The *Bioconductor* Project: Current Status

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Bioconductor

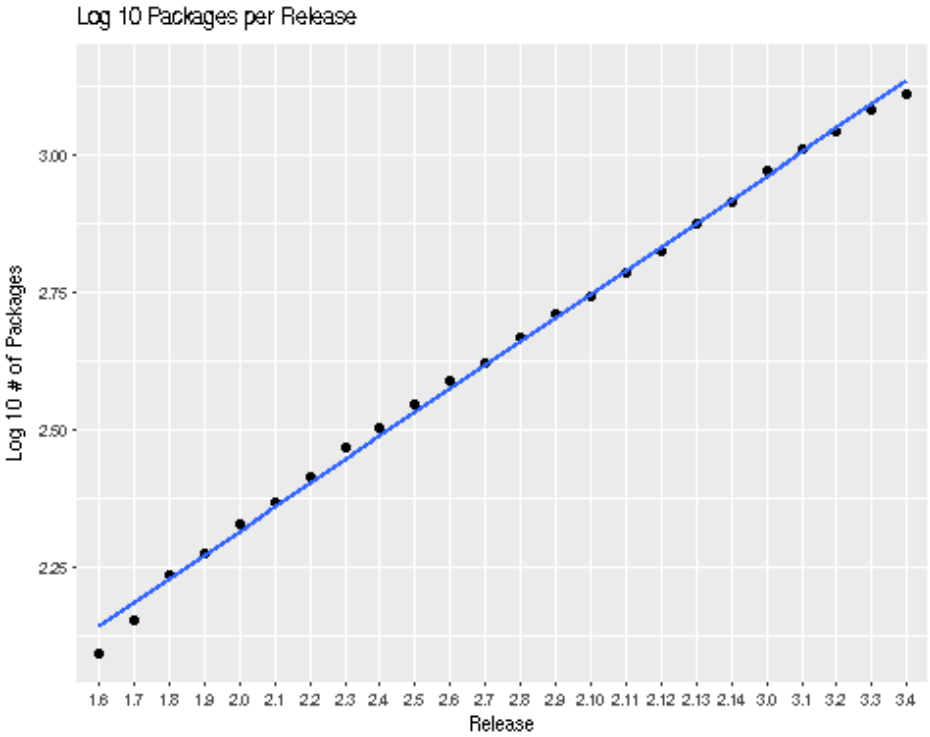
Analysis and comprehension of high-throughput genomic data.

- 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

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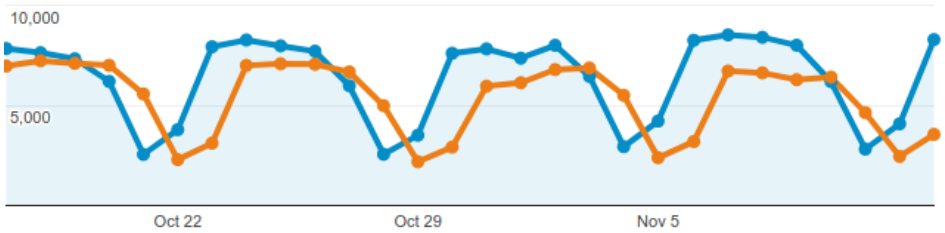

1.	United States	**58,384** (32.78%)
2.	China	**20,910** (11.74%)
3.	United Kingdom	**12,265** (6.89%)
4.	Germany	**10,024** (5.63%)
5.	France	**5,536** (3.11%)
6.	Canada	**4,999** (2.81%)
7.	Spain	**4,864** (2.73%)
8.	Japan	**4,539** (2.55%)
9.	India	**4,397** (2.47%)
10.	Australia	**4,043** (2.27%)

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

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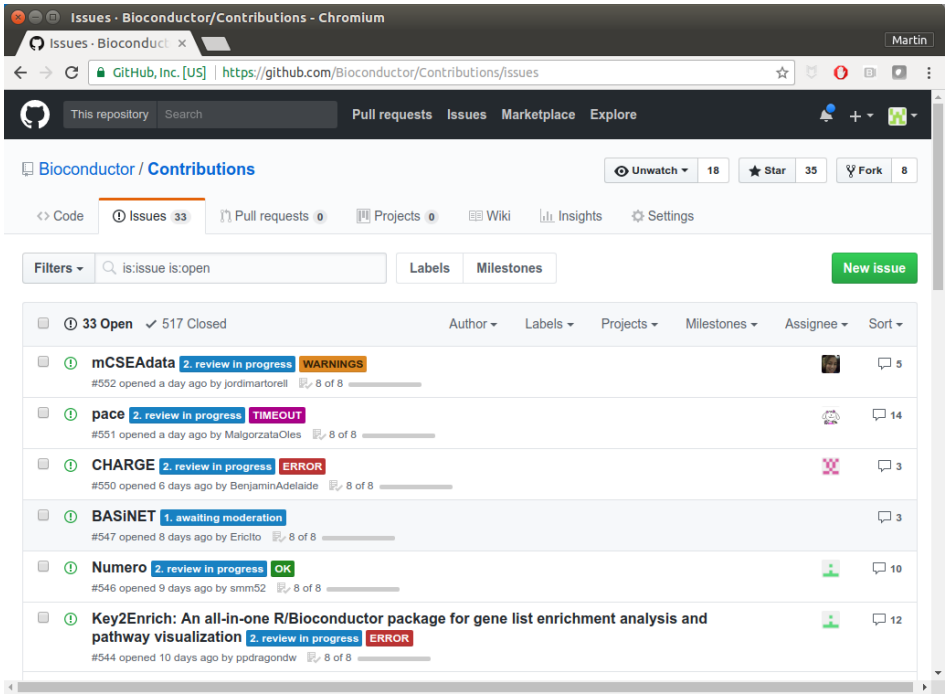

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Recent developments

- 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): 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*.

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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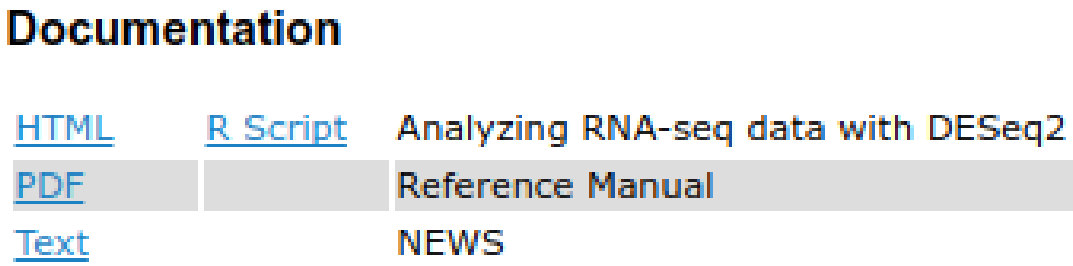

Documentation

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

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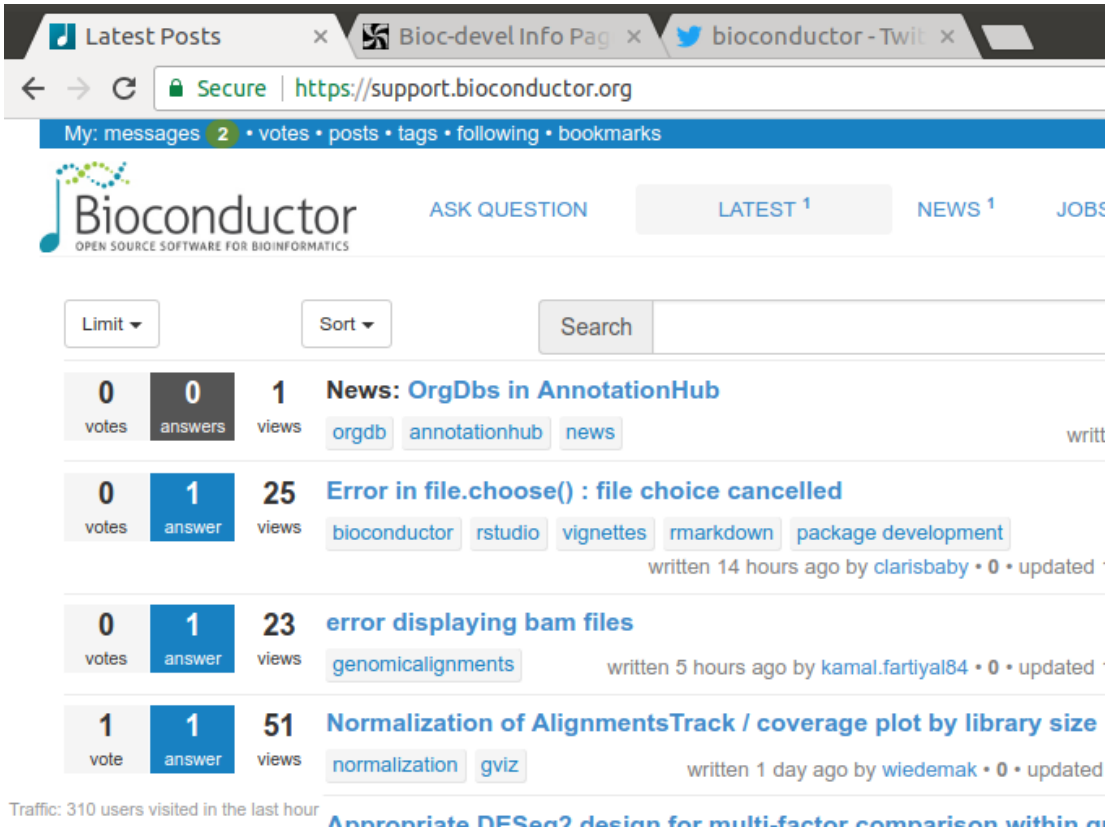

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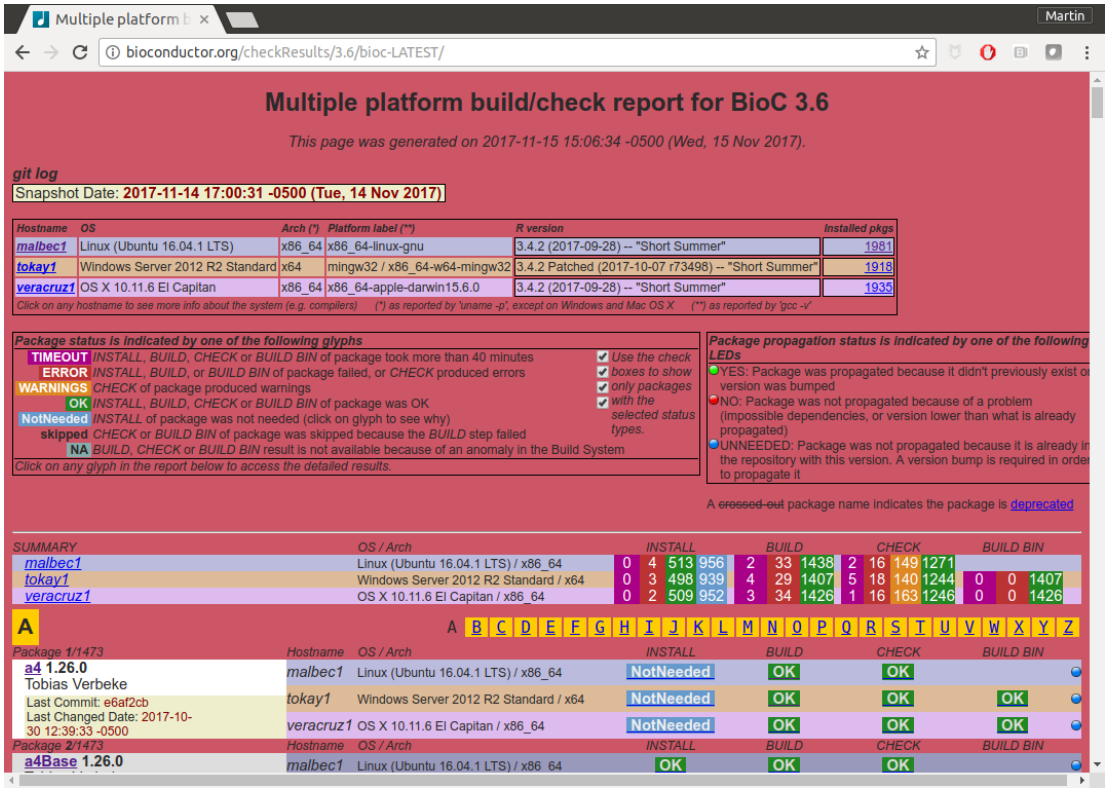

Lessons learned from package reviews I

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.
   - 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

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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