ITCR Training and Outreach Working Group

Thursday, September 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-Sept-2017](https://docs.google.com/document/d/1tioEocs-9BxTYEikhB-Au6fk_k_kUoqtWOIOId4Gtek/edit)

**Attendees: Please sign in!!**

Mike Ryan, JHU / MD Anderson

Mary Goldman, UC Santa Cruz

Mervi Heiskanen, NCI

Tali Mazor, DFCI

Andrey Fedorov, BWH

Anand S. Merchant, NCI

Izumi Hinkson, NCI

Mark Bergman, UPenn

Juli Klemm, NCI

David Hanauer, U of Michigan

Martin Morgan, RPCI

Michael Reich, UCSD

Bradley Broom, UT MD Anderson Cancer Center

Brion Sarachan, GE Global Research

Simina Boca, Georgetown

Hiro Yoshida, MGH/HMS

Sarthak Pati, UPenn

**Agenda/Minutes**

1. General Announcements

ITCR New website live by end of October 2017, Cancer Research Informatics special issue will be released soon.

1. Outreach Activities (type in here)
   * QIICR: DICOM tutorial at the MICCAI 2017 conference <http://qiicr.org/dicom4miccai/> , Sept 10
   * Xena: NCI BTEP workshop on Sept 27
   * *Bioconductor*: [Annual meeting](https://bioconductor.org/BioC2017) (July 25-28); Ohio State training (11-12 September). Transition to git-based version control. [Coursera Bioconductor for Genomic Data Sciences](https://www.coursera.org/learn/bioconductor) (starts Sept 15). Meet-ups -- Buffalo (Sept 7), New York City (Sept 29 -- integrative omics), Boston (Sept 29 -- single-cell RNA-seq), ...
   * GenePattern Notebook:
     + Presentation at [JupyterCon](https://conferences.oreilly.com/jupyter/jup-ny), NYC, August 24
     + Press coverage:
     + BioITWorld: <http://www.bio-itworld.com/2017/08/31/genepattern-notebook-environment-needs-only-web-browser-analyses.aspx>
     + GenomeWeb: <https://www.genomeweb.com/informatics/broads-genepattern-now-has-notebook-aggregation-collaboration-features>
   * NDEx and cBioPortal workshops at NCI on May 22, 2018 - prior to ITCR meeting
2. Overview of TOW Meeting Format
   * TOW [Meeting Planning Document](https://docs.google.com/document/d/1q1t9E74FXQrCLtOfK5uz-Bk8MLhmualzizOoQJyVfjI/edit#heading=h.rt1vjdjjo6ey)
   * Focused Topic Round Table Discussions
   * Speakers
   * Process for Topic/Speaker Selection
3. Effective User Documentation - Round Table Discussion
   * Group Discussion
     + What User Documentation do you provide with your tool?
     + What format / level of information is effective?
       1. Annotated Screen Shots
       2. Written Overviews
       3. Scenario Based Usage Flows
       4. Videos
       5. Wikis
     + To what audience / experience level is documentation targeted?
     + Tips for keeping documentation updated
     + [Summary of Daniele Procida lecture on Effective Documentation](https://docs.google.com/presentation/d/1bs2qb0uYL3OYDpZEDPz7jDTFWdXol1WQsiDxcC9ZspY) (Mary)

Custom javascript / anchors / screenshots

<http://www.cravat.us/CRAVAT/help.jsp>

MediaWiki

Media Wiki format: versioning and creating tables a challenge

<http://bioinformatics.mdanderson.org/main/NG-CHM-V2:Overview>

<https://www.slicer.org/wiki/Documentation/Nightly>

ReadTheDocs

Example of Read the Docs:

<https://docs.readthedocs.io/en/latest/>

Work in progress/under consideration to switch Slicer documentation to readthedocs: <http://slicer.readthedocs.io/en/latest/>

Readthedocs is the platform of choice for pyradiomics library (Hugo Aerts PI, DFCI): <http://pyradiomics.readthedocs.io/en/latest/>

GitBook

<https://www.gitbook.com/book/qiicr/dcmqi-guide/details>

End-user readable view: <https://qiicr.gitbooks.io/dcmqi-guide/content/>

LinkedIn has been useful in building user community

*Bioconductor* notes

* Types of documentation: technical ‘man’ pages; narrative vignettes; Integrative workflows.
* ‘Man’ pages and vignettes integrated with the software itself -- literate programming means that the code, output, and figures are actually generated rather than ‘pictures of code’. Helps avoid bit-rot.
* Facilities provided by the language / project provide some level of structure and standardization -- standard format for man pages; checks that enforce formatting; review of vignettes as part of new package acceptance; ‘brand’ associated with vignettes. Use of standard data sets. Nowadays: markdown.
* Integrative ‘[workflows](https://bioconductor.org/help/workflows/)’ tied to [F1000 Bioconductor channel](https://f1000research.com/gateways/bioconductor); also links to traditional academic citations on package landing pages.
* Nice (awesome!) vignette example: <https://bioconductor.org/packages/release/bioc/vignettes/maftools/inst/doc/maftools.html>
* Some challenges: new user discovery of documentation; translating support site questions into improved documentation; always tempting to make ‘more’ documentation, but that seems to dilute information content, we really want ‘better’ documentation

Tutorials

FYI interesting platform we discovered while developing the latest tutorial that allows to run live python notebook on the cloud: [https://beta.mybinder.org](https://beta.mybinder.org/). And this is how we used it for our tutorial: <https://beta.mybinder.org/v2/gh/qiicr/dicom4miccai-handson/miccai2017?filepath=/src/dicom4miccai-handson/notebooks/headneck.ipynb>