

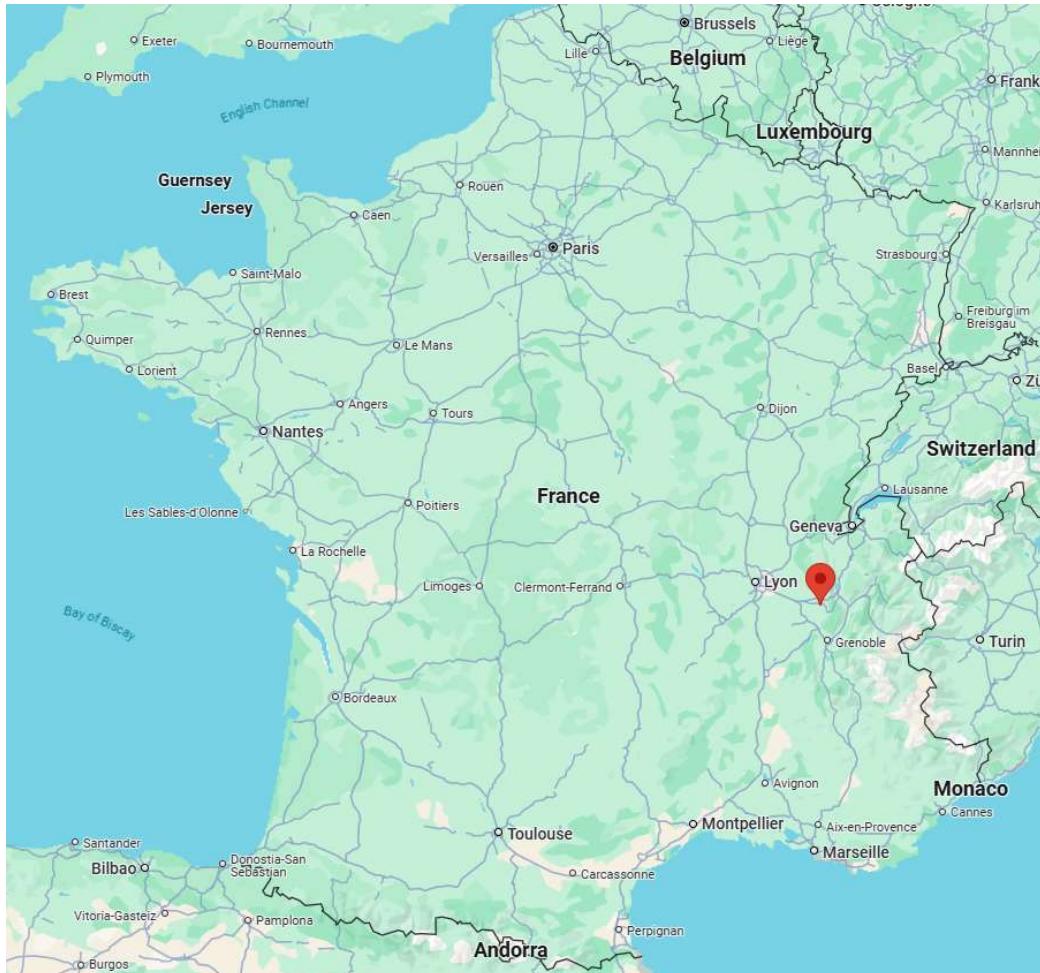
# Reproducible analysis pipelines with {targets}

Olivia Angelin-Bonnet

The New Zealand Institute for Plant and Food Research Ltd

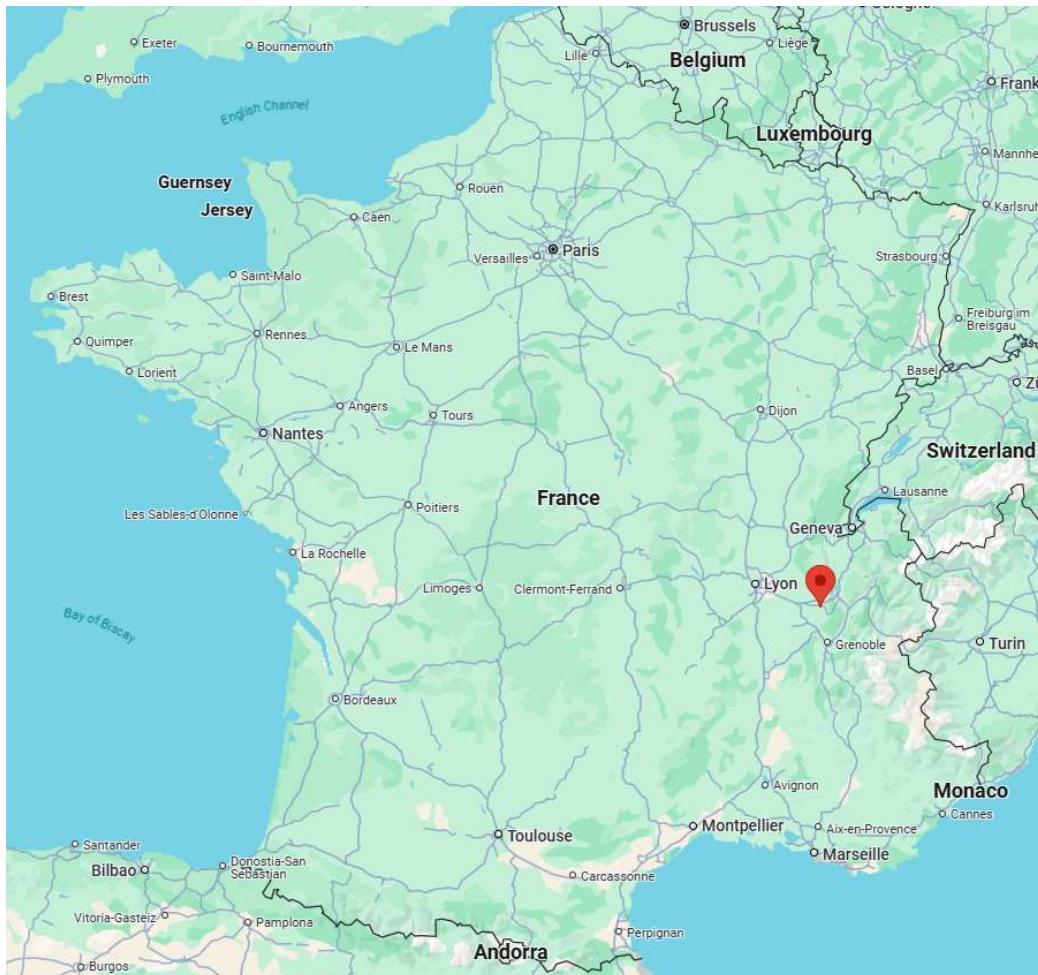
7 April 2025

# Hi! I'm Olivia :)



Location of Le Pont-de-Beauvoisin on a map of France

# Hi! I'm Olivia :)



Location of Le Pont-de-Beauvoisin on a map of France



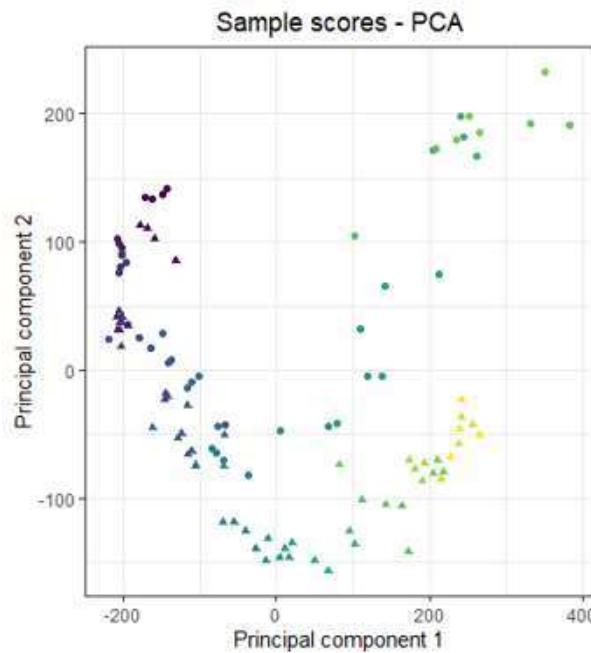
Location of Palmerston North on a map of New Zealand

# Hi! I'm Olivia :)

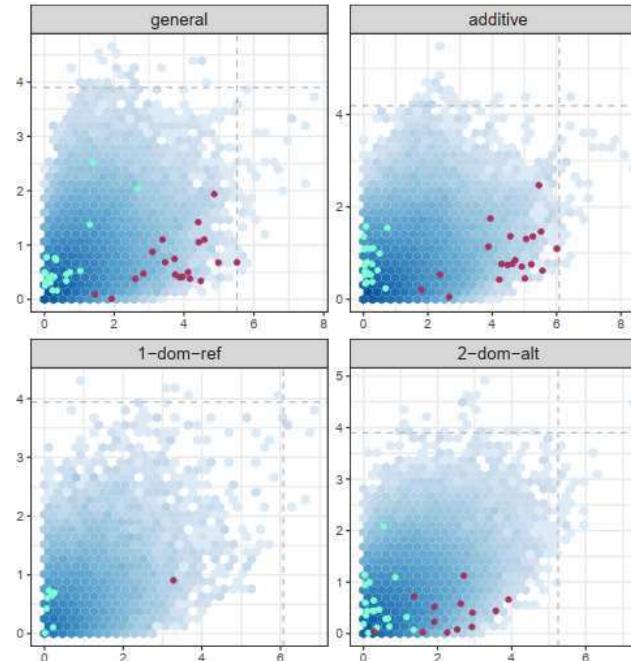


Statistical scientist at Plant & Food Research, working on omics analyses and multi-omics integration

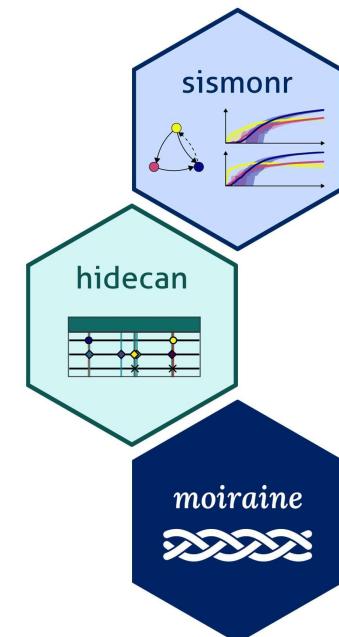
## Multivariate analyses



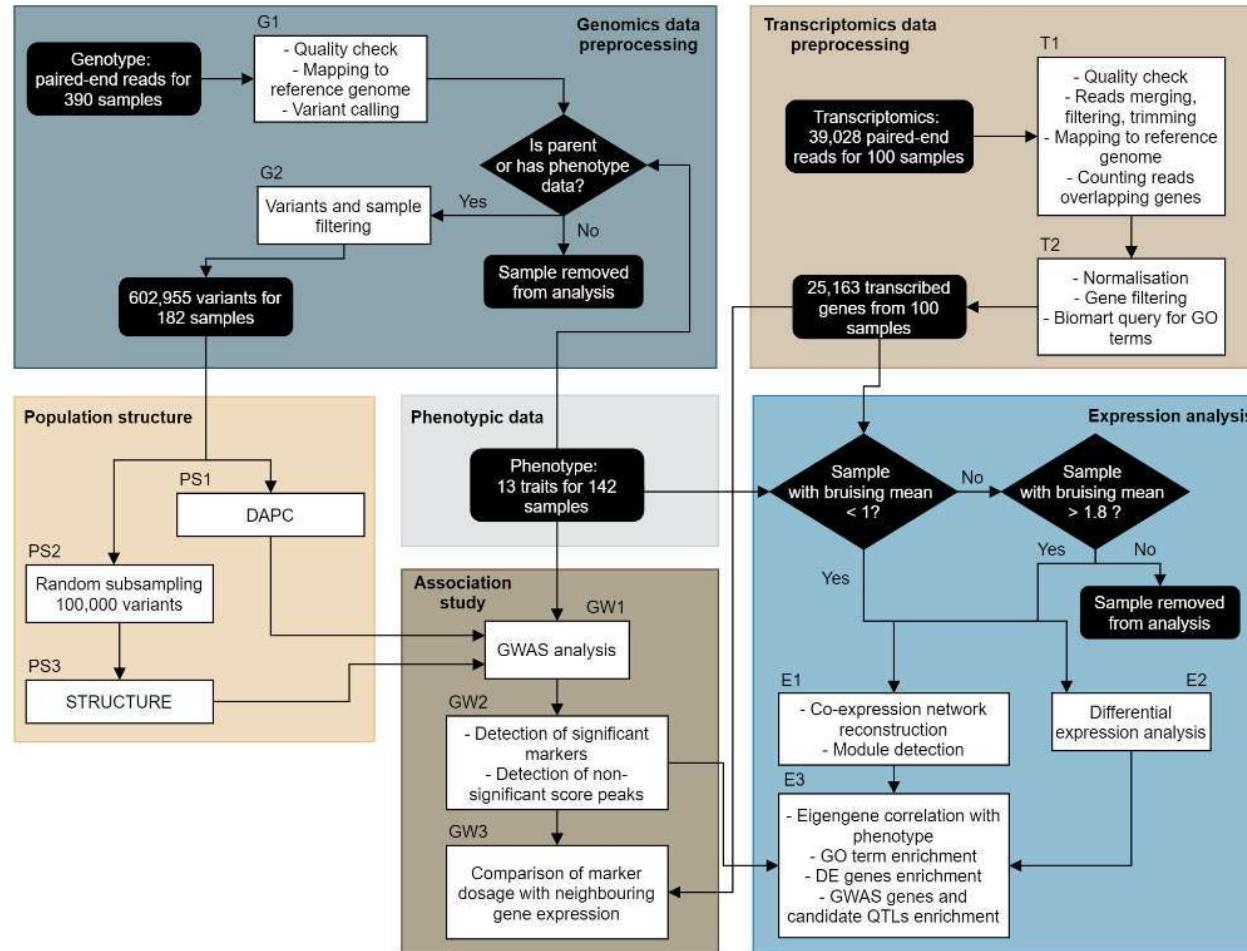
## Visualisations



## R packages



# Developing complex analyses in R



Schema of the analysis for one of my thesis chapters

# Developing complex analyses in R



## Project folder:

```
thesis/chapter4_code
├── genomics_data_analysis
│   ├── 00_genomics_wrangling.Rmd
│   ├── 01_genomics_filtering.Rmd
│   └── 02_genomics_eda.Rmd
└── transcriptomics_data_analysis
    ├── 00_transcriptomics_wrangling.Rmd
    ├── 01_transcriptomics_normalisation.Rmd
    ├── 02_transcriptomics_diff_expr.Rmd
    └── 03_transcriptomics_wgcna.Rmd
...
```

# Developing complex analyses in R



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- Input data has changed; what do I need to re-run?

# Developing complex analyses in R



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- Input data has changed; what do I need to re-run?
- In which order do I need to run these scripts?

# Developing complex analyses in R



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...
```

- Input data has changed; what do I need to re-run?
- In which order do I need to run these scripts?
- I want to change one line of text in my report, how long will it take to re-generate the output?

# Developing complex analyses in R



## Solution

Turn your scripts into pipelines with {targets}!

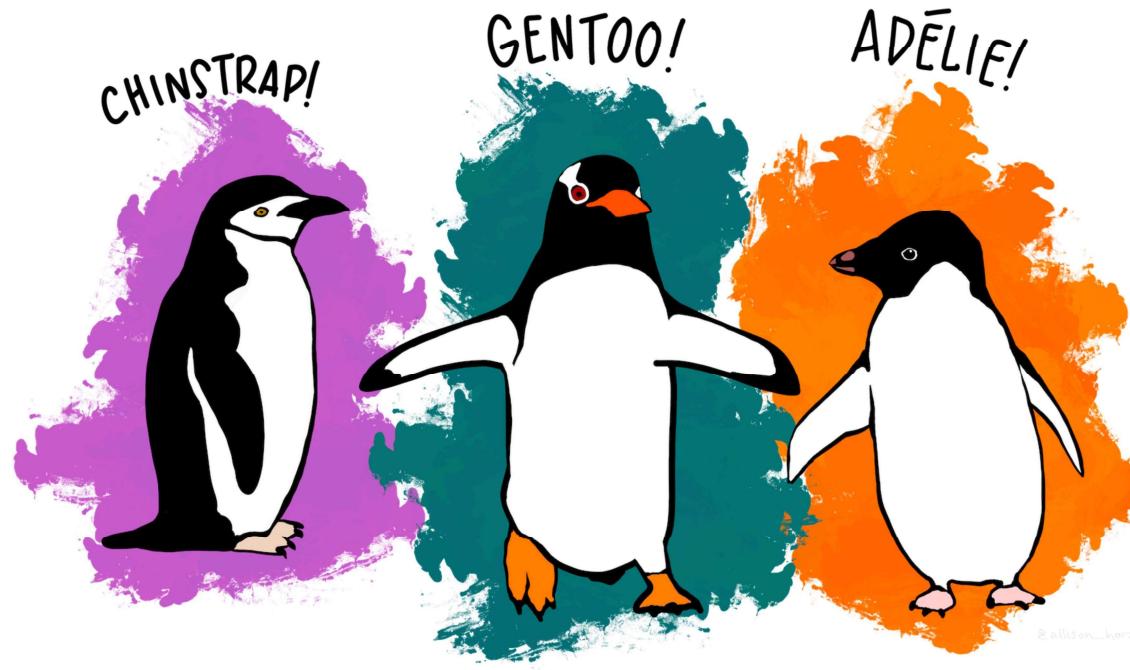


- automatic detection of steps dependencies
- 1-command execution
- automatic caching
- automatic detection of changes in data and/or code

# Learning about {targets}



Let's walk through an example!



Artwork by @allison\_horst

`palmerpenguins` dataset: size measurements for three penguin species observed in the Palmer Archipelago (Antarctica)

# Learning about {targets}



The {targets} R  
package user manual



## 1 Introduction

- How to use {targets} ▼
- 2 A walkthrough to get started
- 3 Help
- 4 Debugging pipelines
- Concepts and best practices ➤
- Data and files ➤
- Heavy workloads ➤
- Branching ➤
- Appendices ➤

# The {targets} R package user manual

AUTHOR

Will Landau

## 1 Introduction

Pipeline tools coordinate the pieces of computationally demanding analysis projects. The [targets](#) package is a [Make](#)-like pipeline tool for statistics and data science in R. The package skips costly runtime for tasks that are already up to date, orchestrates the necessary computation with implicit parallel computing, and abstracts files as R objects. If all the current output matches the current upstream code and data, then the whole pipeline is up to date, and the results are more trustworthy than otherwise.

### 1.1 Motivation

Data analysis can be slow. A round of scientific computation can take several minutes, hours, or even days to complete. After it finishes, if you update your code or data, your hard-earned

<https://books.ropensci.org/targets/>

# Aside – more about setting up R projects



- previous talk: “Setting up a reproducible data analysis project in R-featuring GitHub, `{renv}`, `{targets}` and more”
- see the [slides](#), [recording](#), or [blog post](#) 😊

<b>Project setup</b>	<ul style="list-style-type: none"><li>• Creating a GitHub repository</li><li>• Turning it into an R project</li><li>• Initialising <code>{renv}</code> for the project</li><li>• Setting up the directory structure</li><li>• Populating the README</li></ul>
<b>Tidying code</b>	<ul style="list-style-type: none"><li>• Modularise code into functions</li><li>• Turning code into a <code>{targets}</code> pipeline</li></ul>
<b>Bonus</b>	<ul style="list-style-type: none"><li>• Set up testing of input data with <code>{assertr}</code></li><li>• Automate report rendering with Quarto + <code>{targets}</code></li></ul>



# Let's code!

# I have written some code...



```
library(tidyverse)
library(janitor)
library(ggbeeswarm)
library(here)

# Reading and cleaning data
penguins_df <- read_csv(here("data/penguins_raw.csv"), show_col_types = FALSE) |>
  clean_names() |>
  mutate(
    species = word(species, 1),
    year = year(date_egg),
    sex = str_to_lower(sex),
    year = as.integer(year),
    body_mass_g = as.integer(body_mass_g),
    across(where(is.character), as.factor)
  ) |>
  select(
    species,
    island,
    year,
    sex,
    body_mass_g,
    bill_length_mm = culmen_length_mm,
```

# I have written some code...



Good start, but often:

# I have written some code...



Good start, but often:

- many more steps in the analysis → script becomes long and convoluted

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Good start, but often:

- many more steps in the analysis → script becomes long and convoluted
- harder to get an overview of the analysis, and to find things
- don't want to re-run all the code everytime I make a change

Let's turn it into a {targets} pipeline!

# Step 1: Turn your code into functions

From:

```
# Reading and cleaning data
penguins_df <- read_csv(
  here("data/penguins_raw.csv"),
  show_col_types = FALSE
) |>
  clean_names() |>
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    species = word(species, 1),
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    year = as.integer(year),
    body_mass_g = as.integer(body_mass_g),
    across(where(is.character), as.factor)
) |>
  select(
    ## all relevant columns
) |>
  drop_na()
```

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  ) |>
  drop_na()
```

To:

```
1  read_data <- function(file) {
2    readr::read_csv(
3      file,
4      show_col_types = FALSE
5    ) |>
6    janitor::clean_names() |>
7    dplyr::mutate(
8      species = stringr::word(species, 1),
9      year = lubridate::year(date_egg),
10     sex = stringr::str_to_lower(sex),
11     year = as.integer(year),
12     body_mass_g = as.integer(body_mass_g),
13     dplyr::across(
14       dplyr::where(is.character),
15       as.factor
16     )
17   ) |>
18   dplyr::select(
19     ## all relevant columns
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```

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# Step 1: Turn your code into functions

Don't forget to document your functions! (`{roxygen}`-style)

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Don't forget to document your functions! (`{roxygen}`-style)

```
#' Read and clean data
#'
#' Reads in the penguins data, renames and selects relevant columns. The
#' following transformations are applied to the data:
#' * only keep species common name
#' * extract observation year
#' * remove rows with missing values
#'
#' @param file Character, path to the penguins data .csv file.
#' @returns A tibble.
read_data <- function(file) {
  readr::read_csv(file, show_col_types = FALSE) |>
    janitor::clean_names() |>
    dplyr::mutate(
      ## modifying columns
    ) |>
    dplyr::select(
      ## all relevant columns
    ) |>
    tidyrr::drop_na()
}
```

# Step 1: Turn your code into functions

Improved script:

R/helper\_functions.R

```
#' Read and clean data
#'
#' ...
read_data <- function(file) { ... }

#' Violin plot of variable per species and sex
#'
#' ...
violin_plot <- function(df, yvar) { ... }

#' Scatter plot of bill length vs depth
#'
#' ...
plot_bill_length_depth <- function(df) { ... }
```

analysis/first\_script.R

```
library(here)

source(here("R/helper_functions.R"))

penguins_df <- read_data(
  here("data/penguins_raw.csv")
)

body_mass_plot <- violin_plot(
  penguins_df,
  body_mass_g
)

flipper_length_plot <- violin_plot(
  penguins_df,
  flipper_length_mm
)

bill_scatterplot <- plot_bill_length_depth(
  penguins_df
)
```

# Step 2: Turn your main script into a {targets} pipeline!

From:

```
library(here)

source(here("R/helper_functions.R"))

penguins_df <- read_data(here("data/penguins_raw.csv"))

body_mass_plot <- violin_plot(penguins_df, body_mass_g)

flipper_length_plot <- violin_plot(penguins_df, flipper_length_mm)

bill_scatterplot <- plot_bill_length_depth(penguins_df)
```

# Step 2: Turn your main script into a {targets} pipeline!

To:

```
1 library(targets)
2 library(here)
3
4 source(here("R/helper_functions.R"))
5
6 list(
7   tar_target(penguins_raw_file, here("data/penguins_raw.csv"), format = "file"),
8
9   tar_target(penguins_df, read_data(penguins_raw_file)),
10
11  tar_target(body_mass_plot, violin_plot(penguins_df, body_mass_g)),
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# Step 2: Turn your main script into a **{targets}** pipeline!

Aside: where should my targets script live?

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- to choose a custom folder and file name, need to specify targets configuration:

# Step 2: Turn your main script into a {targets} pipeline!

Aside: where should my targets script live?

- default would be in the `_targets.R` file in the main directory
- to choose a custom folder and file name, need to specify targets configuration:

In the console, run (from main directory):

```
targets::tar_config_set(script = "analysis/_targets.R", store = "analysis/_targets")
```

# Step 2: Turn your main script into a {targets} pipeline!

Aside: where should my targets script live?

- default would be in the `_targets.R` file in the main directory
- to choose a custom folder and file name, need to specify targets configuration:

In the console, run (from main directory):

```
targets::tar_config_set(script = "analysis/_targets.R", store = "analysis/_targets")
```

Will create a `_targets.yaml` file:

```
_target.yaml
main:
  script: analysis/_targets.R
  store: analysis/_targets
```

# Visualise your pipeline



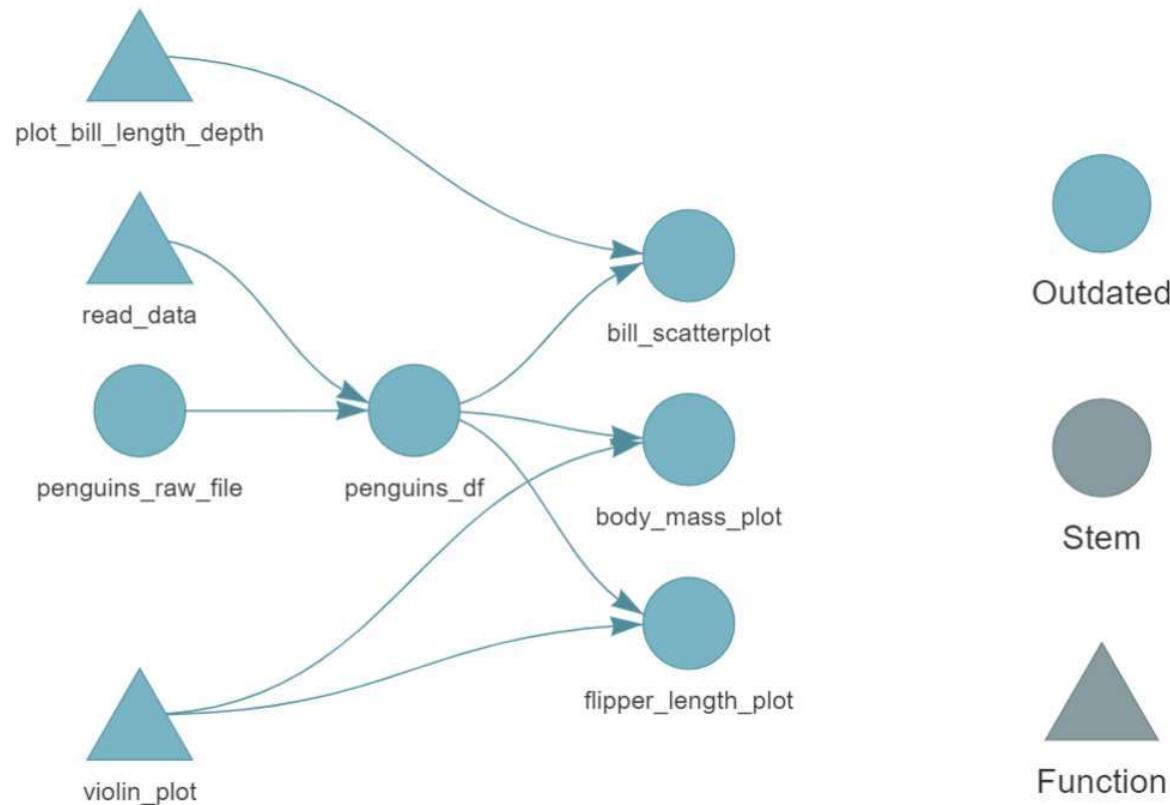
In the console, run:

```
targets::tar_visnetwork()
```

# Visualise your pipeline

In the console, run:

```
targets::tar_visnetwork()
```



# Execute your pipeline



In the console, run:

```
targets::tar_make()
```

# Execute your pipeline



In the console, run:

```
targets::tar_make()
```

```
here() starts at C:/Users/hrpoab/Desktop/GitHub/palmerpenguins_analysis
> dispatched target penguins_raw_file
o completed target penguins_raw_file [0 seconds]
> dispatched target penguins_df
o completed target penguins_df [0.85 seconds]
> dispatched target body_mass_plot
o completed target body_mass_plot [0.16 seconds]
> dispatched target bill_scatterplot
o completed target bill_scatterplot [0.02 seconds]
> dispatched target flipper_length_plot
o completed target flipper_length_plot [0.02 seconds]
> ended pipeline [1.31 seconds]
```



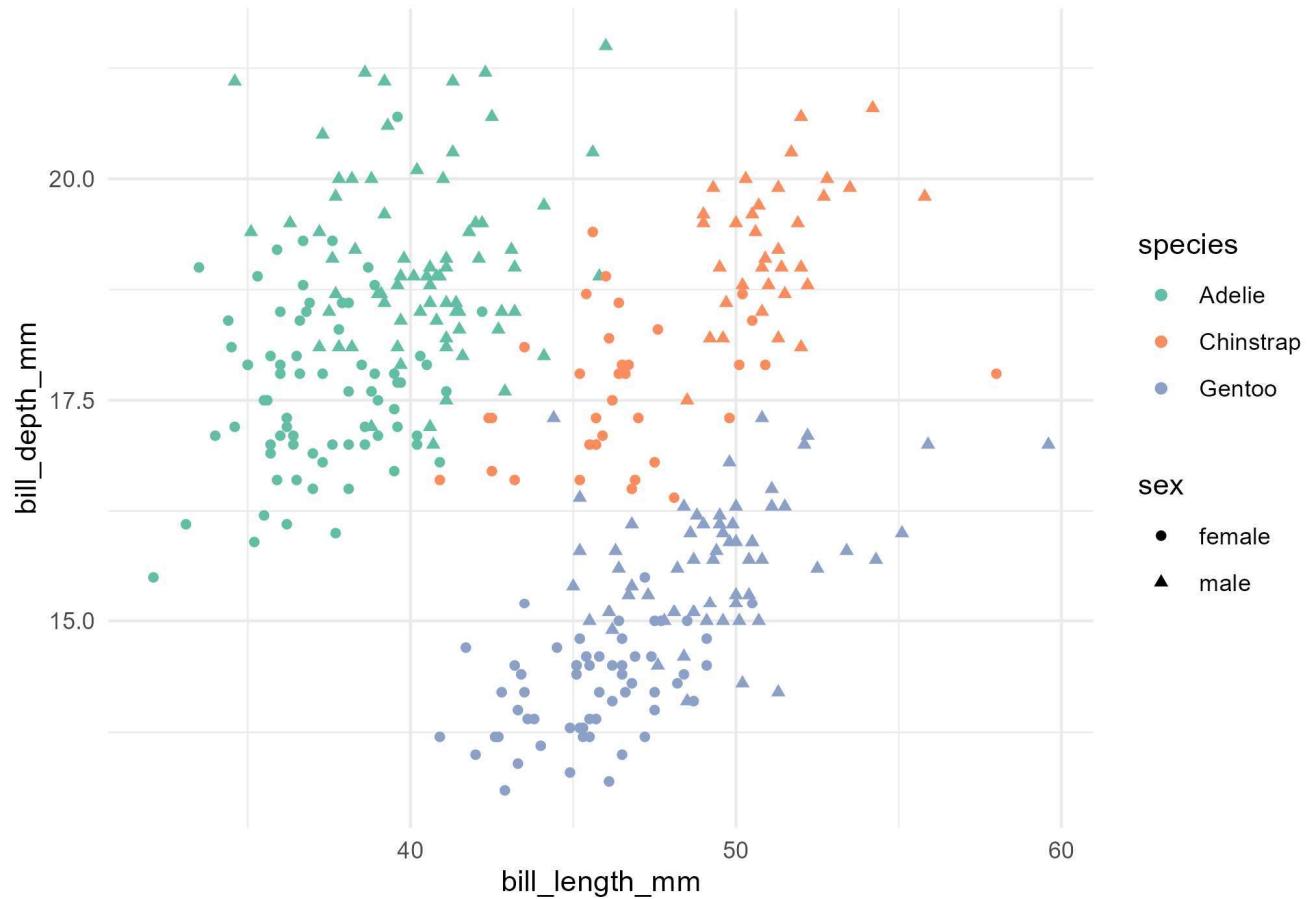
# Get the pipeline results

```
targets::tar_read(bill_scatterplot)
```

# Get the pipeline results



```
targets::tar_read(bill_scatterplot)
```



# Change in a step



*Hi Olivia,*

*Great work! Just a minor comment, could you change the colours in the bill length/depth scatter-plot? It's hard to see the difference between the species.*

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*Hi Olivia,*

*Great work! Just a minor comment, could you change the colours in the bill length/depth scatter-plot? It's hard to see the difference between the species.*

R/helper\_functions.R

```
plot_bill_length_depth <- function(df) {  
  df |>  
    ggplot2::ggplot(  
      ggplot2::aes(  
        x = bill_length_mm,  
        y = bill_depth_mm,  
        colour = species,  
        shape = sex  
      )  
    ) +  
    ggplot2::geom_point() +  
    ggplot2::scale_colour_brewer(palette = "Set2") +  
    ggplot2::theme_minimal()  
}
```

# Change in a step



*Hi Olivia,*

*Great work! Just a minor comment, could you change the colours in the bill length/depth scatter-plot? It's hard to see the difference between the species.*

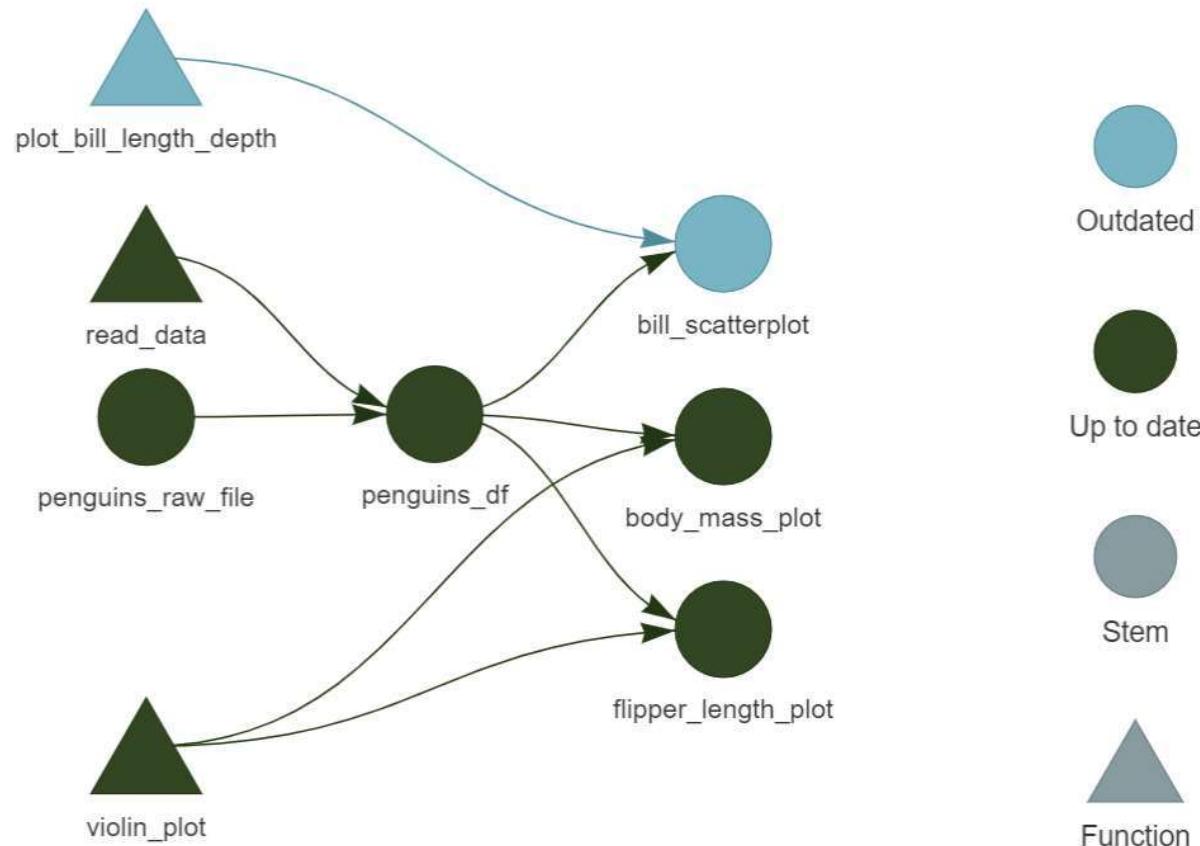
R/helper\_functions.R

```
plot_bill_length_depth <- function(df) {  
  df |>  
    ggplot2::ggplot(  
      ggplot2::aes(  
        x = bill_length_mm,  
        y = bill_depth_mm,  
        colour = species,  
        shape = sex  
      )  
    ) +  
    ggplot2::geom_point() +  
    ggplot2::scale_colour_brewer(palette = "Set1") +  
    ggplot2::theme_minimal()  
}
```

# Change in a step



```
targets::tar_visnetwork()
```



# Change in a step



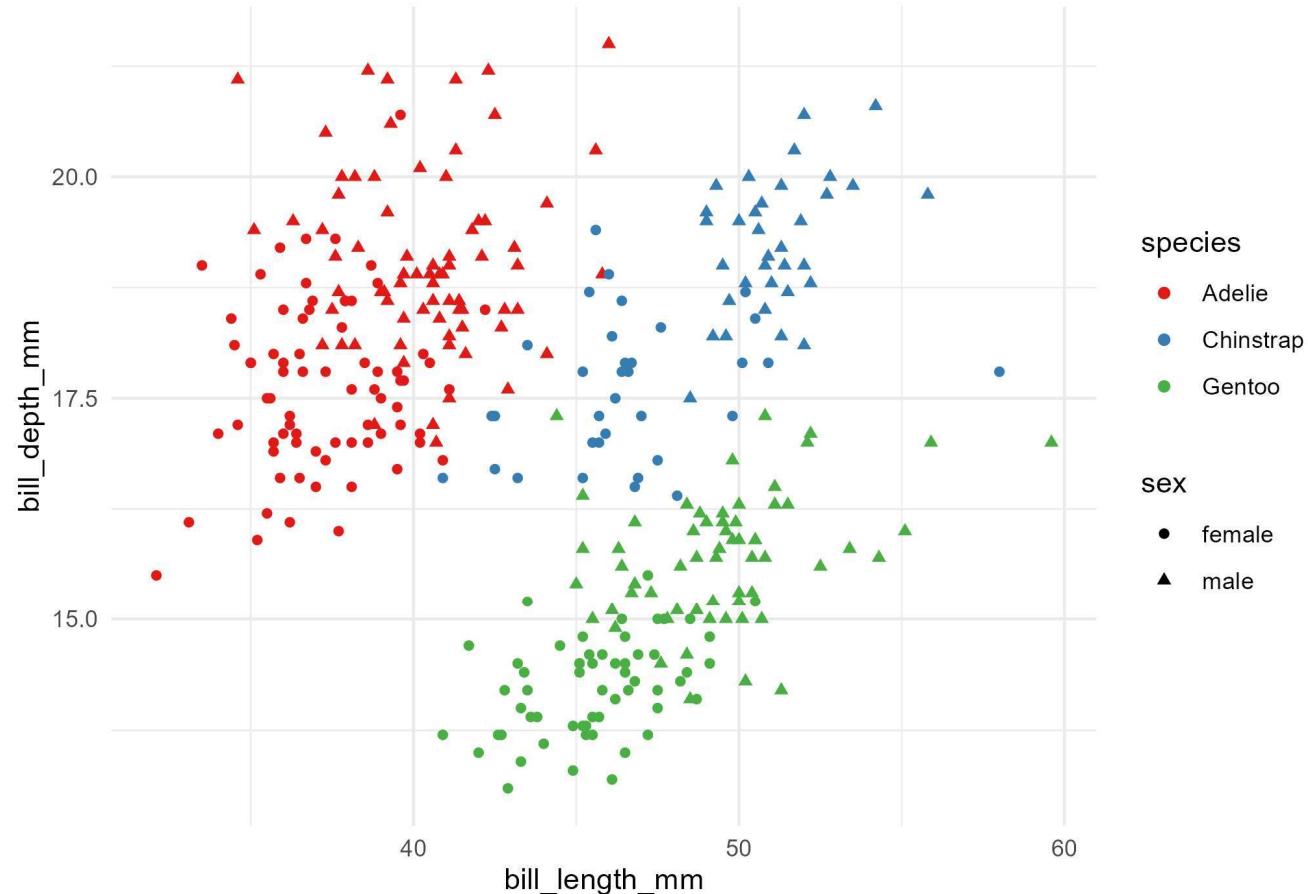
```
targets::tar_make()
```

```
here() starts at C:/Users/hrpoab/Desktop/GitHub/palmerpenguins_analysis
v skipped target penguins_raw_file
v skipped target penguins_df
v skipped target body_mass_plot
> dispatched target bill_scatterplot
o completed target bill_scatterplot [0.35 seconds]
v skipped target flipper_length_plot
> ended pipeline [0.53 seconds]
```

# Change in a step



```
targets::tar_read(bill_scatterplot)
```



# Change in the data



*Hi Olivia,*

*Oopsie! We realised there was a mistake in the original data file. Here is the updated spreadsheet, could you re-run the analysis with this version?*

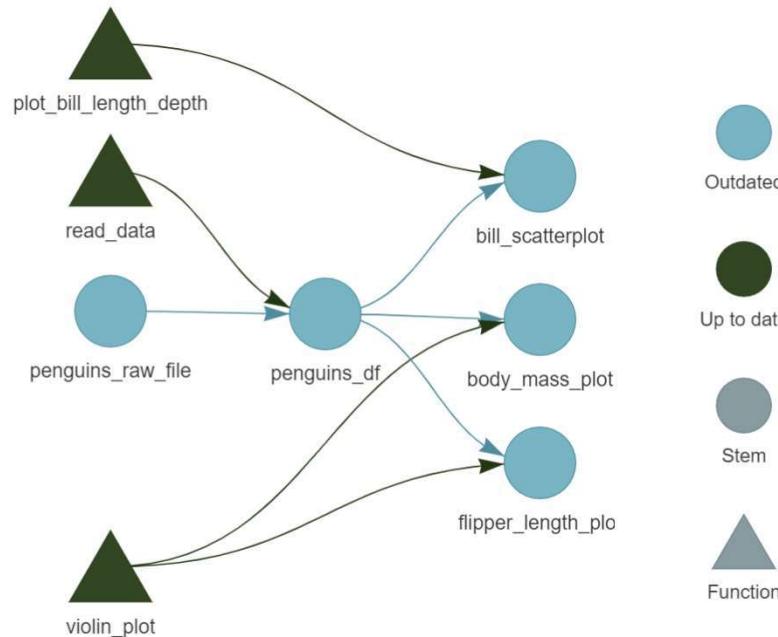
# Change in the data



Hi Olivia,

Oopsie! We realised there was a mistake in the original data file. Here is the updated spreadsheet, could you re-run the analysis with this version?

```
targets::tar_visnetwork()
```



Outdated  
Up to date  
Stem

# Writing a report with Quarto



```
reports/palmerpenguins_report.qmd
```

```
---
```

```
title: |
  Analysis of penguins measurements from the
  palmerpenguins dataset
```

```
author: "Olivia Angelin-Bonnet"
```

```
date: today
```

```
format:
```

```
  docx:
    number-sections: true
```

```
---
```

```
```{r setup}
#| include: false

library(knitr)
opts_chunk$set(echo = FALSE)
```
```

This project aims at understanding the differences between the size of three species of penguins (Adelie, Chinstrap and Gentoo) observed in the Palmer Archipelago, Antarctica, using data collected by Dr Kristen Gorman between 2007 and 2009.

## Analysis of penguins measurements from the palmerpenguins dataset

Olivia Angelin-Bonnet

2024-08-07

This project aims at understanding the differences between the size of three species of penguins (Adelie, Chinstrap and Gentoo) observed in the Palmer Archipelago, Antarctica, using data collected by Dr Kristen Gorman between 2007 and 2009.

### 1 Distribution of body mass and flipper length

Figure 1 shows the distribution of body mass (in grams) across the three penguins species. We can see that on average, the Gentoo penguins are the heaviest, with Adelie and Chinstrap penguins more similar in terms of body mass. Within a species, the females are on average lighter than the males.

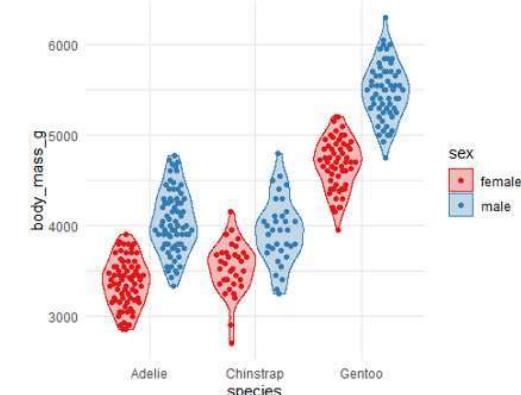


Figure 1: Distribution of penguin body mass (g) across species and sex.

Similarly, Gentoo penguins have the longest flippers on average (Figure 2), and Adelie penguins the shortest. Again, females from a species have shorter flippers on average than the males.

# Quarto + {targets}



Two advantages of using a Quarto document alongside {targets}:

# Quarto + {targets}



Two advantages of using a Quarto document alongside {targets}:

- can read in results from targets pipeline inside the report → no computation done during report generation

# Quarto + {targets}



Two advantages of using a Quarto document alongside {targets}:

- can read in results from targets pipeline inside the report → no computation done during report generation
- can add the rendering of the report as a step in the pipeline → ensures that the report is always up-to-date

# Quarto + {targets}



Two steps to use the `{targets}` pipeline results in a Quarto document:

```
reports/palmerpenguins_report.qmd
```

```
```{r setup}
#| include: false

library(knitr)

opts_chunk$set(echo = FALSE)
```

@fig-body-mass shows...

```{r fig-body-mass}
#| fig-cap: "Distribution ..."

# code for plot
```

```

# Quarto + {targets}



Two steps to use the `{targets}` pipeline results in a Quarto document:

- Make sure the report ‘sees’ the project root directory

```
reports/palmerpenguins_report.qmd
```

```
```{r setup}
#| include: false

library(knitr)
library(here)

opts_chunk$set(echo = FALSE)
opts_knit$set(root.dir = here())
```

@fig-body-mass shows...
```

```
```{r fig-body-mass}
#| fig-cap: "Distribution ..."

# code for plot
```
```

# Quarto + {targets}



Two steps to use the `{targets}` pipeline results in a Quarto document:

- Make sure the report ‘sees’ the project root directory
- Read targets objects with `targets::tar_read()`

```
reports/palmerpenguins_report.qmd
```

```
```{r setup}
#| include: false

library(knitr)
library(here)
library(targets)

opts_chunk$set(echo = FALSE)
opts_knit$set(root.dir = here())
````
```

```
@fig-body-mass shows...
```

```
```{r fig-body-mass}
#| fig-cap: "Distribution ..."

tar_read(body_mass_plot)
````
```

# Quarto + {targets}



Adding the Quarto report as a step in the pipeline (need `{tarchetypes}` and `{quarto}` packages installed):

analysis/\_targets.R

```
1 library(targets)
2 library(tarchetypes)
3 library(here)
4
5 source(here("R/helper_functions.R"))
6
7 list(
8   tar_target(
9     penguins_raw_file,
10    here("data/penguins_raw.csv"),
11    format = "file"
12  ),
13  # etc
14  tar_quarto(
15    report,
16    here("reports/palmerpenguins_report.qmd")
17  )
18 )
```

# Quarto + {targets}

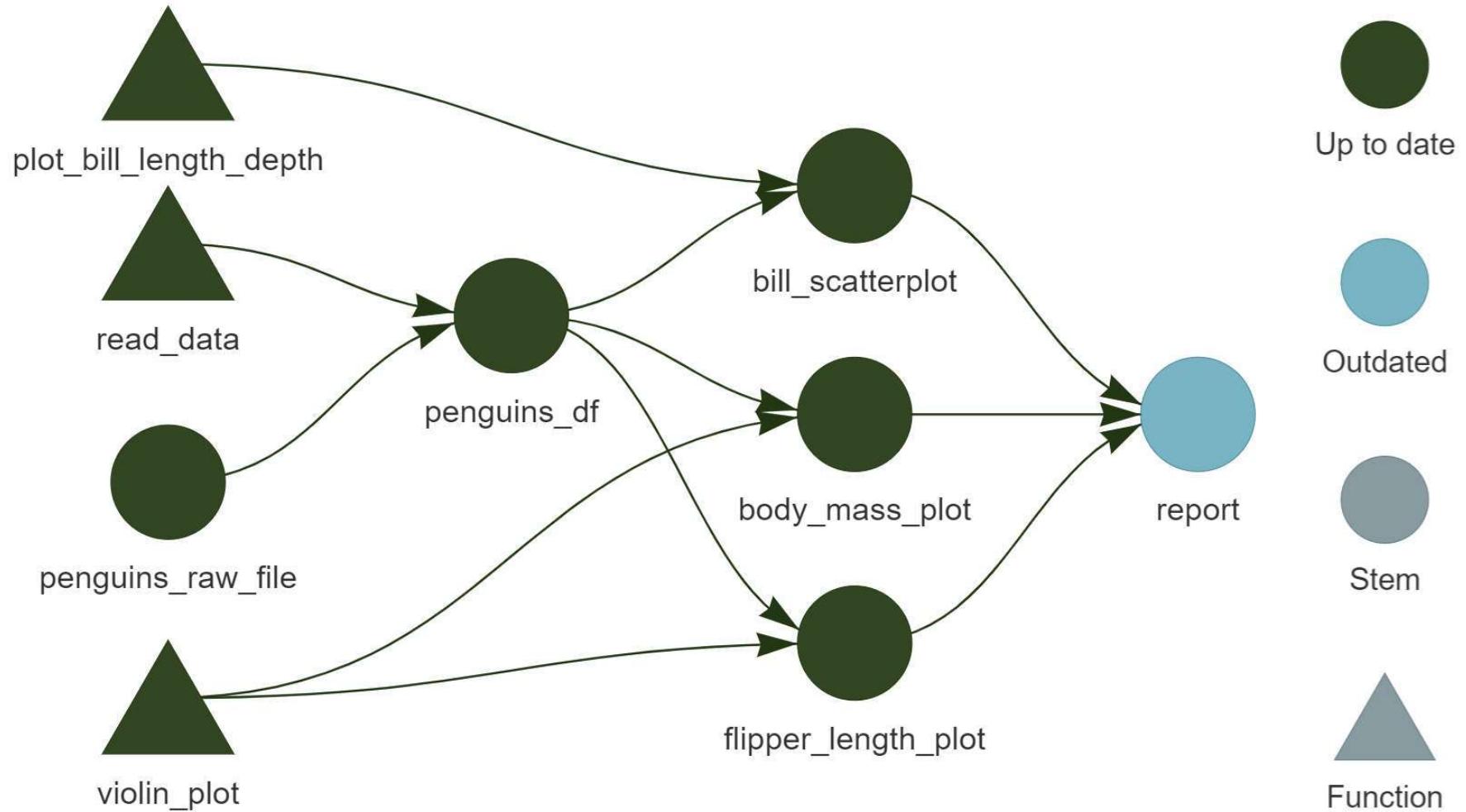


Adding the Quarto report as a step in the pipeline (need `{tarchetypes}` and `{quarto}` packages installed):

`analysis/_targets.R`

```
1 library(targets)
2 library(tarchetypes)
3 library(here)
4
5 source(here("R/helper_functions.R"))
6
7 list(
8   tar_target(
9     penguins_raw_file,
10    here("data/penguins_raw.csv"),
11    format = "file"
12  ),
13  # etc
14  tar_quarto(
15    report,
16    here("reports/palmerpenguins_report.qmd")
17  )
18 )
```

# Quarto + {targets}





# Thank you for your attention!

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# Presentation disclaimer



## Presentation for

Rladies Sydney, online, 7 April 2025

## Publication data:

Angelin-Bonnet O. April 2025. Reproducible analysis pipelines with {targets}. A Plant & Food Research presentation. SPTS No. XXXXX.

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