



## **Bioinformatics Opening Workshop September 8-12, 2014**

### **POSTERS**

**Munni Begum**

Ball State University

“Quantification of Isoforms and Its Impact on Differential Gene Expression Analysis”

**James Brooks and David Edwards**

Virginia Commonwealth

“Discovering Complex Human Health Patterns in Multi-omic Data”

**Mark Burch**

Ohio State University

"2-Step: An Approximate E-M Algorithm for Complex Mixture Models with Applications in Flow Cytometry"

**Hyoyoung Choo-Wosoba and Sandipan Dutta**

University of Louisville

“A Comprehensive Omics Study for the ICGC Cancer Genomes Lung Adenocarcinoma Data”

Co-authors: Younathan Abdia, Sinjini Sikdar, Ryan Gill, Somnath Datta, Susmita Datta

**Hongying Dai**

Children's Mercy Hospital / University of Missouri-Kansas City

“D\_CDF Test of Negative Log Transformed P-values with Application to Genetic Pathway Analysis”

**Z. John Daye**

University of Arizona

“Statistical Network Analysis for Sparse Microbial Abundances”

**Hua Feng**

University of Idaho

“Sample Size Estimation and Type I Error Correction in Genetic Association Studies”

**Jennifer Fettweis**

Virginia Commonwealth University

“Metagenomes of Microbial Populations in the Human Vagina”

**Dayne Filer**

US EPA

“A New Analysis Pipeline for the High-Throughput Toxicity Data Generated by Toxcast”

**Tara Friedrich**

University of California, San Francisco

“Searching for Context Specific Binding of Transcription Factors”

**Emery Goossens**

University of Toronto

“Non-traditional Hypothesis Testing in Genetics”

**Felicia Griffin**

Florida State University

“A Preliminary Examination of the Concept of Frailty in the Elderly”

**Giseon Heo**

University of Alberta

“Applications of Computational Topology to DNA Sequences”

**Zhiguang Huo**

University of Pittsburgh

“A Sparse K-Means Meta-Analysis Framework Combining Multiple Transcriptomic Studies for Disease Subtype Discovery”

**Greg Keele**

University of North Carolina

“Estimating Genetic Haplotype Effects at Quantitative Trait Loci (QTL) using Penalized Regression”

**SungHwan Kim**

University of Pittsburgh

“Integrative Clustering for Feature Discovery and Coherent Samples Identification in Inter-Related Multiple Genomic Datasets”

**Yang Liu**

Pennsylvania State University

“Exploiting Structure to Reduce and Integrate High Dimensional, Under Sampled “Eomics” Data”

**Zhenqiu Liu**

Cedars-Sinai Medical Center

“Causal Network Construction with Latent Regularized Modeling”

**Oleg Makhnin**  
New Mexico Tech

“Multiple Testing for Differential Gene Expression”

**Gabriel Murillo**  
University of California, Riverside

“MultiGeMS: Detection of SNPs from Multiple Samples Using Model Selection on High-Throughput Sequencing Data”. It is A0 size”

**Vahid Noroozi**  
Iowa State University

“Probabilistic Error Correction Using Markov Inference in Erroneous Reads with Insertions, Deletions, and Substitutions”

**Ji Hwan Oh**  
Purdue University

“Kernel Graphical Models”

**Elizabeth Purdom**  
University of California, Berkeley

“Timing Chromosomal Abnormalities in Tumors using Mutation Data”

**Yumou Qiu**  
University of Nebraska, Lincoln

“Thresholding Tests for the Overall Treatment Effect on High-Dimensional Count Distribution”

**Boyu Ren**  
Harvard University

“Hierarchical Graphical Model for Validating Microbial Community Analyses”

**Emma Schwager**  
Harvard School of Public Health

“Discovering Co-variation and Co-exclusion Patterns in Compositional Data from the Human Microbiome”

**Ronglai Shen**  
Memorial Sloan-Kettering Cancer Center

“A Latent Variable Approach for Integrative Clustering of Multiple Genomic Data Types”

**Nihar Sheth**

Virginia Commonwealth University

“Microbiome Research Analytics (MIRA): A Platform for Multi-omics Microbiome Analysis and Visualization”

**Sean Skwerer**

Yale University

“Genome Wide Association Study of Addiction”

**Bin Wang**

University of South Alabama

“A New Distance and Applications for Gene Expression Profiles Analysis”

**Chuanhua Xing**

AstraZeneca -- MedImmune

“A Two Sample Test by Relaxing Classical Assumptions for Testing High Dimensional Data with Dependence”

**Qi Zhang**

University of Wisconsin

“CNV-guided Multi-read Allocation for ChIP-seq”

**Fangyuan Zhang**

Ohio State University

“Detecting Association in a Heterogeneous Sample”

**Yilong Zhang**

New York University

“An Integrated Method for Associating Microbiome Composition with Longitudinal Traits”

**Xiaobei Zhao**

University of North Carolina

“Identification of Copy Number Footprints in Tumor Genomes”