BOOK REVIEWS

Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases. Edited by ROB ELLES. Humana Press Inc., Totowa, NJ, 1996. 356 pp., (comb bound) $69.50.

Molecular Diagnosis of Genetic Diseases is a member of a multivolume collection on *Methods in Molecular Medicine.* Each chapter of this book is contributed by a different author and provides a survey of molecular methods for the diagnosis of a variety of diseases. The individual chapters cover a broad range of diseases including Duchenne/Becker muscular dystrophy, cystic fibrosis, and a number of trinucleotide repeat associated diseases. Within each chapter there is a nice balance between background information and easy-to-use protocols for the analysis of each genetic disease. Within the background information, the underlying mechanisms of mutation for each disease are also clearly explained. Several other chapters focus on individual methods for screening including automated genotyping, pulsed field gel electrophoresis, and single-strand conformation polymorphism analysis. Individual chapters within the text also discuss risk analysis, preimplantation diagnosis, prenatal diagnosis, and X-chromosome inactivation. Thus, the text covers a broad armamentarium for the diagnosis of genetic diseases as well as a number of issues associated with genetic testing. Each chapter is very well written and easy to understand. I believe that the book will serve as a very useful reference to individuals in the field, as well as an excellent introduction for new investigators.

MARK A. BATZER
Louisiana State University Medical Center

ARTICLE NO. AB969924

BOOK REVIEWS

Methods in Enzymology, Vol. 266, **Computer Methods for Macromolecular Sequence Analysis.** Edited by RUSSELL F. DOOLITTLE. Academic Press, San Diego, CA, 1996. 711 pp., $110.00.

This is the second volume of the *Methods in Enzymology* series devoted to the analysis of sequence data. The present volume is divided into five sections covering databases and resources, the use of databases, multiple alignment and phylogenetic considerations, secondary structure considerations, and three-dimensional considerations. Each chapter of this book was contributed by different authors and provides an enormous amount of information ranging from available databases to the design and application of search algorithms. The individual sections of the book are nicely balanced and provide detailed background information as well as outlines of the application and use of many of the programs.

The overall content of the book is slightly skewed to the analysis of proteins. Individual chapters on protein analysis range from protein alignments and phylogenetic trees to a detailed multichapter coverage of secondary structure as well as three-dimensional structure and the detection of structural similarities. In addition, a method for combined DNA and protein alignment is also presented. Additional chapters deal with the discovery and analysis of human genes, protein sequence comparisons at the genomic scale, and protein fold predictions using iterative search and hybrid sequence/structure templates. The coverage of protein structural predictions is excellent and the individual algorithms are explained in sufficient detail.

The book also has a number of chapters on databases and searching through databases. The database section includes chapters on superfamily classification in PIR, TDB: new databases for biological discovery, blocks database and its applications, among others. Additional chapters on gene classification artificial neural system by Cathy Wu, indexing and using sequence databases and SRS: information retrieval system for molecular biology databanks are also included. The coverage of existing resources, while not exhaustive, is still fairly comprehensive and well rounded. A number of the larger database searching programs are also covered including GRAIL, BLAST, and *Entrez.* In addition, large-scale sequence similarity comparisons, detection of distant homologies, and pattern recognition are covered. This section of the book should be particularly useful to new researchers in this area and serve as a reference to those actively involved in the field.

The third section of the book covers multiple alignment and phylogenetic trees. Individual chapters outline parametric and inverse-parametric sequence alignment with XPARAL, local alignment statistics, and CLUSTAL for multiple sequence alignments, methods for estimating evolutionary distances between DNA sequences, reconstruction of gene trees from sequence data, and inferring phylogenies from protein sequences by parsimony, distance, and likelihood methods. Overall, the coverage in this section is outstanding and should serve as a useful reference to individuals interested in multiple alignments and phylogenetic trees. The breadth of topics covered by this volume of *Methods in Enzymology* is outstanding and the book should become very popular among a variety of biological investigators.

MARK A. BATZER
Louisiana State University Medical Center

ARTICLE NO. AB969925