

ISMB/ECCB 2007

Intelligent Systems in Molecular Biology/European Conference on Computational Biology
Austria Center Vienna, 18-25 July

Conference Chairs

Thomas Lengauer (Director, Max-Planck Institut für Informatik, Saarbrücken) is a founder of the International Society for Computational Biology (ISCB), a member of the German Academy of Sciences Leopoldina, and a recipient of the Konrad Zuse Medal of the German Informatics Society and the Karl Heinz Beckurts Award.

Burkhard Rost (Columbia University, New York, USA) is a Heidelberg-educated theoretical physicist who developed the first Internet server for structure prediction and whose objectives in bioinformatics, since 1990, include predicting protein function from sequence and contributing to the effort to construct models of the cell *in silico*.

Peter Schuster (University of Vienna, Austria) is currently President of the Austrian Academy of Sciences. A full professor of theoretical chemistry, Schuster's interests include the study of evolutionary mechanisms via molecular models and the design of special-purpose molecules.

Keynote Speakers and Award Winners: Synopses

Eran Segal, ISCB Overton Prize (Computer Science and Applied Mathematics, Weizmann Institute, Rehovot, Israel): *Quantitative models for chromatin and transcription regulation*. The way DNA wraps around the nucleosomes of chromatin is DNA-sequence-dependent. Alternation and clustering of stronger and weaker binding sites combine to regulate gene transcription.

Temple F. Smith, ISCB Senior Scientist Accomplishment Award (Director, Biomolecular Engineering Research Center, Boston University, Boston, USA): *Computational biology: what is next?* Computational biology was foreshadowed before the Smith-Waterman algorithm—as early as 1964. In its origins, we see how its future will be shaped.

Søren Brunak (Center for Biological Sequence Analysis, BioCentrum DTU, Technical University of Denmark, Lyngby, Denmark): *Understanding interactomes by data integration*. Important protein groups may be classified by their "conservation" of features like chain length and hydrophobicity, and such classification, integrated with expression and interaction data, helps in predicting/constructing functional networks.

Stephen K. Burley (SGX Pharmaceuticals, Inc., San Diego, USA): *Fragment-based discovery of BCR-ABL inhibitors for treatment of chronic myelogenous leukemia*. A highly parallel crystallographic screening technique is used to create a library of fragments of active structures from which small binding compounds with high medicinal activity can be combinatorially constructed to target cancer cell proteins.

Michael Eisen (Center for Integrative Genomics, University of California, Berkeley, USA). *Understanding and exploiting the evolution of the sequences that control gene expression*. Computational and experimental characterization of changes at transcription-factor binding sites enables reconstruction of the evolution of sequences that control gene expression.

Anne-Claude Gavin (European Molecular Biology Laboratory, Heidelberg, Germany): *Interaction networks probed by mass spectrometry*. Spectrometric system-wide analysis of budding yeast is integrated with other data using scoring that yields a more dynamic map of the cell interaction network.

John Mattick (Director, Institute for Molecular Bioscience, University of Queensland, Brisbane, Australia): *The majority of the genome of complex organisms is devoted to an RNA regulatory system that directs differentiation and development*. The "non-protein-coding" RNA that makes up 98 percent of the human genome is in fact a highly parallel genetic "operating system" for development.

Erin K. O'Shea (Director, Center for Systems Biology, Harvard University, Cambridge, USA): *Dissecting transcriptional network structure and function*. A single kinase in budding yeast controls expression of 300 genes by modulating

activity in several transcription factors. Computational analysis of microarray results yields a picture of the overlapping network architecture that enables such fine-tuned responses.

Renée Schroeder (Max F. Perutz Laboratories, University of Vienna, Austria): *Genomic SELEX for the identification of novel non-coding RNAs independent of their expression level.* SELEX (systematic evolution of ligands by exponential enrichment) enables discovery of the functions of "silent" (apparently non-coding) RNAs, in this case of human and *E. coli* RNAs with affinity for important small ligands.

Terry Speed (University of California, Berkeley, USA and Walter & Eliza Hall Institute of Medical Research, Melbourne, Australia): *Genome-wide genotyping: the great classification challenge.* In a few years, we may be able to identify all places at which an individual's genome differs from a reference genome, which poses an enormous statistical challenge. How can it be met?

Special Sessions (half-days throughout the conference)

Private fears in public places? Ethical and regulatory concerns regarding human genome databases - Cheminformatics - Genetic networks: Inferring pathways by combinatorial perturbation - Computational epigenetics and chromatin regulation - Computational approaches to the modern RNA world - Dry work in a wet world: Improving methodology and access for computational methods in systems biology

Highlights Track Areas (Recent work of highest impact)

Systems biology and proteomics - Protein structure and function - RNA world - Genomes and evolution - Networks, interactions, and regulation - Disease - Text mining - Methods and databases

Industry Track

Presentations by researchers in industry lasting 20-25 minutes, describing a business/scientific problem, the approach used, the current state of the project, project demonstration, an evaluation of the benefits, and future developments. Schedule available at the meeting.

Public Library of Science Track

This track, chaired by Barbara Bryant of Millennium Pharmaceuticals with *PLoS Computational Biology* founding editors Steven Brenner and Philip Bourne, features late-breaking news in the following areas: Ecosystems and ecology - Systems biology and networks - Health and disease - Regulation - Protein structure and function - Neuroscience - Multiscale modeling - Evolution - Population genetics and variation - Genomics

Tutorials (all on Saturday, July 21)

Morning (0830 - 1230): Comparative analysis of protein structures: Principles, tools, and applications for establishing evolutionary relationship and predicting function - Workflow approaches to transcriptomics analysis - Ontologies for biomedicine: How to make and use them - Exploring computational biology with a massively parallel high-performance computing environment - Genomes, browsers, and databases: Tools for integrating sequence and annotation data from multiple genomes - Implementing phylogenetic workflows for comparative genomics using BioPerl - Genomic data fusion for gene prioritization and function prediction

Afternoon (1330 - 1730): Gene and protein networks - Automatic text analysis based on Web services - Reverse-engineering mammalian transcriptional regulatory circuits - Systems biology of host-pathogen interactions and microbial communities - Comprehensive analysis of Affymetrix exon expression data using BioConductor - Introduction to phylogenetic networks - Introduction to bioinformatics for glycomics research

Satellite Meetings and Special Interest Groups (SIGs) July 19 and 20

Satellite Meeting: "3Dsig" structural bioinformatics and computational biophysics (both days)

Two-day SIGs: Alternative splicing - Bioinformatics open-source conference - BioPathways - Joint AFP/BioSapiens meeting

One-day SIGs: BioLINK (Thursday) - Bio-Ontologies (Friday) - Comparative genomics, evolution, and regulation in microbes (Friday)