

CONTENTS

Preface	ix
Acknowledgments	xi
Committees	xiii
Part A Full Papers	1
Detection of Monosaccharide Types from Coordinates <i>M. Arita & T. Tokimatsu</i>	3
Mining Super-Secondary Structure Motifs from 3D Protein Structures: A Sequence Order Independent Approach <i>Z. Aung & J. Li</i>	15
FragQA: Predicting Local Fragment Quality of a Sequence-Structure Alignment <i>X. Gao, D. Bu, S. C. Li, J. Xu & M. Li</i>	27
Predicting B Cell Epitope Residues with Network Topology Based Amino Acid Indices <i>J. Huang, W. Honda & M. Kanehisa</i>	40
Comparative Pair-Wise Domain-Combinations for Screening the Clade Specific Domain-Architectures in Metazoan Genomes <i>S. Kawashima, T. Kawashima, N. H. Putnam, D. S. Rokhsar, H. Wada & M. Kanehisa</i>	50
A Conservative Parametric Approach to Motif Significance Analysis <i>U. Keich & P. Ng</i>	61
Recognition of Polyadenylation Sites from <i>Arabidopsis</i> Genomic Sequences <i>C. H. Koh & L. Wong</i>	73

Computational Analysis and Modeling of Genome-Scale Avidity Distribution of Transcription Factor Binding Sites in ChIP-PET Experiments	83
<i>V. Kuznetsov, Y. L. Orlov, C. L. Wei & Y. Ruan</i>	
Linear-Time Reconstruction of Zero-Recombinant Mendelian Inheritance on Pedigrees without Mating Loops	95
<i>L. Liu & T. Jiang</i>	
Computed Protonation Properties: Unique Capabilities for Protein Functional Site Prediction	107
<i>L. F. Murga, Y. Wei & M. J. Ondrechen</i>	
An Accurate and Efficient Algorithm for Peptide and PTM Identification by Tandem Mass Spectrometry	119
<i>K. Ning, H. K. Ng & H. W. Leong</i>	
The Comparative Genomics of Protein Interactions	131
<i>J. M. Peregrín-Alvarez & C. Ouzounis</i>	
Weighted Lasso in Graphical Gaussian Modeling for Large Gene Network Estimation Based on Microarray Data	142
<i>T. Shimamura, S. Imoto, R. Yamaguchi & S. Miyano</i>	
GO Based Tissue Specific Functions of Mouse using Countable Gene Expression Profiles	154
<i>Y. Takenaka, A. Matsumoto & H. Matsuda</i>	
Functional Centrality: Detecting Lethality of Proteins in Protein Interaction Networks	166
<i>K. L. Tew, X.-L. Li, & S.-H. Tan</i>	
The <i>in silico</i> Prediction of Promoters in Bacterial Genomes	178
<i>M. Towsey, J. M. Hogan, S. Mathews & P. Timms</i>	
Part B Keynote Addresses	191
Discovering Biomolecular Mechanisms with Protein Sequence Studies: The Annotator Software Suite	193
<i>F. Eisenhaber</i>	
The p53 Pathway	194
<i>D. Lane</i>	
Regulation of Gene Expression by Small Non-Coding RNAs	195
<i>H. Margalit</i>	

Mapping the Transcriptional Network in Stem Cells Regulated by REST <i>L. W. Stanton</i>	196
Computational Dissection of Mammalian Regulation Networks <i>M. Zhang</i>	197
Author Index	199