

FAIR-BioRS: Actionable Guidelines for Making Biomedical Research Software FAIR

Bhavesh Patel¹, Sanjay Soundarajan¹, Hervé Ménager², Zicheng Hu³

¹CalMI² (San Diego, CA, USA), ²Institut Pasteur (Paris, France), ³UCSF (San Francisco, CA, USA)

What are research software?

- **Software created during the research process or for a research purpose**

- Any format, e.g.:



Python scripts

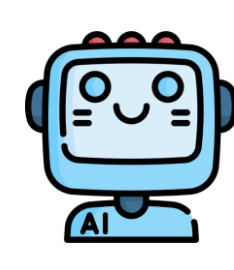


Desktop app

- Any purpose, e.g.:



Data analysis



AI/ML models

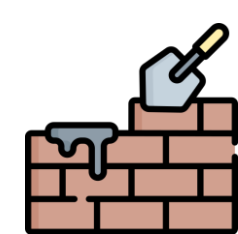
Making them reusable is important!



Ensure reproducibility of research outcomes



Prevent duplicate effort



Enable building on top of existing work



Increase the pace of discoveries and innovations

How to make research software reusable?

- The FAIR principles for research software (FAIR4RS principles) provide a general framework to optimize reusability
- Challenge: The FAIR4RS principles do not provide actionable instructions
- E.g., Principle F1 “Software is assigned a globally unique and persistent identifier” → What identifier? How to get one?

Light version of the FAIR-BioRS guidelines v2.0

Step 1: Prepare prior to the development of the software

- 1.1. Select a version control system platform to work from (e.g., **GitHub**).
- 1.2. Select a license and include the license terms in a file called “**LICENSE**” in **txt** or **md format**. It is highly recommended to use a license approved by the **Open Source Initiative** (OSI). Use choosealicense.com and/or the **SPDX License List** for help.

Step 2: Follow coding standards and best practices during development

- 2.1. Have **code-level documentation** (e.g., in code comments).
- 2.2. Record **dependencies** as per standard practices for the coding language, e.g., in a **requirements.txt** file for Python code.
- 2.3. Follow **language-specific standards** and best practices (e.g., PEP 8 Style Guide for Python Code, Google’s R Style Guide for R code, etc.) and document them (c.f. 3.2).
- 2.4. Ensure that the **inputs/outputs** of the software follow applicable community standards. Use fairsharing.org for finding relevant standards.

Step 3: Document software

- 3.1. Maintain the documentation in a file called “**README**” in **txt** or **md format**. Mature software may require additional, more sophisticated documentation.
- 3.2. Document changes between different versions of the software in a file called “**CHANGELOG**” in **txt** or **md format**. We suggest following the “**Keep a changelog**” conventions for the content and the **Semantic Versioning v2.0.0** for version numbers.

Step 4: Include metadata files

- 4.1. Include a **codemeta.json** metadata file in the root directory of the software.
- 4.2. Similarly include a **CITATION.cff** metadata file.

Step 5: Share software on a repository

- 5.1. If applicable, share on a **deployment repository** e.g., PyPI for Python packages.
- 5.2. Share the software on the **archival repository Zenodo** (suggested) or **Figshare**. The source code and metadata files mentioned above must be archived.
- 5.3. Archive the software repository on **Software Heritage** directly from your version control system platform.

Step 6: Register software on a registry

Register the software on the **bio.tools** registry. Optionally register the software on the **Research Resource Identifiers (RRID) Portal** as well.

Solution: Actionable guidelines

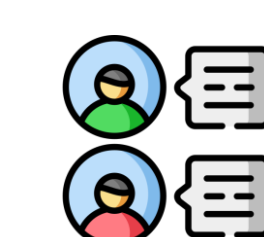
- We established clear actionable guidelines with specific instructions to comply with the FAIR4RS principles
- Method for establishing the guidelines:



Literature review



Our assessment



Community feedback

Cool, what’s next?

We need community support!

Let’s make biomedical research software FAIR together



Like the guidelines?
Use them!



Don’t like the guidelines?
Help improve them!

github.com/fair-biors

Reference: Making Biomedical Research Software FAIR: Actionable Step-by-step Guidelines with a User-support Tool, bioRxiv 2022.04.18.488694 – Accepted for peer-reviewed publication in Nature Scientific Data on July 13th, 2023

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bpatel@fairdataihub.org



fairdataihub.org

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