



GTEX Analysis Working Group Jamboree WEDNESDAY, DECEMBER 2ND, 2015

*Hyatt Regency Bethesda.
One Bethesda Metro Center (7400 Wisconsin Ave)
Bethesda, MD 20814*

AGENDA

All main sessions will be held in the Chesapeake Suites.

- 8:30 a.m. – 9:00 a.m. ***Registration***
- 9:00 a.m. Welcome, opening remarks, & announcements
- 9:00 a.m. Sample and variant QC of GTEX V7 WGS and WES samples *Xiao Li*
- 9:15 a.m. Somatic mutation detection from GTEX data *Don Conrad*
- 9:30 a.m. Tissue transcriptomes and phenotypes *Roderic Guigo*
- 9:45 a.m. Deconvolution of cell-type composition and gene expression
in the human brain *Jie Quan*
- 10:00 a.m. Age effects in the transcriptome *François Aguet*
- 10:15 a.m. Towards a genetic basis of brain aging *Andreas Pfenning*
- 10:30 a.m. – 11:00 a.m. ***Break***
- 11:00 a.m. Statistics right off of full-length RNA molecules: Advances in
deep long read sequencing *Hagen Tigner*
- 11:15 a.m. cis-eQTL analysis: Reconciling Biology, Noise, and Scalability *Pejman Mohammadi*
- 11:30 a.m. The HT-eQTL method for multi-tissue eQTL analysis *Fred Wright*
- 11:45 a.m. Recombination rate variation in regulatory domains and their
application to meQTL/eQTL detection *Yaping Liu*
- 12:00 p.m. Bayesian modeling of DNA methylation variance in the context
of GWAS *Yongjin Park*
- 12:15 p.m. – 1:30 p.m. ***Lunch on own***
- 1:30 p.m. Matrix Ash: Modeling Effect Sizes Across Tissues *Sarah Urbut*
- 1:45 p.m. Identifying co-localized GWAS and eQTL variants using
fine mapping *Eleazar Eskin*
- 2:00 p.m. Multiple testing correction for trans eQTL *Andrew Brown*

- 2:15 p.m. Using mediation analysis to identify trans-regulatory mechanisms shared across tissues *Brandon Pierce*
- 2:30 p.m. Conditional eQTL analysis for multiple eQTLs/GWAS overlaps with eQTLs in all tissues *Manolis Dermitzakis*
- 2:45 p.m. What is the Opposite of Disease? New Fun with PrediXcan in BioVU *Nancy Cox*
- 3:00 p.m. – 3:30 p.m. ***Break***
- 3:30 p.m. Multi-SNP analysis of cis-eQTLs in GTEx data *William Wen*
- 3:45 p.m. Testing the regulatory landscape of a gene for disease loci mapping *Eric Gamazon*
- 4:00 p.m. Integrating GTEx-generated knowledge to millions of samples in GWAS *Haky Im*
- 4:15 p.m. Progress update from Functional and Networks subgroup *Manolis Kellis*
- 4:30 p.m. Variation in Personal Omics Profiles *Michael Snyder*
- 4:45 p.m. – 5:00 p.m. ***Closing remarks and adjourn***