



The 11th International Conference on Molecular Systems Biology

June 21-25, 2009
Shanghai, China

Conference Program

**Conference Venue:
Grand auditorium, Physiological Building, SIBS Campus
320 Yue Yang Road, Shanghai 200031**

Sunday, June 21st (Pre-conference workshops)

Morning workshop (SIBS Physiological Building 300)

8:30-9:30 [What? Why? How? An introduction to modeling biological systems](#)
Eberhart Voit, Department of Biomedical Engineering, Georgia Institute of Technology, USA

9:45-12:45 [Latent variables in high dimensional data](#)
William R. Atchley and Lisa McFerrin, North Carolina State University, USA

Afternoon workshop (SIBS Physiological Building 300)

13:30-14:30 [Molecular diversity analysis of genome-wide human population data](#)
Shuhua Xu, CAS-MPG Partner Institute for Computational Biology, China

14:30-15:30 [Adaptive evolution in Drosophila and humans](#)
Haipeng Li, CAS-MPG Partner Institute for Computational Biology, China

15:30-16:30 [Detecting global evidences of recent positive selection in human](#)
Kun Tang, CAS-MPG Partner Institute for Computational Biology, China

14:00-18:00 **Registration (Grand auditorium)**

18:30-19:30 **Welcome reception (SIBS Physiological Building 300)**

Monday, June 22nd

8:15-8:30	Welcome notes Andreas Dress , CAS-MPG Partner Institute for Computational Biology, China
8:30-9:15	Invited talk: Analysing complex decision-making by regulatory and signalling networks David Rand , Mathematics Institute, University of Warwick, UK
9:15-9:25	Discussion
Morning session: Mathematical modeling of biosystems I (Chair: Albert Sorribas)	
9:25-10:00	Invited talk: Hysteretic and graded responses in bacterial two-component signal transduction Rui Alves , Universidad de Lleida & IRB Lleida Lleida, Spain
10:00-10:25	Global sensitivity analysis of apoptotic signaling networks Wu-Hsiung Wu* , Maw-Shang Chang , Feng-Sheng Wang , University of Chung Cheng, Taiwan
10:25-10:40	Coffee break
10:40-11:05	A system biology approach to L-carnitine biosynthesis in E. coli cultures: signalling pathway involved in metabolic regulation analysis Jose A. Hormiga* , Angel Sevilla , Carlos Alcon , Manuel Canovas , Nestor V. Torres Universidad de La Laguna, Spain
11:05-11:30	Signalling pathway involved in metabolic regulation of L-carnitine biosynthesis in E. coli cultures: optimization of the production from glucose Carlos Gonzalez-Alcon , Jose A. Hormiga , Angel Sevilla , Manuel Canovas , Nestor V. Torres* Universidad de La Laguna, Spain
11:30-11:55	Structural and kinetic analysis of circadian oscillators Xiaoqing Li* , Oliver Ebenhoeh , Alexander Skupin Max Planck Institute of Molecular Plant Physiology, Germany
12:15-13:15	Lunch break (West Canteen)
13:30-14:15	Invited talk: Composition vector approach to phylogeny: success and foundation Bailin Hao , T-Life Research Center and Department of Physics, Fudan University Institute of Theoretical Physics, Academia Sinica, China Santa Fe Institute, USA
14:15-14:25	Discussion
Afternoon session: Molecular interactions and evolution	
14:25-14:50	Gene regulation in circadian rhythm, sleep, and hibernation Jun Yan* , CAS-MPG Partner institute for Computational Biology, China
14:50-15:15	Coevolutionary patterns on HLA class I and class II molecules Xiao-Wei Jiang* , Mario A. Fares , University of Dublin, Trinity College, Ireland
15:15-15:40	The subsequence composition of biosequences Andreas Dress* , Alberto Apostolico , CAS-MPG Partner Institute for Computational Biology, China
15:40-15:55	Coffee break
15:55-16:20	Genome-wide estimation of nucleotide diversity and disequilibrium coefficients from single heterozygous diploid genome Xiang Gao* , Michael Lynch , Indiana University, USA
16:20-16:45	Proto-ubiquitin: Bayesian prediction of an ancient protein Marla A. Endriga* , Lovette F. Cunanan , Richelda A. Galapia , Custer C. Deocaris University of the Philippines Manila, Philippines
16:45-17:10	MSWAT: a multiple sequence web viewer and alignment tool for phylogenetic and molecular evolutionary analyses and its applications Zhengqiu Cai* , Robert K. Jansen , University of Texas at Austin, USA
17:45-19:45	Dinner, West Canteen

Tuesday, June 23rd

8:30-9:15	Invited talk: Parameter estimation revisited (again!): low SSE and speed are not enough Eberhard O. Voit , Integrative BioSystems Institute and Wallace H. Coulter, Georgia Tech University, USA
9:15-9:25	Discussion
Morning session: Mathematical modeling of biosystems II (Chair: Rui Carlos Vaqueiro de Castro Alves)	
9:25-10:00	Rule-based modeling of signal transduction systems Jin Yang , CAS-MPG Partner Institute for Computational Biology, China
10:00-10:25	An ant colony optimization algorithm for the network inference and parameter estimation of S-systems Philip Christian C. Zuniga* , Maia Malonzo , Henry Adorna and Prospero Naval University of the Philippines-Diliman, Philippines
10:25-10:50	Systems analysis of the role of BMP4 and NADPH oxidase in shear stress-induced endothelial inflammation Weiwei Yin* , Eberhard O.Voit , Georgia Institute of Technology and Emory University, USA
10:50-11:00	Coffee break
11:00-11:25	Inverse problems of biochemical systems using time-varying power-law models Feng-Sheng Wang* , Wen-Hung Hunag , National Chung Cheng University, Taiwan
11:25-11:50	Monomial transformations in generalized mass action systems Alberto Marin-Sanguino* , Dieter Oesterhelt , Eduardo Mendoza Max-Planck Institute for Biochemistry and Ludwig-Maximilians-Universitat, Germany
11:50-12:15	Bottleneck ranking using instantaneous and overall indicators in metabolic reaction networks Fumihide Shiraishi* , Kansuporn Sriyudthsak , Kyushu University, Japan
12:15-13:15	Lunch break (West Canteen)
13:30-14:15	Invited talk: Gene regulatory network inference by evolutionary computation Prospero C. Naval , Department of Computer Science, University of the Philippines, Philippines
14:15-14:25	Discussion
Afternoon session: Network inferences (Chair: Rudiyanto Gunawan)	
14:25-15:00	Invited talk: Inferring molecular networks Jing-Dong Jackie Han Chinese Academy of Sciences (CAS) Key Laboratory of Molecular Developmental Biology, Center for Molecular Systems Biology, Institute of Genetics and Developmental Biology, CAS
15:00-15:25	The disease-drug network and its applications in drug discovery Guanghui Hu* , GlaxoSmithKline
15:25-15:50	Sampling Bayesian network with fast mixing MCMC Yongtao Guan* , Matthew Stephens , University of Chicago, USA
15:50-16:05	Coffee break
16:05-16:30	Reconstruction of the NF-κB signalling pathway interactome Paolo Tieri* , Alberto Termanini , Elena Bellavista , Stefano Salvioli , Claudio Franceschi University of Bologna, Italy
16:30-16:55	Detecting complexes from protein interaction networks Sriganesh Srihari* , Hon Wai Leong , National University of Singapore, Singapore
16:55-17:20	Functional evaluation of topological metabolic network properties Georg Basler* , Zoran Nikoloski , Oliver Ebenhoeh University of Potsdam and Max Planck Institute for Molecular Plant Physiology, Germany
17:45-19:45	Dinner, West Canteen

Wednesday, June 24th

8:30-9:15	Invited talk: CoryneRegNet -- a data warehouse containing comprehensive information on the transcriptional regulation of the amino acid producer corynebacterium glutamicum Alf Puehler* , Kalinowski J. , Tauch A. , Center for Biotechnology, Bielefeld University, Germany
9:15-9:25	Discussion
Morning session: Mathematical modeling of biosystems II	
9:25-10:00	Invited talk: Evolution of adaptive responses in metabolic networks: identifying feasible adaptive changes compatible with physiological constraints Albert Sorribas* , Gonzalo Guillen-Gosalbez , Ester Vilaprinyo , Rui Alves , Universitat de Lleida, Spain
10:00-10:25	Identifiability analysis of metabolic networks Sridharan Srinath , Rudiyanto Gunawan* , National University of Singapore, Singapore
10:25-10:40	Coffee break
10:40-11:05	A mathematical model for L-serine metabolism in animal brain with and without expression of 3-phosphoglycerate dehydrogenase gene Kansuporn Sriyudthsak* , Fumihide Shiraishi , Shigeki Furuya , Kyushu University, Japan
11:05-11:30	Modeling breast cancer mortality reduction by early detection Ester Vilaprinyo* , Montserrat Ru , University of Lleida-IRBLleida, Spain
11:30-11:55	A mathematical model of psoriatic pathogenesis Biplab Chattopadhyay* , Priti Kumar Roy , Jadavpur University, India
12:15-13:15	Lunch break (West Canteen)
13:30-14:15	Invited talk: Integrated analysis of regulatory and metabolic intra- and intercellular networks Edgar Wingender , University Medical Center Gottingen, Georg August University, Gottingen, Germany, BIOBASE GmbH, Wolfenbuttel, Germany
14:15-14:25	Discussion
Afternoon session: Gene expression and transcription (Chair: Kun Tang)	
14:25-15:00	Changes of gene expression density profiles during development and disease - data and theory Joerg Galle* , Hans Binder , University of Leipzig, Germany
15:00-15:25	Transcriptional regulation of human brain development and aging Song Guo* , Mehmet Somel , Yuan Yuan , Haiyang Hu , Yan Zeng , Ying Xu , and Philipp Khaitovich , CAS-MPG Partner Institute for Computational Biology, China
15:25-15:40	Coffee break
15:40-16:05	A probabilistic model for gene function and transcription network inference in arabidopsis stress response Qing Zhang , Pui-Man Yu , Dianjing Guo* , Chinese University of Hong Kong, Hong Kong
16:05-16:30	Stress responses in sulfate-reducing bacteria: an integrated genomics approach Qiang He , University of Tennessee Knoxville, USA
16:30-16:55	Increased oxidative stress and antioxidant gene expression in human airway wall after long term response to induced mustard gas Mohammad Nourani* , Majid Ebrahimi , Samaneh Yazdani , and Mostafa Ghanei , Baqiyatallah Medical Sciences University (BMSU), Iran
17:00-18:30	Poster session
18:45-20:45	Dinner, Hope Hotel

Thursday, June 25th

8:30-9:15	Invited talk: Rhythmic brain activities controlled by sub-cellular signaling pathways Jianfeng Feng , Dept. of Computer Science and Centre for Scientific Computing, Warwick University, UK
9:15-9:25	Discussion
Morning session: Mathematical modeling of biosystems IV (Chair: Nestor Torres Darias)	
9:25-10:00	Invited talk: Modelling dopamine systems in neurons and nephrons Eduardo Mendoza , Physics Dept. and Center for NanoScience, Ludwig-Maximilians-University, Germany
10:00-10:25	A hybrid model of dopamine dynamics in Parkinson's disease and Schizophrenia Zhen Qi* , Gary W. Miller , Eberhard O. Voit , Georgia Institute of Technology, USA
10:25-10:40	Coffee break
10:40-11:05	HIV infection in T-lymphocytes and drug induced CTL response of a time delayed model Priti Kumar Roy* , Biplab Chattopadhyay , Jadavpur University, India
11:05-11:30	Mathematical modeling of monolignol biosynthetic pathway Yun Lee* , Eberhard O. Voit , Georgia Institute of Technology, USA
11:30-11:55	Mathematical model for emergence of high pathogenicity avian influenza virus from outbreaks with low pathogenicity avian influenza virus H5N2 Jianjun Paul Tian , College of William and Mary, USA
12:15-13:15	Lunch break (West Canteen)
13:30-14:15	Invited talk: Statistical analyses of high dimensional molecular data (HDMD) William R. Atchley , Department of Genetics, North Carolina State University, USA
14:15-14:25	Discussion
Afternoon session: Molecular systems (Chair: Xinguang Zhu)	
14:25-15:00	Invited talk: Whole-body systems approaches for gut microbiota-targeted health management Liping Zhao , Shanghai Center for Systems Biomedicine, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, China
15:00-15:25	Proteomics, data integration, and protein interactions Jacques Colinge* , Florian Breitwieser , Thomas Burkard , Gerhard Drnberger , Marc Brehme , Lily Rensing Rix , Uwe Rix , Oliver Hantschel , Keiryn L. Bennett , Giulio Superti-Furga Center for Molecular Medicine of the Austrian Academy of Sciences, Austria
15:25-15:40	Coffee break
15:40-16:05	Protein-protein interactions prediction based on protein secondary structure information Lu Cai* , Zhiyong Pei , Sheng Qin , Inner Mongolia University of Science and Technology, China
16:05-16:30	Molecular interaction of the high light-inducible polypeptides (HLIP) with photosynthetic membrane proteins in synechocystis 6803 Qiang Wang , Saowarath Jantaro , Bingshe Lu , Waqar Majeed , Marian Bailey , Qingfang He* University of Arkansas, USA
16:30-16:55	A photorespiratory bypass must shift the release of CO2 from the mitochondrion to the chloroplast in order to maximize the increase of photosynthesis Vincent DevLoo* , Xinguang Zhu , CAS-MPG Partner Institute for Computational Biology, China
16:55-17:20	A new theoretical framework for estimating the mesophyll conductance to carbon dioxide Danny Tholen* , Xinguang Zhu , CAS-MPG Partner Institute for Computational Biology, China
17:30-18:30	Beer session (SIBS Physiological Building 300)