Mini-Symposium

Methods and Applications for Motif Discovery and Next-Gen Sequencing Data Analysis

May 29-30, 2012
NIEHS, Rodbell Auditorium

Tuesday, May 29 (Chair Pierre Bushel, NIEHS)

12:50-12:55	Leping Li, NIEHS Welcome
12:55-1:00	Darryl Zeldin, Scientific Director, NIEHS Opening Remarks
1:00 – 1:45	Gary Stormo (Keynote Lecture), Washington University in St. Louis Modeling Protein-DNA interactions: experimental and computational approaches
1:45 – 2:30	Jun Liu, Harvard University Modeling Protein-DNA binding profiles with protein binding microarray data
2:30 – 3:15	Cliff Meyer, Harvard University Identifying Enhancers through Differential Chromatin Structure Analysis
3:15 – 3:30	Break
3:30 – 4:15	Alex Hartemink, Duke University Toward a Mechanistic Understanding of Transcriptional Regulation: A Systems Perspective on Genome Occupancy
4:15 – 5:00	Leping Li, NIEHS Exploring the functional relevance of constitutively bound CTCF sites across multiple cell lines

Wednesday, May 30 (Chair Jason Lieb, UNC)

9:00 – 9:45	Jason Lieb, University of North Carolina at Chapel Hill Chromatin Dynamics in Cell Fate Specification and Maintenance
9:45 – 10:30	Greg Crawford, Duke University Applications and analysis of DNase-seq data
10:30 – 10:45	Break
10:45 – 11:30	Chip Lawrence, Brown University RNA Motif finding via grouped Gibbs sampler and two efficient recursions
11:30 – 12:15	Jason Ernst, University of California, Los Angeles The genome-wide interplay between chromatin states, transcription factor binding, and regulatory motifs in six human cell types