metaFAIR Task Force

FAANG Metadata, Ontologies and FAIR
Data Sharing Task Force

## Peter Harrison

Genome Analysis Team Leader

EMBL-EBI

peter@ebi.ac.uk

metaFAIR Aims

- Ensure FAANG datasets are richly described and FAIR.

- The task force recommends, develops and reviews metadata rulesets, ontology improvements, data sharing methodologies, FAANG Data Policy and presentation methods.

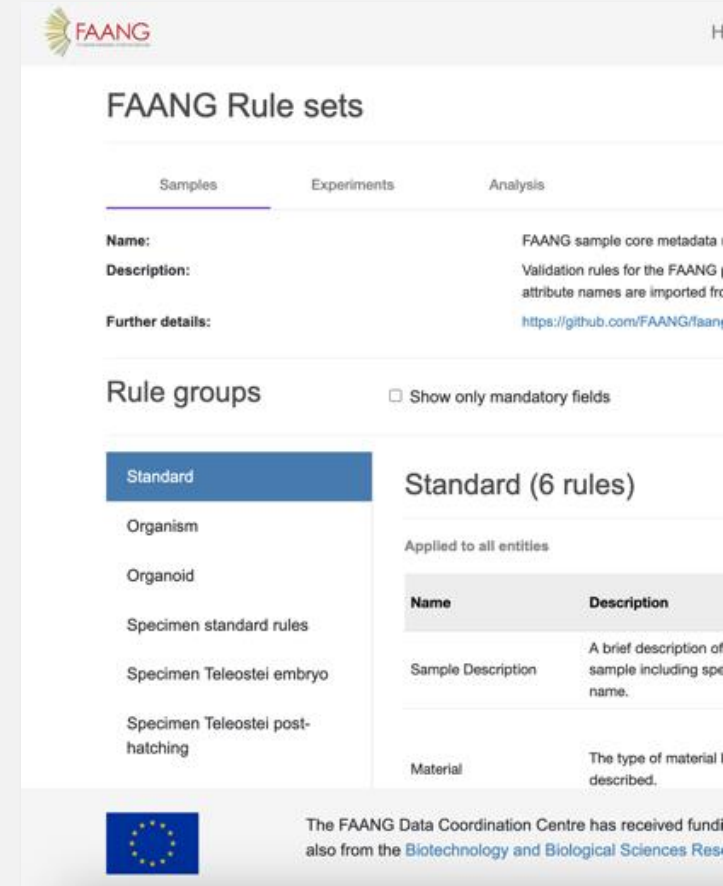- It recommends best practice and promotes open data sharing amongst the FAANG community.

Findable **A**ccessible **I**nteroperable **R**eusable
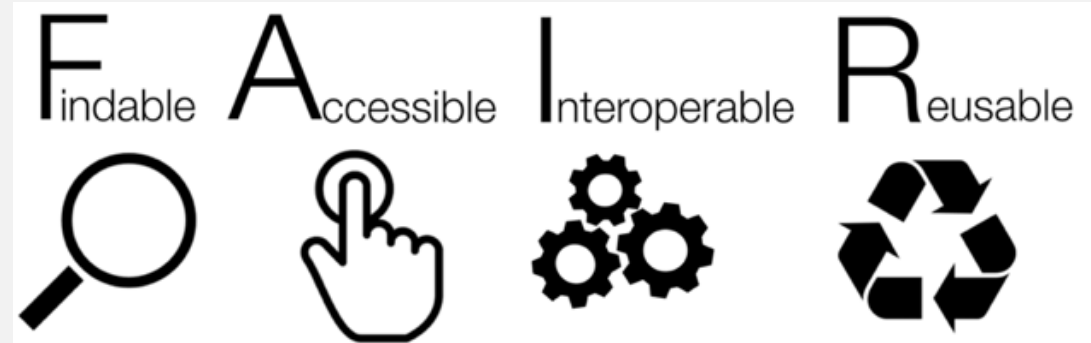
To accelerate genome to phenome research

metaFAIR Goals

Review and recommend development to the FAANG Data Coordination Centre on a range of key areas including:

1. Metadata standards and ontologies.

2. Guidance documentation.

3. Track hub standardisation.

4. How FAIR is FAANG data and what to improve?

5. Developments in single cell atlases, pangenomes and emerging technologies.

6. Training requirements

metaFAIR 2023 highlights

- Meetings held quarterly (will increase frequency in 2024)
- Defined aims and goals
- Identified and delivered training courses on ontology improvements.
- Reviewed and connected with other working groups such as AgBioData working groups on phenotyping and AG2PI single cell.
- Reviewed all metadata changes and voted on major updates.
- Reviewed ontology improvement
- Reviewed FAANG portal updates

Metadata: Mandatory workflow recording

- Task force voted and approved making it **mandatory** to provide link to workflow/pipeline that generated each analysis file.

- Driven by EuroFAANG we are supporting FAANG analysis standardisation through NextFlow nf-core community.

analysis protocol	Link to the description of the analysis protocol, an overview of the full analysis including names, references and versions of any software employed. The protocol can refer to the order in which other protocols were performed and any intermediate steps not covered by any analysis specific protocols.	uri	mandatory	No
analysis code	Link to the repository that contains the code used in the analysis. Ideally this would be formatted and documented for use by others, but even raw or undocumented code is encouraged as it will assist with reproducability.	uri	mandatory	No
analysis version	Version of the analysis code used in the analysis, or if no version is listed then list the date of download in the format YYYY-MM-DD, YYYY-MM, YYYY.	string	mandatory	No

Related Pipelines

Column Selection ▾

Search

Pipeline name	Assay type	Pipeline link	Pipeline documentation	Platform
BovReg/nf-core-rnaseq-bovReg	RNA-seq	https://github.com/BovReg/nf-core-rnaseq-bovreg	https://github.com/BovReg/nf-core-rnaseq-bovreg#readme	nf-core
BovReg/nf-core-rnaseq	RNA-seq	https://github.com/BovReg/nf-core-rnaseq	https://github.com/BovReg/nf-core-rnaseq#readme	nf-core
BovReg/nf-core-smrnaseq	smallRNA-seq	https://github.com/BovReg/nf-core-atacseq	https://github.com/BovReg/nf-core-atacseq#readme	nf-core
BovReg/nf-cage	CAGE-seq	https://github.com/BovReg/nf-cage	https://github.com/BovReg/nf-cage#readme	Nextflow
BovReg/nf-core-chipseq	ChIP-seq	https://github.com/BovReg/nf-core-chipseq	https://github.com/BovReg/nf-core-chipseq#readme	nf-core
BovReg/nf-core-atacseq	ATAC-seq	https://github.com/BovReg/nf-core-atacseq	https://github.com/BovReg/nf-core-atacseq#readme	nf-core
BovReg/nf-core-hic	HIC-seq	https://github.com/BovReg/nf-core-hic	https://github.com/BovReg/nf-core-hic#readme	nf-core
BovReg/nf-core-sarek	Variant Calling	https://github.com/BovReg/nf-core-sarek	https://github.com/BovReg/nf-core-sarek#readme	nf-core
BovReg/BovReg_eQTL	eQTL analysis	https://github.com/BovReg/BovReg_eQTL	https://github.com/BovReg/BovReg_eQTL#readme	Nextflow

nf-core

Metadata: Organoids

- In collaboration with EuroFAANG Research Infrastructure think tank reviewed and enhanced the Organoid and BioBanking metadata rulesets

Standard								
Organism								
Organoid								
Specimen standard rules								
Specimen Teleostei embryo								
Specimen Teleostei post-hatching								
Single cell specimen								
Pool of specimens								
Purified cells								
Cell culture								
Cell line								

Organoid (10 rules)

Applied under these conditions:

Material is "organoid"

Name	Description	Type	Required?	Allow multiple?	Valid values	Valid units	Valid terms	Condition
organ model	Organ for which this organoid is a model system e.g. 'heart' or 'liver'. High level organ term.	ontology id	mandatory	No			UBERON:0001062 BTO:0000042	
organ part model	Organ part for which this organoid is a model system e.g. 'bone marrow' or 'islet of Langerhans'. More specific part of organ.	ontology id	optional	No			UBERON:0001062 BTO:0000042	
freezing date	Date that the organoid was frozen.	string	mandatory	No		YYYY-MM-DD, YYYY-MM, YYYY		
freezing protocol	A link to the protocol for freezing.	uri	mandatory	No				
number of frozen cells	Number of organoids cells that were frozen.	number	optional	No		organoids		
organoid passage	Number of passages. Passage 0 is the plating of cells to create the organoid	number	mandatory	No		passages		

Next steps

1. Set out training requirements for FAANG, particularly from the DCC targeted at major conferences and virtually.

2. Begin work on the whitepaper to state FAANGs position and promote to data providers the FAANG principles and processes

3. Focus on connection to phenotyping metadata in collaboration with expert infrastructures (emerging in Europe) and community specialists.

4. Look at standardisations with crop agriculture through AG2PI and AgBioData, and technology/infrastructure standardisations with ELIXIR.

We need your views

- We are seeking more people to help shape how FAANG strives for rich, FAIR and open datasets.

- Any emerging funded projects should in particular engage to drive the standards and support they need.

Sign up at
www.faang.org

Members
(† Group organizer)

- Adetula, Adeyinka abiola
- Brooks, Samantha
- Chaudhari, Chirag
- Giuffra, Elisabetta
- Gmel, Annik †
- Harrison, Peter †
- Hunter, Christopher
- Kalbfleisch, Ted
- Sokolov, Alexey
- Triant, Deb
- Wang, Ying

FAANG singlecell TF

Purpose

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.

Current Organizers:

Chris Tuggle	Iowa State University
Fernando Biase	Virginia Polytechnic Institute and State University
Alex Clop	Centre for Research in Agricultural Genomics
Richard Crooijmans	Wageningen University
Yvonne Drechsler	Western University of Health Science
Christine Elsik	University of Missouri
Peter Harrison	EMBL-EBI
James Koltes	Iowa State University
Christa Kuehn	Research Institute for Farm Animal Biology

Activities

1. Zoom meetings quarterly in 2022 and 2023

2. 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

3. Small group discussions organized at PAG 2023 and ISAG Capetown 2023

Priorities and future plans

4. New Working group on single cell analysis in AgBioData approved

Peter Harrison, lead, Chris Tuggle co-lead

FAANG singlecell TF

Priorities

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

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

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.*
5. We are currently discussing organizing a conference to combine practical training on SC data analysis and talks by experts and representatives of active groups.

FAANG Prediction Task Force

2022-2023 Annual report

Current Organizers:

Hao Cheng
(University of California Davis, USA)

Daniela Lourenco
(University of Georgia, USA)

Mario Calus
(Wageningen University & Research, Netherlands)

Members:

1. Adebiyi, Marion
2. Adetula, Adeyinka abiola
3. Brito, Luiz
4. Bermann, Matias
5. Calus, Mario
6. Chaudhari, Chirag
7. Cheng, Hao
8. Duenk, Pascal
9. Estellé, Jordi
10. Guan, Dailu
11. Kadarmideen, Haja
12. Kizilaslan, Mehmet
13. Liu, George
14. Lourenco, Daniela
15. Qu, Jiayi
16. Ramon, Manuel
17. Regitano, Luciana
18. Vidal, Rodrigo
19. Wang, Ying
20. Zhao, Tianjing
21. Zhou, Huaijun

The main aim: Unlocking the potential of the generated FAANG data in animal breeding programs in practice.

- Facilitate exchange and collaboration between quantitative geneticists working on routine genomic evaluations and implementation of genomic prediction models that use functional genomics information such as SNP-level functional annotation and individual-level intermediate omics data (e.g., transcriptomics, metabolomics), and molecular geneticists and bioinformaticians involved in producing and interpreting the FAANG data.
- Bridging the gap between molecular and quantitative geneticists by introducing details of FAANG data and genomic evaluation to each other.
- Creating a data repository to convert FAANG data into formats friendly to quantitative geneticists.
- Developing new statistical and machine learning methods for FANNG-enabled genomic prediction.
- Evaluating its potential in routine genomic evaluation.

Current Activities

In the inaugural year of our initiative, we implemented regular meetings among the task force organizers to deliberate on forthcoming activities.

TF priorities were discussed in small group in-person discussions at PAG and ISAG.

A monthly online seminar series has been planned, designed to showcase ongoing progress and brainstorm the next steps.

We have identified several key data resources and practical questions/problems (included in the report).

Priorities identified across the PAG/ISAG meetings.

- Data generation, infrastructure, funding to generate data, broadening scope by integrating expertise and training. => Often the phenotypic and genomic data that we work with is owned by private parties, and this data typically cannot be shared. A common (freely available) dataset could be very useful to compare and benchmark models.
- A major goal is to incorporate farm data as routine practice and to share data across industry, which will be imperative to data access.
- The question 'Can a national effort such as phenotyping be set up?'
- The need to incorporate other areas of expertise complementing the know-how that is already present was identified. This new expertise included molecular geneticists and computer scientists. => Our experience is that to make optimal use of any functional annotation data in genomic or phenotypic prediction, we need to exchange with experts on interpreting this kind of data. In the context of FAANG, it means that we need active exchange with member of other Task Forces.

a. What collaborative projects are being done in your TF that interest you the most? Please provide a short title, and your name if you wish.	GENE-SwitCH (Mario Calus; co-leader of WP4) GEroNIMO (Mario Calus; leader of WP4) Luciana (Brazil): Collaborative Nellore (bos indicus); 400 animals with multiple omics layers (RNA-seq different thesis), WGS imputed, proteomics. Developed a database that will be released next year. Clara Diaz (Spain): beef & dairy cattle, several omics (e.g.+ behavioural traits, also physiological data related to heat stress (400). Smaller: Sequence + transcriptomics diff. tissues. Maria Saura: tarbot (n=800) genotypes + phenotypes + microbiome data (e.g. the skin). Sheep (n=400), genotypes + microbiome, phenotypes. Sebastian (Spain): large database of phenotypes (100k), genotypes (5k). Start to integrate omics to improve predictions. (PhD student): Transcriptome of native breeds of cattle, WGS, pathogen presence Nick Kertz (US): predicting heifer fertility in beef cattle, using transcriptomic data. Luis Varona (Zaragoza): Legarra & Christensen; developing methods to integrate omics data. 300-400 animals with microbiota available. Jordi Estelle (INRAE): host-genetics „Äì microbiote inter; national project funded on modelling this better. Interested to exchange, on sampling and method development. Isidore Houga (Roslin): developing GP for crossbred dairy cattle in Africa (n=2000). No functional genomics data yet. Norman Marwashe: focussing using genomic data in national (beef) cattle evaluations. Large scale national genotyping (& phenotyping for a long time). Just a few small-scale experiments in gene expression. Some collaboration with Brazil & South America on tolerance to ticks, wants to use expression data here. Siriluk Ponsuksili: colleagues already involved in FAANG. Working with omic from microbiome, some data in pigs (embryos?) + some metabolome data. Also some data in chicken. How to use these omics data to integrate in breeding (values)? Summary: EuroFAANG projects that have an explicit WP on genomic prediction (&) Several additional national projects were mentioned, with individual omics data of up to 400 individual animals.
b. What initiatives should our task force undertake to advance that project? What type of effort will this initiative require (grant writing, exchange of materials, organize Zoom calls, etc)?	(Brazil) Main restriction is people available; who is going to do the modelling? Both more people and more skills are needed (those skilled are already occupied). Workshops to train scientists & post-graduate students => building scientists. Developing proposals for funding: networking & discussion to identify possibilities. E.g. Cost networks in EU; could we have one on prediction? OECDE (Spanish funding instrument) also provides funds for networking. Combine datasets across country. General challenge: inclusivity. Commercial breeds are prioritized at the expense of local breeds. Clara: are doing simulation to decide on sampling, in the most informative and useful way, with implications for a breeding program (and to inform experimental set-ups). Local beef cattle breed, huge variability in response to stress (dairy as well). Standardization & harmonization? How to combine expression measured at different time-points? May not always be possible? Example: metabolomics between plasma & serum are very different. Are eQTL in one population good predictors in another breed? Brazil has datasets that may be useful for this. How to combine different datasets? Functional annotation approach could solve this, t Sharing experience of sampling, data generation. Plant people may have shared questions (@ INRAE); something to consider. What kind of omics (and what approach) could be most useful and most feasible? Perhaps microbiome is most robust? Do we reach a plateau across omics layers? Can we accumulate this across different experiments? Get expert opinions on what would be a good omics to start with. Generate meta-data from available data, and share across groups, to identify options to combine/evaluate (this could even include e.g. levels of LD). Do an inventory of available data? Across-species inventory could be very informative. Summary: 1) There are several relatively small datasets on individual omics being identified. Suggested initiative: Inventory of available data (Check with FarmGTEX to avoid & see how to collaborate.) 2) Lack of (availability of) skilled people to undertake the required analyses. Suggested initiative: Organize a Summer School. 3) Build more of a formal network to collaborate and exchange.
c. Who is willing to lead or organize this initiative? Please indicate names and activities volunteered.	1) Inventory of available data (Check with FarmGTEX to avoid & see how to collaborate.) => To be led by Task force leaders (Hao, Daniela & Mario). 2) Summer school? => Will be organized by the GEroNIMO project. 3) Cost Action => Should be a number of (young) people from Europe? UK can participate. Probably needs to be led by an established group in this area.

Future planned activities

- Initiate collaborative research projects between molecular and quantitative geneticists. These projects could utilize FAANG data in innovative ways, fostering inter-disciplinary collaboration.
- Dedicate a portion of the regular meeting to exploring and evaluating potential new data sources.
- Conduct specific workshops or online sessions focused on the evaluation of new data sources. These can cover aspects such as data reliability, applicability to current research needs.

- Through a funded project, organizer Hao Cheng is developing an open database for publicly available AG2P data sets, analysis, and educational resources (e.g., a software package, a GitHub repository).
- The platform will host metadata linked to each data set and analysis resource for at least 100 public AG2P data sets and a similar number of data-analysis resources (currently focusing on genotypes and phenotypes).

- Organize a series of advanced workshops that delve deeper into specific aspects of FAANG data and genomic evaluation. These workshops can be more technical and focused.

High Throughput Phenotyping and Data Storage Task Force (HTP-DS)

organizers
Cedric Gondro, Michigan State University, USA
Raziye Işık, University of Sao Paulo, Brazil
Claudia Kasper, Agroscope, Switzerland
Andreas Kranis, Aviagen/Roslin, UK
Graham Plastow, University of Alberta, Canada

TF priorities

1. Identify and collate information on big data technologies and their uses in animal production
2. Identify community needs on High Performance Computing and develop resources for big data and artificial intelligence analytics
3. Create standards for reusability of data from sensors and imaging
4. Develop blockchain solutions for data integration across supply chains and methods for data sharing protection
5. Develop data storage methods for genomics and computational backbone for analyses (in collaboration with FAANGPredictions and FarmGTEx)
6. Establish a resource to link genotypes, high-throughput phenotypes and environmental parameters for research (in collaboration with metaFAIR)
7. Develop a web server and accompanying portal to host data structures, programs, and resources

Activities

The Task Force's activities have focused on the integration and development of data technologies in livestock, with specific emphasis on community needs assessment, blockchain data integration, genomic data compression and prediction, and the conceptualization of a large-scale phenotyping and genotyping project. The Task Force faces challenges in aligning with parallel initiatives and securing adequate funding. Addressing these issues will be critical for the continued progression of the Task Force's objectives.

Future Direction

• Initiate discussions with other TFs to better identify a focus to re-launch the HTP-DS TF and attract additional participants.

• Seek to identify models from other efforts e.g. plant phenotyping programs such as soyBase or GRIN.

FarmGTEx TF report
2023

Co-coordinators

- Lingzhao Fang: Aarhus University, Denmar
- Huaijun Zhou: University of California, USA
- Albert Tenesa: University of Edinburgh,
- Marta Godia: Wageningen University, Neth

- Total number of members (36)

Specific Aims

- Identify gap information for next phase of FarmGTEx
  - Under-represented tissues, cell types, and species
  - Distinct biological contexts (e.g., development, physiological responses etc.)
  - Novel molecular phenotypes from new technologies
  - Single-cell FarmGTEx
- Develop and benchmark standard bioinformatics pipelines
- Develop a more sustainable infrastructure need for FarmGTEx
  - Loading page for the structure of FarmGTEx and updating news
  - Raw data storage
  - Web portal for visualization and query across species
  - Web server for interactive computational analysis
  - website for developing and maintaining statistical

Summary of pilot phase

- Finished the pilot phase for cattle, pig and chicken

- All the resources have been released and publicly available

http://chicken.farmgtex.org/

https://cgtex.roslin.ed.ac.uk/

http://piggtex.farmgtex.org/

nature genetics

Explore content ∨   About the journal ∨   Publish with us ∨

nature > nature genetics > articles > article

Article | Open access | Published: 04 January 2024

A compendium of genetic regulatory effects across pig tissues

Jinyan Teng, Yahui Gao, Hongwei Yin, Zhonghao Bai, Shuli Liu, Haonan Zeng, The PigGTEx Consortium, Lijing Bai, Zexi Cai, Bingru Zhao, Xiujin Li, Zhiting Xu, Qing Lin, Zhangyuan Pan, Wenjing Yang, Xiaoshan Yu, Dailu Guan, Yali Hou, Brittney N. Keel, Gary A. Rohrer, Amanda K. Lindholm-Perry, William T. Oliver, Maria Ballester, Daniel Crespo-Piazuelo, … Lingzhao Fang ✉   + Show authors

Nature Genetics (2024) | Cite this article

5156 Accesses | 63 Altmetric | Metrics

HOME | SUBMIT | FAQ | BLOG | ALERTS / RSS | ABOUT | CHANNELS

Search

Advanced Search

New Results   🔔 Follow this preprint

The ChickenGTEx pilot analysis: a reference of regulatory variants across 28 chicken tissues

Dailu Guan, Zhonghao Bai, Xiaoning Zhu, Conghao Zhong, Yali Hou, Fangren Lan, Shuqi Diao, Yuelin Yao, Bingru Zhao, Di Zhu, Xiaochang Li, Zhangyuan Pan, Yahui Gao, Yuzhe Wang, Dong Zou, Ruizhen Wang, Tianyi Xu, Congjiao Sun, Hongwei Yin, Jinyan Teng, Zhiting Xu, Qing Lin, Shourong Shi, Dan Shao, Fabien Degalez, Sandrine Lagarrigue, Ying Wang, Mingshan Wang, Minsheng Peng, Dominique Rocha, Mathieu Charles, Jacqueline Smith, Kellie Watson, Albert Johannes Buitenhuis, Goutam Sahana, Mogens Sando Lund, Wesley Warren, Laurent Frantz, Greger Larson, Susan J. Lamont, Wei Si, Xin Zhao, Bingjie Li, Haihan Zhang, Chenglong Luo, Dingming Shu, Hao Qu, Wei Luo, Zhenhui Li, Qinghua Nie, Xiquan Zhang, Zhe Zhang, Zhang Zhang, George E. Liu, Hans Cheng, Ning Yang, Xiaoxiang Hu, Huaijun Zhou, Lingzhao Fang

doi: https://doi.org/10.1101/2023.06.27.546670

This article is a preprint and has not been certified by peer review [what does this mean?].

Working on (will be ready by the end of 2024):

- Sheep (> 8,000 RNA-seq, 40 tissues)
- Goat (> 6,000 RNA-seq, 40 tissues)
- Horse (> 6,000 RNA-seq, 40 tissues)
- Duck (> 4,000 RNA-seq, 40 tissues)
- ...

Additional data are needed for both molQTL discovery and validation

Summary of other activities

- In-person discussions on research priorities and TF organizations at ISAG, July, South Africa

- The FarmGTEx workshop at both PAG30 and PAG31, including 8 invited talks from human genetics and computational biology

- The invited talks from Prof. Jesse Gillis, University of Toronto to at the FarmGTEx meeting

- The FarmGTEx workshop at China National conference of animal breeding and genetics, 19-23th August, Taiyuan, China

Future directions and challenges

- The white paper of FarmGTEx:
  - The first draft: Feb 2024
  - BioRxiv and website: April 2024
  - Submitted to journal: May 2024
- Pilot phase for other species, like rabbits, fish and bees
- Regular FarmGTEx TF meeting (monthly…)
- Funding opportunities for the new phases of FarmGTEx to study context-specific gene regulatory effects, including development and sex
- …

FAANG COMPGEN

FAANG Task Force for comparative genomics and assembly: visualization and analysis of multiple genomes

FAANG_{COMPGEN} Task Force Aims

1. To gather a global picture of pangenome projects and new genome assembly and annotation information being generated for farmed animal species.

2. To provide an overview of which methodologies are being used for genome assembly, annotation, visualization and comparative analysis.

3. To help facilitate sharing of data and results for genome assembly, annotation, pangenome and comparative analyses.

4. To bring together the farmed animal genomics community working on comparative genomics, pangenomes and genome annotation and foster collaboration.

5. To encourage sharing of expertise with others performing comparative genome analysis including the human, bacterial and model organism communities.

FAANG_{COMPGEN} 2023 Highlights

- 27 members in total in the task force

- Zoom calls every two months

- Spreadsheet to gather information on comparative and pangenome projects

- Community building – inviting experts new to FAANG to join the group

- Focused discussions at the PAG and ISAG meetings in 2023

- Invited Talk Glenn Hickey from UC Santa Cruz Genomics Institute – "Building and Using Pangenome Reference Graphs" in December 2023 (90 attendees)

FAANG
Functional Annotation of Animal Genomes
10 Years

FAANG_{COMPGEN} Priorities from 2023 Discussions

- Provision of data visualization and training in comparative and pangenome analysis – training from people involved in the human pangenome (funding needed)

- Potential funding mechanism to support trainings etc.

  o John Williams and Stephanie McKay as a part of the bovine pangenome consortium are planning to hold pangenome use training sessions (funding for this is yet to be determined).

- Using the Ensembl genome browser, and other tools, for comparative analysis of alternate assemblies for breeds/species etc - provision of training required.

- Set up a SLACK channel to facilitate communication.

FAANG~COMPGEN~ Future Planned Activities

- Livestock Genomics course EMBL-EBI 18th-22nd March 2024, training in pangenome and comparative analysis added based on FAANG~COMPGEN~ Task Force discussions.

- Members of the FT FAANGCompGen are also members of the newly formed ruminant T2T consortium and we are exploring opportunities to work with and capitalize on the RT2T efforts.

- We have further planned invited talks from exp̳ the field for this year.

We would be very happy to welcome new members to the task force!

FAANG
Functional Annotation of Animal Genomes
10 years

PANGENOMICS SUMMER SCHOOL

Livestock pangenomics including how to construct and exploit pangenomic information

Piacenza, ITALY ● 21 JULY – 2 AUGUST 2024

The course is organised over 2 weeks with **theoretical** and **practical** sessions:

❑ **Week 1** introduces pangenome construction, quality assessment and annotation

❑ **Week 2** addresses using pangenomes including function, genetic diversity and future applications

Participation can be **both weeks** or **just week 1** or **week 2**

For more information:

pangenome.summerschool@unicatt.it

Department of Animal Science, Food and Nutrition

Genomics

Open access

Celebrating 10 years of the Functional Annotation of Animal Genomes Consortium

Edited by
- Emily Clark
- Christopher Tuggle
- Huaijun Zhou
- Elisabetta Giuffra
Last update 4 July 2023

This special issue aims to highlight the scientific achievements of the international Functional Annotation of Animal Genomes (FAANG) initiative since its foundation 10 years ago. The special issue will cover the annotation and characterisation of genome function and regulatory elements, through integration and comparative analysis of transcriptomic and epigenetic data from farm animals. All manuscripts complying with FAANG data standards are acceptable, while those from the US FAANG and Horizon Europe EuroFAANG projects will be particularly welcome.

Special Issue in Genomics

- we would welcome papers linked to FAANG projects!

- please send Emily (emily.clark@roslin.ed.ac.uk) a potential title and brief description and time frame.

https://www.sciencedirect.com/journal/genomics/special-issue/107QQ5QMRF8

FAANG
Functional Annotation of Animal Genomes
10 Years

Discussion Points

- Are any additional Task Forces required?

- How can we bring new people and expertise into FAANG?

- What should the FAANG workshop at PAG look like next year?

- Facilitating the route to application of FAANG data – linking with industry, the animal space, genome editing?