

## Workshop I: High Throughput Technologies and Methods of Analysis

### Monday March 22, 2004

- 8:00–8:45 *Check-In/Light Breakfast (Hosted by IPAM)*
- 8:45–9:00 *Welcome and Opening Remarks*
- 9:00–10:00 **Vicki H. Wysocki** (University of Arizona)  
*Data-mining a Set of Truth Spectra to Determine Peptide Fragmentation Chemistry*
- 10:00–10:30 *Break*
- 10:30–11:30 **Peter Harrington** (Ohio University)  
*Chemometric Considerations in Proteomic Analyses by Mass Spectrometry*
- 11:30–1:30 *Lunch (on your own)*
- 1:30–2:30 **Shankar Subramaniam** (University of California at San Diego)  
*Contextual Analysis of Biochemical Networks in Mammalian Cells*
- 2:30–3:00 *Break*
- 3:00–4:00 **Joseph Loo** (UCLA)  
*Strategies for Characterizing Proteins in Proteomics Research*
- 4:00–5:00  
*TBA*

### Tuesday March 23, 2004

- 8:00–9:00 *Check-In/Light Breakfast (Hosted by IPAM)*
- 9:00–10:00 **Tim Veenstra** (National Cancer Institute)  
*Analysis of the Human Serum Proteome*
- 10:00–10:30 *Break*
- 10:30–11:30 **Tim Ting Chen** (University of Southern California)  
*Reliability of protein interaction data sets and prediction of protein domain interactions*
- 11:30–1:30 *Lunch (on your own)*
- 1:30–2:30 **Austin Yang** (University of Southern California)
- 2:30–3:00 *Break*

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- 3:00–4:00 **Christoph Borchers** (University of North Carolina)  
*Novel Comprehensive Proteomic Approaches to Address Biological Problems*
- 4:00–5:00 **Nouri Neamati** (University of Southern California)  
*Proteomics and the new frontiers*
- 5:00–6:30 *Wine/Cheese Reception (Hosted by IPAM)*
- 6:30–7:30 **Ruedi Aebersold** (Institute for Systems Biology)  
*Data Collection and Analysis for High Throughput Quantitative Proteomics: Current Status And Challenges*

### Wednesday March 24, 2004

- 8:00–9:00 *Check-In/Light Breakfast (Hosted by IPAM)*
- 9:00–10:00 **Terry Speed** (University of California at Berkeley)  
*Deriving statistical models for predicting peptide tandem MS product ion intensities*
- 10:00–10:30 *Break*
- 10:30–11:30 **Hongyu Zhao** (Yale University)  
*Statistical Issues in the Analysis of Mass Spectrometry Data*
- 11:30–1:30 *Lunch (on your own)*
- 1:30–2:30 **Benno Schwikowski** (Institute for Systems Biology)  
*Algorithms for the Multidimensional Analysis of Multidimensional LC-Mass Spectrometry Data*
- 2:30–3:00 *Break*
- 3:00–4:00 **Fernando Pineda** (Johns Hopkins University)  
*Algorithms and Databases for rapid microorganism identification, Statistical model of proteolytic digestion for improved protein identification*
- 4:00–5:00 **Michael Snyder** (Yale University)  
*Global analysis of Genomes and Proteomes*

### Thursday March 25, 2004

- 8:00–9:00 *Check-In/Light Breakfast (Hosted by IPAM)*
- 9:00–10:00 **Pavel Pevzner** (University of California at San Diego)
- 10:00–10:30 *Break*

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- 10:30–11:30 **Weixiong Zhang** (Washington University)  
*Discovering Temporal Gene Regulatory Networks*
- 11:30–1:30 *Lunch (Hosted by IPAM)*
- 1:30–2:30 **Vineet Bafna** (University of California at San Diego)  
*De novo interpretation of tandem mass spectra*
- 2:30–3:00 *Break*
- 3:00–4:00 **Nathan Edwards** (Applied Biosystems)  
*Generating Peptide Candidates from Protein Sequence Databases for Protein Identification via Mass Spectrometry*
- 4:00–5:00 **Alexander Hartemink** (Duke University)  
*Classification in high-dimensional spaces: joint classification and feature selection*

### Friday March 26, 2004

- 8:00–9:00 *Check-In/Light Breakfast (Hosted by IPAM)*
- 9:00–10:00 **Edward Marcotte** (University of Texas, Austin)  
*The structure and dynamics of genome-wide protein networks*
- 10:00–10:30 *Break*
- 10:30–11:30 **Fengzhu Sun** (University of Southern California)  
*An Integrated Approach for Protein Function Prediction*
- 11:30–1:30 *Lunch (on your own)*
- 1:30–2:30 **William Noble** (University of Washington)  
*A kernel framework for genomic data fusion*
- 2:30–3:00 *Break*
- 3:00–4:00 **Golan Yona** (Cornell University)  
*BIOZON: a unified knowledge resource on DNA sequences, proteins, complexes and cellular pathways*
- 4:00–5:00 **Bin Ma** (University of West Ontario)  
*PEAKS: Accurate de novo sequencing using MS/MS*

