

CONTENTS

Preface	v
Acknowledgments	vi
Committees	vii
Part A Full Papers	1
Predicting Protein-Protein Relationships from Literature Using Latent Topics <i>T. Aso & K. Eguchi</i>	3
Evaluation of DNA Intramolecular Interactions for Nucleosome Positioning in Yeast <i>M. Fernandez, S. Fujii, H. Kono & A. Sarai</i>	13
Quality Control and Reproducibility in DNA Microarray Experiments <i>A. Fujita, J. R. Sato, F. H. L. da Silva, M. C. Galvão, M. C. Sogayar & S. Miyano</i>	21
Comparative Analysis of Topological Patterns in Different Mammalian Networks <i>B. Goemann, A. P. Potapov, M. Ante & E. Wingender</i>	32
Tools for Investigating Mechanisms of Antigenic Variation: New Extensions to varDB <i>C. N. Hayes, D. Diez, N. Joannin, M. Kanehisa, M. Wahlgren, C. E. Wheelock & S. Goto</i>	46

Localized Suffix Array and Its Application to Genome Mapping Problems for Paired-End Short Reads <i>K. Kimura & A. Koike</i>	60
Comparative Analysis of Aerobic and Anaerobic Prokaryotes to Identify Correlation between Oxygen Requirement and Gene-Gene Functional Association Patterns <i>Y. Lin & H. Wu</i>	72
Calculation of Protein-Ligand Binding Free Energy Using Smooth Reaction Path Generation (SRPG) Method: A Comparison of the Explicit Water Model, GB/SA Model and Docking Score Function <i>D. Mitomo, Y. Fukunishi, J. Higo & H. Nakamura</i>	85
Structural Insights into the Enzyme Mechanism of a New Family of D-2-Hydroxyacid Dehydrogenases, a Close Homolog of 2-Ketopantoate Reductase <i>S. Mondal & K. Mizuguchi</i>	98
Comprehensive Analysis of Sequence-Structure Relationships in the Loop Regions of Proteins <i>S. Nakamura & K. Shimizu</i>	106
The Prediction of Local Modular Structures in a Co-Expression Network Based on Gene Expression Datasets <i>Y. Ogata, N. Sakurai, H. Suzuki, K. Aoki, K. Saito & D. Shibata</i>	117
Gradient-Based Optimization of Hyperparameters for Base-Pairing Profile Local Alignment Kernels <i>K. Sato, Y. Saito & Y. Sakakibara</i>	128
A Method for Efficient Execution of Bioinformatics Workflows <i>J. Seo, Y. Kido, S. Seno, Y. Takenaka & H. Matsuda</i>	139
Development of a New Meta-Score for Protein Structure Prediction from Seven All-Atom Distance Dependent Potentials Using Support Vector Regression <i>M. Shiota, T. Ishida & K. Kinoshita</i>	149

Refining Markov Clustering for Protein Complex Prediction by Incorporating Core-Attachment Structure	159
<i>S. Srihari, K. Ning & H. W. Leong</i>	
An Assessment of Prediction Algorithms for Nucleosome Positioning	169
<i>Y. Tanaka & K. Nakai</i>	
Cancer Classification Using Single Genes	179
<i>X. Wang & O. Gotoh</i>	
RECOUNT: Expectation Maximization Based Error Correction Tool for Next Generation Sequencing Data	189
<i>E. Wijaya, M. C. Frith, Y. Suzuki & P. Horton</i>	
Part B Keynote Addresses	203
A New Generation of Homology Search Tools Based on Probabilistic Inference	205
<i>S. R. Eddy</i>	
Representation and Analysis of Molecular Networks Involving Diseases and Drugs	212
<i>M. Kanehisa</i>	
Systems Biotechnology	214
<i>S. Y. Lee</i>	
Strategies Toward CNS-Regeneration Using Induced Pluripotent Stem Cells	217
<i>H. Okano</i>	
Thinking Laterally About Genomes	221
<i>M. A. Ragan</i>	
Author Index	223