Creating targets-based scientific workflows

Reproducible Scientific Workflows in R - Part 2

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Outline

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

Concepts on scientific workflows

Concept #1: Reproducibility, reproducibility, reproducibility!

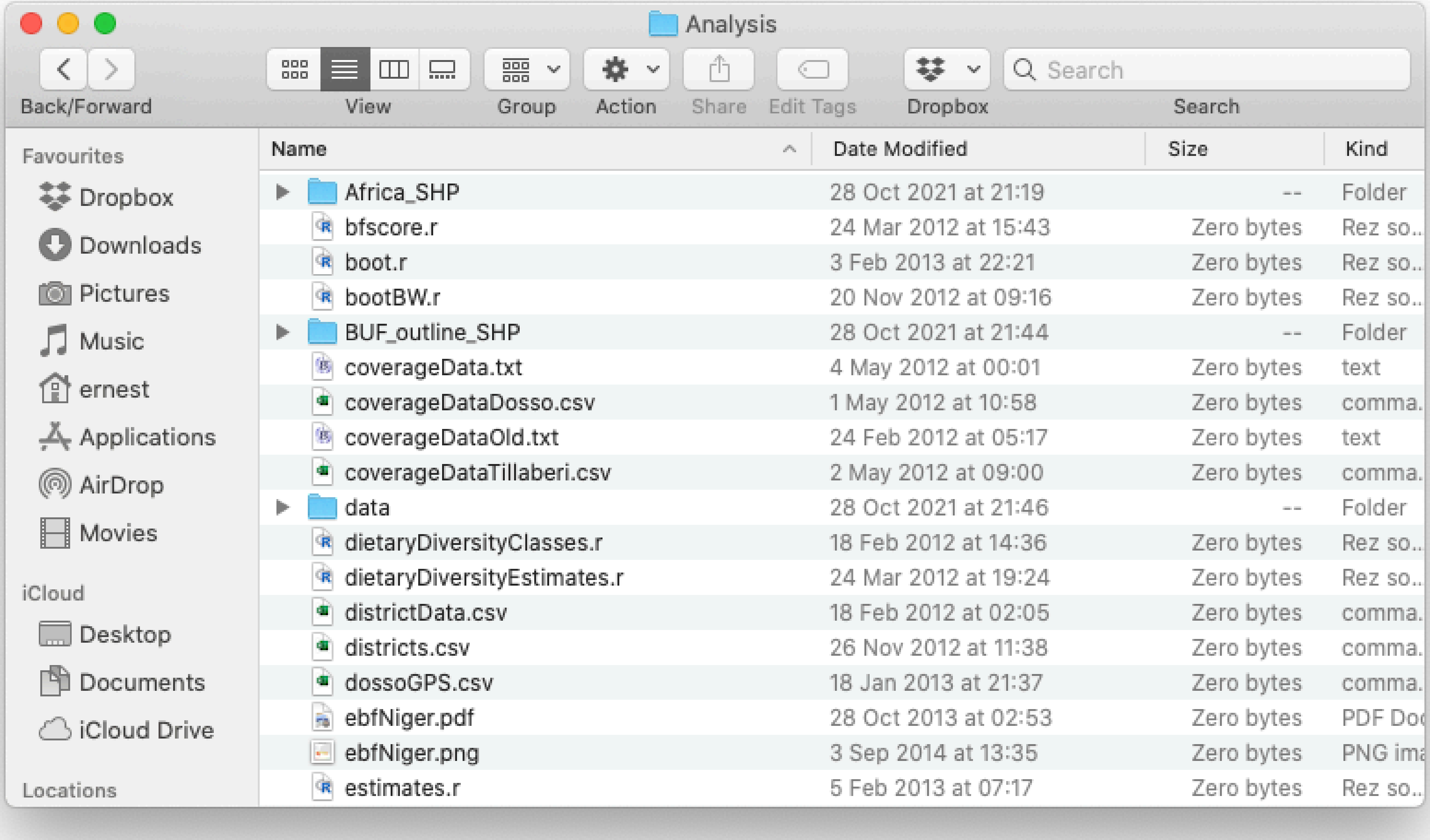
Most important tool for Reproducible Research is the mindset, when starting, taht the end product will be reproducible.

Keith Baggerly, via @kwbroman tweet

Concept #2: Organisation

File organization and naming are powerful weapons against chaos.

@JennyBryan



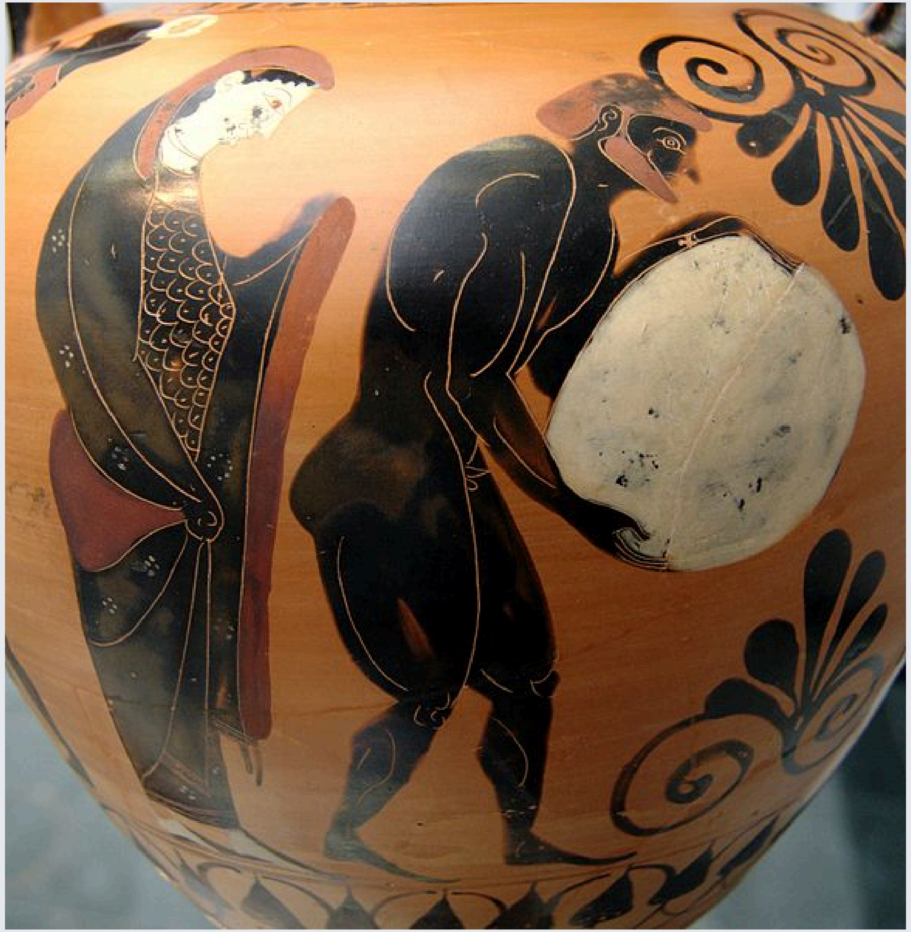
Name	Date Modified	Size	Kind
▶ Africa_SHP	28 Oct 2021 at 21:19	--	Folder
bfscore.r	24 Mar 2012 at 15:43	Zero bytes	Rez so...
boot.r	3 Feb 2013 at 22:21	Zero bytes	Rez so...
bootBW.r	20 Nov 2012 at 09:16	Zero bytes	Rez so...
▶ BUF_outline_SHP	28 Oct 2021 at 21:44	--	Folder
coverageData.txt	4 May 2012 at 00:01	Zero bytes	text
coverageDataDosso.csv	1 May 2012 at 10:58	Zero bytes	comma.
coverageDataOld.txt	24 Feb 2012 at 05:17	Zero bytes	text
coverageDataTillaberi.csv	2 May 2012 at 09:00	Zero bytes	comma.
▶ data	28 Oct 2021 at 21:46	--	Folder
dietaryDiversityClasses.r	18 Feb 2012 at 14:36	Zero bytes	Rez so...
dietaryDiversityEstimates.r	24 Mar 2012 at 19:24	Zero bytes	Rez so...
districtData.csv	18 Feb 2012 at 02:05	Zero bytes	comma.
districts.csv	26 Nov 2012 at 11:38	Zero bytes	comma.
dossoGPS.csv	18 Jan 2013 at 21:37	Zero bytes	comma.
ebfNiger.pdf	28 Oct 2013 at 02:53	Zero bytes	PDF Doc
ebfNiger.png	3 Sep 2014 at 13:35	Zero bytes	PNG ima
estimates.r	5 Feb 2013 at 07:17	Zero bytes	Rez so...

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

```r
# 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

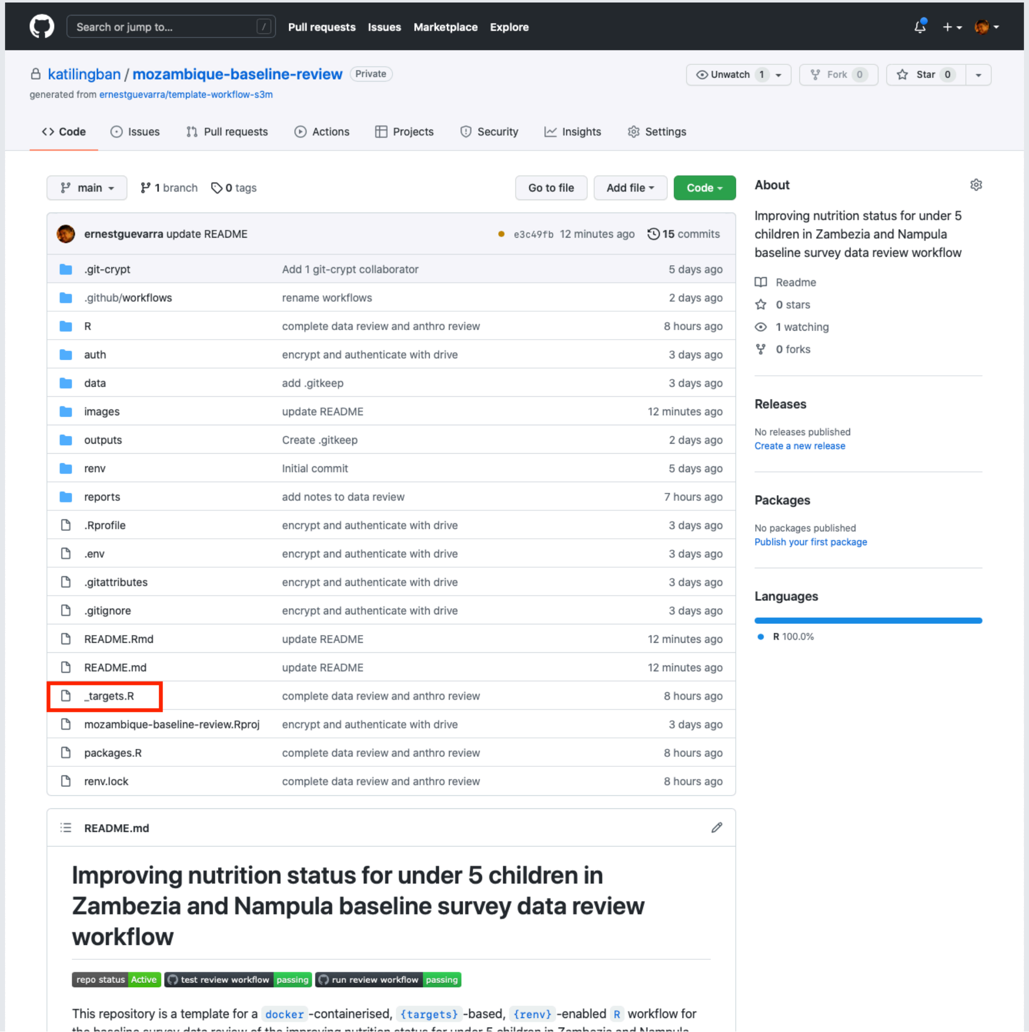
If it hurts, do it more often.

@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 · e3c49fb 12 minutes ago · 15 commits

.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
_targets.R	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

About

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

Readme
0 stars
1 watching
0 forks

Releases

No releases published
Create a new release

Packages

No packages published
Publish your first package

Languages

R 100.0%

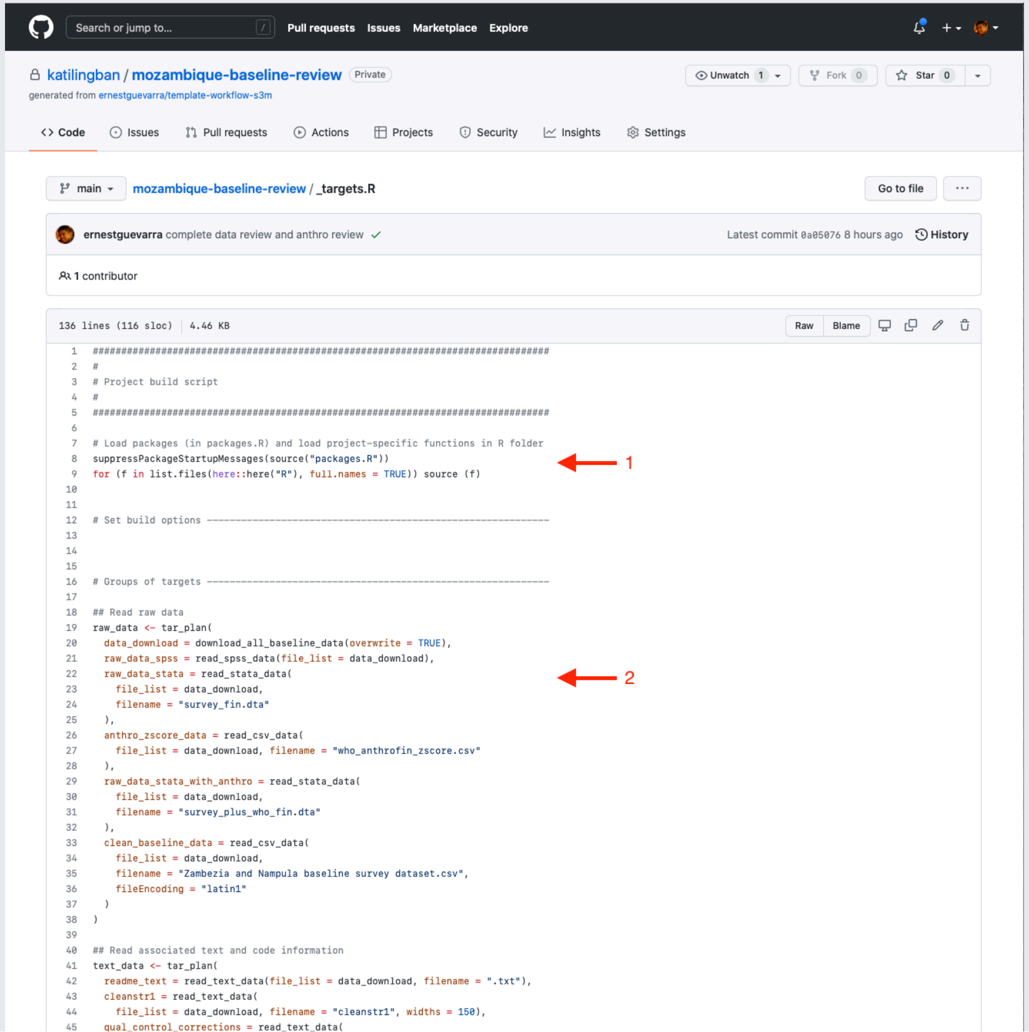
README.md

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

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



katilingban / mozambique-baseline-review Private

generated from ernestguevarra/template-workflow-s3m

mozambique-baseline-review / _targets.R

ernestguevarra complete data review and anthro review ✓ Latest commit 0a05076 8 hours ago History

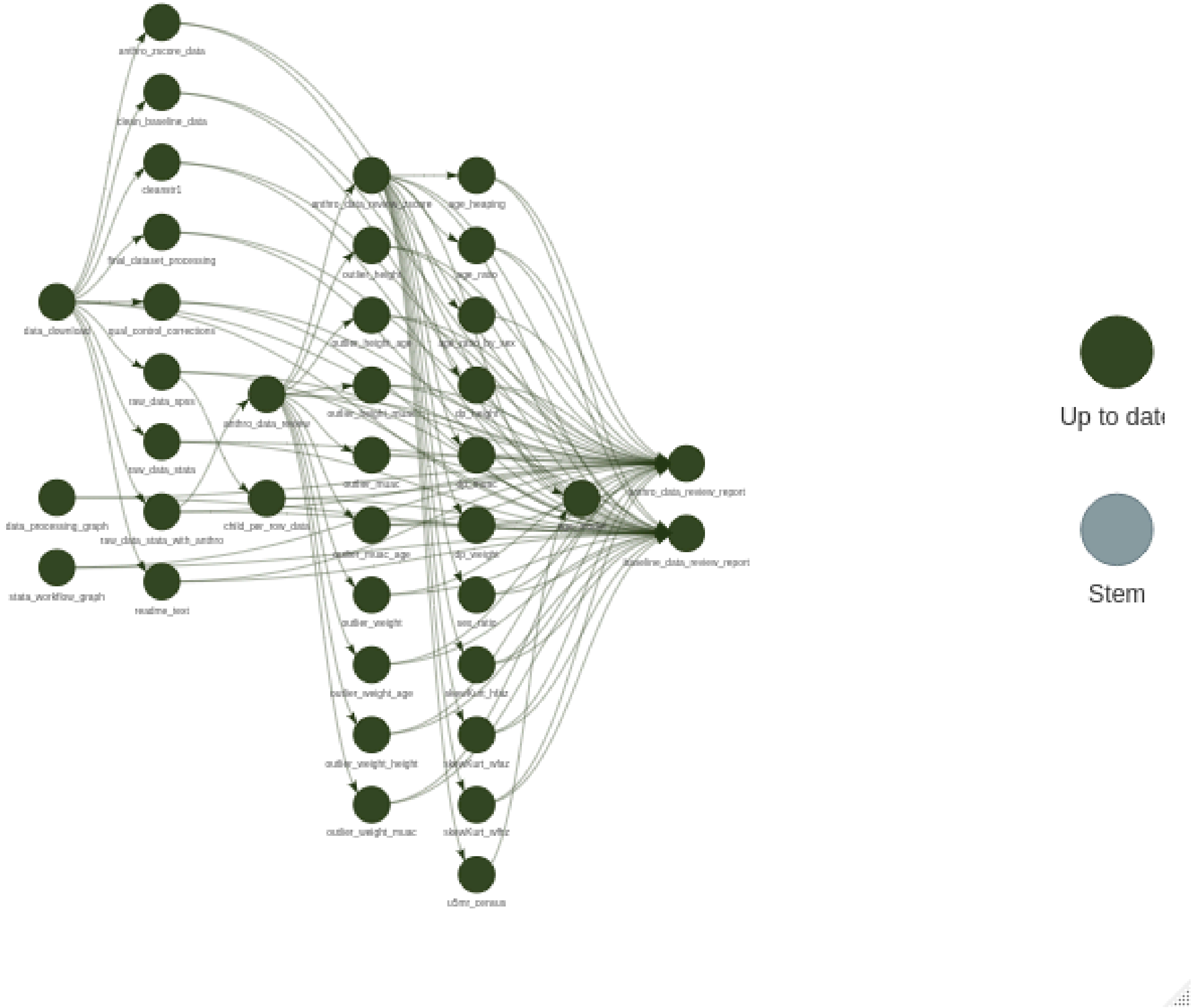
1 contributor

136 lines (116 sloc) | 4.46 KB

```r
################################################################################
#
# Project build script
#
################################################################################

# Load packages (in packages.R) and load project-specific functions in R folder
suppressPackageStartupMessages(source("packages.R"))
for (f in list.files(here::here("R"), full.names = TRUE)) source (f)


# Set build options ------------------------------------------------------------



# Groups of targets ------------------------------------------------------------

## Read raw data
raw_data <- tar_plan(
  data_download = download_all_baseline_data(overwrite = TRUE),
  raw_data_spss = read_spss_data(file_list = data_download),
  raw_data_stata = read_stata_data(
    file_list = data_download,
    filename = "survey_fin.dta"
  ),
  anthro_zscore_data = read_csv_data(
    file_list = data_download, filename = "who_anthrofin_zscore.csv"
  ),
  raw_data_stata_with_anthro = read_stata_data(
    file_list = data_download,
    filename = "survey_plus_who_fin.dta"
  ),
  clean_baseline_data = read_csv_data(
    file_list = data_download,
    filename = "Zambezia and Nampula baseline survey dataset.csv",
    fileEncoding = "latin1"
  )
)

## Read associated text and code information
text_data <- tar_plan(
  readme_text = read_text_data(file_list = data_download, filename = ".txt"),
  cleanstr1 = read_text_data(
    file_list = data_download, filename = "cleanstr1", widths = 150),
  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/session9.html

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

R scripts for slides available here