

DATA SHARING

Share/cite the data

- Your data/code/report should have Digital object identifier (DOI), a unique number that identifies the digital object
- Equivalent of an international standard book number (ISBN) for digital documents
- Allows citation of a dataset

Data repositories

- **Dataverse** (<http://thedata.org>): A repository for research data that takes care of long-term preservation and good archival practices, while researchers can share, keep control of, and get recognition for their data
- **Zenodo** (<http://zenodo.org>): A repository service that enables researchers, scientists, projects, and institutions to share data, publications, posters, images, software etc., with DOI
- **Dryad** (<http://datadryad.org>): A repository that aims to make data archiving as simple and as rewarding as possible through a suite of services not necessarily provided by publishers or institutional websites

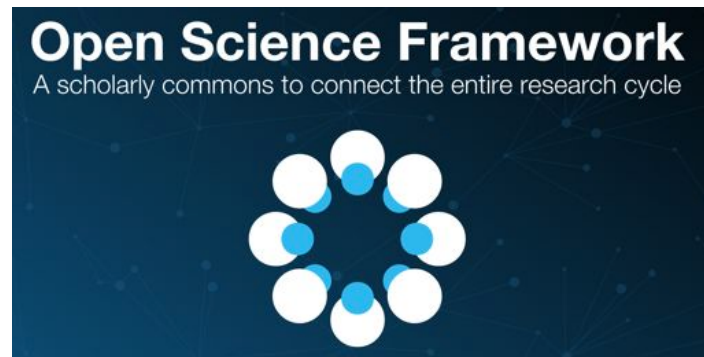
Data repositories

- **Mendeley Data** (<https://data.mendeley.com/>): Share everything, with DOI. Private sharing. *Example:* Genotype data for a set of 163 worldwide populations, <https://data.mendeley.com/datasets/ckz9mtgrjj/1>
- **FigShare** (<http://figshare.com>): Primarily for image data, but users can upload anything
- **SlideShare** (<http://www.slideshare.net/>): Share presentations, viewable and downloadable

Data for reproducible research



<https://cos.io/>



<https://osf.io/>

- Integration with nearly all data/code storage/sharing systems (Google Drive, Dropbox, Github etc.), reference managers (Mendeley, Zotero)

Example: Presentations, <https://osf.io/k39se/>

Publishing with open data/code



Genetic Heterogeneity: Networks and Pathways

CoMEt: Combinations of Exclusive Alterations

CoMEt identifies combinations of exclusive mutations *de novo* using a statistical score for exclusivity.

[More information](#)

[Download \(GitHub\)](#)

[Reference](#)

[Google Group](#)

HotNet2: Network Analysis of Mutation Data

HotNet2 is an algorithm for the discovery of significantly mutated subnetworks in a protein-protein interaction network.

[More information](#)

[Download \(GitHub\)](#)

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MacManes MD, Eisen MB (2013). **Improving transcriptome assembly through error correction of high-throughput sequence reads.**

[Journal](#) [PubMed](#) [PMC](#) [Data:DRYAD](#) [Software:SCRIPTS](#)

Moses AM, Pollard DA, Nix DA, Iyer VN, Li XY et al. (2006). **Large-scale turnover of functional transcription factor binding sites in *Drosophila*.**

[Journal](#) [PubMed](#) [PMC](#) [Software:CisEvolver](#)