

Bioinformatics

Volume II: Structure, Function and Applications

Edited by

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Not only is the quantity of life science data expanding, but new types of biological data continue to be introduced as a result of technological development and a growing understanding of biological systems. Methods for analyzing these data are an increasingly important component of modern biological research. In *Bioinformatics*, leading researchers in the field provide a selection of the most useful and widely applicable methods, able to be applied as is, or with minor variations, to many specific problems. *Volume II: Structure, Function and Applications* contains methods pertinent to the prediction of protein and RNA structures and the analysis and classification of structures, methods for inferring the function of previously identified genomic elements, chiefly protein-coding genes, medical applications in diagnostics and drug discovery, and "meta-methods" for developers of bioinformatics algorithms. As a volume of the highly successful *Methods in Molecular Biology*™ series, this work provides the kind of detailed description and implementation advice that is crucial for getting optimal results.

Comprehensive and cutting-edge, *Bioinformatics: Volume II: Structure, Function and Applications* is an ideal reference for all scientists involved with the ever-growing array of data in the expanding field of life science.

FEATURES

- Encompasses topics from across the diverse field of bioinformatics through its broad scope approach
- Over 80 authors from around the globe contribute to the two volumes, including many leading experts in their respective subjects
- An interdisciplinary collaboration involving biologists, biochemists, physicists, mathematicians, statisticians, and computer scientists
- Contains simplified descriptions, requiring a minimum of background knowledge, amenable to students and beginners in bioinformatics
- References a wide variety of software tools and scripts, available online

CONTENTS

Section I: Structures. UNAFold: Software for Nucleic Acid Folding and Hybridization. Protein Structure Prediction. An Introduction to Protein Contact Prediction. Analysis of Mass Spectrometry Data in Proteomics. The Classification of Protein Domains. **Section II: Inferring Function.** Inferring Function from Homology. The Rosetta Stone Method. Inferring Functional Relationships from Conservation of Gene Order. Phylogenetic Profiling. Phylogenetic Shadowing: Sequence Comparisons of Multiple Primate Species. Prediction of Regulatory Elements. Expression and Microarrays. Identifying Components of Complexes. Integrating Functional Genomics Data. **Section III: Applications and Disease.** Computational Diagnostics with Gene Expression Profiles. Analysis of Quantitative Trait Loci. Molecular Similarity Concepts and Search Calculations.

Optimization of the MAD Algorithm for Virtual Screening. Combinatorial Optimization Models for Finding Genetic Signatures from Gene Expression Datasets. Genetic Signatures for a Rodent Model of Parkinson's Disease Using Combinatorial Optimization Methods. **Section IV: Analytical and Computational Methods.** Developing Fixed-Parameter Algorithms to Solve Combinatorially Explosive Biological Problems. Clustering. Visualization. Constructing Computational Pipelines. Text Mining. Index.

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