Bioc Technical Advisory Board Minutes

3 July 2025

Present: Vince Carey, Charlotte Soneson, Ludwig Geistlinger, Helena Crowell, Stephanie Hicks, Levi Waldron, Rafael Irizarry, Michael Lawrence, Sehyun Oh, Jacques Serizay, Henrik Bengtsson, Marcel Ramos, Alexandru Mahmoud, Lori Kern, Andres Wokaty, Tim Triche, Hervé Pagès
Absent: Laurent Gatto, Davide Risso, Wolfgang Huber, Kasper Hansen

:00 - :04 Previous minutes approved.

:05 - :30 GBCC2025 debrief
- CoFest output (Alex/Charlotte): iSEE server (https://isee.bioconductor.org/).
    - Is there a possibility to have allocations e.g. on de.NBI cloud in addition to Jetstream2?
    - AU resources on Nectar cloud via Galaxy Australia (https://ardc.edu.au/services/ardc-nectar-research-cloud/) in motion (Alex).
    - How much maintenance is expected/what can we commit to?
    - Add Bioconductor branding and grant acknowledgement.
    - Look at error handling, adversarial inputs.
- GPU technology update by Pariksheet Nanda, re: languages that support GPUs.
- Discussion about wrapping Bioconductor packages into Galaxy tools and maintaining those tools (Maria, Gretta Yagudayeva, Charlotte, Marcel, Robert Castelo).
    - Blog post.
    - See also Zulip: "galaxy" channel - "Adding Bioconductor tools into Galaxy" topic.
- Comments:
    - More contributions from Galaxy than from Bioconductor.
    - Virtual platform less elaborate than previous years.
    - Felt less newcomer-friendly content-wise than in previous BioCs (missing introductory workshops for example - how to write a package, unit testing, documentation).
    - SAB suggestion: additional conference/meeting, focused on development and developers.
    - Could also add more technical talks/developer focus to BioC.
    - Should a new conference series be coupled with another conference (Statgen, ASA, ENAR, useR)? Co-hosting with useR could mean more easily having joint workshops such as writing your first package, R Markdown/Quarto.
    - Should we seek some kind of funding support for a conference?
    - Focus on mentoring new developers.
    - One day with two tracks (developer, user beginner)?

    - Seems to be room for both workshops and a contribution-oriented hackathon, which could target a range of expertise (even developers could benefit from certain tutorials).

:30 - :32 TAB Nominations - deadline August 31.

- Charlotte's, Laurent's, Stephanie's terms are ending.
- Probably another one or two haven't met 70% attendance requirement.
- CAB and TAB forms are open on website - Maria will make public announcement.

:32 - :34 Hacktoberfest

- Identify repositories/issues to be tagged with #hacktoberfest, could create a github.com/Bioconductor project board.
    - Continue Sweave -> Rmd conversion.
    - R dev day (Heather Turner) has a repository with issues that is populated over the year: https://github.com/r-devel/r-dev-day.
    - Create a Zulip channel.

:34 - :39 Biostrings maintenance

- Current maintainer Aidan Lakshman is giving up the project in September, need a new maintainer.

:39 - :45 Working group updates

- Spatial (transcript)omics (Helena)
    - OSTA online book
        - Public version at https://lmweber.org/OSTA/ (current developments on another branch).
        - See appendix for who's involved.
        - Recently submitted to Bioc.
        - Got a brief comms-style paper draft.
    - Helmholtz Association grant submitted here.
        - LOS from Wolfgang (Rarr), Cannoodt (AnnDataR, Open Problems), Stegle/Theis (scverse, scan/squidpy, SpatialData), Vince (Bioc).
- Package Build Report Triage and Package Reviews (Lori)
    - 8 active reviewers, 3 occasional ones, 1 in training - always need for more!
- Workflows (Charlotte)
    - Setting up agreement with the Journal of Open Source Education (JOSE) for publication of workflows: create a 'Bioconductor' track with editors from the community (Vince, Laurent, Mike and Charlotte to start with), a workflow that has been reviewed and accepted into Bioconductor will benefit from a simplified review process at JOSE.
- EDAM collaboration (Maria).

:45 - :60 GitHub Actions in Bioconductor

- Slides: GHAs_in_Bioconductor

- Coordinate with the broader R community - are there general actions that we can use/extend?
- Actions are quickly outdated.