

目 录

前言	v
撰稿人	ix

第一部分：相互作用

1. 用 Linguamatics 公司研发的 I2E 软件从发表的文献中挖掘蛋白质相互作用	3
Judith Bandy, David Milward, and Sarah McQuay	
2. 基因组规模实验中转录因子与 DNA 结合的相对亲和力、特异性和敏感度	15
Vladimir A. Kuznetsov	
3. 抑制因子-靶标数据的管理：步骤和在途径分析上的作用	51
Sreenivas Devidas	
4. 用功能蛋白质芯片描绘蛋白质相互作用网络	63
Dawn R. Mattoon and Barry Schweitzer	
5. 蛋白质相互作用的手工注释	75
Svetlana Bureeva, Svetlana Zvereva, Valentin Romanov, and Tatiana Serebryiskaya	

第二部分：分析

6. 基因集富集分析	99
Charles A. Tilford and Nathan O. Siemers	
7. PANTHER 途径：一个整合了数据分析工具且基于本体的途径数据库	123
Huaiyu Mi and Paul Thomas	
8. 采用网络分析优化排序影响途径的基因	141
Aaron N. Chang	
9. 从多样的功能基因组数据中发掘生物学网络	157
Chad L. Myers, Camelia Chiriac, and Olga G. Troyanskaya	
10. 在基于知识的集成平台上对组学数据及小分子化合物的函数分析	177
Yuri Nikolsky, Eugene Kirillov, Roman Zuev, Eugene Rakhmatulin, and Tatiana Nikolskaya	
11. 动力学模型作为一种整合多层次动态实验数据的工具	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	
12. Cytoscape：用于网络建模的一个基于社区的框架	219
Sarah Killcoyne, Gregory W. Carter, Jennifer Smith, and John Boyle	
13. 用语义数据集成和知识管理表示生物网络相关性	241
Sascha Losko and Klaus Heumann	

14. 复杂的、多数据类型及多工具分析的解决方案: 运用工作流程与流水线方法的 原则及应用	259
Robin E. J. Munro and Yike Guo	

第三部分: 应用

15. 高通量 siRNA 筛选结合化合物筛选作为一种干扰生物系统以及识别目标途径的方法	275
Jeff Kiefer, Hongwei H. Yin, Qiang Q. Que, and Spyro Mousses	
16. 用高密度等位基因关联数据进行途径和网络的分析	289
Ali Torkamani and Nicholas J. Schork	
17. miRNAs: 从生物起源到网络	303
Giuseppe Russo and Antonio Giordano	
18. MetaMiner (CF): 疾病导向的生物信息学分析环境	353
Jerry M. Wright, Yuri Nikolsky, Tatiana Serebryiskaya, and Diana R. Wetmore	
19. 转化研究与生物医学信息学	369
Michael Liebman	
20. ArrayTrack: 一个美国食品及药物管理局 (FDA) 和公共基因组工具	379
Hong Fang, Stephen C. Harris, Zhenjiang Su, Minjun Chen, Feng Qian, Leming Shi, Roger Perkins, and Weida Tong	

索引	399
----------	-----

(高友鹤 尹剑锐 译)

Contents

<i>Preface</i>	v
<i>Contributors</i>	ix
SECTION I: INTERACTIONS	
1. Mining Protein–Protein Interactions from Published Literature Using Linguamatics I2E	3
<i>Judith Bandy, David Milward, and Sarah McQuay</i>	
2. Relative Avidity, Specificity, and Sensitivity of Transcription Factor–DNA Binding in Genome-Scale Experiments	15
<i>Vladimir A. Kuznetsov</i>	
3. Curation of Inhibitor–Target Data: Process and Impact on Pathway Analysis	51
<i>Sreenivas Devidas</i>	
4. Profiling Protein Interaction Networks with Functional Protein Microarrays	63
<i>Dawn R. Mattoon and Barry Schweitzer</i>	
5. Manual Annotation of Protein Interactions	75
<i>Svetlana Bureeva, Svetlana Zvereva, Valentin Romanov, and Tatiana Serebryiskaya</i>	
SECTION II: ANALYSIS	
6. Gene Set Enrichment Analysis	99
<i>Charles A. Tilford and Nathan O. Siemers</i>	
7. PANTHER Pathway: An Ontology-Based Pathway Database Coupled with Data Analysis Tools	123
<i>Huaiyu Mi and Paul Thomas</i>	
8. Prioritizing Genes for Pathway Impact Using Network Analysis	141
<i>Aaron N. Chang</i>	
9. Discovering Biological Networks from Diverse Functional Genomic Data	157
<i>Chad L. Myers, Camelia Chiriac, and Olga G. Troyanskaya</i>	
10. Functional Analysis of OMICs Data and Small Molecule Compounds in an Integrated “Knowledge-Based” Platform	177
<i>Yuri Nikolsky, Eugene Kirillov, Roman Zuev, Eugene Rakhmatulin, and Tatiana Nikolskaya</i>	
11. Kinetic Modeling as a Tool to Integrate Multilevel Dynamic Experimental Data	197
<i>Ekaterina Mogilevskaya, Natalia Bagrova, Tatiana Plyusnina, Nail Gizzatkulov, Eugeniy Metelkin, Ekaterina Goryacheva, Sergey Smirnov, Yuriy Kosinsky, Aleksander Dorodnov, Kirill Peskov, Tatiana Karelina, Igor Goryanin, and Oleg Demin</i>	

12.	Cytoscape: A Community-Based Framework for Network Modeling	219
	<i>Sarah Killcoyne, Gregory W. Carter, Jennifer Smith, and John Boyle</i>	
13.	Semantic Data Integration and Knowledge Management to Represent Biological Network Associations	241
	<i>Sascha Losko and Klaus Heumann</i>	
14.	Solutions for Complex, Multi Data Type and Multi Tool Analysis: Principles and Applications of Using Workflow and Pipelining Methods.	259
	<i>Robin E. J. Munro and Yike Guo</i>	
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	275
	<i>Jeff Kiefer, Hongwei H. Yin, Qiang Q. Que, and Spyro Mousset</i>	
16.	Pathway and Network Analysis with High-Density Allelic Association Data	289
	<i>Ali Torkamani and Nicholas J. Schork</i>	
17.	miRNAs: From Biogenesis to Networks	303
	<i>Giuseppe Russo and Antonio Giordano</i>	
18.	MetaMiner (CF): A Disease-Oriented Bioinformatics Analysis Environment.	353
	<i>Jerry M. Wright, Yuri Nikolsky, Tatiana Serebryiskaya, and Diana R. Wetmore</i>	
19.	Translational Research and Biomedical Informatics	369
	<i>Michael Liebman</i>	
20.	ArrayTrack: An FDA and Public Genomic Tool	379
	<i>Hong Fang, Stephen C. Harris, Zhenjiang Su, Minjun Chen, Feng Qian, Leming Shi, Roger Perkins, and Weida Tong</i>	
	Index	399