

Bioinformatics

Volume I: Data, Sequence Analysis and Evolution

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 I: Data, Sequence Analysis and Evolution* examines a selection of methods involving the generation and organization of data, including sequence data, RNA and protein structures, microarray expression data and functional annotations, methods for discovering the functional components of genomes—whether they be genes, alternative splice sites, non-coding RNAs or regulatory motifs—and several of the most interesting methods in phylogenetics and evolution. 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 I: Data, Sequence Analysis and Evolution* 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
- References a wide variety of software tools and scripts, available online

CONTENTS

Section I: Data and Databases. Managing Sequence Data. RNA Structure Determination by NMR. Protein Structure Determination by X-Ray Crystallography. Pre-Processing of Microarray Data and Analysis of Differential Expression. Developing an Ontology. Genome Annotation. **Section II: Sequence Analysis.** Multiple Sequence Alignment. Finding Genes in Genome Sequence. Bioinformatics Detection of Alternative Splicing. Reconstruction of Full-Length Isoforms from Splice Graphs. Sequence Segmentation. Discovering Sequence Motifs. **Section III: Phylogenetics and Evolution.** Modeling Sequence Evolution. Inferring Trees. Detecting the Presence and Location of Selection

in Proteins. Phylogenetic Model Evaluation. Inferring Ancestral Gene Order. Genome Rearrangement by the Double Cut and Join Operation. Inferring Ancestral Protein Interaction Networks. Computational Tools for the Analysis of Rearrangements in Mammalian Genomes. Detecting Lateral Genetic Transfer: A Phylogenetic Approach. Detecting Genetic Recombination. Inferring patterns of Migration. Fixed-Parameter Algorithms in Phylogenetics. Index.

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