Bioc Technical Advisory Board Minutes

3 April 2025

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

:03 - :07. Approve minutes, overview of working groups.

:07 - :08 Joint meeting of CAB/TAB, election timing.

- Tentatively: Announce at GBCC2025; nominations open until end of August; discuss nominees at September meeting; new members joining in October.

:08 - :27 Working group reports.

- Tim Triche: pangenome working group
    - What are the advantages of preprocessing the data in R rather than outside? Infrastructure for doing exploratory analysis related to genomic ranges in R is helpful. Looking for the minimal amount of "glue" to interface with external tools.
    - Community in general needs tools to work on pangenomes (not just in R).
    - Working on many genomes simultaneously vs making *the* pangenome (very context dependent).

:27 - :33 Containers

- Alex built Apptainer container and GitHub Action to build containers. Check #singularity slack channel - feedback welcome.
- Would be useful to have dedicated containers suitable for running R CMD check on packages with minimal effort. In principle making different flavors is straightforward - discuss in GitHub issues.

:33 - :38 Upcoming conference, possible projects for post-conference cofest at Weill Cornell.

- Hackathon-style, but also for other things than code (documentation, training material).
- Prioritize projects that require core team involvement.
- Dataconductor, AHub and EHub futures. AHub may not need separate identity.
- python interop – "venv" vs miniforge. Blending better with posit's Config element DESCRIPTION? Other languages.
- Quarto – what can we do to make it easier to use and benefit from it for various purposes, are there pain points for the BBS? PR open for BiocStyle.

- Alex requested to help organize cofest on Bioc side with Ahmed from Galaxy side. Ok to act as point person, but would love volunteers if anyone is interested to lead subgroups/projects.

:38 - :52 r-universe progress
- https://bioc.r-universe.dev/builds
- Bundling external code inside the package vs having it as a system dependency (graphviz as an example). R Core members reached out to suggest building and using binaries for external dependencies. Centralized/shared dependency management. Is this process relying on 'too few' people? R Foundation/R Core committed to support the process. What would be the process for requesting a new dependency binary? Is there documentation available? Underlying code base/material is largely available.

:52 - :60 Open floor
- Value of code browser & search at code.bioconductor.org?
    - Very valuable, used a lot by TAB members - use it to see what is actually on Bioc, and for packages that don't have a separate GitHub repository.
    - If the switch from gitolite to GitHub goes through we will have the code browser by default.
    - Mirror at https://github.com/bioc (third party).
    - Could we make the code search based on the new tree-sitter parser from Posit (which is now used for GitHub's code search)?