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# **Reproducibility Resources & Tools**

Data management

Harvard University Data Management page <a href="https://datamanagement.hms.harvard.edu">https://kbroman.org/dataorg</a> (Short primer on data storage and handling) Purdue Library <a href="http://guides.lib.purdue.edu/c.php?g=353013&p=2378292">http://guides.lib.purdue.edu/c.php?g=353013&p=2378292</a> (Short primer on data management and file naming conventions) Data One Best Practices <a href="https://www.dataone.org/best-practices">https://www.dataone.org/best-practices</a> (Detailed resource on how to handle data throughout its life-cycle) Best Practices for Biomedical Research Data Management MOOC <a href="http://bit.ly/HMS-RDM-MOOC">http://bit.ly/HMS-RDM-MOOC</a> (Online course aimed at a broad audience on recommended practices for managing research data)

Electronic Lab Notebooks (ELN)

Harvard University ELN guide <a href="https://tinyurl.com/Harvard-ELN">https://tinyurl.com/Harvard-ELN</a> (Great summary about current ELNs and what they do) Benchling <a href="https://benchling.com/">https://benchling.com/</a> (free) Evernote <a href="https://benchling.com/">https://benchling.com/</a> (free) Evernote <a href="https://benchling.com/">https://benchling.com/</a> (free) Evernote <a href="https://benchling.com/">https://benchling.com/</a> (free) Evernote <a href="https://benchling.com/">https://benchling.com/</a> (free and \$\$) Labguru <a href="https://benchling.com/">https://benchling.com/</a> (free and \$\$) SciNote <a href="https://benchling.com/">https://benchling.com/</a> (free) Open Science Framework <a href="https://benchling.com/">https://benchling.com/</a> (\$)

#### Code

Github <a href="https://github.com/">https://github.com/</a> (code repository; free for public repos)

**Jupyter Notebooks** <u>http://jupyter.org/</u> (open source web-app for creating & sharing live code, equations, and more)

**Code Ocean** <u>https://codeocean.com/</u> (computational reproducibility platform; free to upload, share & publish executable code with DOI; pay for more computing time over freemium limit)

**Conda and BioConda** <u>https://conda.io/docs/</u> and <u>https://bioconda.github.io/</u> (A operating system independent package environment manager for the command line) **Docker and Biocontainers** <u>https://docs.docker.com/</u> and <u>http://biocontainers.pro</u> (A container ecosystem to package code and data on the command line.

**Binder** <u>https://mybinder.org/</u> (A tool to make your github repository an online docker image run in the cloud)

**Galaxy** <u>https://usegalaxy.org/</u> (A web and graphic interface based bioinformatics platform. Needs local set-up for larger data handling.)

### Reagents

Addgene <a href="https://www.addgene.org/">https://www.addgene.org/</a> (nonprofit plasmid repository) CiteAb <a href="https://www.citeab.com/">https://www.addgene.org/</a> (antibody search engine with results sorted by citations) Quartzy <a href="https://www.quartzy.com/">https://www.quartzy.com/</a> (manage lab inventory) Resource Identification Portal (RRIDs) <a href="https://scicrunch.org/resources">https://scicrunch.org/resources</a> (unique identifired for antibodies, model organisms, and tools used in PubMed or PMC)

### Methods

**Bio-Protocol** <u>https://bio-protocol.org/</u> (A peer-reviewed protocol journal; free to read & publish)

**protocols.io** <u>http://protocols.io/</u> (an open access repository of science methods; free to read & publish)

### Data

DataDryad <u>http://datadryad.org/</u> (curated digital repository; free to access, \$120 to publish dataset up to 20GB) Figshare <u>http://datadryad.org/</u> (free digital repository, 5GB per file limit) Zenodo <u>https://zenodo.org/</u> (free digital repository; 50GB per dataset limit)

### Authoring

**Zotero** <u>https://www.zotero.org/</u> (free and open-source reference management software to manage bibliographic data and related research materials)

**Mendeley** <u>https://www.mendeley.com/</u> (free desktop & web program reference manager) **RefWorks** <u>https://refworks.proquest.com/</u> (web-based commercial reference management software package)

**Authorea** <u>https://www.authorea.com/</u> (free online real-time collaborative writing & publishing system with unlimited collaborators)

**Overleaf** <u>https://www.overleaf.com/</u> (free online collaborative writing & publishing system)

**Manuscripts** <u>https://www.manuscriptsapp.com/</u> (offline Mac app authoring tool; free unlimited usage)

## Practical tips for reproducibility

- 1. Plan for reproducibility before you start
  - a. Write a study plan or protocol and track new versions.
  - b. **Set-up a reproducible project** using an electronic lab notebook to organize and track your work. Avoid saving proprietary file formats.
- 2. Keep track of things
  - a. **Preregister** important study design and analysis information. Free tools to help you make your first registration include <u>AsPredicted</u>, <u>Open Science Framework</u>, and <u>Registered Reports</u>. Clinical trials use <u>Clinicaltrials.gov</u>.
  - b. **Track changes** to your files using version control.
  - c. **Document** everything done by hand in a README file and data dictionary. **Karl Broman's Data Organization**: <u>http://kbroman.org/dataorg/pages/dictionary.html</u>
- 3. Report your research transparently
  - a. Share your protocols and interventions explicitly and transparently.
  - b. Write a transparent report. Guidelines from the <u>Equator Network</u> or processes like <u>Registered Reports</u> can help.
  - c. **Collect, organize, cite, and share research** with reference management tools <u>Mendeley</u>, <u>RefWorks</u> or <u>Zotero</u>. **Collaborate on manuscripts** using collaborative writing and publishing systems including <u>Authorea</u> and <u>Overleaf</u>.
- 4. Archive & share your materials

#### a. Share and licence your research

- i. Data
  - 1. Avoid supplementary files, licence, and share your data using a repository. **How to License Research Data**:

http://www.dcc.ac.uk/resources/how-guides/license-research-data.

- ii. Materials & reagents
  - 1. Licence your published materials so they can be reused. **Creative Commons License Picker**: <u>https://creativecommons.org/choose/</u>
  - 2. Deposit reagents with repositories like <u>Addgene</u>, <u>The Bloomington</u> <u>Drosophila Stock Center</u>, and <u>ATCC</u> to make them easily accessible to other researchers.
- iii. Software
  - 1. Licence your code using <u>Code Ocean</u> or <u>Github</u>. **Open Source** Licences: <u>https://opensource.org/licenses</u>.

- 5. Further reading:
  - Ten Simple Rules for Reproducible Computational Research: <u>http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1003285</u>
  - Reproducibility in Science: <u>http://ropensci.github.io/reproducibility-guide/</u>
  - Open Science MOOC: <a href="https://opensciencemooc.eu/">https://opensciencemooc.github.io/site/Resources/#three</a>
  - Tools and Resources for Reproducibility Series at protocols.io: <u>goo.gl/r7GKMA</u>
  - Managing Laboratory Notebooks <a href="http://colinpurrington.com/tips/lab-notebooks">http://colinpurrington.com/tips/lab-notebooks</a>
  - General File and Folder Organization
    https://zapier.com/blog/organize-files-folders/
  - File Naming Conventions http://www.exadox.com/en/articles/file-naming-convention-ten-rules-best-practice
- 6. Example studies:
  - Gene family innovation, conservation and loss on the animal stem lineage
    - Paper: https://doi.org/10.7554/eLife.34226
    - Protocols: <u>dx.doi.org/10.17504/protocols.io.kwscxees</u>
    - Data: https://doi.org/10.6084/m9.figshare.5686984.v2
  - A robust method for transfection in choanoflagellates illuminates their cell biology and the ancestry of animal septins
    - Paper: <u>https://doi.org/10.1101/343111</u>
    - Protocols: <u>http://www.protocols.io/groups/king-lab</u>
    - Constructs: <u>http://www.addgene.org/Nicole\_King</u>
  - Implicating candidate genes at GWAS signals by leveraging topologically associating domains
    - Paper: <u>https://dx.doi.org/10.1038/ejhg.2017.108</u>
    - Code: <u>https://zenodo.org/record/163950#.W0hqTdJKjIU</u>
    - Docker workflow: <u>https://zenodo.org/record/166556#.W0hqc9JKjIU</u>
  - mcSCRB-seq: sensitive and powerful single-cell RNA sequencing
    - Protocol: <u>dx.doi.org/10.17504/protocols.io.p9kdr4w</u>
    - Paper: <u>https://doi.org/10.1101/188367</u>
    - Code: <u>https://github.com/cziegenhain/Bagnoli\_2017</u>
  - TransRate: reference-free quality assessment of de novo transcriptome assemblies
    - Paper: <u>https://dx.doi.org/10.1101%2Fgr.196469.115</u>
    - Code: <u>https://github.com/Blahah/transrate</u>
    - Tutorial: <u>http://hibberdlab.com/transrate/</u>
  - Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters
    - Paper: <u>https://doi.org/10.1038/ismej.2016.43</u>

- Code: <u>https://github.com/Kirk3gaard/Publications</u>
- Experimenting with Reproducibility: a case study of Robustness in **Bioinformatics** 
  - Paper: <u>https://doi.org/10.1093/gigascience/giy077</u>
  - Code: https://github.com/sje30/waverepo
- A Bayesian Mixture Modelling Approach For Spatial Proteomics
  - Paper: <u>https://doi.org/10.1101/282269</u>
  - Code: <u>https://github.com/lgatto/2018-tagm-paper</u>

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Code ocean

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