



Emergence

The Ninth Annual BioPathways Meeting

Organized by

Vítor Martins dos Santos
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July 18-19, 2008

ISMB 2008
Toronto, Canada

The 9th BioPathways meeting is organized by the BioPathways Consortium (www.biopathways.org), an open forum aimed at fostering computational approaches to the modeling, reconstruction, analysis and simulation of biological networks.

Previous BioPathways meeting have focused on a variety of themes, such as computational reconstruction of molecular networks, pathway evolution, integration of models and experiments, models and ontologies for pathways, metabolic pathways on modeling of interactions and regulation on a systems scale.

Our special focus this year will be on computational methods for Synthetic Biology and will be organised in collaboration with EMERGENCE, an EU-funded consortium aiming at fostering and consolidating the field of Synthetic Biology in Europe (<http://www.emergence.ethz.ch/>, <ftp://ftp.cordis.europa.eu/pub/nest/docs/5-nest-synthetic-080507.pdf>).

Synthetic Biology addresses the design and fabrication of biological components and systems that do not exist in the natural world as well as the re-design and fabrication of already existing biological systems. Whereas many of the computational methods developed in order to model and analyze natural systems are relevant to the modeling of synthetic living systems, there is also an acute need for new computational methods in order to support the rational design goals and the abstraction/modularity/assembly approach of synthetic biology.

The meeting will include 3 other plenary sessions, touching on the full spectrum of pathways and networks-related themes.

- Network Reconstruction and Analysis
- Database and Software Tools (for pathways and networks)
- Evolution of networks

Each plenary session includes several long invited presentations (30' - 40'). An open discussion will conclude each day.

Looking forward to see you at the BioPathways '08, Toronto

The organizing committee:

Vítor Martins dos Santos, Vincent Danos, Joanne Luciano, Vincent Schachter, Aviv Regev, Eric Neumann

9th BioPathways Meeting Program

METRO TORONTO CONVENTION CENTRE (MTCC). CONFERENCE TO BE HELD IN THE SOUTH BUILDING, Room 714B

Day I – July 18th

7:30 – 8:30	Registration	
8:30-8:45	Vítor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig, DE	Opening remarks
Session 1 & Analysis : Databases & Software Tools Chair: Vítor Martins dos Santos		
8:45-09:30	Trey Ideker, University California San Diego, USA	Mapping pathways through integration of physical and genetic interactions
9:30-10:15	Peter Karp, AI.SRI, Menlo Park, USA	The MetaCyc and BioCyc database collection
10:15-10:45	Coffee Break	
10:45-11:30	Phillip Bourne, University California San Diego, USA	The role of biopathways in drug repositioning and determining side effects
11:30-12:00	Geoffrey Winsor, Simon Fraser University, CA	InnateDB - Facilitating Systems Level Analyses of the Mammalian Innate Immune Response
12:00-12:30	Jennifer Gardy, Centre for Microbial Diseases & Immunity Research, University of British Columbia, CA	Cerebral 2.0: A Cytoscape plugin for the network-based visualization of datasets from multiple experimental conditions
12:30-13:30	Lunch	
Session 2: Network Reconstruction & Analysis Chair: Eric Neumann, Teranode		
13:30-14:10	Rune Linding – Institute for Cancer Research, London, UK	Constructing in vivo phosphorylation networks
14:10-14:50	Terry Gasterland, University California at San Diego, USA	Examining Cell Cycle Control Networks at Single Cell Resolution

14:50-15:30	Kobi Benenson, Harvard University, Cambridge, USA	Molecular automata: from concepts to applications
15:30-16:00	Coffee Break	
16:00-16:35	Ran Kafri, Harvard Medical School, Boston, USA	Functional redundancies - an evolutionarily conserved control element in signal transduction and metabolism
16:35-17:05	Tijana Milenković, Nataša Pržulj, University California Irvine, USA	From network structure to biological function in protein-protein interaction networks
17:05-17:35	Jean Krivine, Harvard Medical School, Boston, USA	Rule-based modeling of large protein networks
17:35-18:15	Peer Bork, EMBL, Heidleberg, DE	Get the most out of your metagenome: computational analysis of environmental sequence data
General Discussion		
18:15-18:30	Network analysis, Databases & Tools	

Day II – July 19th

Session 3 : Computational Methods and Infrastructure for Synthetic Biology		
Chair: Kobi Benenson, Bauer Centre		
8:30-9:00	Vitor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig, DE	EMERGENCE: a Foundation for Synthetic Biology in Europe
9:00-9:40	Randy Rettberg, MIT, Cambridge, USA	Synthetic Biology Based on Standard Parts: Design Competitions and Catalogs
9:40-10:15	Ildefonso Cases, CNIO, Madrid, ES	Bioinformatics tools to help in the design of biological systems
10:15-10:45	Coffee Break	
10:45-11:25	Shoshana Wodak, Hospital Sick Children, Toronto, CA	Identifying meaningful pathways in metabolic networks without the help of chemistry
11:25-12:00	David Gilbert, University of Glasgow, UK	A behaviour driven approach to design and implementation in Synthetic Biology
12:00-12:30	Martijn van Iersel, University of Maastricht, NL	WikiPathways, pathway creation and online collaboration
12:30-13:30	Lunch	
Session 4: Evolution of pathways and networks		
Chair: Joanne Luciano, MITRE		
13:30-14:15	Chris Sander, Sloan-Kettering, New York, USA	System models derived from combinatorial perturbation experiments - the CoPIA method
14:15-14:50	Edwin Wang, National Research Council, McGill University, Montreal, CA	Principles of microRNA regulation of cellular networks
14:50-15:30	Chris Myers, Cornell University, USA	Sloppiness in cellular networks
15:30-16:00	Coffee Break	
15:30-16:05	Matthew de Jongh, Hope College, Holland (MI), USA	Generation and Refinement of Metabolic Reaction Networks in the SEED

16:05-16:35	Andrey Ptitsyn, Colorado State University, Fort Collins, USA	The Structure of Biological Pathways in Time
16:35-17:10	Zhenjun Hu, Boston University, USA	Metagraph: a new graph structure for multiple-scale visualization and modeling of biological networks/pathways
17:10-17:45	Pedro Beltrao, University California San Francisco	Evolution of Cellular Networks
Round Table Discussion		
17:45-18:30	Network Reconstruction, Pathways and Evolution	
End of meeting		