

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

May 29-30, 2012

NIEHS, Rodbell Auditorium

Tuesday, May 29

1:00 – 1:45 Gary Stormo, Ph.D., Washington University in St. Louis
Modeling protein-DNA interactions: experimental and computational approaches

1:45 – 2:30 Jun Liu, Ph.D., Harvard University
Modeling protein-DNA binding profiles with protein binding microarray data

2:30 – 3:15 Clifford Meyer, Ph.D., Harvard University
Identifying enhancers through differential chromatin structure analysis

3:15 – 3:30 Break

3:30 – 4:15 Alexander Hartemink, Ph.D., Duke University
Toward a mechanistic understanding of transcriptional regulation: a systems perspective on genome occupancy

4:15 – 5:00 Leping Li, Ph.D., NIEHS
Exploring the functional relevance of constitutively bound CTCF sites across multiple cell lines

Wednesday, May 30

9:00 – 9:45 Jason Lieb, Ph.D., University of North Carolina at Chapel Hill
Chromatin dynamics in cell fate specification and maintenance

9:45 – 10:30 Greg Crawford, Ph.D., Duke University
Applications and analysis of DNase-seq data

10:30 – 10:45 Break

10:45 – 11:30 Charles Lawrence, Ph.D., Brown University
RNA Motif finding via grouped Gibbs sampler and two efficient recursions

11:30 – 12:15 Jason Ernst, Ph.D., University of California, Los Angeles
The genome-wide interplay between chromatin states, transcription factor binding, and regulatory motifs in six human cell types

