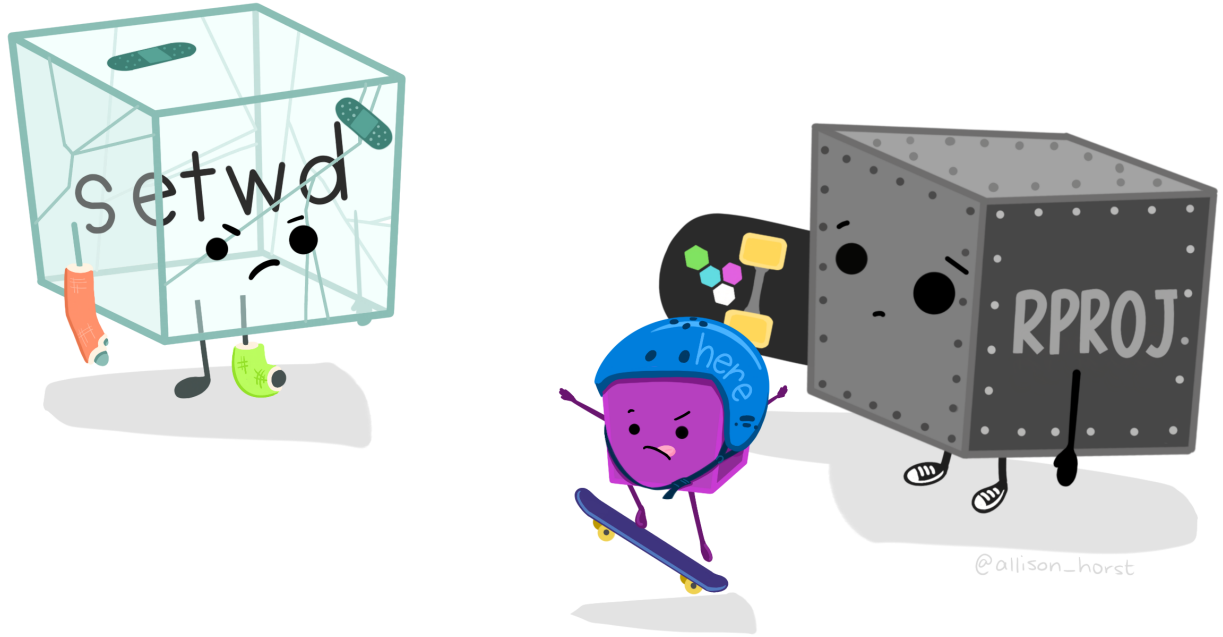
Code pipelines in R

Managing code with targets

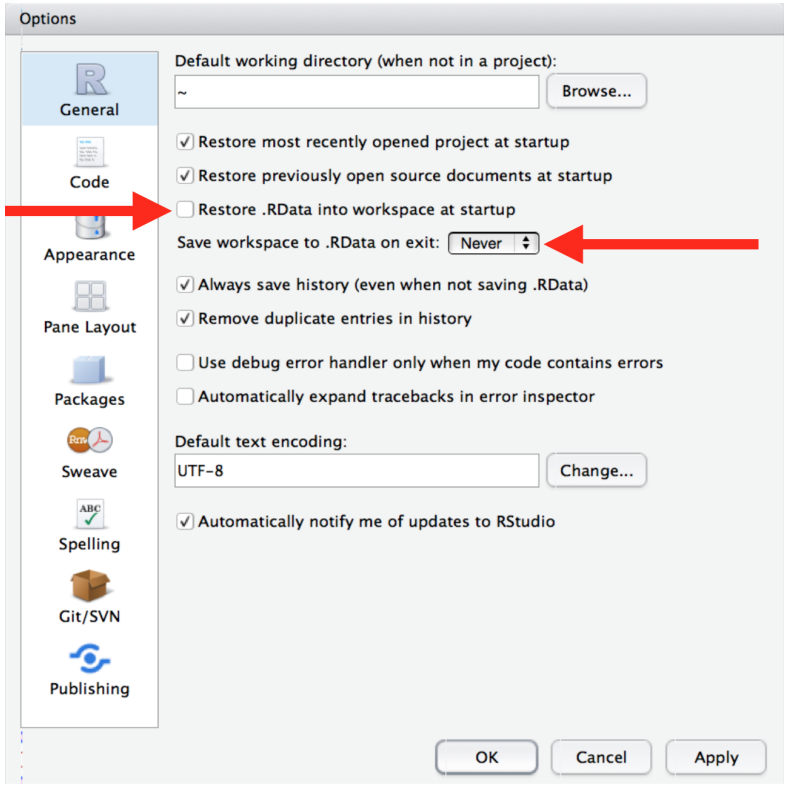
2021-06-04

Strategies for reproduciblity



Project-Oriented Workflows

Strategies for reproduciblity



Use a clean slate; Restart early & often

Strategies for reproduciblity

R Markdown for reproducible documents

renv for package version management

git/GitHub for version control

Script-oriented workflows

```
01-read-data.R
02-clean-data.R
03-decriptive-stats.R
...
n-output.R
report.Rmd
```

Doesn't scale well—in terms of both time and scope

Script-oriented workflows

```
01-read-data.R
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```

Doesn't scale well—in terms of both time and scope

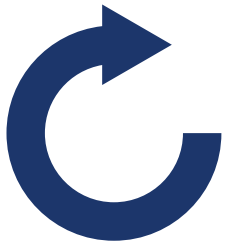
Not clear what we can skip

Function-oriented workflows

```
source("functions.R")
data <- read_data("data.csv") %>%
  clean_data()
table1 <- create_table(data)
...
ggsave("figure3.png")
rmarkdown::render("report.Rmd")
```

Scale the work you need.

Skip the work you don't.



See evidence of reproducibility.

Setting up a pipeline

targets requires a _targets.R file in the root directory of your project

Setting up a pipeline

targets requires a _targets.R **file in the root directory of your project**

Create it with tar_script()**; open it with** tar_edit()

_targets.R

```
library(targets)
options(tidyverse.quiet = TRUE)
tar_option_set(packages = "tidyverse")
source("R/functions.R")

list(
  tar_target(gapminder_file, "gapminder.csv", format = "file"),
  tar_target(gapminder, read_csv(gapminder_file, col_types = cols())),
  tar_target(plot, create_line_plot(gapminder))
)
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  tar_target(plot, create_line_plot(gapminder))
)
```

functions.R **is common for small projects, but targets doesn't care how or from where you source functions.**

R/functions.R

```r
create_line_plot <- function(gapminder) {
  gapminder %>%
    filter(continent != "Oceania") %>%
    ggplot(aes(x = year, y = lifeExp, group = country, color = count
    geom_line(lwd = 1, show.legend = FALSE) +
    facet_wrap(~ continent) +
    theme_minimal(14) +
    theme(strip.text = element_text(size = rel(1.1)))
}
```

_targets.R

```
library(targets)
options(tidyverse.quiet = TRUE)
tar_option_set(packages = "tidyverse")
source("R/functions.R")

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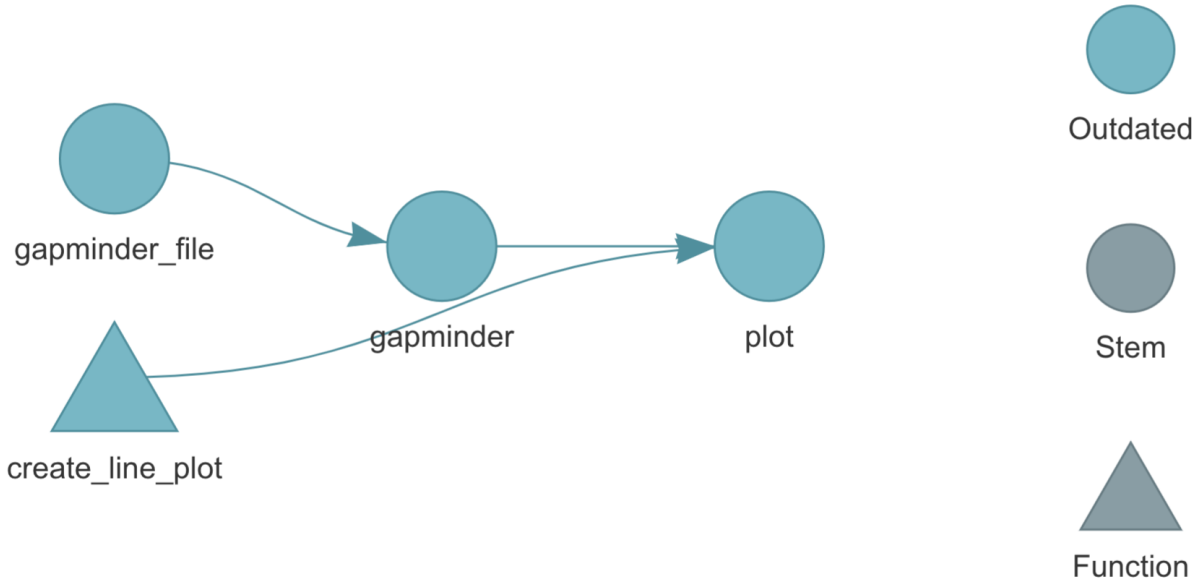
  tar_target(gapminder_file, "gapminder.csv", format = "file"),
  tar_target(gapminder, read_csv(gapminder_file, col_types = cols())),
  tar_target(plot, create_line_plot(gapminder))
)
```

_targets.R **must** end in a list of targets

tar_visnetwork()



Run this in the console! Don't put it in _targets.R or other scripts.

_targets.R

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library(targets)
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tar_option_set(packages = "tidyverse")
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  tar_target(plot, create_line_plot(gapminder))
)
```

Building the pipeline

```
tar_make()
```

- start target gapminder_file
- built target gapminder_file
- start target gapminder
- built target gapminder
- start target plot
- built target plot
- end pipeline

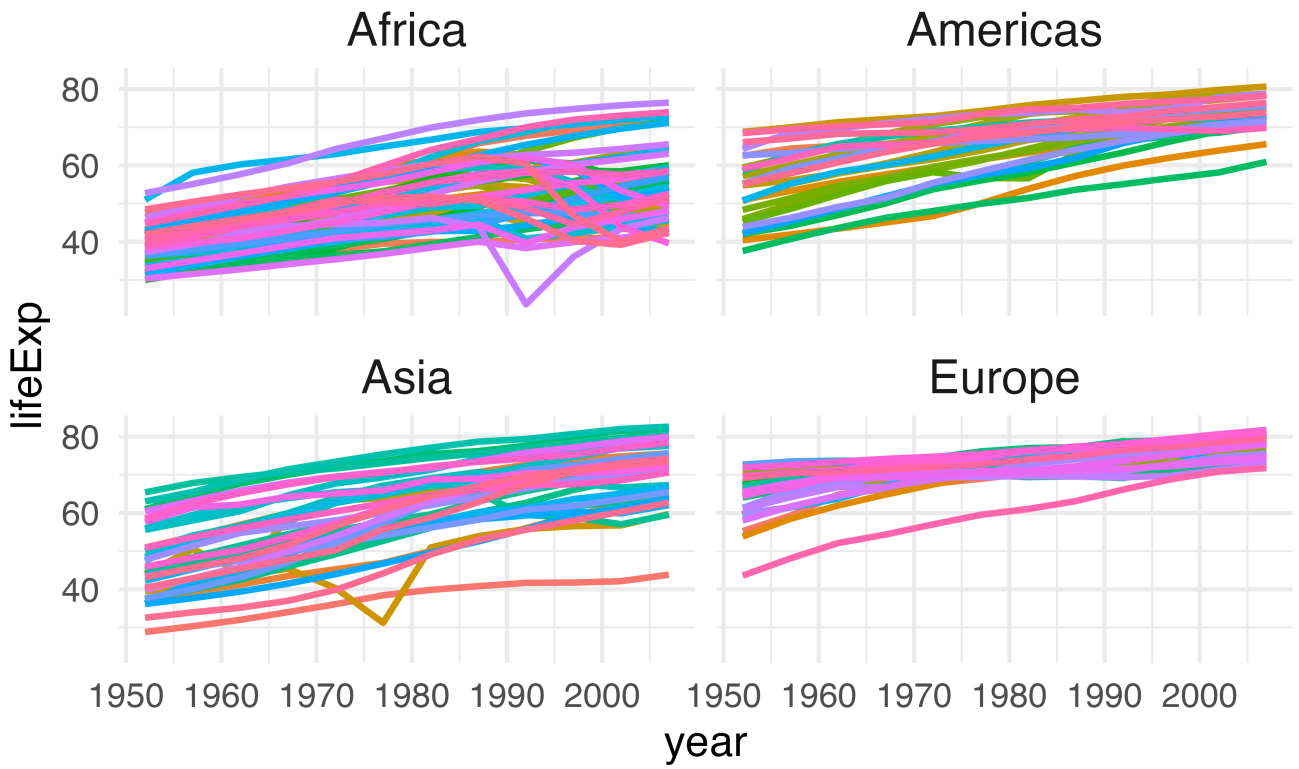
Run this in the console! Don't put it in _targets.R or other scripts.

Where's my output?

`tar_read(target_name)`: return target results

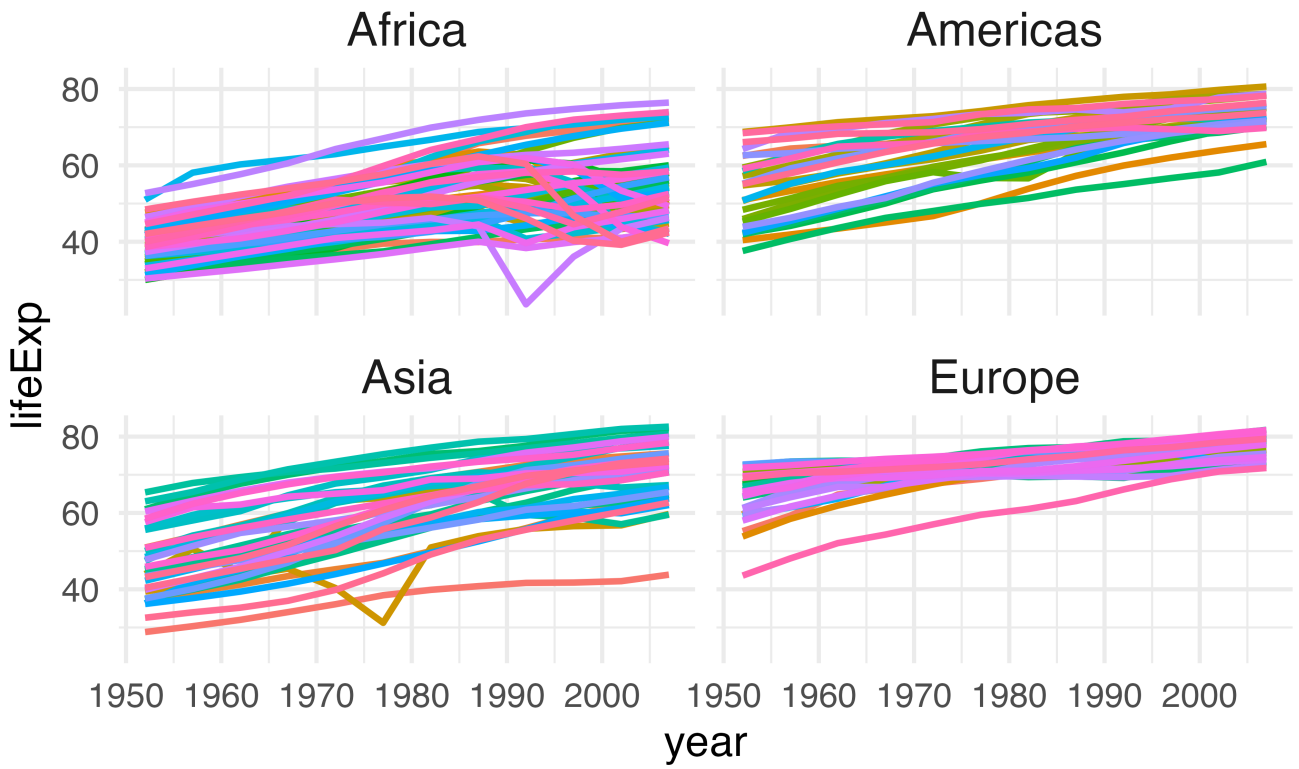
`tar_load(target_name)`: load target_name into global environment

```
tar_read(plot)
```



```
tar_load(plot)

plot
```



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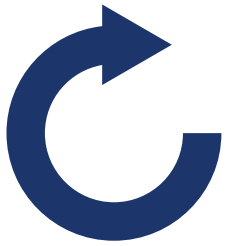
Skip the work you don't.



See evidence of reproducibility.

Your Turn 1

Use tar_script() **in the console, then open** _targets.R **(you can also use** tar_edit() **in the console to open it for you). Read the resulting script.**

Predict how many targets there are, what they are called, and any other dependencies in your code. Run tar_visnetwork() **in the console to check if you were right.**

Run tar_make() **in the console, then run** tar_visnetwork() **again. What's different? Try running** tar_make() **again.**

Building our mental model

```
tar_target(plot, create_line_plot(gapminder))
```

```
plot <- create_line_plot(gapminder)
```

```
list(
  plot = create_line_plot(gapminder)
)
```

tarchetypes

Collection of target and pipeline archetypes for targets

Express complicated pipelines with concise syntax

Need to include library(tarchetypes) **in** _targets.R

Plans

```
list(
  tar_target(gapminder_file, "gapminder.csv", format = "file"),
  tar_target(gapminder, read_csv(gapminder_file, col_types = cols())
  tar_target(plot, create_line_plot(gapminder))
)
```

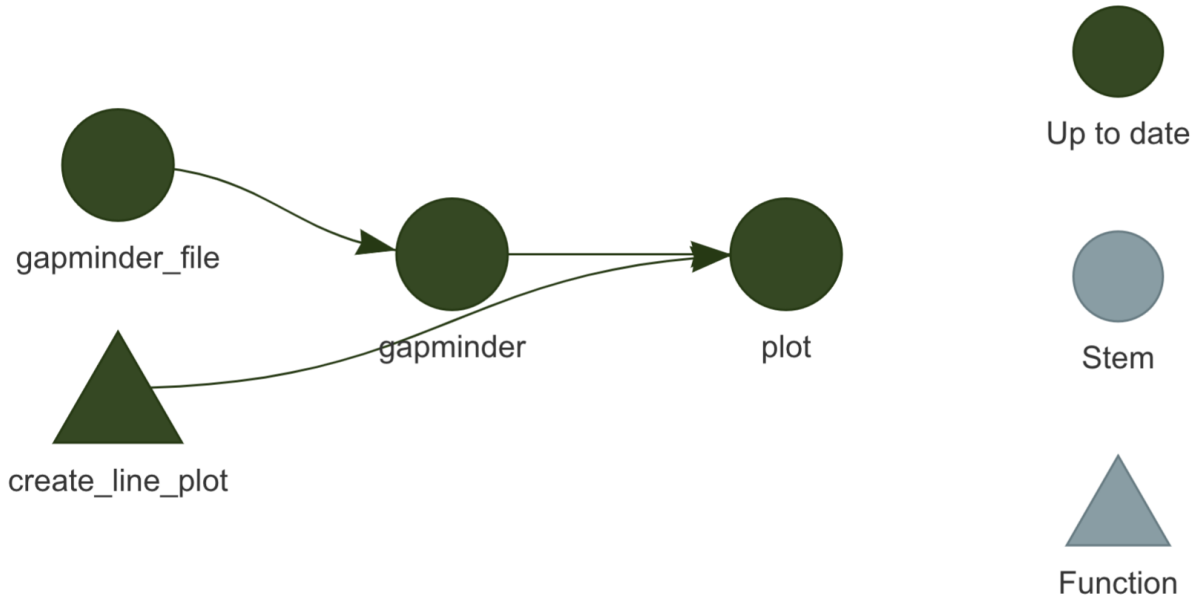
Plans

```
tar_plan(
  tar_target(gapminder_file, "gapminder.csv", format = "file"),
  tar_target(gapminder, read_csv(gapminder_file, col_types = cols())),
  tar_target(plot, create_line_plot(gapminder))
)
```

Plans

```
tar_plan(
  tar_target(gapminder_file, "gapminder.csv", format = "file"),
  gapminder = read_csv(gapminder_file, col_types = cols()),
  plot = create_line_plot(gapminder)
)
```

tar_visnetwork()



Files

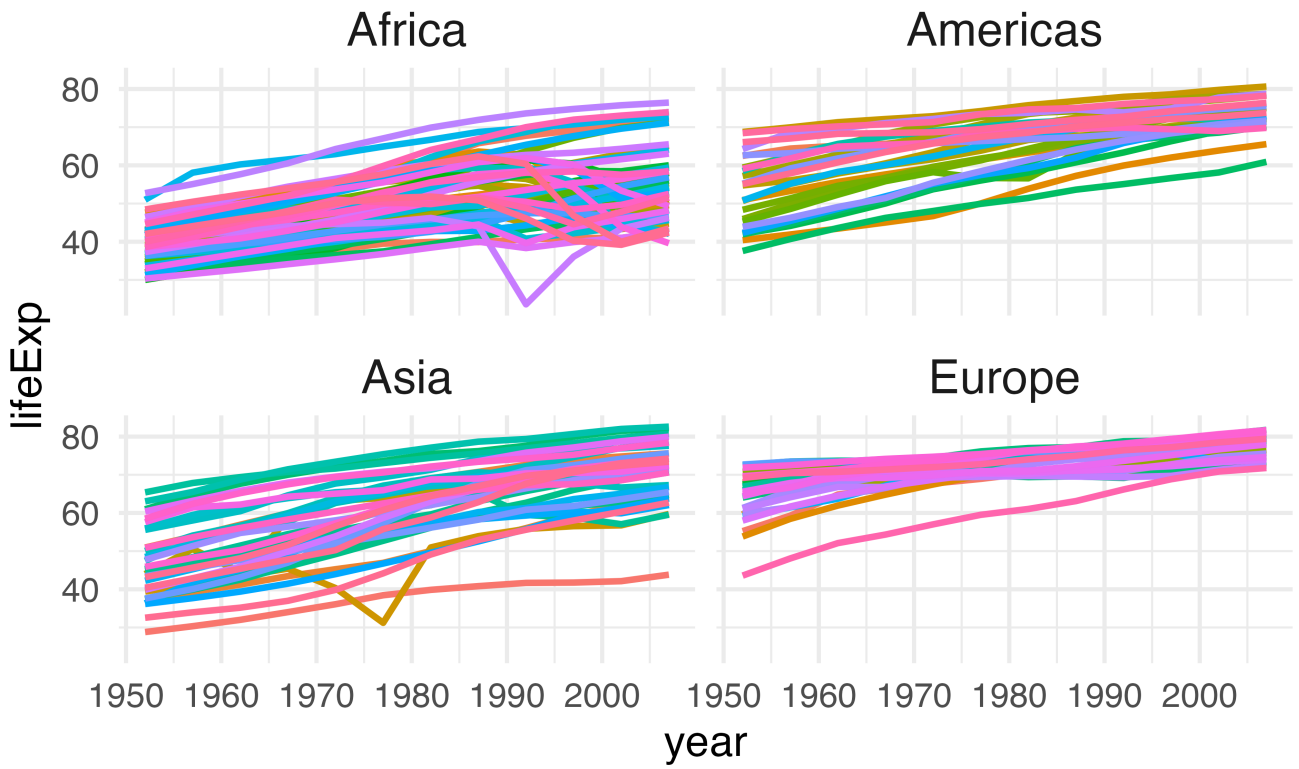
```
tar_plan(
  tar_file(gapminder_file, "gapminder.csv"),
  gapminder = read_csv(gapminder_file, col_types = cols()),
  plot = create_line_plot(gapminder)
)
```

See also tar_url(), tar_parquet(), and other file formats

Your Turn 2

Work through Your Turn 2 in exercises.Rmd

```
tar_read(plot)
```



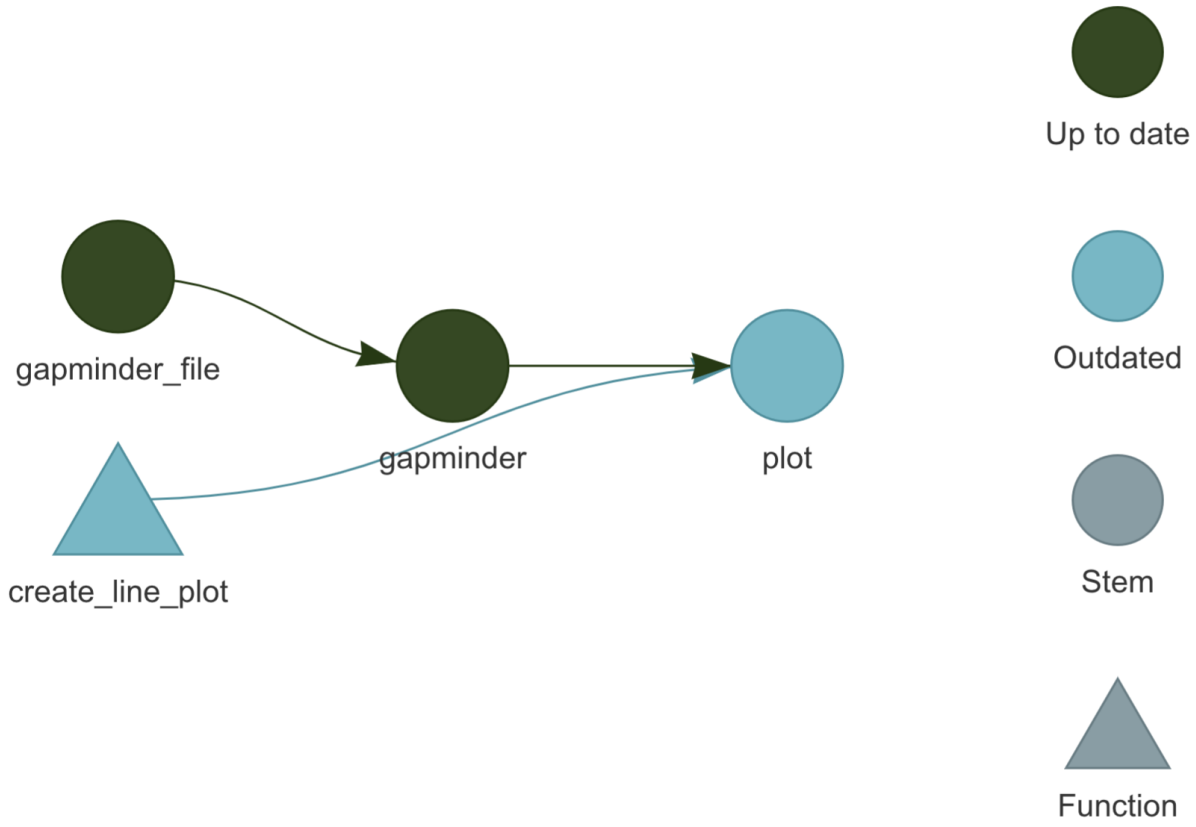
```r
create_line_plot <- function(gapminder) {
  gapminder %>%
    filter(continent != "Oceania") %>%
    ggplot(aes(
      x = year,
      y = lifeExp,
      group = country,
      color = country
    )) +
    geom_line(lwd = 1, show.legend = FALSE) +
    facet_wrap(~ continent) +
    scale_color_manual(values = country_colors) +
    theme_minimal(14) +
    theme(strip.text = element_text(size = rel(1.1)))
}
```

_targets.R

```
library(targets)
library(tarchetypes)
options(tidyverse.quiet = TRUE)
tar_option_set(packages = c("tidyverse", "gapminder"))
source("R/functions.R")

tar_plan(
  tar_file(gapminder_file, "gapminder.csv"),
  gapminder = read_csv(gapminder_file, col_types = cols()),
  plot = create_line_plot(gapminder)
)
```

tar_visnetwork()



Outdated targets

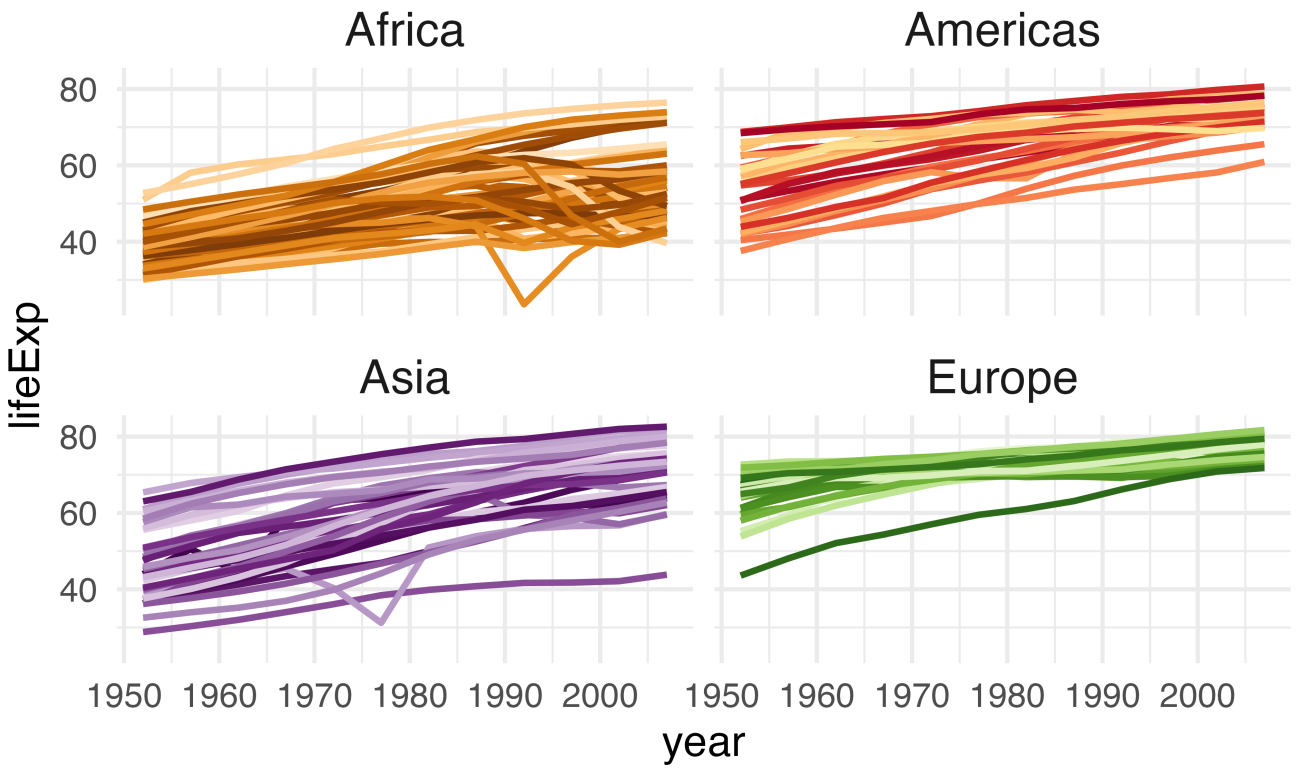
```
tar_outdated()
```

```
## [1] "plot"
```

tar_make()

```
✓ skip target gapminder_file
✓ skip target gapminder
• start target plot
• built target plot
• end pipeline
```

```
tar_read(plot)
```



Your Turn 3

Change diabetes_file **to use** diabetes.csv **instead**

Run tar_outdated() **in the console. What's this telling you? Confirm with** tar_visnetwork()

Predict which targets are going to re-run, then run tar_make()**. Were you right?**

Confirm that diabetes **has changed by looking at it with** tar_read()**. The new dataset should have 403 rows and 20 columns.**

Building up your pipeline

Good targets are meaningful units of your analysis or important dependencies like files

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Add one or two targets at a time

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Run tar_make() **and** tar_visnetwork() **often**

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Good targets are meaningful units of your analysis or important dependencies like files

Add one or two targets at a time

Run tar_make() **and** tar_visnetwork() **often**

Load all targets: tar_load(everything())

Organizing your functions

functions.R **only works well for small pipelines, but targets doesn't have a preference for you organize them**

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functions.R **only works well for small pipelines, but targets doesn't have a preference for you organize them**

> While you're free to arrange functions into files as you wish, [avoid] the two extremes... don't put all functions into one file and don't put each function into its own separate file. —R Packages, 2nd Ed.

What I like to do

1. **Create an** R/ **folder**
2. **Create and open new files in** R/ **with** use_r("file_name") **from the usethis package**
3. **In** _targets.R**:** purrr::walk(fs::dir_ls("R"/), source)

Remember, you need to source() **each file in** _targets.R

Your Turn 4

Add source("R/functions.R") **to** _targets.R

Add "gtsummary" to the packages **argument of** tar_option_set()

Create a new target called table_one **using** create_table_one(diabetes)

Run tar_visnetwork() **and** tar_make()

Take a look at the target you just created

Your Turn 5

Open R/functions.R **and modify** create_table_one()**: Add the argument** missing_text = "(Missing)" **to** tbl_summary()**. Make sure to save your file after you've made the change.**

Run tar_outdated() **in the console, then look at** tar_visnetwork()

Predict which targets are going to re-run, then run tar_make()**. Were you right?**

Including R Markdown files as targets

1. **Create an R Markdown file**
2. **Use** `tar_read()` **or** `tar_load()` **in the Rmd file to access targets**
3. **Include** `tar_render(target_name, "file_name.Rmd")` **in your list of targets**

report.Rmd

````
```{r setup, include = FALSE}
knitr::opts_chunk$set(echo = FALSE)
library(targets)

tar_load(gapminder)
```


These data have `r nrow(gapminder)`
observations.

```{r figure-one, fig.cap = "Figure 1"}
tar_read(plot)
```
````

report.Rmd

````
```{r setup, include = FALSE}
knitr::opts_chunk$set(echo = FALSE)
library(targets)

tar_load(gapminder)
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These data have `r nrow(gapminder)`
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```{r figure-one, fig.cap = "Figure 1"}
tar_read(plot)
```
````
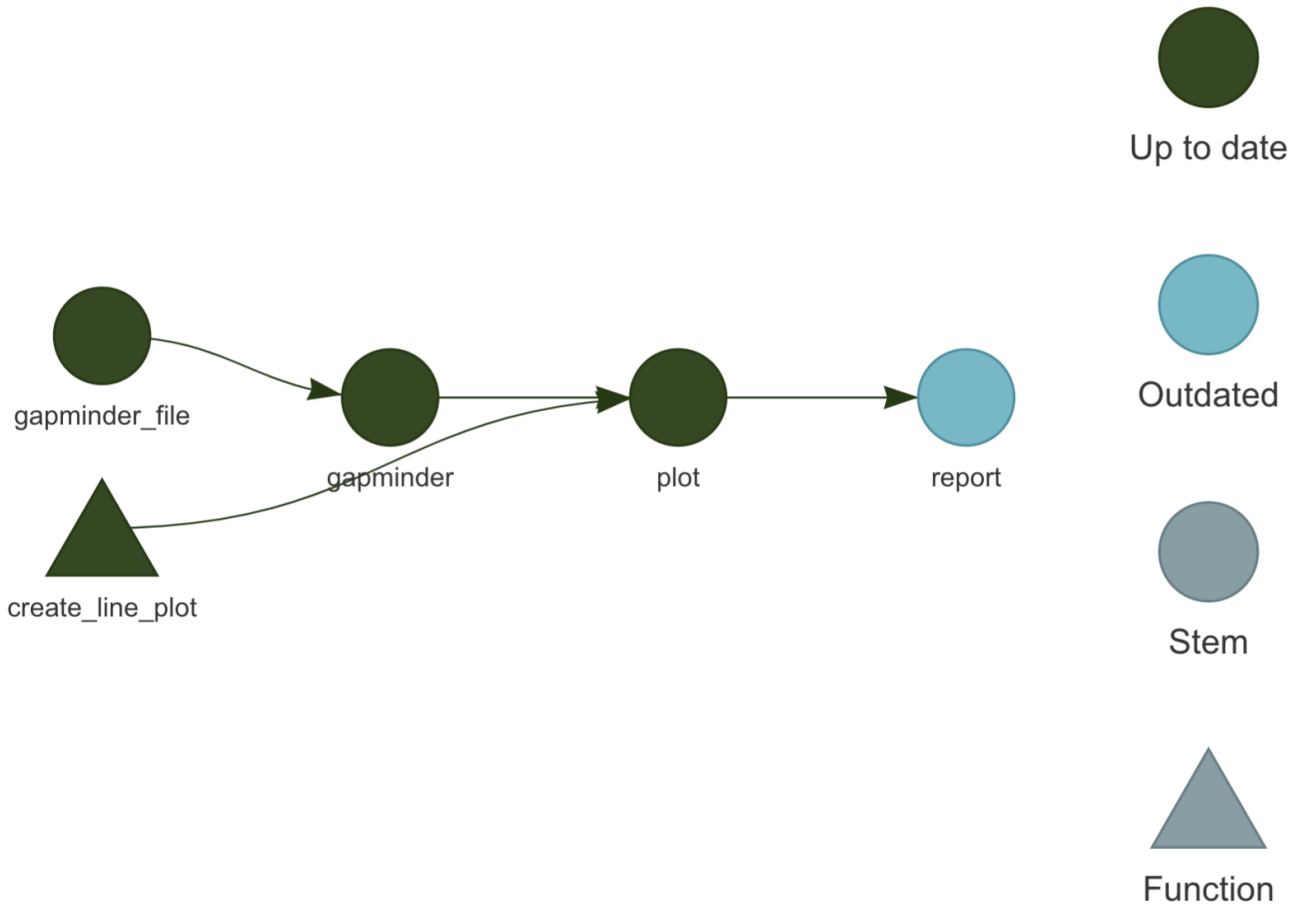

_targets.R

```
library(targets)
library(tarchetypes)
options(tidyverse.quiet = TRUE)
tar_option_set(packages = c("tidyverse", "gapminder"))
source("R/functions.R")

tar_plan(
  tar_file(gapminder_file, "gapminder.csv"),
  gapminder = read_csv(gapminder_file, col_types = cols()),
  plot = create_line_plot(gapminder),
  tar_render(report, "report.Rmd")
)
```

tar_visnetwork()



tar_make()

```
✓ skip target gapminder_file
✓ skip target gapminder
✓ skip target plot
• start target report
• built target report
• end pipeline
```

Your Turn 6

Work through Your Turn 6 in exercises.Rmd

The targets cache: _targets/

tar_destroy(): **Remove everything in the cache**

tar_prune(): **Remove targets that are no longer part of the pipeline**

Your Turn 7

Confirm that you can reproduce your entire pipeline from scratch. In the console:

Run tar_destroy()

Run tar_make()

Other features of targets

Automatic parallelization

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Branching

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Automatic parallelization

Branching

Cloud integration

Resources

The targets User Manual: A comprehensive but friendly introduction to targets. Free online.

The Official targets Short Course: A free short course available on RStudio Cloud or locally

Talks and other targets resources