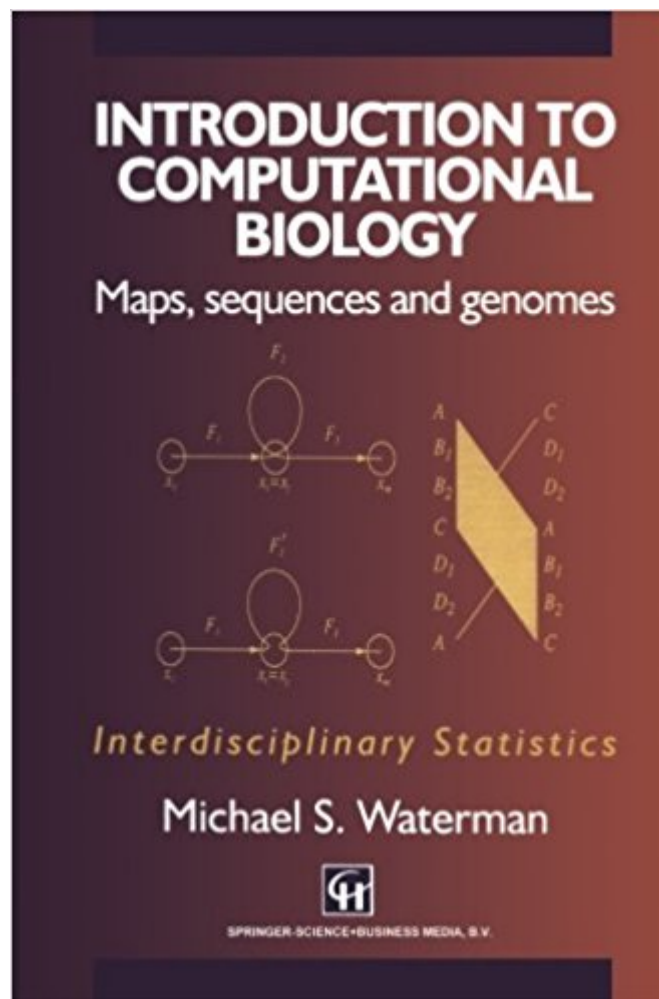


The book was found

Introduction To Computational Biology: Maps, Sequences And Genomes (Chapman & Hall/CRC Interdisciplinary Statistics)



Synopsis

Biology is in the midst of a era yielding many significant discoveries and promising many more. Unique to this era is the exponential growth in the size of information-packed databases. Inspired by a pressing need to analyze that data, *Introduction to Computational Biology* explores a new area of expertise that emerged from this fertile field- the combination of biological and information sciences. This introduction describes the mathematical structure of biological data, especially from sequences and chromosomes. After a brief survey of molecular biology, it studies restriction maps of DNA, rough landmark maps of the underlying sequences, and clones and clone maps. It examines problems associated with reading DNA sequences and comparing sequences to finding common patterns. The author then considers that statistics of pattern counts in sequences, RNA secondary structure, and the inference of evolutionary history of related sequences. *Introduction to Computational Biology* exposes the reader to the fascinating structure of biological data and explains how to treat related combinatorial and statistical problems. Written to describe mathematical formulation and development, this book helps set the stage for even more, truly interdisciplinary work in biology.

Book Information

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Customer Reviews

This book gives a good survey of the different techniques employed by computational biologists.

After a brief review of molecular biology in Chapter 1, the author treats the mathematical modeling of restriction maps in Chapter 2 using graph theory. His presentation is somewhat hurried, but he does give references and gives the reader three exercises at the end of the chapter. Multiple maps are treated in Chapter 3, wherein the author first makes use of probability theory, via the Kingman subadditive ergodic theorem. The proof is omitted but the author does a good job of explaining its use in studying the double digest problem (DDP). The best part of this chapter is the author's explanation of the difficulties of using Kingman's results for solving the DDP, and goes on to discuss multiple solutions of the DDP. Graph theory is again used in the discussion. This sets up the discussion in Chapter 4, which outlines algorithms for the DDP. The author gives a very compact introduction to P- and NP-complete problems in the theory of computation, then proves that DDP is NP-complete. The author does a good job of discussing subsequent approximate methods used for the DDP, such as simulated annealing. Markov chains are introduced in the book here for the first time, but due to the shortness of the presentation, the reader should do outside reading as a back-up. The author does a great job of explaining the difficulties if measurement error is introduced in the DDP at the end of the chapter. Cloning is discussed in Chapter 5, with tools from probability theory used to deal with partial digest libraries. The chapter is really short though, and the working the problems at the end of the chapter is essential for the understanding the results of this chapter.

The first name people learn in bioinformatics is the Smith-Waterman algorithm. Some people never learn anything else. This is by that Waterman. Although written in 1995, it still has some of the best discussion I've seen on the topics it addresses. The first few chapters deal with the "digest problem," reconstructing a DNA or protein sequence from the fragment sizes of enzyme digests. The technique is not used as much now as it was then, but it's always good to know the background of modern techniques. The digest problem doesn't stand alone, though. It introduces concepts - islands, anchors, etc. - that still matter. The problems in reconstructing molecules from digests yield the same kinds of intermediate results and the same ambiguities that arise in modern sequencing. As Waterman advances the discussion, shotgun sequencing appears as a logical extension, at least mathematically, of digest assembly. Sequence assembly involve end matching, perhaps in the presence of sequencing errors. That introduces the topic for which Waterman's name is famous, approximate string matching. The next few chapter progress through dynamic programming and multiple alignments. The logical connections between the techniques shown are so tight that chapter boundaries are almost artificial. It was a real pleasure to see the computational and practical relationships laid out. The final topics, RNA structure and phylogenetic trees, lack the

continuity that characterized the first dozen chapters. The RNA structure may be the weakest chapter in the book, but still a very competent introduction. Throughout, Waterman emphasizes mathematical rigor without insisting on uninformative theorems. Every topic is presented in rich detail, with special attention to scoring and background models.

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