

The Second International Symposium on Optimization and Systems Biology (OSB 2008)

Local Organizer



Organizers



Sponsors



October 31-November 3, 2008
Lijiang Yunnan, China

OSB 2008 Program

October 31-November 3, Lijiang Yunnan, China

October 30 (Thursday) Registration

17:00-20:30 Registration, Participants arrival in Lijiang, check in Lijiang Guanfang Villa Hotel, and Registration package pick up.

18:00-20:00 Dinner

October 31 (Friday) Technical sessions

08:00-08:30 Registration for late arrivals

08:30-08:40 Opening session (Juxian Tang room 1)

08:40-10:20 OSB session A1 (Xianyun Ge)

Topic: Systems Biology I - Bio-molecular networks modeling and analysis

Chair: Eberhard O. Voit

08:40-09:05 *A Genetic Algorithm for Optimal Control of Probabilistic Boolean Networks*

Wai-Ki Ching, **Ho-yin Leung**, Nam-Kiu Tsing and Shu-Qin Zhang

Department of Mathematics, The University of Hong Kong, Hong Kong

09:05-09:30 *Uncovering differentially expressed pathways with protein interaction and gene expression data*

Yu-Qing Qiu, Shihua Zhang

Academy of Mathematics and Systems Science, China

09:30-09:55 *Inferring Gene Regulatory Networks by Incremental Evolution and Network Decomposition*

Wei-po Lee, **Yu-Ting Hsiao**

Department of Information Management, National Sun Yat-sen University, Taiwan

09:55-10:20 *Mass flow model and essentiality of enzymes in metabolic networks*

Zhenping Li, Rui-Sheng Wang, and Xiang-Sun Zhang

Beijing Wuzi University, China

10:20-10:30 Coffee break

10:30-12:35 OSB session A2 (Xianyun Ge)

Topic: Systems Biology II-- Subnetwork and pathway analysis

Chair: Jun Wang

10:30-10:55 *An Algebraic-Numeric Algorithm for the Model Selection in Highly Significant Network Motif in Escherichia coli*

Masahiko Nakatsui, Hiroshi Yoshida, and Katsuhisa Horimoto

Computational Biology Research Center (CBRC), Advanced Industrial Science and Technology (AIST), Japan

10:55-11:20 *Clustering Parameter Values for Differential Equation Models of Biological Pathways*

Dong-Soo Kahng and Doheon Lee

Korea Advanced Institute of Science and Technology, Korea.

11:20-11:45 *Comparative study on a class of evaluation indices for community detection*

Junhua Zhang, Shihua Zhang and Xiang-Sun Zhang

Academy of Mathematics and Systems Science, China

11:45-12:10 *Condition specific subnetwork identification using an optimization model*

Yong Wang and Yu Xia

Academy of Mathematics and Systems Science, China

12:10-12:35 *Identifying differentially activated pathways by augmenting activities of transcription factor target genes*

Hyunchul Jung, Eunjung Lee, Jongwon Kim and Doheon Lee

Department of Bio and Brain Engineering, KAIST, Korea

12:35-13:30 Lunch break

13:30-15:10 OSB session A3 (Xianyun Ge)

Topic: Systems Biology III—Dynamics of molecular networks

Chair: Doheon Lee

13:30-13:55 *Parameter estimation and Stability of equilibrium of Gene Regulatory Network by Piecewise Multi-affine approach*

Jianwei Shen, Zengrong Liu, and Yi Wang

Institute of Systems Biology, Shanghai University, China

13:55-14:20 *Periodic Oscillation of Gene Networks with Forcing and Delay*

Yi Wang, Zhongjun Ma, and Jianwei Shen

Institute of Systems Biology, Shanghai University, China

14:20-14:45 *Dynamical analysis of a biological molecular network including hidden variables by symbolic-numeric approach*

Daisuke tominaga, Yasuhito Tokumoto, Masahiko Nakatsui, Sachiyo Aburatani, Fuyan Sun, and Katsuhisa Horimoto.

National Institute of Advanced Industrial Science and Technology, Japan

14:45-15:10 *Phase Shifts of Circadian Transcripts in Rat Suprachiasmatic Nucleus*

Ryoko Morioka, masanori arita, Katsuhiko Sakamoto, Soshi Kawaguchi, Hajime Tei and

Katsuhisa Horimoto

Computational Biology Research Institute, National Institute of Advanced Industrial Science and Technology, Japan

15:10-15:30 Coffee break

15:30-18:00 OSB A4 (Xianyun Ge)

Topic: Systems Biology IV—Disease systems biology

Chair: Tieqiao Wen

15:30-16:55 *Phylogentic networks: Methods to compute split systems*

Stefan Grünewald

CAS-MPG Partner Institute for Computational Biology, Shanghai, China

15:55-16:20 *Some Infection Models for the Development of AIDS*

Wai-Ki Ching, **Yang Cong**, Tuen Wai Ng and Zheng Jian Bai.

Department of Mathematics, The University of Hong Kong, Hong Kong

16:20-16:45 *Rho-GDI γ inhibits the proliferation of human glioma cells*

Jiao wang, Xiao li, Xing-Ming zhao and Tieqiao wen

Institute of systems biology, Shanghai University, China.

16:45-17:10 Revealing Disease Related Interactions by Correlation Analysis

Zikai Wu, Zhi-Yong Zhang, Lvwen Zhang, and Katsuhisa Horimoto

Institute of systems biology, Shanghai University, China

17:10-17:35 *Establishment of a HCV biological database for epitope-paratope matching using phage display technology*

Te-Fen Kao and **Hao-Teng Chang**

Graduate Institute of Molecular Systems Biomedicine, China Medical University, Taichung,

Taiwan

17:35-18:00 *Time Series Segmentation for Gene Regulatory Process with Time-Window-Extension Technique*

Zhi-Yong Zhang, Katsuhisa Horimoto and Zengrong Liu

Institute of Systems Biology, Shanghai University, China

18:00-19:00 Welcome reception at Guanfang Hotel

19:00-21:00 Ethnic Songs and Dance performance (bus leave at 19:00)

November 1 (Saturday) Technical sessions

08:00-9:40 OSB Plenary session I (Juxian Tang room 1)

Chair: Luonan Chen

08:00-08:50 *Model Identification: A Key Challenge is Computational Systems Biology*

Eberhard O. Voit

Georgia Institute of Technology, USA

08:50-9:40 Combinatorial Optimization in Computational Biology

Dan Gusfield

Computer science department, University of California at Davis, USA

9:40-10:00 Coffee break

10:00-12:30 OSB Plenary session II (Juxian Tang room 1)

Chair: Eberhard O. Voit

10:00-10:50 *Network-based Systems Biology*

Luonan Chen

Institute of Systems Biology, Shanghai University, Shanghai 200444, China

10:50-11:40 *Neurodynamic Optimization: New Models and Selected Application*

Jun Wang

Department of Mechanical & Automation Engineering, The Chinese University of Hong Kong, Shatin, New Territories, Hong Kong

11:40-12:30 *Time-series-based Ensemble Modeling for Bio-Medical Applications*

Maciej Ogorzalek

AGH University of Science and Technology, Poland

12:30-13:30 Lunch break

13:30-15:10 OSB session A5 (Juxian Tang room 1)

Topic: Bioinformatics I - Computational Models & Algorithms

Chair: Xiao-Bo Zhou

13:30-13:55 *Identify SSR Regulators for Functional Gene Sets through Cross-Species Comparison*

Tun-Wen Pai

Department of Computer Science and Engineering, National Taiwan Ocean University, China

13:55-14:20 *A Heuristic Method for Generating Probabilistic Boolean Networks from a Prescribed Transition Probability Matrix*

Wai-Ki Ching, **Xi Chen**, Nam-Kiu Tsing, and Ho-yin Leung

Department of Mathematics, University of Hong Kong, Hong Kong

14:20-14:55 *Sensitivity Analysis of Cis-Regulatory Input Functions*

Aimin Chen

School of Mathematics & Computational Science, Sun Yat-Sen University, China

14:55-15:10 *Structure-based Functional Annotation of Protein Sequences Guided by Comparative Models*

Daron Standley, Akira R. Kinjo, Miesko Lis, Mark van der Giezen, and Haruki Nakamura

Systems Immunology Laboratory, Immunology Frontier Research Center, Osaka University, 3-2 Yamadaoka, Suita, Osaka 565-0871, Japan.

13:30-15:10 OSB session B1 (Juxian Tang room 2)

Topic: Systems Biology V - Dynamics of Molecular Networks

Chair: Zengrong Liu

13:30-13:55 *Effects of multiple parameter variations on biological system behaviors*

Xiao Chang and Ruiqi Wang

Institute of Systems Biology, Shanghai University, China

13:55-14:20. *Dynamics of the Mixed Feedback Loop Integrated with MicroRNA*

Ge Wang and Jin Zhou
Shanghai University, China

14:20-14:45 *Identification of intracellular kinetic parameters in continuous bioconversion of glycerol by *Klebsiella pneumoniae**

En-min Feng, Chongyang liu and Zhaohua Gong
Dalian University of Science and Technology, China

14:45-15:10 *An Algorithm and its Application of Multi-stage Identification Model of Nonlinear Dynamical System*

Caixia Gao and Enmin Feng.
Inner Mongolia University, China.

15:10-15:30 Coffee break

15:30-18:00 Parallel session A6 (Juxian Tang room 1)

Topic: Bioinformatics II-- Computational Models & Algorithms

Chair: Daron Standley

15:30-15:55 *Analysis of the special structure of the Suprachiasmatic Nucleus*

Ying Li and Jianbao Zhang
College of information of Shanghai Ocean University, China

15:55-16:20 *A new algorithm for sequential and non-sequential protein multiple structure alignment*

Lin Wang, WenJuan Zhang
Academy of Mathematics and Systems Science, China

16:20-16:45 *On Distribution and Enumeration of Attractors in Probabilistic Boolean Networks*

Morihiro Hayashida, Takeyuki Tamura, Tatsuya Akutsu, and Wai-Ki Ching
Kyoto University, Japan

16:45-17:10 *Motif based identification of pathogenic patterns for filamentous fungi*

Xing-Ming Zhao, Weihua Tang, and Luonan Chen
Institute of Systems biology, Shanghai University, China

17:10-17:35 *Dynamics and functions of miRNA-mediated incoherent feedforward motifs*

Zengrong Liu, **Fengdan Xu**, and Jianwei Shen
Institute of Systems biology, Shanghai University, China

17:35-18:00 *The Network Biomarker Discovery in Prostate Cancer from Both Genomics and Proteomics Levels*

Guangxu Jin, **Xiaobo Zhou**, Kemi Cui, Stephen T.C. Wong
Center for Bioinformatics and Biotechnology, The Methodist Hospital Research Institute and Cornell University, Houston, TX 77030

15:30-18:00 OSB session B2 (Juxian Tang room 2)

Topic: Bioinformatics III—Machine learning method

Chair: Katsuhisa Horimoto

15:30-15:50 *A Multi-class Algorithm Model Based on p-class Support Vector Ordinal Regression*

Machine

Zhixia Yang

Academy of Mathematics and Systems Science, China

15:50-16:10 *The Imbalanced Problem in Mass-spectrometry Data Analysis*

Hao-Hua Meng, Guo-Zheng Li, Rui-Sheng Wang, Xing-Ming Zhao and Luonan Chen

Shanghai University, China

16:10-16:30 *Mutual Information Based Selective Ensemble Learning*

Tian-Yu Liu and Guo-Zheng Li

Shanghai University, China

16:30-16:50 *Ensemble Non-negative Matrix Factorization for Clustering Biomedical Documents*

Shanfeng Zhu, Wei Yuan, and Fei Wang

Fudan University, China

16:50-17:10 *Analysis of Domain Interactions Among Gamma-secretase Substrates*

Zhiping Liu, Weiming Xia, and **Luonan Chen**

Institute of Systems Biology, Shanghai University, Shanghai 200444, China

17:10-17:30 *Stability of stochastic genetic regulatory networks*

Yonghui Sun and Gang Feng

City University of Hong Kong, Hong Kong

17:30-17:50 *An Integer Linear Programming Approach to Topological Alignments and its Applications*

Axel Mosig

CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, 200031 Shanghai, China

18:00-20:00 Banquet

November 2 (Sunday) One-day excursion to Lijiang Jade Dragon Mountain National Park

8:00 Departure at hotel

17:30-18:00 Back to Hotel

18:00-20:30 Dinner at local restaurant

November 3 (Monday) Check out and back home.

*The above program subjects to revision based on further information and Ad Hoc presentation requests.