

Resource Summary Report

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Git

RRID:SCR_003932

Type: Tool

Proper Citation

Git (RRID:SCR_003932)

Resource Information

URL: <http://git-scm.com/>

Proper Citation: Git (RRID:SCR_003932)

Description: A free and open source distributed version control system designed to handle everything from small to very large projects with speed and efficiency. Git is easy to learn and has a tiny footprint with lightning fast performance. It outclasses SCM tools like Subversion, CVS, Perforce, and ClearCase with features like cheap local branching, convenient staging areas, and multiple workflows.

Resource Type: version source control system, software resource, software application, software development tool

Keywords: version control, distributed, bio.tools

Funding:

Availability: GNU General Public License, v2

Resource Name: Git

Resource ID: SCR_003932

Alternate IDs: nlx_158301, biotools:Git

Alternate URLs: <https://bio.tools/Git>

Record Creation Time: 20220129T080221+0000

Record Last Update: 20250519T203316+0000

Ratings and Alerts

No rating or validation information has been found for Git.

No alerts have been found for Git.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Cougnaud L, et al. (2024) Interactive medical and safety monitoring in clinical trials with clinDataReview: a validated and open-source reporting tool. *Frontiers in medicine*, 11, 1356323.

Hoyt CT, et al. (2024) The O3 guidelines: open data, open code, and open infrastructure for sustainable curated scientific resources. *Scientific data*, 11(1), 547.

Bravo JE, et al. (2024) The TELCoMB Protocol for High-Sensitivity Detection of ARG-MGE Colocalizations in Complex Microbial Communities. *Current protocols*, 4(10), e70031.

Akdeniz BC, et al. (2024) COSGAP: CONtainerized Statistical Genetics Analysis Pipelines. *Bioinformatics advances*, 4(1), vbae067.

Bai W, et al. (2024) Protocol to develop a chemotherapy drug screening process by constructing a cancer prognostic model using public databases. *STAR protocols*, 5(3), 103158.

Bai W, et al. (2024) Protocol to detect immune levels, abnormal metabolism, and signaling pathways in tumor tissue based on scRNA-seq obtained from patient databases. *STAR protocols*, 5(2), 103065.

Kaushal P, et al. (2024) Protocol for mapping differential protein-protein interaction networks using affinity purification-mass spectrometry. *STAR protocols*, 5(4), 103286.

Zhao C, et al. (2023) A reproducible and generalizable software workflow for analysis of large-scale neuroimaging data collections using BIDS Apps. *bioRxiv : the preprint server for biology*.

Liu X, et al. (2023) Applying FAIR4RS principles to develop an integrated modeling environment for the magnetic confinement fusion. *Scientific data*, 10(1), 592.

Li J, et al. (2022) RecombineX: A generalized computational framework for automatic high-throughput gamete genotyping and tetrad-based recombination analysis. *PLoS genetics*, 18(5), e1010047.

Stobbe MD, et al. (2022) Ten simple rules for a successful international consortium in big data omics. *PLoS computational biology*, 18(10), e1010546.

Kulman E, et al. (2022) Reconstructing cancer phylogenies using Pairtree, a clone tree reconstruction algorithm. *STAR protocols*, 3(4), 101706.

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

Amram D, et al. (2022) From P4 medicine to P5 medicine: transitional times for a more human-centric approach to AI-based tools for hospitals of tomorrow. *Open research Europe*, 2, 33.

Domander R, et al. (2021) BoneJ2 - refactoring established research software. *Wellcome open research*, 6, 37.

Leaf AT, et al. (2021) SFRmaker and Linesink-Maker: Rapid Construction of Streamflow Routing Networks from Hydrography Data. *Ground water*, 59(5), 761.

Halchenko YO, et al. (2021) DataLad: distributed system for joint management of code, data, and their relationship. *Journal of open source software*, 6(63).

Li F, et al. (2021) A protocol for transposon insertion sequencing in *Schizosaccharomyces pombe* to identify factors that maintain heterochromatin. *STAR protocols*, 2(2), 100392.

Grothausmann R, et al. (2021) Combination of μ CT and light microscopy for generation-specific stereological analysis of pulmonary arterial branches: a proof-of-concept study. *Histochemistry and cell biology*, 155(2), 227.

Schölzel C, et al. (2021) Characteristics of mathematical modeling languages that facilitate model reuse in systems biology: a software engineering perspective. *NPJ systems biology and applications*, 7(1), 27.