

# 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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# Temporary Slide with links

## Background

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

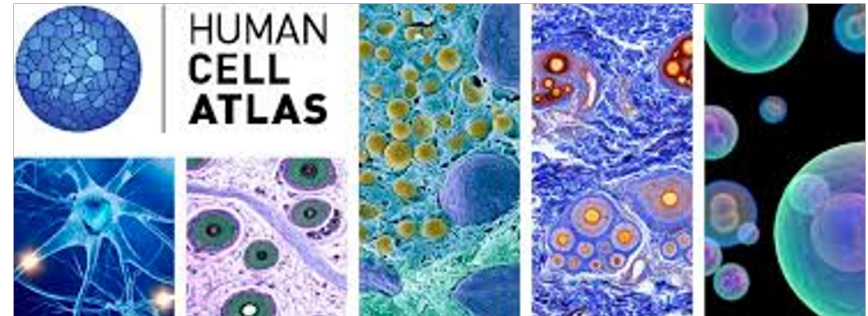
Bias in AI Danger of Poor Quality Software - Arifacts magnified  
<https://news.rice.edu/news/2024/breaking-mad-generative-ai-could-break-internet>

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



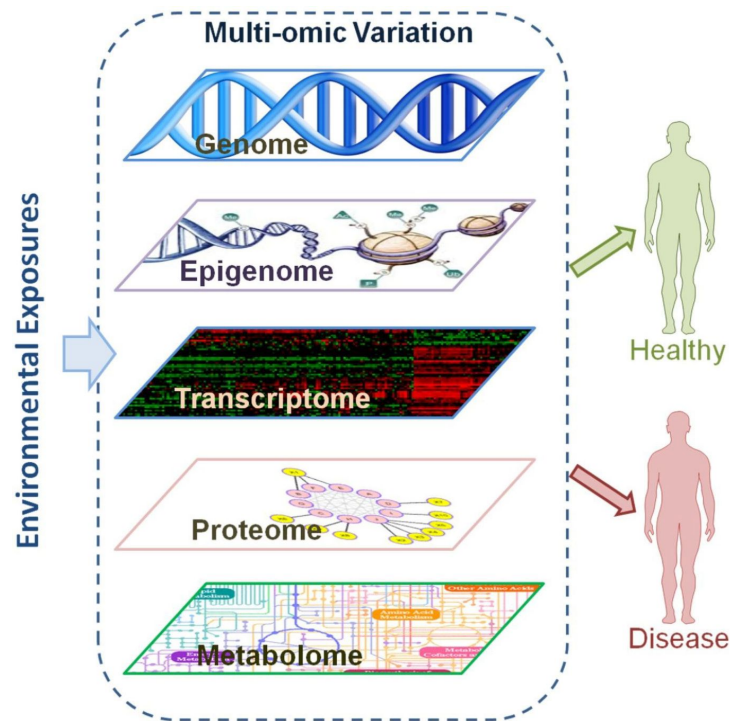
In the past 2 decades, life sciences has been revolutionized by the capacity to measure biology molecules in vast detail



# Why Bioconductor Matters

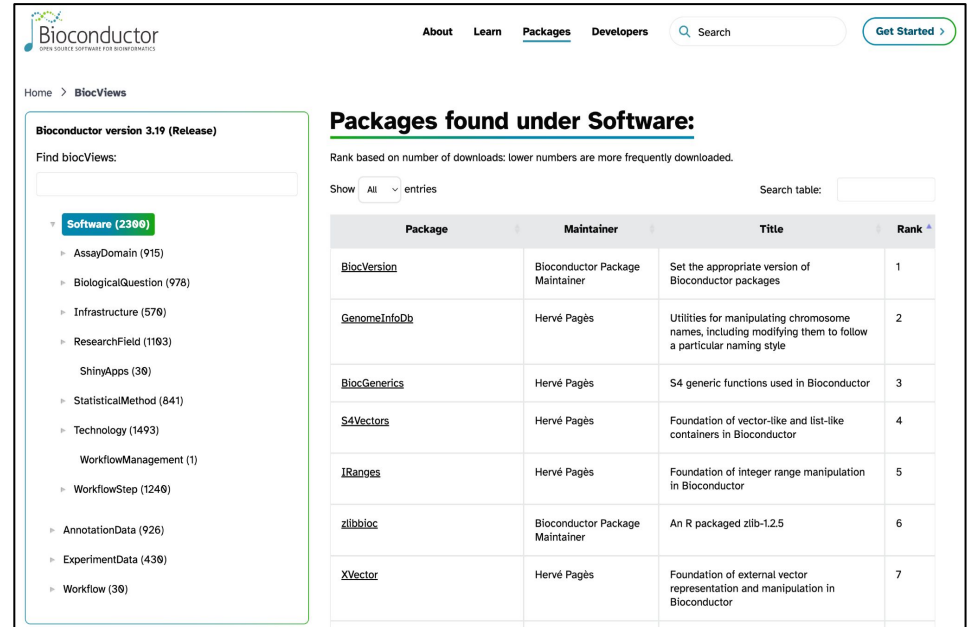
Large volumes of complex data require advanced, efficient, fast, user-friendly statistical & AI tools

- 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



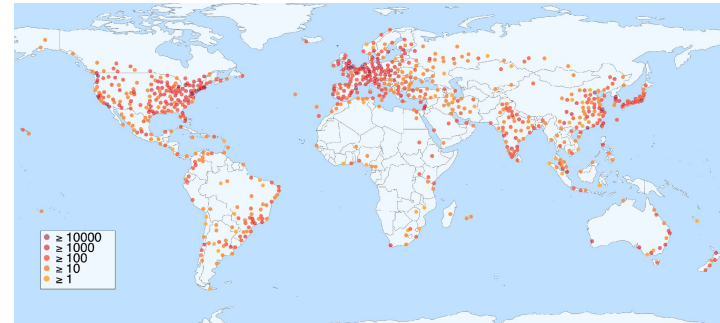
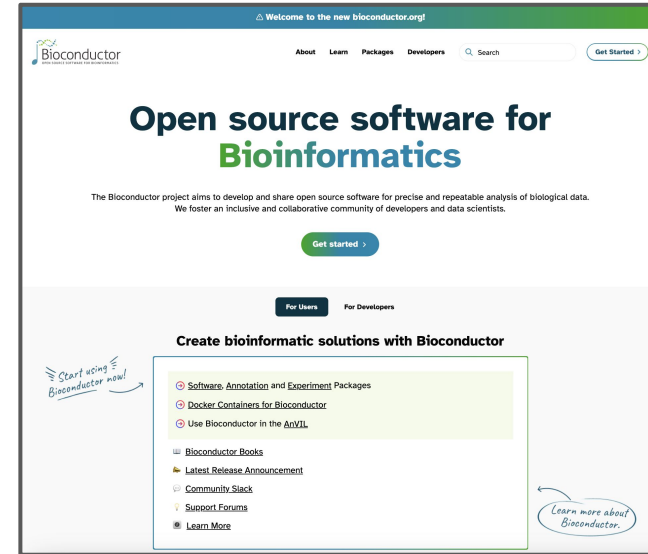
The screenshot shows the Bioconductor website interface. On the left, there's a sidebar with a search bar and a list of categories under 'Find bioViews:'. The 'Software (2380)' category is highlighted. The main content area is titled 'Packages found under Software:' and includes a note about ranking based on downloads. Below this is a table listing various packages.

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



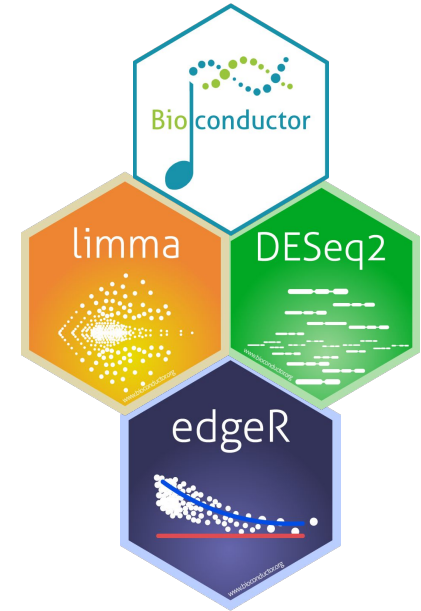
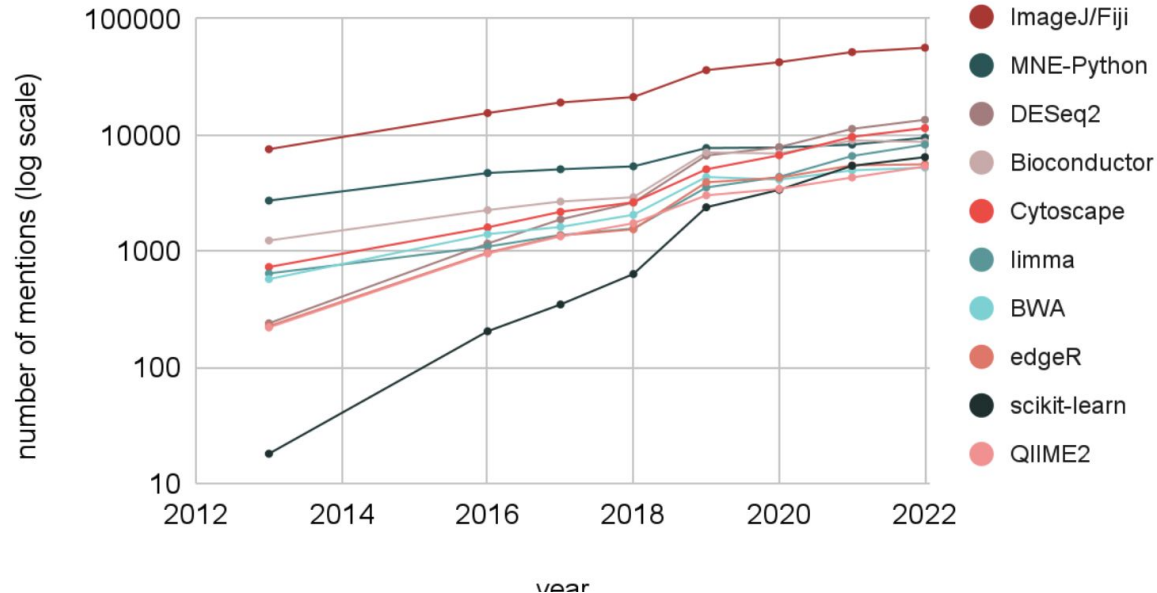
# Bioconductor in 2026

- 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

Switch to long report

Build/check report for BioC 3.23

This page was generated on 2020-02-05 11:32 -0500 (Thu, 05 Feb 2020)

Approx. Package Snapshot Date/Time (git pull): 2020-02-04 13:40 -0500 (Wed, 04 Feb 2020)

See this page for all the Bioconductor builds and their schedule.

Package status is indicated by one of the following glyphs:

<b>IN PROGRESS</b>	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package took more than 40 minutes
<b>ERROR</b>	<input checked="" type="checkbox"/> Bad DESCRIPTION file, or INSTALL, BUILD or BUILD BIN of package failed, or CHECK produced errors
<b>WARNINGS</b>	<input checked="" type="checkbox"/> CHECK of package produced warnings
<b>OK</b>	<input checked="" type="checkbox"/> INSTALL, BUILD, CHECK or BUILD BIN of package went OK
<b>NA</b>	INSTALL, BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System

Click on any glyph in the report below to access the detailed report.

Package	Maintainer	INSTALL/BUILD/CHECK
1/0247 <b>af</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
9/0248 <b>afBase</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
9/0249 <b>afClassif</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
4/0249 <b>afCorg</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
9/0247 <b>afPreproc</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
9/0247 <b>afReporting</b> 1.59.0 (android.aspx)	Laure Cougnard	OK
7/0247 <b>afReray</b> 1.79.0 (android.aspx)	Yongming Andrew Sun	OK
9/0247 <b>afSeedR</b> 1.29.0 (android.aspx)	Jiahong Fong	OK
9/0247 <b>afSSeq</b> 1.65.0 (android.aspx)	Wentao Yang	OK
19/0247 <b>afode</b> 1.41.0 (android.aspx)	Juan Pablo Acosta	OK
19/0247 <b>afCE</b> 1.29.0 (android.aspx)	Jon B Poel	OK
12/0247 <b>afGHI</b> 1.89.0 (android.aspx)	Peter Dimitrov	OK
13/0247 <b>afGME</b> 2.67.0 (android.aspx)	Sean Davis	WARNINGS
14/0247 <b>afGCH2</b> 2.51.1 (android.aspx)	Ramon Diaz-Ularte	OK



# 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 diversity funding and engage with industry

- EU Horizon, Digital Europe
- IHI, DTIF