



# Hit your reproducibility {targets}

UK Gov Data Science Festival, 2020-09-30

 [mattdray](#)  [matt-dray](#)  [rostrum.blog](#)

## Revisit materials:

- these slides
- source including demo code
- blog post
- {drake} talk and blog post

**Reproducevangelism**

		Data	
		Same	Different
Analysis	Same	Reproducible	Replicable
	Different	Robust	Generalisable

From **The Turing Way** by The Alan Turing Institute



Reproducible Analytical Pipelines

Can I recreate what you did:

- from scratch?
- on a different machine?
- in the future?
- without you present?

R has many reproducibility tools, like:

- RStudio Projects to keep everything together
- R Markdown for reproducible docs
- packages for reusable functions
- {here} for relative filepaths
- {renv} for dependency management

Today's focus:

1. Make workflows reproducible
2. Try {targets}



**1. Make workflows reproducible**

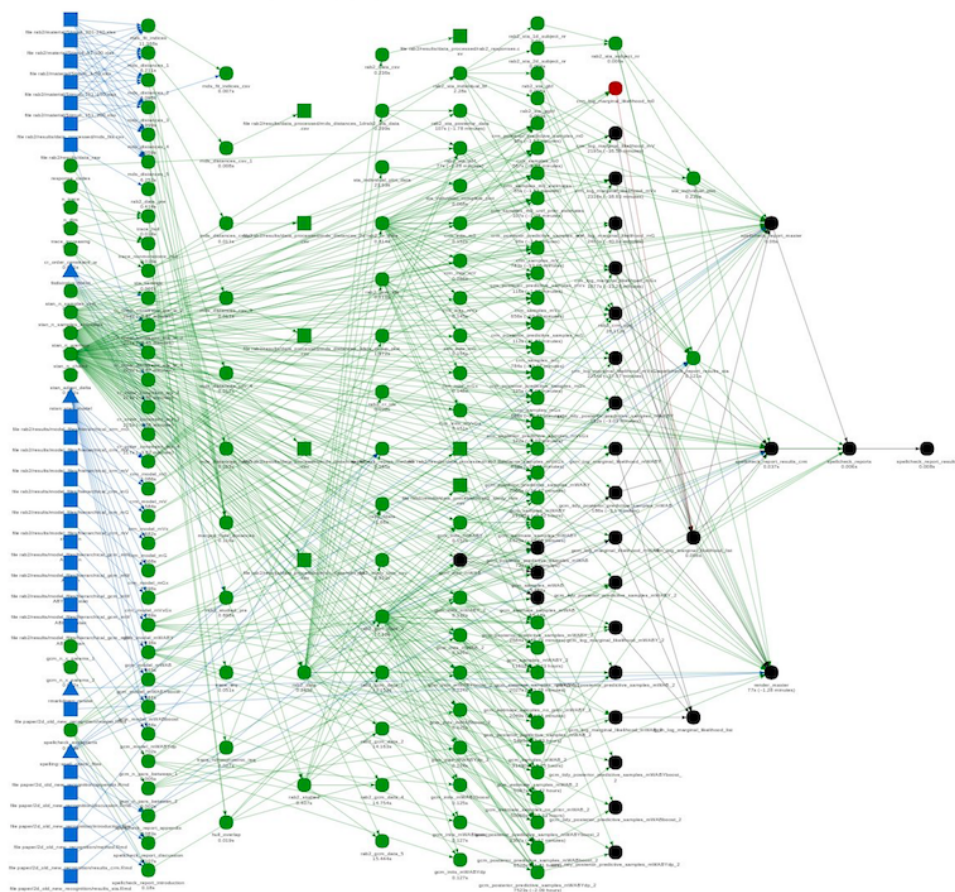
What about the relationships between functions, files and outputs?

Is your workflow reproducible?

What if:

- you haven't recorded the steps?
- the interdependencies become complex?
- some steps are computationally intensive?
- something changes?

# You can't remember this



# Let a workflow manager handle it

- [Dagobah](#) - Simple DAG-based job scheduler in Python.
- [Dagr](#) - A scala based DSL and framework for writing and executing bioinformatics pipelines as Directed Acyclic GRaphs.
- [Dagster](#) - Python-based API for defining DAGs that interfaces with popular workflow managers for building data applications.
- [DataJoint](#) - an open-source relational framework for scientific data pipelines.
- [Dask](#) - Dask is a flexible parallel computing library for analytics.
- [Dockerflow](#) - Workflow runner that uses Dataflow to run a series of tasks in Docker.
- [Doit](#) - Task management & automation tool.
- [Drake](#) - Robust DSL akin to Make, implemented in Clojure.
- [Drake R package](#) - Reproducibility and high-performance computing with an easy R-focused interface. Unrelated to Factual's Drake.
- [Dray](#) - An engine for managing the execution of container-based workflows.
- [eHive](#) - System for creating and running pipelines on a distributed compute resource.
- [Fission Workflows](#) - A fast, lightweight workflow engine for serverless/FaaS functions.
- [Flex](#) - Language agnostic framework for building flexible data science pipelines (Python/Shell/Gnuplot).
- [Flower](#) - Robust and efficient workflows using a simple language agnostic approach (R package).



[pditommaso/awesome-pipeline](#)

## 2. Try {targets}



{targets} by Will Landau

From **the manual**, it:

- learns how your pipeline fits together
- skips costly runtime
- runs only the necessary computation
- supports parallel computing
- abstracts files as R objects
- evidence that results match the code and data



It also has excellent docs:

- the [site](#) and [source](#)
- the [{targets} R package user manual](#)
- [minimal example](#) (can be run in RStudio Cloud)
- [targetsketch](#): a Shiny app for learning {targets} and setup new projects

More resources in [the {targets} README](#).

Supersedes {drake} by Will Landau



...major user-side limitations regarding data management, collaboration, and parallel efficiency

At its simplest:

1. Write a pipeline script
2. Execute the script
3. Change stuff
4. Go to 2



Contrived, simple demo

The goal is a {targets} pipeline that:

- creates a chart
- creates a table
- renders them in an R Markdown report

Then we'll change something and re-run it.

Generate `_targets.R` in your working directory

```
tar_script()
```

## Set up functions and options in `_targets.R`

```
tar_option_set(  
  packages = c(  
    "targets", "tarchetypes", "knitr",  
    "dplyr", "ggplot2", "rphylopic",  
  )  
)
```

```
b_plot <- function(data, image) {  
  ggplot(data, aes(id, temp)) +  
    geom_boxplot() +  
    labs(title = "Weasel temperatures") +  
    add_phylopic(image)  
}
```

## Set up pipeline in `_targets.R`

```
targets <- list(  
  tar_target(b1, mutate(beaver1, id = "A")),  
  tar_target(b2, mutate(beaver2, id = "B")),  
  tar_target(beavers, bind_rows(b1, b2)),  
  tar_target(uid, "be8670c2-a5bd-4b44-88e8-92f8b0c7f4"),  
  tar_target(png, image_data(uid, size = "512")[[1]]),  
  tar_target(plot, b_plot(beavers, png)),  
  tar_target(table, b_table(beavers)),  
  tarchetypes::tar_render(report, "report-beavers.Rmd")  
)  
  
tar_pipeline(targets)
```

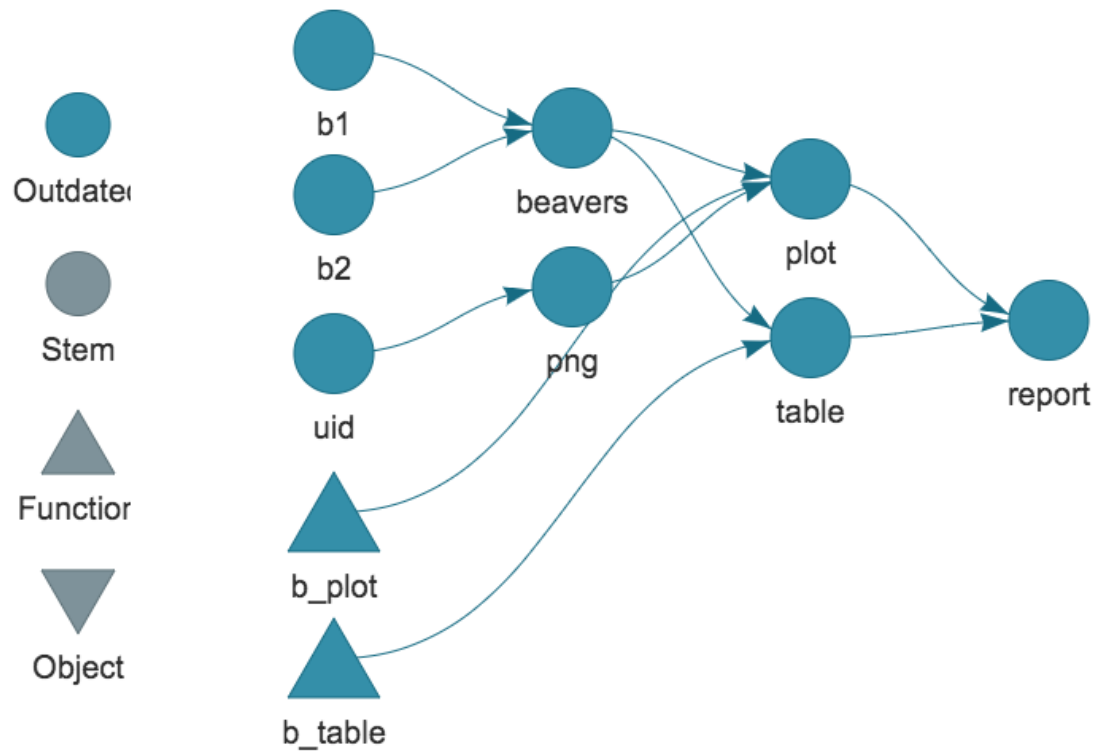


# View your targets

```
tar_manifest(fields = "command")
```

	name	command
	<chr>	<chr>
1	uid	"\"be8670c2-a5bd-4b44-88e8-92f8b0c7f4c6\""
2	report	"tarchetypes::tar_render_run(path = \"beave
3	beavers	"bind_rows(b1, b2)"
4	table	"b_table(beavers)"
5	plot	"b_plot(beavers, png)"
6	b1	"mutate(beaver1, id = \"A\")"
7	b2	"mutate(beaver2, id = \"B\")"
8	png	"image_data(uid, size = \"512\")[[1]]"

```
tar_visnetwork()
```



# Execute the pipeline

```
tar_make()
```

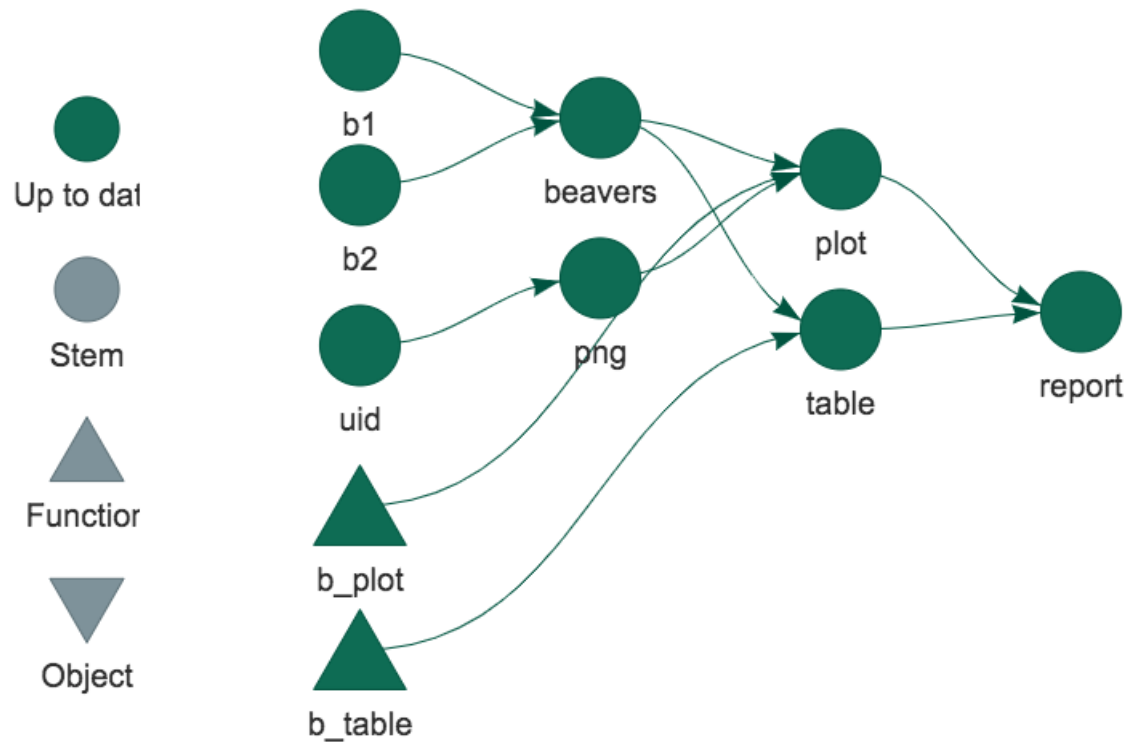
- run target uid
- run target b1
- run target b2
- run target png
- run target beavers
- run target plot
- run target table
- run target report

This created a `_targets/` cache

This is like a 'memory' for {targets}

`tar_load()` and `tar_read()` to fetch objects

```
tar_visnetwork()
```



# The rendered R Markdown

## R's built-in beavers dataset

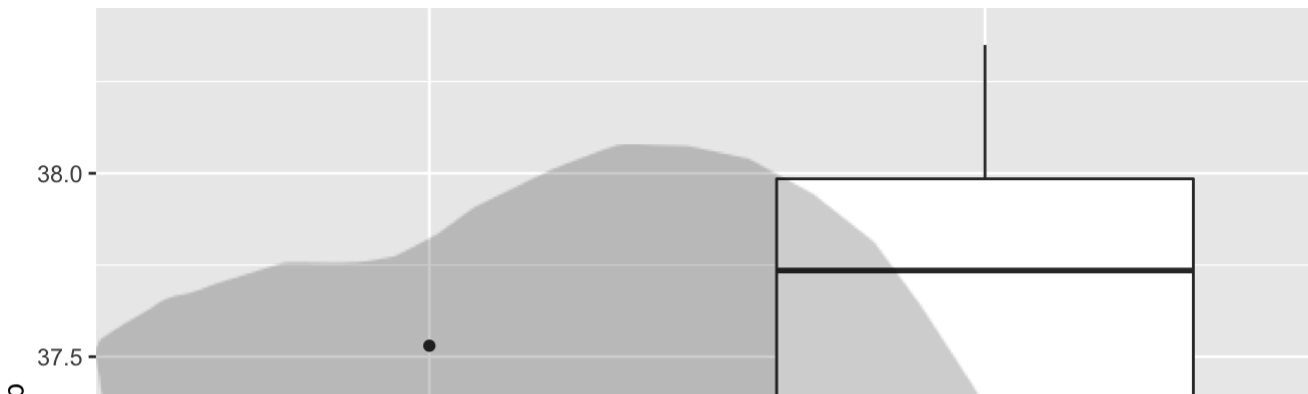
Matt Dray

26 September 2020

## Results

What does the distribution of body temperatures look like?

Weasel temperatures



Whoops...

- labs(title = "Weasel temperatures")

+ labs(title = "Beaver temperatures")

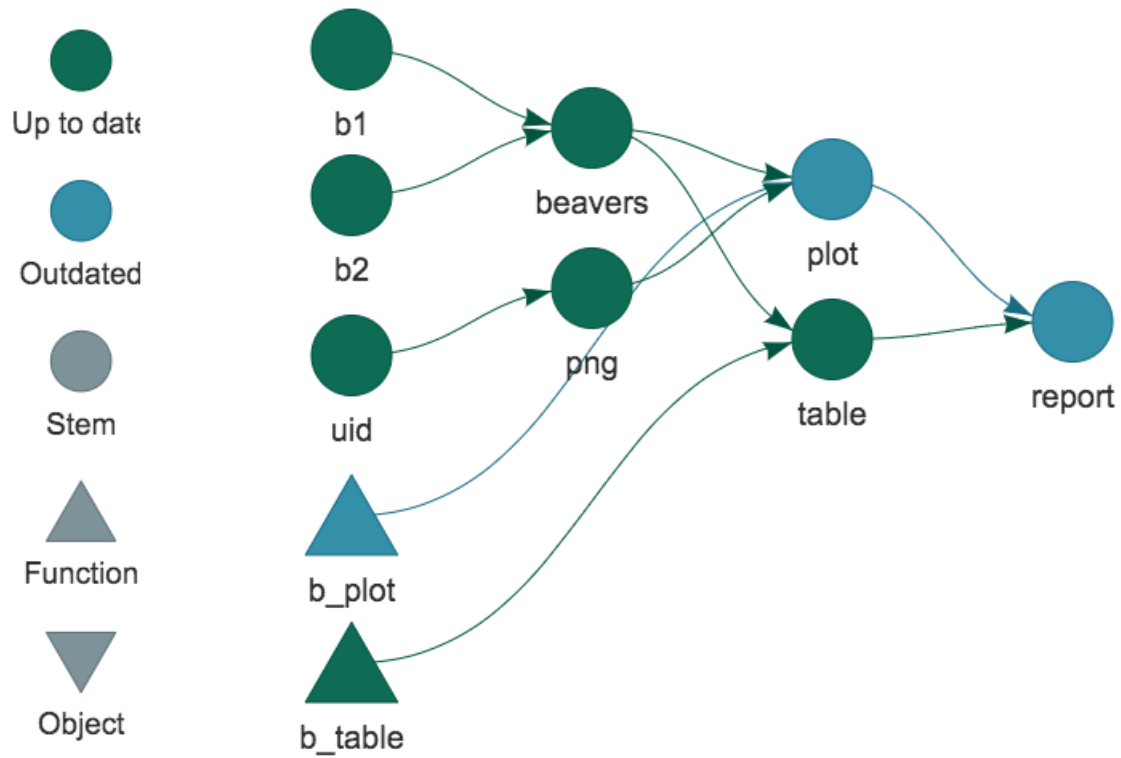
Check what has become outdated as a result

```
tar_outdated()
```

```
[1] "report" "plot"
```



```
tar_visnetwork()
```

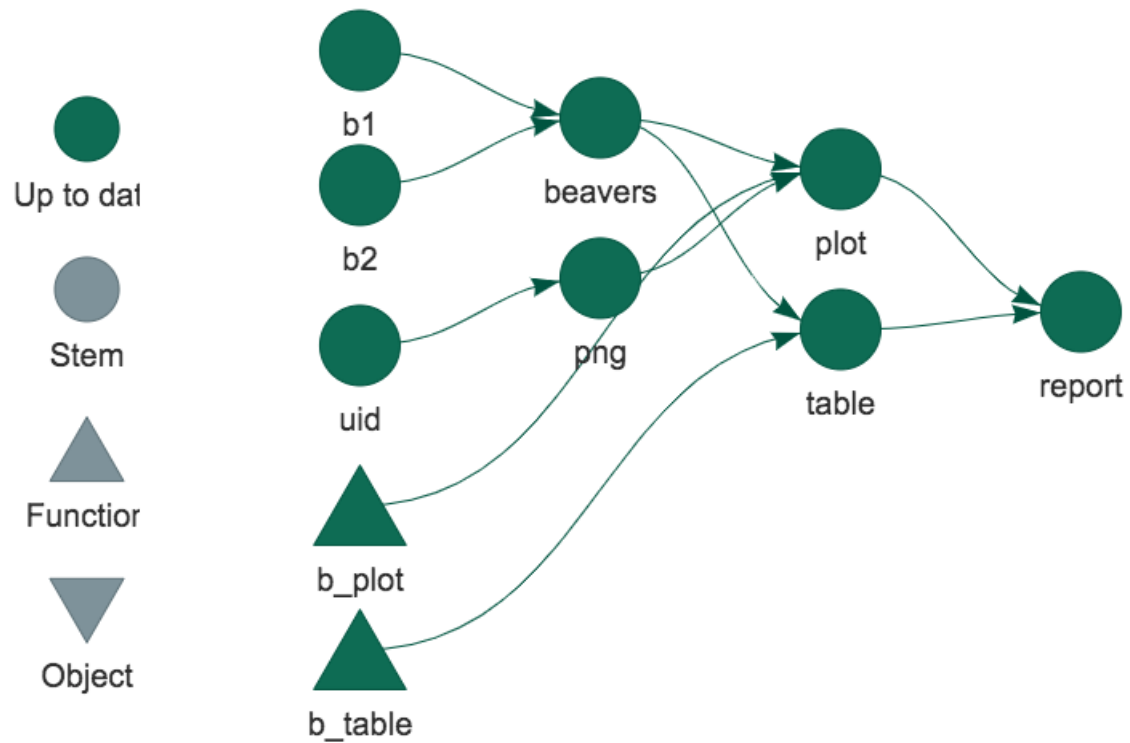


# Only outdated targets are re-run

```
tar_make()
```

- ✓ skip target uid
- ✓ skip target b1
- ✓ skip target b2
- ✓ skip target png
- ✓ skip target beavers
- run target plot
- ✓ skip target table
- run target report

```
tar_visnetwork()
```



# The final product

## R's built-in beavers dataset

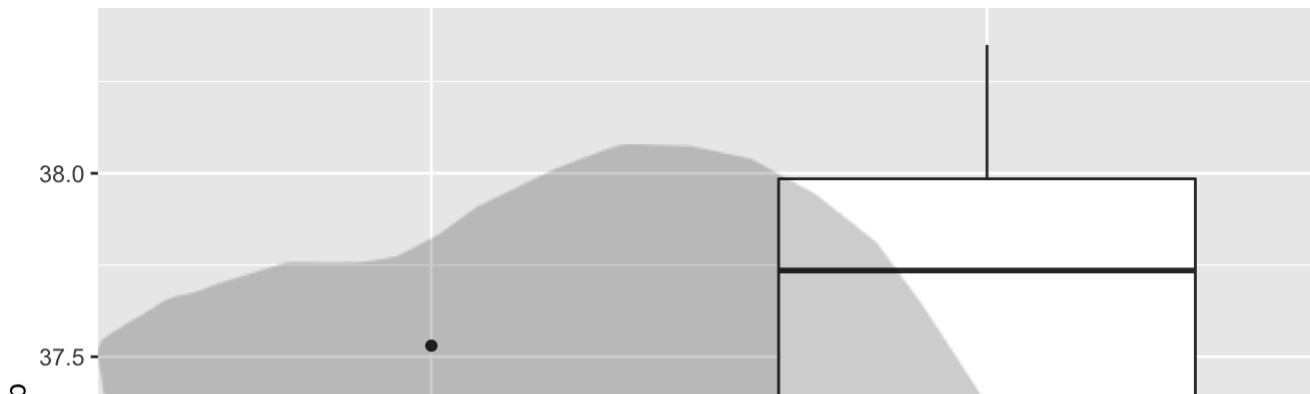
Matt Dray

26 September 2020

## Results

What does the distribution of body temperatures look like?

Beavers temperatures



To recap:

1. `tar_script()` creates `_targets.R`
2. Add `tar_targets()`
3. Check `tar_manifest()`
4. `tar_visnetwork()` to visualise
5. Execute with `tar_make()`
6. Change stuff, check `tar_outdated()`
7. Go to 4

And again, at its simplest:

1. Write a pipeline script
2. Execute the script
3. Change stuff
4. Go to 2



# Hit your reproducibility {targets}

1. Make *workflows* reproducible
2. Try {targets}



mattdray



matt-dray



rostrum.blog

## Image sources:

- RAP hex logo
- {targets} hex logo
- {drake} hex logo
- {drake} hairball by Frederik Aust
- *Castor canadensis* from PhyloPic