AGENDA

7.30 a.m. Registration and Breakfast (Lobby)

Moderator: Kristin Ardlie

8.00 a.m. Welcome – GTEx LDACC

8.05 a.m. NIH introduction – GTEx program updates

Simona Volpi

8.20 a.m. GTEx LDACC: Project overview, data and analysis updates

Kristin Ardlie

8.45 a.m. GTEx LDACC: Data production pipeline – Raw data to portal

Gad Getz

9.00 a.m. Using eQTLs from a range of normal human tissues to provide insights into the biological causes of common genetic diseases

Ayellet Segrè

9.20 a.m. Accurate and fast multiple testing correction to identify eGenes in eQTL studies

Jae Hoon Sul

9.40 a.m. Sparse Bayesian latent factor decompositions for identifying trans-eQTLs

Victoria Hore

10.00 a.m. An empirical Bayes approach for multiple tissue eQTL analysis

Gen Li

10.20 a.m. Coffee Break and Open Poster Viewing (Lobby)

Moderator: Barbara Engelhardt

10.50 a.m. The multi-tissue cis-eQTL landscape in coronary artery bypass grafting patients: the STokholm Atherogenesis and Gene Expression (STAGE) study

Khanh-Dung ‘KD’ H. Nguyen

11.10 a.m. Identification of long intergenic non-coding RNA QTLs in four tissue types reveals association with metabolic phenotypes

Barbara Engelhardt
11.30 a.m. Sources of somatic mosaicism in the human body
           Donald Conrad

11.50 a.m. The contribution of STRs to the genetic architecture of gene expression
           Melissa Gymrek

12.10 p.m. Genetic control of chromatin in a human population
           Olivier Delaneau

12.30 p.m. Lunch Break. Open Poster Viewing and Workshops
           Workshops run from 12.45 p.m. – 1.30 p.m.

1. RNA-Seq: eQTLs, Transcriptome Variation, ASE, and other Analysis Methods (Main Auditorium)
2. GTEx Data: Data types, availability, and how and where to access it (Yellowstone Room)
3. Pristine to FFPE: Assessing RNA quality and library prep methods for optimal RNA sequencing (Galapagos Room)

Moderator: Gad Getz
1.40 p.m. GTEx and Cancer – Overview of integrated analyses
          Gad Getz

1.55 p.m. GTEx and Cancer – Single cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma
          Itay Tirosh

2.15 p.m. PathSeq analysis of microbial sequences detectable in GTEx data
          Chandra Sekhar Pedamallu

2.35 p.m. GTEx, ENCODE & Roadmap Epigenomics – Fine-mapping, networks and disease
          Manolis Kellis

2.55 p.m. GTEx and ENCODE – Preliminary transcriptome analyses
          Roderic Guigo

3.05 p.m. Coffee Break and Open Poster Viewing

Moderator: Tuuli Lappalainen
3.35p.m. Tissue-specific patterns of imprinting revealed by analysis of monoallelic expression in human populations
         Tuuli Lappalainen

3.55 p.m. Bayesian regression models for inferring allelic imbalanced expression from RNA-seq data
          Daniel Fernandez

4.15 p.m. Impact of protein-coding loss-of-function variants on the human transcriptome
          Manuel Rivas

4.35 p.m. Integrative mining of GTEx data for drug discovery
          Simon Xi

4.55 p.m. Wrap-up and closing
          Kristin Ardlie, Gad Getz

5.10 p.m. Adjourn