Introduction to the FAANG project

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ENCODE project

- Purpose: to determine the functional elements of the human genome
- **Rationale for project**
- SNPs associated with disease/traits are often inter-genic
- evolutionary comparisons have shown that some inter-genic and non-translated regions are strikingly well-conserved



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ENCODE described

To understand function:

- a) what part is transcribed into RNA? - **RNAseq**
- b) what regulatory mechanisms control this transcription:



- Landmarks bound by regulatory proteins
- Chromatin modifications also mark transcription and "openness"
- Methylation of DNA is associated with regulation as well
- Chromatin interactions



ENCODE results

Collecting all these data (hundreds of experiments) allowed *predictive models* for genome function to be developed

- Predicts <u>Chromatin State</u> in the genome- OPEN or CLOSED, function
- Created a <u>Segmentation map of</u> <u>function</u> across the genome



Success in ENCODE required:

- High quality reference genome sequence
- <u>Standardized</u> infrastructure providing
 - Biological resources
 - Bioinformatics tools
 - Databases
- Effective coordination and communication

FAANG needs all these to succeed!





Main current activities

- Establish set of Core assays, begin to develop ENCODE-type functional data
- Develop tissue description, storage and sharing protocols
- Develop computational tools to analyze data
- Develop bioinformatics infrastructure
- Develop communication mechanisms



FAANG Pilot and FAANG-related projects

Species

Leading Inst. & country

pig, cattle, goat, chicken	INRA	France
pig, cattle, chicken	UC-Davis	US
horse	UC-Davis & Univ. Nebraska	US
cattle	Leibniz Inst. for Farm Anim. Biology	Germany
Sheep	Int. Sheep Genome Consortium & others	Australia & US
pig, chicken	Wageningen Univ.	The Netherlands
cattle	Dairy Futures Coop. Res. Centre, AgriBio & others	Australia
cattle, pig	Alberta & Guelph Univ. & others	Canada
cattle and zebu	Adelaide Univ.	Australia
sheep, buffalo	Roslin- Edinburgh Univ.	UK
cattle	Washington State Univ.	US
'Arctic Ark'	Natural Resources Institute	Finland

Joint ASAS/ISAG FAANG Symposium, 23 July 2016, Salt Lake City

Global FAANG Consortium

Organic growth of FAANG during 2015-2017 Current FAANG contributors= >350



2014 membership- GB authors

FAAANG Functional Annotation of Animal Genomes 2017 membership

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