

Reproducibility

What's Reproducibility

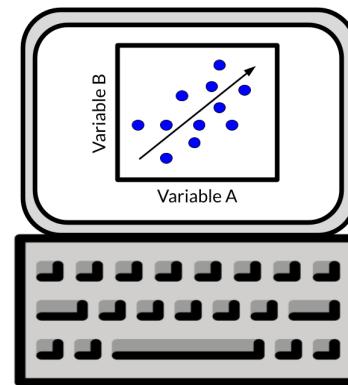
Reproducibility:

a different analyst re-performs the analysis with
the **same code** and
the **same data** and obtains
the **same result**.

Patil, Peng, Leek (2016) <https://www.biorxiv.org/content/10.1101/066803v1>

Content adapted from [Candace Savonen](#).

My data analysis is showing a pattern that is very informative for the ongoing research in my field.

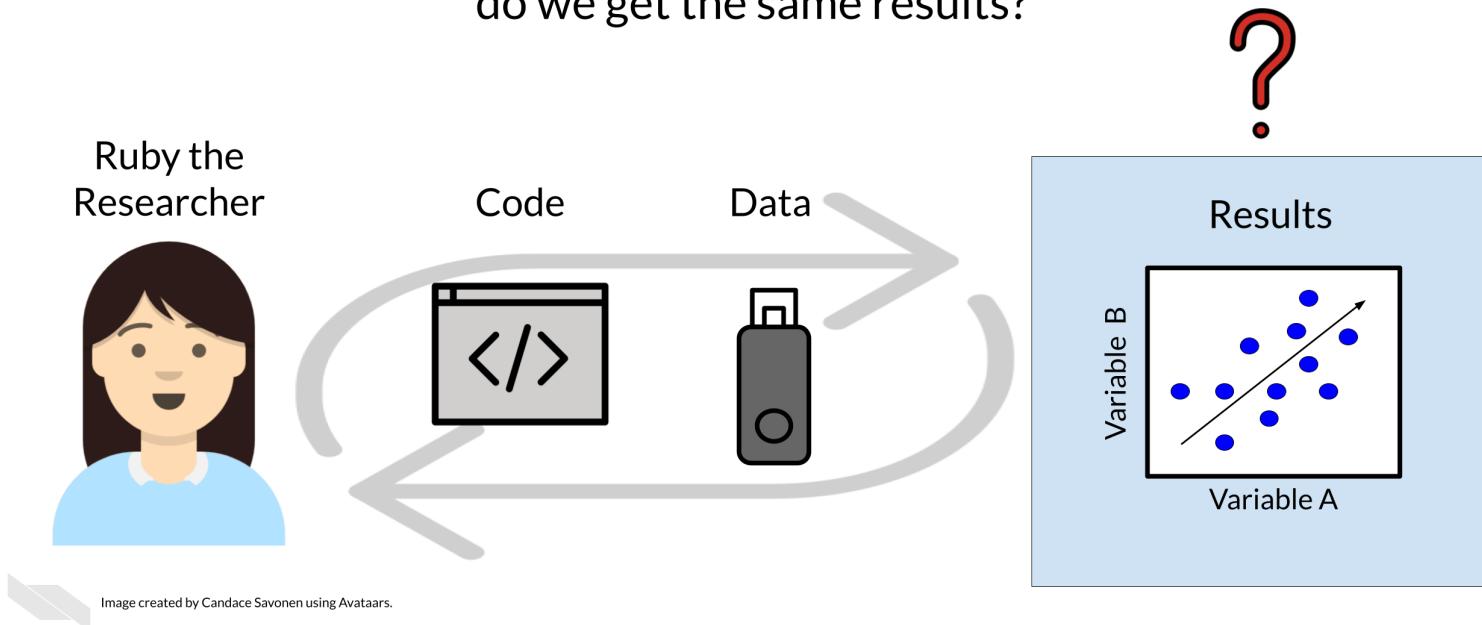


Ruby the Researcher

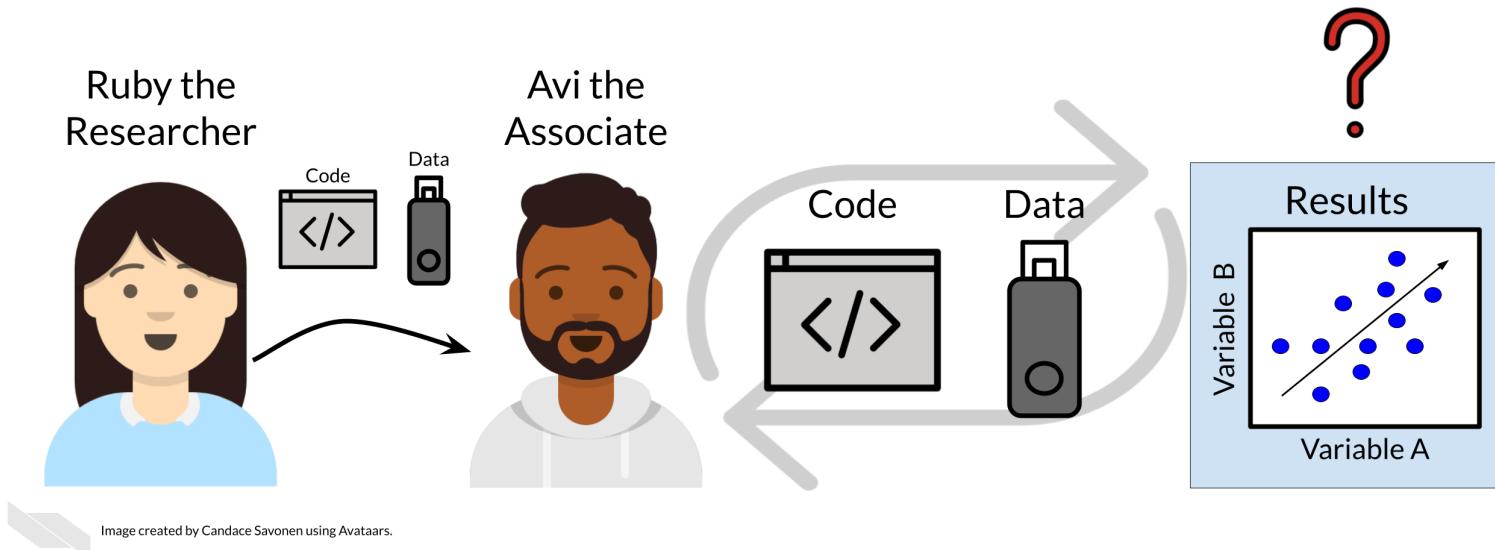


Image created by Candace Savonen using Avataars.

Repeatable: keeping everything the same but repeating the analysis - do we get the same results?

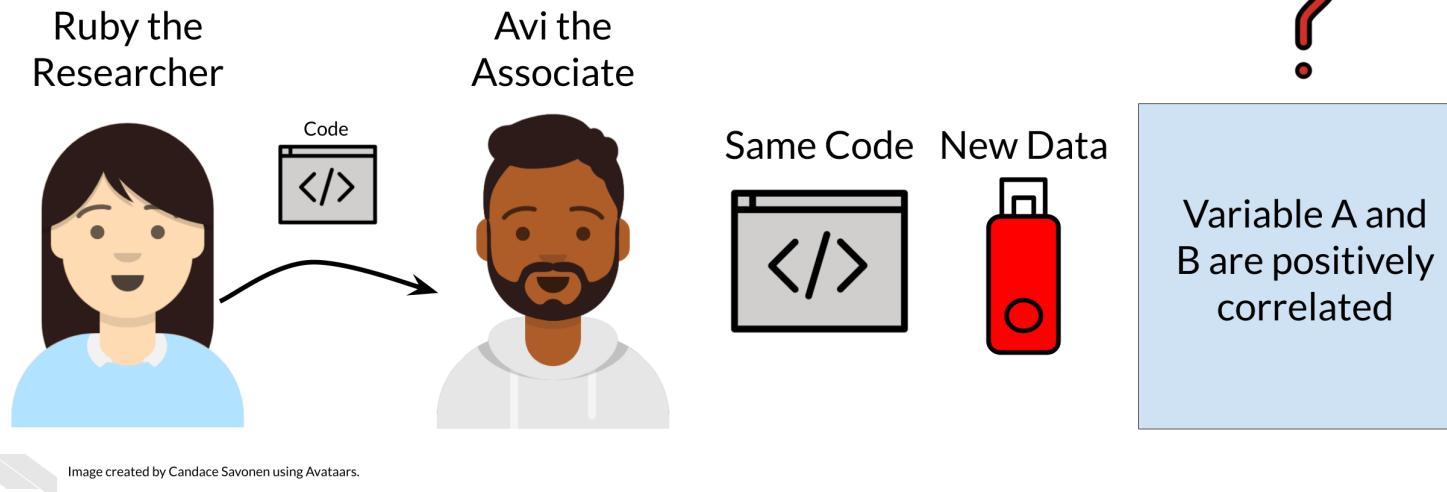


Reproducible: using the same data and analysis but in the hands of *another researcher* - do we get the same results?

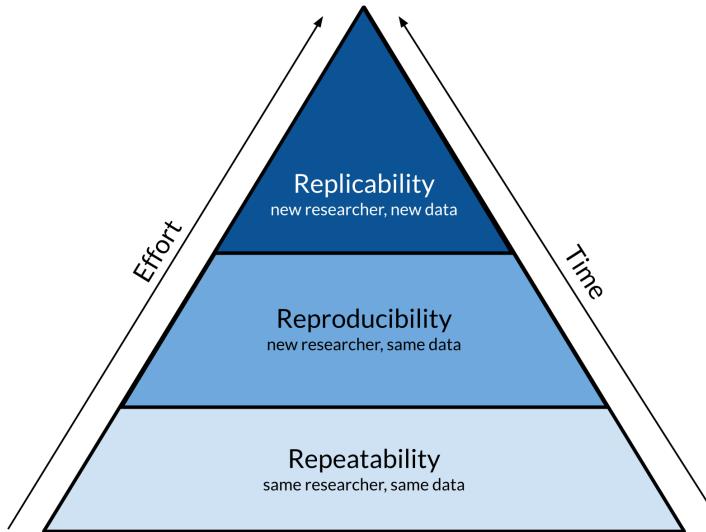


Replicable:

with new data do we obtain the same inferences?



Reproducibility vs Repeatability vs Replicability



Based off of a figure from Essawy et al, 2020 <https://doi.org/10.1016/j.envsoft.2020.104753>

Why Reproducibility is important...

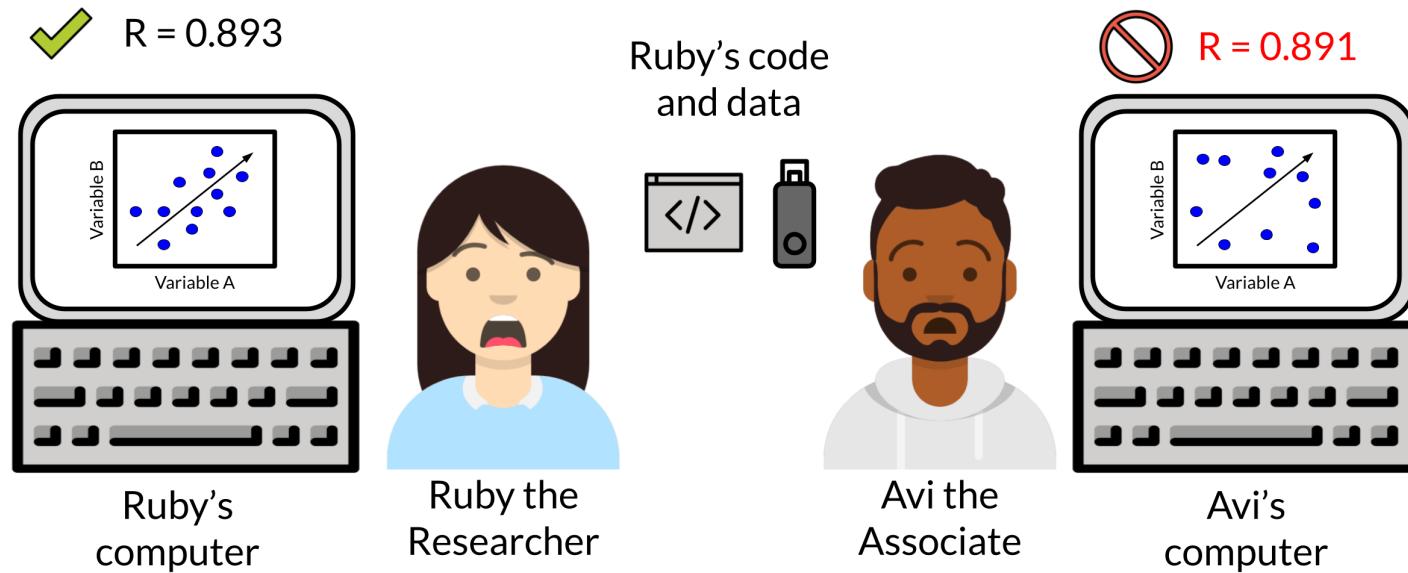
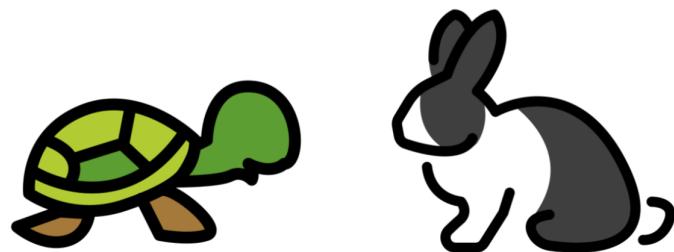


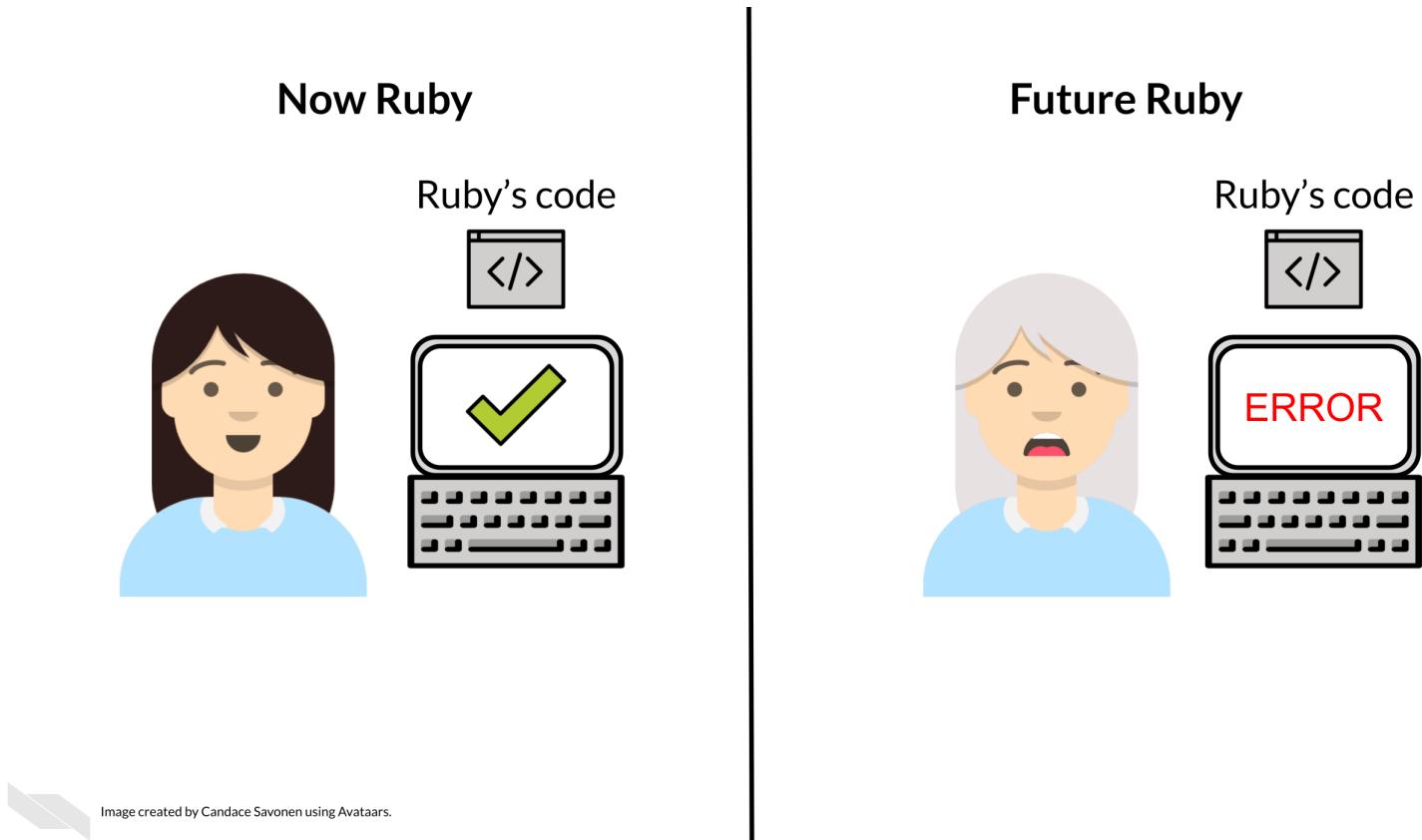
Image created by Candace Savonen using Avataars.

It's worth the wait

Reproducibility is a tortoise's game - it's an incremental and slow process **but it has high payoffs!**



Reproducibility can also be for your future self!



The process

Step 1) Get your code to work once

Step 2) Get your code to work reliably for you

Step 3) Get your code to work for someone else

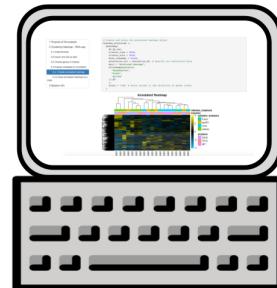
R Markdown

R Markdown notebooks are a handy
tool for reproducibility!



R Markdown lets you test your work

Working from this notebook allows me to interactively develop on my data analysis and write down my thoughts about the process all in one place!



RMarkdown is conducive to interactive development!

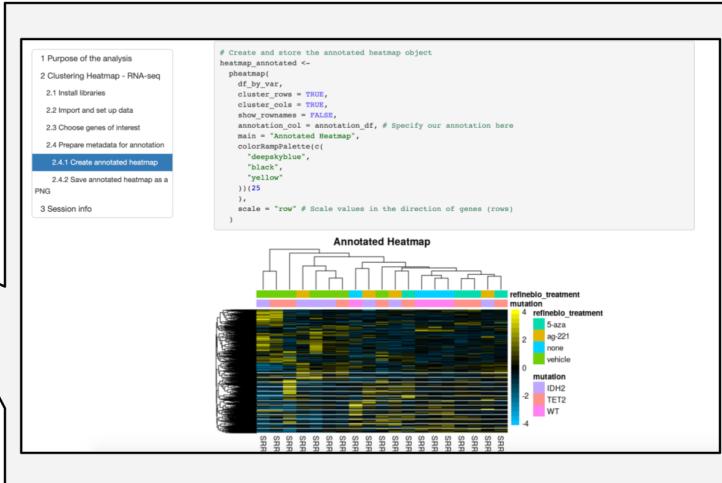
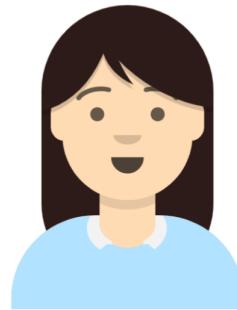


Image created by Candace Savonen using Avataars.

R Markdown allows you to more clearly show what you did

Avi, here's some output from this scientific notebook I've been developing from!

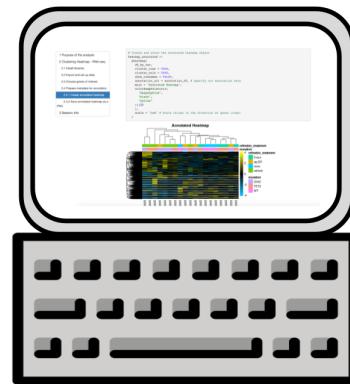


Ruby the Researcher

This is so easy to follow and read, even though I didn't write the code. Thanks for sharing your exciting results!



Avi the Associate



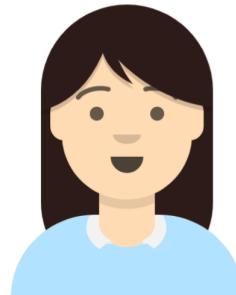
RMarkdown creates easily shareable output!



Image created by Candace Savonen using Avataars.

R Markdown makes it easier to update code and see results

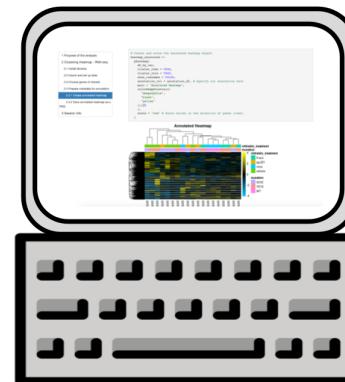
Yay! I just got the data for 5 more samples. Because of my handy notebook set up, I can easily call one command and re-run the analysis so it is updated with the new samples included!



Ruby the
Researcher



Image created by Candace Savonen using Avataars.

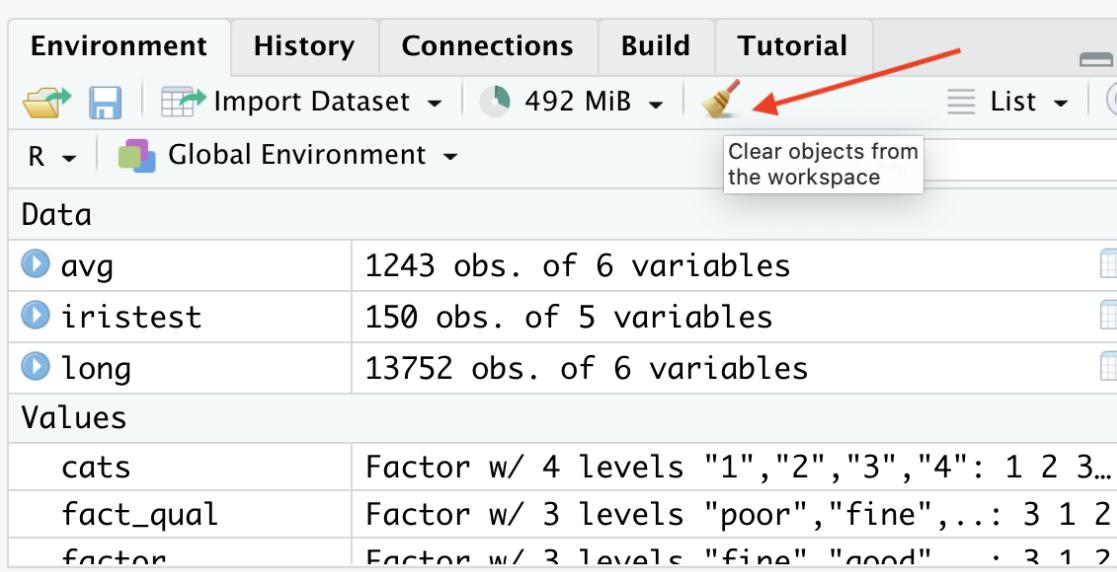


**RMarkdown is handy for
creating updateable reports!**

Clean your environment

Regularly cleaning your environment and trying your code again, can help ensure that your code is running as expected.

Occasionally we might forget to save a step of our code in our R Markdown file that we ran only in the console. This will help us figure that out.



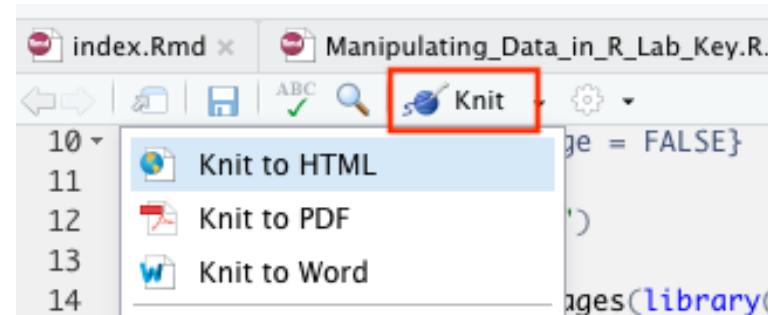
The screenshot shows the RStudio interface with the 'Environment' tab selected. The top bar includes tabs for Environment, History, Connections, Build, and Tutorial. Below the tabs are icons for Import Dataset, 492 MiB (memory usage), and a brush icon. A red arrow points to the brush icon, which has a tooltip 'Clear objects from the workspace'. The Global Environment dropdown is set to 'Global Environment'. The main area displays the workspace contents:

Data	
avg	1243 obs. of 6 variables
iristest	150 obs. of 5 variables
long	13752 obs. of 6 variables

Values	
cats	Factor w/ 4 levels "1", "2", "3", "4": 1 2 3...
fact_qual	Factor w/ 3 levels "poor", "fine", ...: 3 1 2
factor	Factor w/ 3 levels "fine", "good", ...: 3 1 2

Check if your file knits regularly

Regularly checking if your file knits will help you spot a missing step or error earlier when you have less code to try to identify where your code might have gone wrong.



Tell your future self and others what you did!

Provide sufficient detail so that you can understand what you did.

R Markdown syntax

Before:

```
# Header - biggest font created by hashtag and space
## SubHeader Second Biggest created by 2 hashtags and space

**bold** text
*italicized* text

`code` referenced outside of a chunk needs backticks
```

After knit:

Header - biggest font created by hashtag and space

SubHeader Second Biggest created by 2 hashtags and space

bold text *italicized* text

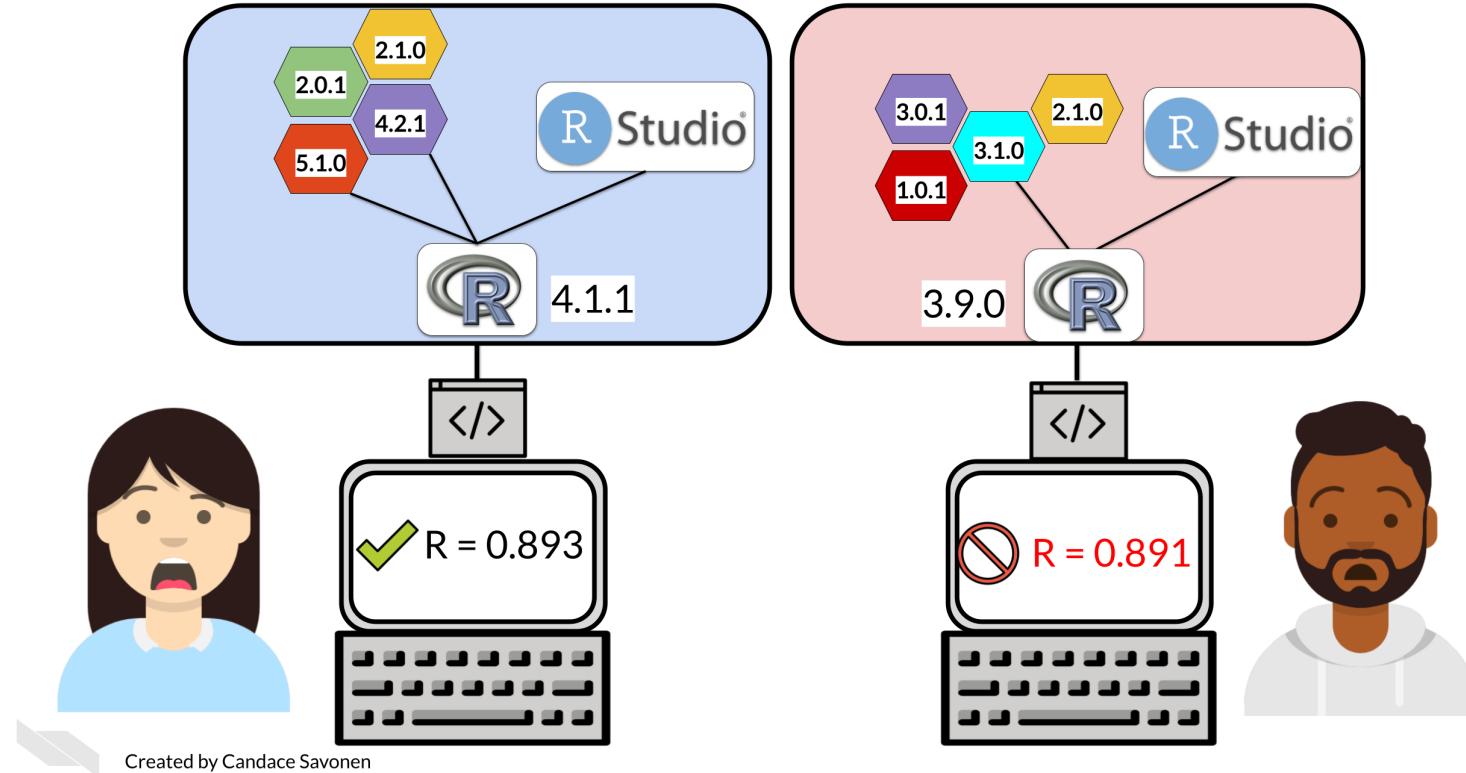
`code` referenced outside of a chunk needs backticks

R Markdown syntax

Go to Help > Cheatsheets > R Markdown Cheatsheet or our website!

Versions matter

Ruby's local computing environment Avi's local computing environment



Session info can help

sessionInfo()

Ruby's session info print out	Avi's session info print out
<pre>R version 4.0.2 (2020-06-22) Platform: x86_64-pc-linux-gnu (64-bit) Running under: Ubuntu 20.04.2 LTS Matrix products: default BLAS/LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-r0.3.8.so locale: [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C [4] LC_COLLATE=en_US.UTF-8 LC_MONETARY=en_US.UTF-8 [7] LC_PAPER=en_US.UTF-8 LC_NAME=en_US.UTF-8 [10] LC_TELEPHONE=C LC_MEASUREMENT=en_US.UTF-8 attached base packages: [1] stats graphics grDevices utils datasets methods base other attached packages: [1] rmarkdown_2.4 loaded via a namespace (and not attached): [1] rstudioapi_0.11 knitr_1.39 magrittr_1.5 hms_0.5.3 [6] R6_2.4.1 rlang_0.4.7 fansi_0.4.1 dplyr_1.0.2 [11] xfun_0.18 sessioninfo_1.1.1 tinytex_0.26 cli_2.0.2 [16] htmltools_0.5.0 ellipsis_0.3.1 assertthat_0.7.1 withr_2.3.0 [21] tibble_3.0.3 lifecycle_0.2.0 crayon_1.4.1 digest_0.6.27 [26] vctrs_0.3.4 glue_1.4.2 evaluate_0.14 magrittr_2.0.1 [31] generics_0.0.2 isnan_1.2 lubridate_1.7.1 rlang_0.4.11</pre>	<pre>R version 4.0.5 (2021-03-31) Platform: x86_64-apple-darwin17.0 (64-bit) Running under: macOS Big Sur 10.16 Matrix products: default LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib locale: [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8 attached base packages: [1] stats graphics grDevices utils datasets methods base other attached packages: [1] rmarkdown_2.10 loaded via a namespace (and not attached): [1] lembuild_0.1.2 BioManager_1.30.16 compiler_4.0.5 magrittr_2.0.1 [5] fastmap_1.1.0 htmltools_0.5.2 tools_4.0.5 yaml_2.2.1 [9] tinytex_0.33 knitr_1.33 digest_0.6.27 xfun_0.25 [13] rlang_0.4.11 evaluate_0.14</pre>
<p>R version 4.0.2 vs 4.0.5</p> <p>Different operating systems!</p> <p>rmarkdown 2.4 vs 2.10</p>	<p>R version 4.0.5</p> <p>Locale:</p> <p>attached base packages:</p> <p>other attached packages:</p>

If Avi and Ruby have discrepancies in their results, the session info print out gives a record which may have clues to why that might be!

Image by Candace Savonen

More resources

These are just some quick tips, for more information:

- [Reproducibility in Cancer Informatics course](#)
- [Advanced Reproducibility in Cancer Informatics course](#)
- [The RMarkdown book](#)
- [Jenny Bryan's organizational strategies.](#)
- [Write efficient R code for science.](#)

Summary

To help make your work more reproducible:

- Use RMarkdown
- Clean your environment regularly
- Check the knit of your RMarkdown regularly
- Tell your future self and others what you did!
- Print session info!

□ [Class Website](#)