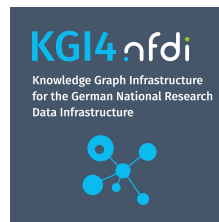
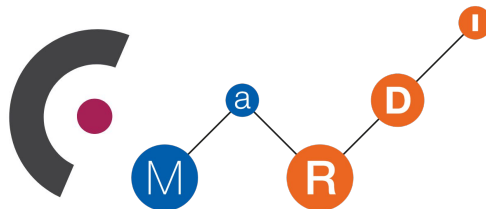


Analyzing the reproducibility of research-related Jupyter notebooks at scale



[Daniel Mietchen](#) ([FIZ Karlsruhe](#) & [MaRDI](#) & [KGI4NFDI](#)) & [Sheeba Samuel](#) ([TU Chemnitz](#))



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Outline

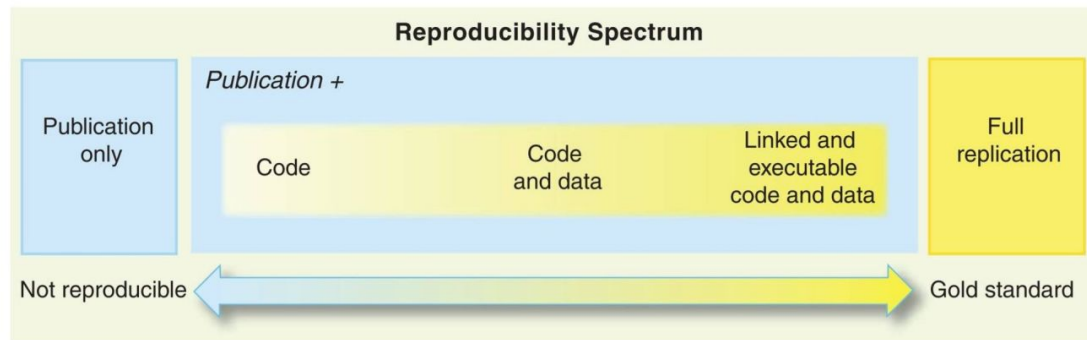
- What did we do?
- Why did we do this?
- How did we do this?
- Results
- What's next?
- Discussion

What did we do?

- We studied
 - the computational reproducibility
 - of 27,271 Jupyter notebooks
 - from 2,660 public GitHub repositories
 - associated with 3,467 peer-reviewed biomedical publications
 - from 740 journals

- Key concepts here

- computational reproducibility
- Jupyter notebook
- GitHub repository
- peer-reviewed publication
- PubMed Central
 - full-text XML of biomedical papers
 - <https://pmc.ncbi.nlm.nih.gov/>



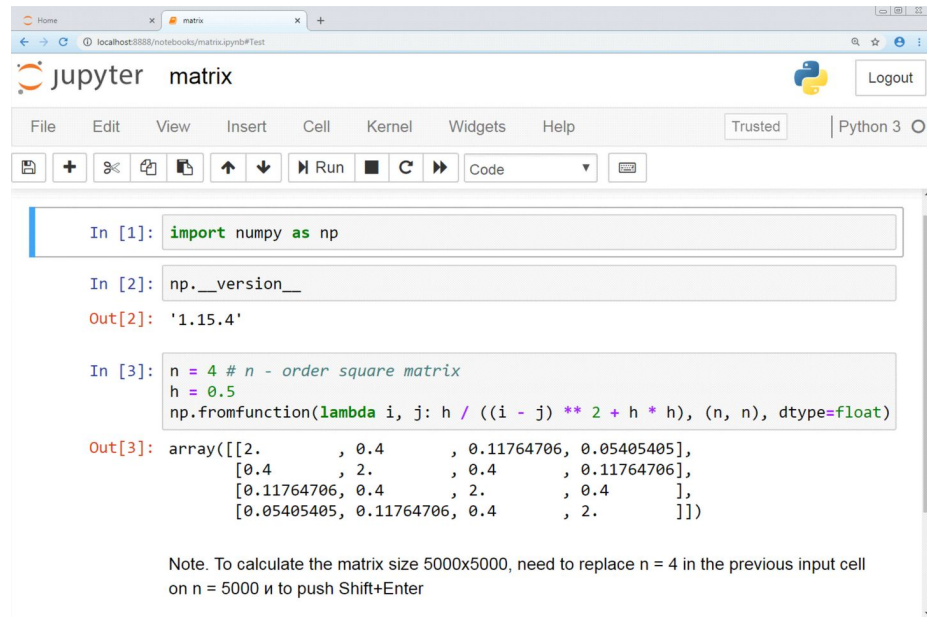
[Reproducible Research in Computational Science, Roger D. Peng, 2011]

What are Jupyter notebooks?

- They
 - provide a shared environment for
 - code
 - code execution
 - code comments
 - Markdown-based documentation
 - run on free and open-source software
 - can be shared conveniently
 - have been the subject of guidelines
 - can assist in enhancing computational reproducibility
 - prior studies found problems for generic Jupyter notebooks
 - perhaps this works better for Jupyter notebooks associated with peer-reviewed papers?

Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks

Adam Rule¹, Amanda Birmingham², Crista Zuniga³, Ilkay Altintas⁴, Shih-Cheng Huang^{4*}, Rob Knight^{3,5}, Niema Moshiri⁶, Mai H. Nguyen⁴, Sara Brin Rosenthal², Fernando Pérez⁷, Peter W. Rose^{4*}



The screenshot shows a Jupyter Notebook interface in a web browser. The browser address bar shows 'localhost:8888/notebooks/matrix.ipynb#Test'. The Jupyter logo and 'matrix' title are at the top. The interface includes a menu bar (File, Edit, View, Insert, Cell, Kernel, Widgets, Help) and a toolbar with icons for saving, opening, and running cells. The notebook content shows three input cells and one output cell. The first cell imports numpy as np. The second cell prints the numpy version, which is 1.15.4. The third cell defines a function to create a matrix of size n by n, where n is 4, and prints the result. The output shows a 4x4 matrix of floating-point numbers. A note at the bottom states: 'Note. To calculate the matrix size 5000x5000, need to replace n = 4 in the previous input cell on n = 5000 n to push Shift+Enter'.

```
In [1]: import numpy as np

In [2]: np.__version__
Out[2]: '1.15.4'

In [3]: n = 4 # n - order square matrix
        h = 0.5
        np.fromfunction(lambda i, j: h / ((i - j) ** 2 + h * h), (n, n), dtype=float)
Out[3]: array([[2.         , 0.4        , 0.11764706, 0.05405405],
               [0.4        , 2.         , 0.4        , 0.11764706],
               [0.11764706, 0.4        , 2.         , 0.4        ],
               [0.05405405, 0.11764706, 0.4        , 2.         ]])
```

Note. To calculate the matrix size 5000x5000, need to replace n = 4 in the previous input cell on n = 5000 n to push Shift+Enter

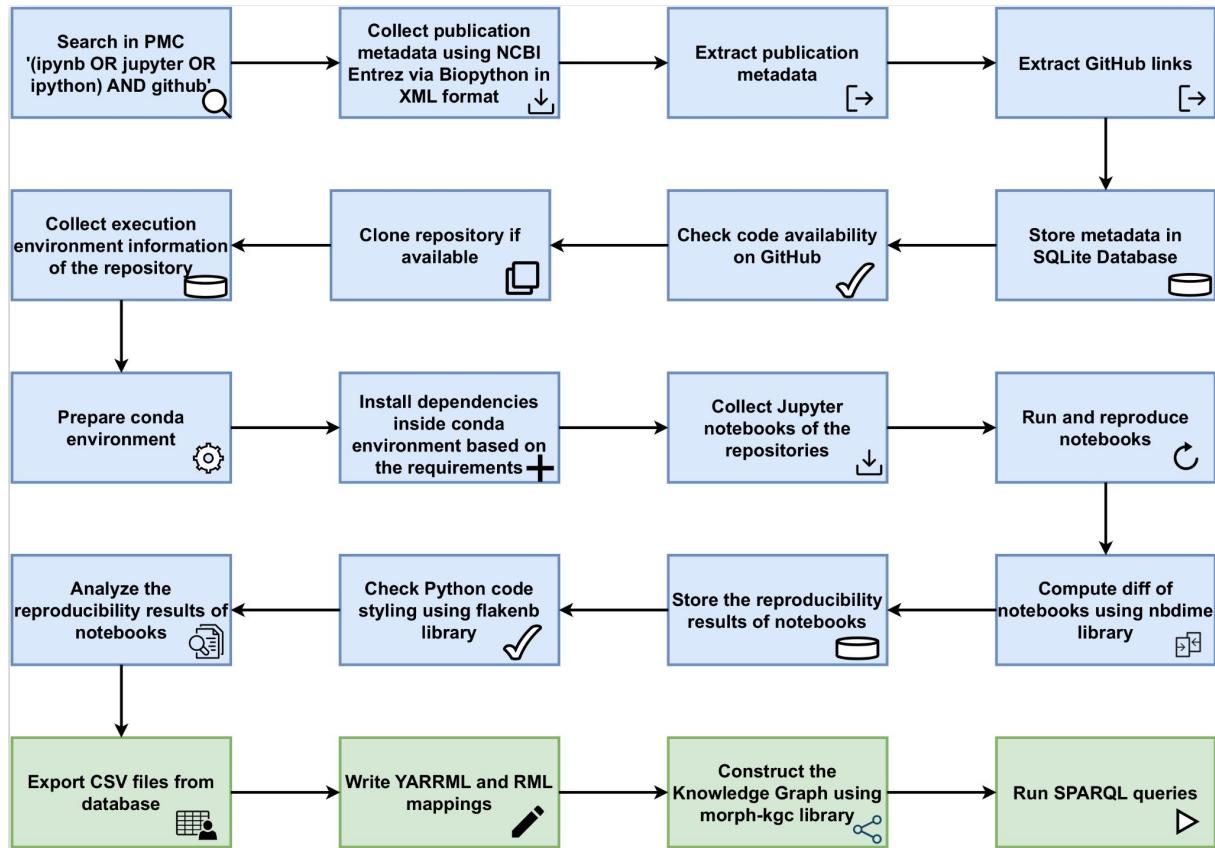
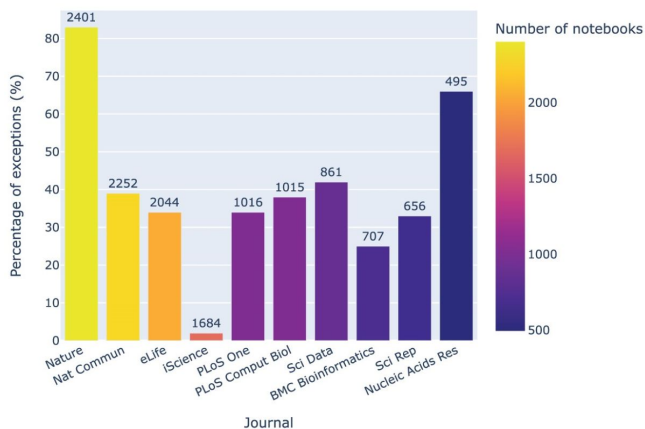
A Large-scale Study about Quality and Reproducibility of Jupyter Notebooks

João Felipe Pimentel*, Leonardo Murta*, Vanessa Braganholo*, and Juliana Freire†

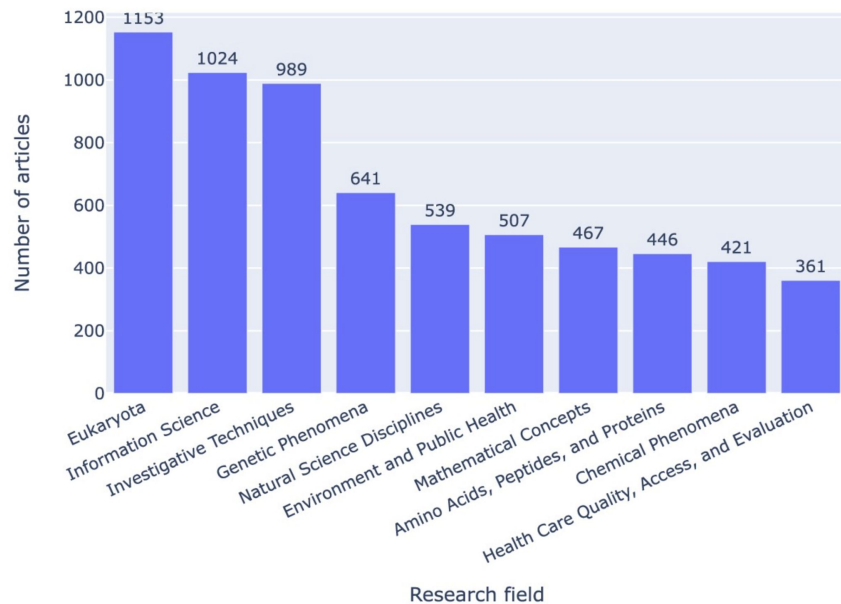
Why did we do this?

- We wanted to find out
 - How does the computational reproducibility of Jupyter notebooks work in practice?
 - What are common issues?
 - What are best practices?
 - How does computational reproducibility vary
 - by research field
 - by journal
 - over time
 - ...
 - because insights into these questions might affect research and education around
 - computational reproducibility
 - scientific reproducibility
 - (research) software engineering
 - software documentation
 - and related matters

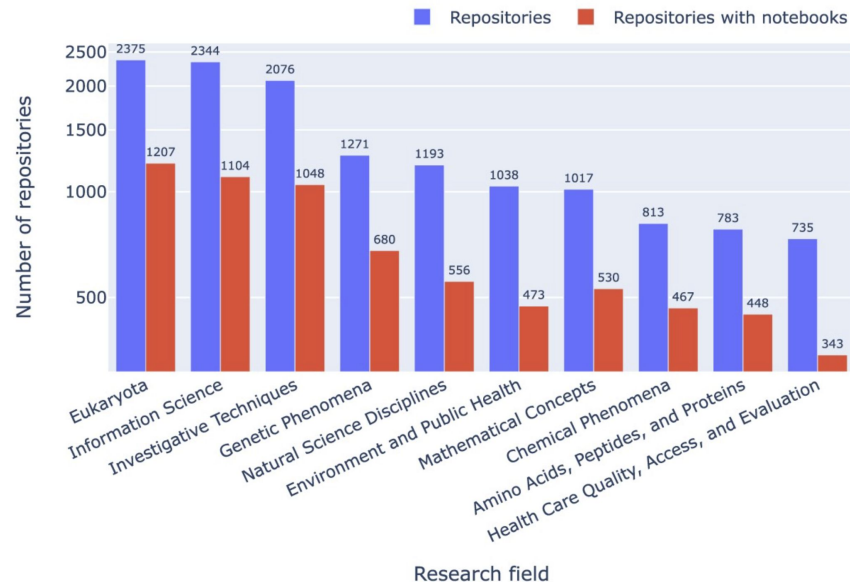
How did we do it?



Results - Research Field



SPARQL Query to reproduce the figure:
[Research articles by research field](#)



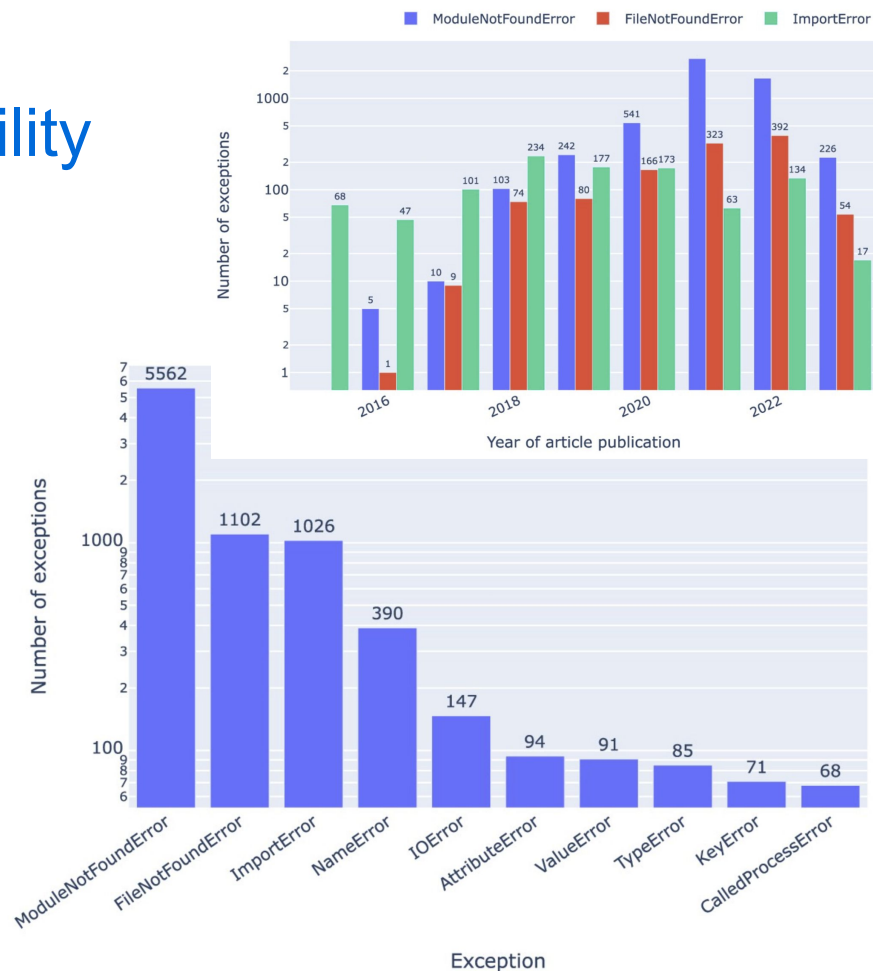
SPARQL Query: [Research field \(MeSH terms\) by the number of GitHub repositories that contain at least one Jupyter notebook.](#)

Results - Programming Languages of Jupyter notebooks

Notebook language	Rerun	Initial run	Ratio rerun/initial
Matlab	134	9	14.9
Julia	295	59	5.0
Unknown	3,112	720	4.3
Python	22,578	8,160	2.8
R	891	461	1.9
Bash	36	24	1.5
Sos	29	24	1.2
Groovy	95	95	1.0
Scala	29	29	1.0
Java	8	8	1.0

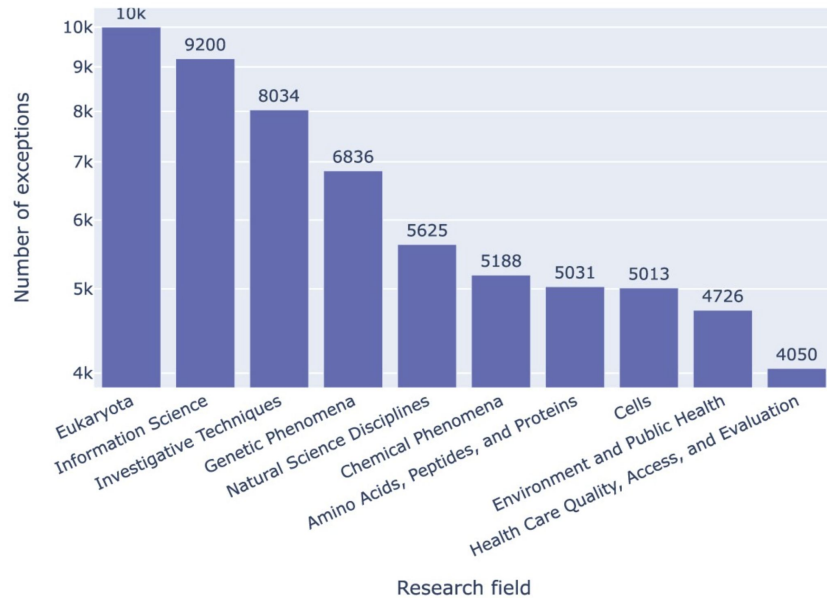
Results - Notebook Reproducibility

Features	Notebooks with different results	Notebooks with identical results
Number of notebooks	324 (151)	879 (245)
setup.py	0 (0)	344 (98)
requirement.txt	1 (0)	353 (107)
pipfile	0 (0)	0 (0)
Total cells	23 (17.9)	19.6 (17.1)
Code cells	15.4 (12.3)	11.3 (9.8)
Markdown cells	7.6 (5.6)	8.3 (6.7)
Ratio of Markdown vs. code cells	0.49 (0.46)	0.73 (0.68)
Empty cells	0.9 (0.7)	0.7 (0.7)
Differences	6.3 (5.3)	0 (0)
Execution time (s)	18.3 (22.1)	57.6 (16.4)
Execution time per code cell (s)	1.88 (1.80)	5.09 (1.67)

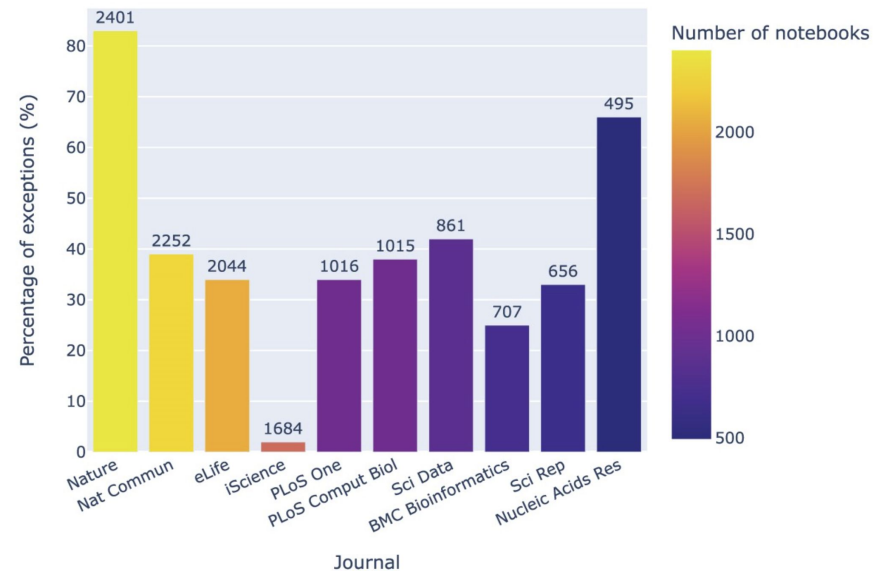


SPARQL Query: [Exceptions occurring in Jupyter notebooks in our corpus.](#)

Results - Notebook Reproducibility



SPARQL Query: [Jupyter notebook exceptions by research field, taking as a proxy the highest-level MeSH terms of the article associated with the notebook.](#)

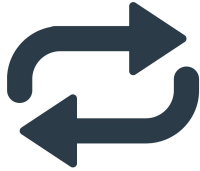


Effect of peer review and editorial workflows: Nature has about 50 *percent* more notebooks than iScience, but Nature's fail about 40 *times* more often

Environmental Footprint

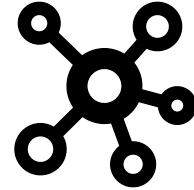
Simplified calculation: carbon footprint = energy needed * carbon intensity

(<http://calculator.green-algorithms.org/>)



373.78 kWh

126.58 kg CO₂e



65.97 Wh

7.33 g CO₂e

Limitations

- only computational reproducibility
- only for Jupyter notebooks from articles available through PubMed Central
- only ran notebooks written in Python
- fully automated pipeline not using LLMs, ignoring non-FAIR instructions
- stops at first error, does not attempt fixes
- ecological footprint only assessed for running the pipeline, not developing it

Further details

- Analyzing the reproducibility of research-related Jupyter notebooks at scale
- Initial Run
 - 2021
 - Preprint: <https://doi.org/10.48550/arXiv.2209.04308>
- Rerun
 - 2023
 - Code : <https://github.com/fusion-jena/computational-reproducibility-pmc>
 - Data : <https://doi.org/10.5281/zenodo.8226725>
 - Paper : <https://doi.org/10.1093/gigascience/giad113>
- Knowledge graph ([see also deRSE25 talk today at 16:00](#))
 - Website: <https://w3id.org/fairjupyter>
 - SPARQL Endpoint: <https://reproduceme.uni-jena.de/#/dataset/fairjupyter/query>
 - Knowledge Graph Browser: <https://reproduceme.uni-jena.de/fj/>
 - Sample query: [PLOS Comp Bio articles and associated GitHub repos and Jupyter notebooks](#)
 - Preprint: <https://doi.org/10.48550/arXiv.2404.12935>
 - Paper: <https://doi.org/10.4230/TGDK.2.2.4>

What's next?

- Assessments of Jupyter notebooks in single GitHub repos
 - focus here is on evaluations before submission to journals/ conferences
- Assessments of dockerized Jupyter notebooks
- Assessments of non-Python notebooks
- Assessments of Jupyter notebooks from publications not in PubMed Central
- Software/ Data Carpentry course based on FAIRJupyter
- FAIRJupyter as a continuous service
- Your ideas here - collaborations welcome

Thank you

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- Ara Cluster of Friedrich Schiller University Jena under DFG grants INST 275/334-1 FUGG and INST 275/363-1 FUGG.
- [BASE4NFDI/KGI4NFDI](#): DFG 521453681
- **Contact:** sheeba.samuel@informatik.tu-chemnitz.de & daniel.mietchen@fiz-karlsruhe.de

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