



Institute for Pure and Applied Mathematics  
University of California, Los Angeles presents

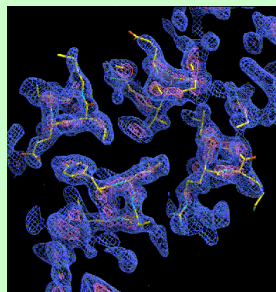
# Proteomics: Sequence, Structure, Function

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

March 22 - 26, 2004

Members of the organizing committee include **Tim Ting Chen**, Chair (USC), **Vineet Bafna** (UCSD), **Joseph Loo** (UCLA) and **Pavel Pevzner** (UCSD)

**Workshop I: High Throughput Technologies and Methods of Analysis** is part of an active program of research activities, seminars and workshops throughout the **March 8 – June 11, 2004** period and core participants will be in residence at IPAM continuously for these fourteen weeks. The program will open with tutorials, and will be punctuated by 4 major workshops and a culminating workshop at UCLA's Lake Arrowhead Conference Center. Numerous distinguished researchers will be participating. Between the workshops there will be a program of activities involving the long-term and short-term participants, as well as visitors.



### Scientific Overview

**Focus:** New technologies such as mass spectrometry and protein arrays; methods of analysis, both analysis of experiments and analysis leading to an understanding of protein networks.

The workhorse of proteomics is 2-D gel electrophoresis. This technology spreads out proteins in a sample differentially in the plane, producing a collection of spots, each of which contains one protein. A comparatively new technology has come on line – mass spectrometry – that promises to be to proteomics what automated sequencing machines were to genomics. The basic modality is protein mass fingerprinting – a protein is cut into segments and then the fragment masses measured very precisely using mass spec. By comparison with protein databases, the composition of the fragments can be determined, and from this the entire protein reconstructed.

There are numerous challenges to making this an effective high-throughput method. Mass spec facilities are springing up at research facilities worldwide. In addition, a number of new technologies coming on line will provide even more information. Each technology raises interesting issues of analysis, ranging from comparatively familiar issues of image analysis to the much more open issues of how to use the information generated to reconstruct networks of protein interactions.

### Confirmed Speakers:

Ruedi Aebersold (Inst for Systems Bio)	Bin Ma (Univ of W. Ontario)	Shankar Subramaniam (UCSD)
Vineet Bafna (UCSD)	Edward Marcotte (U. of Texas, Austin)	Fengzhu Sun (USC)
Christoph Borchers (U. of North Carolina)	Nouri Neamati (USC)	Tim Veenstra (NCI)
Tim Ting Chen (USC)	William Noble (U. of Washington)	Vicki H. Wysocki (U. of Arizona)
Nathan Edwards (Applied Biosystems)	Pavel Pevzner (UCSD)	Austin Yang (USC)
Mark Gerstein (Yale)	Fernando Pineda (Johns Hopkins)	John Yates (Scripps Res Inst)
Peter Harrington (Ohio U.)	Benno Schwikowski (Inst for Systems Bio)	Golan Yona (Cornell)
Alex Hartemink (Duke)	Michael Snyder (Yale)	Weixiong Zhang (Washington U., St. Louis)
Joseph Loo (UCLA)	Terry Speed (UC Berkeley)	Hongyu Zhao (Yale)

### Participation

Financial support for this workshop is available for participants at all academic levels, and recent PhD's, graduate students, and researchers in the early stages of their career are especially encouraged to apply. An online application for support is available at <http://www.ipam.ucla.edu/programs/protws1>. Encouraging the careers of women and minority mathematicians and scientists is an important component of IPAM's mission and we welcome their applications. Applicants who are interested in becoming core participants and participating in the semester program (March 8 – June 11, 2004) should apply at <http://www.ipam.ucla.edu/programs/prot2004>.

Please visit our website at

<http://www.ipam.ucla.edu/programs/protws1>

or email questions to [protws1@ipam.ucla.edu](mailto:protws1@ipam.ucla.edu)

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