R-eproducible workflows

1-day workshop
Morning practical session





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Inconsistent function names, inconsistent syntax

- R is a very versatile language
 - Sometimes it can be too versatile
 - Do you want to use...

```
row.names or rownames rowSums or rowsum
Sys.time, system.time
```

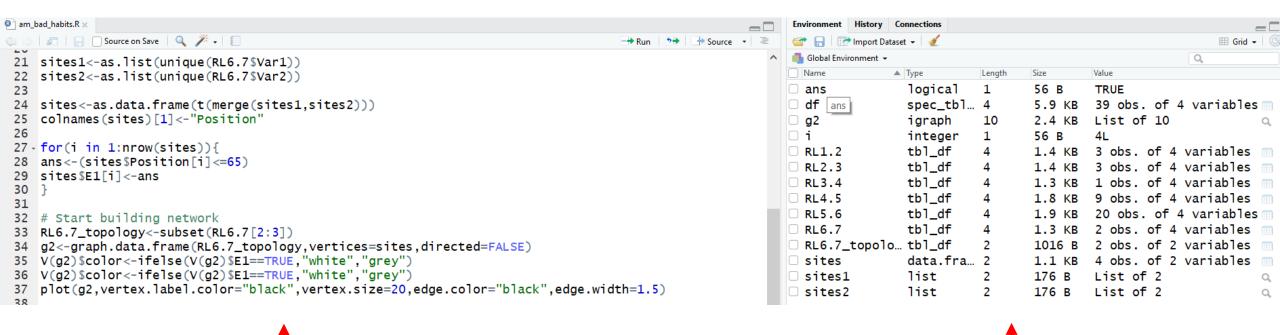
- Should it be written as...

```
newobject or new.Object
x = 5 or x <- 5
mapping=aes(x,y) or mapping = aes(x, y)</pre>
```

Variable selection

```
summary(starwars$name)
              summary(starwars$"name")
              summary(starwars["name"])
              summary(starwars[ , "name"])
              summary(starwars[1])
              summary(starwars[ , 1])
              summary(starwars[[1]])
- Open the R-project file reproducible-workflows 2019. Rproj
- Open the script am too much.choice.R
```

Motivation to move on from poorly written code



Lack of annotation
Poor naming conventions
Poor readability
Spacing absent

- Open the script am bad habits.R

Cluttered environment Intermediate objects

Writing clearer code

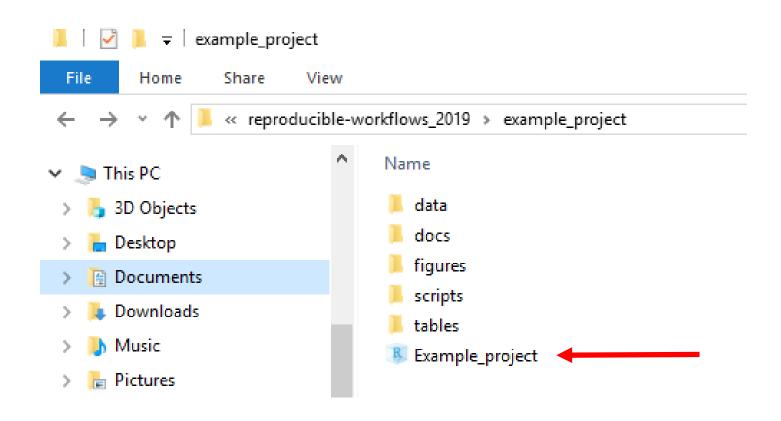
- Annotation
- Object names
 - should use only lowercase letters, numbers, and " $_$ "
- Spacing
 - Put a space before and after =
 - Put a space after a ,
 - Operators should be surrounded by spaces e.g. ==, <-, +
- For a more complete list visit
 - http://style.tidyverse.org/syntax.html

- Open the script am good habits.R

Navigating RStudio – some useful tips

- Open the script am_rstudio_ide_tricks.R

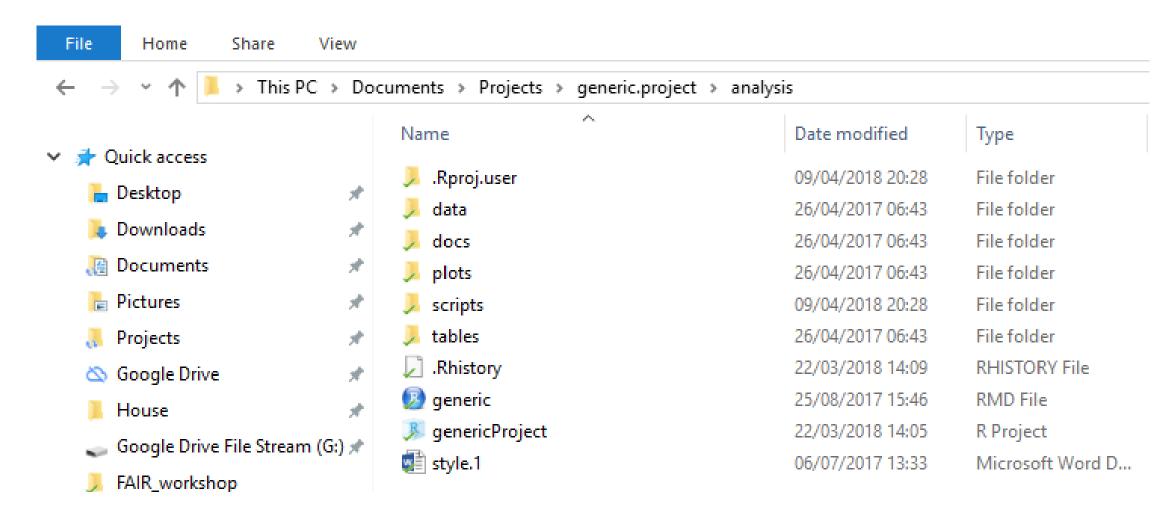
B: R-projects - everything in its right place



- Switch to the R-project file example project. Rproj
- Open the scripts 01_eg_clean_data.R, 02_eg_figures.R and 03 eg analysis.R

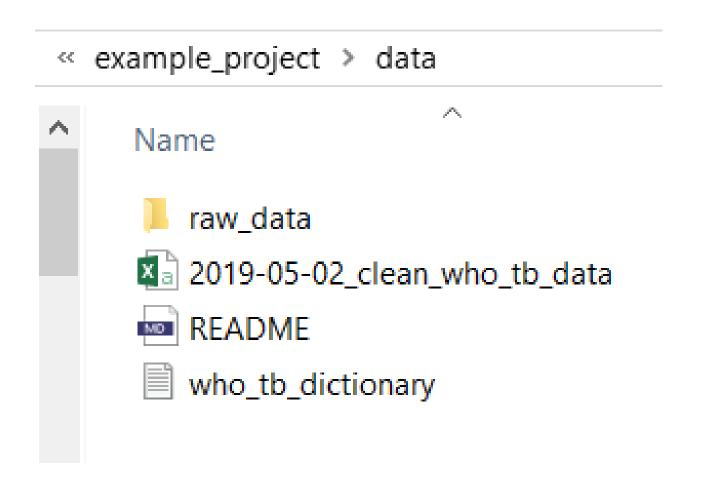
Define a generic project structure

- STEP 1: Give your research projects a shared structure



Give your files informative names

- STEP 2: Include metadata in the file names



Come back to what you know

- STEP 3: Make you file names machine readable, human readable and work with default ordering

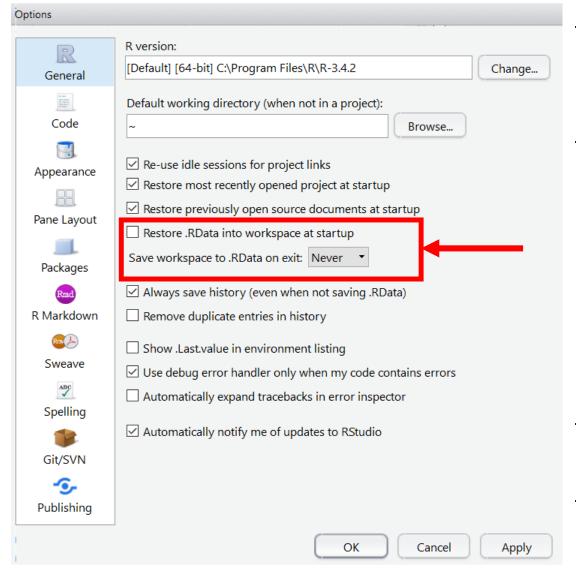
NO

- Epistatic_change
- Epistatic_change_match_discovery
- Epistatic_change_match_discovery_fig_2_point_1
- Epistatic_change_v2
- 😰 epistatic_codon _change_tracking
- Epistatic_connection_network
- Meatmap_for_epistatic_syn
- Meatmap1_for_epi_site_co-change
- Meatmap2_for_epi_fdr_adjusted_p-value
- Meatmap2_for_epi_p-value

Yes

Doc	uments > Projects > 18.04.27-WP3_Feeding_Trial	analysis > scripts
	Name	Date modified
_	01_data_import_and_tidying_master_file	02/10/2018 18:51
*	02_data_import_and_tidying_nutritics_grouped	19/10/2018 19:47
*	03_figures	17/10/2018 16:40
*	04_tables	22/05/2018 12:26
*	05_study_overview	19/10/2018 23:06
яř	functions	13/05/2018 23:13

Other points to note



- You might consider your environment as "real"
- If you continue to use R, it is better for you to consider your R scripts as "real", as these should recreate the environment

- You may suffer short term pain
- This will prevent long term agony