ITCR Training and Outreach Working Group

Thursday, December 14, 2017 Meeting Notes

4pm Eastern

Toll-free: 855-259-6342; \*\*Conference Code: 40152#; \*\* Security PIN: 256871#

WebEx When it's time, [Join Meeting.](https://cbiit.webex.com/cbiit/e.php?MTID=m5142a86eb7872cc8b8e671a3075c1e6d)

**Google Doc for the Meeting:**

[ITCR-TOW-Dec-2017](https://docs.google.com/document/d/1LX9NhlQ8NxcI0rTet6FkSUqDmHbNDscG9szob8ivUEc/edit)

**Attendees: Please sign in!!**

Mike Ryan, JHU / MD Anderson

Mary Goldman, UC Santa Cruz

Mervi Heiskanen, NCI

Leah Mechanic, NCI

David Hanauer, U of Michigan

Juli Klemm, NCI

Michael Reich, UCSD

Bradley Broom, UT MD Anderson Cancer Center

Martin Morgan, Roswell Park Cancer Institute

Andrey Fedorov, BWH/HMS

Izumi Hinkson, NCI

**Agenda/Minutes**

1. General Announcements
   * ISMB 2018 Special Session proposals due 1/30.
     + July 6-10 in Chicago https://www.iscb.org/ismb2018
   * January meeting - is a time change possible?
   * Fill in your preference now for next discussion topic [here](https://docs.google.com/forms/d/e/1FAIpQLSeuyy7OC577W6JxRt7M_8mYDhPNODrZDKGZQMR7EkLI2tzfOQ/viewform).
2. Outreach Activities (type in here)
   * CRAVAT (Mike Ryan), TRINITY (Aviv Regiv), and CIViC (Obi Griffith) presented their ITCR tools to the SeqSpace Webinar <https://epi.grants.cancer.gov/events/seqSPACE/>.
   * *Bioconductor* Asia (Nov 16-17, Adelaide, Australia) and [European](https://bioconductor.github.io/EuroBioc2017/) (Dec 4-6, Cambridge, UK) user conferences; [Boston](https://www.meetup.com/Boston-R-Bioconductor-for-genomics/events/240111912/) and [New York City](https://www.meetup.com/BiocNYC/events/243813429) meet-ups;  nice *Nature* [publicity](https://www.nature.com/articles/d41586-017-07833-1?WT.mc_id=TWT_NA_1712_FHTOOLBOXDNACLOUD_PORTFOLIO) and [video](https://youtu.be/cP5rvWoJDOQ).
   * GenePattern talk at Cancer Tools 101 BroadE seminar at the Broad Institute, Cambridge MA, 12/4.
   * [DICOM connectathon](https://qiicr.gitbooks.io/dicom4qi/content/), 3D Slicer booth, and a talk at a mini-course at the [Radiological Society for North America (RSNA)](https://rsna2017.rsna.org/) annual meeting, Dec
3. Round Table Discussion - How to Get, Keep and Manage Outside Contributors to Your Code Base.
   * What is the experience of your tool with external code contributors?
     + Have you had external code contributions?
       1. If not, do you plan to try to get contributions in the future? Why? How?
       2. If yes, how did you encourage participation?  How do you vet contributions? How do end users get externally developed features - are they part of the base product or available as a plugin?
     + *Bioconductor*

* Extensive outside contributors (maintainers) -- >1500 packages, about 1100 ‘maintainers’. Core development team with much more restricted outside collaborations.
* ‘Modular’ -- packages developed by individual contributors, mostly ‘edges’ so consequences of bad implementations limited to their own contribution.
* Most developers are [‘new’](https://github.com/Bioconductor/BiocTalks/blob/BiocEuro-2017/vignettes/packages-per-developer.pdf) -- power-law, where most developers contribute one or a few packages.
* Review process -- [open github issue](https://github.com/Bioconductor/Contributions/issues), comments from the community / assigned reviewer, automated quality control (‘single package builder’), acceptance to ‘devel’ branch -- goal to increment quality rather than hold to absolute standard. Maybe 5% (revised estimate!) of each team member’s time spent on review.
* Available packages: organized via [‘biocViews’](https://bioconductor.org/packages) ontology. Individual package ‘[landing pages](https://bioconductor.org/packages/DESeq2)’ describing author, contact, doi, etc.; usage and quality metrics badges (at top of landing page; badges in a state of flux at the moment) as well as download statistics
* [Support site](https://support.bioconductor.org/) questions tagged with packages, maintainers ‘subscribe’ to relevant tags

3D Slicer

* Core platform: <https://github.com/slicer/slicer> (github stats don’t reflect contributors properly due to svn still being used as primary, github repo is just a mirror) (on ohloh: <https://www.openhub.net/p/slicer>)
* Extensions: <https://github.com/slicer/extensionsindex> (122 extensions, 74 contributors)

Gene pattern [www.gparc.org](http://www.gparc.org/)

UCSC Xena - Google Summer of Code

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