

Resource Summary Report

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Binder

RRID:SCR_016437

Type: Tool

Proper Citation

Binder (RRID:SCR_016437)

Resource Information

URL: <https://mybinder.org/>

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Description: Open-source web application for managing digital repositories. Allows to create custom computing environments that can be shared and used by many remote users. Turns a GitHub repository containing a collection of Jupyter Notebooks into a collection of interactive notebooks. With Binder, open those notebooks in an executable environment, making your code immediately reproducible by anyone, anywhere.

Resource Type: web application, service resource, storage service resource, data repository, software resource

Keywords: managing, digital, repository, Jupyter Notebook, interactive notebook, code, reproducible

Resource Name: Binder

Resource ID: SCR_016437

License: Public

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260813T055131+0000

Ratings and Alerts

No rating or validation information has been found for Binder.

No alerts have been found for Binder.

Data and Source Information

Usage and Citation Metrics

We found 40 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Sinha A, et al. (2025) The NeuroML ecosystem for standardized multi-scale modeling in neuroscience. eLife, 13.

Bayarri G, et al. (2024) Using interactive Jupyter Notebooks and BioConda for FAIR and reproducible biomolecular simulation workflows. PLoS computational biology, 20(6), e1012173.

Xu J, et al. (2024) PyAMARES, an Open-Source Python Library for Fitting Magnetic Resonance Spectroscopy Data. Diagnostics (Basel, Switzerland), 14(23).

Sipakov R, et al. (2024) Leveraging Quadratic Polynomials in Python for Advanced Data Analysis. F1000Research, 13, 490.

Padilla DK, et al. (2024) Preparing the Next Generation of Integrative Organismal Biologists. Integrative and comparative biology, 64(3), 1007.

Ber??nek J, et al. (2024) Analysis of metadynamics simulations by metadynminer.py. Bioinformatics (Oxford, England), 40(10).

Moore J, et al. (2023) OME-Zarr: a cloud-optimized bioimaging file format with international community support. bioRxiv : the preprint server for biology.

Fabbris G, et al. (2023) Resonant inelastic x-ray scattering data for Ruddlesden-Popper and reduced Ruddlesden-Popper nickelates. Scientific data, 10(1), 174.

Khanal P, et al. (2023) Gas7 Is a Novel Dendritic Spine Initiation Factor. eNeuro, 10(4).

Moore J, et al. (2023) OME-Zarr: a cloud-optimized bioimaging file format with international community support. Histochemistry and cell biology, 160(3), 223.

Fanton S, et al. (2023) NetPlotBrain: A Python package for visualizing networks and brains. Network neuroscience (Cambridge, Mass.), 7(2), 461.

Rocca-Serra P, et al. (2023) The FAIR Cookbook - the essential resource for and by FAIR doers. Scientific data, 10(1), 292.

Stall S, et al. (2023) Journal Production Guidance for Software and Data Citations. Scientific data, 10(1), 656.

de Vries SEJ, et al. (2023) Sharing neurophysiology data from the Allen Brain Observatory. eLife, 12.

DuPre E, et al. (2022) Beyond advertising: New infrastructures for publishing integrated research objects. PLoS computational biology, 18(1), e1009651.

Maboudian SA, et al. (2022) Visualizing and Quantifying Longitudinal Changes in Verbal Fluency Using Recurrence Plots. Frontiers in aging neuroscience, 14, 810799.

Bayarri G, et al. (2022) BioExcel Building Blocks Workflows (BioBB-Wfs), an integrated web-based platform for biomolecular simulations. Nucleic acids research, 50(W1), W99.

Kolpakov F, et al. (2022) BioUML-towards a universal research platform. Nucleic acids research, 50(W1), W124.

Gomes DGE, et al. (2022) Why don't we share data and code? Perceived barriers and benefits to public archiving practices. Proceedings. Biological sciences, 289(1987), 20221113.

Juavinett AL, et al. (2022) The next generation of neuroscientists needs to learn how to code, and we need new ways to teach them. Neuron, 110(4), 576.