BIT-GHTF Symposium || IGB-GHTF 12th anniversary || BIT 10th anniversary

HIGH-THROUGHPUT SEQUENCING AND OTHER METHODS FROM TECHNOLOGY TO DISCOVERY

When: June 7, 2012
Where: Donald Bren Hall, 6011

10:25-10:30: Introductory Remarks - Pierre Baldi
10:30-10:35: Introductory Remarks - Hal Stern, Dean of Donald Bren School of ICS
  - Stan Nelson, University of California, Los Angeles
11:25-11:45: GHTF Sequencing from Front to Back
  - Christophe Magnan and Melanie Oakes

Faculty Presentations on Challenges of Executing and Interpreting NGS Experiments

11:45-12:00: Deriving Alternative Splicing Information from RNA-seq
  - Klemens Hertel
12:00-12:15: Adventures in Functional Sequencing
  - Ali Mortazavi
12:15-12:30: Deciphering the "Polyadenylation Code"
  - Yongsheng Shi
12:30-12:45: Illumina's Nextera Technology for Highly-Multiplexed Libraries: Strengths, Limitations, and Optimization - Molly Burke, Anthony Long’s Group

Pizza Lunch with Discussions for High-End Users, Chalk Talks, and Open Problems
2:00-2:30: Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space
   - Stefano Lonardi, University of California, Riverside

BIT Student Presentations

2:30-2:55: Mapping Protein Complex Interaction Networks by Quantitative Mass Spectrometry - Robyn M. Kaake

2:55-3:20: A Lineage-Hidden Markov Model for Genomic Annotation from Epigenetic Modifications - Jacob Biesinger


3:35-3:50: Computational Prediction of MAPK Substrates and Integrations with Phosphoproteomes - Elizabeth A. Gordon


4:05-4:20: Computational Modeling of Regulatory Networks in Skin Wounding Response - Michael Zeller

4:20-4:35: Genome-Wide Analysis of Cohesin in a Cornelia de Lange Syndrome mouse model - Daniel A Newkirk

4:35—4:45: Closing Remarks (GHTF) - Suzanne Sandmeyer

4:45—4:55: Closing Remarks (BIT) - Wes Hatfield

Posters and Social Hour
Wine | Food | Entertainment
starting at 5:00 PM