

# Creating targets-based scientific workflows

## Reproducible Scientific Workflows in R - Part 2

Ernest Guevarra

2024-02-12

# Outline

- Concepts on scientific workflows
- The `{targets}` package
- Practical session

# Concepts on scientific workflows

**Concept #1: Reproducibility, reproducibility,  
reproducibility!**

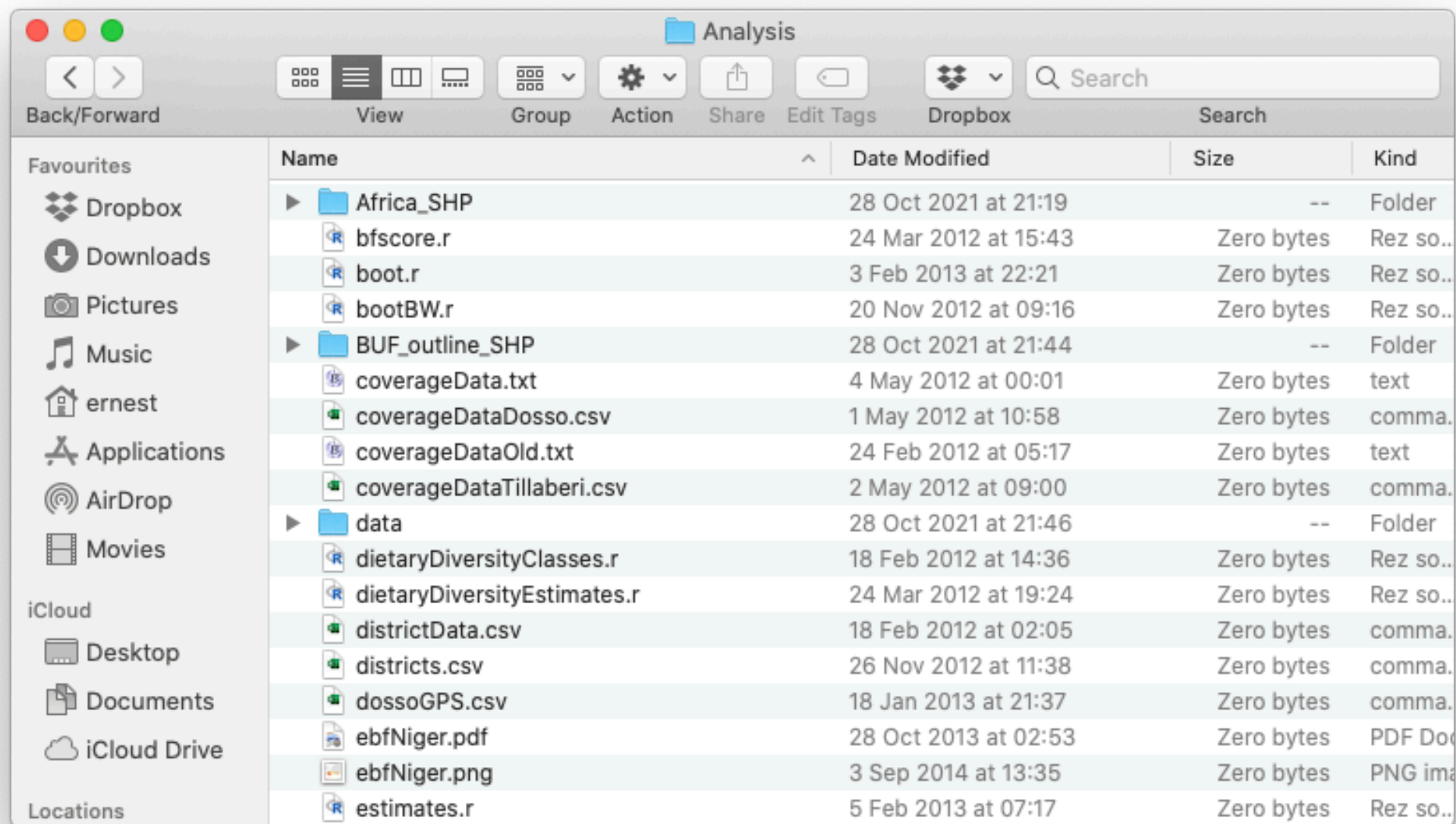
**Most important tool for Reproducible Research  
is the mindset, when starting, that the end  
product will be reproducible.**

Keith Baggerly, via [@kwbroman](#) tweet

# Concept #2: Organisation

**File organization and naming are powerful weapons against chaos.**

@JennyBryan





**Concept #3: DRY - Don't repeat yourself**

**Don't repeat yourself. It's not only repetitive,  
it's redundant, and people have heard it before.**

Lemony Snicket

```
# Overlay maps of Niger and Nigeria to clean-up the map
par(new=TRUE)
plot(nigeria, axes = FALSE, xlim = mapXLimits, ylim = mapYLimits, border = "white", col = "white")

par(new = TRUE)
plot(boundaries, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.5, border = "black")

par(new = TRUE)
plot(n1, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

par(new = TRUE)
plot(n4, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

par(new = TRUE)
plot(n5, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

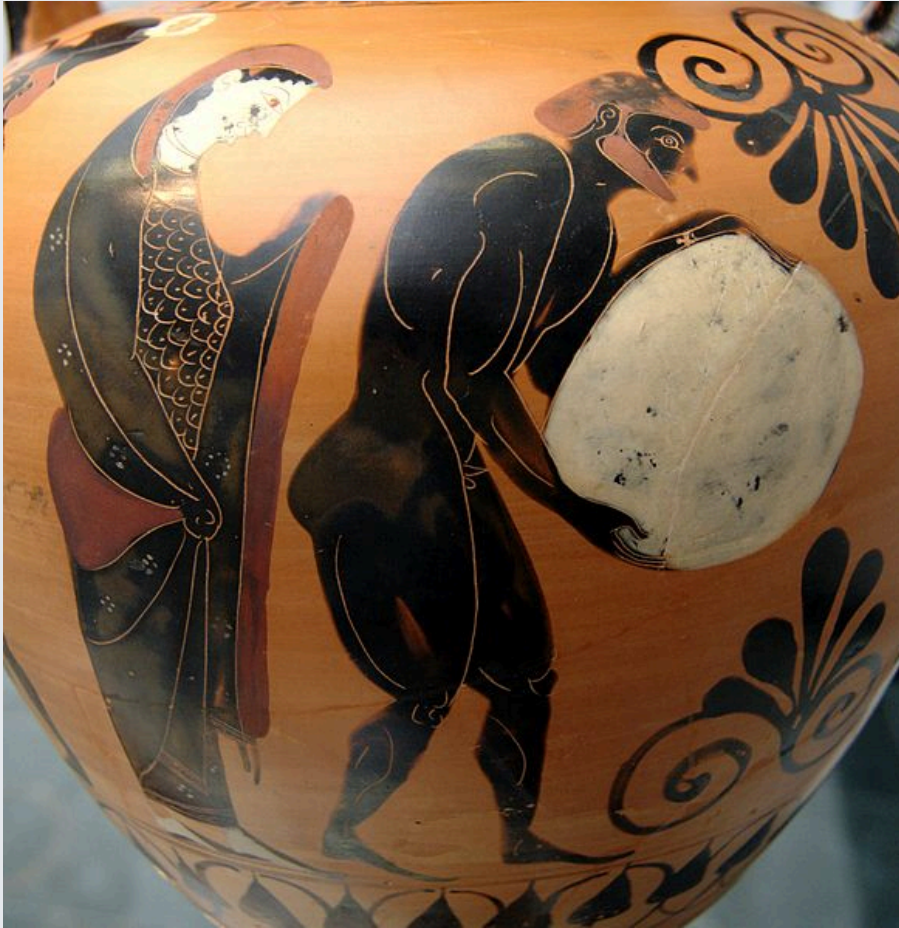
par(new = TRUE)
plot(n6, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

par(new = TRUE)
plot(n6.27, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

par(new = TRUE)
plot(n7, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

par(new = TRUE)
plot(n14, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")
```

# Sisyphean loop



1. Launch the code.
2. Wait while it runs.
3. Discover an issue.
4. Restart from scratch.

**Concept #3: Frequency reduces difficulty**

**If it hurts, do it more often.**

@martinfowler, via @JennyBryan tweet

# The {targets} package



- a pipeline toolkit for Statistics and data science in R
- maintain a reproducible workflow without repeating yourself
- learns how your workflow fits together
- skips costly runtime for tasks that are already up-to-date
- runs only the necessary computation
- supports implicit parallel computing
- abstracts files as R objects
- shows tangible evidence that the results match the underlying code and data

# {targets} file organisation

ernestguevarra update README

File	Description	Commit Time
.git-crypt	Add 1 git-crypt collaborator	5 days ago
.github/workflows	rename workflows	2 days ago
R	complete data review and anthro review	8 hours ago
auth	encrypt and authenticate with drive	3 days ago
data	add .gitkeep	3 days ago
images	update README	12 minutes ago
outputs	Create .gitkeep	2 days ago
renv	Initial commit	5 days ago
reports	add notes to data review	7 hours ago
.Rprofile	encrypt and authenticate with drive	3 days ago
.env	encrypt and authenticate with drive	3 days ago
.gitattributes	encrypt and authenticate with drive	3 days ago
.gitignore	encrypt and authenticate with drive	3 days ago
README.Rmd	update README	12 minutes ago
README.md	update README	12 minutes ago
<b>_targets.R</b>	complete data review and anthro review	8 hours ago
mozambique-baseline-review.Rproj	encrypt and authenticate with drive	3 days ago
packages.R	complete data review and anthro review	8 hours ago
renv.lock	complete data review and anthro review	8 hours ago

**README.md**

## Improving nutrition status for under 5 children in Zambezia and Nampula baseline survey data review workflow

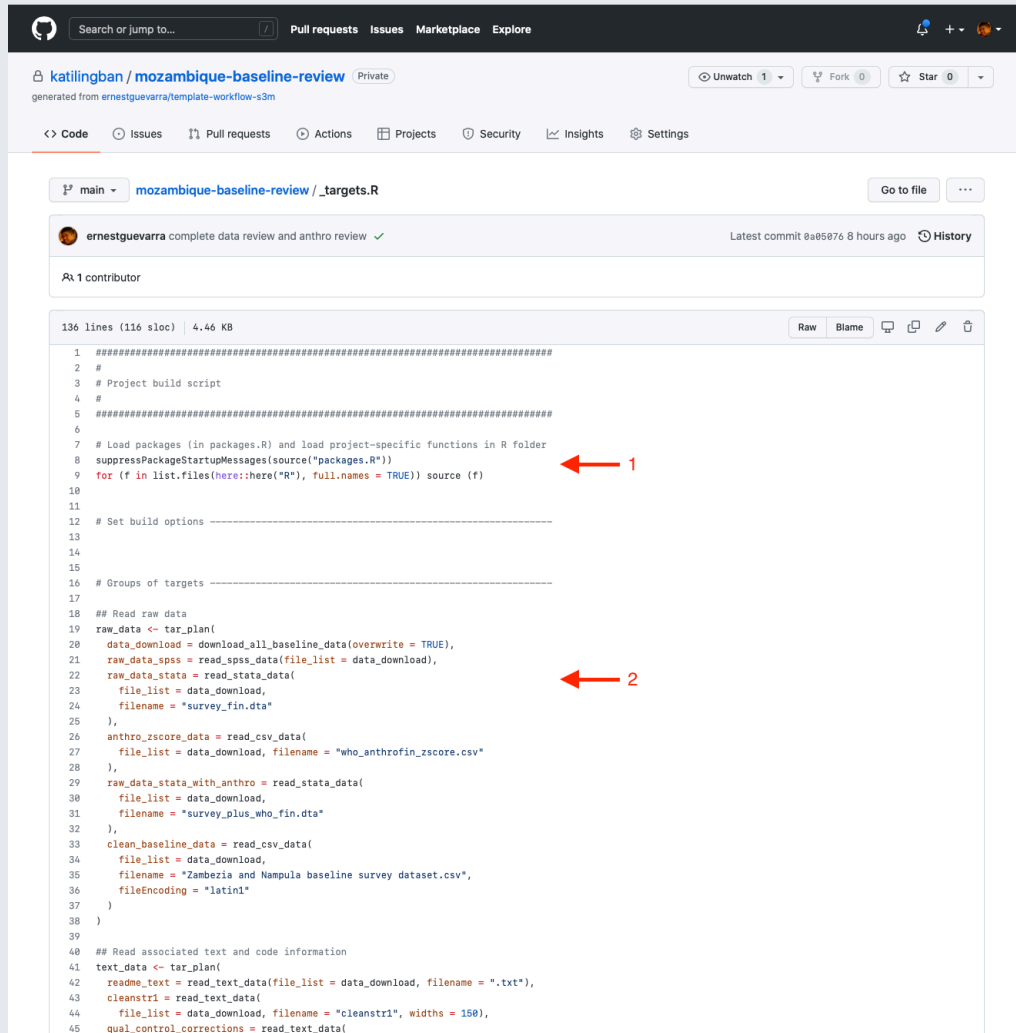
repo status **Active** test review workflow **passing** run review workflow **passing**

This repository is a template for a `docker`-containerised, `{targets}`-based, `{renv}`-enabled `R` workflow for the baseline survey data review of the improving nutrition status for under 5 children in Zambezia and Nampula.

- this is a typical file structure with user-defined components of any project-oriented workflow
- the `_targets.R` file, however, is special and specific to a `{targets}` workflow - it is the target script file
- the target script file should be in the project's root directory



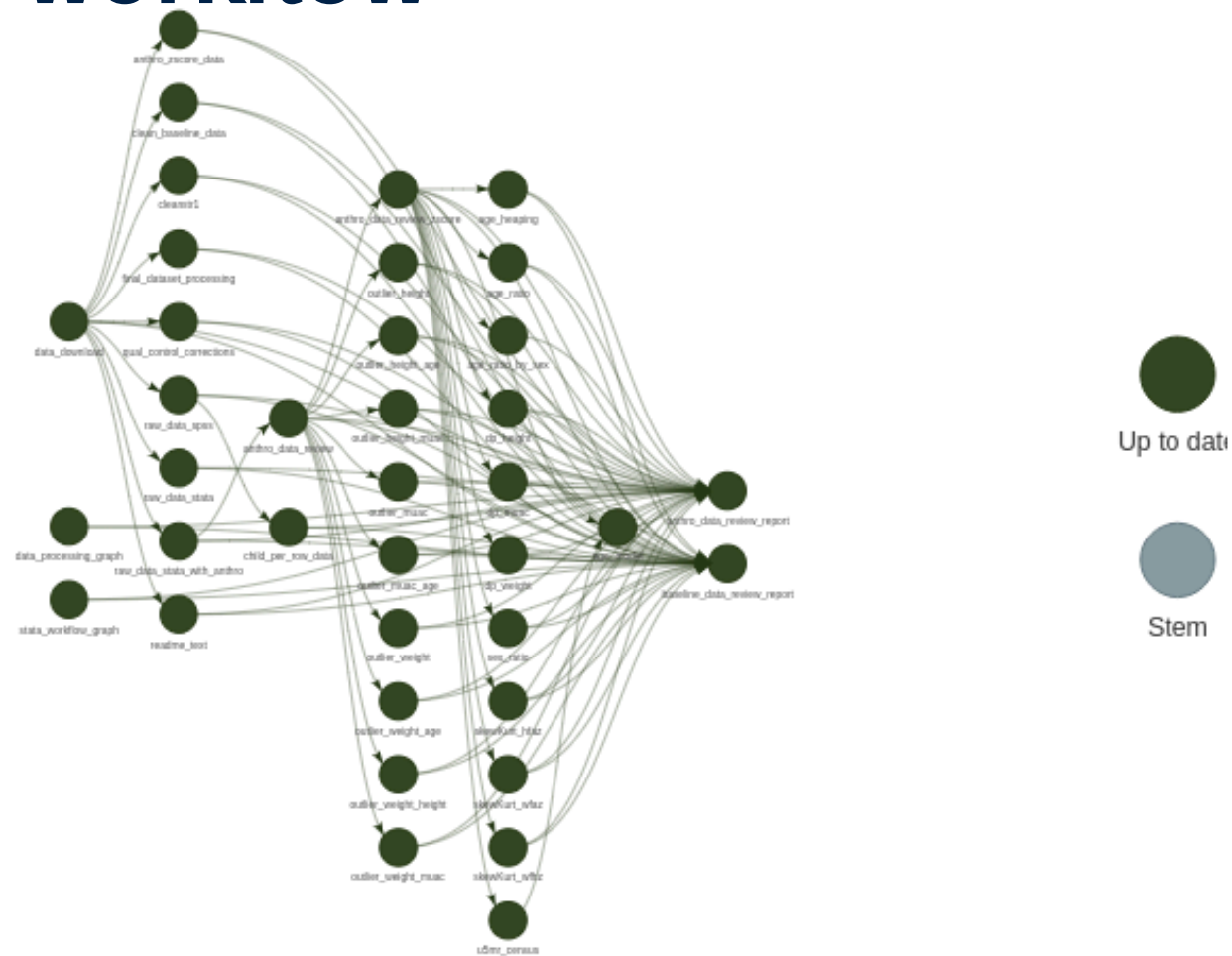
# {targets} script file



```
1 #####
2 #
3 # Project build script
4 #
5 #####
6
7 # Load packages (in packages.R) and load project-specific functions in R folder
8 suppressPackageStartupMessages(source("packages.R"))
9 for (f in list.files(here::here("R"), full.names = TRUE)) source(f)
10
11
12 # Set build options -----
13
14
15
16 # Groups of targets -----
17
18 ## Read raw data
19 raw_data <- tar_plan(
20   data_download = download_all_baseline_data(overwrite = TRUE),
21   raw_data_spss = read_spss_data(file_list = data_download),
22   raw_data_stata = read_stata_data(
23     file_list = data_download,
24     filename = "survey_fin.dta"
25   ),
26   anthro_zscore_data = read_csv_data(
27     file_list = data_download, filename = "who_anthrofin_zscore.csv"
28   ),
29   raw_data_stata_with_anthro = read_stata_data(
30     file_list = data_download,
31     filename = "survey_plus_who_fin.dta"
32   ),
33   clean_baseline_data = read_csv_data(
34     file_list = data_download,
35     filename = "Zambia and Nampula baseline survey dataset.csv",
36     fileEncoding = "latin1"
37   )
38 )
39
40 ## Read associated text and code information
41 text_data <- tar_plan(
42   readme_text = read_text_data(file_list = data_download, filename = ".txt"),
43   cleanstr1 = read_text_data(
44     file_list = data_download, filename = "cleanstr1", widths = 150),
45   qual_control_corrections = read_text_data(
```

- Load the packages required (1)
- Load custom functions (1)
- Define individual targets - intermediate step of the workflow (2)
- End with a list of targets objects

# {targets} workflow



Questions?

# Practical session

We will all continue to go through Exercise #1 in the  
**Practical R for Epidemiologists** book

Questions?

# Thank you!

Slides can be viewed at <https://oxford-ihm.io/open-reproducible-science/session9.html>

PDF version of slides can be downloaded at <https://oxford-ihm.io/open-reproducible-science/pdf/session9-reproducible-scientific-workflows.pdf>

R scripts for slides available [here](#)