

CONTENTS

Preface	v
Committees	vii
Referees	ix
Genomics	
An ORFome Assembly Approach to Metagenomics Sequences Analysis <i>Yuzhen Ye and Haixu Tang</i>	3
A Probabilistic Coding Based Quantum Genetic Algorithm for Multiple Sequence Alignment <i>Hongwei Huo, Qiaoluan Xie, Xubang Shen, and Vojislav Stojkovic</i>	15
Scalable Computation of Kinship and Identity Coefficients on Large Pedigrees <i>En Cheng, Brendan Elliott, and Z. Meral Ozsoyoglu</i>	27
Voting Algorithms for the Motif Finding Problem <i>Xiaowen Liu, Bin Ma, and Lusheng Wang</i>	37
Proteomics	
A Max-Flow Based Approach to the Identification of Protein Complexes Using Protein Interaction and Microarray Data <i>Jianxing Feng, Rui Jiang, and Tao Jiang</i>	51
MSDash: Mass Spectrometry Database and Search <i>Zhan Wu, Gilles Lajoie, and Bin Ma</i>	63
Estimating Support for Protein-Protein Interaction Data with Applications to Function Prediction <i>Erliang Zeng, Chris Ding, Giri Narasimhan, and Stephen R. Holbrook</i>	73
GaborLocal: Peak Detection in Mass Spectrum by Gabor Filters and Gaussian Local Maxima <i>Nha Nguyen, Heng Huang, Soontorn Oraintara, and An Vo</i>	85
Structural Bioinformatics	
Optimizing Bayes Error for Protein Structure Model Selection by Stability Mutagenesis <i>Xiaoduan Ye, Alan M. Friedman, and Chris Bailey-Kellogg</i>	99

Feedback Algorithm and Web-Server for Protein Structure Alignment <i>Zhiyu Zhao, Bin Fu, Francisco J. Alanis, and Christopher M. Summa</i>	109
Predicting Flexible Length Linear B-Cell Epitopes <i>Yasser EL-Manzalawy, Drena Dobbs, and Vasant Honavar</i>	121
Fast and Accurate Multi-class Protein Fold Recognition with Spatial Sample Kernels <i>Pavel Kuksa, Pai-Hsi Huang, and Vladimir Pavlovic</i>	133
Designing Secondary Structure Profiles for Fast ncRNA Identification <i>Yanni Sun and Jeremy Buhler</i>	145
Matching of Structural Motifs Using Hashing on Residue Labels and Geometric Filtering for Protein Function Prediction <i>Mark Moll and Lydia E. Kavradi</i>	157
A Hausdorff-based NOE Assignment Algorithm Using Protein Backbone Determined from Residual Dipolar Couplings and Rotamer Patterns <i>Jiayang (Michael) Zeng, Chittaranjan Tripathy, Pei Zhou, and Bruce R. Donald</i>	169
Iterative Non-sequential Protein Structural Alignment <i>Saeed Salem and Mohammed J. Zaki</i>	183
Combining Sequence and Structural Profiles for Protein Solvent Accessibility Prediction <i>Rajkumar Bondugula and Dong Xu</i>	195
Extensive Exploration of Conformational Space Improves Rosetta Results for Short Protein Domains <i>Yaohang Li, Andrew J. Bordner, Yuan Tian, Xiuping Tao, and Andrey A. Gorin</i>	203
Improving Homology Models for Protein-Ligand Binding Sites <i>Chris Kauffman, Huzefa Rangwala, and George Karypis</i>	211
Pathways, Networks, and Biological Systems	
Using Relative Importance Methods to Model High-Throughput Gene Perturbation Screens <i>Ying Jin, Naren Ramakrishnan, Lenwood S. Heath, and Richard F. Helm</i>	225
Consistent Alignment of Metabolic Pathways Without Abstraction <i>Ferhat Ay, Tamer Kahveci, and Valerie de Crécy-Lagard</i>	237
Detecting Pathways Transcriptionally Correlated with Clinical Parameters <i>Igor Ulitsky and Ron Shamir</i>	249

Computational Genomics

The Effect of Massive Gene Loss Following Whole Genome Duplication on the Algorithmic Reconstruction of the Ancestral Populus Diploid <i>Chunfang Zheng, P. Kerr Wall, Jim Leebens-Mack, Victor A. Albert, Claude dePamphilis, and David Sankoff</i>	261
Error Tolerant Sibship Reconstruction in Wild Populations <i>Saad I. Sheikh, Tanya Y. Berger-Wolf, Mary V. Ashley, Isabel C. Caballero, Wanpracha Chaovalitwongse, and Bhaskar DasGupta</i>	273
On the Accurate Construction of Consensus Genetic Maps <i>Yonghui Wu, Timothy J. Close, and Stefano Lonardi</i>	285
Efficient Haplotype Inference from Pedigrees with Missing Data Using Linear Systems with Disjoint-Set Data Structures <i>Xin Li and Jing Li</i>	297
Computational Methods	
Knowledge Representation and Data Mining for Biological Imaging <i>Wamiq M. Ahmed</i>	311
Fast Multisegment Alignments for Temporal Expression Profiles <i>Adam A. Smith and Mark Craven</i>	315
Graph Wavelet Alignment Kernels for Drug Virtual Screening <i>Aaron Smalter, Jun Huan, and Gerald Lushington</i>	327
Author Index	339