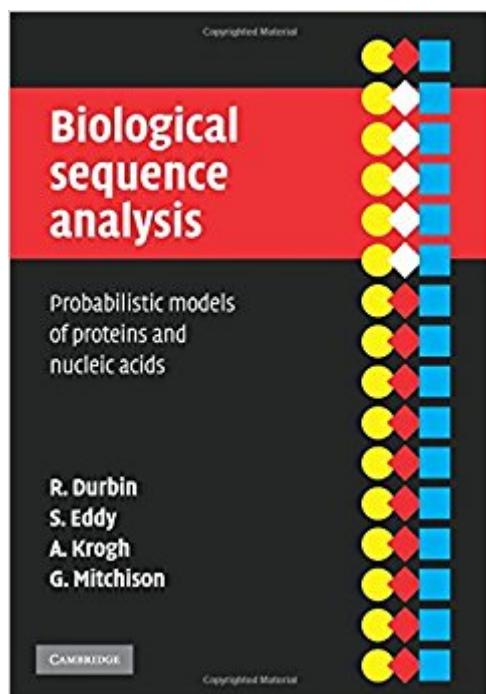The book was found

Biological Sequence Analysis: Probabilistic Models Of Proteins And Nucleic Acids

Synopsis

Probablistic models are becoming increasingly important in analyzing 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 analyzing 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 is accessible to molecular biologists, computer scientists, and mathematicians with no formal knowledge of the other fields, and at the same time presents the state of the art in this new and important field.

Book Information

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Customer Reviews

"The book is amply illustrated with biological applications and examples." Cell"...successfully integrates numerous probabilistic models with computational algorithms to solve molecular biology problems of sequence alignment...an excellent textbook selection for a course on bioinformatics and a very useful consultation book for a mathematician, statistician, or biometrician working in sequence alignment." Bulletin of Mathematical Biology"This is one of the more rewarding books I have read within this field. My overall evaluation is that this book is very good and a must read for active participants in the field. In addition, it could be particularly useful for molecular biologists"

Theoretical Population Biology

Probabilistic methods are assuming greater significance in the analysis of nucleotide sequence data. This book provides the first unified, up-to-date and self-contained account of such methods, and more generally of probabilistic methods of sequence analysis, presented in a Bayesian framework.

This 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.

Although 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.

I 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.

I will agree and submit: this is an invaluable introduction to the field of bioinformatics. With introductions to everything from sequence analysis to hidden markov models and even a primer on grammars, this is a useful introduction both to biological applications for computer scientists *as well as* computational methods for biologists.I am in a joint graduate-level biology/computer science class and we are using this book as a foundation to bring both groups up to speed and it seems to be working out nicely.However, one criticism is that sometimes Durbin et al jump into subjects without an adequate introduction or with one that is overcomplexified. In other words, they sometimes break Einstein's the rule of "make everything as simple as possible but not simpler". Durbin et al do not always make things as simple as possible. And it is annoying when they do not. Especially when I see them confusing the bejebus out of the biology people over computer science concepts that are really not that complicated through overly technical jargon.But this is rare and they provide many insightful diagrams to clear up their algorithms as well as lucid ways to introduce biological concepts. Sometimes the introduction of an algorithm/theory *and* a biological concept molds together beautifully such that the reader is simultaneously being infused with both. An example of this phenomenon is their dual introduction to CpG islands and markov models.

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids The Biophysical Chemistry of Nucleic Acids and Proteins Nucleic Acids in Chemistry and Biology: RSC Nucleic Acids in Chemistry and Biology Project Economics and Decision Analysis: Probabilistic Models The Dark Is Rising Sequence, Book One: Over Sea, Under Stone (Dark Is Rising Sequence (Audio)) The Dark Is Rising Sequence, Book Two: The Dark Is Rising (Dark Is Rising Sequence (Audio)) Probabilistic Graphical Models: Principles and Techniques (Adaptive Computation and Machine Learning series) Chemical Approaches to the Synthesis of Peptides and Proteins (New Directions in Organic & Biological Chemistry) Sequence Alignment: Methods, Models, Concepts, and Strategies Probability and Computing: Randomization and Probabilistic Techniques in Algorithms and Data Analysis Data Analysis and Graphics Using R: An Example-Based Approach (Cambridge Series in Statistical and Probabilistic Mathematics) Probabilistic Methods of Signal and System Analysis (The Oxford Series in Electrical and Computer Engineering) Choosing Safety: A Guide to Using Probabilistic Risk Assessment and Decision Analysis in Complex, High-Consequence Systems Choosing Safety: A Guide to Using Probabilistic Risk Assessment and Decision Analysis in Complex, High-Consequence Systems (Rff Press) HPLC in Nucleic Acid Research: Methods and Applications (Chromatographic Science Series) Bioinformatics: A Practical Guide To The Analysis Of Genes And Proteins, 3Rd Ed Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Bioinformatics: Sequence and Genome Analysis Amino Acids: The Way to Health and Wellness: Find Health and Healing from Depression, Addictions, Obesity, Anxiety, Sexual Issues, and Fill Nutritional Needs of Vegetarian and Vegan Diets

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