Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids

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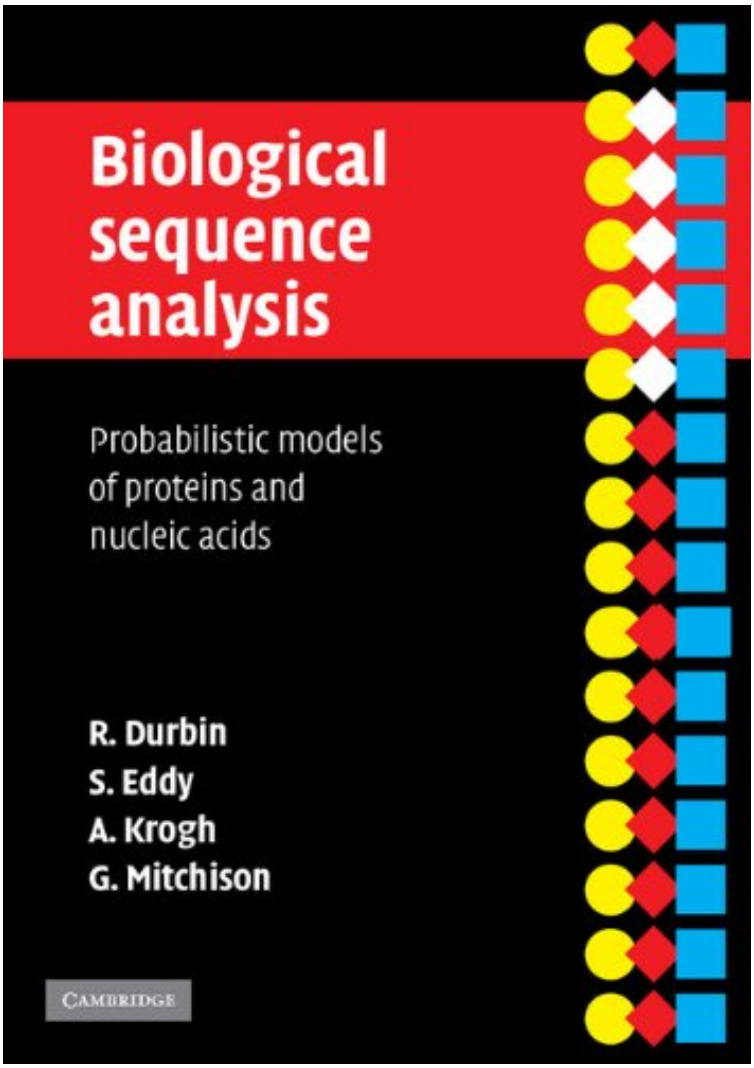

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Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison : Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids before purchasing it in order to gage whether or not it would be worth my time, and all praised Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids:

2 of 2 people found the following review helpful. a defining text for bioinformaticsBy RidahoanThis is an old book now, and I don't know if its been supplanted, but when published it was by far the best book in its field. I think it still has much to offer. No, it's not an easy read for those of us coming from a biological background, but it is accessible, thorough, and self-contained, and a much gentler read than what one will confront in the literature. Unlike more theoretical treatments, this provides examples, and trots (if not walks) the reader through them, which is a huge step up

for those texts assuming the reader has a strong mathematical background. It also builds on itself in explicit and thoughtful ways, so that the reader does not feel confronted with a jumble of different analytical techniques. For me it was an excellent introduction to methods of sequence analysis, and to some extent, probabilistic perspectives on modelling in general.0 of 0 people found the following review helpful. One of the best availableBy RobertAlthough this book is based primarily on work that was completed in 1998, and therefore somewhat out of date, it is the best book I have found for teaching bioinformatics. I selected this as the best of the available books on the subject for use in my bioinformatics and numerical methods course which is to be taught in the fall of 2007 at Univ. of Conn. This course is an upper division undergraduate and first year graduate course. That is roughly the level of this text and the comparative advantage of this book is the excellent presentation and thorough discussion of the algorithms. A student armed with Matlab or MathScriptor can take this book and start writing algorithms for sequence alignment and Hidden Markov Method (HMM) analysis after only the first three or four chapters. This book is in its 11th printing and is nearly error free (I found only a few in the figures). This book is strongly recommended for both students and researchers, particularly those interested in protein alignment, phylogenic analysis or an introduction to Hidden Markov Methods.4 of 5 people found the following review helpful. Brief and clearBy wiredweirdI keep coming back to this book for its readable, applicable summaries of basic algorithms.One chapter covers the basics of dynamic programming for string matching: a staple of bioinformatics computing. The authors come back to it a number of times as they introduce new variations on the string-matching theme. They give about the clearest description of the Needleman-Wunsch and basic variants (including Smith-Waterman) of any book I know.The bulk of the book is devoted to Hidden Markov Models (HMMs), as one might have guessed in a book with Eddy as co-author. It covers the basics of model construction, motif finding, and various uses for decoding. Again, it covers all the basics so clearly you'll want to start coding as soon as you read it.The later sections of the book cover phylogeny and tree building, along with the relationships to multiple alignment. Good, solid, clear writing prepares the reader for texts that may be more specialized, but possibly less transparent.The next-to-last chapter, on RNA folding, is weaker than the ones before, in my opinion. It ties to the other chapters reasonably well in terms of algorithms, but I don't think it does justice to the thermodynamic models of RNA folding. If there is any weakness in this chapter, though, it does not detract from the strengths elsewhere.The final chapter, the "background on probability", is the one that I think needs the most support. If you don't already understand its topics, I doubt that this will help very much. (If you do understand them, you won 't need the help.) There's nothing inherently tricky about probability, but individual distributions carry many assumptions, and I did not see those spelled out well.This shouldn't be the only book in your bioinformatics library. If you really want algorithms, though, it's a good book to have in the collection and one you'll keep coming back to.

Probabilistic models are becoming increasingly important in analysing the huge amount of data being produced by large-scale DNA-sequencing efforts such as the Human Genome Project. For example, hidden Markov models are used for analysing biological sequences, linguistic-grammar-based probabilistic models for identifying RNA secondary structure, and probabilistic evolutionary models for inferring phylogenies of sequences from different organisms. This book gives a unified, up-to-date and self-contained account, with a Bayesian slant, of such methods, and more generally to probabilistic methods of sequence analysis. Written by an interdisciplinary team of authors, it aims to be accessible to molecular biologists, computer scientists, and mathematicians with no formal knowledge of the other fields, and at the same time present the state-of-the-art in this new and highly important field.