Bioconductor Community Advisory Board (CAB) Agenda

Feb 12, 2026

Members: Aedin, Eliana, Enis, Fabricio, Izabela, Johannes, Kevin, Kozo, Laurent, Lluís, Lori, Maria, Martha, Mengbo, Oluwatobilola (Tobi), Stevie, Tuomas, Umar, Zahraa, Zuguang

Attending: Kozo, Lluís, Lori, Izabela, Kevin, Laurent, Johannes, Tuomas, Stevie, Eliana, Martha, Zahraa, Fabricio
Regrets: Maria
Guests:

Sign Up for CAB lead discussion

:00 - :5 Welcome + Review minutes from previous meeting for posting

Jan 2026

NEW TIME SWITCH NEXT MONTH! MARCH
Proposed new time: Will send a voting link post meeting. Please vote by Feb 20th.

:5–10 Managing Ongoing Tasks

https://github.com/orgs/Bioconductor/projects/15
We understand that this is volunteer but to keep track of ideas and TODOs and try to push things forward that we feel are important

- Two issue kanbans (about the new event management system [and Champion program]) have been moved from "In Progress" to "Done." This progress has been summarized in a biocblog post on pull request https://github.com/Bioconductor/biocblog/pull/103/changes .

:10-30: CAB Led Discussion: Kevin SSI Fellowship

For the CAB CAB Feb 2026 SSI fellowship
Original application SSI fellowship 2026 Kevin Rue-Albrecht

How should we coordinate with the EDAM Metabolomics Working Group?

- Kevin and the group are planning to meet together. (That group meets on Zoom every other week.)

Possible Remote interactions for EuroBioc2026 since Kevin is unable to attend in person
biocViews visibility possibly added by conversion to obo format (already investigated by Sean Davis)

:30-40 Support site & Zulip forums (Tuomas)

Tuomas comment on Zulip:
Discussion forums
Currently, we have a Zulip and Bioconductor support site. They both currently have their own purpose; Zulip is for general community discussion, while the support site is for users to seek help. Questions and information on the support site can also be searched through search engines.
My concern is that Bioconductor has expanded a lot, and it has become difficult -- in my opinion -- to find information when all questions appear in a single stream. Dedicated topics or channels, e.g., one for microbiome analysis, would make navigation much easier. Currently, one can add tags, but I think that does not solve the issue completely.
Because of this issue, we have created our own GitHub forum for microbiome analysis, but that is not optimal either.
Question: Is it possible to add channels to Support forum? (We could also discuss the discussion forums in general. Single forum fulfilling the aforementioned aspects could be the most optimal solution.)

- Lluis comment in Zulip: the support site is built using the biostars engine. But it is not well supported and the core team is considering moving away from it.

As the core team investigates moving to a new platform please continue to give feedback on what is current short comings or ideal features. Suggestions welcome:

- Forums would be useful

:41-50 Guix Consensus Documents (Laurent):

https://codeberg.org/guix/guix-consensus-documents/src/branch/main/001-gcd-process.md

:50-:55 Other language discussion (Tuomas)

Tuomas discussion on Zulip:
Bioconductor is not limited to any programming language. However, for historical and other reasons, R is the main language.
I talked with many people, for instance in ABACBS/BioCAsia, and many of them said that they are not using Bioconductor because they are using Python. So they did not know that Bioconductor is not limited to R (especially now when there is more activity in Python).
Bioconductor's main points are the community of bioinformaticians and the standards / quality of software. These can be transferred to any language. I think we

should highlight these aspects more and educate the community that there are development in other languages also.
Lots of AI/ML development is happening in Python which draws people from R. In the future, this could become a vital issue for Bioconductor if less people use R and the community starts to shrink. If we educate people more and developers see active Bioconductor efforts in other languages, this could encourage growth in those languages as well.

- Lluis comment: I think Bioconductor is focused on R, from the web page:

  > About Bioconductor
  > Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community.

  Of course this can change if the community wants that as the main description says: "The Bioconductor project aims to develop and share open source software for precise and repeatable analysis of biological data." which I think is what you alluded to.
  There are similar projects on different languages with biopython, biojava, bioperl, ... each with different focus based on the interests of their communities. I'd like to know how AI will you make ethical open source AI, and the analysis precise and repeatable. Last time I read about repeatable work with AI it involved rebuilding the linux kernel. R has already tools to deal with AI, MCP, A2A and other new developments. In addition I am not sure we need something specific for biological data. The tools work well for Bioconductor already:
  https://lawremi.github.io/wizrd/articles/biomart-mcp.html

Support from/for Bioconductor and external collaborator funding / collaborative efforts between groups

- Python, Julia, Rust have all had interest
- Short example for combined R + Python analysis of LC-MS metabolomics data https://rformassspectrometry.github.io/Metabonaut/articles/SpectriPy-tutorial-metabonaut.html

This seems like an excellent conversation for a joint CAB/TAB meeting

:55-:00 Any Other Business

Nick and Lori created a new organization to organize/centralize Bioconductor hackathon ideas. More details coming soon….