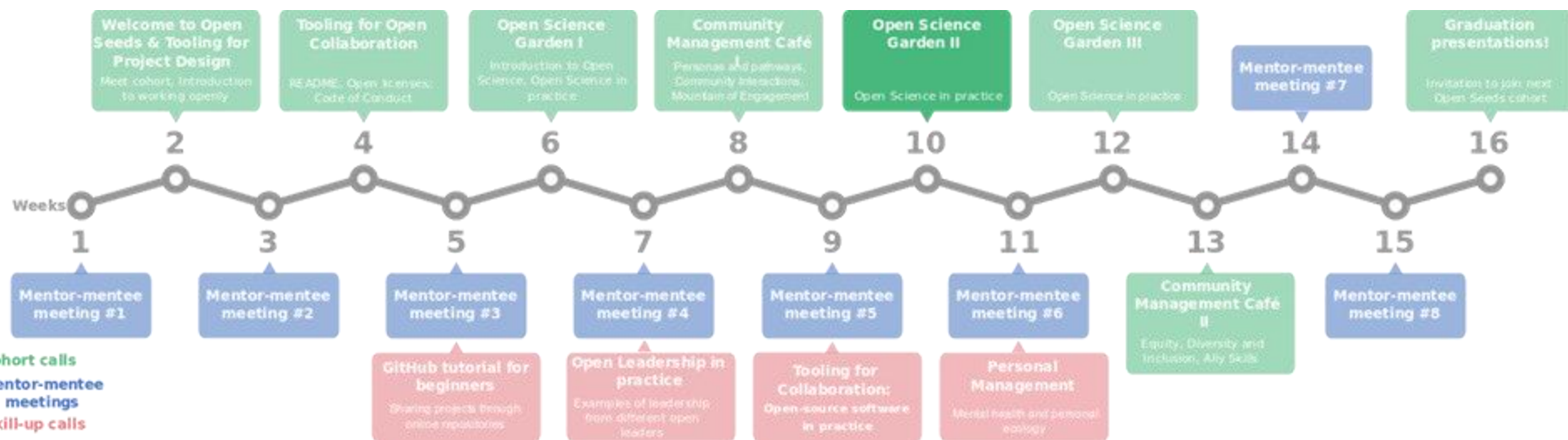




Open Seeds by OLS

Open Science
Garden(s)





Open Science in Open Seeds

3 calls: **Open Science Gardens**

- 3 talks per calls covering each 1 Open Science Element
- Discussion and reflections around Open Science practice



Illustration by The Turing Way and Scriberia shared under a CC 4.0 licence.

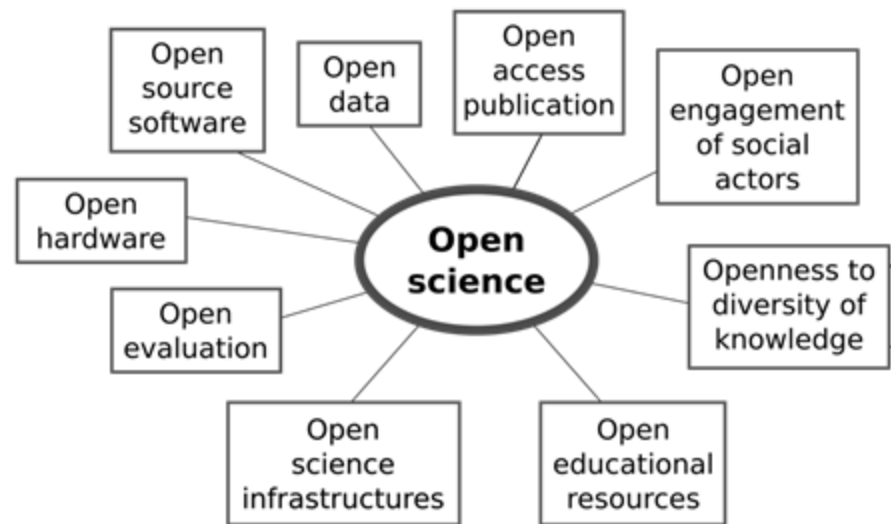


Illustration by Robbielan Morrison. Used under a CC 4.0 licence.

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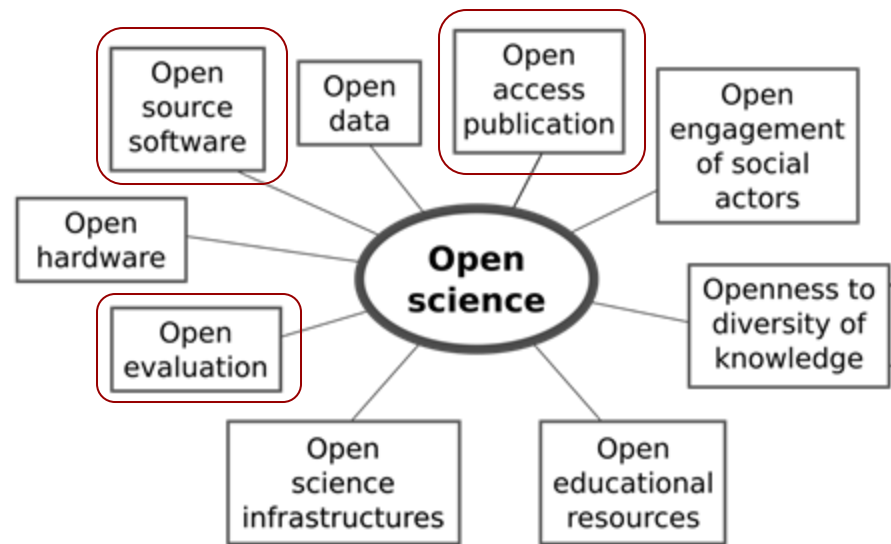


Illustration by Robbielan Morrison. Used under a CC 4.0 licence.

Additional slides on other aspects of research outcomes
that are reviewed / evaluate

Reporting guidelines

Resources that **guide authors in reporting** the minimum information needed to ensure a **manuscript can be understood and replicated**.

- **Checklists**, flow diagrams or text summaries.
- Domain-specific, e.g. **ARRIVE** guides the reporting of research involving animals.
- The EQUATOR library of reporting guidelines: www.equator-network.org

Is the information provided in a manuscript sufficiently comprehensive to inform the review process?

Percie du Sert et al. The ARRIVE guidelines 2.0: Updated guidelines for reporting animal research (2020) PMID: 32663219

ARRIVE Essential 10		
Study design	1	For each experiment, provide brief details of study design including: a. The groups being compared, including control groups. If no control group has been used, the rationale should be stated. b. The experimental unit (e.g., a single animal, litter, or cage of animals).
Sample size	2	a. Specify the exact number of experimental units allocated to each group, and the total number in each experiment. Also indicate the total number of animals used. b. Explain how the sample size was decided. Provide details of any a priori sample size calculation, if done.
Inclusion and exclusion criteria	3	a. Describe any criteria used for including and excluding animals (or experimental units) during the experiment, and data points during the analysis. Specify if these criteria were established a priori. If no criteria were set, state this explicitly. b. For each experimental group, report any animals, experimental units, or data points not included in the analysis and explain why. If there were no exclusions, state so. c. For each analysis, report the exact value of n in each experimental group.
Randomisation	4	a. State whether randomisation was used to allocate experimental units to control and treatment groups. If done, provide the method used to generate the randomisation sequence. b. Describe the strategy used to minimise potential confounders such as the order of treatments and measurements, or animal/cage location. If confounders were not controlled, state this explicitly.
Blinding	5	Describe who was aware of the group allocation at the different stages of the experiment (during the allocation, the conduct of the experiment, the outcome assessment, and the data analysis).
Outcome measures	6	a. Clearly define all outcome measures assessed (e.g., cell death, molecular markers, or behavioural changes). b. For hypothesis-testing studies, specify the primary outcome measure, i.e., the outcome measure that was used to determine the sample size.
Statistical methods	7	a. Provide details of the statistical methods used for each analysis, including software used. b. Describe any methods used to assess whether the data met the assumptions of the statistical approach, and what was done if the assumptions were not met.
Experimental animals	8	a. Provide species-appropriate details of the animals used, including species, strain and substrain, sex, age or developmental stage, and, if relevant, weight. b. Provide further relevant information on the provenance of animals, health/immune status, genetic modification status, genotype, and any previous procedures.
Experimental procedures	9	For each experimental group, including controls, describe the procedures in enough detail to allow others to replicate them, including: a. What was done, how it was done, and what was used. b. When and how often. c. Where (including detail of any acclimatisation periods). d. Why (provide rationale for procedures).
Results	10	For each experiment conducted, including independent replications, report: a. Summary/descriptive statistics for each experimental group, with a measure of variability where applicable (e.g., mean and SD, or median and range). b. If applicable, the effect size with a confidence interval.
<p>Explanations and examples for items 1 to 10 are available in the E&E document [42] and on the website at https://www.arriveguidelines.org.</p> <p>Abbreviations: ARRIVE, Animal Research: Reporting of In Vivo Experiments; E&E, Explanation and Elaboration</p> <p>https://doi.org/10.1371/journal.pbio.3000410.t001</p>		

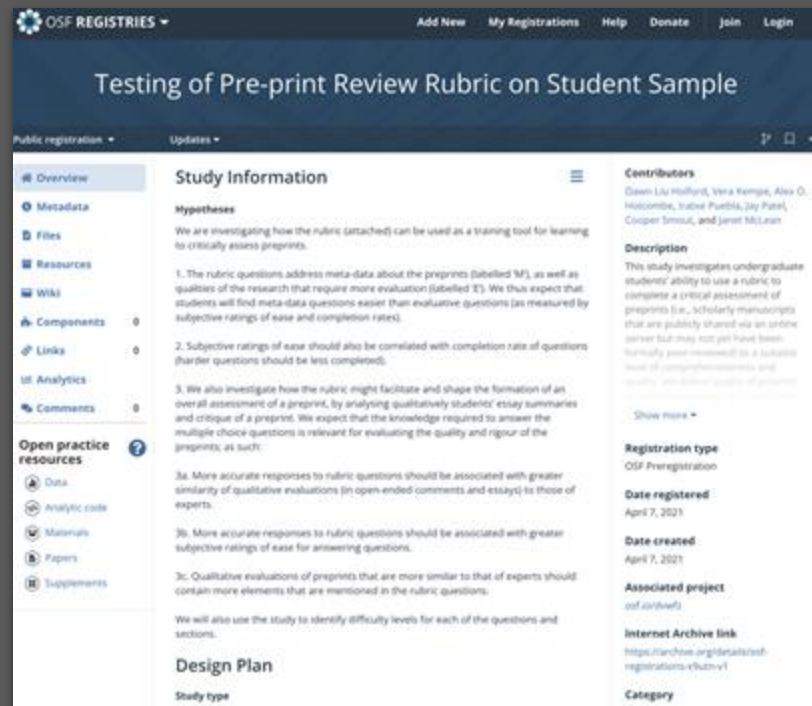
Preregistrations

Specifying research plan and sharing on an open registry (like OSF Registry) before the study occurs.

Trial registration

Clinical trials must be registered in a public registry (like clinicaltrials.gov) at or before the time of first patient enrollment. The manuscript should report the trial registration number.

Recommendations by the International Committee of Medical Journal Editors (ICMJE)



When reviewing a paper, if the study is preregistered, it is useful to look at the preregistration record, to check that the stated hypothesis and analytical approach followed the plans.

Registered Reports

Registered Reports (RR)

Manuscript that reports the study rationale and design prior to data collection, such as Introduction and Methods, but no Results

Some journals consider RR for publication:
*If accepted, the **journal commits to publishing the manuscript reporting the findings**, independent of the direction of the results, provided the study was completed as outlined in the initial plan*



www.cos.io/initiatives/registered-reports

A review of a stage 1 Registered Report is restricted to the **rationale and methodology**.

A review of stage 2 Registered Report, the focus lies on checking that the **study was completed** as initially outlined.

Thanks to **Dr. Priya Silverstein** for Q&A with me: <https://www.priyasilverstein.com>

Protocols

Researchers may share the **full description of their methodologies or protocols** separately from the main paper:

- Protocols.io, a platform dedicated to sharing protocols, make them available under a CC BY license
- Preprint or online under open license
- Openly shared repository

When reviewing a paper, check if the protocol has been shared and see if it is cited in the manuscript. This is the most relevant to the Methods section.

The screenshot shows the Protocols.io website interface. At the top, there is a navigation bar with the Protocols.io logo, a cat icon, and links for FEATURES, PLANS, BLOG, and CASE STUDY. Below the navigation bar, the main content area displays a protocol titled "De novo transcriptome assembly workflow" by Jared Mamrot et al. The protocol is associated with Scientific Reports and has a DOI of dx.doi.org/10.17504/protocols.io.ghebt3e. The protocol was published on March 06, 2017. The authors listed are Jared Mamrot, Roxane Legale, Stacey J Elery, Trevor Wilson, Tarsten Seemann, David Gardner, David W Walker, Peter Temple-Smith, Anthony T Papenfuss, and Hayley Dickinson. The protocol is associated with the Hudson Institute of Medical Research. The protocol is available under a CC BY license. The protocol is categorized under "OTHER". The protocol is available in the "STEPS" tab, which shows the abstract and the first step of the protocol. The abstract describes the production of a reference-quality de novo transcriptome assembly for the spiny mouse (Acomys cahirinus). The first step of the protocol is "Import and organise raw data", which involves downloading raw data from the NCBI to a working directory and archiving a copy (read-only). The step includes a list of commands and a link to the Aspera connect software.

www.protocols.io/view/de-novo-transcriptome-assembly-workflow-ghebt3e

Data and code

Authors should share **data and code** for their study

- Best practice is to share on repository in citable format - **persistent identifier**
- As supporting information files: “**As open as possible**, as closed as necessary”
- **FAIR framework**: FIndable, Accessible, Interoperable, Reusable

When reviewing a paper, **check that datasets and code are FAIR**: Are the reused datasets & code cited? Are data generated in the study shared online / in supporting information files?

Raise any issues of availability, completeness or accuracy.

