The *Bioconductor* Project: Current Status

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Bioconductor

Analysis and comprehension of high-throughput genomic data.

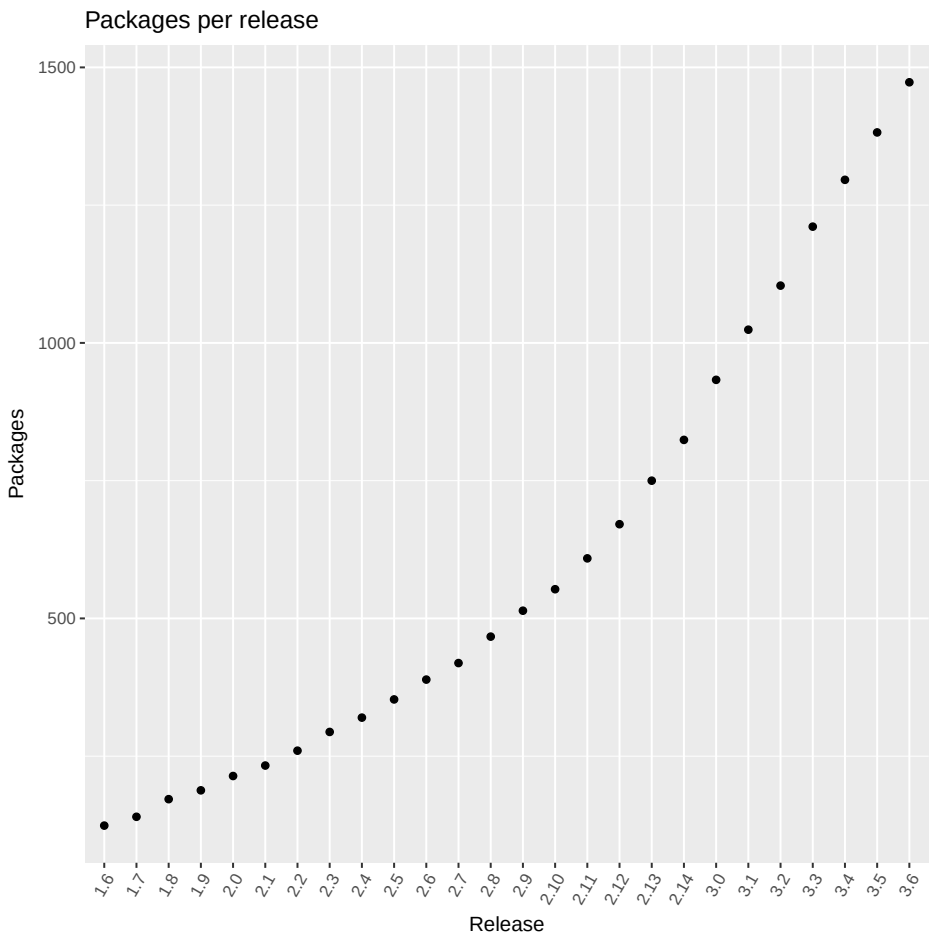
- Started 2002
- 1473 *R* packages – developed by 'us' and user-contributed.

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

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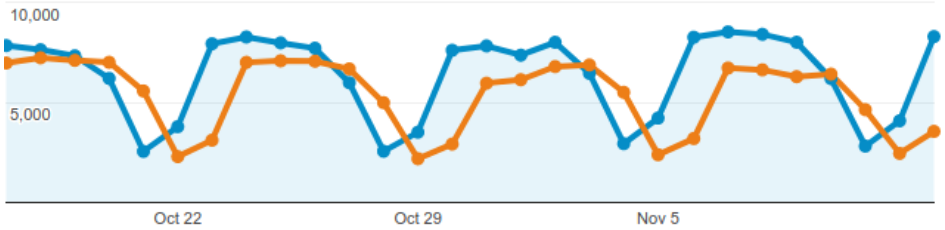

1.	United States	58,384 (32.78%)
2.	China	20,910 (11.74%)
3.	United Kingdom	12,265 (6.89%)
4.	Germany	10,024 (5.63%)
5.	France	5,536 (3.11%)
6.	Canada	4,999 (2.81%)
7.	Spain	4,864 (2.73%)
8.	Japan	4,539 (2.55%)
9.	India	4,397 (2.47%)
10.	Australia	4,043 (2.27%)

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https://bioconductor.org
https://support.bioconductor.org

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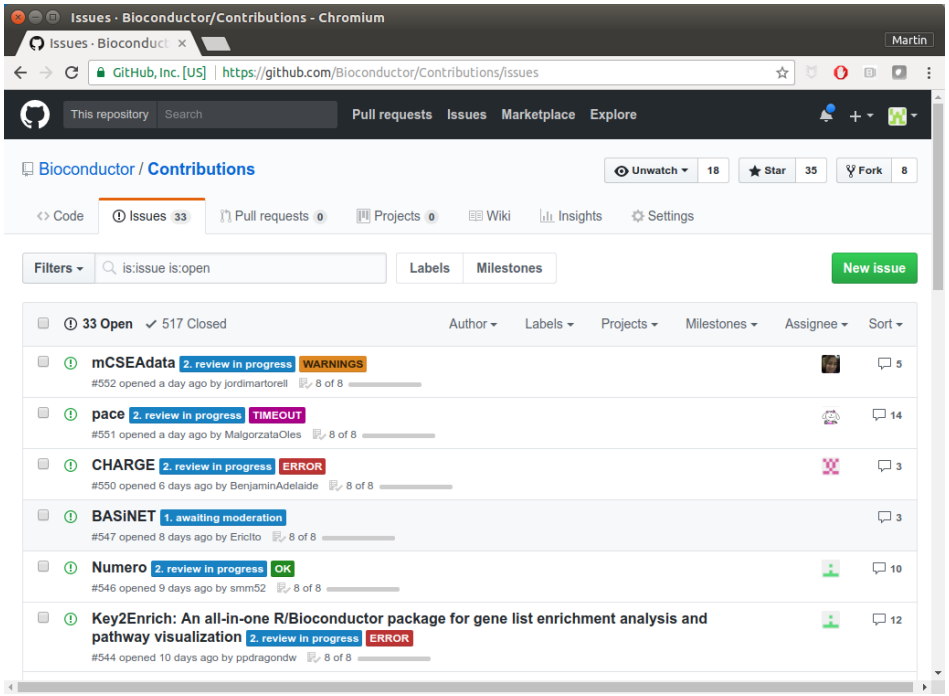

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Why use or contribute to *Bioconductor*?

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

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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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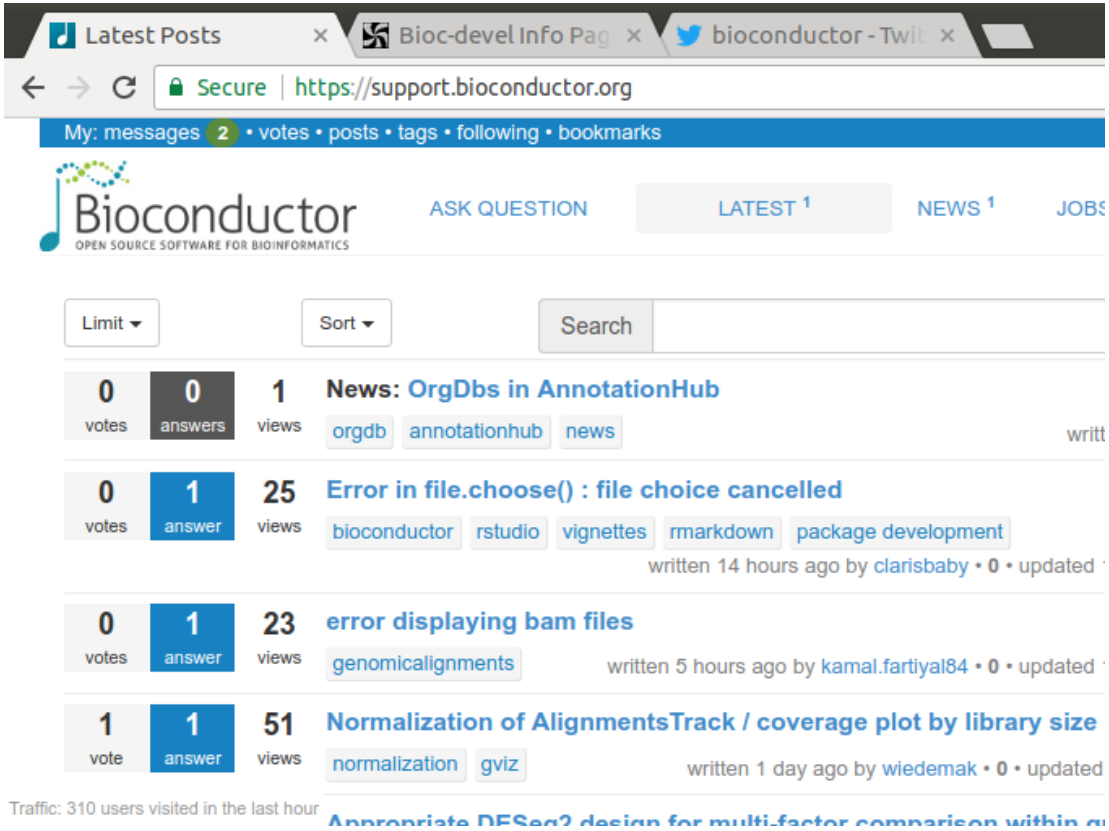

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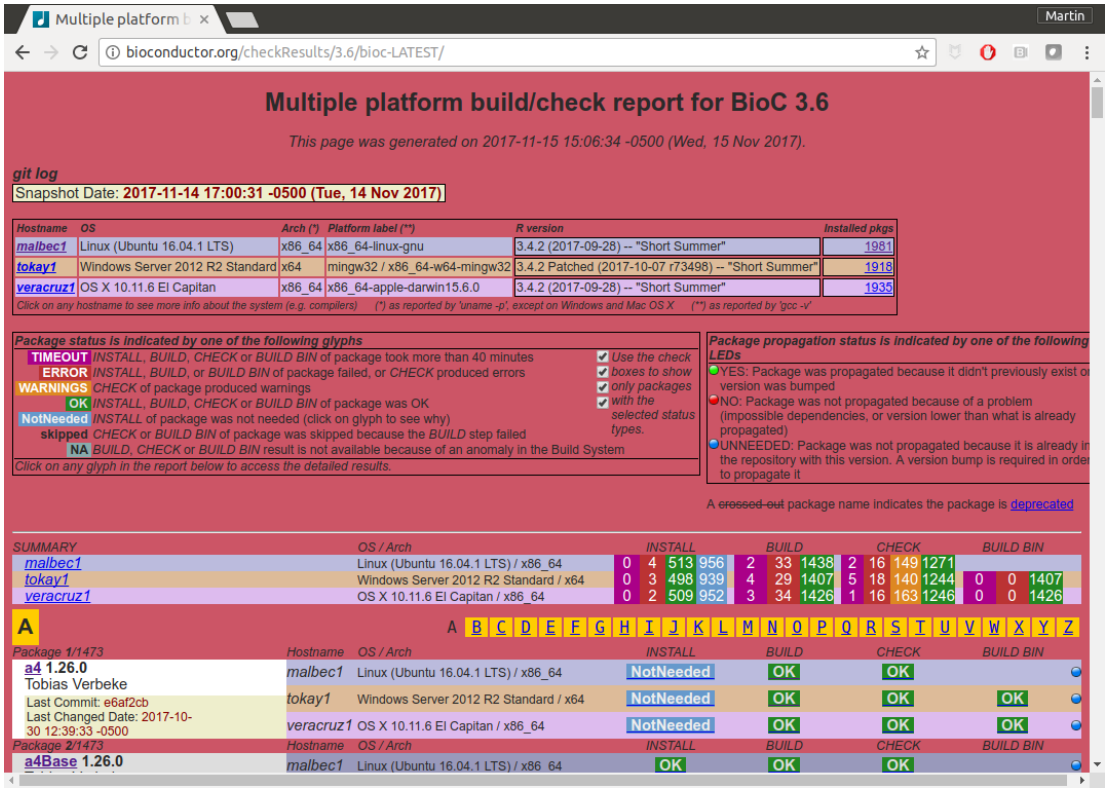
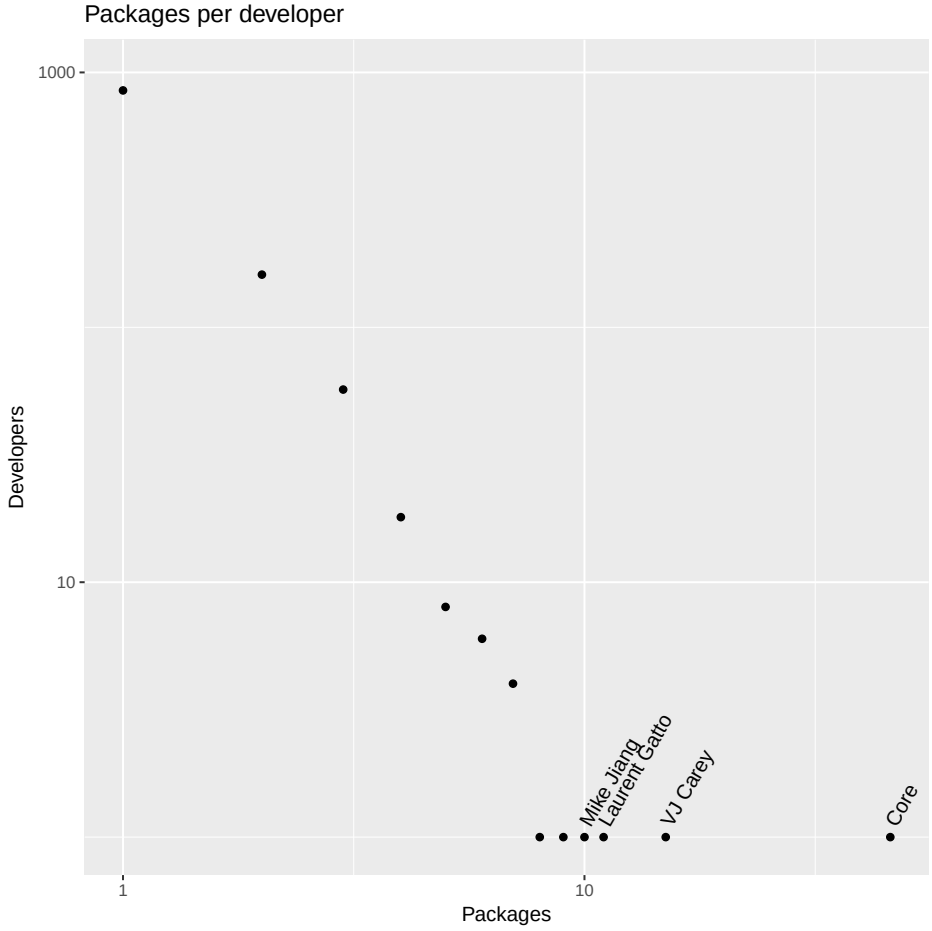


Our contributors



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

Lessons learned from package reviews I

1. Interoperability
   - Use feature × sample `SummarizedExperiment`, not sample × 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.
   - Desireable: 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): AAACCTGAGATAGGAG-1 AAACCTGAGCGGCTTC-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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