

## CONTENTS

<b>Preface</b>	vii
<b>Committees</b>	ix
<b>Referees</b>	xi
<b>Keynote Address</b>	
Quantitative Aspects of Gene Regulation in Bacteria: Amplification, Threshold, and Combinatorial Control <i>Terry Hwa</i>	3
Whole-Genome Analysis of Dorsal Gradient Thresholds in the <i>Drosophila</i> Embryo <i>Julia Zeitlinger, Rob Zinzen, Dmitri Papatsenko et al.</i>	5
<b>Invited Talks</b>	
Learning Predictive Models of Gene Regulation <i>Christina Leslie</i>	9
The Phylofacts Phylogenomic Encyclopedias: Structural Phylogenomic Analysis Across the Tree of Life <i>Kimmen Sjölander</i>	11
Mapping and Analysis of the Human Interactome Network <i>Kavitha Venkatesan</i>	13
Gene-Centered Protein-DNA Interactome Mapping <i>A.J. Marian Walhout</i>	15
<b>Proteomics</b>	
Algorithm for Peptide Sequencing by Tandem Mass Spectrometry Based on Better Preprocessing and Anti-Symmetric Computational Model <i>Kang Ning and Hon Wai Leong</i>	19
Algorithms for Selecting Breakpoint Locations to Optimize Diversity in Protein Engineering by Site-Directed Protein Recombination <i>Wei Zheng, Xiaoduan Ye, Alan M. Friedman and Chris Bailey-Kellogg</i>	31
An Algorithmic Approach to Automated High-Throughput Identification of Disulfide Connectivity in Proteins Using Tandem Mass Spectrometry <i>Timothy Lee, Rahul Singh, Ten-Yang Yen and Bruce Macher</i>	41

## Biomedical Application

- Cancer Molecular Pattern Discovery by Subspace Consensus Kernel Classification  
*Xiaoxu Han* 55
- Efficient Algorithms for Genome-Wide tagSNP Selection Across Populations via the Linkage Disequilibrium Criterion  
*Lan Liu, Yonghui Wu, Stefano Lonardi and Tao Jiang* 67
- Transcriptional Profiling of Definitive Endoderm Derived from Human Embryonic Stem Cells  
*Huiqing Liu, Stephen Dalton and Ying Xu* 79

## Pathways, Networks and Systems Biology

- Bayesian Integration of Biological Prior Knowledge into the Reconstruction of Gene Regulatory Networks with Bayesian Networks  
*Dirk Husmeier and Adriano V. Werhli* 85
- Using Indirect Protein-Protein Interactions for Protein Complex Predication  
*Hon Nian Chua, Kang Ning, Wing-Kin Sung et al.* 97
- Finding Linear Motif Pairs from Protein Interaction Networks: A Probabilistic Approach  
*Henry C.M. Leung, M.H. Siu, S.M. Yiu et al.* 111
- A Markov Model Based Analysis of Stochastic Biochemical Systems  
*Preetam Ghosh, Samik Ghosh, Kalyan Basu and Sajjal K. Das* 121
- An Information Theoretic Method for Reconstructing Local Regulatory Network Modules from Polymorphic Samples  
*Manjunatha Jagalur and David Kulp* 133
- Using Directed Information to Build Biologically Relevant Influence  
*Arvind Rao, Alfred O. Hero III, David J. States and James Douglas Engel* 145
- Discovering Protein Complexes in Dense Reliable Neighborhoods of Protein Interaction Networks  
*Xiao-Li Li, Chuan-Sheng Foo and See-Kiong Ng* 157
- Mining Molecular Contexts of Cancer via In-Silico Conditioning  
*Seungchan Kim, Ina Sen and Micheal Bittner* 169

## Genomics

- Prediction of Transcription Start Sites Based on Feature Selection Using AMOSA  
*Xi Wang, Sanghamitra Bandyopadhyay, Zhenyu Xuan et al.* 183
- Clustering of Main Orthologs for Multiple Genomes  
*Zheng Fu and Tao Jiang* 195
- Deconvoluting the BAC-Gene Relationships Using a Physical Map  
*Yonghui Wu, Lan Liu, Timothy J. Close and Stefano Lonardi* 203

A Grammar Based Methodology for Structural Motif Finding in ncRNA Database Search <i>Daniel Quest, William Tapprich and Hesham Ali</i>	215
IEM: An Algorithm for Iterative Enhancement of Motifs Using Comparative Genomics Data <i>Erliang Zeng, Kalai Mathee and Giri Narasimhan</i>	227
MANGO: A New Approach to Multiple Sequence Alignment <i>Zefeng Zhang, Hao Lin and Ming Li</i>	237
Learning Position Weight Matrices from Sequence and Expression Data <i>Xin Chen, Lingqiong Guo, Zhaocheng Fan and Tao Jiang</i>	249
<b>Structural Bioinformatics</b>	
Effective Labeling of Molecular Surface Points for Cavity Detection and Location of Putative Binding Sites <i>Mary Ellen Bock, Claudio Garutti and Conettina Guerra</i>	263
Extraction, Quantification and Visualization of Protein Pockets <i>Xiaoyu Zhang and Chandrajit Bajaj</i>	275
Uncovering the Structural Basis of Protein Interactions with Efficient Clustering of 3-D Interaction Interfaces <i>Zeyar Aung, Soon-Heng Tan, See-Kiong Ng and Kian-Lee Tan</i>	287
Enhanced Partial Order Curve Comparison Over Multiple Protein Folding Trajectories <i>Hong Sun, Hakan Ferhatosmanoglu, Motonori Ota and Yusu Wang</i>	299
fRMSDPred: Predicting Local RMSD Between Structural Fragments Using Sequence Information <i>Huzefa Rangwala and George Karypis</i>	311
Consensus Contact Prediction by Linear Programming <i>Xin Gao, Dongbo Bu, Shuai Cheng Li et al.</i>	323
Improvement in Protein Sequence-Structure Alignment Using Insertion/Deletion Frequency Arrays <i>Kyle Ellrott, Jun-Tao Guo, Victor Olman and Ying Xu</i>	335
Composite Motifs Integrating Multiple Protein Structures Increase Sensitivity for Function Prediction <i>Brian Y. Chen, Drew H. Bryant, Amanda E. Cruess et al.</i>	343
<b>Ontology, Database and Text Mining</b>	
An Active Visual Search Interface for Medline <i>Weijian Xuan, Manhong Dai, Barbara Mirel et al.</i>	359
Rule-Based Human Gene Normalization in Biomedical Text with Confidence Estimation <i>William W. Lau, Calvin A. Johnson and Kevin G. Becker</i>	371

CBioC: Beyond a Prototype for Collaborative Annotation of Molecular Interactions from the Literature <i>Chitta Baral, Graciela Gonzalez, Anthony Gitter et al.</i>	381
<b>Biocomputing</b>	
Supercomputing with Toys: Harnessing the Power of NVIDIA 8800GTX and Playstation 3 for Bioinformatics Problem <i>Justin Wilson, Manhong Dai, Elvis Jakupovic et al.</i>	387
Exact and Heuristic Algorithms for Weighted Cluster Editing <i>Sven Rahmann, Tobias Wittkop, Jan Baumbach et al.</i>	391
Method for Effective Virtual Screening and Scaffold-Hopping in Chemical Compounds <i>Nikil Wale, George Karypis and Ian A. Watson</i>	403
<b>Transcriptomics and Phylogeny</b>	
Improving the Design of Genechip Arrays by Combining Placement and Embedding <i>Sérgio Anibal de Carvalho Jr. and Sven Rahmann</i>	417
Modeling Species-Genes Data for Efficient Phylogenetic Inference <i>Wenyuan Li and Ying Liu</i>	429
Reconciliation with Non-Binary Species Trees <i>Benjamin Vernot, Maureen Stolzer, Aiton Goldman and Dannie Durand</i>	441
<b>Author Index</b>	453