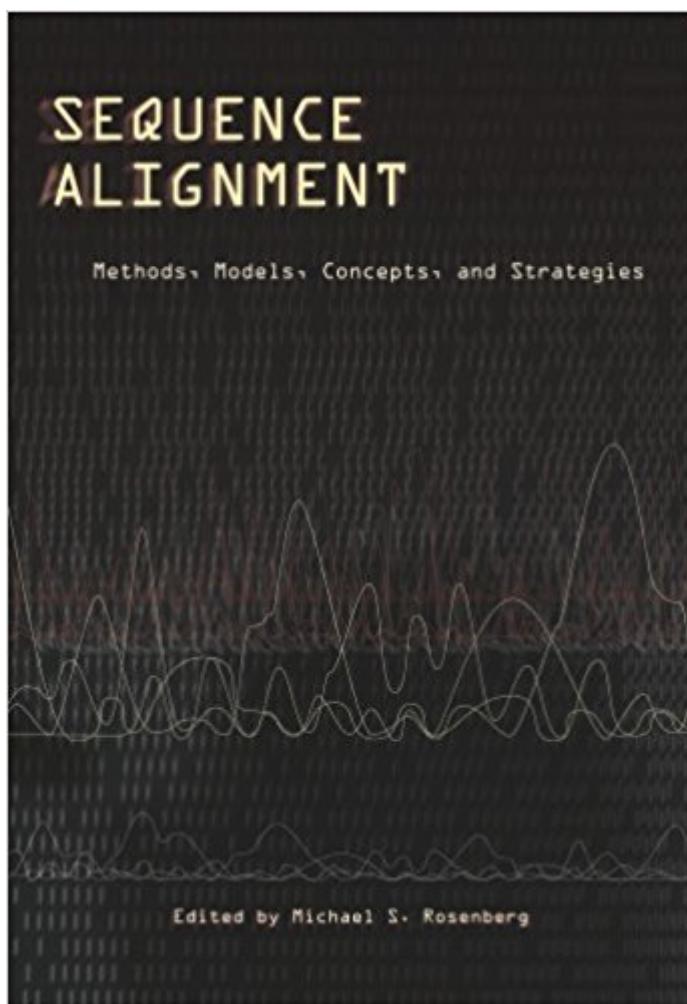


The book was found

Sequence Alignment: Methods, Models, Concepts, And Strategies



Synopsis

The sequencing of the human genome involved thousands of scientists but used relatively few tools. Today, obtaining sequences is simpler, but aligning the sequences—making sure that sequences from one source are properly compared to those from other sources—remains a complicated but underappreciated aspect of comparative molecular biology. This volume, the first to focus on this crucial step in analyzing sequence data, is about the practice of alignment, the procedures by which alignments are established, and more importantly, how the outcomes of any alignment algorithm should be interpreted. Edited by Michael S. Rosenberg with essays by many of the field's leading experts, *Sequence Alignment* covers molecular causes, computational advances, approaches for assessing alignment quality, and philosophical underpinnings of the algorithms themselves.

Book Information

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Customer Reviews

"Sequence alignment represents the final frontier in the development of repeatable, comprehensive methods for phylogenetic analysis. This book will inform readers about the current status of alignment methods and will help stimulate additional work in the field."—David M. Hillis, University of Texas "Sequence Alignment provides an in-depth treatment of the prerequisite to many evolutionary analyses by presenting a diversity of opinions on the best way to align complex molecular sequence data. Topics covered include the basic algorithms used, global versus local procedures, the robustness alignment error detection, and a description of the programs now available. Sequence Alignment is a reassuring companion, guiding the reader through a large and

complicated field." John Huelsenbeck, Department of Integrative Biology, University of California, Berkeley

Michael S. Rosenberg is Associate Professor of Computational Evolutionary Biology and Bioinformatics in the School of Life Sciences and the Center for Evolutionary Functional Genomics of the Biodesign Institute at Arizona State University.

This was my 1st book in sequence analysis. At first I did not appreciate the book and gave it 3 stars. Maybe that's because I needed some introduction into the topic first. But after some time, I re-read it again, and found it pretty good and informative.

This book is written by several authors, each presenting a paper in a particular topic related to sequence alignment. When I received the book, the first thing I opened was page 142, where I found a description of how one can import RNA alignments into Microsoft Word and edit them there. There are instructions to change the colors, font, and the page size to be able to comfortably work. I couldn't believe my eyes! At least list one of the many many many tools (and procedures) far better suited for the task described in that chapter. After going over some other papers in the book, their quality varies tremendously from one to another. More than serving as a reference (as the title suggested me first), the book contains the opinions of many people. Unfortunately the first paper I opened already gave me a very negative impression, difficult to overcome.

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