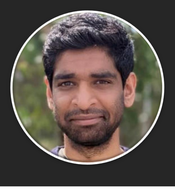
Making Biomedical Research Software FAIR with FAIRshare



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We all agree, biomedical research software must be made reusable

- Biomedical research software (Python scripts, R code, Jupyter notebooks, etc.) are integral part of research projects
- Making them reusable is therefore crucial to:
  - Ensure reproducibility of research results
  - Increase the pace of scientific progress

Cool, what's the problem then?

- No actionable guidelines are available to make software reusable!
- The FAIR Principles for research software (FAIR4RS) only provide a general framework to optimize reusability
- 4,000+ biomedical-related repos created on GitHub in 2021:

97% No license specified

100% No high-level metadata files

Solution: FAIR-BioRS guidelines

- First 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)

Step 1: Follow best practices during development — E.g., work from **GitHub**, include a **README** doc, etc.

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Step 2: Collect files to share — Include the **source code** when possible

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Step 3: Include metadata files — Include the standard **codemeta.json** and **CITATION.cff** metadata files

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Step 4: Choose a license — Use an **OSI-approved license**, preferably MIT or Apache 2.0

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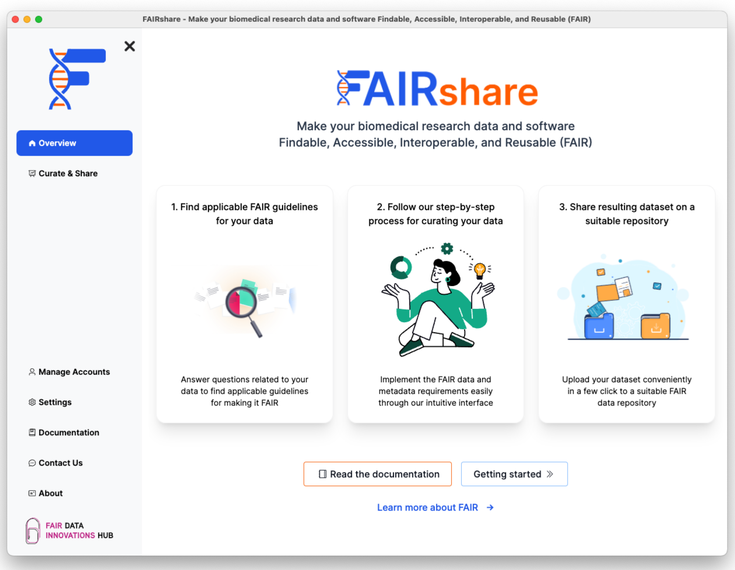
Step 5: Share software on a repository — Share on **Zenodo** or **Figshare** to obtain a DOI and make your software citable

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

User-support tool: FAIRshare



Like a tax filling tool but for "filling" FAIR research software and data

- Open source, free cross-platform desktop software
- Goal: Simplify the process of implementing the FAIR-BioRS guidelines for researchers
- How? Guide users through the process step-by-step via an intuitive user interface
- Include automation to take-over time-consuming and complex tasks

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Find this poster, references, and more here