8                     | T2      | 0    | 0            | 0      |         |       | 8         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 31 | 9                     | T2      | 0    | 1    | 1           |         |     |       | 9                     | T2      | 0    | 0           | 0      |         |      |          | 9                     | T2      | 3    | 0            | 3      |         |       | 9         | T2                    | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 32 | 10                    | T2      | 0    | 0    | 0           |         |     |       | 10                    | T2      | 0    | 0           | 0      |         |      |          | 10                    | T2      | 2    | 0            | 2      |         |       | 10        | T2                    | 0    | 2    | 2           |        |         |         |        |        |  |  |
| 33 | 11                    | control | 0    | 0    | 0           |         |     |       | 11                    | control | 1    | 0           | 1      |         |      |          | 11                    | control | 0    | 5            | 5      |         |       | 11        | control               | 0    | 2    | 2           |        |         |         |        |        |  |  |
| 34 | 12                    | control | 0    | 1    | 1           |         |     |       | 12                    | control | 0    | 0           | 0      |         |      |          | 12                    | control | 1    | 1            | 2      |         |       | 12        | control               | 1    | 0    | 1           |        |         |         |        |        |  |  |
| 35 | 13                    | control | 0    | 1    | 1           |         |     |       | 13                    | control | 0    | 0           | 0      |         |      |          | 13                    | control | 0    | 0            | 0      |         |       | 13        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 36 | 14                    | control | 1    | 1    | 1           |         |     |       | 14                    | control | 0    | 1           | 0      |         |      |          | 14                    | control | 0    | 5            | 5      |         |       | 14        | control               | 0    | 0    | 0           |        |         |         |        |        |  |  |
| 37 | 15                    | control | 0    | 2    | 2           |         |     |       | 15                    | control | 0    | 1           | 1      |         |      |          | 15                    | control | 0    | 2            | 2      |         |       | 15        | control               | 1    | 0    | 0           |        |         |         |        |        |  |  |
| 38 |                       |         |      |      |             |         |     |       |                       |         |      |             |        |         |      |          |                       |         |      |              |        |         |       |           |                       |      |      |             |        |         |         |        |        |  |  |
| 39 |                       |         |      |      |             |         |     |       |                       |         |      |             |        |         |      |          |                       |         |      |              |        |         |       |           |                       |      |      |             |        |         |         |        |        |  |  |

## Multiple tabs

Could you avoid new tab by adding a column to original spreadsheet?

## Using formatting, comments, etc to convey information

| Plot: 2                           |         |     |        |
|-----------------------------------|---------|-----|--------|
| Date collected                    | Species | Sex | Weight |
| 1/8/14                            | NA      |     |        |
| 1/8/14                            | DM      | M   | 44     |
| 1/8/14                            | DM      | M   | 38     |
| 1/8/14                            | OL      |     |        |
| 1/8/14                            | PE      | M   | 22     |
| 1/8/14                            | DM      | M   | 38     |
| 1/8/14                            | DM      | M   | 48     |
| 1/8/14                            | DM      | M   | 43     |
| 1/8/14                            | DM      | F   | 35     |
| 1/8/14                            | DM      | M   | 43     |
| 1/8/14                            | DM      | F   | 37     |
| 1/8/14                            | PF      | F   | 7      |
| 1/8/14                            | DM      | M   | 45     |
| 1/8/14                            | OT      |     |        |
| 1/8/14                            | DS      | M   | 157    |
| 1/8/14                            | OX      |     |        |
| 2/18/14                           | NA      | M   | 218    |
| 2/18/14                           | PF      | F   | 7      |
| 2/18/14                           | DM      | M   | 52     |
| measurement device not calibrated |         |     |        |

| Date collected | Species | Sex | Weight | Calibrated |
|----------------|---------|-----|--------|------------|
| 1/8/14         | NA      |     |        |            |
| 1/8/14         | DM      | M   | 44     | Y          |
| 1/8/14         | DM      | M   | 38     | Y          |
| 1/8/14         | OL      |     |        |            |
| 1/8/14         | PE      | M   | 22     | Y          |
| 1/8/14         | DM      | M   | 38     | Y          |
| 1/8/14         | DM      | M   | 48     | Y          |
| 1/8/14         | DM      | M   | 43     | Y          |
| 1/8/14         | DM      | F   | 35     | Y          |
| 1/8/14         | DM      | M   | 43     | Y          |
| 1/8/14         | DM      | F   | 37     | Y          |
| 1/8/14         | PF      | F   | 7      | Y          |
| 1/8/14         | DM      | M   | 45     | Y          |
| 1/8/14         | OT      |     |        |            |
| 1/8/14         | DS      | M   | 157    | N          |
| 1/8/14         | OX      |     |        |            |
| 2/18/14        | NA      | M   | 218    | N          |
| 2/18/14        | PF      | F   | 7      | Y          |
| 2/18/14        | DM      | M   | 52     | Y          |

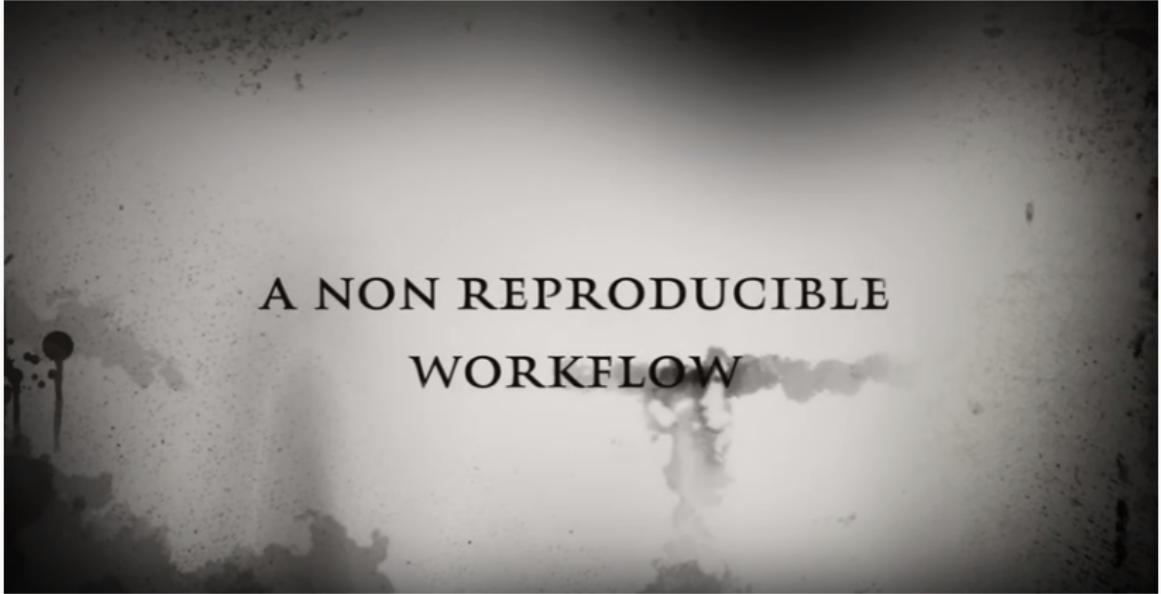
Your turn: tidy up this messy dataset

<https://ndownloader.figshare.com/files/2252083>

## Reproducible dynamic documents with Rmarkdown

---

A scary movie... with happy ending



A NON REPRODUCIBLE  
WORKFLOW

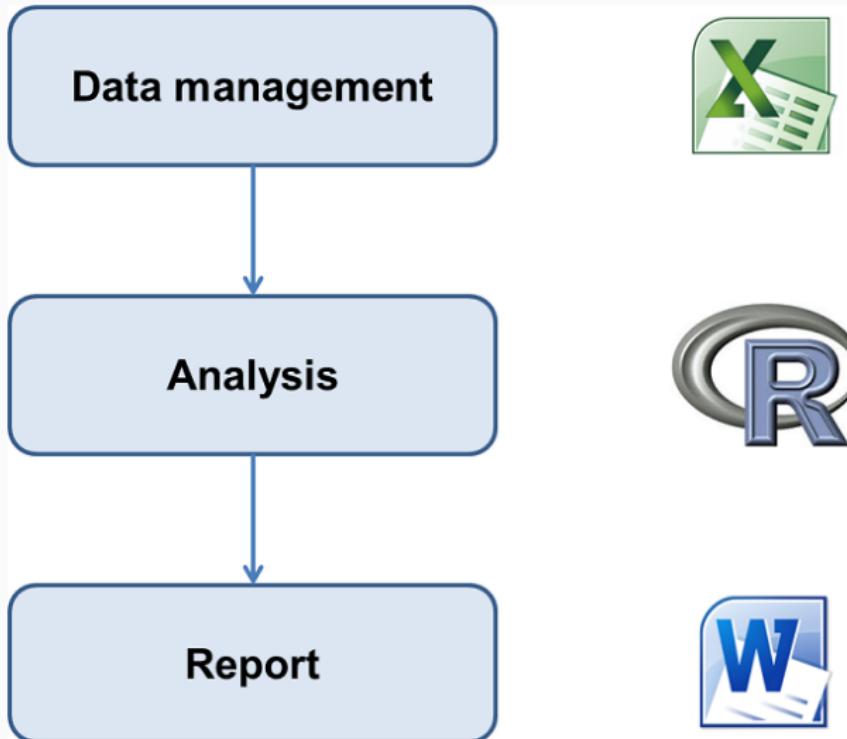
<https://youtu.be/s3JldKoA0zw>

## A typical research workflow

1. Prepare data (spreadsheet)
2. Analyse data (R)
3. Write report/paper (Word)
4. Start the email attachments  
nightmare...



This workflow is broken



## Problems of a broken workflow

- How did you do this? What analysis is behind this figure? Did you account for ...?

## Problems of a broken workflow

- How did you do this? What analysis is behind this figure? Did you account for ...?
- What dataset was used? Which individuals were left out? Where is the clean dataset?

## Problems of a broken workflow

- How did you do this? What analysis is behind this figure? Did you account for ...?
- What dataset was used? Which individuals were left out? Where is the clean dataset?
- Oops, there is an error in the data. Can you repeat the analysis? And update figures/tables in Word!

Manual copy-paste is tedious & problematic

Coefficients:

|             | Estimate   | Std. Error | t value | Pr(> t ) |
|-------------|------------|------------|---------|----------|
| (Intercept) | -0.0651657 | 0.4264970  | -0.153  | 0.879    |
| sunshine    | 0.0100228  | 0.0004232  | 23.683  | <2e-16   |

'Transcribing numbers from stats software by hand was the largest source of errors'

(Eubank 2016)



**Trevor A. Branch**

@TrevorABranch

 Follow

My rule of thumb: every analysis you do on a dataset will have to be redone 10–15 times before publication. Plan accordingly. **#Rstats**

Your **closest collaborator** is you 6 months ago,  
and you don't respond to emails.

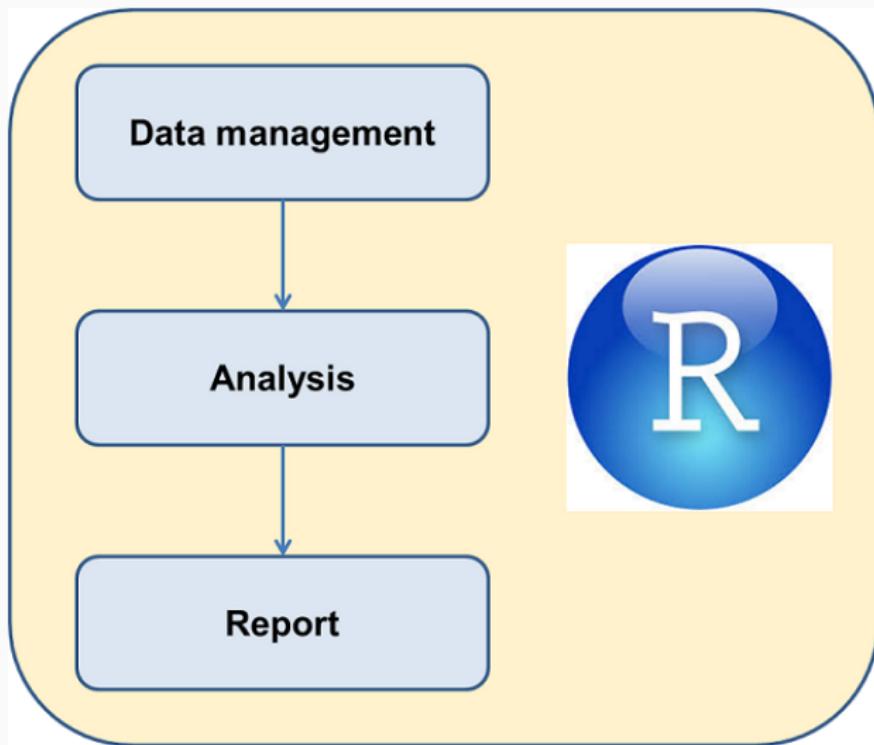
(P. Wilson)

Even **you** will struggle to reproduce  
**your own results** from a few weeks/months ago.

Writing reproducible manuscripts is hard

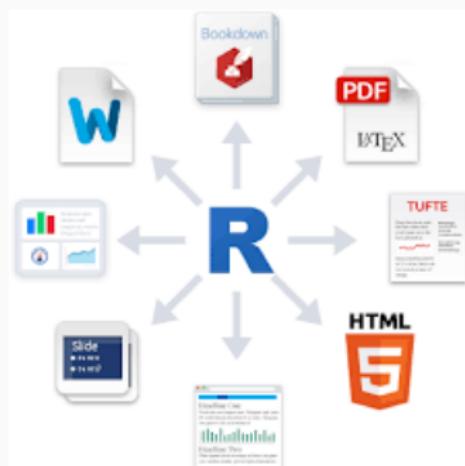
Revising non-reproducible manuscripts is even harder

Also, please note that because rev#1  
asked to re-calculate effect sizes (...)  
we need to change every single  
number in the main text.

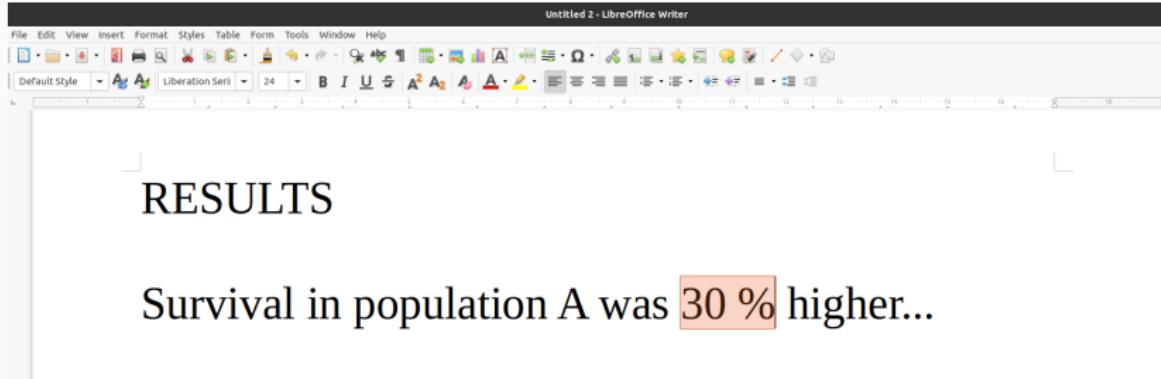


## Rmarkdown documents

- Fully reproducible (trace all results inc. tables and plots)
- Dynamic (regenerate with 1 click)
- Multiple outputs:
  - documents (HTML, Word, PDF)
  - presentations (HTML, PDF, PowerPoint)
  - books
  - websites...



Where does this value come from?



RESULTS

Survival in population A was 30 % higher...

The image shows a screenshot of the LibreOffice Writer application. The title bar reads "Untitled 2 - LibreOffice Writer". The menu bar includes File, Edit, View, Insert, Format, Styles, Table, Form, Tools, Window, and Help. The toolbar below the menu bar contains icons for various document operations like opening, saving, and printing. The text "RESULTS" is written in a large, bold, black font. Below it, the sentence "Survival in population A was 30 % higher..." is written in a smaller black font. The word "30 % higher..." is highlighted with a light orange rectangular box. The background of the slide is white.

# Dynamic documents with Rmarkdown

*Rmarkdown:*

Survival in population A was `r surv.diff` % higher

*Output:*

Survival in population A was **30** % higher

# Dynamic documents with Rmarkdown

```
mydata <- read.csv('data.txt')
```

*Rmarkdown:*

We measured `r nrow(mydata)` individuals

*Output:*

We measured **100** individuals

*Much better than copy-paste!*

# Rmarkdown: code (R, Python, etc) + text (Markdown)

```
---
```

```
title: "Does sunshine make people happy?"  
author: "FRS"  
output: word_document  
---  
  
## Introduction  
  
It is well known that individual well-being can be influenced by climatic conditions.  
  
## Methods  
  
```{r echo=FALSE}  
## Read data  
data <- read.table("data.txt", header = TRUE)  
  
# Fit linear model  
model <- lm(happiness ~ sunshine, data = data)  
```
```

Metadata  
(YAML)

Text  
(Markdown)

Code  
(R, Python...)

We collected data on `r nrow(data)` individuals and fitted a linear model.

## Code chunk options

```
```{r echo=FALSE, eval=TRUE, cache=TRUE, fig.height=3}
plot(iris)
```
```

<https://yihui.org/knitr/options/>

## Code chunk options

```
```{r}
#| echo = FALSE
#| eval = TRUE
#| fig.cap = 'My figure caption'

plot(iris)
```
```

# Naming chunks helps debugging

```
processing file: test.Rmd
|.....
ordinary text without R code | 14%

|.....
label: setup (with options) | 29%
List of 1
$ include: logi FALSE

|.....
ordinary text without R code | 43%

|.....
label: read.data | 57%
|.....
ordinary text without R code | 71%

|.....
label: plot (with options) | 86%
List of 1
$ echo: logi FALSE

Quitting from lines 28-29 (test.Rmd)
Error in eval(predvars, data, env) : object 'specie' not found
Calls: <Anonymous> ... plot.formula -> eval -> eval -> <Anonymous> -> eval -> eval
Execution halted
```

## Naming chunks helps navigating long docs

```
1 ---  
2 title: "My Analysis"  
3 author: "FRS"  
4 output: html_document  
5 ---  
6  
7 ```{r setup, include=FALSE}  
8 knitr::opts_chunk$set(echo = TRUE)  
9 ```  
10  
11 This is an R Markdown document. Markdown is a simple  
12 My Analysis for authoring HTML, PDF, and MS Word  
Chunk 1: setup  
Chunk 2: read.data  
Chunk 3: plot  
more details on using R Markdown see  
.rstudio.com>.
```

11:60

(Top Level) ▾

R Markdown ▾

## Naming chunks: figure files take chunk name

|   |                       |
|---|-----------------------|
|  | unnamed-chunk-1-1.png |
|  | unnamed-chunk-1-2.png |
|  | unnamed-chunk-1-3.png |
|  | unnamed-chunk-1-4.png |

;Not only R! Python, Julia, C++, SQL, Stan, etc

**knitr** engines:

```
[1] "asis"      "asy"       "awk"        "bash"       "block"      "block2"      "bslib"      "c"          "cat"        "cc"         "coffee"     "comment"    "css"        "dita"      "dot"        "embed"      "eviews"     "exec"       "fortran"    "fortran95" "gawk"       "go"         "groovy"     "haskell"    "highlight"  "js"         "julia"      "lein"       "mysql"      "node"       "octave"     "perl"       "php"        "pgsql"      "python"     "R"          "Rcpp"       "Rscript"    "ruby"       "sas"        "sass"       "scala"      "scss"       "sed"        "sh"         "sql"        "stan"       "stata"      "targets"    "tikz"       "verbatim"   "zsh"
```

# Markdown: easy text formatting

```
# Header  
## Subheader  
*italic*  
**bold**  
[a link](https://example.com)
```

.

Handy: <https://thinkr-open.github.io/remedy/>

Or use [Visual Markdown Editor](#)

# Regenerate Word/PDF/HTML with one click

```
---
```

```
title: "Does sunshine make people happy?"
```

```
output: pdf_document
```

```
bibliography: refs.bib
```

```
---
```

```
# Introduction
```

```
Climate influences individual well-being [Rehdanz_2005].
```

```
However, ...
```

```
# Methods
```

```
```{r echo=FALSE}
```

```
# read data
```

```
data <- read.table("data.txt", header=T)
```

```
data[10,1] <- 11 # correct error
```

```
# fit linear model
```

```
model <- lm(happiness ~ sunshine, data=data)
```

we collected data on `r nrow(data)` individuals and fitted a linear model.

## # Results

We found that...

```
```{r echo=FALSE, results='asis'}
```

```
# make table with model output
```

```
print(xtable::xtable(model), comment = FALSE)
```

```
```{r echo=FALSE, fig.height=3, fig.width=3, fig.align='center'}
```

```
visreg::visreg(model) # plot
```

## # Discussion

Our results confirm that happiness is related to sunshine (`slope = r coef(model)[2]`).

## # References

**a**

# Does sunshine make people happy?

**b**

## Introduction

Climate influences individual well-being (Rehdanz and Maddison 2005). However, ...

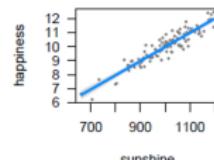
## Methods

We collected data on 100 individuals and fitted a linear model.

## Results

We found that...

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.0986	0.4271	-0.23	0.8180
sunshine	0.0101	0.0004	23.75	0.0000



## Discussion

Our results confirm that happiness is related to sunshine ( $slope = 0.0100652$ ).

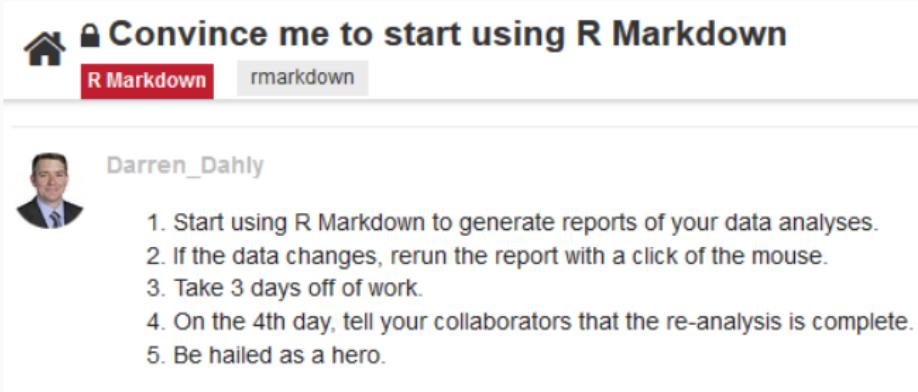
## References

Rehdanz, Katrin, and David Maddison. 2005. "Climate and Happiness." *Ecological Economics* 52 (1). Elsevier BV: 111–25. doi:10.1016/j.ecolecon.2004.06.015.

Spotted error in the data? No problem!

- Make changes in Rmarkdown document
- Click **Knit** in Rstudio
- Report will **update automatically!**

# Why Rmarkdown?



**Convince me to start using R Markdown**

R Markdown rmarkdown

 Darren\_Dahly

1. Start using R Markdown to generate reports of your data analyses.
2. If the data changes, rerun the report with a click of the mouse.
3. Take 3 days off of work.
4. On the 4th day, tell your collaborators that the re-analysis is complete.
5. Be hailed as a hero.

<https://community.rstudio.com/t/convince-me-to-start-using-r-markdown/1636/12>

Your turn

---

# Create, edit and share Rmarkdown document

File > New File > Rmarkdown

Write text

Insert code chunks

Change chunk options (echo, eval, etc)

HTML/Word/PDF output

PDF generation requires LaTeX

```
library('tinytex')  
  
install_tinytex()
```

## Rmarkdown bells and whistles

---

# 'Visual RMarkdown': Rmd as in word processor

The editor toolbar includes buttons for the most commonly used formatting commands:



Additional commands are available on the **Format**, **Insert**, and **Table** menus:

Format	Insert	Table
<b>B</b> Bold ⌘B <i>I</i> Italic ⌘I «» Code ⌘D Text ▾ Bullets & Numbering ▾ Blockquote Line Block Div Block... Code Block... Raw ▾ Clear Formatting ⌘\br/>Edit Attributes... F4	Rmd Chunk ⌘I Image... ⌘I Link... ⌘K Horizontal Rule ⌘_ Definition ▾ Inline Math Display Math Footnote ⌘F7 Citation... Div Block... Code Block... YAML Block Comment ⌘C	Insert Table... ⌘T <input checked="" type="checkbox"/> Table Header Table Caption Align Column ▾ Insert Row Above Insert Row Below Insert Column Left Insert Column Right Delete Row Delete Column Delete Table

<https://rstudio.github.io/visual-markdown-editing>

## Automatic table generation

```
model <- lm(happiness ~ sunshine, data = mydata)
xtable(model)
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.0652	0.4265	-0.15	0.8789
sunshine	0.0100	0.0004	23.68	0.0000

Many alternatives: `gtsummary`, `modelsummary`, `huxtable`, etc

## equatiomatic describes model structure

We fitted a linear model:

```
library('equatiomatic')
model <- lm(happiness ~ sunshine, data = mydata)
extract_eq(model)
```

$$\text{happiness} = \alpha + \beta_1(\text{sunshine}) + \epsilon \quad (1)$$

## Models that describe themselves!

```
library('report')
model <- lm(happiness ~ sunshine, data = mydata)
report(model)
```

We fitted a linear model (estimated using OLS) to predict happiness with sunshine (formula: `happiness ~ sunshine`). The model explains a statistically significant and substantial proportion of variance ( $R^2 = 0.85$ ,  $F(1, 98) = 560.90$ ,  $p < .001$ , adj.  $R^2 = 0.85$ ). The model's intercept, corresponding to `sunshine = 0`, is at -0.07 (95% CI [-0.91, 0.78],  $t(98) = -0.15$ ,  $p = 0.879$ ). Within this model:

- The effect of sunshine is statistically significant and positive (beta = 0.01, 95% CI [9.18e-03, 0.01],  $t(98) = 23.68$ ,  $p < .001$ ; Std. beta = 0.92, 95% CI [0.85, 1.00])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

## Insert equations with LaTeX

Using LaTeX:

```
$$
y \sim N(\mu, \sigma^2)
$$
```

$$y \sim N(\mu, \sigma^2)$$

- Mathpix: <https://github.com/jonocarroll/mathpix>

# Citing bibliography

Insert Citation

My Sources

- Bibliography
- Zotero
- My Library
- From DOI
- Crossref
- DataCite
- PubMed

Search for citation

 @boghizadehfini2020	What dentists need to know about COVID-19	Baghizadeh Fini, M 2020	
 @bostanciklioglu2020	Severe Acute Respiratory Syndrome Coronavirus 2 is Penetrating to Dementia Re...	Bostanciklioglu, M 2020	
 @fran	Functional reactive animation	Elliott, C, and Hudak, P 1997	
 @guo2020	Guo, Y, Cao, Q, Hong, Z, Tan, Y, Chen, et al. 2020	The origin, transmission and clinical therapies on coronavirus disease 2019 (CO...	
 @hu2020	The cytokine storm and COVID-19	Hu, B, Huang, S, and Yin, L 2020	
 @malik2020	Malik, Y, Kumar, N, Sircar, S et al. 2020	Coronavirus Disease Pandemic (COVID-19): Challenges and a Global Perspective	
 @R-bose	R: A language and environment for statistical computing	R Core Team 2017	

Selected Citation Keys

Add to bibliography: book.bib 

<https://rstudio.github.io/visual-markdown-editing/#/citations>

## Using BibTeX file with references

```
---
```

```
title: "My awesome Rmd"
```

```
output: html_document
```

```
bibliography: references.bib
```

```
---
```

## Format bibliography for any journal

```
---
```

```
title: "Does sunshine make people happy?"
```

```
author: "FRS"
```

```
output: word_document
```

```
bibliography: myrefs.bib
```

```
csl: ecology-letters.csl
```

```
---
```

Thousands of Citation Styles:

<https://www.zotero.org/styles>

<https://github.com/citation-style-language/styles>

# Rmarkdown templates

- rticles
- papaja
- rrttools
- pinp
- rmdTemplates
- pagedreport
- GitHub!

## My cool paper written in Rmarkdown

F. Rodriguez-Sánchez<sup>a,1,2</sup> and And Prinsen<sup>a,3</sup>

<sup>a</sup>Some Institute of Technology, Department, Street, City, State, Zip; <sup>1</sup>Another University Department, Street, City, State, Zip

This manuscript was compiled on September 18, 2018.

Please provide an abstract of no more than 250 words in a single paragraph. Abstracts should explain to the general reader the major contributions of the article. References in the abstract must be cited in the text. We strongly insist and insist on this.

[one](#) | [two](#) | [option 1](#) | [option 2](#) | [option 3](#)

This PNAS journal template is provided to help you write your work in the correct journal format. Instructions for use are provided below.

Note: please start your introduction without including the word "Introduction" as a section heading (except for math articles in the Physical Sciences section); this heading is implied in the first paragraph.

### Guide to using this template

Please note that while this template provides a preview of the typesetting for a journal article, it is not a definitive guide. It is not necessary to use the first author's instructions. For more detailed information please see the PNAS Instructions for Authors.

**Author Affiliations.** Include departments, institutions, and complete address, with the ZIP/postal code, for each author. Use lower case letters to denote the order of contribution of authors in the manuscript. Authors with an ORCID ID may supply this information at submission.

**Submitting Manuscripts.** All authors must submit their article to PNASonline. If you are using Overleaf to write your article, please use the "Submit to PNAS" option in the top bar of the editor window.

**Format.** Many authors find it useful to organize their manuscripts with the following order of sections: Title, Author Affiliation, Keywords, Abstract, Significance Statement, Results, Discussion, Materials and Methods, Acknowledgments, and References. Other orders and headings are acceptable.

**Manuscript Length.** PNAS generally uses a two-column format averaging 67 characters, including spaces, per line. The maximum length of a Direct Submission research article is six pages and a PNAS PLUS research article is ten pages including all figures, tables, and equations. When submitting tables, figures, and/or equations in addition to text, keep the text less than 2000 words under 30,000 characters (including spaces) for Direct Submission and 77,000 characters (including spaces) for PNAS PLUS.

**References.** References should be cited in numerical order as they appear in text; this will be done automatically via bibtex, e.g. (1) and (2, 3). All references, including for the SI, should be included in the main manuscript file. References appearing in footnotes should not be digitized. All references



Fig. 1. Photograph of a bright green tree frog captured in the wild.

included in tables should be included with the main reference section.

**Data Availability.** PNAS must be able to archive the data essential to a published article. Where such archiving is not possible, deposition of data in public databases, such as GenBank, ArXiv, or PNAS Data Bank, University of California, and others outlined in the Instructions for Authors, is acceptable.

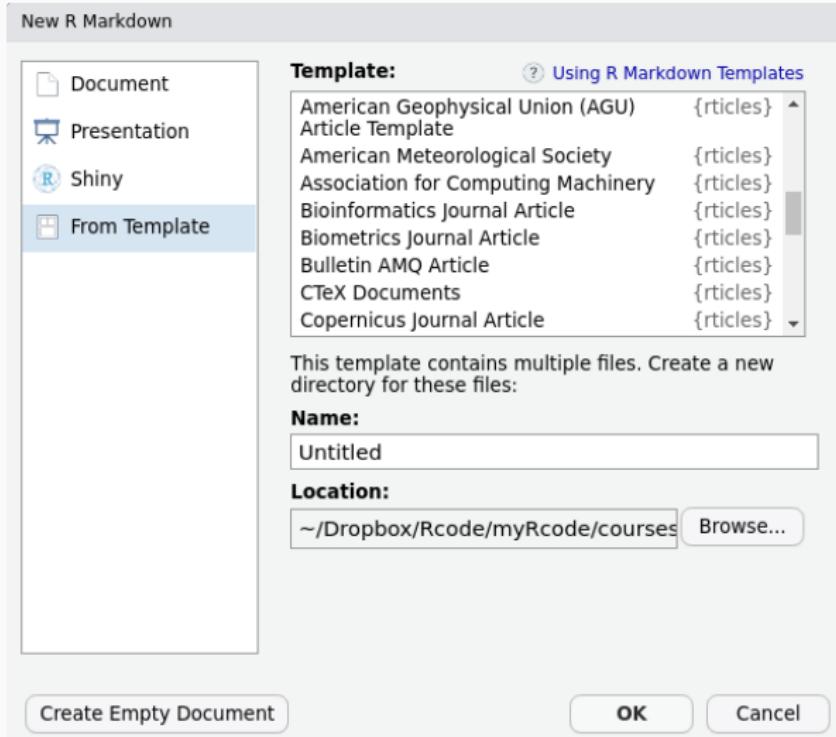
**Language Editing Services.** Prior to submission, authors who believe their manuscript would benefit from professional editing are encouraged to use a language-editing service (see list at [www.pnas.org/site/authors/language-editing.shtml](http://www.pnas.org/site/authors/language-editing.shtml)). PNAS does not accept responsibility or liability for any changes made and their use has no bearing on acceptance of a manuscript for publication.

### Significance Statement

Authors must submit a 120-word maximum statement about the significance of their research paper written at a level understandable to a general scientific audience and not limited to the field of specialty. The primary goal of the Significance Statement is to explain the relevance of the work in broad context to a broad readership. The Significance Statement appears in the paper, later and is required for all submitted papers.

[one](#) | [two](#) | [option 1](#) | [option 2](#) | [option 3](#)

# Accessing Rmd templates



## Revise writing style: gramr

**Ignore**

- Passive Voice
- Duplicate words (the the)
- 'So' at start of sentence
- 'There is/are; at start of sentence
- Avoid weasel words
- Wordiness
- Problematic Adverbs
- Cliches
- Avoid 'Being' words

[Next](#) [Finish](#)

**Text to Check**

So the cat was stolen. 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>>.

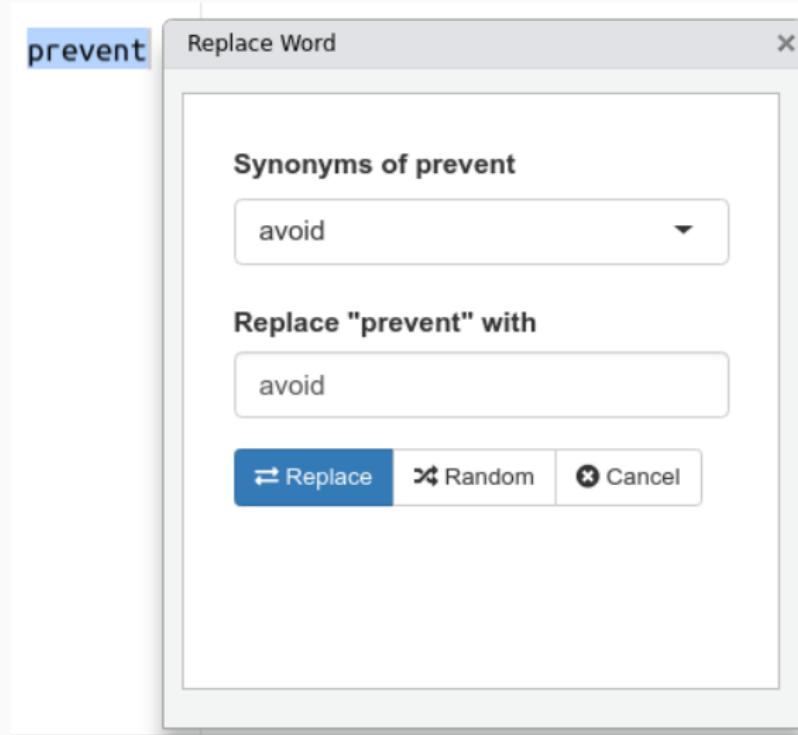
"was stolen" may be passive voice

<https://github.com/ropenscilabs/gramr>

## Spell and grammar checking

<https://github.com/nevrome/wellspell.addin>

## Find synonyms



<https://github.com/gadenbuie/synamyn>

## Word count and readability

Method	koRpus	stringi
Word count	107	104
Character count	604	603
Sentence count	10	Not available
Reading time	0.5 minutes	0.5 minutes

<https://github.com/benmarwick/wordcountaddin>

# Automated reproducibility checks

<https://github.com/brandmaier/reproducibleRchunks>

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

Here is a computation:

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

Code Chunk Reproduction Report

- ✓ my\_sum: REPRODUCTION SUCCESSFUL

Here is a computation:

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

Code Chunk Reproduction Report

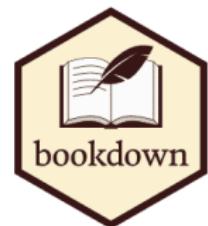
- ✗ my\_sum: REPRODUCTION FAILED Fingerprints are not identical.

## BOOKDOWN

### Write HTML, PDF, ePub, and Kindle books with R Markdown

The `bookdown` package is an [open-source R package](#) that facilitates writing books and long-form articles/reports with R Markdown. Features include:

- Generate printer-ready books and ebooks from R Markdown documents.
- A markup language easier to learn than LaTeX, and to write elements such as section headers, lists, quotes, figures, tables, and citations.
- Multiple choices of output formats: PDF, LaTeX, HTML, EPUB, and Word.
- Possibility of including dynamic graphics and interactive applications (HTML widgets and Shiny apps).
- Support a wide range of languages: R, C/C++, Python, Fortran, Julia, Shell scripts, and SQL, etc.
- LaTeX equations, theorems, and proofs work for all output formats.
- Can be published to GitHub, bookdown.org, and any web servers.
- Integrated with the RStudio IDE.
- One-click publishing to <https://bookdown.org>.



[https://bookdown.org/](https://bookdown.org)

# Presentation Ninja

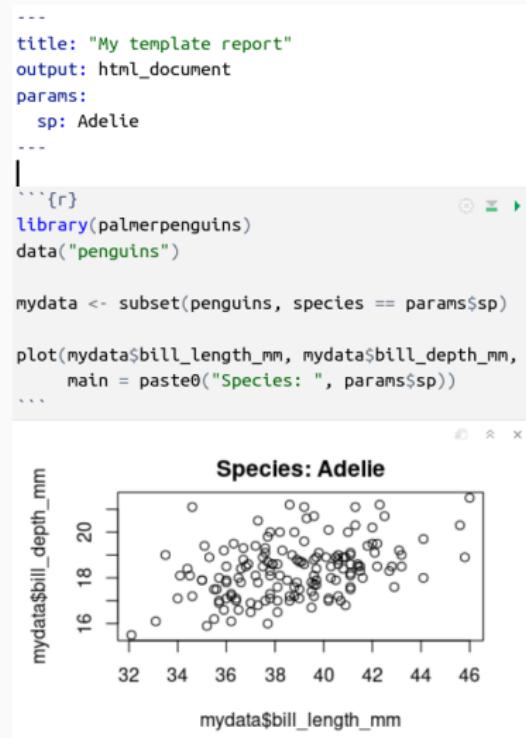
with xaringan

Yihui Xie

RStudio, PBC

<https://slides.yihui.org/xaringan/>

# Parameterised reports



<https://bookdown.org/yihui/rmarkdown/parameterized-reports.html>

## Render thousands of individual reports from Rmd template

```
library('rmarkdown')

for (i in unique(penguins$species)) {

  render('template_report.Rmd',
        params = list(sp = i))

}
```

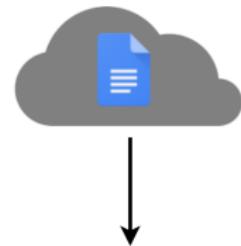
# Collaborative writing

- GitHub, GitLab, etc
- Google Docs ([trackdown](#))
- [redoc](#)

Locally



Google Docs



Share link with collaborators



## Rmarkdown resources

---

# Rmarkdown website

<http://rmarkdown.rstudio.com/>

R Markdown

from  Studio

Get Started    Gallery    Formats    Articles    



**More Examples**

The rest of this document consists of a few test cases to make sure everything still works well to display more complicated scenarios. First we generate some data in our RStudio environment with the classic option `knitr::opts_chunk$set(echo = TRUE)`:

```
y = approx(x = rnorm(100), y = rnorm(100), xout = seq(0, 1, by = 0.01))
y = approx(x = rnorm(100), y = rnorm(100), xout = seq(0, 1, by = 0.01))
y = gene_somethin()
```

Analyze. Share. Reproduce.

Your data tells a story. Tell it with R Markdown.  
Turn your analyses into high quality documents, reports, presentations and dashboards.

## Rmarkdown cheat sheet

# R Markdown Cheat Sheet

learn more at [rmarkdown.rstudio.com](http://rmarkdown.rstudio.com)

## 1 Open a new Rmd file

If you’re new to R Markdown, use the wizard that populates the file with a template.

## 2 Write document

By editing template

## 3 Knit document to create report

Use knit button or render() to knit.

## 4 Preview Output

In IDE window

## 5 Publish document

to web or server

## 6 Examine build log

in RStudio

## Reproducible Research

At the click of a button, or the type of a command, you can turn any R code in an R Markdown file to reproduce your work and export the results as a finished report.

## Dynamic Documents

You can choose to export the report to a variety of formats, including PDF, MS Word, ODT, RTF, or markdown document, or as a html or pdf file or plain text.

## Rmd structure

YAML Header  
Optional section of the header (in a .yaml file) that specifies key values (e.g., `title`, `author`, `date`, `output`).

## Text

Narration formatted with `text` blocks.

## Code chunks

Chunks of embedded code. Each chunk:

- has its own `id`
- ends with `---`

If `Markdown` will run the code, it will also run the results to the doc.

## Working directory

It will use the location of the file as the working directory.

## Inline code

Insert with `[[r code]]` or `[[r code]]` to preview as text without code.

## Code chunks

One or more lines of code enclosed with `---` and `---`. Place chunk options within curly braces, after `---` with `---`.

## Embed code with knitr syntax

Global options

Set with `knitr::opts_chunk$set()`, e.g.

`---`  
`cache: true`  
`echo: false`  
`eval: true`  
`error: true`  
`highlight: true`  
`include: true`  
`message: true`  
`results: 'asis'`  
`warning: true`

## Global options

Set with `knitr::opts_chunk$set()`, e.g.

`---`  
`cache: true`  
`echo: false`  
`eval: true`  
`error: true`  
`highlight: true`  
`include: true`  
`message: true`  
`results: 'asis'`  
`warning: true`

`---`  
`cache: true`  
`echo: false`  
`eval: true`  
`error: true`  
`highlight: true`  
`include: true`  
`message: true`  
`results: 'asis'`  
`warning: true`

## Important check options

`cache` - cache results for future knits  
`default = FALSE`

`cache.path` - directory to save cached documents  
`default = "cache"`

`child` - file to run and then include  
`default = NULL`

`collapse` - collapse all output into single block  
`default = FALSE`

`comment` - prefix for each line of results  
`default = "##"`

`dependencies` - chunk dependencies for caching (default = `NULL`)

`echo` - display code in output document (default = `TRUE`)

`engine` - code language used in chunk (default = `"R"`)

`error` - display error messages in document (default = `TRUE`) or stop when an error occurs (default = `FALSE`)

`eval` - Run code in chunk (default = `TRUE`)

`include` - Include chunk in document after rendering (default = `TRUE`)

`message` - display code messages in document (default = `TRUE`)

`results` (default = `"markup"`)  
`asis`  
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[https://www.rstudio.org/links/r\\_markdown\\_cheat\\_sheet](https://www.rstudio.org/links/r_markdown_cheat_sheet)

# Rmarkdown reference guide



## R Markdown Reference Guide

Learn more about R Markdown at [rmarkdown.rstudio.com](http://rmarkdown.rstudio.com)  
Learn more about Interactive Docs at [rstudio.com/articles](http://rstudio.com/articles)

### Syntax

Make a code chunk with three back ticks followed by an R in braces. End the chunk with three back ticks:

```
```{r}
paste("Hello", "World")
````
```

Place code below with a single back ticks. The first back tick must be followed by an R, like this: `r paste("Hello", "World")` .

Add chunk options within braces. For example, `echo=FALSE` will prevent source code from being displayed:

```
```{r eval=TRUE, echo=FALSE}
paste("Hello", "World")
````
```

Learn more about chunk options at <http://yihui.name/knitr/options>

### Chunk options

| option                       | default value | description                                                                                                                                                                                                                                                           |
|------------------------------|---------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>child</code>           | NULL          | A character vector of filenames. Knitr will knit the files and place them into the main document.                                                                                                                                                                     |
| <code>code</code>            | NULL          | Set to R code. Knitr will replace the code in the chunk with the code in the code option.                                                                                                                                                                             |
| <code>engine</code>          | "R"           | Knitr will evaluate the chunk in the named language, e.g. <code>engine = "python"</code> . See <code>names(knitr\$knit_engines\$engine)</code> to see supported languages.                                                                                            |
| <code>eval</code>            | TRUE          | If FALSE, knitr will not run the code in the code chunk.                                                                                                                                                                                                              |
| <code>include</code>         | TRUE          | If FALSE, knitr will run the chunk but not include the chunk in the final document.                                                                                                                                                                                   |
| <code>part</code>            | TRUE          | If FALSE, knitr will not include the chunk when running <code>part()</code> to extract the source code.                                                                                                                                                               |
| <code>results</code>         |               |                                                                                                                                                                                                                                                                       |
| <code>collapse</code>        | FALSE         | If TRUE, knitr will collapse all the source and output blocks created by the chunk into a single block.                                                                                                                                                               |
| <code>echo</code>            | TRUE          | If FALSE, knitr will not display the code in the code chunk above it's results in the final document.                                                                                                                                                                 |
| <code>engine</code>          | "R"           | If "YAML", knitr will not display the code's results in the final document. If "Rmd", knitr will delay displaying all output pieces until the end of the chunk. If "asis", knitr will pass through results without reformatting them (useful for results extraction). |
| <code>error</code>           | TRUE          | If FALSE, knitr will not display any error messages generated by the code.                                                                                                                                                                                            |
| <code>message</code>         | TRUE          | If FALSE, knitr will not display any messages generated by the code.                                                                                                                                                                                                  |
| <code>warning</code>         | TRUE          | If FALSE, knitr will not display any warning messages generated by the code.                                                                                                                                                                                          |
| <code>Code Definition</code> |               |                                                                                                                                                                                                                                                                       |
| <code>background</code>      | "#FFFFFF"     | A background color for chunks in LaTeX output.                                                                                                                                                                                                                        |
| <code>comment</code>         | "%"           | A character string. Knitr will append the string to the start of each line of results in the final document.                                                                                                                                                          |
| <code>highlight</code>       | TRUE          | If TRUE, knitr will highlight the source code in the final output.                                                                                                                                                                                                    |
| <code>prompt</code>          | FALSE         | If TRUE, knitr will add a > to the start of each line of code displayed in the final document.                                                                                                                                                                        |
| <code>size</code>            | "normal"      | Fontsize for LaTeX output.                                                                                                                                                                                                                                            |
| <code>strip.white</code>     | TRUE          | If TRUE, knitr will remove white spaces that appear at the beginning or end of a code chunk.                                                                                                                                                                          |
| <code>tab</code>             | FALSE         | If TRUE, knitr will tidy code chunks for display with the <code>tidy_source()</code> function in the <code>formatR</code> package.                                                                                                                                    |

Updated 03/03/2014

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<https://github.com/rstudio/cheatsheets/blob/main/old/pdfs/rmarkdown-reference.pdf>

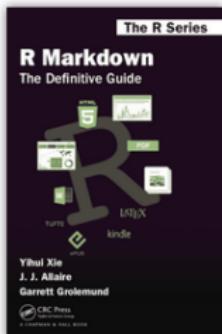
## R Markdown: The Definitive Guide

by Yihui Xie, J. J. Allaire, Garrett Grolemund

2018-09-11

Star

239



The first official book authored by the core R Markdown developers that provides a comprehensive and accurate reference to the R Markdown ecosystem. With R Markdown, you can easily create reproducible data analysis reports, presentations, dashboards, interactive applications, books, dissertations, websites, and journal articles, while enjoying the simplicity of Markdown and the great power of R and other languages. *Read more →*

<https://bookdown.org/yihui/rmarkdown/>

<https://bookdown.org/yihui/rmarkdown-cookbook/>

Quarto

---

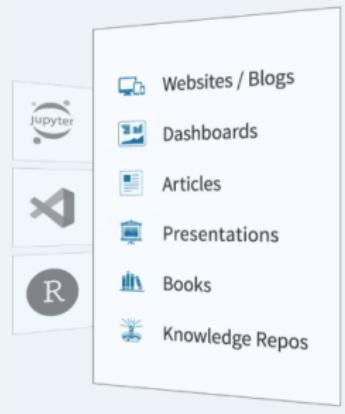
# Quarto: 2nd generation Rmarkdown

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# Quarto manuscripts

## La Palma Earthquakes

### AUTHORS

Steve Purves  

Rowan Cockett  

### PUBLISHED

February 23, 2024

### AFFILIATION

Curvenote

Curvenote

### OTHER FORMATS

 MS Word

 PDF (agu)

 MECA Bundle

### ABSTRACT

In September 2021, a significant jump in seismic activity on the island of La Palma (Canary Islands, Spain) signaled the start of a volcanic crisis that still continues at the time of writing. Earthquake data is continually collected and published by the Instituto Geográfico Nacional (IGN). ....

### KEYWORDS

La Palma, Earthquakes

### Table of contents

-  [1 Introduction](#)
- [2 Data & Methods](#)
- [3 Conclusion](#)
- [References](#)

### Notebooks

-  [Article Notebook](#)
-  [Data Screening](#)

## 1 Introduction

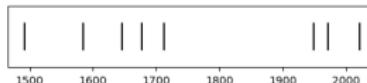


Figure 1: Timeline of recent earthquakes on La Palma

 [Source: Article Notebook](#)

Based on data up to and including 1971, eruptions on La Palma happen every 79.8 years on average.

Studies of the magma systems feeding the volcano, such as Marrero et al. (2019), have proposed that there are two main magma reservoirs feeding the Cumbre Vieja volcano; one in the mantle (30-40km depth) which charges and in turn feeds a shallower crustal reservoir (10-20km depth).

Eight eruptions have been recorded since the late 1400s ([Figure 1](#)).

Data and methods are discussed in [Section 2](#).

<https://quarto-ext.github.io/manuscript-template-jupyter/>

<https://quarto.org/docs/manuscripts/>

## Hundreds of Quarto extensions

<https://m.canouil.dev/quarto-extensions/>

Journal templates: <https://quarto.org/docs/extensions/listing-journals.html>

Your turn

---

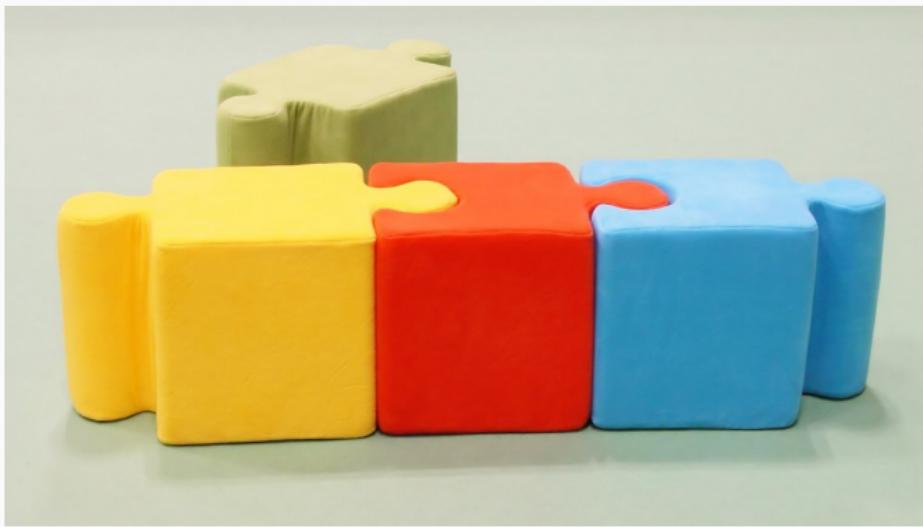
## Your turn

- Try visual markdown editor
- Add bibliography
- Try templates (rticles, rmdTemplates)
- Parameterised reports (e.g. different iris or penguin species)

## Workflow management

---

In complex projects we must keep pieces organised

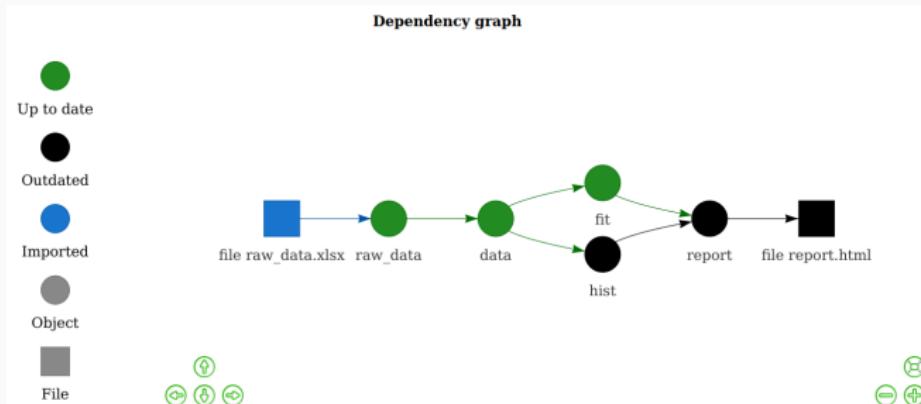


makefile runs all code in right order

makefile.R

```
source('clean_data.R')  
  
source('fit_model.R')  
  
render('report.Rmd')
```

# targets: advanced workflow management



<https://docs.ropensci.org/targets/>

Your turn

---

- Write makefile.R for your project
- Try **targets** minimal example
- <https://github.com/wlandau/targets-minimal>

## Controlling software dependencies

---



Package changes can break your analysis

How to reproduce your analysis in a year,  
or different computer?

# sessionInfo records OS & used packages

```
sessionInfo()
```

```
R version 4.4.2 (2024-10-31)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 20.04.6 LTS

Matrix products: default
BLAS:    /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
LAPACK:  /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3;  LAPACK version 3.9.0
```

```
locale:
[1] LC_CTYPE=en_GB.UTF-8      LC_NUMERIC=C
[3] LC_TIME=es_ES.UTF-8      LC_COLLATE=en_GB.UTF-8
[5] LC_MONETARY=es_ES.UTF-8    LC_MESSAGES=en_GB.UTF-8
[7] LC_PAPER=es_ES.UTF-8      LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=es_ES.UTF-8 LC_IDENTIFICATION=C
```

```
time zone: Europe/Madrid
tzcode source: system (glibc)
```

```
attached base packages:
[1] stats      graphics   grDevices  utils      datasets   methods    base
```

```
other attached packages:
[1] report_0.5.9      equatiomatic_0.3.3 xtable_1.8-4      knitr_1.49
```

```
loaded via a namespace (and not attached):
[1] sandwich_3.1-1    generics_0.1.3    tidyverse_1.3.1    lattice_0.22-6
```

checkpoint reconstructs packages in given date

```
library('checkpoint')

options(checkpoint.mranUrl="https://packagemanager.posit.co/")

checkpoint('2019-10-08')

source('analysis.R')
```

1. Detects packages used
2. Installs version from given date (only CRAN)
3. Independent install (not messing w/ main library)

## automagic records & install packages (CRAN + GitHub)

```
automagic::make_deps_file()
```

File `deps.yaml` records dependencies:

```
- Package: equatiomatic
  Repository: CRAN
  Version: 0.1.0

- Package: report
  GithubUsername: easystats
  GithubRepo: report
  GithubRef: HEAD
  GithubSHA1: c48a4bb0a40df7116bc502aa3ce2cbbc9d70b7e2
```

To install all those dependencies:

```
automagic()
```

## renv: recommended to control dependencies

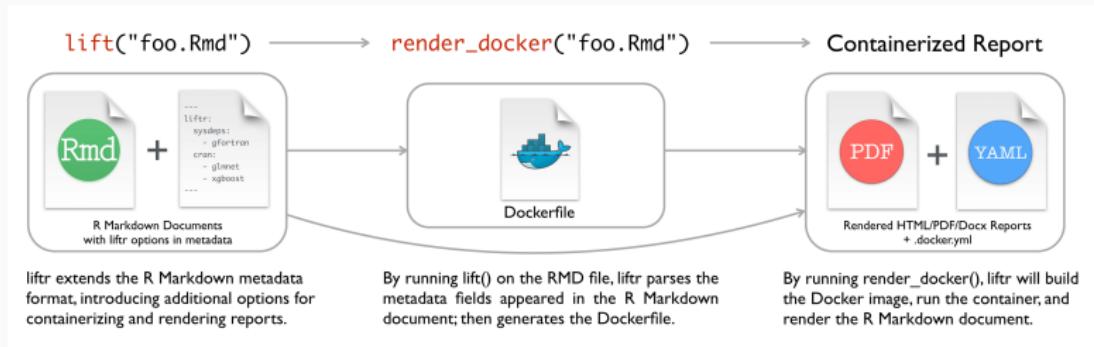
```
renv::init()  
# Create private package library for project  
  
renv::snapshot()  
# Capture dependencies in lockfile  
  
renv::restore()  
# Regenerate dependencies from lockfile
```

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

To ensure reproducibility,  
besides R packages  
we also need to control  
computational environment

Docker recreates virtual systems  
from a Dockerfile

# liftr: process Rmd in Docker container



<https://liftr.me/>

containerit creates Dockerfile

```
library('containerit')

dockfile <- dockerfile(from = 'mypaper.Rmd')
```

<https://o2r.info/containerit>

## tugboat created Dockerfile w/ entire software environment

### tugboat



A simple R package to generate a Dockerfile and corresponding Docker image from an analysis directory. `tugboat` uses the `renv` package to automatically detect all the packages necessary to replicate your analysis and will generate a Dockerfile that contains an exact copy of your entire directory with all the packages installed.

`tugboat` transforms an unstructured analysis folder into a `renv.lock` file and constructs a Docker image that includes all your essential R packages based on this lockfile.

`tugboat` may be of use, for example, when preparing a replication package for research. With `tugboat`, you can take a directory on your local computer and quickly generate a Dockerfile and Docker image that contains all the code and the necessary software to reproduce your findings.

```
library(tugboat)
create()
build()
```

<https://www.dmolitor.com/tugboat/>

Your turn

---

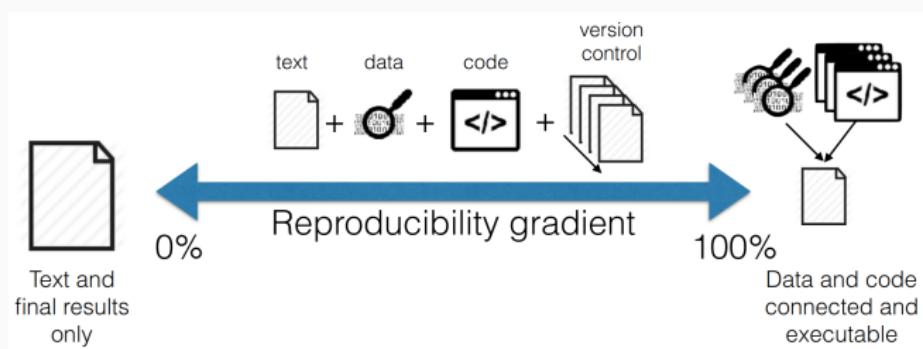
- Create script/Rmd using different packages
- Call `checkpoint` on former date
- Record dependencies:
  - `renv::snapshot`
- Recreate packages
  - `restore()`

## How to write more reproducible code

- BES guide to reproducible code
- Turing Way
- Building reproducible analytical pipelines with R
- Good enough practices in scientific computing
- Ciencia reproducible: qué, por qué, cómo
- <https://rstats.wtf>
- **fertile** package
- CodeCheck

# Reproducibility

- Good for you, good for science
- Requires systemic changes
- Reproducibility gradient: step by step



# Happy collaboration!

