Single Cell Task Force 2022-2023 Annual report

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52. White, Stephen
53. Wiarda, Jayne
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Activities

The FAANGsinglecell TF (SCTF) has met as a group via Zoom 4 times in 2022 and 2023:

March 30, 2022	February 6, 2023
May 16, 2022	April 3, 2023
Sept 15, 2022	June 5, 2023
Nov 17, 2022	November 28, 2023

Approximately 12-25 people participated in these calls. In early 2022, the calls focused on developing planned activities and providing the organizing text to the FAANG Steering Committee. In addition, 12-15 members of the SCTF group participated in the two face-to-face small group discussions at the PAG meeting in January 2023 and the ISAG meeting in July 2023. The priorities identified by Zoom discussions and the PAG/ISAG discussions is detailed below.

Speakers scFAANG seminar series (arranged by Gabriella Lindgren)

Fernando Biase, Virginia Tech "Single-cell transcriptome data produced with the SMART-seq framework" Monday, Sept 12, 2022

Amanda Raine, SciLifeLab, Uppsala University "scSPLAT, a method for single-cell DNA methylation profiling" Oct 10, 2022

Peter Harrison at EMBL-European Bioinformatics Institute (EMBL-EBI) "EMBL-EBI standardisation and archiving of single cell metadata and datasets. Current and Future". Feb 13, 2023

Alex Stretton, Parse Biosciences. "10x More Cost Effective than the Competition – How Parse Biosciences' Instrument-free single cell transcriptomics kits enable your projects to scale!" May 8, 2023

Ole Madsen, Wageningen University "Single cell sequencing at Wageningen University: Preliminary assessment of cell composition in intestinal organoids Jun 12, 2023

Hervé Acloque "Gene networks controlling functional cell interactions in the pig embryo revealed by scRNAseq and scOmics studies" Sep 11, 2023

Single cell TF priorities

The purpose of the groups will be identifying current projects and protocols and respective future needs, as well as further common interests and approaches with the overall goal of improving protocol sharing and standardization for both data creation, storage and analysis. Development of mechanisms and tools to exchange such information is needed to advance each component of single cell analysis.

1. **FAIR Data creation, storage and sharing**
    a. Sample acquisition and processing protocols
    b. Sample description/metadata schema
    c. Raw data (pre-analytical) data storage and sharing
    d. Cross-lab training in protocols
2. **Biological Analysis, Interpretation and Sharing**
    a. Raw data processing protocols

b. Query-specific analysis tools- benchmarking/sharing
c. Results visualization, storage and sharing
d. Public data exploratory tools
e. Experimental/biological validation of findings
f. Cross-lab exchanges of methods and training in use of tools
g. Cyber-infrastructure needs for extremely large/comparative projects

SCTF Priorities identified across the PAG/ISAG meetings.

PAG:

1. Infrastructure and funding to generate data and submit data/metadata to the FAANG data portal
   - especially to establish experimental data creation standards, as there are several competing technologies in sc analysis, in order to generate a cell atlas.
   - validate existing FAANG data portal infrastructure to submit and store sc data
2. Infrastructure to coordinate data visualization and meta-analysis across groups
3. Coordinate and organize opportunities for training in new wet-lab or computational training within the task force or within FAANG
   - priority high for workshops in data submission standards and protocols
   - EuroFAANG to do a training session. Use animal published data.
4. Identify methods and protocols members are working in

ISAG:

1. Collect community information
   - Tissues, species, objectives, protocols and technologies. These will need to be standardized.
2. Infrastructure for data sharing and data analysis
   - This will include established and newly developed tools as well as other related analytical information.
3. Training on bioinformatics and computational analysis
   - EuroFAANG to do a training session.
   - AgBioData Single Cell Working group is being formed to work on plant and animal data curation and standards.
4. Sharing data with EBI for single cell annotation in a standardized manner
5. Carry bi-monthly online talks
   - the contributors will be both, external experts on single cell protocols and data analysis as well FAANG's single cell task force members to present their related research.

Future planned activities identified across all group members, both short and long term. Those to be addressed in 2024 priorities are labeled as such.

1. Organization of small groups focused on specific aspects of the two main topics (group on single cell data curation in line with AgBioData and the FAIR principles; group on cell annotation).

2. Identification of existing resources for data sharing and analysis from other single cell consortia. (ADDRESSED IN TOP PRIORITY LIST #4)
3. Establishment of spaces for collections of shared protocols and analytical pipelines.
4. Test of additional technologies in addition to 10x Genomics: PIPseq (Fluid BioSciences), Splitseq (Parse Biosciences), Singleron (All steps in one single plate. Richard C, WUR:), BD Biosciences (interrogates a custom set of genes. Chris T, ISU). Compare to 10x Genomics.
5. Identification of the most affordable technologies for single cell omics studies.
6. Publication of an article benchmarking existing technologies. (ADDRESSED IN TOP PRIORITY LIST #4)
7. Search for potential funding for a SC Atlas data portal. A component of this is expected to be collaboration with EBI in meta-analysis and data integration for automated annotation to integrate FAANG data into the EBI gene expression atlas. (ADDRESSED IN TOP PRIORITY LIST #3)
9. Share data with EBI for cell annotation.
10. Investigate approaches to translate, integrate, compare data from different platforms/protocols/technologies. (ADDRESSED IN TOP PRIORITY LIST #4)
11. Investigate how to deal with batch effects. (ADDRESSED IN TOP PRIORITY LIST #4)
12. Meet with the metaFAIR Task Force to discuss current data standards. (ADDRESSED IN TOP PRIORITY LIST #4)
13. Carry a survey to include all protocols used by the community (FAANG and others working on animals). (ADDRESSED IN TOP PRIORITY LIST #1)
14. Carry a similar survey to include the tools for data analysis and data structure used by the community. (ADDRESSED IN TOP PRIORITY LIST #4)
15. Identify possibilities and encourage additional data training:
    -EuroFAANG
    -FAANG meta-data workshop at PAG'24
16. TF communication.
17. Continue with the talks from external experts (e.g., Saket Choudhary) and FAANG members on single cell methodologies.

Activities that have been identified as top priority (and will be undertaken in 2024):

1. To conduct surveys of the community working on single-cell studies in farm animals, regarding the protocols and technologies being used.
    OUTCOME: a list of protocols and technologies that the community is using.
2.To carry a technology benchmarking to identify the most affordable – but still of high quality and satisfactory throughput – technology/assay for single cell studies:
    OUTCOME: a list of these technologies.

The results from these two activities will lead to the publication of an article benchmarking all these technologies in comparison to the 10X Genomics gold standard.

3.To develop a community resource for cell type annotation.
4. Identify the community members that are interested in sharing their single cell data and in collaborating with the aim to test existing pipelines and annotation tools to identify the optimal ones. This will be partly addressed in the surveys we are already conducting.