Book Review

Introduction to Mathematical Methods in Bioinformatics

Alexander Isaev, Springer, Heidelberg, Germany
2004, pp. 294
ISBN 3–540–21973–0

This book is exactly what the title suggests: an introduction to the mathematics needed for bioinformatics or at least, some bioinformatics areas. The mathematical treatment is extremely thorough and the book is aimed at university lecturers (and their undergraduate students) in mathematics departments giving courses in bioinformatics. This gives an emphasis on theory and mathematical background and rigour rather than practical details. As such, it is not a book to be used in order to gain experience of a wide variety of topics or of practical details. Rather it can be used for teaching or for bioinformaticists who wish to learn more about the theory behind the use of probability in alignment and especially to learn about hidden Markov models (HMMs).

The book is divided into two equal sized sections. The first covers a small range of bioinformatics topics in some detail. These deal with (1) sequence alignment; (2) profile HMMs; (3) protein folding, and (4) phylogenetic reconstruction. The sections on alignment and phylogenetic reconstruction are thorough and deal with standard methods and their theory. The mathematics will be challenging to non-numerate readers but the topics that are covered are standard and well established. Similar treatments and topics, albeit with different emphases, are given by other textbooks it has to be said. The narrow range of topics will be fine for introductory university courses where it is better to cover the classic areas in detail. However, the small range does mean that there is no coverage of proteomics of any kind beyond sequence alignment or protein folding. The only machine learning method that is covered in detail is the HMM and there is little or no mention of SNPs, genomics, transcriptomics, RNA structure, databases or ontologies.

The second section is more mathematically rigorous and detailed and is designed for a more advanced undergraduate course in probability theory and how these are used in bioinformatics. This contains two general chapters on probability and statistics and two chapters on specific topics: significance of alignment scores and on substitution matrices.

Professor Des Higgins
Conway Institute
University College Dublin
Ireland
September 2005