

Software Heritage: the universal archive of source code

Pierre Poulain



Software Heritage
THE GREAT LIBRARY OF SOURCE CODE

ANF workflow & reproductibilité 2025 | 2025-11-27

Outlook



1. Why is archiving software source code important?
2. What is Software Heritage?
3. How to archive source code in Software Heritage?
4. What are the best practices for archiving source code?

This presentation is guaranteed code-free

Software is everywhere!



NEWS FEATURE

THE TOP 100 PAPERS

Nature explores the most-cited research of all time.

BY RICHARD VAN NOORDEN,
BRENDAN MAHER AND REGINA NUZZO

The discovery of high-temperature superconductors, the determination of DNA's double-helix structure, the first observations that the expansion of the Universe is accelerating — all of these breakthroughs won Nobel prizes and international acclaim. Yet none of the papers that announced them comes anywhere close to ranking among the 100 most highly cited papers of all time.

Citations, in which one paper refers to earlier works, are the standard means by which authors acknowledge the source of their methods, ideas and findings, and are often used as a rough measure of a paper's importance. Fifty years ago, Eugene Garfield published the Science Citation Index (SCI), the first systematic effort to track citations in the scientific literature. To mark the anniversary, *Nature* asked Thomson Reuters, which now owns the SCI, to list the 100 most highly cited papers of all time. (See the full list at www.nature.com/top100.) The search covered all of Thomson Reuters' Web of Science, an online version of the SCI that also includes databases covering the social sciences, arts and humanities, conference proceedings and some books. It lists papers published from 1900 to the present day.

The exercise revealed some surprises, not least that it takes a staggering 12,119 citations to rank in the top 100 — and that many of the world's most famous papers do not make the cut. A few that do, such as the first observation¹

of carbon nanotubes (number 36) are indeed classic discoveries. But the vast majority describe experimental methods or software that have become essential in their fields.

The most cited work in history, for example, is a 1951 paper² describing an assay to determine the amount of protein in a solution. It has now gathered more than 305,000 citations — a recognition that always puzzled its lead author, the late US biochemist Oliver Lowry. "Although I really know it is not a great paper ... I secretly get a kick out of the response," he wrote in 1977.

The colossal size of the scholarly literature means that the top-100 papers are extreme outliers. Thomson Reuters' Web of Science holds some 58 million items. If that corpus were scaled to Mount Kilimanjaro, then the 100 most-cited papers would represent just 1 centimetre at the peak. Only 14,499 papers — roughly a metre and a half's worth — have more than 1,000 citations (see 'The paper mountain'). Meanwhile, the footfalls comprise works that have been cited only once, if at all — a group that encompasses roughly half of the items.

Nobody fully understands what distinguishes the sliver at the top from papers that are merely very well known — but researchers' customs explain some of it. Paul Wouters, director of the Centre for Science and Technology Studies in Leiden, the Netherlands, says that many methods papers "become a standard reference that one cites in order to make clear

to other scientists what kind of work one is doing". Another common practice in science ensures that truly foundational discoveries — Einstein's special theory of relativity, for instance — get fewer citations than they might deserve: they are so important that they quickly enter the textbooks or are incorporated into the main text of papers as terms deemed so familiar that they do not need a citation.

Citation counts are riddled with other confounding factors. The volume of citations has increased, for example — yet older papers have had more time to accrue citations. Biologists tend to cite one another's work more frequently than, say, physicists. And not all fields produce the same number of publications. Modern bibliometricians therefore recoil from methods as crude as simply counting citations when they want to measure a paper's value: instead, they prefer to compare counts for papers of similar age, and in comparable fields.

Nor is Thomson Reuters' list the only ranking system available. Google Scholar compiled its own top-100 list for *Nature*. It is based on many more citations because the search engine calls references from a much greater (although poorly characterized) literature base, including from a large range of books. In that list, available at www.nature.com/top100, economics papers have more prominence. Google Scholar's list also features books, which Thomson Reuters did not analyse. But among the science papers, many of the same titles show up.

Yet even with all the caveats, the old-fashioned hall of fame still has value. If nothing else, it serves as a reminder of the nature of scientific knowledge. To make exciting advances, researchers rely on relatively unused papers to describe experimental methods, databases and software.

Here *Nature* tours some of the key methods that tens of thousands of citations have hoisted to the top of science's Kilimanjaro — essential, but rarely thrust into the limelight.

BIOLOGICAL TECHNIQUES

For decades, the top-100 list has been dominated by protein biochemistry. The 1951 paper² describing the Lowry method for quantifying protein remains practically unreachable at number 1, even though many biochemists say that it and the competing Bradford assay³ — described by paper number 3 on the list — are tad outdated. In between, at number 2, is Laemmli buffer⁴, which is used in a different kind of protein analysis. The dominance of these techniques is attributable to the high volume of citations in cell and molecular biology, where they remain indispensable tools.

At least two of the biological techniques described by top-100 papers have resulted in Nobel prizes. Number 4 on the list describes the DNA-sequencing method⁵ that earned the late Frederick Sanger his share of the 1980 Nobel Prize in Chemistry. Number 63 describes polymerase chain reaction ▶

PHOTO BY KYLE BEAN, DESIGN BY MICHELLE FERNANDES/NATURE

« But the vast majority describe experimental methods or software that have become essential in their fields. »

Source: van Noorden et al, *Nature*, 2014
DOI: 10.1038/514550a

The 3 pillars of open science



- Open access to scientific publications
- Open (research) data
- Open source

Open science: share your code!



JCIM
JOURNAL OF
CHEMICAL INFORMATION
AND MODELING

ACS EDITORS'
CHOICE

pubs.acs.org/jcim

Viewpoint

Code Sharing in the Open Science Era

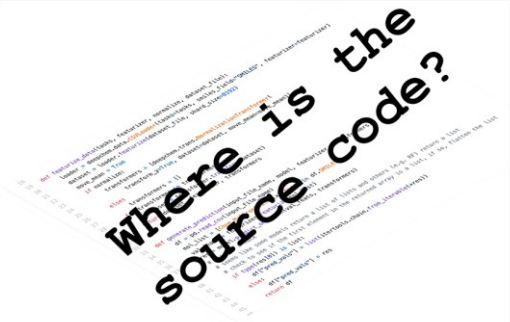
W. Patrick Walters*

Cite This: *J. Chem. Inf. Model.* 2020, 60, 4417–4420

Read Online

ACCESS | Metrics & More | Article Recommendations

ABSTRACT: Many high-profile scientific journals have established policies mandating the release of code accompanying papers that describe computational methods. Unfortunately, the majority of journals that publish papers in Computational Chemistry and Cheminformatics have yet to define such guidelines. This Viewpoint reviews the current state of reproducibility for the field and makes a case for the inclusion of code with computational papers.



Source: Walters, JCI, 2020, DOI: 10.1021/acs.jcim.0c01000

Open science: share your code!



nature

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COMMENT | 07 October 2025

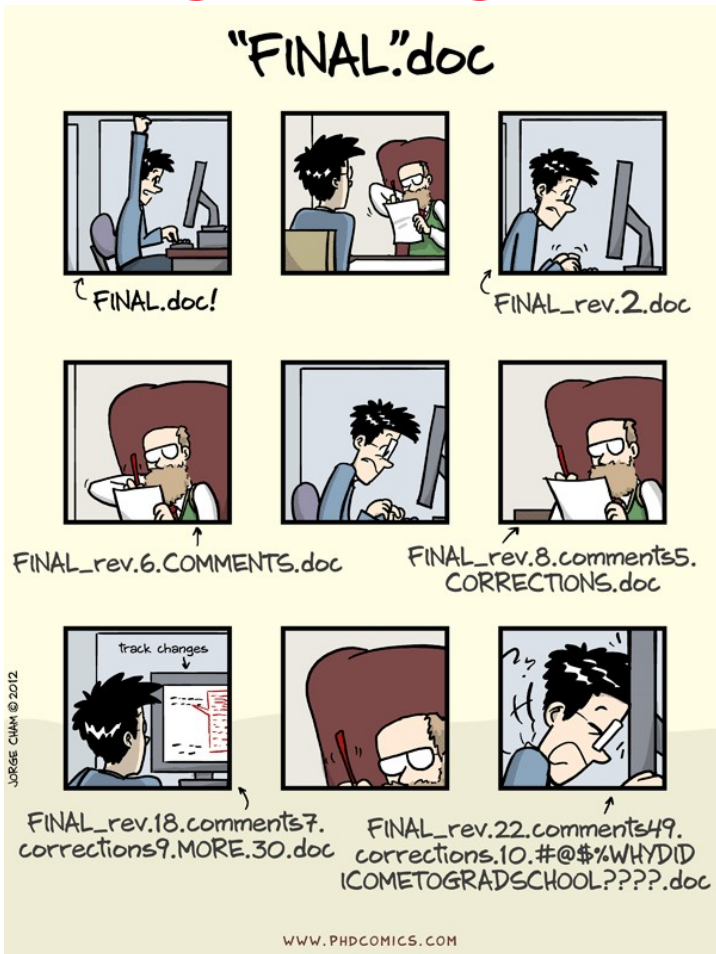
Stop treating code like an afterthought: record, share and value it

Scientists, research institutions, funders, libraries and publishers must all improve software practices.

By [Roberto Di Cosmo](#), [Sabrina Granger](#), [Konrad Hinsén](#), [Nicolas Jullien](#), [Daniel Le Berre](#), [Violaine Louvet](#), [Camille Maumet](#), [Clémentine Maurice](#), [Raphaël Monat](#) & [Nicolas P. Rougier](#) ✉

Source: Di Cosma, Nature, 2025, DOI: 10.1038/d41586-025-03196-0

The growing adoption of version control



OPINION ARTICLE



Four simple recommendations to encourage best practices in research software [version 1; peer review: 3 approved]

✉ Rafael C. Jiménez ¹, ✉ Mateusz Kuzak², Monther Alhamdoosh ³, Michelle Barker⁴, Bérénice Batut ⁵, Mikael Borg⁶, Salvador Capella-Gutierrez ⁷, Neil Chue Hong⁸, Martin Cook¹, ¹⁰

Source: Jiménez et al, F1000 Research, 2017
DOI: 10.12688/f1000research.11407.1

PLOS BIOLOGY

OPEN ACCESS

COMMUNITY PAGE

Best Practices for Scientific Computing

Greg Wilson , D. A. Aruliah, C. Titus Brown, Neil P. Chue Hong, Matt Davis, Richard T. Guy, Steven H. D. Haddock, Kathryn D. Huff, Ian M. Mitchell, Mark D. Plumbley, Ben Waugh, Ethan P. White, Paul Wilson

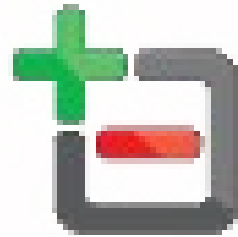
Published: January 7, 2014 • <https://doi.org/10.1371/journal.pbio.1001745>

Source: Wilson et al, PLOS Biology, 2014
DOI: 10.1371/journal.pbio.1001745

Together with the use of free
development platforms



GitLab



GITORIOUS



Together with the use of free gone development platforms



Google Kills Off Codelabs Code

Natasha Lomas @riptari / 10 March 13, 2015

Source: TechCrunch

1,4 million de projects 😱

Sunsetting Mercurial support in Bitbucket

April 21, 2020 | 3 min read



Denise Chan

[Update Aug 26, 2020] Mercurial repositories have now been disabled and cannot be accessed.

[Update Jan 2021] Today, mercurial repositories, snippets, and wikis will turn to read-only mode. After July 8th, 2020 they will no longer be accessible.

Source: BitBucket blog

250 000 dépôts 😭

Reproducibility in science requires long-term access to source code



You must prepare for the unavailability of your software repository (closure of the platform, deletion of the repository)



Source: Geralt, Pixabay

Quick note on French academic development platforms



Journal of Bioinformatics and Computational Biology | Vol. 13, No. 02, 1550006 (2015) | Research Papers

No Access

Pantograph: A template-based method for genome-scale metabolic model reconstruction

Nicolas Lolra, Anna Zhukova, and David James Sherman

<https://doi.org/10.1142/S0219720015500067> | Cited by: 23 (Source: Crossref)

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Tools



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Abstract

Genome-scale metabolic models are a powerful tool to study the inner workings of biological systems and to guide applications. The advent of cheap sequencing has brought the opportunity to create metabolic maps of biotechnologically interesting organisms. While this drives the development of new methods and automatic tools, network reconstruction remains a time-consuming process where extensive manual curation is required. This curation introduces specific knowledge about the modeled organism, either explicitly in the form of molecular processes, or indirectly in the form of annotations of the model elements. Paradoxically, this knowledge is usually lost when reconstruction of a different organism is started. We introduce the Pantograph method for metabolic model reconstruction. This method combines a template reaction knowledge base, orthology mappings between two organisms, and experimental phenotypic evidence, to build a genome-scale metabolic model for a target organism. Our method infers implicit knowledge from annotations in the template, and rewrites these inferences to include them in the resulting model of the target organism. The generated model is well suited for manual curation. Scripts for evaluating the model with respect to experimental data are automatically generated, to aid curators in iterative improvement. We present an implementation of the *Pantograph* method, as a toolbox for genome-scale model reconstruction, curation and validation. This open source package can be obtained from:

<http://pathtastic.gforge.inria.fr>.

Non sécurisé pathtastic.gforge.inria.fr



Ce site est inaccessible

Vérifiez si l'adresse pathtastic.gforge.inria.fr est correcte.

DNS_PROBE_FINISHED_NXDOMAIN

Actualiser

Quick note on French academic development platforms



 **Europe PMC**

AboutToolsDevelopersHelp

Search life-sciences literature (45 737 437 articles, preprints and more)

Advanced search | Try the new Advanced search!

Free full text access ⓘ

☐ Full text in Europe PMC (14)

☐ Link to free full text (0)

Type ⓘ

☐ Research articles (14)

☐ Review articles (0)

☐ Preprints (0)

☐ Books & documents (0)

Date published



1-14 of 14 results

Sort by: ☒ Relevance ⓘ ☐ Times cited ☐ Date

Neural field simulator: two-dimensional spatio-temporal dynamics involving finite transmission speed.

Nichols EJ, Hutt A

Front Neuroinform, 9:25, 20 Oct 2015

agreement No. 257253 (MATHANA project). 1 <https://gforge.inria.fr/projects/nfsimulator/> . 2 <http://nfsimulator.gforge.inria.fr...show3d.gforge.inria.fr/Index.html> . 5 <https://gforge.inria.fr/projects/show3d/> . 6 <http://www.wxpython.org>

Cited by: 2 articles | PMID: 26539105 ⓘ | PMCID: PMC4611063

SpaCEM3: a software for biological module detection when data is incomplete, high dimensional and dependent.

Vignes M, Blanchet J, Leroux D, Forbes F

Bioinformatics, 27(6):881-882, 03 Feb 2011

datasets are available from <http://spacem3.gforge.inria.fr/>.

Cited by: 1 article | PMID: 21296754 ⓘ | PMCID: PMC3051335

Quick note on French academic development platforms



Source: Forges de l'Enseignement supérieur et de la Recherche, 2023

Archive your code in



Software Heritage

THE GREAT LIBRARY OF SOURCE CODE

Software Heritage archives all open source code, forever and for free

- Non-profit organization
- Launched in 2016 at INRIA (Roberto Di Cosmo & Stefano Zacchiroli)
- Supported by UNESCO, the CNRS, UPCité, Microsoft, Google, Huawei, Intel.



Source: Software Heritage 5 years anniversary (2021)

Software Heritage & French open science



- Soutenir **Software Heritage** et recommander son adoption pour l'archivage et le référencement des codes sources.
- Proposer la standardisation du **Software Heritage Identifier (SWHID)**, qui complètera les DOI pour les logiciels.

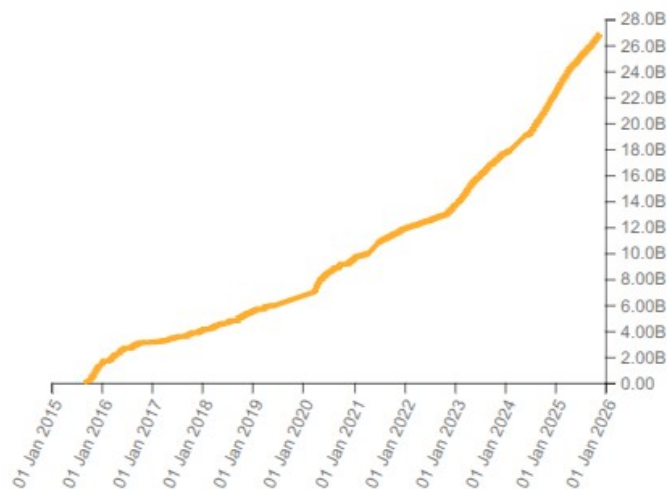
Source: Ouvrir la science, 2021

A very large archive



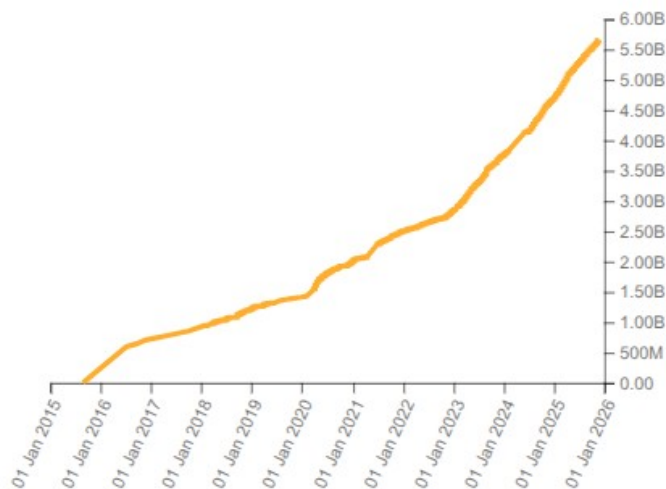
Source files

26 821 223 962



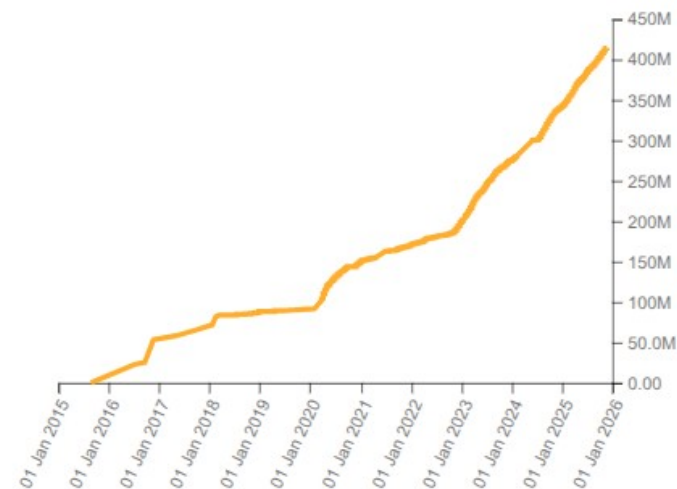
Commits

56 531 594 75



Projects

414 129 039



Source: Software Heritage

Archiving source code



 Bitbucket 2,957,824 origins <	 56,983 origins <	git 33,367 origins <
 30,473 origins <	 debian 145,437 origins <	 97,078 origins <
GitHub 309,156,541 origins <	gitiles 25,163 origins <	 GitLab 5,896,888 origins <
 3,969 origins <	 Gogs 493 origins <	 2,297,328 origins <
 Guix 72,253 origins <	 GNU 354 origins <	 heptapod 1,383 origins <
 launchpad 660,952 origins <	Maven™ 876,288 origins <	 NixOS 62,988 origins <
 4,290,683 origins <	 5,146 origins <	 Packagist The PHP Package Repository 383,534 origins <
 PAGURE 72,459 origins <	 Phabricator 203 origins <	 pub.dev 71,696 origins <
 699,495 origins <	 SOURCEFORGE 382,364 origins <	stagit 344 origins <

Source: Software Heritage

Rescuing source code



Discontinued hosting

Discontinued hosting services. Those origins have been archived by Software Heritage.



122,014 origins



790,026 origins



336,795 origins



Source: Software Heritage

“Google Code content now safely collected”, 2016

“Rescuing 250000+ endangered Mercurial repositories”, 2020

Save your code now!



<https://archive.softwareheritage.org/save/>

 Software Heritage Archive

 **Save code now**

Enter a SWHID to resolve or keyword(s) to search for in origin URLs 

Features

 Search

 Downloads

 **Save code now**

 Help

You can contribute to extend the content of the Software Heritage archive by submitting an origin save request. To do so, fill the required info in the form below:

Origin type

git 



Origin url 

Submit 

Help

Browse save requests

A "Save code now" request takes the following parameters:

Let's save some code



ptools / heligeom_webserver

Search: Type to search

Code Issues Pull requests Actions Projects Wiki Security 1 Insights Settings

heligeom_webserver Public

Edit Pins Unwatch 3 Fork 1 Star 0

master 2 Branches 3 Tags

Go to file Add file Code

File/Folder	Modification	Time Ago
HubLot add AUTHORS file ✓	979cba4 · 2 weeks ago	210 Commits
.github/workflows	Side modifications:	3 months ago
heligeom	Add publication link	2 weeks ago
ptools-python @ a5e091c	Handle alternate location (take A one by default)	last month
tests	update test	last month
.gitignore	update dependencies	4 years ago
.gitlab-ci.yml	Update to Python 3.12	5 months ago
.gitmodules	clean adjust function	3 months ago
AUTHORS	add AUTHORS file	2 weeks ago
CHANGELOG.md	finish 4ESV flatten example	last month
LICENSE	Add GPL LICENSE	last month
Pipfile	add missing dependencies with new ptools version	last month

About

Heligeom is a tool, part of Ptools, for characterizing, manipulating and assembling structural units with a screw organization.

heligeom.galaxy.ibpc.fr/

- Readme
- GPL-3.0 license
- Activity
- Custom properties
- 0 stars
- 3 watching
- 1 fork

Report repository

Releases

3 tags

[Create a new release](#)

https://github.com/ptools/heligeom_webserver

Let's save some code



<https://archive.softwareheritage.org/save/>

 **Save code now**

Enter a SWHID to resolve or keyword(s) to search

You can contribute to extend the content of the Software Heritage archive by submitting an origin save request. To do so, fill the required info in

Origin type	Origin url	
git ▼	https://github.com/ptools/heligeom_webserver	Submit

This stunt was NOT performed by a professional; TRY it at work!

Let's save some code



Help		Browse save requests				
10	▼	entries per page		Search:		
Date	Type	Url	Request	Status	Info	
19/03/2025 18:37:03	git	https://github.com/ptools/heligeom_webserver	accepted	succeeded	ⓘ	Save again
19/03/2025 18:13:19	git	https://github.com/aappleby/pinwheel	accepted	succeeded	ⓘ	Save again
19/03/2025 18:13:19	git	https://github.com/NyaMisty/ghidra_mod	accepted	succeeded	ⓘ	Save again

<https://archive.softwareheritage.org/save/list/>

Let's save some code



https://github.com/ptools/heligeom_webserver visit type git

16 March 2025, 17:06:49 UTC

<> Code Branches (6) Releases (3) Visits

★ Branch: HEAD ▾ 3a90521 / History Download Save again

 Tip revision: 979cba4f58f153ad5cddb7a4187958bf97doe71 authored by Hubert on 03 March 2025, 10:03:16 UTC
add AUTHORS file

File	Mode	Size
📁 .github		
📁 heligeom		
📁 ptools-python@ a5e091c		
📁 tests		
📄 .gitignore	-rW-r--r--	480 bytes
📄 .gitlab-ci.yml	-rW-r--r--	513 bytes
📄 .gitmodules	-rW-r--r--	109 bytes
📄 AUTHORS	-rW-r--r--	48 bytes

Permalinks

https://archive.softwareheritage.org/browse/origin/directory/?origin_url=https://github.com/ptools/heligeom_webserver

What code?



Any *code* is welcome in Software Heritage:

- 10,000 lines software
- (small, medium, large) R, Python, Bash scripts
- Workflows (Make, Nextflow, Snakemake)
- (Jupyter) notebooks
- ...

GOOD NEWS EVERYONE



**SOFTWARE HERITAGE
ARCHIVES ANY OPEN-SOURCE CODE!**

Best practices: beyond the code



Metadata for humans

- **README**
<https://readme.so/fr/editor>
- **AUTHORS**
Ada Lovelance <ada@programming.org>
Margaret Hamilton <margaret@nasa.com>
- **LICENSE**
Open-source **SPDX** license
<https://choosealicense.com/>
<https://reuse.software/>

Metadata for machines

- **codemeta.json**
with a human-friendly generator:
CodeMeta Generator

See also: “**HOWTO** archive and reference your code”

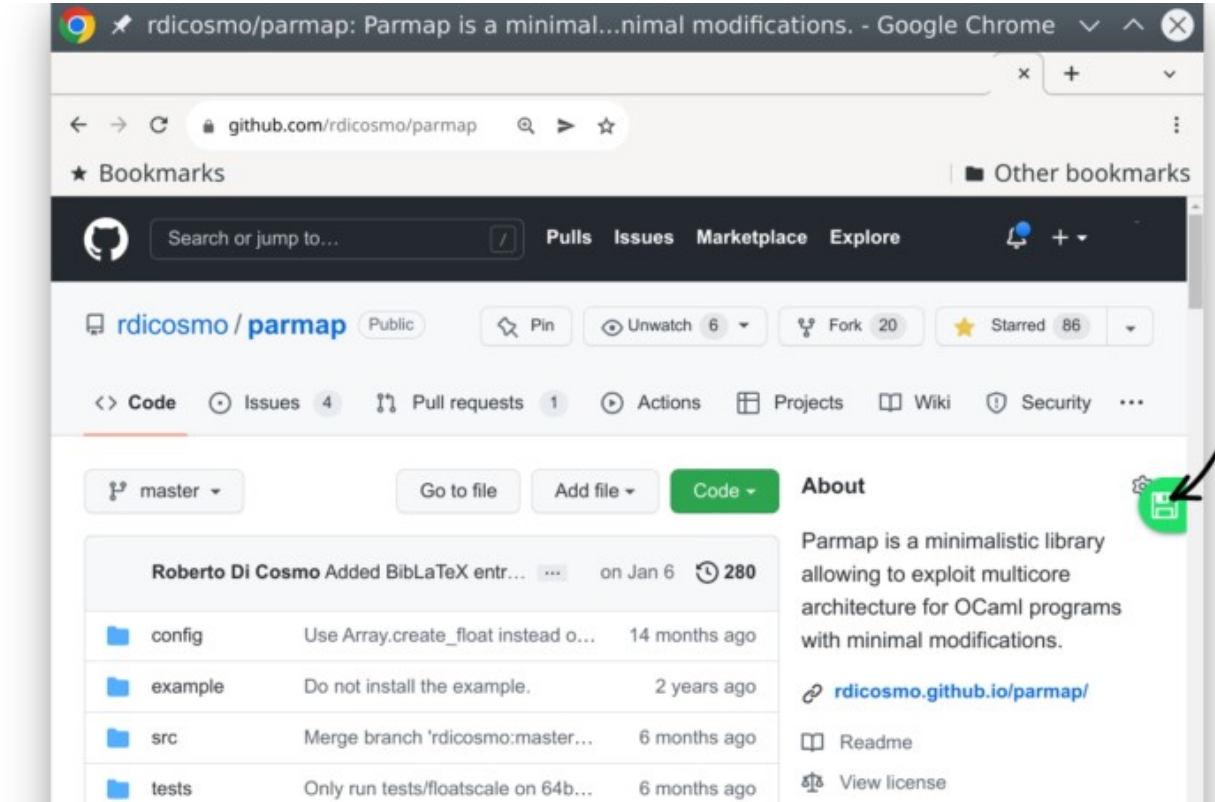
Save your code (browser extension)



Manually but fun

The screenshot shows the GitHub interface for the repository 'ptools / heligeom_webserver'. The repository is public and has 210 commits. The file list on the left includes .github/workflows, heligeom, ptools-python @ a5e091c, tests, .gitignore, .gitlab-ci.yml, .gitmodules, AUTHORS, CHANGELOG.md, LICENSE, Pipfile, Pipfile.lock, README.rst, config.py, pyproject.toml, and requirements.txt. The right sidebar contains an 'About' section with a description of Heligeom, a link to heligeom.galaxy.ibpc.fr, and sections for 'Releases' and 'Contributors'. A green extension icon is located on the right edge of the repository view, and a pink arrow points to it from the right side of the image.

Save your code (browser extension)



This tab shows
the archival status
of the repository

Green up to date
Yellow not up to date
Grey not archived yet
Red not archivable (private)

Source : Browser extensions, Software Heritage

See: “Archive access and update in just one click with the updateswh browser extension”, 2022

Save your code (webhook)



Setting up Webhooks on GitLab (and its instances)

Here is an example of how to configure the save code webhook on GitLab.
For your convenience, this is the URL that you can copy/paste directly:

```
https://archive.softwareheritage.org/api/1/origin/save/webhook/gitlab/
```

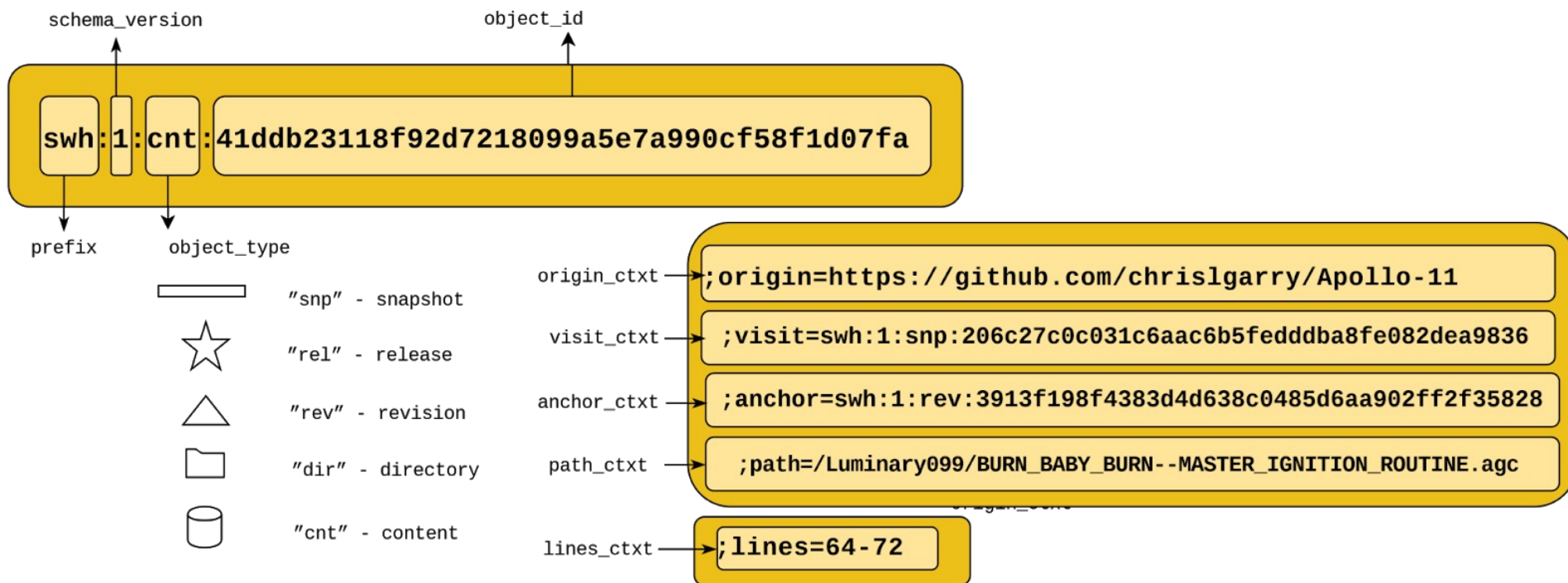
The recommended settings for GitLab are: **trigger archival on tag push and release creation, and not on every push event**.

See: “Webhooks are here: Integrate Software Heritage with Your Development Workflow!”, 2023

Reference source code



~~DOI~~ SWHID (SoftWare Hash Identifier): persistent and intrinsic identifier



Source: Software Heritage

SWHID (SoftWare Hash Identifier)



Home

[What are SWHIDs?](#)

[Key Benefits](#)

[The SWHID Working Group](#)

[Quick Access](#)

[Participation and Governance](#)

[Getting Started](#)

[For Developers](#)

[For Researchers](#)

[Onboarding Materials](#)

SWHID: International Standard for Software Artifact Identification

SWHIDs (from "SoftWare Hash Identifiers") are persistent, intrinsic identifiers for software source code artifacts such as source code files, source trees, commits, and other objects typically found in version control systems.

SWHID is an ISO International Standard

SWHID has been officially adopted as ISO/IEC 18670:2025 on April 23, 2025.

The first international standard for persistent, content-based identification of software artifacts.

[View ISO Standard](#)

[Read Public Specification](#)

[FAQ](#)

Source: <https://www.swhid.org/>

Reference source code



https://github.com/ptools/heligeom_webserver

visit type git

📅 16 March 2025, 17:06:49 UTC

<> Code 🔑 Branches (6) 📦 Releases (3) 📅 Visits

★ Branch: HEAD ▾ 3a90521 / 🕒 History ⬇️ Download 📷 Save again

Tip revision: **979cba4f58f153ad5cdbdb7a4187958bf97d0e71** authored by **Hubert** on **03 March 2025, 10:03:16 UTC**
add AUTHORS file

File	Mode	Size
📁 .github		
📁 heligeom		
📁 ptools-python @ a5e091c		
📁 tests		
📄 .gitignore	-rw-r--r--	480 bytes
📄 .gitlab-ci.yml	-rw-r--r--	513 bytes
📄 .gitmodules	-rw-r--r--	109 bytes
📄 AUTHORS	-rw-r--r--	48 bytes

🔗 Permalinks

Reference source code



https://github.com/ptools/heligeom_webserver visit type git

16 March 2025, 17:06:49 UTC

<> Code Branches (6) Releases (3) Visits

★ Branch: HEAD 3a90521 / History Download Save again

Permalinks

To reference or cite the objects present in the Software Heritage archive, permalinks based on SoftWare Hash IDentifiers (SWHIDs) must be used.
Select below a type of object currently browsed in order to display its associated SWHID and permalink.

directory revision snapshot

archived repository archived swh:1:dir:3a905213f26d1a70fbdecc30d331c9d1d177d304 Iframe embedding

```
swh:1:dir:3a905213f26d1a70fbdecc30d331c9d1d177d304;  
origin=https://github.com/ptools/heligeom_webserver;  
visit=swh:1:snp:aad2c1acf7e5eceb9d5f2337d0a46d9d188d140d;  
anchor=swh:1:rev:979cba4f58f153ad5cdbdb7a4187958bf97d0e71
```

☒ Add contextual information Copy identifier Copy permalink

File

.github

heligeom

ptools-python

tests

.gitignore

.gitlab-ci.yml

.gitmodules

AUTHORS

-rw-r--r--

513 bytes

-rw-r--r--

109 bytes

-rw-r--r--

48 bytes

SWHID alone (useless)



swh:1:dir:3a905213f26d1a70fbdecc30d331c9d1d177d304

Browse the archive

Enter a SWHID to resolve or keyword(s) to search for in origin URLs

3a90521 /

Download

File	Mode	Size
.github		
heligeom		
ptools-python @ a5e091c		
tests		
.gitignore	-rW-r--r--	480 bytes
.gitlab-ci.yml	-rW-r--r--	513 bytes
.gitmodules	-rW-r--r--	109 bytes
AUTHORS	-rW-r--r--	48 bytes
CHANGELOG.md	-rW-r--r--	701 bytes

SWHID + context (useful)



```
swh:1:dir:3a905213f26d1a70fbdecc30d331c9d1d177d304;  
origin=https://github.com/ptools/heligeom_webserver;  
visit=swh:1:snp:aad2c1acf7e5eceb9d5f2337d0a46d9d188d140d;  
anchor=swh:1:rev:979cba4f58f153ad5cdbdb7a4187958bf97d0e71
```

≡ Browse the archive

Enter a SWHID to resolve or keyword(s) to search for in origin URLs

🔍

 https://github.com/ptools/heligeom_webserver 

visit type git

🕒 16 March 2025, 17:06:49 UTC

<> Code

🔗 Branches (6)

📦 Releases (3)

📅 Visits

★ Branch: HEAD ▾

3a90521 /

🕒 History

📄 Download

📷 Save again

🔑 Tip revision: 979cba4f58f153ad5cdbdb7a4187958bf97d0e71 authored by Hubert on 03 March 2025, 10:03:16 UTC

add AUTHORS file

File	Mode	Size
📁 .github		
📁 heligeom		
📁 ptools-python @ a5e091c		
📁 tests		
📄 .gitignore	-rw-r--r--	480 bytes

Reference source code (recap)



The URL of the repo in the development platform (GitHub, GitLab):
https://github.com/ptools/heligeom_webserver

The URL of the archive in SWH (for your README file):  archived repository
https://archive.softwareheritage.org/browse/origin/directory/?origin_url=https://github.com/ptools/heligeom_webserver

The reference of the archive in SWH for a paper,
with the appropriate contexte:

```
swh:1:dir:3a905213f26d1a70fbdecc30d331c9d1d177d304;  
origin=https://github.com/ptools/heligeom_webserver;  
visit=swh:1:snp:aad2c1acf7e5eceb9d5f2337d0a46d9d188d140d;  
anchor=swh:1:rev:979cba4f58f153ad5cdbdb7a4187958bf97d0e71
```

Cite code source (as a link)



Example:

Link to:

https://github.com/ptools/heligeom_webserver

*“Heligeom source code is available on GitHub
(https://github.com/ptools/heligeom_webserver)
and archived in Software Heritage
([swh:1:dir:af308bc8009c2d889d6cd42c29198ecb50e7fd25](https://archive.softwareheritage.org/swh:1:dir:af308bc8009c2d889d6cd42c29198ecb50e7fd25)).”*

Link to:

[https://archive.softwareheritage.org/swh:1:dir:af308bc8009c2d889d6cd42c29198ecb50e7fd25;
origin=https://github.com/ptools/heligeom_webserver;
visit=swh:1:snp:17e03b8881aa89e8fdda8727b572f3897a9eac9c;
anchor=swh:1:rev:e07989aa780a79ae6a602d7d30e1081b3d6b2fc7](https://archive.softwareheritage.org/swh:1:dir:af308bc8009c2d889d6cd42c29198ecb50e7fd25;origin=https://github.com/ptools/heligeom_webserver;visit=swh:1:snp:17e03b8881aa89e8fdda8727b572f3897a9eac9c;anchor=swh:1:rev:e07989aa780a79ae6a602d7d30e1081b3d6b2fc7)

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buildH: Build hydrogen atoms from united-atom molecular dynamics of lipids and calculate the order parameters

Python Submitted 08 July 2021 • Published 19 September 2021

Background

Statement of Need

Overview

Acknowledgements

References

Some notebooks are provided in the GitHub repository to explain how buildH works and how to analyze the data produced. In case of trouble, any user can post an issue on GitHub.

buildH is available in the Python Package Index (PyPI) as well as in the Bioconda repository. The current version 1.6.0 of buildH is archived in the Zenodo repository (<https://zenodo.org/record/5356246>) and in the Software Heritage archive ([swh:1:dir:4c63d5ca3497726a1e54ac152ce1667d7c004d2b](https://archive.softwareheritage.org/swh:1:dir:4c63d5ca3497726a1e54ac152ce1667d7c004d2b)).

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Zoom automatique

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<https://joss.theoj.org/papers/10.21105/joss.03521>

Cite code source (as a reference)



Data availability

Data files produced from the data collection and processing are available in Parquet format in Zenodo. They are freely available

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search and index MD files, and to download and parse them. The code is open-source (under the AGPL-3.0 license), freely available and archived in Software Heritage (Poulain et al., 2023).

Full documentation is provided along the scripts to ease data collection and processing. Jupyter notebooks used to create the figures of this paper are open-source (under the AGPL-3.0 license), freely available on GitHub and archived in Software Heritage (Poulain, 2023). The code of the MDverse data exploration is open-source (under the BSD 3-Clause license), freely available and archived in Software Heritage (Poulain and Oussarek, 2023).

Pohjolainen E, Chen X, Malola S, Groenhof G, Häkkinen H (2016) **A Unified AMBER-compatible molecular mechanics force field for thiolate-protected gold nanoclusters** *Journal of Chemical Theory and Computation* 12:1342–1350.

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Software

Poulain P (2023) **MDverse data analysis, version 1.0.0** *Software Heritage*. swh:1:rev:4562c50d1b51a51fdf952ae6e9efaa407dd06e20

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buildH

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MÉTADONNÉES

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Hubert Santuz, Amélie Bâcle, Pierre Poulain, Patrick Fuchs. buildH. 2019, (swh:1:dir:4c63d5ca3497726a1e54ac152ce1667d7c004d2b;origin=https://github.com/patrickfuchs/buildH/;visit=swh:1:snp:a63a8d07dbebeb442a06707be476817cec44ac72;anchor=swh:1:rev:9f05672515e1c0b0064eeb34f63844296193bc0d). (hal-03467422)

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Reference code in HAL



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Réf. DGDS-D-2025-24

Paris, le 27 octobre 2025

Chères et chers collègues,

La prochaine campagne des comptes rendu d'activités des chercheurs (CRAC) sera ouverte aux chercheurs et aux chercheuses du 3 novembre 2025 au 12 décembre 2025. Je vous encourage à remplir vos CRAC sans attendre les derniers jours de la campagne.

Comme les années précédentes, l'application CRAC sera alimentée pour les articles à partir de l'archive ouverte HAL. Seuls seront déposés les textes mais également les textes de dépôt dans le serveur.

Ces modalités vous sont présentées par les chercheurs et les chercheuses.

Notre politique d'accès ouvert a décidé cette année de la publication est déposée dans HAL, et si elle est liée à un jeu de données qui possède un identifiant (un DOI différent de celui de la publication), il est possible de mettre cet identifiant dans HAL en lien avec la publication. La même chose est rendue possible avec un logiciel de recherche lié à une publication et déposé dans l'archive internationale Software Heritage, ce qui lui donne un identifiant SWHID (SoftWare Heritage persistent Identifiers) qui peut également être renseigné dans HAL afin d'être lié à la publication.

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Notre politique d'accès ouvert concerne également les données et les logiciels de la recherche. Nous avons décidé cette année de les mettre en valeur dans le CRAC. Ceci est rendu possible par le fait que lorsqu'une publication est déposée dans HAL, et si elle est liée à un jeu de données qui possède un identifiant (un DOI différent de celui de la publication), il est possible de mettre cet identifiant dans HAL en lien avec la publication. La même chose est rendue possible avec un logiciel de recherche lié à une publication et déposé dans l'archive internationale Software Heritage, ce qui lui donne un identifiant SWHID (SoftWare Heritage persistent Identifiers) qui peut également être renseigné dans HAL afin d'être lié à la publication.

Cite source code



BibLaTeX style extension for software

[Software Release] B. Langmead and S. L. Salzberg, *Bowtie2* version 2.4.2, Oct. 2022. LIC: GPL. URL: <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>, VCS: <https://github.com/BenLangmead/bowtie2>, SWHID: `<swh:1:rel:97bacfffeaa6e7c3f574ce5b566daba82aa18a11f;origin=https://github.com/BenLangmead/bowtie2;visit=swh:1:snp:c25778cfefc086c63c6f78eed230d0b9c88876ee>`.

[Software excerpt] MIT Instrumentation Laboratory, “AGC Luminary routine for changing LEM asset during landing”, from *Apollo 11 Guidance Computer (AGC) source code for the command and lunar module* 1967. VirtualAGC project. LIC: Public Domain. URL: <https://www.ibiblio.org/apollo>, VCS: <https://github.com/virtualagc/virtualagc>, SWHID: `<swh:1:cnt:64582b78792cd6c2d67d35da5a11bb80886a6409;origin=https://github.com/virtualagc/virtualagc;anchor=swh:1:rev:007c2b95f301f9438b8b74d7993b7a3b9a66255b;lines=245-261>`.

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