

# The *Bioconductor* Project: Current Status

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Analysis and comprehension of high-throughput genomic data.

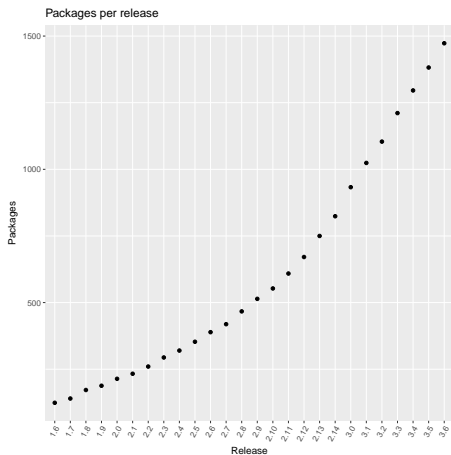
- Started 2002
- 1473 *R* packages – developed by 'us' and user-contributed.

Well-used and respected.

- 53k unique IP downloads / month.
- 21,700 PubMedCentral citations.

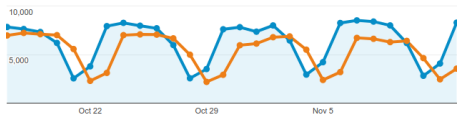
More than 1000 maintainers!

# State of the project



- Packages
- Users
- Web & support sites
- Training, workflows, & meetings
- New package submission
- Release & devel builders
- Funding
- Governance: (annual) Scientific Advisory Board; (monthly) Technical Advisory Board

# State of the project



1.	United States	<b>58,384</b> (32.78%)
2.	China	<b>20,910</b> (11.74%)
3.	United Kingdom	<b>12,265</b> (6.89%)
4.	Germany	<b>10,024</b> (5.63%)
5.	France	<b>5,536</b> (3.11%)
6.	Canada	<b>4,999</b> (2.81%)
7.	Spain	<b>4,864</b> (2.73%)
8.	Japan	<b>4,539</b> (2.55%)
9.	India	<b>4,397</b> (2.47%)
10.	Australia	<b>4,043</b> (2.27%)

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<https://bioconductor.org>

<https://support.bioconductor.org>

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The screenshot displays the GitHub interface for the Bioconductor/Contributions repository. It shows a list of 33 open issues. The top issue is 'mcSEAdata' with a 'review in progress' label and a 'WARNING' badge. Other issues include 'pace', 'CHARGE', 'BASINET', 'Numero', and 'KeyZEnrich: An all-in-one R/Bioconductor package for gene list enrichment analysis and pathway visualization'. The interface includes navigation tabs for Code, Issues, Pull requests, Projects, Wiki, Insights, and Settings. A 'New Issue' button is visible in the top right.

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# State of the project



SOUND

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# Why use or contribute to *Bioconductor*?

- Recognition.
- Access & permanence.
- Interoperability.
- Documentation.
- Support.
- Tested.





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in Bioc > 12.5 years

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```
git$ grep -l SummarizedExperiment \  
*/DESCRIPTION | wc -l  
165
```

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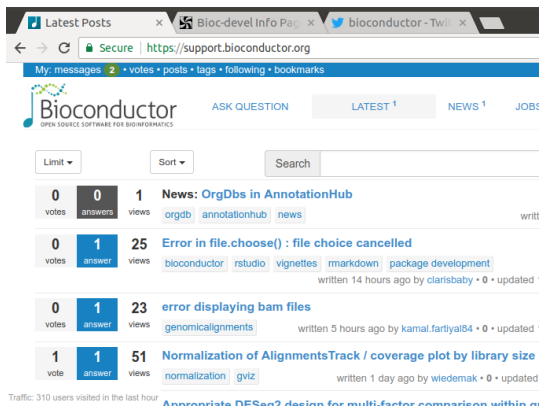
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## Documentation

<a href="#">HTML</a>	<a href="#">R Script</a>	Analyzing RNA-seq data with DESeq2
<a href="#">PDF</a>		Reference Manual
<a href="#">Text</a>		NEWS

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The screenshot shows the Bioconductor support forum interface. At the top, there are navigation tabs for 'Latest Posts', 'Bioc-devel Info Page', and 'bioconductor - Twitter'. The browser address bar shows the URL 'https://support.bioconductor.org'. Below the navigation, there are links for 'My: messages', 'votes', 'posts', 'tags', 'following', and 'bookmarks'. The Bioconductor logo is prominently displayed, along with the tagline 'OPEN SOURCE SOFTWARE FOR BIOINFORMATICS'. There are buttons for 'ASK QUESTION', 'LATEST 1', 'NEWS 1', and 'JOBS'. A search bar is located below the navigation. The main content area displays a list of posts with the following details:

Votes	Answers	Views	Title	Tags	Author	Updated
0	0	1	News: OrgDbs in AnnotationHub	orgdb, annotationhub, news		written 14 hours ago by clarisbaby • 0 • updated
0	1	25	Error in file.choose(): file choice cancelled	bioconductor, rstudio, vignettes, markdown, package development		written 14 hours ago by clarisbaby • 0 • updated
0	1	23	error displaying bam files	genomicalignments		written 5 hours ago by kamal.fartiyal84 • 0 • updated
1	1	51	Normalization of AlignmentsTrack / coverage plot by library size	normalization, gviz		written 1 day ago by wiedemak • 0 • updated

Traffic: 310 users visited in the last hour

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Multiple platform build/check report for BioC 3.6

This page was generated on 2017-11-15 15:06:34 -0500 (Wed, 15 Nov 2017).

git log  
Snapshot Date: 2017-11-14 17:00:31 -0500 (Tue, 14 Nov 2017)

hostname	OS	Arch	Platform label (P)	R session	Installed pkg
malbecT	Linux (Ubuntu 16.04.1 LTS)	x86_64	x86_64-linux-gnu	3.4.2 (2017-09-28) -- "Short Summer"	1951
tokayT	Windows Server 2012 R2 Standard	x64	mingw32/x86_64-w64-mingw32	3.4.2 Patched (2017-10-07 r73456) -- "Short Summer"	1918
veracruzT	OS X 10.11.6 El Capitan	x86_64	x86_64-apple-darwin15.6.0	3.4.2 (2017-09-28) -- "Short Summer"	1930

Package status is indicated by one of the following glyphs

- TIMEOUT** INSTALL, BUILD, CHECK or BUILD BIN of package took more than 60 minutes
- ERROR** INSTALL, BUILD, or BUILD BIN of package failed, or CHECK produced errors
- WARNING** CHECK of package produced warnings
- OK** INSTALL, BUILD, CHECK or BUILD BIN of package was OK
- NotNeeded** INSTALL of package was not needed (click on glyph to see why)
- NA** CHECK or BUILD BIN of package was skipped because the BUILD step failed
- NA** BUILD, CHECK or BUILD BIN result is not available because of an anomaly in the Build System

Package propagation status is indicated by one of the following LEDs

- GREEN** Package was propagated because it didn't previously exist or version was bumped
- RED** Package was not propagated because of a problem (impossible dependencies, or version lower than what is already propagated)
- NA** Package was not propagated because it is already in the repository with this version. A version bump is required in order to propagate it

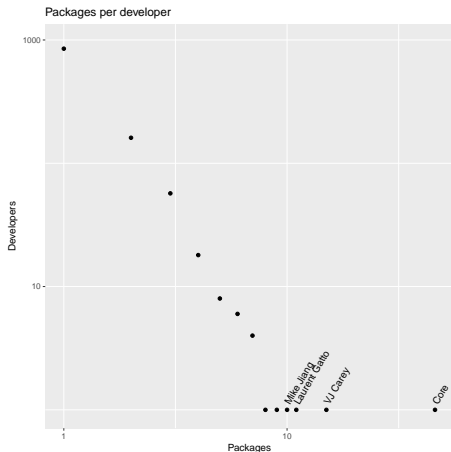
A crossed-out package name indicates the package is [deprecated](#)

SUMMARY	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
ma4base	Linux (Ubuntu 16.04.1 LTS) / x86_64	0 4 513 856 2	33 1438	2 16 146 1271	
tokayT	Windows Server 2012 R2 Standard / x64	0 3 458 330 4	29 1407	5 18 144 1244	0 0 1407
veracruzT	OS X 10.11.6 El Capitan / x86_64	0 2 509 882 3	34 1426	1 16 163 1246	0 0 1426

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

Package	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
ma4 1.26.0	malbecT Linux (Ubuntu 16.04.1 LTS) / x86_64	NotNeeded	OK	OK	
Tobias Verbeke	tokayT Windows Server 2012 R2 Standard / x64	NotNeeded	OK	OK	OK
Last Commit e6af2dc Last Changed Date: 2017-10-30 12:39:23 -0500	veracruzT OS X 10.11.6 El Capitan / x86_64	NotNeeded	OK	OK	OK
ma4base 1.26.0	malbecT Linux (Ubuntu 16.04.1 LTS) / x86_64	OK	OK	OK	

# Our contributors



- 1060 unique maintainers.
- 791 'first time' authors.

# Lessons learned from package reviews I

## 1 Interoperability

- ▶ Use feature  $\times$  sample `SummarizedExperiment`, not sample  $\times$  feature matrix.
- ▶ Use paradigms familiar to *Bioconductor* users.

## 2 Reuse

- ▶ Use `rtracklayer::import.bed()`, not custom parser.

## 3 Robust code

- ▶ Edge cases: `seq_len()` / `seq_along()`, not `1:n`.
- ▶ Code complexity: `vapply()`, not `sapply()`.

## 4 Performant code

- ▶ *Vectorize* rather than *iterate* (`for`, `lapply()`, `apply()` are all iterative).
- ▶ Reuse (e.g., `matrixStats`) before C / C++ implementation.

# Lessons learned from package reviews II

- 5 Tested code
  - ▶ Essential: evaluated example and vignette code chunks.
  - ▶ Desirable: unit tests, e.g., *testthat*.
- 6 Time and space limits.
  - ▶ Excessive computation may represent inefficient code.
  - ▶ Challenging to identify rich but modest data for illustration.
  - ▶ Experiment data packages, work flows, F1000 papers as venues for more expensive / comprehensive reproducible analysis.
- 7 Ambition
  - ▶ Implement essential features well.
  - ▶ Avoid dependencies on packages for marginal value.
- 8 Pretty
  - ▶ 'Poetry' with short lines, consistent and ample spacing, standard formatting.



# Recent developments

- Git!

```
git clone https://git.bioconductor.org/packages/limma  
git clone git@git.bioconductor.org:packages/DESeq2
```

- Large Single Cell

- ▶ *SingleCellExperiment*
- ▶ *HDF5Array*

## Large single-cell data

```
> sce = TENxBrainData::TENxBrainData()
snapshotDate(): 2017-10-30
> sce
class: SingleCellExperiment
dim: 27998 1306127
metadata(0):
assays(1): counts
rownames: NULL
rowData names(2): Ensembl Symbol
colnames(1306127): AACCTGAGATAGGAG-1 AACCTGAGCGGCTTC-1 ...
  TTTGTCAGTTAAAGTG-133 TTTGTCATCTGAAAGA-133
colData names(4): Barcode Sequence Library Mouse
reducedDimNames(0):
spikeNames(0):
```

# Large single-cell data

- Chunk-wise iteration (often transparent to the user / developer).
- Marginal summaries in `rowData`, `colData`.
- Supporting infrastructure: *ExperimentHub*, *rhdf5*, *HDF5Array*, *DelayedMatrixStats*, *beachmat*.

# Cloud computing

## Possible visions

- As now, but 'in the cloud' – <https://rstudio.cloud>.
- Exploit cloud services, e.g., BigQuery.
- Pay-as-you-play – use existing *Bioconductor* AMIs or docker containers.
- Integrated with 'third party' compute efforts, e.g., NCI, NIH in the United States.
- Federated data access.

# Events

- CSAMA (training), Brixen / Bressanone, Italy, 8 - 13 July.
- *Bioc2018* Toronto, Canada, 25 - 27 July.

# Acknowledgments

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Technical advisory board: Vincent Carey, Kasper Hansen, Wolfgang Huber, Robert Gentleman, Rafael Irizzary, Levi Waldron, Michael Lawrence, Sean Davis, Aedin Culhane

Scientific advisory board: Vincent Carey (Brigham & Women's), Wolfgang Huber (EBI), Rafael Irizzary (Dana Farber), Jan Vitek (Northeastern University), Robert Gentleman (23andMe).

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