# Contents

Preface ............................................................ v
Contributors ........................................................ ix

## SECTION I: INTERACTIONS

1. Mining Protein–Protein Interactions from Published Literature Using Linguamatics I2E ................................. 3
   Judith Bandy, David Milward, and Sarah McQuay
2. Relative Avidity, Specificity, and Sensitivity of Transcription Factor–DNA Binding in Genome-Scale Experiments ......................................................... 15
   Vladimir A. Kuznetsov
3. Curation of Inhibitor-Target Data: Process and Impact on Pathway Analysis .......................................................... 51
   Sreenivas Devidas
4. Profiling Protein Interaction Networks with Functional Protein Microarrays ......................................................... 63
   Dawn R. Mattoon and Barry Schweitzer
5. Manual Annotation of Protein Interactions .......................................................... 75
   Svetlana Bureeva, Svetlana Zvereva, Valentin Romanov, and Tatiana Serebryiskaya

## SECTION II: ANALYSIS

6. Gene Set Enrichment Analysis .......................................................... 99
   Charles A. Tilford and Nathan O. Siemers
7. PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools ......................................................... 123
   Huaiyu Mi and Paul Thomas
8. Prioritizing Genes for Pathway Impact Using Network Analysis .......................................................... 141
   Aaron N. Chang
9. Discovering Biological Networks from Diverse Functional Genomic Data .......................................................... 157
   Chad L. Myers, Camelia Chiriac, and Olga G. Troyanskaya
10. Functional Analysis of OMICs Data and Small Molecule Compounds in an Integrated “Knowledge-Based” Platform .......................................................... 177
    Yuri Nikolsky, Eugene Kirillov, Roman Zuev, Eugene Rakhmatulin, and Tatiana Nikolskaya
11. Kinetic Modeling as a Tool to Integrate Multilevel Dynamic Experimental Data .......................................................... 197
    Ekaterina Mogilevskaya, Natalia Bagrova, Tatiana Plyusnina, Nail Gizzatkulov, Eugeni Metelkin, Ekaterina GoryACHEVA, Sergey Smirnov, Yuriy Kosinsky, Aleksander Dorodnov, Kirill Peskov, Tatiana Karelina, Igor Goryanin, and Oleg Demin
Sarah Killecoyne, Gregory W. Carter, Jennifer Smith, and John Boyle

13. Semantic Data Integration and Knowledge Management to Represent Biological Network Associations
Sascha Losko and Klaus Heumann

14. Solutions for Complex, Multi Data Type and Multi Tool Analysis: Principles and Applications of Using Workflow and Pipelining Methods
Robin E. J. Munro and Yike Guo

SECTION III: APPLICATIONS

15. High-Throughput siRNA Screening as a Method of Perturbation of Biological Systems and Identification of Targeted Pathways Coupled with Compound Screening
Jeff Kiefer, Hongwei H. Yin, Qiang Q. Que, and Spyro Mousses

16. Pathway and Network Analysis with High-Density Allelic Association Data
Ali Torkamani and Nicholas J. Schork

17. miRNAs: From Biogenesis to Networks
Giuseppe Russo and Antonio Giordano

18. MetaMiner (CF): A Disease-Oriented Bioinformatics Analysis Environment
Jerry M. Wright, Yuri Nikolsky, Tatiana Serebryiskaya, and Diana R. Wetmore

19. Translational Research and Biomedical Informatics
Michael Liebman

20. ArrayTrack: An FDA and Public Genomic Tool
Hong Fang, Stephen C. Harris, Zhenjiang Su, Minjun Chen, Feng Qian, Leming Shi, Roger Perkins, and Weida Tong

Index

Contents
Protein Networks and Pathway Analysis
Nikolsky, Y.; Bryant, J. (Eds.)
2009, XIV, 410 p. 118 illus., Hardcover
A product of Humana Press