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**Making Biomedical Research
Software Findable, Accessible,
Interoperable, Reusable (FAIR)
with FAIRshare**

**fairdataihub.org
calmi2.org**

Why Make Software Reusable?

Software has become an essential part of biomedical research

Data processing, analysis, visualization, computational modeling, etc.



Research software: Python scripts, Jupyter notebooks, R code, Web apps, etc. that are integral parts of a research outcome.

Making research software reusable is therefore crucial to:



Ensure reproducibility of research results



Increase the pace of scientific progress

What's the Problem?

No clear actionable guidelines are available to make software reusable!

The FAIR4RS Principles provide a framework but remain general, for example:

- “Software is described with **rich metadata**”
- “Software must have a **clear and accessible license**”

Review of the 4,000+ biomedical repositories created in 2021 on GitHub:



97%

Don't have a
license specified



100%

Don't have any standard
high-level metadata files
(codemeta.json or
CITATION.cff)

Our Solution: FAIR-BioRS guidelines

Actionable guidelines for making biomedical research software FAIR as per the FAIR4RS Principles

- Based on a review of relevant literature and resources (including NIH guidelines)

Details available in our preprint: <https://doi.org/10.1101/2022.04.18.488694>



- Open for community feedback
<https://github.com/fairdataihub/FAIR-BioRS-guidelines>

Our Solution: FAIRshare



Cross-platform desktop software

<https://github.com/fairdataihub/FAIRshare>



Open source and free (MIT license)



Goal: Simplify for researchers the process of making biomedical research data and software FAIR



How? Combine intuitive user interface and automation

Our Solution: FAIRshare

Includes a workflow for guiding users step-by-step into making their biomedical research software FAIR as per the FAIR-BioRS guidelines

- Works with software files located on the computer or on GitHub
- Provides convenient interface to enter metadata and automatically create codemeta.json and CITATION.cff files
- Provides intuitive interface to select a license and view license terms
- Supports sharing on Zenodo and Figshare
- And much more!

The screenshot displays the FAIRshare web application interface. At the top, the title bar reads "FAIRshare - Make your biomedical research data and software Findable, Accessible, Interoperable, and Reusable (FAIR)". Below the title bar is a navigation menu with "Edit", "View", "Window", and "Help". The main content area features a sidebar on the left with a DNA helix icon and a list of menu items: "Overview", "Curate & Share", "Manage Accounts", "Settings", "Documentation", "Contact Us", and "About". The main content area shows a workflow progress bar with eight steps: 1. Select data files, 2. Review standards, 3. Provide metadata, 4. Select a license, 5. Select repository, 6. Upload dataset, 7. Publish dataset, and 8. Register application. The current step is "Select repository", which is highlighted with a blue border. Below the progress bar, the text "Provide the location of the files you want to include in your research software dataset" is displayed. A question "Where are your research software files located?" is followed by two options: "My computer" (represented by a monitor icon) and "On GitHub" (represented by the GitHub logo). The "On GitHub" option is selected, indicated by an orange border. Below the options, the text "Continue to select the repository you want to use." is shown. At the bottom, there are two buttons: "« Back" and "Continue »". The FAIR DATA INNOVATIONS HUB logo is visible in the bottom left corner of the sidebar.

Takeaways

What do we need to do?

Optimize the **reusability** of biomedical research software

How do we do it?

Follow the **FAIR-BioRS guidelines**

What can make our life easy?

FAIRshare is available to assist

How can everyone help in this effort?

Use **FAIRshare** and **provide feedback** on the FAIR-BioRS guidelines!

Thank you!



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