Minutes Steering Committee Call 11 April 2017 (10 AM CDT)

On call: CKTuggle, EGiuffra, MGroenen, HZhou, PHarrrison, LClarke, CSchmidt, JReecy, HCheng, GTosser-Klopp, Yaling Zhu (LHuang group)
Regrets: GPlastow, SWhite, MWatson

Minutes from 7 Feb 2017 call- approved with one change

Announcements

Reports from Standing Committee Chairs

- *Animals/Samples/Assays:*

No call since Nov 22 as they transitioned to fewer calls and no requests to meet. However, the ASA committee has discussed the future structure of their committee, and developed a description of the purpose and function of this committee. The currently drafted version is appended at the end of the minutes. This could be discussed at the ISAG Seq+Annotation Workshop?
Should an Instruction booklet be developed?
EG asked whether protocols are still mandatory for Biosample submission…
HZ asked about protocols for cell lines…
The ASA committee was asked to provide an update at next call.

- *Metadata and Data Sharing:*

The Metadata and Data Sharing committee is continuing to meet on an as required basis, our last meeting being in January. The FAANG Data Coordination Centre (DCC) has extended the validation and conversion tooling (http://www.ebi.ac.uk/vg/faang) to support users submitting experimental data to the European Nucleotide Archive. This offers similar functionality to the existing service for submitting sample metadata to BioSamples. FAANG users are now able to complete a FAANG experimental excel metadata template (available from https://www.ebi.ac.uk/seqdb/confluence/display/FAANG/Submission+of+sequencing+data) validate it against the FAANG experimental metadata standards, fix any highlighted errors and then convert the file to the XML format accepted by the ENA. This should make it far easier for FAANG members to submit to the ENA and ensure they are meeting FAANG standards. This new service is currently being tested by 5 sets of submitters, if all goes well it will be advertised more widely to the FAANG metadata and sampling lists.
We also would like to survey the FAANG membership to ascertain who is currently generated and who already has generated samples and experimental data. The FAANG DCC does not currently have a good handle on which groups have data and why it has not yet been submitted to an appropriate archive. This will also help us to plan our support capacity and potentially on an quarterly basis contact responders to the survey to offer help and ascertain progress with submissions.
It was agreed that this was a good idea, and was suggested that it also be posted to AnGenMap, and also to directly target groups that presented at PAG and known to have data. It was suggested that progress be reported on the June Steering call with results fed back as part of the FAANG reporting in July at ISAG.

- *Bioinformatics and Data Analysis:*

The website is being organized for the tools and resources ther with Zhiliang Hu. Currently the following pipelines/protocols are available:

1. *DNA Methylation*
2. *RNAseq*
3. *ChIPseq*

   EG asked: how to simplify access to tools/pipelines? Jim responded that BDA pipeline should be on GitHub; will look into linking that on our website… Laura responded that these pipelines are on Confluence.

- Communication:

  Had call 5 April 2017.

Meetings:

1. FAANG Workshop for PAG 2018 will be scheduled for Friday afternoon to avoid conflicts with other species Workshops.

2. FAANG at ISAG 2017 (Scientific Program: http://www.isag.us/2017/scientific-programme.aspx)

ISAG 2017 organizers have organized the Wednesday plenary session for talks related to FAANG goals, so this will be an excellent showcase for functional annotation. David MacHugh requested help from FAANG with speakers to round out the Wednesday morning Plenary. Chris organized an email suggestion and voting preferences from Communication Committee members, and provided that to David on Feb 15. Diane Dickel and James Kijas have accepted, along with Leif Andersson, to give plenary talks. There is currently a suggestion that FAANG Comm Comm to organize the 30 minutes that remain in the scheduled time.** See Update below

Jim Reecy is planning to include a short time (15 min) for group discussion on FAANG activities at the Genome Sequencing and Annotation Workshop to be held Monday afternoon.

3. The report of the H2020 Animal Genomics Workshop held in Brussels; Alan Archibald provided the near-final report at the 5 April Com Com call.

4. USDA AFRI Tools and Resources proposal development

Lakshmi Matukumalli sent an email out indicating that the release of AFRI Foundational RFA has slipped to the end of April, but expects this is an accurate timeline.

Old Business

1. Monthly newsletters?   *Any volunteers to provide content will be welcome.*

2. Further discussion on working together to foment increased opportunities for FAANG-related projects H2020, FFAR, etc.

New business

1. Laura Clarke would like to add to the agenda for tomorrow promoting Peter Harrison to chair of the Metadata and Data Sharing committee to replace her. Laura would like to keep her spot on the steering group but Peter will be responsible for the operations of the M&DS group with Carl.

Approved with thanks to Laura for her service on MDA.

2. **The 30 minute time slot remaining to be organized (12:30-13:00) for the Wednesday July 19 FAANG Plenary session will be filled by Laura Clarke, who agreed to talk about Metadata standards and Biosamples, etc.

3. EG indicated that the H2020 report on Animal Genomics will be online soon; she will ask JC Cavitte to notify us when it is available.

Future Steering Committee calls
June 6 10 AM US Central time

ASA committee text on Committee Function/purpose

Posted on FAANG.org website:

Animals, Samples and Assays (ASA) Committee

The overall objective of the Animals, Samples and Assays Working Committee (ASA) is to achieve and share standardized protocols for adequate sample collection, storage, processing, and respective assays as required for FAANG core assays. Standardization of the different steps involved is the essential prerequisite for integration of multiple datasets.

- Foster potential collaborations in order to avoid redundancies and optimize synergies in terms of sample collection.
- Set-up and standardize assays to be carried out on the same tissues/species, in order to obtain suitable datasets for the work of the FAANG "Metadata and Sharing Working group" and "Bioinformatics and Analysis Working Group".
- Contribute to the organized scientific dissemination to the whole community (FAANG Communication Working Group).

Group’s activities

Discussions among members take place i) over email via the faang-sample@animalgenome.org mailing list.

ASA members can meet by video-conference (Zoom) around specific topics upon members’ request to co-chairs (Giuffra, Zhou).

Sharing protocols to FAANG FTP site

The FAANG sample and experiment metadata specification (see M&DA webpage) requires your protocols to be publicly available. It is best these are hosted in a location which will be available in the long term so locations such as lab pages are inadvisable as web addresses change and hosting goes away.

FAANG hosts protocols on its FTP site protocols directory ftp://ftp.faang.ebi.ac.uk/ftp/protocols/ In the 'Samples' sub-directory you will find existing protocols in use for sample collection and treatment suited for long term storing; in the 'Assays' sub-directory you will find protocols in use for FAANG assays optimized on specific cells or tissues.

Protocols by definition evolve in time, thus improved versions (i.e. yielding datasets of better quality) should be uploaded as often as necessary. Therefore, each protocol on the FTP 'Sample' and 'Assay' directories includes a date stamp, so if protocols are subsequently updated then you can submit the same protocol name with a different date stamp to indicate an updated version. Any modification of an existing file will be recorded as a new file with an updated timestamp.

For the coordinated improvement of existing protocols, as well as to exchange views, questions and related draft files on new protocols you are testing, we strongly recommend discussion via email to keep everyone informed of progress faang-sample@animalgenome.org