

CONTENTS

Preface	vii
Program Committee	ix
Kinetic Modelling of DNA Replication Initiation in Budding Yeast <i>M. Barberis, T. W. Spiesser and E. Klipp</i>	1
Predicting Protein Complex Geometries with Linear Scoring Functions <i>O. Demir-Kavuk, F. Krull, M.-H. Chae and E.-W. Knapp</i>	21
Characterizing Common Substructures of Ligands for GPCR Protein Subfamilies <i>B. Erguner, M. Hattori, S. Goto and M. Kanehisa</i>	31
A Systems Biology Approach: Modelling of Aquaporin-2 Trafficking <i>M. Fröhlich, P. M. T. Deen and E. Klipp</i>	42
Comparison of Gene Expression Profiles Produced by Cage, Illumina Microarray and Real Time RT-PCR <i>A. Fujita, M. Nagasaki, S. Imoto, A. Saito, E. Ikeda, T. Shimamura, R. Yamaguchi, Y. Hayashizaki and S. Miyano</i>	56
On the Performance of Methods for Finding a Switching Mechanism in Gene Expression <i>M. Kayano, I. Takigawa, M. Shiga, K. Tsuda and H. Mamitsuka</i>	69
Gene Regulatory Network Clustering for Graph Layout Based on Microarray Gene Expression Data <i>K. Kojima, S. Imoto, M. Nagasaki and S. Miyano</i>	84
FluxViz — Cytoscape Plug-In for Visualization of Flux Distributions in Networks <i>M. König and H.-G. Holzhütter</i>	96

Comprehensive Genomic Analysis of Sulfur-Relay Pathway Genes <i>M. Kotera, T. Kobayashi, M. Hattori, T. Tokimatsu, S. Goto, H. Mihara and M. Kanehisa</i>	104
Phylogenetic Analysis of Lipid Mediator GPCRs <i>S. Mizutani, M. Tanaka, C. E. Wheelock, M. Kanehisa and S. Goto</i>	116
Genome-Wide Analysis of Plant UGT Family Based on Sequence and Substrate Information <i>Y. Nishimura, T. Tokimatsu, M. Kotera, S. Goto and M. Kanehisa</i>	127
Robust Gene Network Analysis Reveals Alteration of the STAT5a Network as a Hallmark of Prostate Cancer <i>A. Reddy, C. C. Huang, H. Liu, C. DeLisi, M. T. Nevalainen, S. Szalma and G. Bhanot</i>	139
Analyzing Gene Coexpression Data by an Evolutionary Model <i>M. Schütte, M. Mutwil, S. Persson and O. Ebenhöf</i>	154
Collocation-Based Sparse Estimation for Constructing Dynamic Gene Networks <i>T. Shimamura, S. Imoto, M. Nagasaki, M. Yamauchi, R. Yamaguchi, A. Fujita, Y. Tamada, N. Gotoh and S. Miyano</i>	164
Different Groups of Metabolic Genes Cluster Around Early and Late Firing Origins of Replication in Budding Yeast <i>T. W. Spiesser and E. Klipp</i>	179
Integer Programming-Based Method for Completing Signaling Pathways and Its Application to Analysis of Colorectal Cancer <i>T. Tamura, Y. Yamanishi, M. Tanabe, S. Goto, M. Kanehisa, K. Horimoto and T. Akutsu</i>	193
G1 and G2 Arrests in Response to Osmotic Shock are Robust Properties of the Budding Yeast Cell Cycle <i>C. Waltermann, M. Floettmann and E. Klipp</i>	204
A Dynamic Programming Algorithm to Predict Synthesis Processes of Tree-Structured Compounds with Graph Grammar <i>Y. Zhao, T. Tamura, M. Hayashida and T. Akutsu</i>	218
Author Index	231