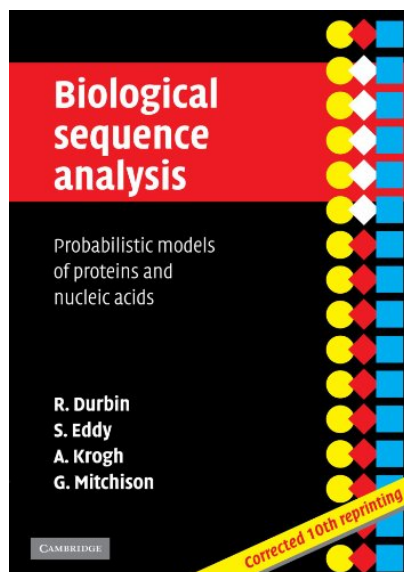


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Probabilistic models are becoming increasingly important in analyzing the huge amount of data being produced by large-scale DNA-sequencing efforts such as the Human Genome Project. For example, hidden Markov models are used for analyzing biological 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.

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