

Minutes Steering Committee 1 December 2015

Attending call: CKTuggle, HZhou, EGiuffra, JReecy, BHayes, G. Plastow, HCheng

Minutes of Nov 5 call- approved pending some edits- Chris will work on this.

Announcements

Reports from Standing Committee Chairs

- *Animals/Samples/Assays: not much new; Call is scheduled for Dec 16. The plan is to discuss the minimal number of assays to add a sample (tissues may be specified), as discussed at GO-FAANG Workshop. They will also discuss instructions on how to collect and store samples. They are working on a ChIP seq assay SOP. They are also discussing more assays on core samples and more tissues in “phase 2”. The DNAase is a very difficult assay and requires fresh tissue. ATAC-seq is potentially a replacement but there are few papers or data on this method yet in the literature. Moreover, many of the se assays have to be optimized for each tissue. Ben Hayes asked if a Table of Assays could be assembled and shared--to be discussed as well Dec 16.*
- *Metadata and Data Sharing: David Richardson is taking on some responsibilities here, along with Laura. No report at this call.*
- *Bioinformatics and Data Analysis: Jim Reecy reporting- they had a call Nov 30. In response to previous questions about possible fragmentation of the analysis groups (RNAseq analysis versus a LncRNA analysis group); this was discussed and the RNAseq analysis group intends to integrate the lncRNA group as part of the RNAseq group; there should be good communication. An example analysis was discussed- de novo assembly and genome-guided assembly; they groups may initially work separately so as to compare the differences between such disparate analyses, but the intent would be to come back together and compare the results. This integration is vital. Jim indicated that the Metadata group made a presentation (David R?), asking to be involved early and to discuss what information does the BDA analyses groups need so they can ask for such information from sample collectors/submitters. The RNA and methylation structure groups updated their work. The lncRNA group is having a hackathon December 9. There was a request to be able to make changes to the Wiki pages- Laura and/or David will check on this. The RNA analysis group will be meeting at PAG after the FAANG Workshop.*
- *Communication*
PAG Workshop- Huaijun will send out the detailed schedule.
ISAG-ASAS July 2016 Symposium Workshop plenary Speakers are complete:
- Tom Gingeras, Barbara Stranger, Ben Hayes, George Mias, Wes Warren
Funding Opportunity webpage progressing- see old business

Old Business

1. Monthly newsletters?

Any volunteers to provide content will be welcome.

2. Infrastructure call from EC: Elisabetta is working on this; INRA has contracted with an external company to manage the project; they will meet at PAG. The call for proposals requires a very complex structure but we have some advantages in that the RCN and the new funded COST action should be able to nicely integrate with the IF structure in the proposal. This COST action will be advertised in 2016. Discussion with Carl Schmidt is ongoing as well for integration with the RCN.

3. ISAG-ASAS FAANG Symposium.

We need suggestions for invitations for the short talks.

4. Funding opportunities information webpage

It was discussed whether only funded projects should be listed here, or if proposed projects or submitted projects should be included? Or potentially provide at a different location? While there may be some reluctance in "revealing" unfunded projects, the main point was to share ideas, cooperatively plan, avoid potential duplication-- and long lead times for projects means it is best to provide such information as early as possible. There was no resolution of this issue; to be further discussed.

New business?

Scheduling next calls- see below- a call before PAG was viewed positively.

Graham has secured support from Affymetrix for the FAANG Workshop; a couple additional potential sponsors were mentioned, and Graham will follow up.

Ben Hayes will contact Laura Clarke about her group getting access to the RNAseq data mentioned in a previous call.

Reminders

Future Steering Committee calls

A Doodle will be sent out.