

Keystone Symposia: Biomolecular Interaction Networks: Function and Disease

March 7–12, 2010 • Fairmont Le Château Frontenac • Québec City, Québec • Canada

Scientific Organizers: Anna Panchenko, Teresa Przytycka and Andrea Califano

PROGRAM FACULTY & TALKS

- M. Madan Babu**, University of Cambridge, UK
Evolution of Transcriptional Regulatory Networks
- Aviv Bergman**, Albert Einstein College of Medicine, USA
Evolutionary Capacitance as a General Feature of Complex Gene Networks
- Rachel Brem**, University of California, Berkeley, USA
*Expression Variation and Regulatory Feedback in *Saccharomyces**
- Andrea Califano**, Columbia University, USA
Molecular Interaction Networks to Dissect Master Regulators of Malignant Transformations
- Eric H. Davidson**, California Institute of Technology, USA
Evolutionary Plasticity of Developmental Gene Regulatory Network Architecture
- Aimee Dudley**, Institute for Systems Biology, USA
Systems Approaches to Spatial Dynamics in Posttranscriptional Networks
- Hunter B. Fraser**, Stanford University, USA
Quantitative Genetics of Phenotypic Robustness
- Anne-Claude Gavin**, European Molecular Biology Laboratory, Germany
Biomolecular Networks from Proteins to Small Molecules
- Barry Honig**, Columbia University/HHMI, USA
On the Nature of Protein Fold Space: Extracting Functional Information from Apparently Remote Structural Neighbors
- Trey G. Ideker**, University of California, San Diego, USA
Comparative Analysis of Protein Networks
- Nevan J. Krogan**, University of California, San Francisco, USA
High-Throughput Genetic Interaction Mapping
- Douglas A. Lauffenburger**, Massachusetts Institute of Technology, USA
Integrated Experimental and Computational Approaches to Dissect Cell Response to Stimuli
- Edward M. Marcotte**, University of Texas at Austin, USA
Linking Genes to Traits Using Network-Guided Genetics
- Ruth Nussinov**, National Cancer Institute and Tel Aviv University, USA
Modular Architecture of Protein Structures and Allosteric Communications: Potential Implications for Signaling Proteins and Regulatory Linkages
- Anna Panchenko**, National Center for Biotechnology Information, NIH, USA
Evolution of Protein Binding Modes
- Tony Pawson**, Samuel Lunenfeld Research Institute, Canada
Proteomic Analysis of Bidirectional Signaling Networks
- Dana Pe'er**, Columbia University, USA
Genetic Regulatory Complexity: Lessons from Yeast to Cancer
- Yitzhak Pilpel**, Weizmann Institute of Science, Israel
Adaptive Prediction of Environmental Changes by Microorganisms
- Teresa Przytycka**, NCBI, NLM, National Institutes of Health, USA
New Approaches to Uncovering Differentially Regulated Genes and Pathways
- Eric Schadt**, Pacific Biosciences, USA
Variations in DNA Elucidate Molecular Networks that Cause Disease
- Mona Singh**, Princeton University, USA
Analyzing and Interrogating Protein Interaction Maps via Network Schemas
- Michael Snyder**, Stanford University School of Medicine, USA
Interacting and Modification Networks
- Gustavo Stolovitzky**, IBM, USA
Systems Biology of Small and Large Scale Gene Regulatory Networks
- Sarah Teichmann**, MRC Laboratory of Molecular Biology, UK
Evolution of Protein Complexes by Duplication of Homomeric Interactions
- Anna Tramontano**, University of Rome, La Sapienza, Italy
Mapping Epitopes on Protein Surface: Mining Annotated Proteins
- Olga G. Troyanskaya**, Princeton University, USA
From Integrated Functional Networks to Understanding Disease
- Alfonso Valencia**, Spanish National Cancer Research Centre, Spain
Coevolutionary Information in the Prediction of Global Interactomes and Interaction Regions
- Shoshana Wodak**, Hospital for Sick Children, Research Institute, Canada
Modularity of the Transcriptional Response of Protein Complexes in Yeast

Program subject to change. Current as of October 12, 2009



The aim of this symposium is to bring together researchers from different fields of computational and experimental biology to discuss the use of biomolecular interaction networks to study cell function in both physiological and pathological contexts. These interaction maps, also known as interactomes, model protein-protein, protein-DNA and protein-small molecule interaction networks either within an organism or within specific cellular contexts. Regulatory interactions play a key role in determining cellular differentiation, in maintaining cellular and organism homeostasis and in triggering abnormal differentiation events leading to human disease including cancer. Not surprisingly, even slight genetic and epigenetic perturbations of these regulatory pathways can trigger macroscopic changes in normal cell physiology and lead to disease. Due to the abundance of experimental data, researchers are starting to uncover some general rules and principles underlying molecular interaction networks: their topological properties, the relationships between their components, evolutionary conservation and divergence and their role in maintaining specific cellular functions and processes. Despite significant advances, however, knowledge about the distinct functional roles of many proteins is still elusive. Thus, interaction networks have emerged as exceedingly useful tools in predicting context-specific molecular function based on knowledge of upstream regulators, cognate binding partners and downstream regulated targets. Furthermore, molecular interaction networks are starting to provide a unique integrative context to study additional disease-related genetic and epigenetic data, including single nucleotide mutations and polymorphisms, gene copy number alterations and complex, polygenic diseases.

PROGRAM PLENARY SESSIONS:

- Experimental Identification, Characterization and Verification of Interaction Data
- Biomolecular Interaction Networks: Topological Structure and Properties
- Protein Interaction Interfaces: General Principles of Molecular Recognition
- From Molecular Interaction Networks to Function Prediction
- Evolution of Biomolecular Networks
- Disease Interactome: Disease-Associated Genes, Disease Mutations and Protein Interactions
- Linking Regulatory Networks to Cellular Function
- Regulatory Networks and Genetic Polymorphism

DEADLINES:

Abstract & Scholarship: November 9, 2009
Late-Breaking Abstract: December 7, 2009
Early Registration: January 7, 2010

www.kestonesymposia.org/10C1

KEYSTONE SYMPOSIA[®]
on Molecular and Cellular Biology
Accelerating Life Science Discovery

PO Box 1630 • Silverthorne, CO 80498 • USA
www.kestonesymposia.org • 1-800-253-0685 • 1-970-262-1230