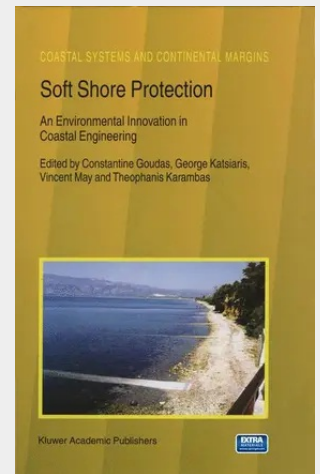


Hidden Markov Models for Bioinformatics

The purpose of this book is to give a thorough and systematic introduction to probabilistic modeling in bioinformatics. The book contains a mathematically strict and extensive presentation of the kind of probabilistic models that have turned out to be useful in genome analysis. Questions of parametric inference, selection between model families, and various architectures are treated. Several examples are given of known architectures (e.g., profile HMM) used in genome analysis. Audience: This book will be of interest to advanced undergraduate and graduate students with a fairly limited background in probability theory, but otherwise well trained in mathematics and already familiar with at least some of the techniques of algorithmic sequence analysis.

This text is based on a set of notes produced for courses given for graduate students in mathematics, computer science and biochemistry during the academic year 1998-1999 at the University of Turku in Turku and at the Royal Institute of Technology (KTH) in Stockholm. The course in Turku was organized by Professor Mats Gyllenberg's group and was also included within the postgraduate program ComBi, a Graduate School in Computational Biology, Bioinformatics, and Biometry, directed by Professor Esko Ukkonen at the University of Helsinki. The purpose of the courses was to give a thorough and systematic introduction to probabilistic modelling in bioinformatics for advanced undergraduate and graduate students who had a fairly limited background in probability theory, but were otherwise well trained in mathematics and were already familiar with at least some of the techniques of algorithmic sequence analysis. Portions of the material have also been lectured at shorter graduate courses and seminars both in Finland and in Sweden. The initial set of notes circulated also for a time outside those two countries via the World Wide Web. The intermediate course in probability theory and techniques of discrete mathematics held by the author at the University College of Södertörn (Huddinge, Sweden) during the academic year 1997-1998 has also influenced the presentation. The opportunity to give this course is hereby gratefully acknowledged.



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