
Contents

<i>Preface</i>	<i>v</i>
<i>Contributors</i>	<i>xi</i>

PART I DATABASES

1 Update on Genomic Databases and Resources at the National Center for Biotechnology Information	3
<i>Tatiana Tatusova</i>	
2 Protein Structure Databases	31
<i>Roman A. Laskowski</i>	
3 The MIntAct Project and Molecular Interaction Databases	55
<i>Luana Licata and Sandra Orchard</i>	
4 Applications of Protein Thermodynamic Database for Understanding Protein Mutant Stability and Designing Stable Mutants.	71
<i>M. Michael Gromiha, P. Anoosha, and Liang-Tsung Huang</i>	
5 Classification and Exploration of 3D Protein Domain Interactions Using Kbdock.	91
<i>Anisah W. Ghoorah, Marie-Dominique Devignes, Malika Smaïl-Tabbone, and David W. Ritchie</i>	
6 Data Mining of Macromolecular Structures.	107
<i>Bart van Beusekom, Anastassis Perrakis, and Robbie P. Joosten</i>	
7 Criteria to Extract High-Quality Protein Data Bank Subsets for Structure Users	139
<i>Oliviero Carugo and Kristina Djinović-Carugo</i>	
8 Homology-Based Annotation of Large Protein Datasets	153
<i>Marco Punta and Jaina Mistry</i>	

PART II COMPUTATIONAL TECHNIQUES

9 Identification and Correction of Erroneous Protein Sequences in Public Databases	179
<i>László Pattthy</i>	
10 Improving the Accuracy of Fitted Atomic Models in Cryo-EM Density Maps of Protein Assemblies Using Evolutionary Information from Aligned Homologous Proteins	193
<i>Ramachandran Rakesh and Narayanaswamy Srinivasan</i>	
11 Systematic Exploration of an Efficient Amino Acid Substitution Matrix: MIQS.	211
<i>Kentaro Tomii and Kazunori Yamada</i>	

12	Promises and Pitfalls of High-Throughput Biological Assays	225
	<i>Greg Finak and Raphael Gottardo</i>	
13	Optimizing RNA-Seq Mapping with STAR	245
	<i>Alexander Dobin and Thomas R. Gingeras</i>	
PART III PREDICTION METHODS		
14	Predicting Conformational Disorder	265
	<i>Philippe Lieutaud, François Ferron, and Sonia Longhi</i>	
15	Classification of Protein Kinases Influenced by Conservation of Substrate Binding Residues	301
	<i>Chintalapati Janaki, Narayanaswamy Srinivasan, and Malini Manoharan</i>	
16	Spectral-Statistical Approach for Revealing Latent Regular Structures in DNA Sequence	315
	<i>Maria Chaley and Vladimir Kutyrkin</i>	
17	Protein Crystallizability	341
	<i>Pawel Smialowski and Philip Wong</i>	
18	Analysis and Visualization of ChIP-Seq and RNA-Seq Sequence Alignments Using ngs.plot	371
	<i>Yong-Hwee Eddie Loh and Li Shen</i>	
19	Datamining with Ontologies	385
	<i>Robert Hoehndorf, Georgios V. Gkoutos, and Paul N. Schofield</i>	
20	Functional Analysis of Metabolomics Data	399
	<i>Mónica Chagoyen, Javier López-Ibáñez, and Florencio Pazos</i>	
21	Bacterial Genomic Data Analysis in the Next-Generation Sequencing Era	407
	<i>Massimiliano Orsini, Gianmauro Cuccuru, Paolo Uva, and Giorgio Fotia</i>	
22	A Broad Overview of Computational Methods for Predicting the Pathophysiological Effects of Non-synonymous Variants	423
	<i>Stefano Castellana, Caterina Fusilli, and Tommaso Mazza</i>	
23	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning	441
	<i>Salvatore Alaïmo, Rosalba Giugno, and Alfredo Pulvirenti</i>	
24	Protein Residue Contacts and Prediction Methods	463
	<i>Badri Adhikari and Jianlin Cheng</i>	
25	The Recipe for Protein Sequence-Based Function Prediction and Its Implementation in the ANNOTATOR Software Environment	477
	<i>Birgit Eisenhaber, Durga Kuchibhatla, Westley Sherman, Fernanda L. Sirota, Igor N. Berezovsky, Wing-Cheong Wong, and Frank Eisenhaber</i>	

PART IV BIG DATA

26	Big Data, Evolution, and Metagenomes: Predicting Disease from Gut Microbiota Codon Usage Profiles	509
	<i>Maja Fabijanić and Kristian Vlahoviček</i>	
27	Big Data in Plant Science: Resources and Data Mining Tools for Plant Genomics and Proteomics.	533
	<i>George V. Popescu, Christos Noutsos, and Sorina C. Popescu</i>	
	<i>Index</i>	549

Data Mining Techniques for the Life Sciences

Carugo, O.; Eisenhaber, F. (Eds.)

2016, XIII, 552 p. 97 illus., 84 illus. in color., Hardcover

ISBN: 978-1-4939-3570-3

A product of Humana Press