

Introduction to the {targets} package

Reproducible Scientific Workflows in R - Part 1

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Outline

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

Concepts on scientific workflows

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



Karl Broman

@kwbroman



Keith Baggerly: Most important tool for [#ReproducibleResearch](#) is the *mindset*, when starting, that the end product will be reproducible.

♡ 11 4:07 PM - Nov 20, 2015



 [See Karl Broman's other Tweets](#)

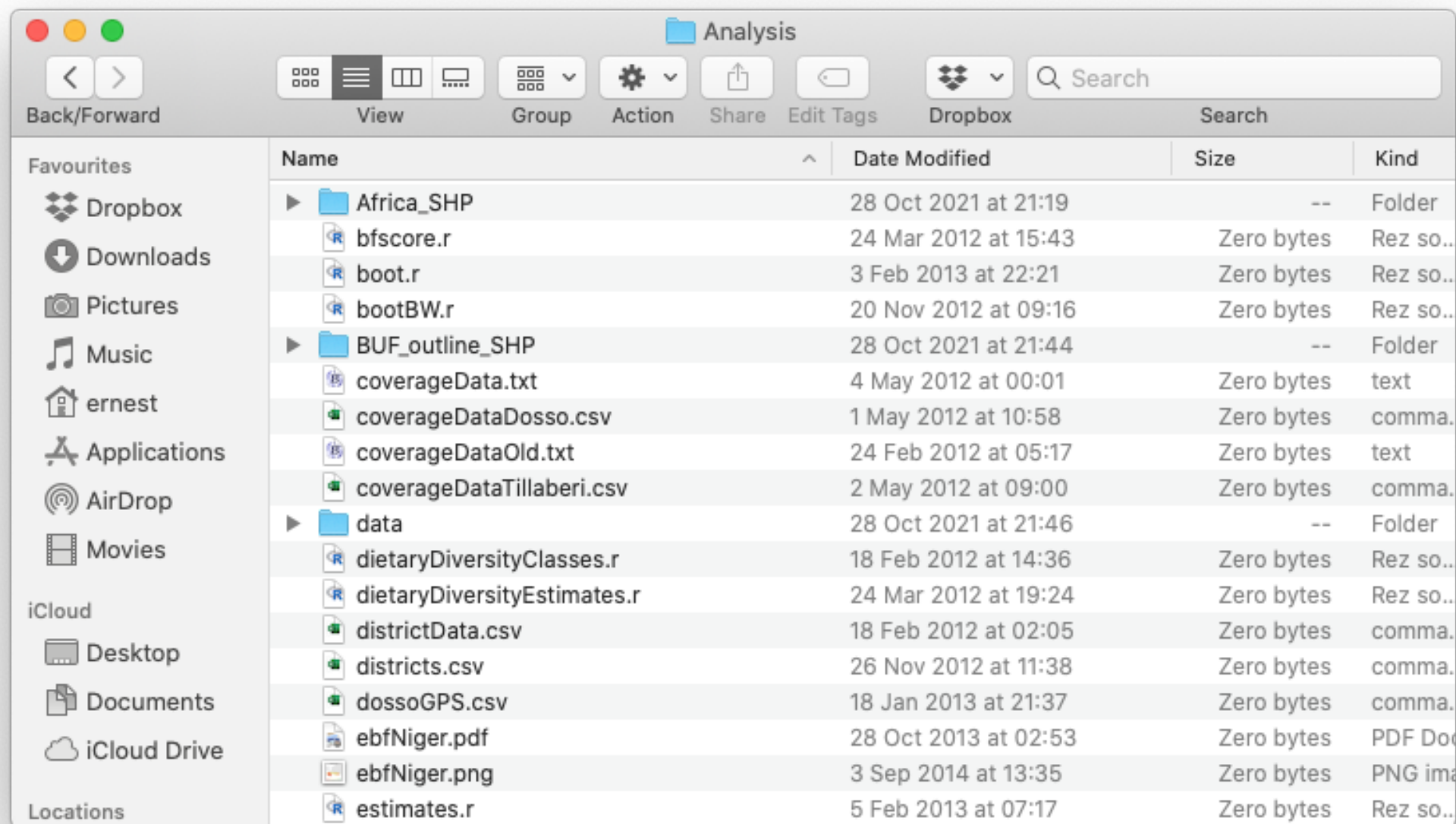


Keith Baggerly, via @kwbroman tweet

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")

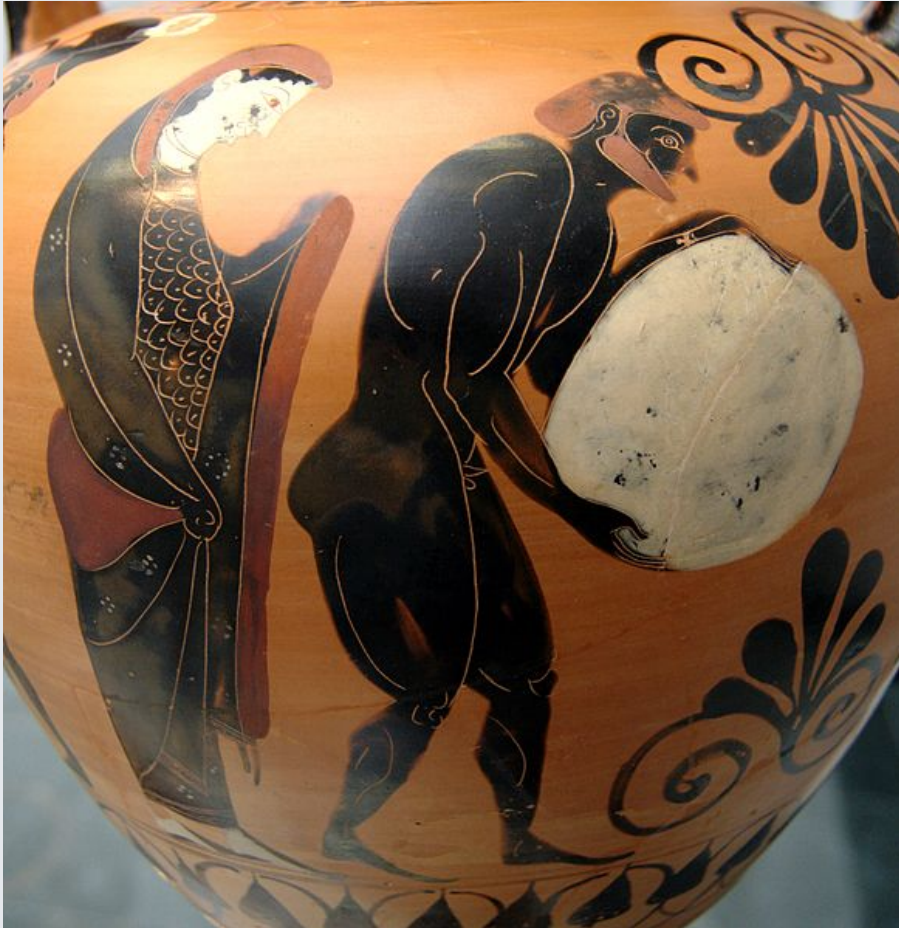
par(new = TRUE)
plot(n6, axes = FALSE, xlim = mapXLimits, ylim=mapYLimits, lwd = 0.25, col = "blue")

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



Jenny Bryan ✓

@JennyBryan



If it hurts, do it more often. — @martinfowler

We shared this idea in a recent workshop and it resonated with many. Applies to all sorts of things: git tasks (pushing & pulling), keeping your s/w stack current, sharing your work with others, etc.

[martinfowler.com/bliki/Frequenc...](https://martinfowler.com/bliki/Frequency.html)

♡ 150 7:32 PM - Jan 22, 2019



💬 49 people are talking about this



@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

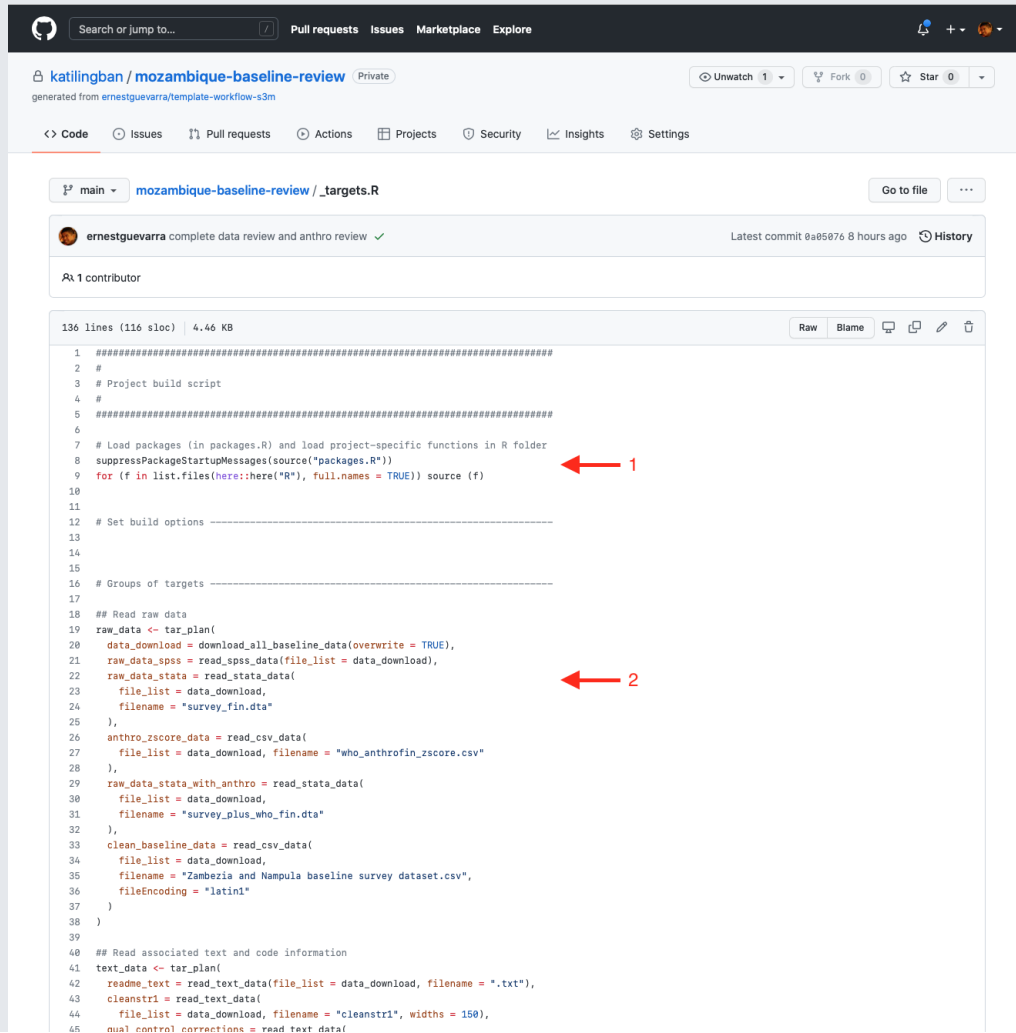
The screenshot shows a GitHub repository page for 'katilingban / mozambique-baseline-review'. The repository is private and was generated from 'ernestguevarra/template-workflow-s3m'. The file list on the left includes:

- .git-crypt
- .github/workflows
- R
- auth
- data
- images
- outputs
- renv
- reports
- .Rprofile
- .env
- .gitattributes
- .gitignore
- README.Rmd
- README.md
- _targets.R** (highlighted with a red box)
- mozambique-baseline-review.Rproj
- packages.R
- renv.lock

The right sidebar shows the repository's description: 'Improving nutrition status for under 5 children in Zambezia and Nampula baseline survey data review workflow'. It also includes sections for Releases, Packages, and Languages, with a progress bar for R at 100.0%.

- 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

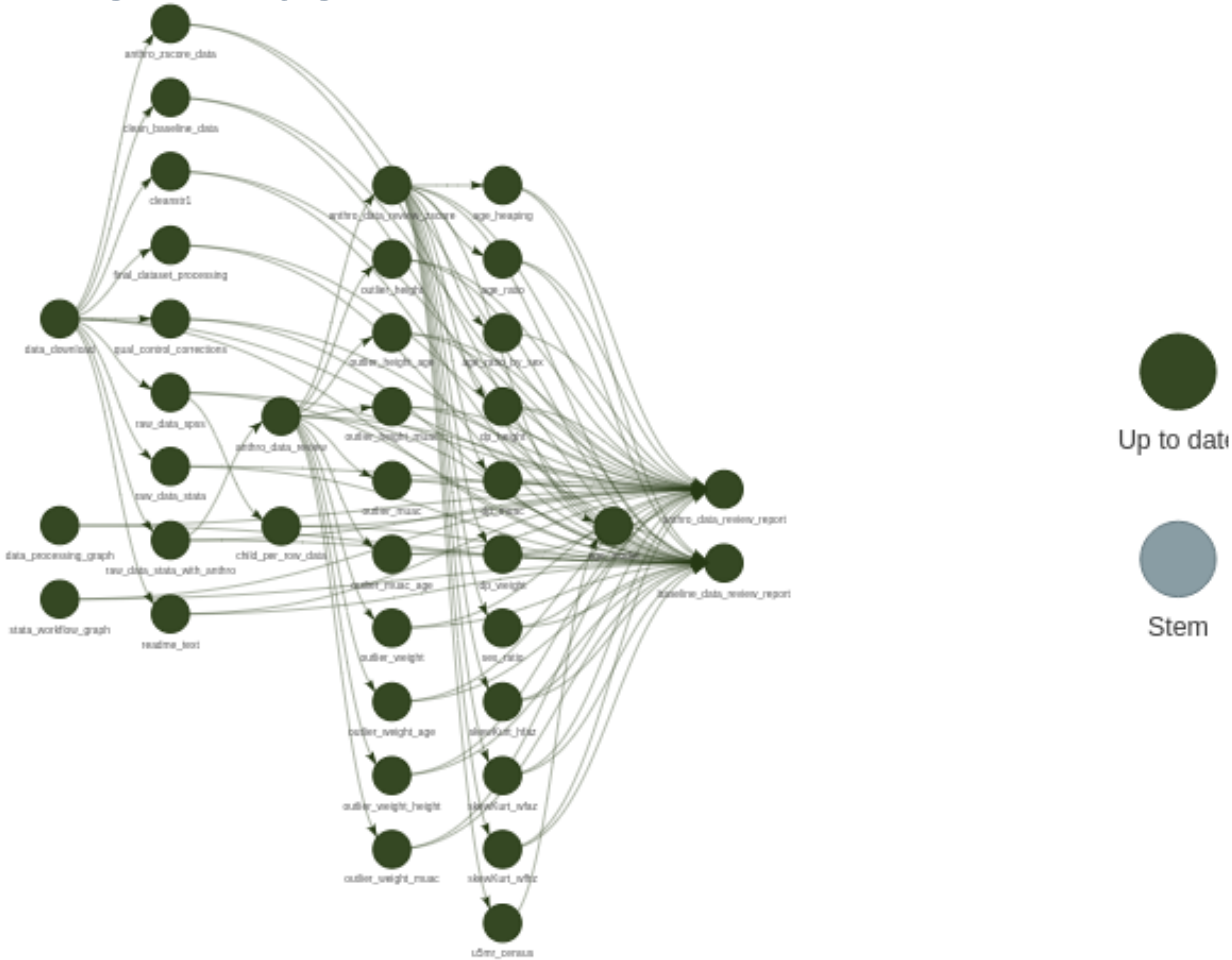
{targets} script file



```
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 = "Zambezi 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-ihtm.io/open-reproducible-science/session8.html>

PDF version of slides can be downloaded at <https://oxford-ihtm.io/open-reproducible-science/pdf/session8-reproducible-scientific-workflows.pdf>

R scripts for slides available [here](#)