

Bioc Technical Advisory Board Minutes

5 February 2026

Present: Laurent Gatto, Gabriele Sales, Vince Carey, Lori Kern, Helena Crowell, Hugo Gruson, Robert Castelo, Michael Lawrence, Hervé Pagès, Levi Waldron, Marcel Ramos, Kasper Hansen, Rafael Irizarry, Ludwig Geistlinger, Henrik Bengtsson, Gabriele Sales, Andres Wokaty, Alex Mahmoud

Absent: Wolfgang Huber, Jacques Serizay

:00 - :05 December [minutes](#) approved.

:05 - :30 Hugon Gruson “pass the microphone” [[slides](#)].

- Proposal to extend current Bioc testing stack (R CMD check + BiocCheck) with rchk + lintr; “Bioconductor” lintr tag would be available to the wider community
- Comments:
 - Long tests in Bioc available, but underused.
 - Initial adoption via SPB for newly submitted packages?
 - Implementation of lintr in Rust underway, with significant performance gains.
 - R-universe offers a flag to include BiocCheck.

:30 - :35 Brief note by Levi on governance considerations related to Software Sustainability Institute opportunity.

:35 - :45 Working group updates.

- **Spatial omics:** two hackathons to take place in April (Italy) – one joint with scverse, the other Bioconductor-centric; OSTA [book](#) online, [paper](#) under review.
- **Conference planning/hackathon management:** Work underway to include hackathons as a regular component in parallel/preceeding (Euro)BioC.
- **EDMA ontology/BiocViews:** BiocViews has been given an OBO representation by Sean Davis to facilitate new methods of cross-ontology mapping.

:45 - :50 GitHub actions for Bioconductor developers.

- [biocthis](#) is great, but creates a complex workflow based on commodity actions outside our control.
- An alternate approach is for Bioconductor to define actions (Mike Smith has done some of this), which are used in a simple workflow oriented towards developer needs.

- This needs to be consistent with R-universe procedures; see this [tech note](#) for new capability of R-universe oriented actions. [Implications are noted for package review/SPB]
- New working group on GHA to be formed, chaired by Hugo. Leo Collado-Torres (biocthis) would be good to include; various TAB members also expressed interest.

:50 - :55 Update on large matrix methods.

- Rafa will share a dataset that reaches current limitations as a use-case.
- Current sparse matrix representation = indices + values, however, length $2^{*}31$ vectors (in R) too small for the number of non-zero entries.
- New representation would require reimplementing of, e.g., SparseMatrixStats. (Hervé has been/is working on some of this, but need to consider long-term viability)

:55 - :60 R-universe and other topics.

- Large investigation by Lori on packages that need [intervention](#):
New site to collect packages that have been deprecated, but might be saved, As well as packages with large files (to be deprecated with the next release).
- View of link to R-universe build outcomes:

To the developers/maintainers of the Biostrings package:

- Allow up to 24 hours (and sometimes 48 hours) for your latest push to `git@github.com:bioconductor/packages/Biostrings.git` to reflect on this report. See [Troubleshooting Build Report](#) for more information.
- Use the following [Renviron settings](#) to reproduce errors and warnings.
- If 'R CMD check' started to fail recently on the Linux builder(s) over a missing dependency, add the missing dependency to 'Suggests:' in your DESCRIPTION file. See [Renviron.bioc](#) for more information.

[raw results](#)

Package 7/20	Hostname	OS / Arch	INSTALL	BUILD	CHECK	BUILD BIN
Biostrings 2.77.0 (landing page) Hervé Pagès Snapshot Date: 2025-05-06 18:16 -0000 (Tue, 06 May 2025) git_url: https://git.bioconductor.org/packages/Biostrings git_branch: devel git_last_commit: 504fc67 git_last_commit_date: 2025-04-15 13:17:28 -0000 (Tue, 15 Apr 2025)	bbstest2	Linux (Ubuntu 24.04.1 LTS) / x86_64	OK	OK	ERROR	

See [other builds for Biostrings](#) in R Universe.

:50 - :90 Discussion on large matrix methods continued.

- Row- vs. column-major vs. triplet representation (most flexible, but insufficient)
- Current workaround by Hervé: non-zero values as separate vectors for each column
- Not a Bioconductor-specific issue; should this be brought to R core instead?

Appendix: Food for thought (not discussed).

Hervé Pagès 10:07 PM
1,879,397 downloads (distinct IPs) in 2025 vs 1,139,800 in 2024. That's a 65% increase! Does this reflect the growth of our user base or is there something else? BTW the number reported here <https://bioc.2026.bioconductor.org/sponsors/> is for 2024, not 2021. (edited)

