{targets}

What is `{targets}`?

“a Make-like pipeline tool for statistics and data science in R”

- manage a sequence of computational steps
- only update what needs updating
- ensure that the results at the end of the pipeline are still valid

Script-based workflow

`01-data.R`

```r
library(tidyverse)
data <- read_csv("data.csv", col_types = cols()) %>%
    filter(!is.na(Ozone))
write_rds(data, "data.rds")
```

`02-model.R`

```r
library(tidyverse)
data <- read_rds("data.rds")
model <- lm(Ozone ~ Temp, data) %>%
    coefficients()
write_rds(model, "model.rds")
```

`03-plot.R`

```r
library(tidyverse)
model <- read_rds("model.rds")
data <- read_rds("data.rds")
ggplot(data) +
    geom_point(aes(x = Temp, y = Ozone)) +
    geom_abline(intercept = model[1], slope = model[2])
ggsave("plot.png", plot)
```

Problems with script-based workflow

- **Reproducibility**: if you change something in one script, you have to remember to re-run the scripts that depend on it
- **Efficiency**: that means you'll usually rerun all the scripts even if they don't depend on the change
- **Scalability**: if you have a lot of scripts, it's hard to keep track of which ones depend on which
- **File management**: you have to keep track of which files are inputs and which are outputs and where they're saved

Based on example in https://books.ropensci.org/targets

{targets} workflow

R/functions.R

```r
get_data <- function(file) {
  read_csv(file, col_types = cols()) %>%
    filter(!is.na(Ozone))
}

fit_model <- function(data) {
  lm(Ozone ~ Temp, data) %>%
    coefficients()
}

plot_model <- function(model, data) {
  ggplot(data) +
    geom_point(aes(x = Temp, y = Ozone)) +
    geom_abline(intercept = model[1], slope = model[2])
```

{targets} workflow

_targets.R

```r
library(targets)

tar_source()
tar_option_set(packages = c("tidyverse"))

list(
  tar_target(file, "data.csv", format = "file"),
  tar_target(data, get_data(file)),
  tar_target(model, fit_model(data)),
  tar_target(plot, plot_model(model, data))
)
```

Run `tar_make()` to run pipeline

`use_targets()` will generate a `_targets.R` script for you to fill in.

`{targets}` workflow

Targets are “hidden” away where you don’t need to manage them

```
├── _targets.R
├── data.csv
├── R/
│   ├── functions.R
├── _targets/
│   ├── objects
│          ├── data
│          ├── model
│          ├── plot
```

You can of course have multiple files in `R/`; `tar_source()` will source them all

My typical workflow with `{targets}`

1. Read in some data and do some cleaning until it's in the form I want to work with.
2. Wrap that in a function and save the file in `R/`.
3. Run `use_targets()` and edit `_targets.R` accordingly, so that I list the data file as a target and `clean_data` as the output of the cleaning function.
4. Run `tar_make()`.
5. Run `tar_load(clean_data)` so that I can work on the next step of my workflow.
6. Add the next function and corresponding target when I've solidified that step.

I usually include `library(targets)` in my project `.Rprofile` so that I can always call

_targets.R tips and tricks

```r
list(
  tar_target(
    data_file,
    "data/raw_data.csv",
    format = "file"
  ),
  tar_target(
    raw_data,
    read.csv(data_file)
  ),
  tar_target(
    clean_data,
    clean_data_function(raw_data)
  )
```

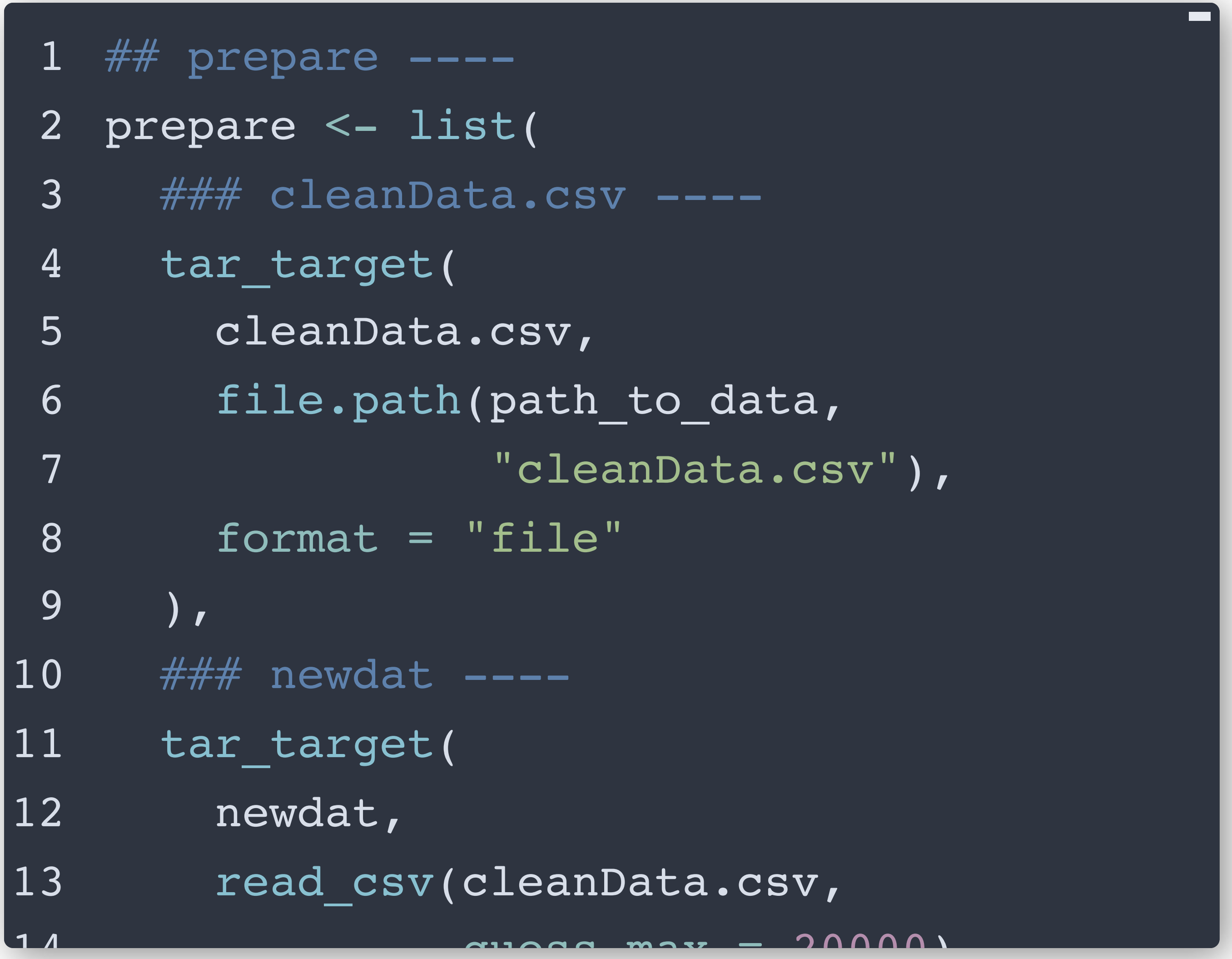
I like to pair my functions/targets by name so that the workflow is clear to me

`_targets.R` tips and tricks

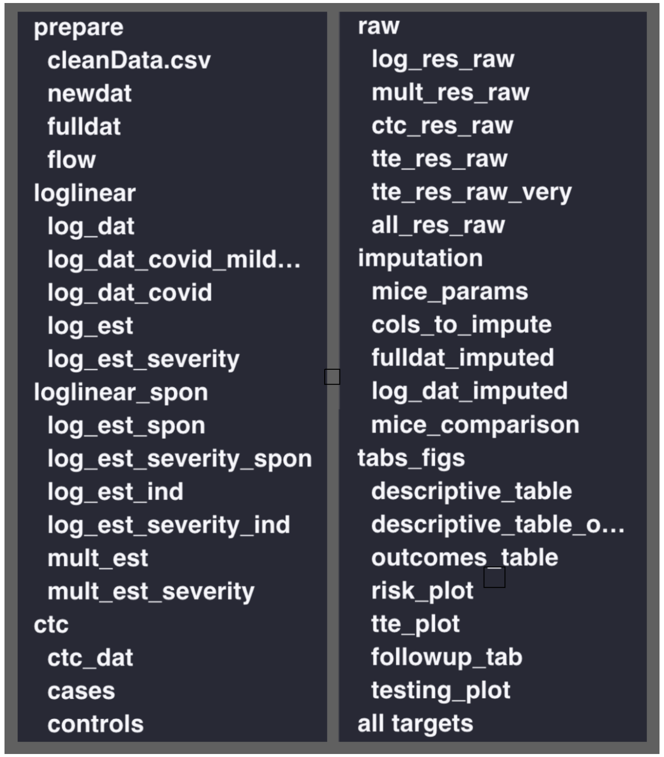
```r
preparation <- list(
  ...,
  tar_target(
    clean_data,
    clean_data_function(raw_data)
  )
)
modeling <- list(
  tar_target(
    linear_model,
    linear_model_function(clean_data)
  ),
  ...
)
```

By grouping the targets into lists, I can easily comment out chunks of the pipeline

_targets.R tips and tricks



```r
## prepare ----
prepare <- list(
  ### cleanData.csv ----
  tar_target(
    cleanData.csv,
    file.path(path_to_data,
              "cleanData.csv"),
    format = "file"
  ),
  ### newdat ----
  tar_target(
    newdat,
    read_csv(cleanData.csv,
             guess_max = 20000)
```



```
prepare
  cleanData.csv
  newdat
  fulldat
  flow
loglinear
  log_dat
  log_dat_covid_mild...
  log_dat_covid
  log_est
  log_est_severity
loglinear_spon
  log_est_spon
  log_est_severity_spon
  log_est_ind
  log_est_severity_ind
  mult_est
  mult_est_severity
ctc
  ctc_dat
  cases
  controls
raw
  log_res_raw
  mult_res_raw
  ctc_res_raw
  tte_res_raw
  tte_res_raw_very
  all_res_raw
imputation
  mice_params
  cols_to_impute
  fulldat_imputed
  log_dat_imputed
  mice_comparison
tabs_figs
  descriptive_table
  descriptive_table_o...
  outcomes_table
  risk_plot
  tte_plot
  followup_tab
  testing_plot
all targets
```

In big projects, I comment my _targets.R file so that I can use the RStudio outline

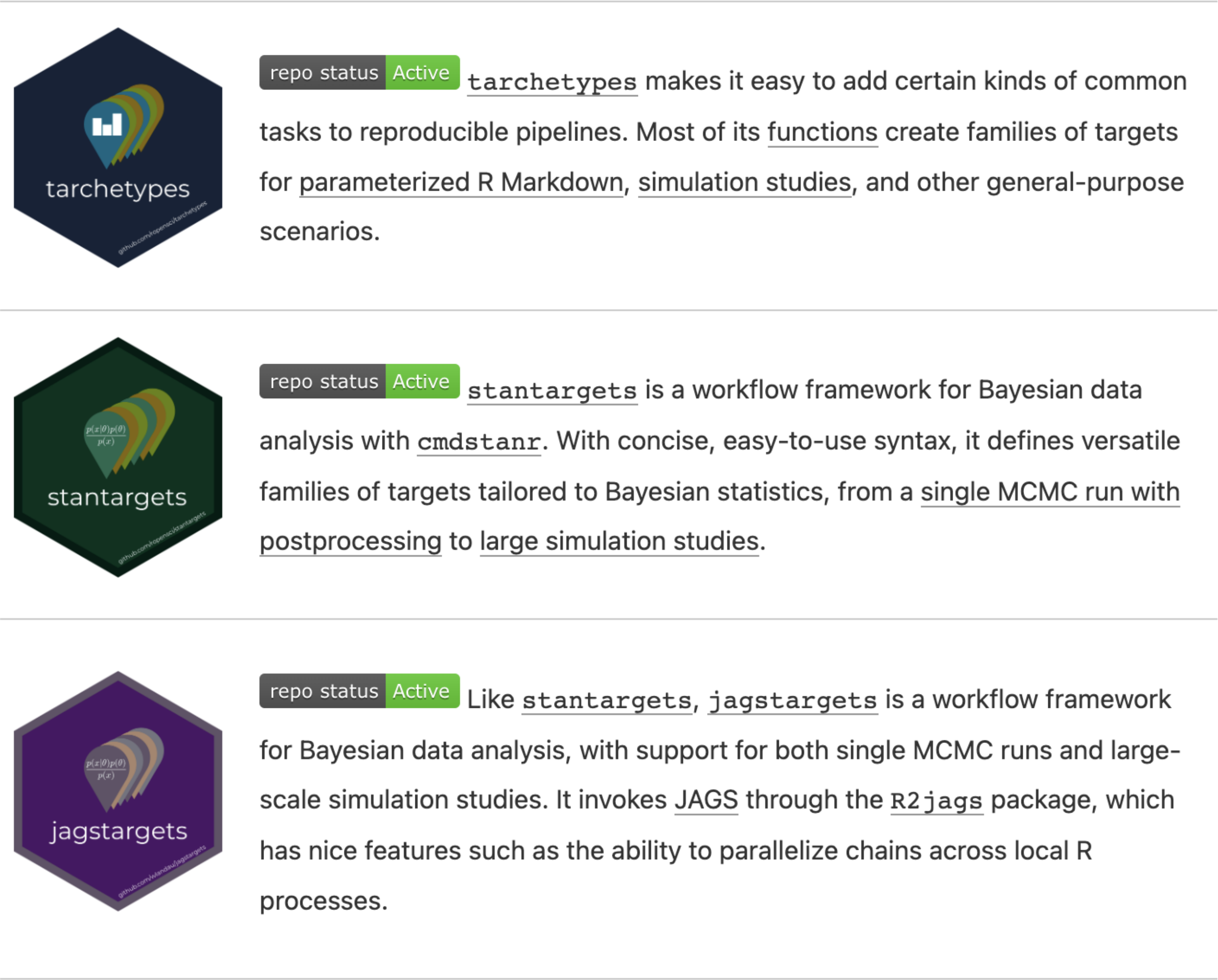
Key {targets} functions

- `use_targets()` gets you started with a `_targets.R` script to fill in
- `tar_make()` runs the pipeline and saves the results in `_targets/objects/`
- `tar_make_future()` runs the pipeline in parallel[1]
- `tar_load()` loads the results of a target into the global environment (e.g., `tar_load(clean_data)`)
- `tar_read()` reads the results of a target into the global environment (e.g., `dat <- tar_read(clean_data)`)
- `tar_visnetwork()` creates a network diagram of the pipeline
- `tar_outdated()` checks which targets need to be updated
- `tar_prune()` deletes targets that are no longer in `_targets.R`
- `tar_destroy()` deletes the `.targets/` directory if you need to burn everything down and start again

[1] Note: `{targets}` is moving to a new distributed computing strategy using `{crew}`

Advanced `{targets}`

“target factories”



repo status Active `tarchetypes` makes it easy to add certain kinds of common tasks to reproducible pipelines. Most of its functions create families of targets for parameterized R Markdown, simulation studies, and other general-purpose scenarios.

repo status Active `stantargets` is a workflow framework for Bayesian data analysis with `cmdstanr`. With concise, easy-to-use syntax, it defines versatile families of targets tailored to Bayesian statistics, from a single MCMC run with postprocessing to large simulation studies.

repo status Active Like `stantargets`, `jagstargets` is a workflow framework for Bayesian data analysis, with support for both single MCMC runs and large-scale simulation studies. It invokes JAGS through the `R2jags` package, which has nice features such as the ability to parallelize chains across local R processes.

`{tarchetypes}`: reports

Render documents that depend on targets loaded with `tar_load()` or `tar_read()`.

- `tar_render()` renders an R Markdown document
- `tar_quarto()` renders a Quarto document (or project)

It can’t detect dependencies like `tar_load(ends_with("plot"))`

What does `report.qmd` look like?

~~~
---
title: "My report"
---
```{r}
library(targets)
tar_load(results)
tar_load(plots)
~~~
There were `r results$n` observations with a mean age of `r result
```{r}
library(ggplot2)
plots$age_plot
```
```

Because `report.qmd` depends on `results` and `plots`, it will only be re-rendered if either of those targets change.
```

# {tarchetypes}: branching

Using data from the National Longitudinal Survey of Youth,

_targets.R

```r
library(targets)
library(tarchetypes)
tar_source()

targets_setup <- list(
  tar_target(
    csv,
    "data/nlsy.csv",
    format = "file"
  ),
  tar_target(
    dat,
    readr::read_csv(csv,
      show_col_types = FALSE)
  )
)
```

R/functions.R

```r
model_function <- function(outcome_var,
                           sex_val, dat) {

  lm(as.formula(paste(outcome_var,
      " ~ age_bir + income + factor(region)")) ,
     data = dat,
     subset = sex == sex_val)
}

coef_function <- function(model) {
  coef(model)[["age_bir"]]
}
```

we want to investigate the relationship between age at first birth and hours of sleep on weekdays and weekends among moms and dads separately

Option 1

Create (and name) a separate target for each combination of sleep variable ("sleep_wkdy", "sleep_wknd") and sex (male: 1, female: 2):

```r
targets_1 <- list(
  tar_target(
    model_1,
    model_function(outcome_var = "sleep_wkdy", sex_val = 1, dat =
  ),
  tar_target(
    coef_1,
    coef_function(model_1)
  )
)
```

… and so on…

Option 2

Use `tarchetypes::tar_map()` to map over the combinations for you (static branching):

```r
targets_2 <- tar_map(
  values = tidyr::crossing(
    outcome = c("sleep_wkdy", "sleep_wknd"),
    sex = 1:2
  ),
  tar_target(
    model_2,
    model_function(outcome_var = outcome, sex_val = sex, dat = dat
  ),
  tar_target(
    coef_2,
    coef_function(model_2)
  )
)
```

Option 2, cont.

Use `tarchetypes::tar_combine()` to combine the results of a call to `tar_map()`:

```r
combined <- tar_combine(
  combined_coefs_2,
  targets_2[["coef_2"]],
  command = vctrs::vec_c(!!!.x),
)
tar_read(combined_coefs_2)
```

`command = vctrs::vec_c(!!!.x)` is the default, but you can supply your own function to combine the results

Option 3

Use the `pattern =` argument of `tar_target()` (dynamic branching):

```r
targets_3 <- list(
  tar_target(
    outcome_target,
    c("sleep_wkdy", "sleep_wknd")
  ),
  tar_target(
    sex_target,
    1:2
  ),
  tar_target(
    model_3,
    model_function(outcome_var = outcome_target, sex_val = sex_tar
    pattern = cross(outcome_target, sex_target)
  )
```

Branching

Dynamic	Static
Pipeline creates new targets at runtime.	All targets defined in advance.
Cryptic target names.	Friendly target names.
Scales to hundreds of branches.	Does not scale as easily for tar_visnetwork() etc.
No metaprogramming required.	Familiarity with metaprogramming is helpful.

From https://books.ropensci.org/targets/dynamic.html#branching

Branching

- The book also has an example of using metaprogramming to map over different functions
  - i.e. fit multiple models with the same arguments
- Static and dynamic branching can be combined
  - e.g. `tar_map(values = ..., tar_target(..., pattern = map(...)))`
- Branching can lead to slowdowns in the pipeline (see book for suggestions)

{tarchetypes}: repetition

tar_rep() repeats a target multiple times with the same arguments

```r
targets_4 <- list(
  tar_rep(
    bootstrap_coefs,
    dat |>
      dplyr::slice_sample(prop = 1, replace = TRUE) |>
      model_function(outcome_var = "sleep_wkdy", sex_val = 1, dat
      coef_function(),
    batches = 10,
    reps = 10
  )
)
```

The pipeline gets split into batches x reps chunks, each with its own random seed

{tarchetypes}: mapping over iterations

```r
sensitivity_scenarios <- tibble::tibble(
  error = c("small", "medium", "large"),
  mean = c(1, 2, 3),
  sd = c(0.5, 0.75, 1)
)
```

`tar_map_rep()` repeats a target multiple times with different arguments

```r
targets_5 <- tar_map_rep(
  sensitivity_analysis,
  dat |>
    dplyr::mutate(sleep_wkdy = sleep_wkdy + rnorm(nrow(dat), mean,
    model_function(outcome_var = "sleep_wkdy", sex_val = 1, dat =
    coef_function() |>
    data.frame(coef = _),
  values = sensitivity_scenarios,
  batches = 10,
  reps = 10
)
```

{tarchetypes}: mapping over iterations

```r
tar_read(sensitivity_analysis) |> head()
```

Ideal for sensitivity analyses that require multiple iterations of the same pipeline with different parameters

```r
tar_read(sensitivity_analysis) |>
  dplyr::group_by(error) |>
  dplyr::summarize(q25 = quantile(coef, .25),
                   median = median(coef),
                   q75 = quantile(coef, .75))
```

Summary

- `{targets}` is a great tool for managing complex workflows
- `{tarchetypes}` makes it even more powerful
- The user manual is a great resource for learning more

Exercises

We’ll clone a repo with `{targets}` already set up and add some additional steps to the analysis.