

# Bioc Technical Advisory Board Minutes

5 September 2019

Bluejeans: <https://bluejeans.com/272538961>

Attending: Martin Morgan, Stephanie Hicks, Charlotte Soneson, Laurent Gatto, Vince Carey, Rafael Irizarry, Aaron Lun, Kasper Hansen, Matt Ritchie, Aedin Culhane, Levi Waldron, Sean Davis, Robert Gentleman

Regrets: Wolfgang Huber, Michael Lawrence

## Schedule

:00 - :05 Minutes and action items from previous meetings

- [Minutes](#) approved
- Code of Conduct Committee. Levi will chair, Stephanie also volunteers
- Community Advisory Board -- [preliminary governance document](#); discussed below

:05 - :35 Material for review

- Overview of current Bioconductor funding
  - [U41](#): Vince, Rafa, Martin preliminary meeting to discuss renewal; will meet with Program Officer
  - [U24](#): Original renewal resurrected & funded! Levi, Martin, Vince, Davide Risso
  - [AnVIL](#): <https://anvilproject.org> cloud computing
  - [CZI seed network](#): monthly telecons scheduled
- Events
  - BiocAsia: Sydney Dec 5-6. Website is live (<https://bioconductor.github.io/BiocAsia/>) and registration will open soon. Speakers confirmed: Martin Morgan, Helena Crowell, Elana Fertig (international) and Simon Poon (local). Rafa Irizarry and John Marioni will also be in Sydney for the BioInfoSummer symposium (<https://bis.amsi.org.au/>) which BioC Asia is part of and may attend.
  - [BiocEurope](#) (<http://eurobioc2019.bioconductor.org/>): Brussels Dec 9-10; Organisers: Laurent Gatto and Axelle Lorient (local organizers), Mark Robinson, Charlotte Soneson, Wolfgang Huber, Lieven Clement, Martin Morgan.
  - Meetups
- Committees
  - U.S. Conference (Levi)
    - Next meeting Fri Sept 6 9:30am EDT. Will establish roles and prepare for call for organizing members.
    - Planned for Boston, dates tentatively July 29-31 (Weds - Fri)
  - Emerging Topics (Vince)

- nuc-seq/spatial transcriptomics queries from Stephanie - Deep Ganguli
- scalability metrics on a [new Slack channel](https://community-bioc.slack.com/messages/CM8TCBMH6)  
(<https://community-bioc.slack.com/messages/CM8TCBMH6>)
- [ensembl APIs](https://gist.github.com/vjcitr/7295067e6592213823c28b9421eb5fdc)  
(<https://gist.github.com/vjcitr/7295067e6592213823c28b9421eb5fdc>)
- Working groups
  - Developer forum: first session (Mike Smith talking about biomaRt; Aaron Lun about single-cell). [YouTube](#). 31 people listened for 1000 minutes; 17 - 18 participating at any one time.
- Other:
  - Biostars working on an [updated support site](#) -- updated back-end; consistent deployment of Bioc / Biostars so better opportunities for support. Feedback welcome at [#support-site-update](#).
  - [DFrame](#) (make DataFrame a virtual class, with DFrame a concrete installation)
    - Discussion about whether technical justification for this change outweighs work it creates
    - This has made a lot of work for the core team, and likely many others where there are serialized S4 objects and ``new("DataFrame", )`` code.
    - TODO: What is the governance process for making a significant change like this? There was an internal discussion among Martin's group, but it's difficult to know when a change needs to be aired to the community. This is a topic for discussion and report back in the next meeting.
  - NCI image analysis [workshop & hackathon](#).
  - Rsamtools CRAM support imminent. gs / aws remote access foreseeable.
  - NEED: BigWig reader doesn't work reliably on windows -- should we invest in this?
  - Rsubread [now works on Windows!](#)

#### :35 - :45 Serialization

- Serializing S4 challenges: serialized complex S4 objects can be subject to bit rot or can limit the ability to re-design and improve classes.
  - One approach is to avoid serializing, instead serialize base R objects and use constructors.
  - One reason to keep data formats in as simple as possible (vs serialized S4) is to allow data (e.g. ExperimentHub) accessible to outside the R community (e.g. Python)
  - Another is to make sure `updateObject()` will work. Versioned classes may be part of this. Argument: if we are committed to S4 we should be able to serialize it.
  - Heard strong opinions for/against both approaches.
- Current state (Michael -- loading serialized objects in base R)
  - Discussions with R core and Gabe Becker indicate that a hook called on object load would be feasible. To do it right, we would want to attach the package

version, but that would require a change in serialization format, at least for S3 objects. Gabe is working on a proposal.

- Better approaches to serializing as S4 ? `serializeS4()`. API for serialization / deserialization
- Best practices?
  - Communication of best practices, whatever they are, to the community
  - Will be further discussion in Developer's Forum
- Action item: need technical solutions for conversion between S4 and more primitive entities.

:50 - :59 Community Advisory Board

- [Preliminary governance document](#) presented
- Idea is to separate out non-technical responsibilities currently done by technical advisory board, e.g. training, education, conference oversight, code of conduct
- Additional ideas: organize communities of interest around topical areas. E.g. single-cell RNAseq, ..., how to foster participation through recognition (F1000 publication; funding; ...)