

<b>ISAG-ASAS Joint FAANG Symposium</b>
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**STANDING COMMITTEES / WORKSHOPS**

**Organised by a standing committee      yes      and      no**

This Symposium was organized by an ad hoc group, with input from the Genome Sequencing Workshop Committee (GSWC), and was held in a time slot that overlapped with GSWC and therefore replaced the GS Workshop.

**Date and meeting time: July 22, 2016      8 AM-4:40 PM**

**Chair, name and contact email: Christopher K. Tuggle, [cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)**

**Agenda / programme attached      yes**

**Number of participants at meeting:**

Approximately 500 at start; 450 counted just before lunch, 270 counted at 4 PM

**Summary of the meeting** including votes, decisions taken and plans for future conferences

Please see program below. The format of this Symposium was primarily full-length or short talks by scholars in the field of functional genomics, as well as short descriptions of the FAANG project (introductory or current progress summaries). There were a number of questions for each speaker and the talks were well-received.

The current progress summary was followed by a short business meeting where it was proposed that the name of the current committee be replaced with Genome Sequencing and Annotation Workshop. This proposal passed by acclamation. This proposal was then agreed to be presented at the ISAG Business meeting. The current officers of the GSW Committee were proposed to continue as there was no GSW per se in 2016.

**Committee members** (the new committee)

Chair	term of service	E mail address:
James Reecy		<a href="mailto:jreecy@iastate.edu">jreecy@iastate.edu</a>
Other members	term of service	E mail address:
Dave Burt		<a href="mailto:dave.burt@roslin.ed.ac.uk">dave.burt@roslin.ed.ac.uk</a>
George Liu		<a href="mailto:George.Liu@ARS.USDA.GOV">George.Liu@ARS.USDA.GOV</a>

**Final Program**  
**Functional Annotation of Animal Genomes (FAANG)**  
**Joint ASAS-ISAG Symposium**  
**July 23, 2016, Salt Lake City, Utah**

Morning Session 1 Co-Chairs: Chris Tuggle, Debora Hamernik

- 8:30-8:40 Welcome and Introduction  
What is FAANG and why should you be interested in it?  
Christopher Tuggle (Iowa State University, USA)
- 8:40-9:20 Plenary Lecture 1  
Transcriptional landscape and epigenetics in mammalian cells: The multiple lives of an RNA  
Tom Gingeras, (Cold Spring Harbor Laboratory, USA)
- 9:20-9:35 Discussion
- 9:35- 10:00 Short talk 1: Causal inference of molecular networks integrating multi-omics data  
Francisco Penãgaricano (U of Florida)
- 10:00- 10:30 Coffee Break

Morning Session 1 Co-Chairs: Hans Cheng, Martien Groenen

- 10:35-11:15 Plenary lecture 2  
Genotypes to phenotypes: Lessons from functional variation in the human genome and transcriptome  
Barbara Stranger (University of Chicago, USA)
- 11:15-11:30 Discussion
- 11:30-11:55 Short talk 2: Common recurrent chimeras between human and mouse  
Sarah Djebali (INRA, France)

**Lunch 12:00-1:00**

Afternoon Session 1 Co-Chairs: Stephen White, Fiona McCarthy

- 1:00-1:40 Plenary lecture 3  
Improving genomic selection across breeds and across generations with functional annotation  
Ben Hayes (Victoria, AUS)
- 1:40-1:55 Discussion
- 1:55-2:35 Plenary lecture 4  
Integration of Dynamic Omics Data for Personalized Medicine.  
George Mias (Michigan State, USA)
- 2:35-2:50 Discussion
- 2:50 to 3:20 Break

Afternoon Session 2 Co-Chair: Jim Reecy

3:20-4:00 Plenary Lecture 5  
Genomic Tools: the use of the new sequencing methods for genome assembly and re-assembly.  
Wes Warren (St. Louis, USA)

4:00-4:30 Business meeting and Updates on ongoing FAANG activities  
Elisabetta Giuffra, Chair

Updates (20 min)

- Ongoing projects, metadata collections, late-breaking results
- FAANG vs. existing networking actions (COST, NSF)

Business meeting (10 min)

4:30 End