



Reproducibility in health data research

Dr Arron Lacey (he/him)

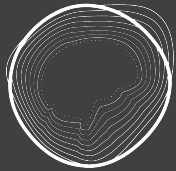
Senior Community Manager -EDoN Initiative

Dr Emma Karoune (she/her)

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DECOVID

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- **Senior Community Manager** - [EDoN Initiative](#) [@The Alan Turing Institute](#)



EDoN
Early Detection of
Neurodegenerative
diseases

The
Alan Turing
Institute

- **Core team member** [@The Turing Way](#)



- **Honorary Lecturer Swansea University**



Swansea University
Prifysgol Abertawe



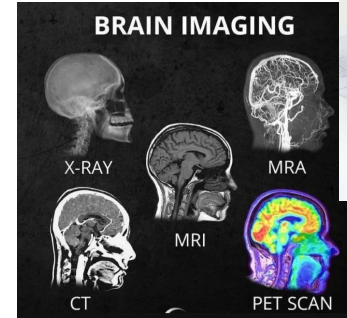
SAIL DATABANK

[@turingway](#), [@arronlacey](#), [@ekaroune](#), Zenodo: <https://doi.org/10.5281/zenodo/6895192>

EDoN: Using digital tools to detect dementia 15-20 years early

Two main challenges:

- **Variety of multi-modal data**
 - Apps, Fitbits, Geolocation, EEG, Imaging
 - No one-size-fits-all data warehouse + modelling solutions



- Hardware / Software evolves
- Newer products come to market
- Lack of data / algorithm standards¹

- Large data
- 1 sleep cycle ~ GBs
- Feature extraction with Deep Learning
- Even larger lack of data algorithm standards²

- Range of imaging modalities
- Hardware configurations
- NIFTI / BIDS?
- Medical ontologies
- Over 100 tests for cognitive decline - do they map?

Main themes: Changing methodologies, Data warehousing, Data Harmonization

1 RAPIDS - Reproducible Analysis Pipelines for Data Streams <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8636712/>

2 <https://academic.oup.com/sleep/article/43/11/zsaa097/5841249>

EDoN: Using digital tools to detect dementia 15-20 years early

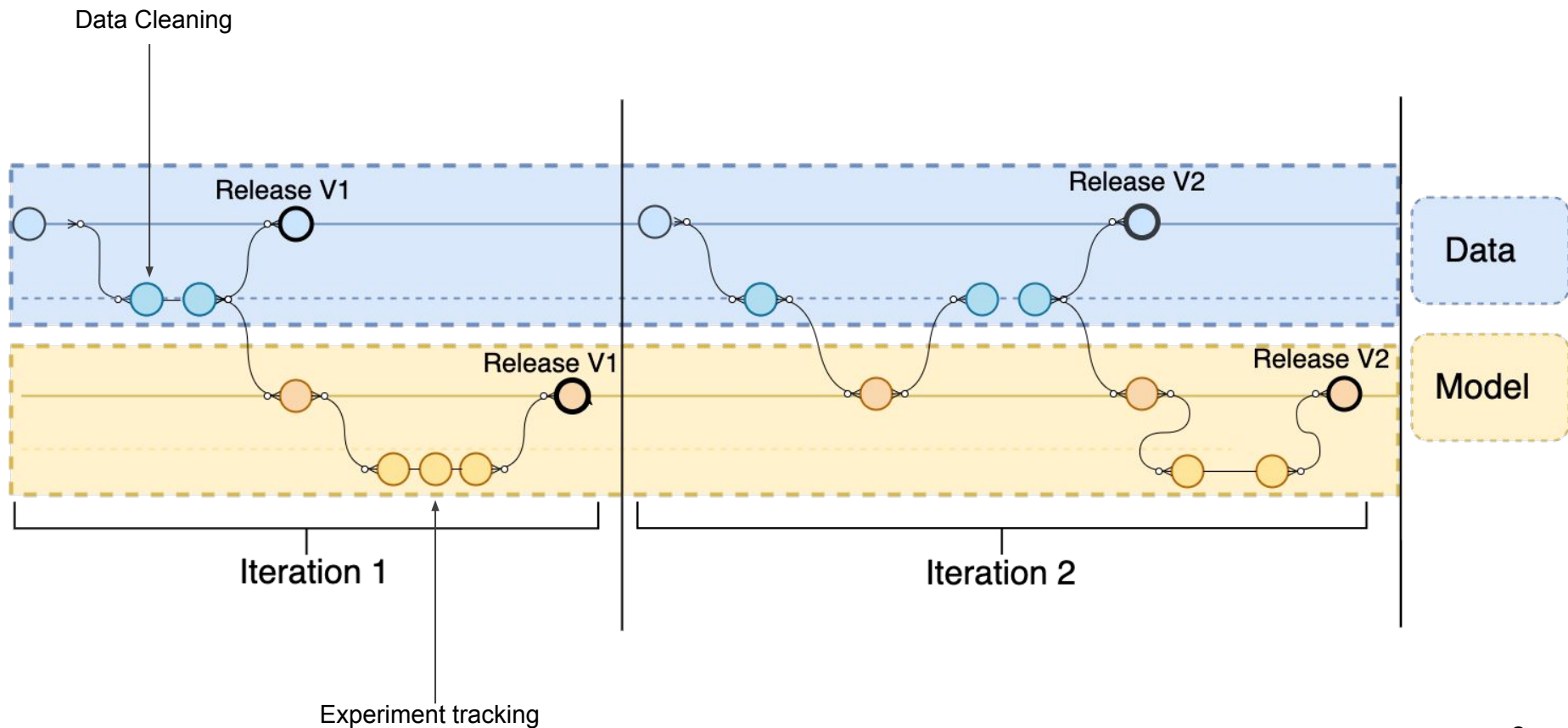
Two main challenges:

1. Variety of multi-modal data

- Apps, Fitbits, Geolocation, EEG, Imaging, NLP
- No one-size-fits-all data warehouse + modelling solutions

2. Modelling sustained longitudinally

- 5 year initiative with iterative development
- Real world: confirmation of modelling > 15-20 years
- Revisit data, models and codebase



REPRODUCIBLE



REPLICABLE



ROBUST



GENERALISABLE



Scriberia 

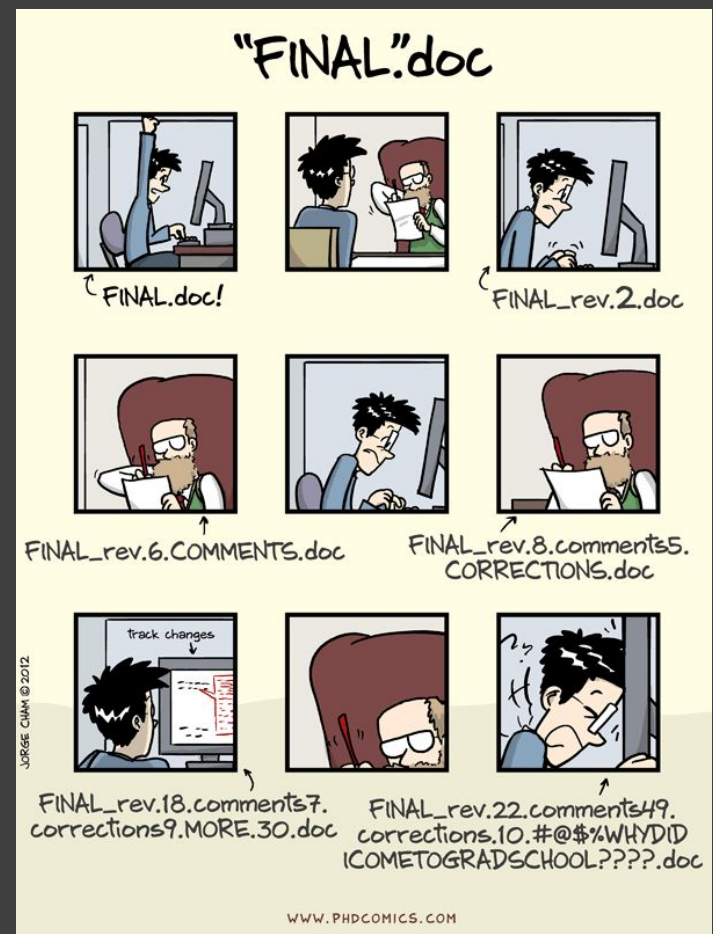
Version control

- **Version control** your schemas for:
 - Adding data
 - Correcting data
 - Deleting data
- **Version control** your analysis / models
 - Code
 - Model weights
 - Reports

Is model V2.XXX interacting with data V3.XXX?



- version control system
- records changes to a file or set of files over time
- provides access to any specific version





arronlacey added audio to final slide



6cae85c

10 days ago



22 commits

📁 .github/workflows	Update main.yml	13 days ago
📁 bivariate	added audio to final slide	10 days ago
📁 code-slide_files	added initial dependencies and .qmd	13 days ago
📁 images	added audio to final slide	10 days ago
📁 index_files	removed unneeded files	11 days ago
📁 mini	added initial dependencies and .qmd	13 days ago
📁 scripts	added initial dependencies and .qmd	13 days ago
📄 .DS_Store	added audio to final slide	10 days ago
📄 .gitignore	added initial dependencies and .qmd	13 days ago
📄 LICENSE	Initial commit	13 days ago
📄 README.md	Update README.md	13 days ago
📄 _config.yml	Set theme jekyll-theme-slate	13 days ago
📄 actors.js	added initial dependencies and .qmd	13 days ago
📄 code-slide.Rmd	updated with html fragments	11 days ago

...	@@ -1,7 +1,5 @@		
1	---	1	---
2	- title: "code-slide"	2	+ title: "Coding Minimum Working Example"
3	- author: "Arron Lacey"		
4	- date: '2022-07-11'		
5	output:	3	output:
6	html_document:	4	html_document:
7	self_contained: false	5	self_contained: false
↓	@@ -35,4 +33,26 @@ a		
↑			
35	test_object("a")	33	test_object("a")
36	test_output_contains("a", incorrect_msg = "Make sure to print `a`.")	34	test_output_contains("a", incorrect_msg = "Make sure to print `a`.")
37	success_msg("Great!")	35	success_msg("Great!")
38	- ```	36	+ ```
		37	+
		38	+ ```{r ex="summarise", type="sample-code"}
		39	+ # View the first 6 rows of mtcars
		40	+
		41	+
		42	+ # get the mean and total samples per cycle group
		43	+
		44	+ ```
		45	+
		46	+
		47	+ ```{r ex="summarise", type="solution"}
		48	+ # View the first 6 rows of mtcars
		49	+ head(mtcars)
		50	+
		51	+ library(dplyr)
		52	+ # get the mean and total samples per cycle group
		53	+ mtcars %>%
		54	+ group_by(cyl) %>%
		55	+ summarise(mean = mean(displ), n = n())

*“An article about computational science in a scientific publication is not the scholarship itself, it is merely advertising of the scholarship. The actual scholarship is the **complete software development environment** and the complete set of instructions which generated the figures.”*

— *Buckheit and Donoho (paraphrasing John Claerbout)*

WaveLab and Reproducible Research, 1995

(slide courtesy of Chris Holdgraf and the Jupyter Team)

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

Take home message

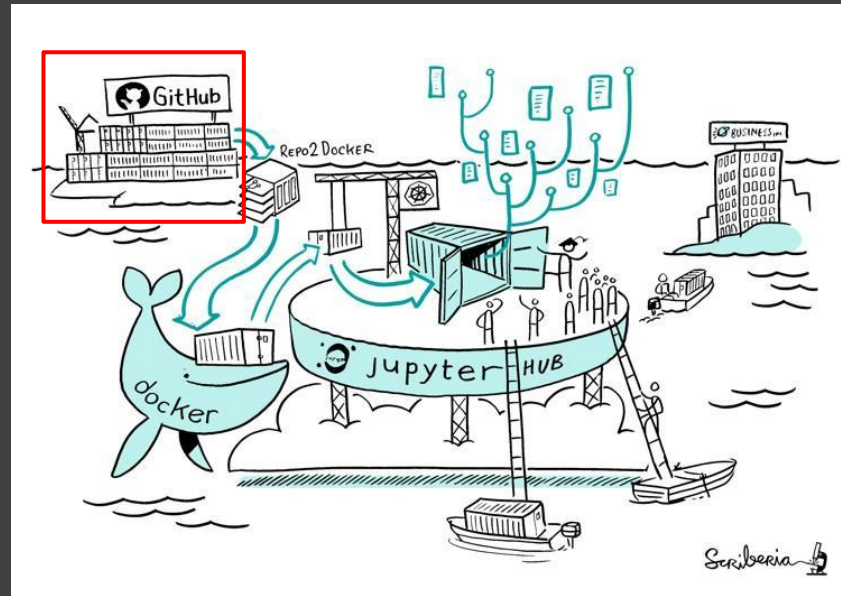
sharing your code and
data isn't enough



Make sure your work works for everyone

Committing code to Github isn't enough on it's own. Why?

Your code might work on your machine...



master 2 branches 0 tags

Go to



Fixed a typo in a comment!

2cacea4 on 5 Jan 2021 12 commits

https	Initial commit	4 years ago
misc	Initial commit	4 years ago
src	Fixed a typo in a comment!	2 years ago
.dockerignore	Made many updates to get to v1.1.0	3 years ago
.gitignore	Initial commit	4 years ago
Dockerfile	Updated R and Python and switched from pip to conda in http docke...	2 years ago
Dockerfile.https	Changed HTTPS dockerfile to reflect changes to HTTP file and updat...	2 years ago
LICENSE	Initial commit	4 years ago
NEWS.md	Changed HTTPS dockerfile to reflect changes to HTTP file and updat...	2 years ago
NOTICE.txt	Initial commit	4 years ago
README.md	Changed HTTPS dockerfile to reflect changes to HTTP file and updat...	2 years ago



Dockerfile

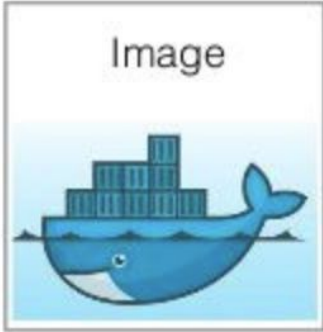
```
1  ENV http_proxy=http://192.168.10.15:8080
2  ENV https_proxy=http://192.168.10.15:8080
3
4  FROM openanalytics/r-base
5
6  MAINTAINER
7
8  # system libraries of general use
9  RUN apt-get update && apt-get install -y \
10     sudo \
11     pandoc \
12     pandoc-citeproc \
13     libcurl4-gnutls-dev \
14     libcairo2-dev \
15     libxt-dev \
16     libssl-dev \
17     libssh2-1-dev \
18     libssl1.0.0
19
20 # system library dependency for the euler app
21 RUN apt-get update && apt-get install -y \
22     libmpfr-dev
23
24 # basic shiny functionality
25 RUN R -e "install.packages(c('shiny', 'rmarkdown','data.table','SQLite','DT','shinythemes','dplyr'), repos='https://cloud.r-project.org/')
```



```
FROM ubuntu:14.04
MAINTAINER Docker docker@docker.com
WORKDIR /app
ADD . /app
RUN apt-get update \
    && apt-get install -y \
    python-pip \
    && pip install Flask
EXPOSE 5000
CMD ["python", "app.py"]
```

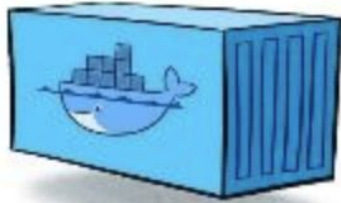
Dockerfile

build



Docker Image

run



Docker Container

Binder



choldgraf Distinguished Contributor

3  Nov '18

The Binder Project helps you create one-click, sharable, live code environments from public code repositories that runs entirely in the cloud.

<https://github.com/binder-examples>

<https://discourse.jupyter.org/t/about-the-binder-category/200>


@turingway, CC-BY 4.0, The Turing Way, DOI: 10.5281/zenodo.6346555







master 1 branch 0 tags

Go to file

Add file


Code

 **choldgraf** Merge pull request #3 from btel/fix-link ... 4a93712 on 23 Jan 2020 16 commits

 logs/20200116-182258	adding sample training logs	3 years ago
 README.md	fix link to jupyter-server-proxy issue	3 years ago
 environment.yml	added environment	3 years ago
 postBuild	lanuch tensorboard by jupyter server	3 years ago
 tensorboardserverextension.py	update README and remove reference to bokeh	3 years ago
 train_model.ipynb	fix link to tensorboard interface	3 years ago

☰ README.md

Serving Tensorboard UI on startup

 launch binder (Tensorboard)

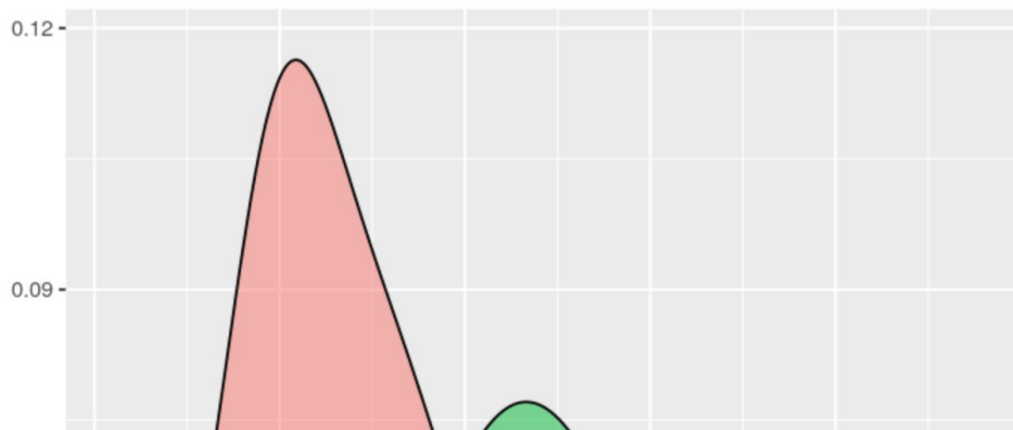
 launch binder (notebook)

```
In [1]: # ggplot2 examples
library(ggplot2)
```

```
In [2]: # create factors with value labels
mtcars$gear <- factor(mtcars$gear,levels=c(3,4,5),
  →labels=c("3gears","4gears","5gears"))
mtcars$am <- factor(mtcars$am,levels=c(0,1),
  →labels=c("Automatic","Manual"))
mtcars$cyl <- factor(mtcars$cyl,levels=c(4,6,8),
  labels=c("4cyl","6cyl","8cyl"))
```

```
In [3]: # Kernel density plots for mpg
# grouped by number of gears (indicated by color)
ggplot(mpg, data=mtcars, geom="density", fill=gear, alpha=I(.5),
  main="Distribution of Gas Milage", xlab="Miles Per Gallon",
  ylab="Density")
```

Distribution of Gas Milage



Cheat code for reproducible work - collaboration!



Feature request: nicer error message for coord_cartesian #4601



petyaracz opened this issue on 2 Sep 2021 · 1 comment · May be fixed by #4894



petyaracz commented on 2 Sep 2021



I would like `coord_cartesian` to return a more human-readable error when I mess up the syntax:

example

```
library(ggplot2)

ggplot(iris, aes(Petal.Length, Petal.Width)) +
  geom_point() +
  coord_cartesian(xlim(2,6))
```

observed behaviour

```
Error in rep(no, length.out = len) :
  attempt to replicate an object of type 'environment'
In addition: Warning message:
In is.na(coord_limits) :
  is.na() applied to non-(list or vector) of type 'environment'
```

expected behaviour

```
Error in coord_cartesian: did you mean "xlim = c()"?
```



1

Submit Issues


Nicer error message in coord-cartesian #4894

 Open

92amartins wants to merge 3 commits into `tidyverse:main` from `92amartins:4601-nicer-error-message-in-coord-cartesian`

 Conversation **3**

 Commits **3**

 Checks **11**

 Files changed **4**



92amartins commented 25 days ago

Contributor




This is an attempt to fix [#4601](#)



thomasp85 reviewed 19 days ago

[View changes](#)

R/coord-cartesian-.r Outdated

 Show resolved



thomasp85 requested changes 19 days ago

[View changes](#)

thomasp85 left a comment

Member



Thanks. Can I get you to update to match the style guide (suggested change), as well as add a unit test for the two errors



1



92amartins force-pushed the `4601-nicer-error-message-in-coord-cartesian` branch 2 times, most recently from

`04cb6fc` to `3759a9a` 17 days ago

[Compare](#)

Pull Requests

Testing!



Changes requested

Hide all reviewers

1 review requesting changes by reviewers with write access. [Learn more.](#)



1 change requested



thomasp85 requested changes



1 pending reviewer



thomasp85 was requested for review



All checks have passed

Hide all checks

11 successful checks



R-CMD-check / macOS-latest (release) (pull_request) Successful in 14m — macOS-latest (relea...

[Details](#)



pkgdown / pkgdown (pull_request) Successful in 11m

[Details](#)



test-coverage / test-coverage (pull_request) Successful in 6m

[Details](#)



R-CMD-check / windows-latest (release) (pull_request) Successful in 16m — windows-latest (re...

[Details](#)



R-CMD-check / windows-latest (3.6) (pull_request) Successful in 13m — windows-latest (3.6)

[Details](#)



R-CMD-check / ubuntu-latest (devel) (pull_request) Successful in 11m — ubuntu-latest (devel)

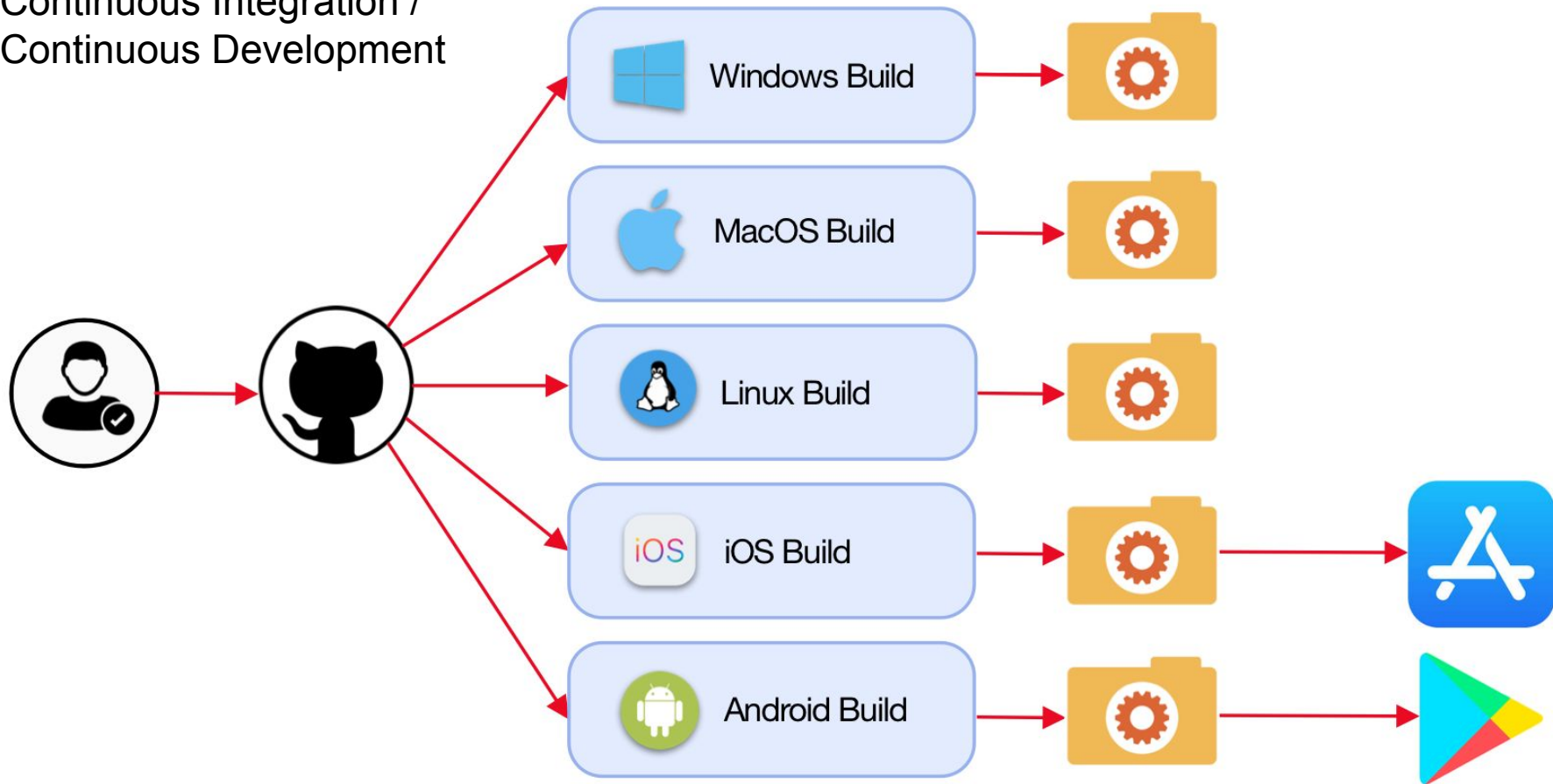
[Details](#)



Merging is blocked

Merging can be performed automatically once the requested changes are addressed.

Continuous Integration / Continuous Development



arronlacey Create r.yml ✖ c9478af 5 minutes ago 🕒 34 commits

📁 .github/workflows	r-ubuntu-install.yaml	9 months ago
📁 R	edit wandb_agent	8 months ago
📁 man	put params into config() in wandb_init	9 months ago
📄 .Rbuildignore	initial commit	9 months ago
📄 .gitignore	updated .gitignore	9 months ago
📄 DESCRIPTION	updated DESCRIPTION	9 months ago
📄 LICENSE	initial commit	9 months ago
📄 LICENSE.md	initial commit	9 months ago
📄 NAMESPACE	added documentation to wand_init and wand_agent	9 months ago
📄 README.md	attempt 1: pass list to wandb_init()	9 months ago
📄 r.yml	Create r.yml	5 minutes ago
📄 wandbR.Rproj	initial commit	9 months ago

```
name: R

on:
  push:
    branches: [ main ]
  pull_request:
    branches: [ main ]

jobs:
  build:
    runs-on: macos-latest
    strategy:
      matrix:
        r-version: ['3.6.3', '4.1.1']

    steps:
      - uses: actions/checkout@v2
      - name: Set up R ${ matrix.r-version }
        uses: r-lib/actions/setup-r@f57f1301a053485946083d7a45022b278929a78a
        with:
          r-version: ${ matrix.r-version }
      - name: Install dependencies
        run: |
          install.packages(c("remotes", "rcmdcheck"))
          remotes::install_deps(dependencies = TRUE)
        shell: Rscript {0}
      - name: Check
        run: rcmdcheck::rcmdcheck(args = "--no-manual", error_on = "error")
        shell: Rscript {0}
```

How to ask a question on



How to pass hex codes to geom_hline in ggplot?

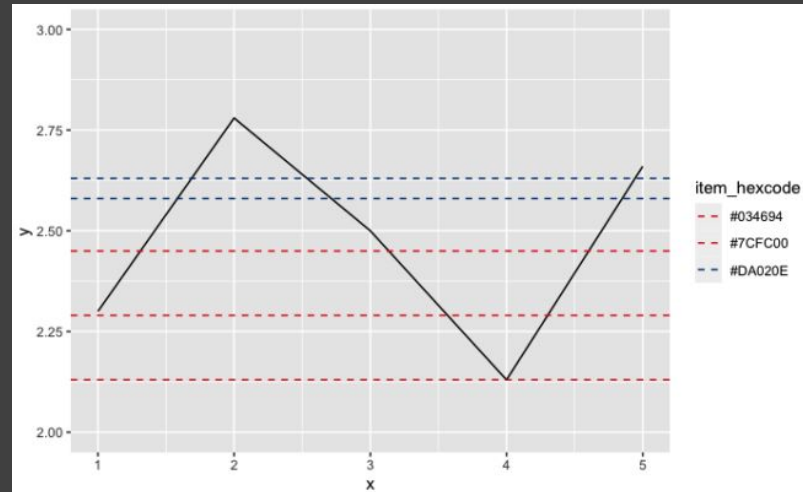
In the code below I create a ggplot, `p1`, using data from `df1`. I would like to add a horizontal line at the `score` value for each item in `df2`, and colour each line using the corresponding hexcode for each item, contained in column `item_hexcode`.

```
library(tidyverse)
# create example dataframes
set.seed(123)
df1 <- tibble(x = 1:5, y = (sample(200:300, 5, replace = TRUE)/100))
df2 <- tibble(item = c("a", "a", "b", "c", "b"),
              score = c(2.58, 2.63, 2.45, 2.13, 2.29),
              item_hexcode = c("#DA020E", "#DA020E", "#034694", "#7CFC00", "#034694"))

# initial plot
p1 <- ggplot(df1, aes(x, y)) + geom_line() + ylim(2, 3)
p1

# overlay horizontal lines on first plot, and colour lines according to hexcodes
p2 <- p1 + geom_hline(data = df2, aes(yintercept = score,
                                     colour = item_hexcode), linetype = "dashed" ) +
  scale_color_manual(values = df2$item_hexcode)

p2
```



Reproducibility with sensitive data

Project Report: Wales Multimorbidity Machine Learning (WMML)
Collaboration with The Alan Turing Institute

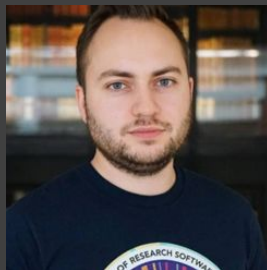
Developing and Publishing Code for Trusted Research Environments: Best Practices and Ways of Working

Ed Chalstrey, Research Data Scientist

Research Engineering Group, The Alan Turing Institute

October 2021

<https://arxiv.org/pdf/2111.06301.pdf>



Ed Chalstrey

Report Summary:

- Develop methods code as scripts/modules in a GitLab/GitHub repository
- Developing code in a public repository external from the TRE should be considered
- Test code to ensure it works as expected
- Where possible, automate tests and code quality checks with Continuous Integration
- Jupyter/Rmd notebooks should be used for data analysis, but not code development
- Adopt a consistent development workflow and coding style for the project duration
- Publish research code with a DOI, citation file and software licence
- Optionally, explore synthetic data and executable papers to enhance reproducibility

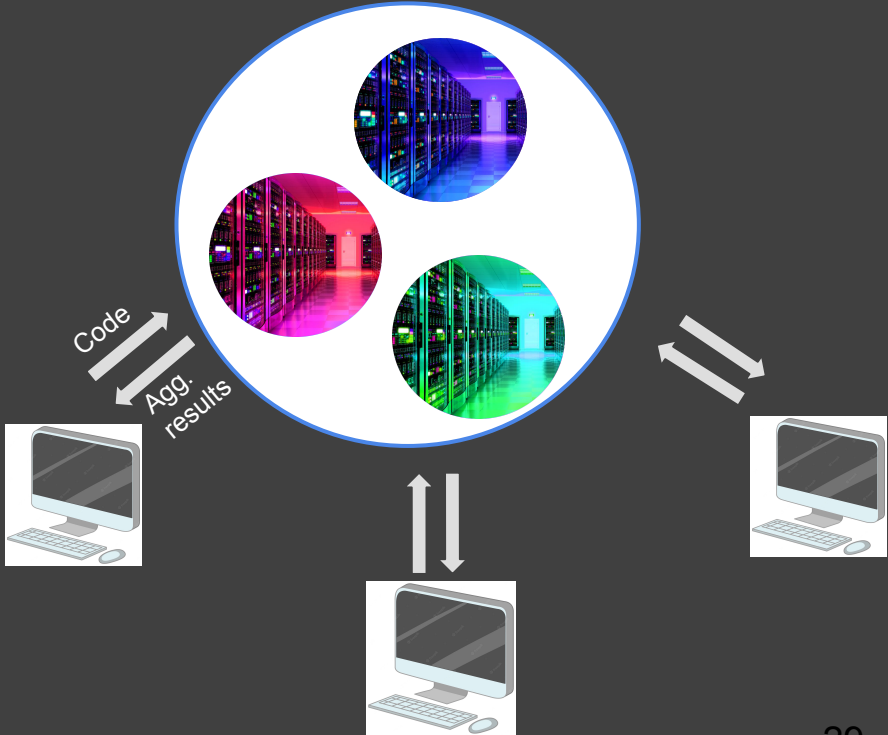
<https://the-turing-way.netlify.app/project-design/sdpw/trew.html>

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

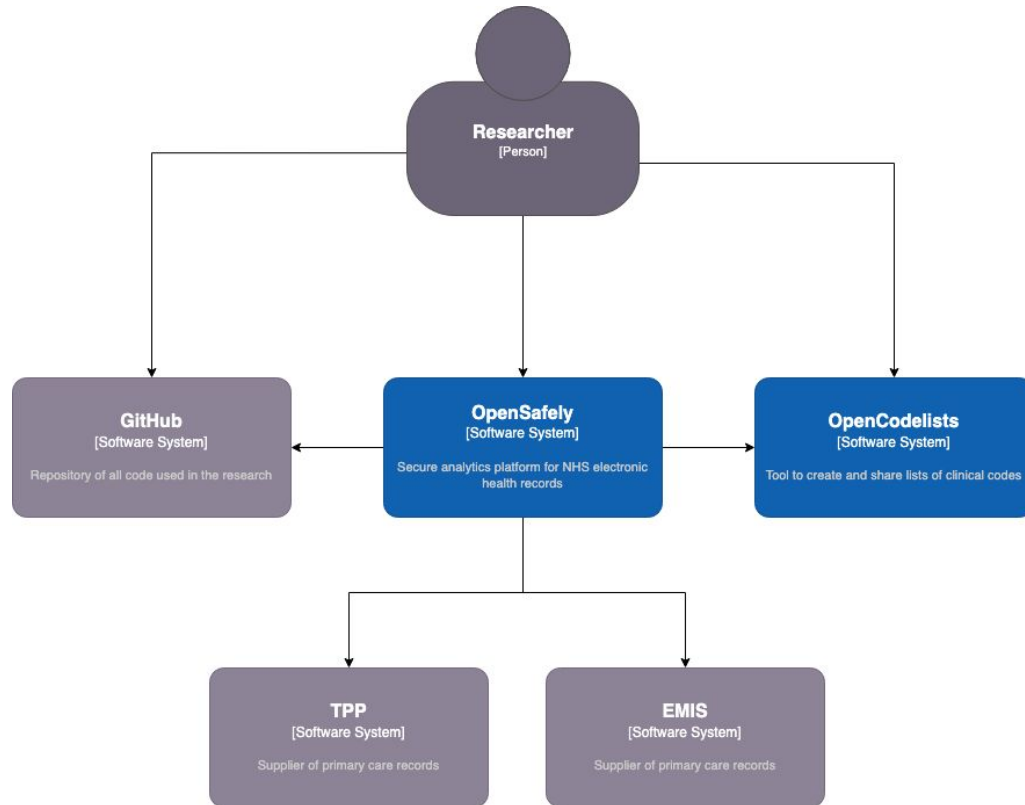
Trusted Research Environment



Federated Environment



OpenSAFELY



[Published: 25 May 2016](#)

1,500 scientists lift the lid on reproducibility

[Monya Baker](#)

[Nature](#) **533**, 452–454 (2016) | [Cite this article](#)

49k Accesses | **1640** Citations | **4227** Altmetric | [Metrics](#)

Out of 1579 researchers, more than **70%** of have tried and failed to reproduce another scientist's experiments, and **more than half** have failed to reproduce their own experiments.

The reproducibility debate is an opportunity, not a crisis

[Marcus R. Munafò](#) , [Chris Chambers](#), [Alexandra Collins](#), [Laura Fortunato](#) & [Malcolm Macleod](#)

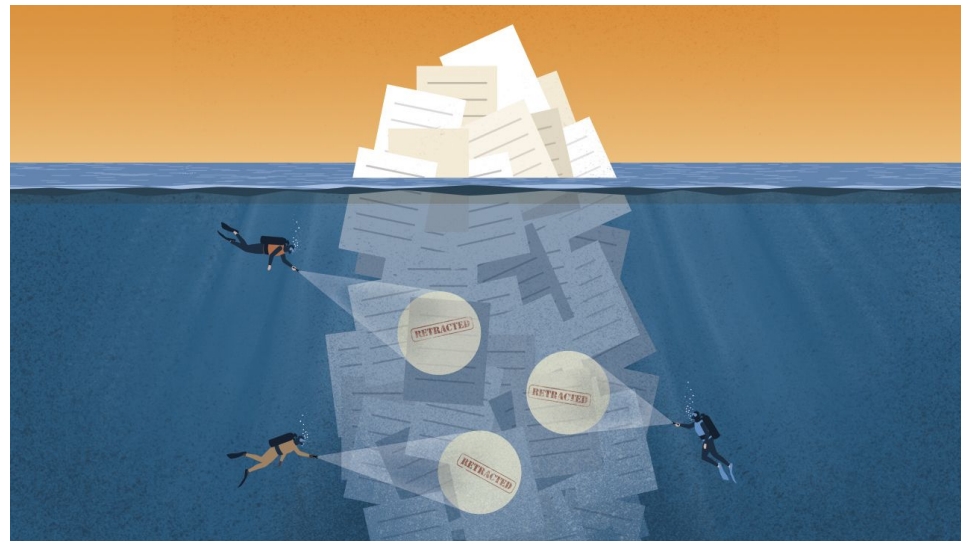
[BMC Research Notes](#) **15**, Article number: 43 (2022) | [Cite this article](#)

1881 Accesses | **2** Citations | **62** Altmetric | [Metrics](#)

Reproducibility can mitigate falsified research

Critical research on the causes of Alzheimer's may have been falsified

Scientists could have been led down blind alleys for more than a decade



<https://retractionwatch.com/>

- 1. Reproducibility is necessary**
- 2. Reproducibility is currency**
- 3. Reproducibility is an opportunity**

Emma Karoune

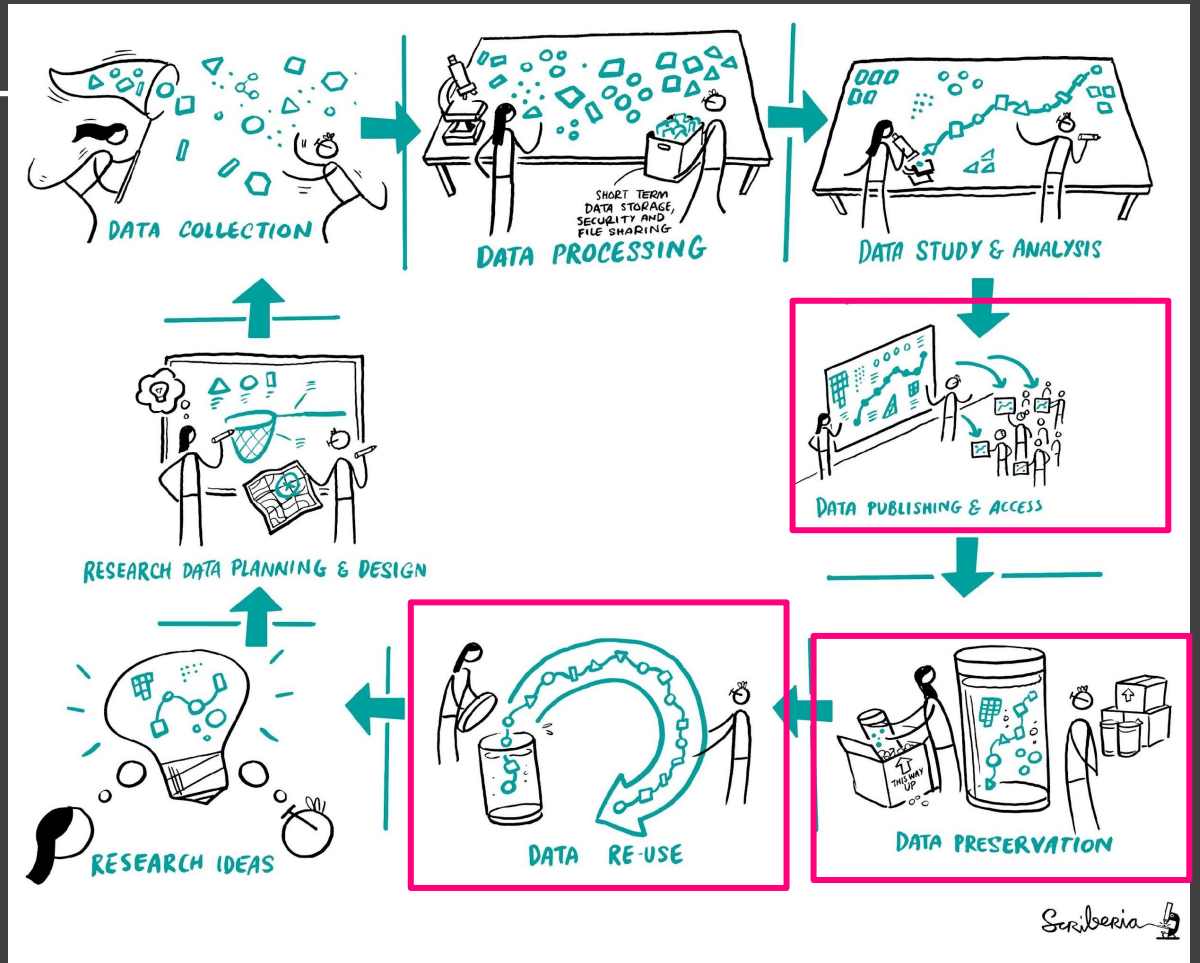
The
Alan Turing
Institute

- she/her/ ekaroune@turing.ac.uk / [@ekaroune](https://twitter.com/ekaroune) / [0000-0002-6576-6053](tel:0000-0002-6576-6053)
- **Senior Community Manager** - Turing-RSS Lab & DECOVID [@The Alan Turing Institute](https://twitter.com/TheAlanTuringInstitute)
- **Core team member** [@The Turing Way](https://twitter.com/TheTuringWay)
- **SSI Fellow**
- ELIXIR-UK **FAIR Data Fellow**
- **Mentor** [@Open Life Science](https://twitter.com/OpenLifeScience)
- **Research Associate** [@Historic England](https://twitter.com/HistoricEngland)
 - FAIR Phytoliths Project
 - Open reference collections



Reproducibility

		Data	
		Same	Different
Analysis	Same	Reproducible	Replicable
	Different	Robust	Generalisable





- Findable,
- Accessible
- Interoperable
- Reusable

FAIR does not mean open!

- FAIR does not require data to be open
- FAIR requires open metadata
- Detailed information about research/data should be open
- FAIR applies open standards for interoperability

Metadata = information about the “data descriptors” that facilitate cataloguing data and data discovery

Box 2 | The FAIR Guiding Principles

To be Findable:

- F1. (meta)data are assigned a globally unique and persistent identifier
- F2. data are described with rich metadata (defined by R1 below)
- F3. metadata clearly and explicitly include the identifier of the data it describes
- F4. (meta)data are registered or indexed in a searchable resource

To be Accessible:

- A1. (meta)data are retrievable by their identifier using a standardized communications protocol
 - A1.1 the protocol is open, free, and universally implementable
 - A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- A2. metadata are accessible, even when the data are no longer available

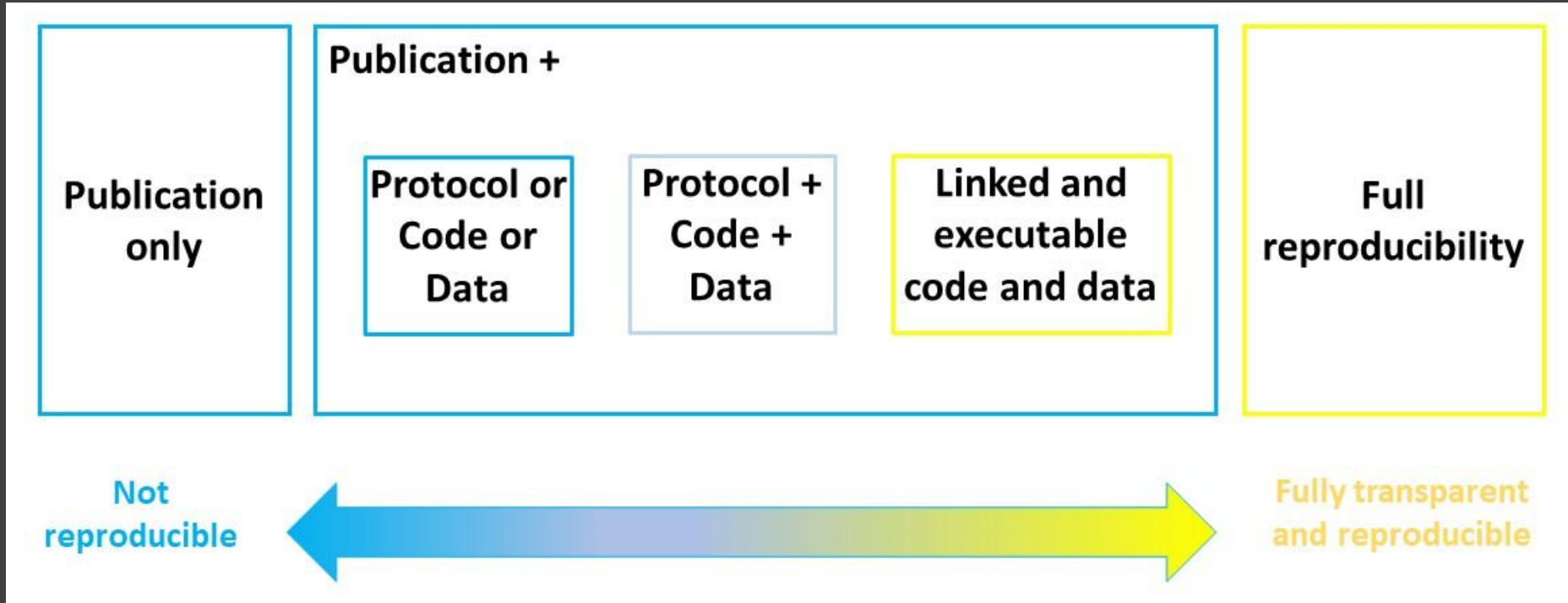
To be Interoperable:

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles
- I3. (meta)data include qualified references to other (meta)data

To be Reusable:

- R1. meta(data) are richly described with a plurality of accurate and relevant attributes
 - R1.1. (meta)data are released with a clear and accessible data usage license
 - R1.2. (meta)data are associated with detailed provenance
 - R1.3. (meta)data meet domain-relevant community standards

Reproducible articles



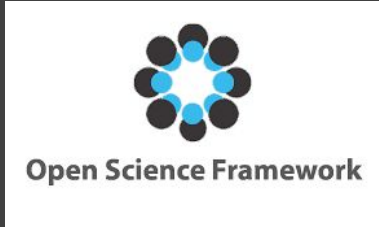
From Karoune & Plomp (2022) - an adapted reproducible spectrum (Peng 2011) with the addition of protocols.

Publishing reproducibly

Your research workflow needs to be transparent and accessible to others!

- Use a repository for data, code and other documentation
 - Get a **DOI** for all your outputs
- Link to your article using the **data and code availability statements**
 - Give clear statement of where other outputs are and how they can be accessed.
 - **Cite** your own dataset
- Publish other types of articles too! data, software, methods papers

Upload outputs to free openly accessible online digital repositories



- Trustworthy digital repository (TDR)
- Allows to generate shareable **DOI-**Digital Object Identifier

- **Not** a TDR
- cannot ensure long-term access

Repositories with restricted access

- Findable - Depositing datasets for long term sustainability - DOI
- Enabling accessibility
 - Different levels of access - how secure does it need to be?
 - Clear access procedure
- Interoperability
 - Standardised dataset
- Enabling reuse
 - Understanding of data collection - transparent recording

https://rdmkit.elixir-europe.org/uk_resources



Turing-RSS Health Data Lab

Our mission




“To support the UKHSA in UK health security through an embedded data science collaboration, working towards an **interoperable framework** that provides trusted quantitative evidence to decision makers.”

Reproducibility is one of our key goals:

- Reproducibility lead
- Planning for reproducibility - code and data management/version control
- FAIR data and reproducible publishing

<https://www.turing.ac.uk/research/research-projects/turing-rss-health-data-lab>

Improving local prevalence estimates of SARS-CoV-2 infections using a causal debiasing framework

[George Nicholson](#) , [Brieuc Lehmann](#) , [Tullia Padellini](#), [Koen B. Pouwels](#), [Radka Jersakova](#), [James Lomax](#), [Ruairidh E. King](#), [Ann-Marie Mallon](#), [Peter J. Diggle](#), [Sylvia Richardson](#), [Marta Blangiardo](#) & [Chris Holmes](#) 

Nature Microbiology **7**, 97–107 (2022) | [Cite this article](#)

Data availability

The data underlying the Alpha VoC 202012/01 analysis were accessed via the UK Health Security Agency Data Science Hub (DaSH) data platform; they are not publicly available and can only be accessed using approved UK government email domains such as @test-and-trace.nhs.uk. For the remainder of the results presented here, the data are publicly available. Randomized surveillance data comes from the REACT study²⁸ (<https://github.com/mrc-ide/reactidd/tree/master/inst/extdata>). From REACT, we create weekly test counts at the spatially coarse-scale level (PHE region) and, for validation purposes but not model fitting, use round-aggregated counts at the fine-scale level (LTLA), for rounds 7–11. The combined weekly Pillar 1+2 data are publicly available for download (<https://www.gov.uk/government/publications/nhs-test-and-trace-england-statistics-14-january-to-20-january-2021>; note that LFD results are not included in these weekly summaries). We downloaded R_t estimates outputted by the Imperial College team's Epidemia model^{28,39} from https://imperialcollegelondon.github.io/covid19local/downloads/UK_hotspot_Rt_estimates.csv on 13 October 2021, and we provide a copy of that downloaded file in our Zenodo repository at <https://doi.org/10.5281/zenodo.5784718>.

All our articles:

- Open access
- Links to code and data

Code availability

The R scripts⁴⁰ used to generate the results in this manuscript are available in the following Git repository: <https://github.com/alan-turing-institute/jbc-turing-rss-testdebiasing>.

December 15, 2021

Software **Open Access**

alan-turing-institute/jbc-turing-rss-testdebiasing: v1.0.0

Brieuc lehmann; Radka Jersakova

Version of scripts and data used to generate results and figures for 'Improving local prevalence estimates of SARS-CoV-2 infections using a causal debiasing framework', to appear in Nature Microbiology.

Preview

jbc-turing-rss-testdebiasing-Publication.zip

alan-turing-institute-jbc-turing-rss-testdebiasing-798ac3a

o .gitignore	174 Bytes
o LICENSE	1.1 kB
o README.md	5.5 kB
o data	
o example.RData	1.7 kB
o northhamptonshire_pop_nomis.csv	309 Bytes
o samples_pcr.csv	22.1 MB
o jbc-turing-rss-testdebiasing.Rproj	205 Bytes
o renv.lock	13.7 kB
o scripts	
o 00_download_data.R	5.9 kB
o 01_preprocess_data.R	8.3 kB
o 02_calculate_infectiousness_estimates.R	3.9 kB
o 03_prevalence_comparisons.R	3.2 kB
o 04a_main_run.R	4.0 kB
o 04b_main_cut.R	3.0 kB
o 05_supp_run.R	3.6 kB



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Projects

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Code

About

Brieuc lehmann Update README... on Dec 15, 2021 21

data	Update README with demo	11 months ago
scripts	Remove sf from renv depende...	11 months ago
transmats	Update scripts pre submission	12 months ago
.gitignore	Update README with demo	11 months ago
LICENSE	Initial commit	15 months ago
README.md	Update README.md	7 months ago
jbc-turing-rs...	Update scripts pre submission	12 months ago
renv.lock	Update prevdebiar version	10 months ago
testdebiasin...	Update scripts pre submission	12 months ago

Debiasing targeted testing

hut23 hut23-744

Readme

MIT license

4 stars

5 watching

3 forks

Releases 1

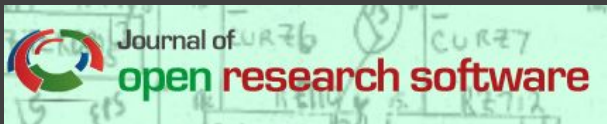
v1.0.0 Latest

on Dec 15, 2021

Data papers

- Describes a dataset
- Does not include analysis or findings
- Data usually in an open repository
- Use a template to write it
- Data journals

Software and methods papers too!



The Turing Way

An Open Science and community-led guide on Data Science

We involve a **diverse community** to make research **reproducible, ethical, collaborative and inclusive** for everyone.



<https://github.com/alan-turing-institute/the-turing-way>,

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

The Turing Way Book on Reproducibility



Kirstie Whitaker
Lead of Tools,
Practices & Systems
Programme



Malvika Sharan
TPS Senior researcher:
Open research &
Community



Anne Lee Steele
Community Manager,
The Turing Way

The Turing Way is a lightly opinionated guide to reproducible data science.

Our goal is to provide all the information that researchers need at the start of their projects to ensure that they are easy to reproduce at the end.

This also means making sure PhD students, postdocs, PIs, and funding teams know which parts of the "responsibility of reproducibility" they can affect, and what they should do to nudge data science to being more efficient, effective, and understandable.



Book: <https://the-turing-way.netlify.app/welcome>,

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

Guide for Reproducible research

Guide for Reproducible Research

Overview

Open Research

Version Control

Licensing

Research Data Management

Reproducible Environments

BinderHub

Code quality

Code Testing

Code Reviewing Process

Reusable Code

Continuous Integration (CI)

Reproducible Research with

Make

Research Compendia

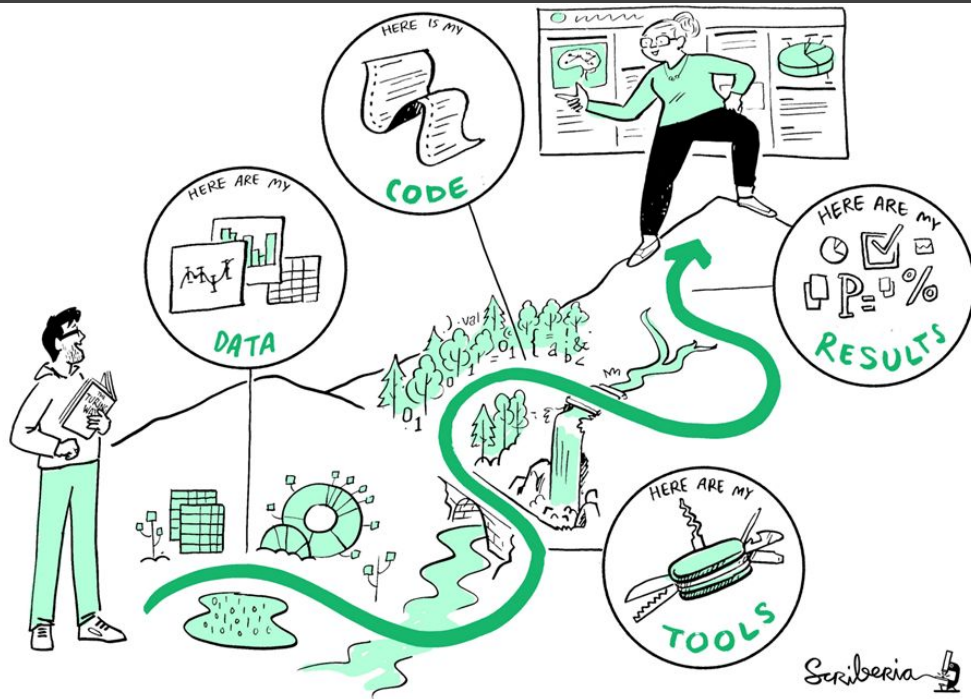


Fig. 3 The Turing Way project illustration by Scriberia. Used under a CC-BY 4.0

licence. DOI: [10.5281/zenodo.3332807](https://doi.org/10.5281/zenodo.3332807).

The Turing Way Guides



Reproducibility



Project Design



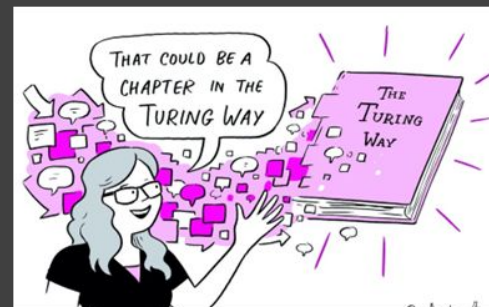
Communication



Collaboration



Ethical Research



Community Handbook



Book:
the-turing-way.netlify.app/

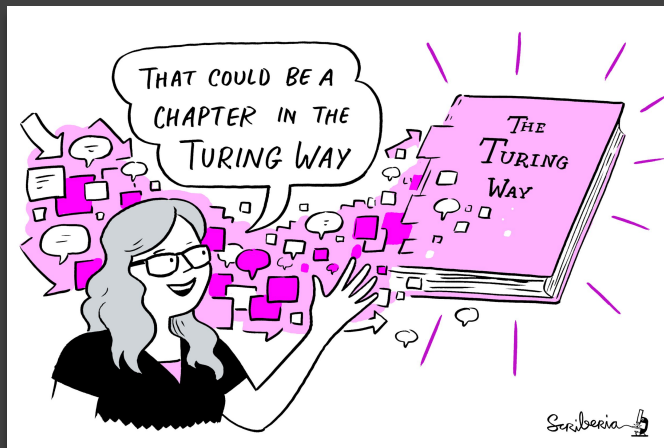
GitHub:
github.com/alan-turing-institute/the-turing-way

Twitter:
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Email:
theturingway@gmail.com

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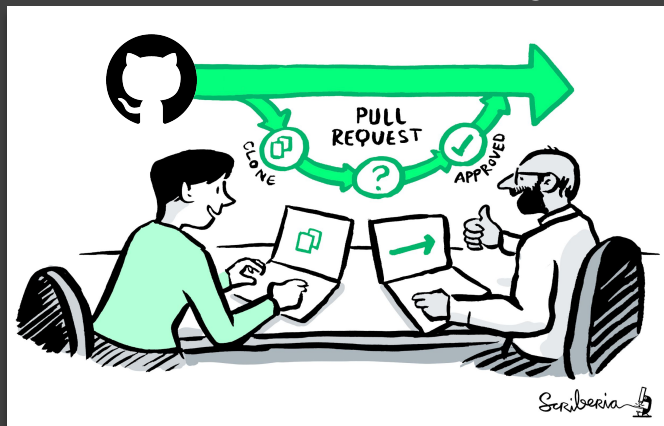
A Book



A Community

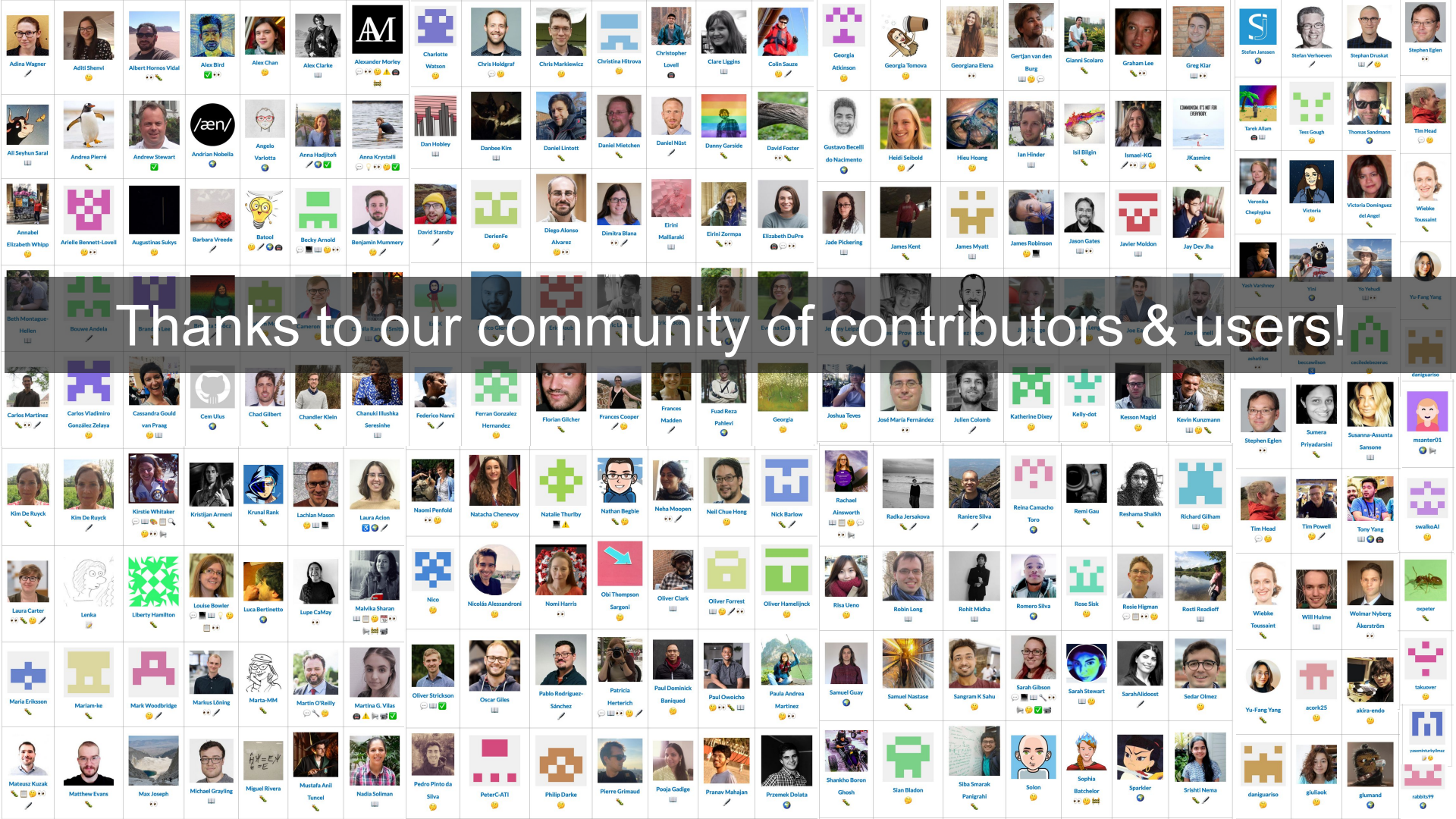


An Open Source Project



A Culture of Collaboration





Thanks to our community of contributors & users!

📁 .github	Remove prettier configuration
📁 book	minor update
📁 communications	Fix typos
📁 conferences	Add KW formatting pedantry
📁 project_management	Update online-collaboration-cafe.md
📁 templates	Updating Github templates
📁 tests	Add "et cetera" as a deprecated Latinism
📁 workshops	Remove mis-pasted text
📄 .all-contributorsrc	Merge pull request #991 from alan-turing-institute/all-contributors/a...
📄 .gitignore	ignore pptx in workshop folder
📄 .travis.yml	add html-proof file again
📄 <u>CODE_OF_CONDUCT.md</u>	her -> their
📄 <u>CONTRIBUTING.md</u>	Update CONTRIBUTING.md
📄 GOVERNANCE.md	Read through months later
📄 LICENSE.md	Fix typo in licence
📄 <u>README.md</u>	Merge pull request #991 from alan-turing-institute/all-contributors/a...
📄 book_skeleton.md	Update book_skeleton.md
📄 contributors.md	Add myself to contributors.md
📄 tips_and_tricks_survey.md	Update tips_and_tricks_survey.md
📄 ways_of_working.md	Adjust team contact section



all contributors 322

13 days ago
5 days ago
9 months ago
last month
6 months ago
2 months ago
5 months ago
2 months ago

GitHub:
<https://github.com/alan-turing-institute/the-turing-way>

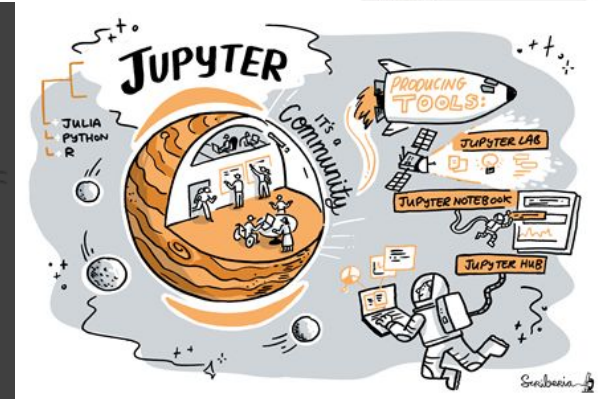
Cite as: *The Turing Way Community*. (2021). *The Turing Way: A handbook for reproducible, ethical and collaborative research* (1.0.1). Zenodo. <https://doi.org/10.5281/zenodo.5671094>

An open source project

- Everyone can freely read, reuse, distribute, modify and help develop.
- The project belongs to *The Turing Way* community.
- Built on open-source infrastructure: Git, Jupyter Book, Binder, project bots etc.
 - Netlify: the-turing-way.netlify.app/welcome



A screenshot of the Zenodo website. The header is blue with the Zenodo logo, a search bar, and links for 'Upload' and 'Communities'. The main content area is titled 'The Turing Way' and shows a list of 'Recent uploads'. Each upload entry includes a date, a title, a presenter, and a 'View' button. The entries are: 1. 'Challenges in Assessing Contributions to Reproducible Research and Open Science' by Sharan, Malvika, dated September 3, 2020. 2. 'FSCI2020 Lightning Talk: The Turing Way' by Esther Plomp and Kirstie Whitaker, dated August 11, 2020. 3. 'The Turing Way workshop on Boost your reproducibility with Binder' by Sharan, Malvika, dated August 6, 2020. On the right side, there is a 'New upload' button and a section titled 'The Turing Way' with a paragraph of text about the project's goals and a link to the GitHub repository.



Opportunities for connections



Collaboration Cafes and
weekly coworking

bit.ly/turingway

Book Dash Events
(in-person & virtual)

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

Fireside chat: Monthly informal Events

Navigating Growth and Scale to Sustain Open Communities

29 July 2022, 15:00 UTC

Hosted by



Register on Eventbrite



Selena Yang

Co-founder and Coordinator
of Geochicas



Patrick Mineault

Founder, xcorr Consulting
for neuroAI



Geoffrey Kateregga

Community Manager,
Humanitarian OpenStreetMap
Team



Alycia Crall

Director of Community,
The Carpentries



Anne Lee Steele

Community Manager,
The Turing Way

Fireside Chat Series

The July 2022 event is hosted with The Carpentries organisation. Fireside Chat series features people, ideas & projects in open and reproducible research.



bit.ly/turingway

29 July 2022, 15:00 UTC

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>

Notable impact

Resources are being used & replicated by learners, educators, community builders, policy makers and researchers globally

- Featured in **Goldacre Review** (2022)
- Highly commended project in **The Hidden REF** Competition (2022)
- Reproducibility of scientific results in the **EU 2020** (report)
- An Emerging Technology Charter by **Mayor of London** (policy)
- **Cited by 30+ peer-reviewed articles** & 100+ online publications

Community replication of project by:

- FAIR cookbook - Uni of **Oxford**
- **UCL** Institute of Health Informatics Coding Club handbook
- **ONS** - Quality assurance of code
- LIBER Citizen Science working group

Acknowledgements

- The Turing Way team, Kirstie Whitaker, Malvika Sharan, Anne Lee Steele
- *The Turing Way* community, contributors & collaborators

Book: the-turing-way.netlify.com **Twitter:** twitter.com/turingway

Newsletter: tinyletter.com/TuringWay

GitHub: github.com/alan-turing-institute/the-turing-way

Original artwork by Scriberia: <https://doi.org/10.5281/zenodo.3332807>



Turing-RSS Health Data Lab

Web: <https://www.turing.ac.uk/research/research-projects/turing-rss-health-data-lab>

Twitter: https://twitter.com/turingrss_hdlab

EDoN

Web: <https://edon-initiative.org/>

@turingway, @arronlacey, @ekaroune, Zenodo: <https://doi.org/10.5281/zenodo/6895192>