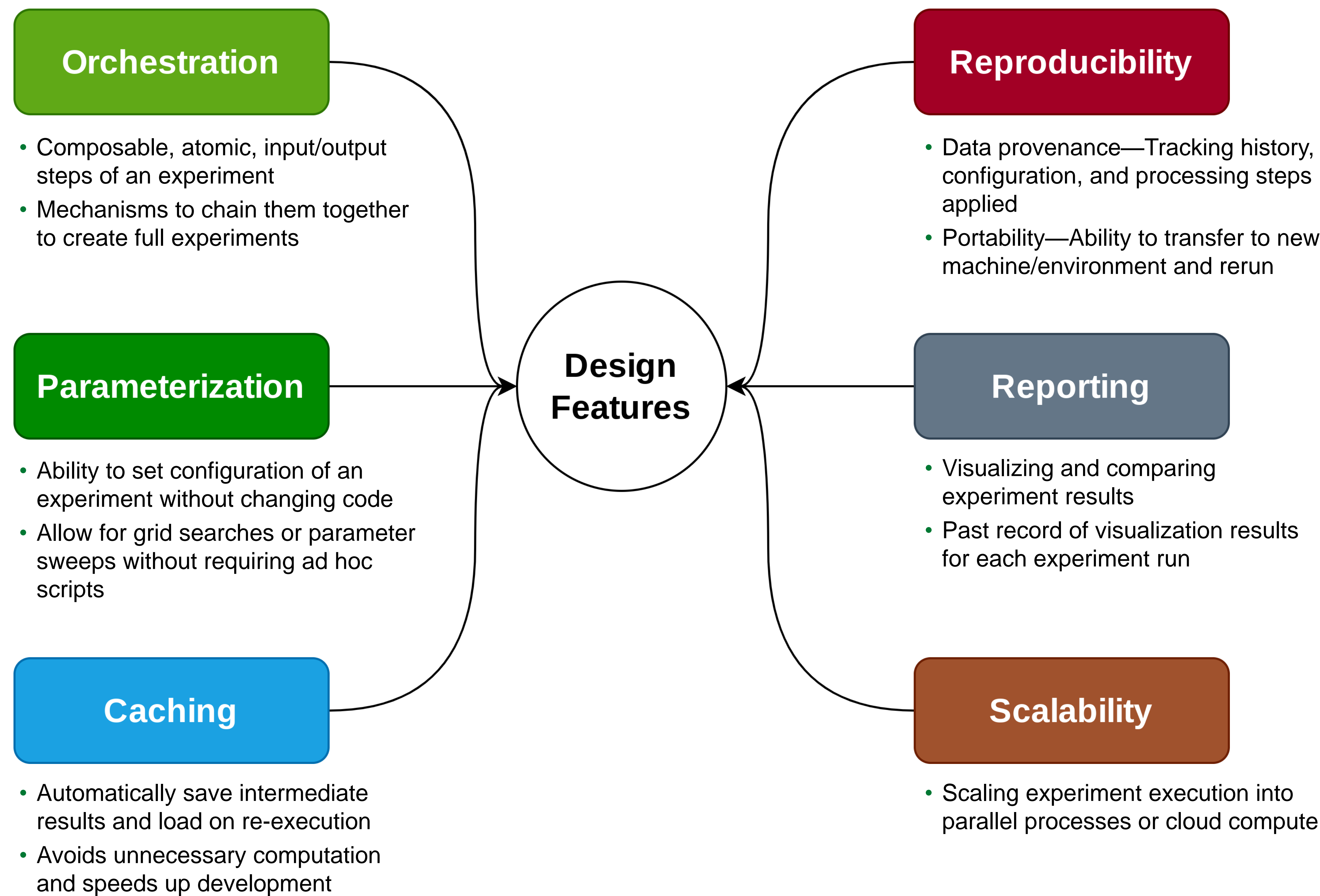
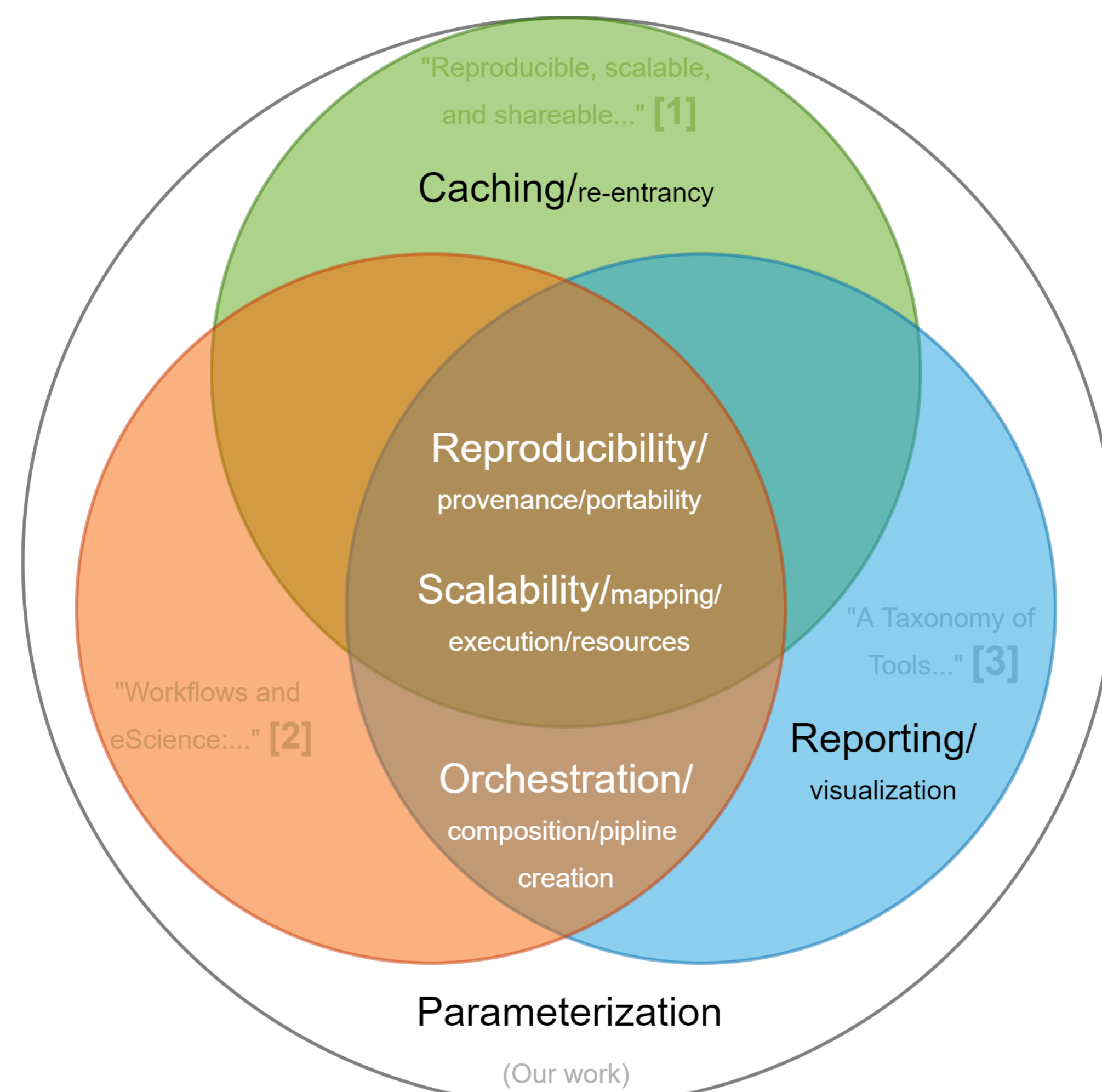


Reproducibility Crisis

- Complexity in software, environments, and lack of good software engineering principles in scientific domains has led to a reproducibility crisis in many computational research-based fields
- Resolving this requires infrastructure that supports good scientific and software practices
- Our work
 - surveys the literature for necessary design features and proposes a combination
 - analyzes design features of existing tools and proposes a new open-source tool, Curifactory

Concepts from Literature

- FAIRness principles
- Software engineering principles (testing, version control, agile)
- Compiled suggested design features from three other works on workflow/experiment management systems [1,2,3]



Existing Tooling

- DVC— Git-like interface for versioning datasets. Every compute input/output is a file, and caching/provenance is free
- MLFlow—STRONG MLOps tool, supporting entire data science life cycle, includes a powerful reporting dashboard and distributed computing
- Sacred—Allows parameterization directly in Python functions, user specification of observers for tracking metadata and artifacts
- Kedro—Ability to deploy to clusters, excellent web dashboard reporting and experiment visualization, ability to export entire project to docker container

	Orchestration	Parameterization	Caching	Provenance	Portability	Reporting	Scalability
DVC							
MLFlow							
Sacred							
Kedro							
Curifactory							

<https://github.com/ORNLCurifactory>

Curifactory

- **Orchestration**—Atomic level abstraction “stage,” a function with defined inputs and outputs. Stages chained/composed into experiment scripts
- **Parameterization**—Parameters defined and instantiated in Python scripts, allowing inheritance, composition, looping
- **Caching**—Stages provide easy mechanism to store and reload every output to disk. Re-running same experiment will reload rather than recompute
- **Reproducibility**—Metadata tracked every run. Ability to create full store of an experiment containing all information, output report, and every intermediate artifact. Ability to build docker container for specific run
- **Reporting**—Every run outputs HTML report with metadata and user-definable graphics
- **Scalability**—Runs with multiple parameter sets can be run in multiple processes
- Published with BSD-3 clause license, available on PyPI and GitHub

References

- [1] Laura Wratten, Andreas Wilm, and Jonathan Göke. Reproducible, scalable, and shareable analysis pipelines with bioinformatics workflow managers. *Nature Methods* 18(10):1161–1168, October 2021. doi:10.1038/s41592-021-01254-9.
- [2] Ewa Deelman, Dennis Gannon, Matthew Shields, and Ian Taylor. Workflows and e-Science: An overview of workflow system features and capabilities. *Future Generation Computer Systems*, 25:524–540, May 2009. doi:10.1016/j.future.2008.06.012.
- [3] Luigi Quaranta, Fabio Calefato, and Filippo Lanubile. A Taxonomy of Tools for Reproducible Machine Learning Experiments.

Acknowledgments

The authors would like to acknowledge the US Department of Energy, National Nuclear Security Administration's Office of Defense Nuclear Nonproliferation Research and Development (NA-22) for supporting this work