

Workshop IV: Search and Knowledge Building for Biological Datasets

Monday November 26, 2007

- 8:00–8:50 *Check-In/Light Breakfast (Hosted by IPAM)*
- 8:50–9:00 *Welcome and Opening Remarks*
- 9:00–10:00 **Olga Troyanskaya** (Princeton University)
- 10:00–10:30 *Break*
- 10:30–11:30 **Vipin Kumar** (University of Minnesota, Twin Cities)
Association Analysis-based Extraction of Functional Information from Protein-Protein Interaction Data
- 11:30–1:00 *Lunch (on your own)*
- 1:00–2:00 **Chris Wiggins** (Columbia University)
Defining, Inferring, and Encoding modularity
- 2:00–2:30 *Break*
- 2:30–3:30 **William Noble** (University of Washington)
Consistent probabilistic outputs for gene function prediction
- 3:30–4:00 *Coffee Break*
- 4:00–5:00 **Alexandre Morozov** (Rutgers University)
A biophysical approach to predicting intrinsic and extrinsic nucleosome positioning signals
- 5:00–6:30 *Reception (Location: IPAM Lobby)*

Tuesday November 27, 2007

- 8:00–8:30 *Continental Breakfast*
- 8:30–9:30 **Srinivasan Parthasarathy** (Ohio State University)
Integrated Mining of Protein Interaction Networks: A Case for Ensemble Clustering
- 9:30–10:30 **Alexander Urban** (Yale University)
Integrated approaches for the analysis of complex human genomic sequence variation and its correlation to complex phenotypes
- 10:30–11:00 *Break*

(Tuesday schedule continued on next page)



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- 11:00–12:00 **Christina Leslie** (Memorial Sloan-Kettering Cancer Center)
Learning predictive models of gene regulation
- 12:00–1:30 *Lunch (on your own)*
- 1:30–2:30 **Trey G. Ideker** (University of California, San Diego (UCSD))
Protein Network Comparative Genomics
- 2:30–3:30 **Jiawei Han** (University of Illinois at Urbana-Champaign)
Mining, Indexing, and Searching Graphs in Biological Databases
- 3:30–4:00 *Coffee Break*
- 4:00–5:00 **Andrey Rzhetsky** (University of Chicago)
Computational analysis of complex traits: text- and network- and phenotype-mining

Wednesday November 28, 2007

- 8:00–9:00 *Continental Breakfast*
- 9:00–10:00 **Ronen Basri** (Weizmann Institute of Science)
Multiscale Edge Detection and Segmentation Algorithms for Biomedical Image Analysis
- 10:00–10:30 *Break*
- 10:30–11:30 **Yoav Freund** (University of California, San Diego (UCSD))
From microscopy images to models of cellular processes
- 11:30–1:00 *Lunch (on your own)*
- 1:00–2:00 **Amit Singer** (Yale University)
Cryo-EM and NMR Structure Determination through Eigenvectors of Sparse Matrices
- 2:00–2:30 *Break*
- 2:30–3:30 **Leon Glass** (McGill University)
Using Logical Circuits to Analyze and Model Genetic Networks
- 3:30–4:00 *Coffee Break*
- 4:00–5:00 **Richard Bonneau** (New York University)
Learning global transcriptional dynamics with the Inferelator and cMonkey

Thursday November 29, 2007

- 8:00–8:30 *Continental Breakfast*
- 8:30–9:30 **Alexander Krasnitz** (Cold Spring Harbor Laboratory)
Epicenter Analysis in Cancer
- 9:30–10:30 **Gilad Lerman** (University of Minnesota, Twin Cities)
Defining functional distance using manifold embeddings of gene ontology annotations
- 10:30–11:00 *Break*
- 11:00–12:00 **John Storey** (University of Washington)
Harnessing Naturally Randomized Transcription to Infer Causal Regulatory Relationships Among Genes
- 12:00–1:30 *Lunch (on your own)*
- 1:30–2:30 **Petros Drineas** (Rensselaer Polytechnic Institute)
Identifying Ancestry Informative Markers via Principal Components Analysis
- 2:30–3:30 **Stephen Altschul** (National Center for Biotechnology Information)
Protein Sequence Database Searches Using Compositionally Adjusted Amino Acid Substitution Matrices
- 3:30–4:00 *Coffee Break*
- 4:00–5:00 **Weixiong Zhang** (Washington University in St. Louis)
Integrative computational analysis of microRNA transcriptional regulation

Friday November 30, 2007

- 8:00–9:00 *Continental Breakfast*
- 9:00–10:00 **Laxmi Parida** (IBM Research)
Combinatorics and Statistics of Gene Clusters
- 10:00–10:30 *Break*
- 10:30–11:30 **John Doyle** (California Institute of Technology)
- 11:30–1:00 *Lunch (on your own)*
- 1:00–2:00 **Avi Ma'ayan** (Mount Sinai School of Medicine, CUNY)
Graph Theory Based Querying to Identify Novel Functions of Components and Pathways in Mammalian Cells
- 2:00–2:30 *Break*
- 2:30–3:30 **Jeffrey Morris** (University of Texas M. D. Anderson Cancer Center)
Applications of Wavelet-Based Functional Mixed Models to Proteomics and Genomics Data
- 3:30–4:00 *Coffee Break*

