Computational Molecular Biology: An Algorithmic Approach (Computational Molecular Biology)

Pavel A. Pevzner
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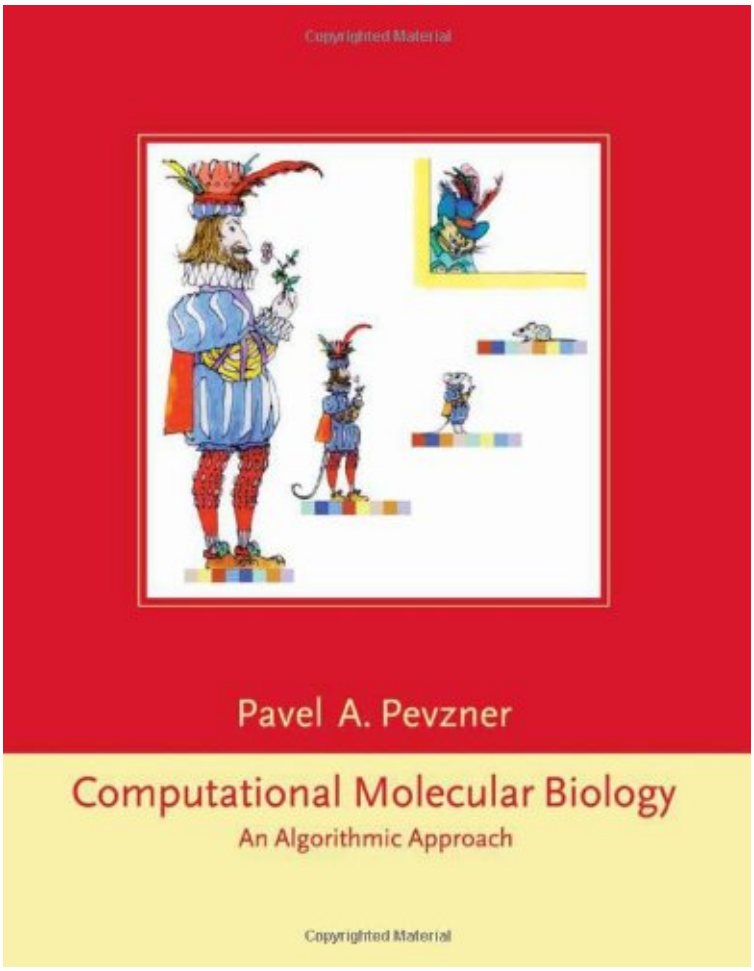

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Pavel A. Pevzner : Computational Molecular Biology: An Algorithmic Approach (Computational Molecular Biology) before purchasing it in order to gage whether or not it would be worth my time, and all praised Computational Molecular Biology: An Algorithmic Approach (Computational Molecular Biology):

9 of 9 people found the following review helpful. Readable and practicalBy wiredweirdPevzner has written a very useful book on bioinformatics algorithms, and one that seems reasonably up to date. The table of contents follows a classic plan: restriction maps, assembly and sequencing, 2- and N- way string comparisons, and analysis of rearrangements. There's a good but brief section on mass spec analysis - unfortunately, that chapter is called "Proteomics" even though the term covers a lot more than MS. Other sections skim the surface of hidden Markov models and Gibbs sampling for finding patterns ("motifs") in DNA.A few chapters have unusual strengths. The

"Conway Equation" gives more insight in analysis of motif significance than other introductory books do. The section in sequence comparison pays a lot more attention to BLAST-like algorithms than other books do, also - modern material you'd normally see only in the journals. Also, the section on rearrangements gives some ideas about using rearrangement data for phylogenetic analysis. That really gives the material meaning. Rearrangements aren't just string operations, they're features of evolution, and they can be compared to each other. No matter what the discussion, Pevzner keeps maintains a readable and enjoyably informal tone.The book does have some weaknesses, though. It's a bit advanced for an undergrad intro, but bottoms out before the Baum-Welch algorithm, for example. Discussion of microarrays for sequencing seems dated. Pevnzer describes their use in sequencing, a rarity now, but skips their use in functional gneomics, where they are used most often. Illustration style is erratic and many diagrams are oddly stretched (3.5, 5.7, 8.3, and others, some much worse). Formal analysis of the algorithms is weak, but Pevzner somewhat makes up for that with better statistical analysis than many authors give. Also, even though the book was reprinted in 2001, it still estimates 100K genes in the human genome.This is a good second book, maybe the one to read after Pevzner's newer "Introduction". It covers most of the basics and gives fairly usable pseudocode. Most of all, it always keeps the biology in mind. That, by itself, makes this book stand out.//wiredweird0 of 2 people found the following review helpful. the used book was rated as very good condition but it was notBy faegheh jafarifarthe book itself is a very good book to read but the condition of the book as a used book was not "very good" as it was mentioned. the cover was actually pretty damaged and there was some writing inside book too.48 of 48 people found the following review helpful. Nice book for expertsBy A CustomerThe title is somewhat misleading because the book is primarily devoted to combinatorial methods that could be used in genome sequencing and genomics. The selection of methods is arbitrary and does not seem to be dictated by either pedagogical or scientific vision. It mainly reflects the author's own work and interests. Contrary to what the editorial review states I find this text quite abstract and formal. I like the book very much but I don't think it should be recommended to the beginners in computational biology. Readers who have a taste for mathematics and a strong background in combinatorics could benefit the most from reading this book. Anybody who looks for a textbook-level guidance in computational biology should probably rely on better designed texts such as Don Gusfield's "Algorithms on strings trees and sequences" or "Biological sequence analysis" by Durbin and co-authors. However, the readers who are interested in mathematics behind designs of DNA arrays (chapter 5) or in mathematical treatment of genome rearrangements (chapter 10) should certainly read this book in detail.

In one of the first major texts in the emerging field of computational molecular biology, Pavel Pevzner covers a broad range of algorithmic and combinatorial topics and shows how they are connected to molecular biology and to biotechnology. The book has a substantial "computational biology without formulas" component that presents the biological and computational ideas in a relatively simple manner. This makes the material accessible to computer scientists without biological training, as well as to biologists with limited background in computer science. Computational Molecular Biology seriesComputer science and mathematics are transforming molecular biology from an informational to a computational science. Drawing on computational, statistical, experimental, and technological methods, the new discipline of computational molecular biology is dramatically increasing the discovery of new technologies and tools for molecular biology. The new MIT Press Computational Molecular Biology series provides a unique venue for the rapid publication of monographs, textbooks, edited collections, reference works, and lecture notes of the highest quality.

About the AuthorPavel Pevzner is Ronald R. Taylor Professor of Computer Science at the University of California, San Diego. He is the author of Computational Molecular Biology: An Algorithmic Approach (MIT Press, 2000).