Statistical Modeling and Analysis of Whole Genome Methylation and Chromatin Interaction (Epigenetics) Workshop

March 9-10, 2015

Posters

Hao Feng
Emory University Rollins School of Public Health

"A Bayesian Hierarchical Model to Detect Differentially Methylated Loci from Single Nucleotide Resolution Sequencing Data"

Brigitte Hofmeister
University of Georgia

"Read-Resolution Analysis of Whole-Genome Bisulfite Sequencing"

Lexiang Ji
University of Georgia

"Methylated DNA is Over-Represented in Whole-Genome Bisulfite Sequencing Data"

Jora Lin
National Chung Cheng University

"A Novel Statistical Approach to Estimate Methylation Level of Individual Cpg Site from Mbdcap-Seq"

Eric Lock
University of Minnesota - Twin Cities

"Bayesian Screening for Group Differences in Methylation Array Data"

Oswaldo Lozoya
NIEHS

"The Impact of Mitochondrial Dysfunction on the Epigenome"

Frank Shen
Pennsylvania State University

"Exploring the Structure of Hi-C Data using Nonnegative Matrix Factorization"

Han Zhang
Ohio State University

“Quantitative Bayesian Lasso for Detecting Effects of Rare Haplotype Variants and Environmental Factors on Complex Diseases”

Chenchen Zou
Jackson Laboratory for Genomic Medicine

“Multi-Track Structure Inference Model for Genome-Wide Chromatin Conformation-Capturing Data”