

The *Bioconductor* Project: Current Status

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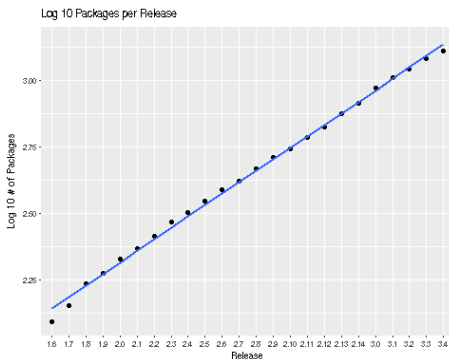
Analysis and comprehension of high-throughput genomic data.

- Started 2002
- 14736 *R* packages – developed by 'us' and user-contributed.

Well-used and respected.

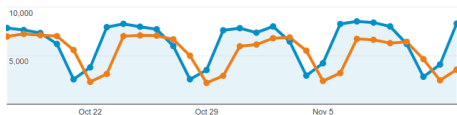
- 53k unique IP downloads / month.
- 21,700 PubMedCentral citations.

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

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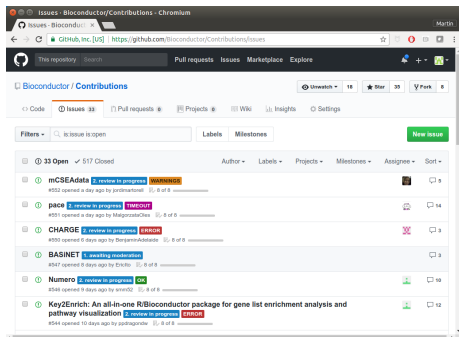
State of the project

<https://bioconductor.org>

<https://support.bioconductor.org>

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The screenshot displays the GitHub interface for the Bioconductor/Contributions repository. The main content area shows a list of 33 open issues. The issues are:

- mcSEAdata**: review in progress, WARNING (opened 1 day ago by jorntermont)
- pace**: review in progress, TIMEOUT (opened 1 day ago by MajoristaChia)
- CHARGE**: review in progress, ERROR (opened 6 days ago by BenjaminAdelaide)
- BASINET**: awaiting moderator (opened 8 days ago by EricCh)
- Numero**: review in progress, OK (opened 9 days ago by svenh2c)
- KeyZEnrich: An all-in-one R/Bioconductor package for gene list enrichment analysis and pathway visualization**: review in progress, ERROR (opened 10 days ago by pathogenesis)

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State of the project



SOUND

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Recent developments

- Git!

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

- Large Single Cell

- ▶ *SingleCellExperiment*
- ▶ *HDF5Array*

- Lessons from 100's of package reviews

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*.

Why use or contribute to *Bioconductor*?

- Recognition.
- Access & Permanance.
- 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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Documentation

HTML	R Script	Analyzing RNA-seq data with DESeq2
PDF		Reference Manual
Text		NEWS

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

Votes	Answers	Views	Title	Tags	Author
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
malbec7	Linux (Ubuntu 16.04.1 LTS)	x86_64	x86_64-linux-gnu	3.4.2 (2017-09-28) -- "Short Summer"	1951
tokay7	Windows Server 2012 R2 Standard	x64	mingw32/x86_64-w64-mingw32	3.4.2 Patched (2017-10-07 r73456) -- "Short Summer"	1918
veracruz7	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)
- skipped** 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

Click on any glyph to see more info about the system (e.g. compiler) (*) as reported by 'uname -s', except on Windows and Mac OS X (*) as reported by 'gcc -v'

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
- NO** Package was not propagated because of a problem (impossible dependencies, or version lower than what is already propagated)
- UNNEEDED** 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	0 0 1407	0 0 1407
tokay7	Windows Server 2012 R2 Standard x64	0 3 488 330 4 29 1407	5 18 144 1244	0 0 1407	0 0 1407
veracruz7	OS X 10.11.6 El Capitan x86_64	0 2 509 882 3 34 1426	1 16 183 1246	0 0 1426	0 0 1426

A 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	Linux (Ubuntu 16.04.1 LTS) x86_64	NotNeeded	OK	OK	
Tobias Verbeke	tokay7 Windows Server 2012 R2 Standard x64	NotNeeded	OK	OK	OK
Last Commit e6af2dc Last Changed Date: 2017-10-30 12:39:23 -0500	veracruz7 OS X 10.11.6 El Capitan x86_64	NotNeeded	OK	OK	OK
ma4Base 1.26.0	malbec7 Linux (Ubuntu 16.04.1 LTS) x86_64	OK	OK	OK	

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

Future challenges

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

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

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