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Systems Biology and Computational Proteomics

Volume Editors

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Preface

The RECOMB Satellite Conferences on Systems Biology and Computational Proteomics were held December 1–3, 2006, at La Jolla, California. The Systems Biology meeting brought researchers together on various aspects of systems biology, including integration of genome-wide microarray, proteomic, and metabolomic data, inference and comparison of biological networks, and model testing through design of experiments. Specific topics included:

- Pathway mapping and evolution in protein interaction networks
- Inference of protein signaling networks for understanding cellular responses and developmental programs
- Model prediction of drug mechanism of action and toxicity
- Multi-scale methods which bridge abstract and detailed models
- Systematic design of genome-scale experiments
- Modeling and recognition of regulatory elements
- Identification and modeling of *cis*-regulatory regions
- Modeling the structure and function of regulatory regions
- Comparative genomics of regulation

With the sequencing of the genome, and subsequent identification of the parts list (the gene and their protein products), there is a renewed emphasis on studying the proteome. This year, the computational proteomics meeting focused on on computational mass spectrometry. Mass spectrometry is emerging as a key technology for proteomics. The last few years have seen tremendous improvement in the quality and quantity of available peptide mass spectrometry data, as well as the realization that advanced computational approaches are critical to the success of this technology. The conference explored the use of this technology in various proteomic applications, including, but not limited to: protein identification and quantification in specific cellular environments; structural genomics; networks of protein interaction; post-translational modifications; and others.

We received approximately 50 full paper submissions to the joint workshops. After review, a total of 20 were invited for oral presentations, adding to 14 plenary talks. These papers appear either as extended abstracts in this volume or are published in the journal *Molecular Systems Biology*.

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Vineet Bafna
Trey Ideker

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