

Bioconductor: possibly the world's most impactful bioinformatics open source project

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National Open Source Innovation
Summit 2026



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Global Developer Manager



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Temporary Slide with links

Background

Bioconductor. (common R) - OHDSI (impossible to find packages)- Open not structured and not quality No review/Documentation/Many githubs

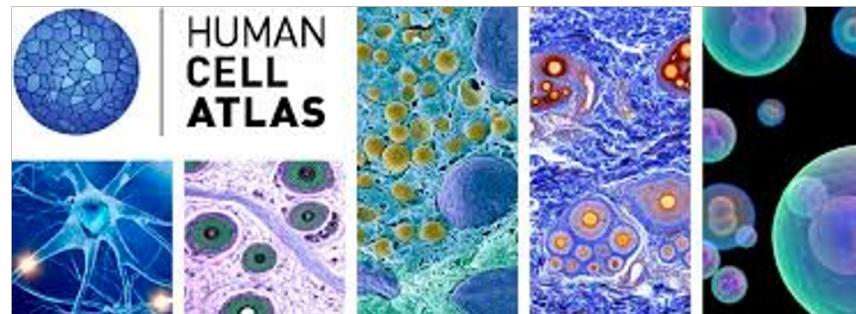
Bias in AI Danger of Poor Quality Software - Arifacts magnified
<https://news.rice.edu/news/2024/breaking-mad-generative-ai-could-break-internet>

AI continent and Data Spaces/Data Labs
Ethical, cost of AI - Better Software
RSQkit ELIXIR (organization thinking about data mgt/software quality)

Our body has 37,000,000,000,000 Cells



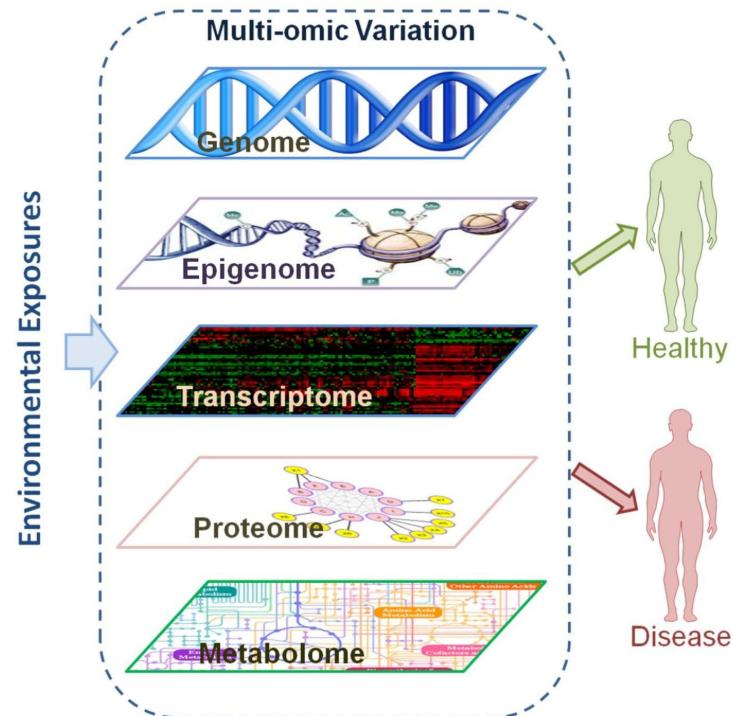
In the past 2 decades, life sciences has been revolutionized by the capacity to measure biology molecules in vast detail



Why Bioconductor Matters

Large volumes of complex data require advanced, efficient, fast, user-friendly statistical & AI tools

- Biology data impact Medicine, Biodiversity, Agriculture, Marine
- Plants, Pathogens, Biodiversity, Microbiology, food
- Understanding Disease
- Discovery of biomarkers, new therapeutic targets
- 80% new cancer medicines are targeted



A ecosystem for health & life sciences

- Supports analysis of many biological data (genomics, transcriptomics, proteomics, ...)
- >2,000 packages; data wrangling, statistical analysis & AI, reporting, visualization, interactive tools
Written in R.
- Optimized underlying methods in multiple languages including C++, Fortran
- Strong methods for interoperability with other 4GL Python, Julia

Bioconductor version 3.19 (Release)

Find bioViews:

Software (2369)

- AssayDomain (915)
- BiologicalQuestion (978)
- Infrastructure (578)
- ResearchField (1163)
- ShinyApps (39)
- StatisticalMethod (641)
- Technology (1493)
- WorkflowManagement (1)
- WorkflowStep (1246)
- AnnotationData (926)
- ExperimentData (430)
- Workflow (30)

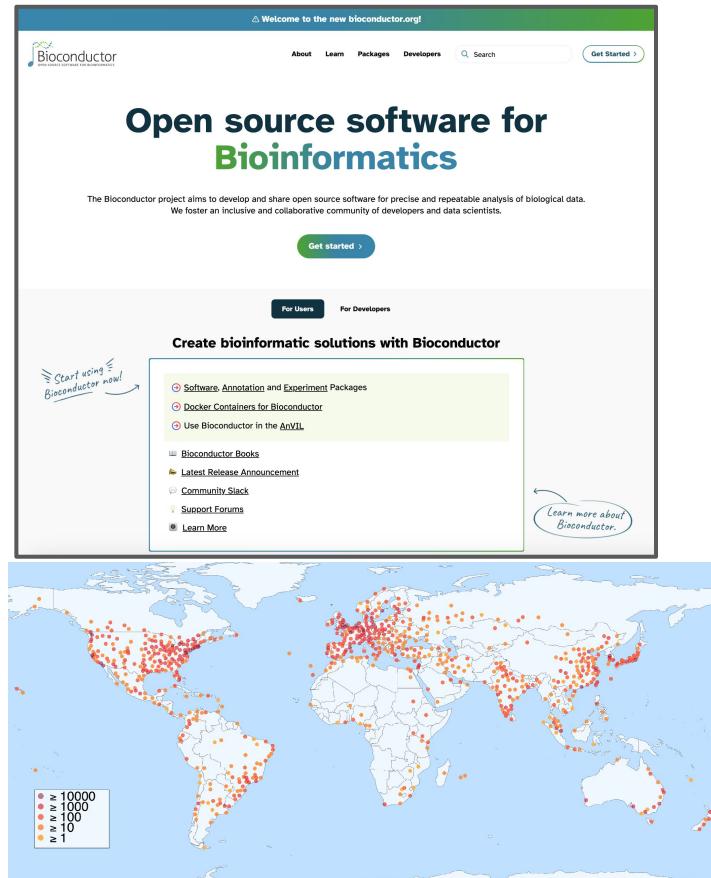
Packages found under Software:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Package	Maintainer	Title	Rank
BiocVersion	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	1
GenomeInfoDb	Hervé Pagès	Utilities for manipulating chromosome names, including modifying them to follow a particular naming style	2
BiocGenerics	Hervé Pages	S4 generic functions used in Bioconductor	3
S4Vectors	Hervé Pagès	Foundation of vector-like and list-like containers in Bioconductor	4
IRanges	Hervé Pagès	Foundation of integer range manipulation in Bioconductor	5
zlibbioc	Bioconductor Package Maintainer	An R packaged zlib-1.2.5	6
XVector	Hervé Pagès	Foundation of external vector representation and manipulation in Bioconductor	7

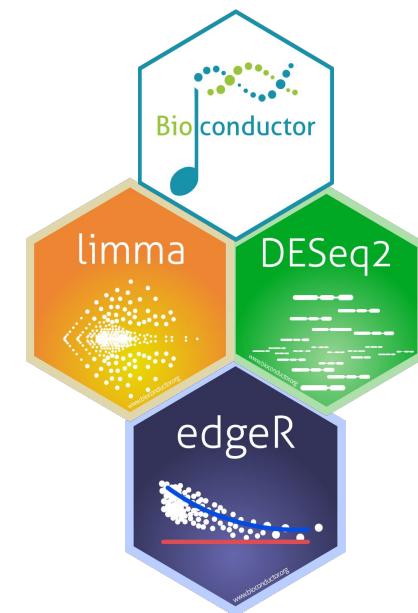
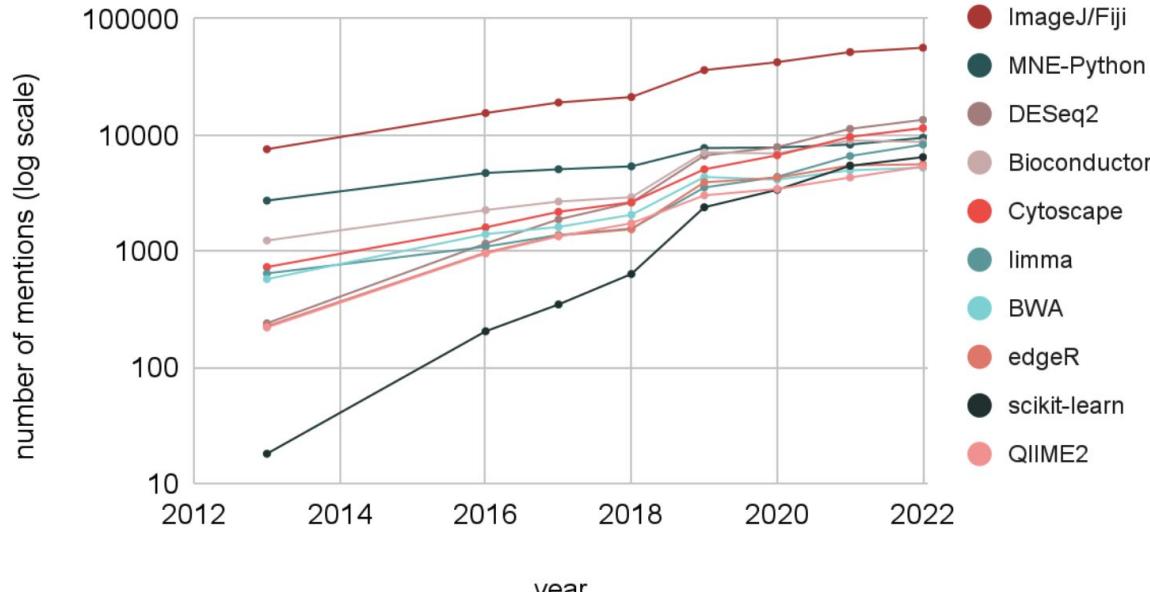
Bioconductor in 2026

- Open source, open development
- Now version 3.22
- Community-driven
- Core value supporting users to become developers.
- 2,000+ contributed packages,
- Downloads >1 million per year
- Global



Data shows Bioconductor is essential software

A. Total number of papers



4/10 top cited
biomedical OSS are
Bioconductor

Bioconductor as Software Infrastructure

Challenges at the intersection of biology and computer science

- Data scale - DNA sequencing data alone (in individual institution repositories!) is on the petabyte scale
- Complex hardware landscape
- Difficulty retaining talent and institutional knowledge

Bioconductor Strengths

- Historically robust maintenance and governance
- Metronomic versioning and release schedule emphasizing reliability
- Diverse community with strong and mixed technical backgrounds

Reproducibility, Reusability and Efficiency

- Bioconductor is package **repository** (SVN -> github)
- **Rigorous review** process* for packages (both automated and manual)
- **Daily build and check*** of all packages on multiple OS platforms. Issues reported to developers
- **Standardized data structures** and interoperability
- Rigour in **documentation** & vignette tutorial with examples*
- FAIR before FAIR
- Software quality -> Accepted by Pharma Regulatory
- **Connected** to Global OSS projects, Galaxy, Python scVerse, OHDSI, ELIXIR

* Stable, Quality, Trusted, Respected

Build/check report for BioC 3.23																																																	
This page was generated on 2020-02-05 11:32 -0600 (Thu, 05 Feb 2020).																																																	
See this page for all the Bioconductor builds and their schedule.																																																	
Package status is indicated by one of the following glyphs:																																																	
■ TIMEOUT	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes																																																
■ ERROR	<input checked="" type="checkbox"/> Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors																																																
■ WARNING	<input checked="" type="checkbox"/> CHECK of package produced warnings																																																
■ OK	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package went OK																																																
	<input type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System																																																
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Partner with us...

How can our learnings help you

- Build global community
- Increase Robustness, rigour and quality
- Software for vast data

Our Challenges

Distributed & Federated Compute

European Health Data Space (EHDS)

Software quality for EU AI Data Lab, AI Test Beds

GPU native

Funding is currently USA centred

- NIH U54, NCI
- CZI EOSS 4.0, 6.0
- Small PI grants

Seeking to diversify funding and engage with industry

- EU Horizon, Digital Europe
- IHI, DTIF



Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS