FAANG Single Cell Task Force 2024-2025 Report

Status & plans: Is your TF currently active or planning to be active in early 2026? If inactive, do you recommend sunsetting it?

The FAANG Single Cell TF is active. We have been collaborating with the AgBioData scRNAseq Data Biocuration Working Group (WG) for the past 1.5-2 years. We have two categories of activities, split between the different interests of these two groups. First, the FAANG TF have held quarterly Webinars of the TF members to discuss techniques and methods to generate and analyze scRNAseq data. Second, in collaboration with the AgBiodata WG which includes plant and animal-interested researchers, we obtained a USDA AG2PI Workshop grant (EMPOWERING G2P IN AGRICULTURE: BUILDING A COLLABORATIVE ENVIRONMENT FOR SINGLE-CELL APPLICATIONS) (https://portal.nifa.usda.gov/web/crisprojectpages/1033123-empowering-g2p-in-agriculture-building-a-collaborative-environment-for-single-cell-applications.html).
We used these funds for four major activities. A) Organize and hold a series of four ninety-minute Webinars on single cell technology topics (available on YouTube; i.e., https://www.youtube.com/watch?v=5lZjMNIZtGk); B) develop and circulate a survey to understand the needs of the agricultural single cell community; C) hold an in-person Workshop March 29-30, 2025 (https://www.agbt.org/home/home/agbt-ag/agworkshops/); and D) summarize these activities and distribute the outcomes via a number of modalities.

The March 2025 workshop featured a blend of keynote presentations, breakout sessions, and collaborative discussions aimed at developing a transdisciplinary and community-driven approach to single-cell data management in agriculture. The workshop's primary goal was to foster a community of agricultural researchers and data infrastructure specialists to address the unique challenges posed by single-cell data management, particularly in ensuring that data are Findable, Accessible, Interoperable, and Reusable (FAIR). These discussions laid the groundwork for strategic planning and actionable next steps, including developing genotype-to-phenotype (G2P) frameworks at the single-cell level. The workshop also underscored the critical role of the AgBioData Single Cell Biocuration Working Group in facilitating ongoing efforts to resolve challenges in data integration, sharing, and curation. This workshop represents a pivotal moment in agricultural genomics, mobilizing expertise across domains and species to build a robust, collaborative ecosystem for single-cell research.

We don't recommend sunsetting this TF. We are currently following up these activities by summarizing the community-led suggestions and outcomes from the survey and Workshop.

Early 2026 activities: Specific goals, deliverables, or events you intend to kick off in Q1–Q2 2026.

2025 Workshop Outcomes: We are working with the AgBioData WG members to write a White paper that will summarize the community-led suggestions and outcomes from the survey and Workshop (USDA-funded activity D above). We are also intending to further organize teams to create group resources for cell annotations and data/sample resources.

Seminar Series: We will increase the frequency of our seminars, aiming for ten meetings per year. Each seminar will feature a presentation by a member of the task force or an invited external expert, covering diverse topics in single-cell wet-lab protocols and data analysis. The typical format will consist of a 40–45 minute presentation, followed by 15–20 minutes of questions and open discussion.

We will actively encourage participation from the community, both as speakers and attendees. For example, on January 10, 2026, Prof. Clarissa Strieder-Barboza (Texas Tech

University) will deliver a seminar on her current research applying single-cell technologies to investigate dairy cattle metabolism and to characterize tissues relevant to the beef industry.

Training Sessions: We plan to organize two to three training sessions in 2026 to support the professional development of our community members and other interested scientists if funding is available, with priority given to early-career researchers. These sessions will focus on different aspects of the bioinformatics analysis of single-cell datasets, primarily—but not exclusively—scRNA-Seq.
Training will cover:
-Data quality control and filtering
-Standardization and normalization
-Batch correction and data integration
-Cell-level analyses (clustering, annotation)
-Gene-level analyses (differential gene expression, etc.)

Potential providers include public institutions such as the European Molecular Biology Laboratory (EMBL; https://www.embl.org/about/info/course-and-conference-office/events/sic19-01), the ELIXIR Single-Cell community (https://www.singlecellomics.org), and individual experts experienced in training delivery (e.g., Dr Giuseppe A. Saldi, bioinformatician at NYU Abu Dhabi).

Training may be delivered online or on-site, potentially as a satellite session at one of the major international conferences for the animal science community (e.g., ISAG, PAG, WCGALP). We are currently scouting and evaluating suitable training providers.

Web presence: Are your TF webpages on the FAANG site up to date? Note any updates needed.

We need to update the website to include prior reports as well as this report. We need to establish/prune members who are no longer active.

Coordination with other groups: Many TFs are embedded in international efforts. Please outline practical steps to unify/align efforts and how interested researchers could access/join via the FAANG site.

We are currently collaborating globally as a TF, in that there are 56 listed TF members (not all active) from US, Canada, Asian and European countries. We are also collaborating with the AgBioData group, which is primarily US based Agricultural researchers interested in genome data curation and reuse.

The TF has been working with the Functional Annotation Team at EBI, led by Christina Ernst, and the Genome Analysis Team led by Emily Clark, to improve interoperability across EBI resources. For example, creating a FAANG submission template for Annotare, based on the FAANG metadata standard, for submission to Array Express will ensure that new datasets that are submitted are compatible with downstream visualisation in the single cell Expression Atlas, and FAANG Data Portal (A paper describing early successes, with previous team leads at EBI, has been published in this reporting period (Kapoor, M. et al., 2024, Front Genet. 2024 Nov 29;15:1460351. doi: 10.3389/fgene.2024.1460351). INRAE are also discussing with Garth Ilsley in the Ensembl Regulation team on incorporating single cell ATAC-Seq and RNA-Seq data in their annotation workflows.

Interested researchers can join via the FAANG website.

New TF needs (for broader PAG discussion): Comment on potential gaps. (From the earlier 2022 survey: *Training for standardisation and future generation of scientists*; *Biorepositories of tissues/complex cell systems*; *High-throughput in vitro modeling and genome editing*.)

There are several active members very interested in working with other groups to develop training modules (see above for the current plan), this is a priority for 2026. As well, members are interested in collaborating with other TF. One area of interest is how to move to cell-level molecular phenotype – we would like to work to improve deconvolution to take current tissue-level phenotypes to cell type level across available RNAseq data. This goal should be of interest to multiple TF such as Farm-GTEx and FAANGprediction.

In August 2025 the Functional Genomics Team and Training Team at EMBL-EBI released a series of short videos for submission of functional genomics data, including single cell datasets to Annotare; e.g., adding sample attributes, bulk file assignments. All EMBL-EBI training videos for Annotare are available here https://www.youtube.com/@EMBL-EBI/search?query=annotare. These resources will be of relevance to the TF, and could be developed further to suit community priorities and include additional resources, depending on demand and usage.