

# Report on activities of FAANG Steering and Communication Committees and ISAFG/FAANG Workshop in Australia

*Christopher K Tuggle*  
*Iowa State University*



# *Update on FAANG Committee Work*

## *Steering Committee*

- **Developed plan for two committees to advise FAANG as a whole through the Steering Committee:**
- **Scientific Advisory Committee**
- **Animal Breeding Industry Liaison Committee**
- **The members will be invited to attend the 2020 FAANG Workshop at PAG**

# *Current planned FAANG meetings*

- **Annual Workshop(s) at PAG**
  - **Need for training on data handling and analysis**
    - **Hands-on training session by Peter Harrison on Metadata/data submission to data portal**
    - **next Wednesday January 16, 2019- 5 days!**
    - **Additional training sessions being developed- data analysis**
      - **Workshop at PAG 2020: target offering**
      - **'input requested'**
- **Midwest ASAS FAANG Session March 2019**
  - **See next slide**
- **Activities at ISAG2019**
  - **Being developed....**
  - **PH Metadata Training session planned**
- **ISAFG in the future????**



**March 11, 2019 -- Omaha, Nebraska**  
***Symposium: Benefits and Implication of  
the FAANG project to the Animal Science community***

**Speakers Include:**

**Chris Tuggle, Iowa State University**  
**Brenda Murdoch, University of Idaho**  
**Sylvain Foissac, INRA**  
**Gota Morota, Virginia Tech University**  
**Jessica Petersen, University of Nebraska**

For more information, contact James Koltes at: [jekoltes@iastate.edu](mailto:jekoltes@iastate.edu)

# *Current planned FAANG meetings*

- Annual Workshop(s) at PAG
  - Need for training on data handling and analysis
    - Hands-on training session by Peter Harrison on Metadata/data submission to data portal
    - next Wednesday January 16, 2019- 5 days!
    - Additional training sessions being developed- data analysis
      - Workshop at PAG 2020: target offering
      - 'input requested'
- Midwest ASAS FAANG Session March 2019
  - See next slide
- **Activities at ISAG2019**
  - **Being developed....**
  - **PH Metadata Training session planned**
- **ISAFG in the future????**

# Report on ISAFG/FAANG Workshop



**November 14, 2018**

**Adelaide, SA, AUS**

# Overview of ISAFG/FAANG 2018 program

	Monday, 12th Nov	Tuesday, 13th Nov	Wednesday, 14th Nov	Thursday, 15th Nov
7:30 AM	Registration Plenary Session 1 (Chair: Stefan Hiendleder)	Registration Plenary Session 2 (Chair: Dave Burt)	Registration Joint ISAFG - FAANG Plenary (Chair: Paolo Ajmone-Marsan)	Registration FAANG Workshop: breakout sessions
8:30 AM Plenary	David Gorkin: "Navigating the genome with epigenome maps: insights from the systematic mapping of chromatin state and accessibility across mouse fetal development"	Peter Dearden: "The architecture of a plastic trait"	Christine Wells: "Cell identity in the era of single cell profiling" (Sponsored by Illumina)	Data: transcriptomes (Nathan Watson-Haigh) Wet lab: histone modification (Stephanie McKay + Brenda Murdoch)
9:15 AM Plenary	Michael Skinner: "Environmentally induced epigenetic transgenerational inheritance of health and disease: ancestral ghosts in your genome"	Sue Lamont: "Some like it hot: functional genomics of response to heat stress in poultry"	Brian Dalrymple: "Genetics and genomics pathways to form and function: point and counterpoint"	Data: genomes (Lloyd Low) Wet lab: transcriptomics (miRNA, RNA, IsoSeq: Brenda Murdoch + Stephanie McKay)
10:00 AM	Morning tea	Morning tea	Morning tea	Morning tea
10:30 AM	Session 1: Disease & immunity (Chair: Paul Coussens)	Session 4: Gene regulation (Chair: Steve Moore)	Joint ISAFG - FAANG Session: New technology applications (Chair: Ben Hayes)	FAANG WORKSHOP: plenary discussions (Chair: Chris Tuggle)
Keynote	David MacHugh: "Functional and integrative genomics of bovine and human tuberculosis: a One Health perspective"	Amanda Chamberlain: "Identification of regulatory variation in dairy cattle with RNA sequence data"	Tim Smith: "Advances in genome technology"	Summary of breakout sessions
11:15 AM	Laura Miller: "e-PIG-enetics: porcine sncRNA response to highly pathogenic PRRSV"	Stephanie McKay: "A neuroepigenomic investigation of DNA methylation in cattle with extreme measures of docility"	Tad Sonstegard: "Discovery and editing of adaptive traits in livestock" (sponsored by Recombinetics Inc)	Recommendations for FAANG
11:45 AM	Lunch	Lunch	Lunch	CLOSE
12:30 PM	Poster Session (even numbers)	Neogen Australasia Sponsor Session: Russell Lyons "Neogen Agrigenomics: Global Innovation   Local service"; Kylie Munyard "Shades of alpaca grey: the causative mutation for grey in alpacas"; Iona MacLeod "Ovine sequencing and functional annotation: the future for genomic selection in sheep"; George Sofronidis "Meet the Laboratorydoodle, a genetically innovative breed"	Weatherbys Scientific Australia Sponsor Session: Delivering animal genomics to drive research and profitability in livestock production, Romy Morrin-O'Donnell "Welcome and Introduction to Weatherbys Scientific: our contribution to the Irish cattle industry and beyond"; Wayne Pitchford "Incorporating functional genomics into the selection of tropically adapted beef cattle"	
1:30 PM	Session 2: Reproduction & fertility (Chair: Brenda Murdoch)	Session 5: Functional genomics (Chair: Clare Gill)	FAANG Workshop (Chair: Chris Tuggle)	SHORT COURSES:
Keynote	Claire Wade: "Evolution of reproductive behaviour in the dog"	James Kijas: "Functional genomics in atlantic salmon: a trait specific investigation generating multiple FAANG datatypes"	FAANG overview: Chris Tuggle	Venue @ North Terrace Campus, University of Adelaide
2:15 PM	Marina Fortes: "The landscape of bovine retrotransposon polymorphisms and its association with fertility and production traits in Australian tropical beef cattle"	Chris Tuggle: "An improved functional annotation of the domestic pig genome"	FAANG project updates: Chris Tuggle, Colin Kern, Brenda Murdoch, David MacHugh, Amanda Chamberlain, Ben Hayes	
2:45 PM	Vanmathy Kasimanickam: "Serum miRNA profiling in pregnant and non-pregnant beef heifers"	Terry Bertozzi: "Functional genomics without a genome: the phototransduction pathway of blind beetles"	Open Discussion/ Q & A on FAANG Future	Introduction to R (Thursday 1:00 - 5:00 pm)
3:15 PM	Afternoon tea	Afternoon tea	Afternoon tea	
3:45 PM	Session 3: Environmental interactions (Chair: Carl Schmidt)	Session 6: Quick fire poster talks (Chair: Cindy Bottema)	FAANG Workshop: breakout sessions	Gene annotation with R (Friday, 9:00 am - 5:00 pm)
Keynote	Yanfeng Wang: "Genetic regulation of cold-induced WAT browning in pigs"	5 x 15' talks: Adetula Abiola Adeyinka, Thomas Hall, Min Wang, Luciana Regitano, Tomasz Sadkowski	Data: retrieval (Carl Schmidt + Peter Harrison) Wet lab: methylation (Bastien Llamas)	
4:30 PM	Daniela Lourenco: "How genomics can help to identify resilient animals under environmental stress conditions"		Data: submission (Peter Harrison + Carl Schmidt) Wet lab: chromatin structure (HiC, ATACseq; Monique Rijnkels)	
5:00 PM	Raluca Mateescu: "Current insights into genomics of thermotolerance in beef cattle"	CLOSE	CLOSE	
5:30 PM	Poster Session (odd numbers)			
6:00 PM	Welcome Reception (6:00 - 7:30 pm):			
6:30 PM	National Wine Centre Concourse	Conference dinner (6:30 - 11:00 pm):		
7:00 PM		Adelaide Zoo - please meet at entrance by 6:25 pm		

# Overview of ISAFG/FAANG 2018 program

Home About FAANG Projects & Fundings Publications Meetings / Events more



Functional Annotation of ANimal Genomes (FAANG) Project  
— A coordinated international action to accelerate Genome to Phenome

Previous Meetings ← • • • ⇒ Upcoming Events

## Archives from previous meetings

- 7th International Symposium on Animal Functional Genomics & Functional Annotation of Animal Genomes Workshop 2018
  - Dates:** Nov. 12-15, 2018
  - Location:** Adelaide, Australia
  - Archives:** [Proceedings \(PDF\)](#)
  - Status:** Held as planned
- FAANG at PAG-XXVI (PAG 2018)
  - Dates:** Jan. 12, 2018
  - Location:** Town & Country, San Diego, CA
  - Archives:** [Power point slides](#), [PDF](#), etc.
  - Status:** Held as planned
- FAANG at PAG-XXIV (PAG 2016)
  - Dates:** Jan. 8, 2016
  - Location:** Town & Country, San Diego, CA
  - Archives:** [Power point slides](#)
  - Status:** Held as planned
- Gathering On Functional Annotation of ANimal Genomes (GO-FAANG Workshop)
  - Dates:** Oct. 7-8, 2015
  - Location:** National Academy of Sciences (NAS) Building, Washington, DC
  - Archives:** [Videos](#), [Power point slides](#), [PDF](#), etc.
  - Status:** Held as planned

Thursday, 15th Nov

Registration

FAANG Workshop: breakout sessions

“...ing”

Data: transcriptomes (Nathan Watson-Haigh)  
Wet lab: histone modification (Stephanie McKay + Brenda Murdoch)

...rm

Data: genomes (Lloyd Low)  
Wet lab: transcriptomics (miRNA, RNA, IsoSeq: Brenda Murdoch + Stephanie McKay)

Morning tea

FAANG WORKSHOP: plenary discussions (Chair: Chris Tuggle)

Summary of breakout sessions

...in

Recommendations for FAANG

CLOSE

...ng  
...estock

...o the

SHORT COURSES:

Venue @ North Terrace Campus, University of Adelaide

...gh,

Introduction to R  
(Thursday 1:00 - 5:00 pm)

Gene annotation with R  
(Friday, 9:00 am - 5:00 pm)

...nkels)



*4 FAANG Breakout sessions:  
charge to 2 small groups meeting  
simultaneously*

- **Data creation: 1) methylation, 2) chromatin structure, 3) histone modifications, 4) transcriptomics**
- **Data analysis: 1) retrieval, 2) submission, 3) transcriptomes, 4) genomes**

# ***FAANG Discussions***

- **Breakout Chairs wrote up main discussion points and recommendations**
- **Summarized quickly at joint session with discussion**

# ***Small group recommendations to FAANG***

- **Slides will be send to Steering Committee**
- **Summarized here for discussion and further input from the community**
- **Information available at [faang.org](http://faang.org) soon**

# Data Creation breakout sessions

## - distilled comments/recommendations

### 1. Transcriptomics:

- Move toward total RNA-seq rather than mRNA-seq?
- Suggest use RSeQC for QC metrics for Publication
  - <http://rseqc.sourceforge.net/>

### 2. QC checking during early data creation stage for ChIP-seq and ATAC-seq

- Some groups doing light Illumina sequencing of initial samples
- Others using qPCR of specific control loci
- **REQUESTS**
  - Facilitate sharing of validated primers for such qPCR work
  - Facilitate sequencing data sharing for early QC testing
    - Repository site
    - Parameters for minimum quality standards
    - Data analysis computation tools

# Data Analysis breakout sessions

## - distilled comments/recommendations

### 1. Legacy data

- Recommendation is that you update existing legacy datasets to meet the FAANG standard and FAANG DCC can help you with this ([faang-dcc@ebi.ac.uk](mailto:faang-dcc@ebi.ac.uk)).
- If there are external datasets please tell us and we will import them!
- FAANG DCC will be identifying relevant legacy datasets, clearly labelled in the data portal.
- We will have a Metadata and Data Sharing working group call on what the minimum standards for legacy data should be in new year.

### 2. Flagging data or data analyses for quality.

- FAANG DCC will not flag data or analyses for not meeting QC; that is for peer review.
- They will provide data quality metrics for meta-analysis.

# Data Analysis breakout sessions

## - distilled comments/recommendations- cont'd

3. **Discussed whether FAANG should request, or even require, bioinformatics analysis code to be placed in a public accessible repository?**
  - **FAANG DCC will provide option to supply your analysis code, will not be mandatory.**
    - Plan for the analysis metadata standard to have an option to link to your analysis code in GitHub. FAANG can also host code for users if required in our community GitHub. Supplying analysis code is encouraged but not mandatory. A protocol describing your analysis, similar to that of a published paper, and as we also require for sampling and experiments, will be mandatory.
4. **Discussed updating metadata standard to record how much processing is done on 'raw' data.**
  - Will be included in the upcoming analysis metadata standard. Peter would welcome comments and suggestions on what is best to record here. What are the controlled terms?

# Data Analysis breakout sessions

## - distilled comments/recommendations- cont'd

### 5. Genome assembly – it's a moving target

- Transition from previous to improved build is somewhat random and can be unfair to researchers – *“when is an analysis too stale for publication?”*
- Need a transition plan for species assemblies
- **REQUESTS:**
  - FAANG designate a “consortium reference” assembly that will apply to FAANG groups
  - Locate this list of reference assemblies on FAANG website?

# *To discuss in general session*

- **Distilled recommendations from ISAFG discussions:**
  - Useful to set up means to record/share primers for QC of CHIP results, ATAC-seq, etc? Would it be used?
  - Useful to set up place to obtain examples of datasets blessed as gold standard, also poor standard for QC?
  - Protocols for QC analysis needed?
  - Protocols for data analysis should be organized/clarified?
  - “Consortium reference assembly”?
- **Need to create summary FAANG information display**
  - Data generated? Samples collected?
  - A resource for upholding Toronto rules, integrating projects...
  - Start with existing spreadsheet... send out announcements for updating info.
- **Other?**