8:45-8:55 Opening Remarks by Pierre Baldi
8:55-9:00 Symposium Format by Augustin Dunn

Session 1: High-Throughput Sequencing and Applications

9:00-9:20 AREM: aligning short reads from ChIP-Sequential by expectation maximization.
Daniel Newkirk, Jacob Biesinger, Alvin Chon, Kyoko Yokomori and Xiaohui Xie

Julie M. Cridland and Kevin R. Thornton

9:40-10:00 RNA-seq analyses of blood-induced changes in gene expression in *Aedes aegypti.*
Bonizzoni, Mariangela, Dunn, W Augustin, Campbell, Corey L, Olson, Ken E, Dimon, Michelle T, Marinotti, Osvaldo, James, Anthony A

Session 2: Gene Regulation and Disregulations

10:00-10:20 High-throughput analysis of cohesin-mediated gene regulation in the CdLS mouse model.
Daniel Newkirk, Richard Chien, Aniello Infante, Kyoko Yokomori, Xiaohui Xie

10:20-10:40 Transcriptional regulation of mammary gland development as a model for breast cancer.
Michael L Salmans, Padhraic Smyth, Bogi Andersen

10:40-11:00 Learning Epigenetic Markers of Cell-Specific Gene Expression.
Corey Schaninger, Padhraic Smyth, Bogi Andersen

11:00-11:20 Requirement of chromatin modifications for epigenetic switching in *Candida albicans.*
Zhiyun Guan, Su Zhao, Qing Nie, Haoping Liu

Session 3: Protein-Protein Interactions and Target Identification

Elizabeth A. Gordon, Vishal R. Patel, Thomas C. Whisenant, Robyn M Kaake, Lan Huang, Pierre Baldi and Lee Bardwell

11:40-12:00 Developing an integrated cross-linking mass spectrometry approach to analyze the structure and topology of the dynamic yeast 26S proteasome. Athit Kao, Scott Rychnovsky, Pierre Baldi, Lan Haung

12:00-1:00 Lunch

Session 4: Chemoinformatics and Drug Discovery

1:00-1:20 Learning to predict chemical reactions.

1:20-1:40 When is chemical similarity significant? The statistical distribution of chemical similarity scores and its extreme values.  
Ramzi Nasr and Pierre Baldi.

1:40-2:00 Virtual high-throughput screening for Annexin A2 and metastasin  
Paul Rigor, Gabe Ozorowski, Harmut Luecke and Pierre Baldi

2:00-2:20 High-Throughput 3D Structure Prediction of Small Molecules.  
Peter Sadowski, Arlo Randall, Pierre Baldi

David R. Fooshee, Tran B. Nguyen, David L. Bones, Sergey A. Nizkorodov, Patrick J. Roach, Julia Laskin, Alex Laskin, and Pierre Baldi

2:40-2:50 Coffee Break

Session 5: Modeling Systems and Diseases

2:50-3:10 Computational prediction of NOTCH targets in the C. elegans stem cell niche.  
Michael Zeller, Olivier Cinquin, Pierre Baldi

3:10-3:30 Extensions to the Sigmoid Modeling System and kMech: An Enzyme Mechanism Modeler.  
B. Compani, T. Su, I. Chang, P. Baldi, E. Mjolsness

3:30-3:45 Closing