



# Reproducible systematic reviews and meta-analyses

A 3-hour, hands-on workshop

---

April Clyburne-Sherin  
*Instructor & Open Research Consultant*  
Website: [aprilcs.com](http://aprilcs.com)  
Email: [aprilcs@pm.me](mailto:aprilcs@pm.me)

## **Purpose**

To introduce methods and tools in organization, documentation, automation, and dissemination of systematic reviews and meta-analyses that nudge it further along the reproducibility spectrum.

## **Outcome**

Participants feel more confident applying reproducibility methods and tools to their next systematic review or meta-analysis.

## **Process**

Participants practice new methods and tools with code and data during the workshop to explore what they do and how they might work in a project workflow. Participants can compare benefits of new practices and ask questions to help clarify which would provide them the most value to adopt.



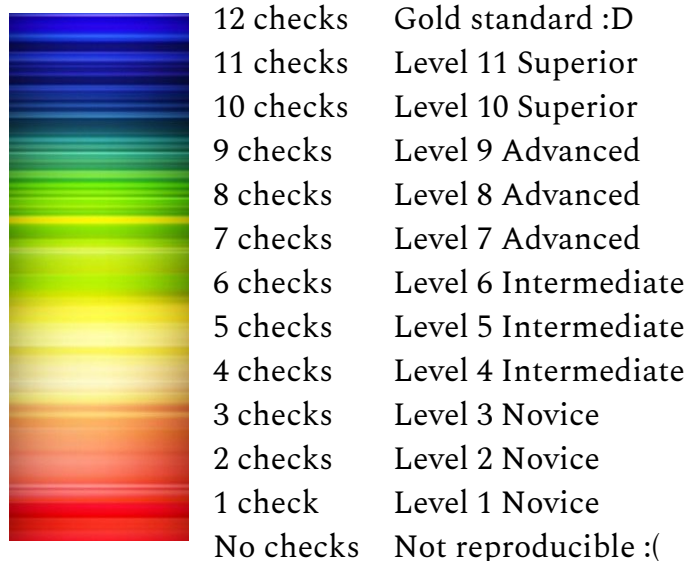
Licensed under the Creative Commons Attribution 4.0 International License.

# Reproducibility as a spectrum

Remember that reproducibility is a spectrum - it is not all or nothing! Integrating one new best practice into your research nudges it up the spectrum. Let's see where we land on the spectrum today with a reproducibility check-up!

Reproducibility check-up:

- ☐ My project workspace is structured and organized, with a file naming convention.
- ☐ I have an updated project level README file that includes a file inventory.
- ☐ I have documented my data, such as a data dictionary or codebook.
- ☐ I register my study plan before I start (on PROSPERO, OSF, or other registry).
- ☐ I automate my analysis when I can, such as with a master script or using make.
- ☐ I have documented my software and computational environment with versions.
- ☐ I track the versions of my materials manually or using version control.
- ☐ All my research materials are backed-up in three locations.
- ☐ I share my analysis code.
- ☐ I share my data in a data repository.
- ☐ I share my study protocol.
- ☐ I follow reporting guidelines when writing my protocol and my report.



When considering which practice to bring into your workflow, adopt the practice that will benefit yourself first - as your future self is the most frequent reuser of your research.

# Workshop materials

## Links to recommended resources

Good enough practices in scientific computing. Wilson G, Bryan J, Cranston K, Kitze J, Nederbragt L, et al. (2017) Good enough practices in scientific computing. PLOS Computational Biology 13(6): e1005510. <https://doi.org/10.1371/journal.pcbi.1005510>

The Practice of Reproducible Research: Case Studies and Lessons from the Data-Intensive Sciences. Kitze J, Turek D, & Deniz F. (Eds.). (2018). Oakland, CA: University of California Press.

<https://www.gitbook.com/book/bids/the-practice-of-reproducible-research/details>

Jupyter Notebooks and reproducible data science. Woodbridge M, Sanz D, Mietchen D, & Mounce R (2017).

<https://markwoodbridge.com/2017/03/05/jupyter-reproducible-science.html>.

## Lessons learned: testing reproducibility

Following Open Data Day 2017, Mark Woodbridge, Daniel Sanz, Daniel Mietchen, & Ross Mounce published a blog post called “Jupyter Notebooks and reproducible data science”. Their informal experiment was:

- Search PMC for papers that include research notebooks called Jupyter Notebooks -> 107 papers
- Attempt to rerun the notebook to reproduce the findings of the published paper.
- Only able to reproduce one research notebook.
- “My initial thought was that analysing the validity of the notebooks would simply involve searching the text of each article for a notebook reference, then downloading and executing it ... It turned out that this was hopelessly naive...”
- Sharing alone does not guarantee reproducibility.
- The lessons they outline in the blog post are the framework for our workshop.

# Organization

“It takes some effort to organize your research to be reproducible... the principal beneficiary is generally the author herself.” - Jon Claerbout

Source: <http://sepwww.stanford.edu/oldsep/matt/join/redoc/web/iris.html>

## Woodbridge et al. identified organizational barriers to reproducibility.

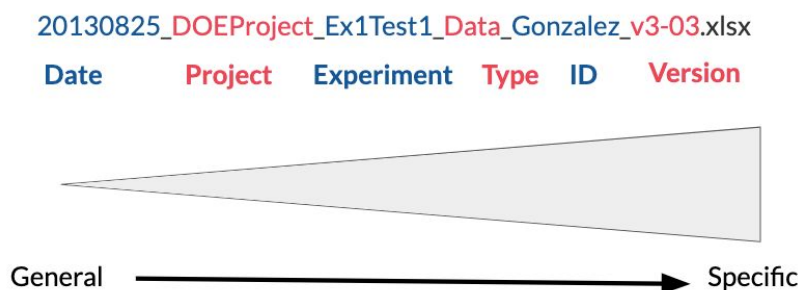
1. Files, data, dependencies needed to reproduce the findings were often missing.
2. Difficulty locating and identifying necessary materials.

## We can organize for reproducibility:

- ❑ Create a structured and centralized workspace for your project.  
Source: Karl Broman: <http://kbroman.org/steps2rr/pages/organize.html>
- ❑ Create subdirectories for like materials: separate data, code, and results.

- ❑ Always keep raw data.
- ❑ Always backup materials in three unique locations.
- ❑ Adopt an informative naming convention for your files. Source: <http://guides.lib.purdue.edu/c.php?g=353013&p=2378292>

```
.
|-- CITATION
|-- README
|-- LICENSE
|-- requirements.txt
|-- data
|   -- birds_count_table.csv
|-- doc
|   -- notebook.md
|   -- manuscript.md
|   -- changelog.txt
|-- results
|   -- summarized_results.csv
|-- src
|   -- sightings_analysis.py
|   -- runall.py
```



- ❑ Create a protocol using PRISMA-P (<http://www.prisma-statement.org/>).
  - ❑ Reporting guidelines by the Equator Network are developed through consensus by stakeholders to contain bias, maximize transparency, and create more useful research reports. <https://www.equator-network.org/>
  - ❑ Have your search strategy peer-reviewed and report it following PRISMA-S (<https://osf.io/ygn9w/wiki/home/>).
  - ❑ Include your analysis plan: how will you analyse your results?

- ❑ Submit your protocol for peer-review using Registered Reports:  
<https://osf.io/registries/discover?provider=OSF&q=systematic%20review&type=Registered%20Report%20Protocol%20Preregistration>
- ❑ Finding multiple data sources, guidance on how to:  
<https://onlinelibrary.wiley.com/doi/full/10.1002/jrsm.1277>
- ❑ Register the study plan with the OSF or PROSPERO before data extraction.
- ❑ Review available free systematic review tools to help organize your review:
  - ❑ Systematic Review Accelerator: <http://sr-accelerator.com/#/sra-helper>
  - ❑ Abstrackr: <http://abstrackr.cebm.brown.edu/>
  - ❑ CADIMA: <https://www.cadima.info/>
  - ❑ Find more at the Systematic Review Toolbox:  
<http://systematicreviewtools.com/index.php>

# Organization

Let's create a structured, centralized workspace for a research project. It will hold our data, code, research notebooks, documentation, etc.

Examples of OSF systematic reviews: <https://osf.io/vr94u/> and <https://osf.io/4k7zv/>.

## **Exercise 1: Create a workspace for your research.**

What tool we will use: Open Science Framework, [www.osf.io](http://www.osf.io). OSF is free, open source, and discipline agnostic. It allows private and public research projects and is integrated with commonly used organization and research tools such as Github, Google Drive, and Box.

1. Place a pink sticky note on your laptop.
2. Create an account at [www.osf.io](http://www.osf.io).
3. Click "Create New Project".
4. Type a title for your project. If you are practicing with your own research, choose a title based on your project. If you want to follow with an example, type "Ebola virus safety systematic review and meta-analysis".
5. Storage location should default to select United States.
6. Click "Create" and then "Go to project".
7. Place a green sticky note on your laptop when you have a project created.

## **Exercise 2: Centralize your research materials into your workspace.**

1. Place a pink sticky note on your laptop.
2. Go to <https://github.com/aprilcs/sr-ma>. These are adapted materials from a very simplified step-by-step Ebola virus systematic review paper: <https://link.springer.com/article/10.1186/s41182-019-0165-6>.
3. Click "Clone or download" and select "Download ZIP".
4. Once they have downloaded, unzip your materials.
5. Now navigate back to your OSF project.
6. Under "Files", select OSF Storage (United States).
7. Click "Upload" and select the files you downloaded.
8. Place a green sticky note on your laptop when you have uploaded your materials.

## **Exercise 3: Create subdirectories for like materials.**

1. Place a pink sticky note on your laptop.

2. Click “Add Components” and create components named “Code”, “Data”, and “Documents”.
3. From the file tree, drag and drop the protocol and PROSPERO template documents into “Documents”.
4. Place a green sticky note on your laptop when you have moved the materials.

**Exercise 4: Explore pre-registration and Registered Reports.**

1. Before you extract data, you should create a complete and transparent protocol using PRISMA-P guidelines. Planning your review in advance and registering your full plan combats publication bias, researcher degrees of freedom, and allows for feedback on your plan before you begin. Take a look at some Registered Reports:  
<https://osf.io/registries/discover?provider=OSF&q=systematic%20review&type=Registered%20Report%20Protocol%20Preregistration>
2. In your project, click “Registrations” and then click “New Registrations”. If you submitted your protocol for peer-review in a journal, you would register using the Registered Reports option. Otherwise, you can register using an Open-Ended OSF registration or using PROSPERO: <https://www.crd.york.ac.uk/PROSPERO/>.
3. Place a green sticky note on your laptop when you have reviewed the registration options.

# Documentation

## Woodbridge et al. identified missing documentation as a barrier to reproducibility

1. Dependencies were often not documented.
2. Documentation on how to reproduce the results was missing or inadequate.

### We can create documentation that improves reproducibility:

- ❑ Create a project level README file.
  - i. Resources on making a great README file from Cornell University (includes a template): [data.research.cornell.edu/content/readme](https://data.research.cornell.edu/content/readme)
  - ii. An example of a reproducible README in an AJPS Replication Package:  
[dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/EZSJ1S](https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/EZSJ1S)
  - iii. Resource on using markdown to create your README:  
[github.com/adam-p/markdown-here/wiki/Markdown-Cheatsheet](https://github.com/adam-p/markdown-here/wiki/Markdown-Cheatsheet)
- ❑ Document each element or variable in your dataset with a data dictionary.

Resources on making a great data dictionary:

  - i. DataONE:  
<https://www.dataone.org/best-practices/create-data-dictionary>
  - ii. McGill Codebook Cookbook:  
<http://www.medicine.mcgill.ca/epidemiology/joseph/pbelisle/CodebookCookbook.html>
  - iii. UPenn: <https://guides.library.upenn.edu/datamgmt/documentation>
  - iv. Karl Broman: <http://kbroman.org/dataorg/pages/dictionary.html>
- ❑ Track versions of materials manually, using version control systems like git, or by choosing a tool that has built in versioning such Google Docs or the OSF.
- ❑ Document analyses, software, computational environment, packages, and other dependencies with versions.
  - i. Specify your packages and dependencies with versions. Resource on documenting dependencies:  
[https://mybinder.readthedocs.io/en/latest/config\\_files.html](https://mybinder.readthedocs.io/en/latest/config_files.html)  
Python:      `pip freeze > ../code/requirements.txt`  
              `conda list --export > ../code/requirements.txt`  
R:             `install.R` and `runtime.txt`



- ❑ Consider using container technology. Source: Boettiger, Carl. An introduction to Docker for reproducible research. <https://doi.org/10.1145/2723872.2723882>. Containers solve:
  - i. Dependency Hell - Provides other researchers with a binary image in which all the software has already been installed, configured, and tested.
  - ii. Imprecise documentation - Provides a human readable summary of the necessary software dependencies needed to execute the code.
- ❑ Consider using literate programming to document the analysis narrative with the code in an executable document.
  - i. Shows what you did and why you did it in one document.
  - ii. Easily shared.
  - iii. Best start: Jupyter Notebooks or RMarkdown in RStudio.

**Exercise 5: Keep your files up-to-date.**

1. Place a pink sticky note on your laptop.
2. Upload and organize the rest of the materials you downloaded from Github (<https://github.com/aprilcs/sr-ma>).
3. Click on the README.md file in the file tree of your OSF project.
4. Click “Edit” and update the “Contact” section with your details.
5. Click “Save”.
6. Place a green sticky note on your laptop.

**Exercise 5: Collaborate using version control.**

1. Place a pink sticky note on your laptop.
2. While in your README file, click “Revisions”.
3. View and download the previous version of your README.
4. “Checkout” your protocol document.
5. Make a change to your protocol document locally on your computer, and upload it with the same name. How does the OSF track those changes?
6. Check it back in so others can edit if they wish.
7. Place a green sticky note on your laptop.

**Exercise 6: Explore literate programming.**

8. Place a pink sticky note on your laptop.
9. Join the Meta-analysis in R project using this link: [https://rstudio.cloud/spaces/50013/join?access\\_code=a1BbeJBM1srSePWE%2B2fbYH%2BKWTzwpRIuDYV5UcYS](https://rstudio.cloud/spaces/50013/join?access_code=a1BbeJBM1srSePWE%2B2fbYH%2BKWTzwpRIuDYV5UcYS).
  - a. Create a free account, and “join” the space.

- b. Click “Projects” -> meta-analysis
- 10. Add some narrative and a code chunk to the RMarkdown document:
  - a. Narrative in markdown: “We want a variable which only contains information if a study is a mindfulness intervention or not. The code above should have created a new variable of TRUE and FALSEs from the character intervention variable. The code below will compare the two and see if it worked correctly.”
  - b. R code chunk
    - c. ````{r check logical factors}`
    - d. `n <- data.frame(intervention.type.logical,metadata$`intervention type`)`
    - e. `names <- c("New", "Original")`
    - f. `colnames(n) <- names`
    - g. `head(n)`
    - h. `````
- 11. Click Knit to view the notebook in HTML or PDF.
- 12. Place a green sticky note on your laptop.

**Exercise 7: Explore documentation of computational environments.**

- 13. Place a pink sticky note on your laptop.
- 14. Return to <https://github.com/aprilcs/sr-ma>, click on “install.R” and then “runtime.txt”
- 15. Brainstorm what you think the runtime.txt file means.
- 16. Place a green sticky note on your laptop.

# Automation

## What Woodbridge et al. found:

1. Manual manipulation or setup was needed to reproduce results, often without documentation of how the results were produced.

## We can automate the execution of our analyses to improve reproducibility:

- ❑ Reproduce results automatically as a function of the data & the code.
- ❑ Use scripting languages when possible. Doing Meta-Analysis in R is a good starting guide: [https://bookdown.org/MathiasHarrer/Doing\\_Meta\\_Analysis\\_in\\_R/](https://bookdown.org/MathiasHarrer/Doing_Meta_Analysis_in_R/).
- ❑ Create a master script to execute all analyses in order. Resource on automation using a master script: [practicereproducibleresearch.org/core-chapters/3-basic.html](https://practicereproducibleresearch.org/core-chapters/3-basic.html)
  - ❑ Create a master script that executes your analysis scripts in order.
    - ❑ In R, use a run.r or main.r master script
      - ❑ Use source() to run your scripts
      - ❑ Run your install.r script
      - ❑ In your master script, use rmarkdown::render to render your RMarkdown document into your results directory.
    - ❑ In Python, use a main.py or run.sh master script
      - ❑ In your run.sh script, use nbconvert to execute your notebook into the results directory.
      - ❑ In your master script, use nbconvert to execute your notebook into your results directory.
- ❑ Use relative file paths rather than absolute file paths. Resource explaining paths by Karl Broman: <http://kbroman.org/steps2rr/pages/organize.html>.

## Exercise 8: Explore a master script

- Place a pink sticky note on your laptop.
- Join the Ebola virus vaccine R project using this link:  
[https://rstudio.cloud/spaces/50013/join?access\\_code=a1BbeJBM1srSePWE%2B2fbYH%2BKWTzwpRIuDYV5UcYS](https://rstudio.cloud/spaces/50013/join?access_code=a1BbeJBM1srSePWE%2B2fbYH%2BKWTzwpRIuDYV5UcYS).
  - Create a free account, and “join” the space.
  - Click “Projects” -> ebola-vaccine
- Create a new file (R Script).
  - Create a master script named “main.R” that runs your R scripts in this order: install.R, meta-analysis-ebola.R, and subgroup-analysis.R.
- Run and trouble-shoot the file until it works.
- Place a green sticky note on your laptop.

**Exercise 9: Create a reproducible repository with Binder.**

- Place a pink sticky note on your laptop.
- Go to <https://github.com/aprilcs/sr-ma> and click “Launch Binder”.
- Go to <https://mybinder.org/> and type “<https://github.com/aprilcs/sr-ma>” into the “GitHub repository name or URL” field.
- Place a green sticky note on your laptop.

# Dissemination

## What Woodbridge et al. found:

1. There is no standardized way of attaching materials to published articles.
2. Therefore it is difficult to discover and retrieve necessary materials.

We can share using repositories to make our research FAIR (findable, accessible, interoperable, and reusable):

- ❑ Write a report following PRISMA: <http://www.prisma-statement.org>
- ❑ Share data, such as in the Systematic Review Data Repository (SRDR.) <https://srdrr.ahrq.gov/>. It is a powerful and easy-to-use tool for the extraction and management of data for systematic review or meta-analysis. It is also an open and searchable archive of systematic reviews and their data.
- ❑ Share a link to a trusted repository that contains all our materials.
  - ❑ Obtain a DOI for your repository and use this link throughout your article.
    - ❑ Example: Github -> Binder -> Zenodo -> DOI linked in article.
  - ❑ Cross link repository with published article in metadata of each.
  - ❑ Mint a persistent identifier for your repository such as a DOI. This is unique and citable and persistent.
  - ❑ Archive the exact versions of the materials used for published findings.
  - ❑ Find & compare repositories through Repository of Research Data Repositories: <https://www.re3data.org/>.
- ❑ Specify a license for your data and your code and materials.
  - ❑ Creative Commons licenses are appropriate for data and text. CC-0 or CC-BY are recommended if you want reuse. Resource: <https://creativecommons.org/>.
  - ❑ Resource on choosing a data licence is the Digital Curation Center: <http://www.dcc.ac.uk/resources/how-guides/license-research-data>.
  - ❑ For software, permissive open source licenses such as the MIT, BSD, or Apache licenses promote reuse. Resource on choosing a code licence by Karl Broman: <http://kbroman.org/steps2rr/pages/licenses.html>.
    - ❑ Open Source Initiative: <https://opensource.org/licenses>
    - ❑ License picker: <https://choosealicense.com/>
- ❑ Consider new publishing models that counter publication bias in the research literature.
  - ❑ Preprints - Before you submit your paper for publication, post it for free on a preprint server such as arXiv: <https://arxiv.org/>. Peers can review your work, provide feedback, and you can ensure access to your work.

- ❑ Registered Reports - Before you start your study, a journal peer-reviews your pre-registration. Feedback to improve your study is provided before you begin. Journal accepts the study in principle based on theory, design, analyses. The study is published when done.
- ❑ Publish your methods and protocol. Source:  
<https://www.aje.com/en/arc/how-to-write-an-easily-reproducible-protocol/>
  - ❑ Think of protocol as brief, modular, self-contained scientific publication. Include 3-4 sentence abstract that puts methodology in context, include as much detail as possible.
  - ❑ Resources: A protocol sharing tool like [www.protocols.io](http://www.protocols.io) allows publish sharing, versioning, and commenting on scientific protocols.

**Exercise 11: Learn to mint a DOI for your repository.**

- Place a pink sticky note on your laptop.
- Return to your OSF project.
- Select “Make Public” if you wish to see how to mint a DOI. Do not do this if you uploaded your own data.
- Now you will see a “Create DOI” option for your project.
- Place a green sticky note on your laptop when you see the “Create DOI” option.

**Exercise 12: Pick a licence for your data and code and materials.**

- Place a pink sticky note on your laptop.
- Return to your OSF project.
- Select “Add a licence” for your top level project as well as your Data and Code components, one by one.
- From the licence picker, select the licenses you wish.
- Place a green sticky note on your laptop when you have chosen your licenses.