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

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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](image)

<table>
<thead>
<tr>
<th>HTML</th>
<th>R Script</th>
<th>Analyzing RNA-seq data with DESeq2</th>
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Our contributors

- 1060 unique maintainers.
- 791 'first time' authors.
Interoperability
- Use feature × sample SummarizedExperiment, not sample × feature matrix.
- Use paradigms familiar to Bioconductor users.

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

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

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): 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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