Currently, this biological sequence analysis probabilistic models of proteins and nucleic acids, as one of the most working sellers here will no question be among the best options to review. You may not be perplexed to enjoy every ebook collections biological sequence analysis probabilistic models of proteins and nucleic acids that we will certainly offer. It is not vis–vis the costs. Its approximately what you dependence currently. This biological sequence analysis probabilistic models of proteins and nucleic acids, as one of the most working sellers here will no question be among the best options to review.

Biological Sequence Analysis - Richard Durbin - 1998-04-23
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.

Biological Sequence Analysis - Richard Durbin - 2005-02-01
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Problems and Solutions in Biological Sequence Analysis - Mark Borodovsky - 2006-09-04
This book is the first of its kind to provide a large collection of bioinformatics problems with accompanying solutions. Notably, the problem set includes all of the problems offered in Biological Sequence Analysis (BSA), by Durbin et al., widely adopted as a required text for bioinformatics courses at leading universities worldwide. Although many of the problems included in BSA as exercises for its readers have been repeatedly used for homework and tests, no detailed solutions for the problems were available. Bioinformatics instructors had therefore frequently expressed a need for fully worked solutions and a larger set of problems for use on courses. This book provides just that: following the same structure as BSA and significantly extending the set of workable problems, it will facilitate a better understanding of the contents of the chapters in BSA and will help its readers develop problem-solving skills that are vitally important for conducting successful research in the growing field of bioinformatics. All of the material has been class-tested by the authors at Georgia Tech, where the first ever M.Sc. degree program in Bioinformatics was held.

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Biological Sequence Analysis - 1998
Introduction to Computational Biology - Michael S. Waterman - 2018-05-02

Biological Sequence Analysis is in the midst of a era yielding many significant discoveries and promising many more. Unique to this era is the exponential growth in the size of information-packed databases. Inspired by a pressing need to analyze such data, Introduction to Computational Biology explores a new area of expertise that emerged from this fertile field - the combination of biological and information sciences. This introduction describes the mathematical structure of biological data, especially from sequences and chromosomes. After a brief survey of molecular biology, it studies restriction maps of DNA, rough landmark maps of the underlying sequences, and clones and clone maps. It examines problems associated with reading DNA sequences and comparing sequences to finding common patterns. The reader then considers that statistics of pattern counts in sequences, RNA secondary structure, and the inference of evolutionary history of related sequences. Introduction to Computational Biology exposes the reader to the fascinating structure of biological data and explains how to treat related combinatorial and statistical problems. Written to describe mathematical formulation and development, this book helps set the stage for even more, truly interdisciplinary work in biology.

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Algorithms on Strings, Trees and Sequences - Dan Gusfield - 1997-05-28

String algorithms are a traditional area of study in computer science. In recent years their importance has grown dramatically with the huge increase of electronically stored text and of molecular sequence data (DNA or protein sequences) produced by various genome projects. This 1997 book is a general text on computer algorithms for string processing. In addition to pure computer science, the book contains extensive discussions on biological problems that are cast as string problems, and on methods developed to solve them. It emphasises the fundamental ideas and techniques central to today's applications. New approaches to this complex material simplify methods that up to now have been for the specialist alone. With over 400 exercises to reinforce the material and develop additional topics, the book is suitable as a text for graduate or advanced undergraduate students in computer science, computational biology, or bio-informatics. Its discussion of current algorithms and techniques also makes it a reference for professionals.

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Advances in computers and biotechnology have had a profound impact on biomedical research, and as a result complex data sets can now be generated to address extremely complex biological questions. Correspondingly, advances in the statistical methods necessary to analyze such data are following closely behind the advances in data generation methods. The statistical methods required by bioinformatics present many new and difficult problems for the research community. This book provides an introduction to some of these new methods. The main statistical techniques covered include sequence analysis, BLAST, microarray analysis, gene finding, and the analysis of evolutionary processes. The main statistical techniques covered include sequence analysis, BLAST, microarray analysis, and on statistical inference, including a discussion of ANOVA, and discussions of the statistical theory of motifs and methods based on the hypergeometric distribution. Much material has been clarified and reorganized. The book is written so as to appeal to biologists and computer scientists who wish to know more about the statistical methods of the field, as well as to trained statisticians who wish to become involved with bioinformatics. The earlier chapters introduce the concepts of probability and statistics at an elementary level, but with an emphasis on material relevant to later chapters and often not covered in standard introductory texts. Later chapters should be immediately accessible to the trained statistician. Sufficient mathematical background consists of introductory courses in calculus and linear algebra. The basic biological concepts that are used are explained, or can be understood from the context, and standard mathematical concepts are summarized in an Appendix. Problems are provided at the end of each chapter allowing the reader to develop aspects of the theory outlined in the main text. Warren J. Ewens holds the Christopher H. Brown Distinguished Professorship at the University of Pennsylvania. He is the author of two books, Population Genetics and Mathematical Population Genetics. He is a senior editor of Annals of Human Genetics and has served on the editorial boards of Theoretical Population Biology, GENETICS, Proceedings of the Royal Society B and SIAM Journal in Mathematical Biology. He is a fellow of the Royal Society and the Australian Academy of Science. Gregory R. Grant is a senior bioinformatics researcher in the University of Pennsylvania Computational Biology and Informatics Laboratory. He obtained his Ph.D. in number theory from the University of Maryland in 1995 and his Masters in Computer Science from the University of Pennsylvania in 1999. Comments on the first edition: "This book would be an ideal text for a postgraduate course and is equally well suited to individual study. I would recommend the book highly." (Biometrics) "Ewens and Grant have given us a very welcome introduction to what is behind those very [graphical user] interfaces." (Naturewissenschafte) "The authors do an excellent job of presenting the essence of the material without getting bogged down in mathematical details." (Journal American Statistical Association) "The authors have restructured classical material to a great extent and the new organization of the different topics is one of the outstanding services of the book." (Metraka)


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Computational Genome Analysis - Richard C. Deonier - 2005-12-27

This book presents the foundations of key problems in computational molecular biology and bioinformatics. It focuses on computational and statistical principles applied to genomes, and introduces the mathematics and statistics that are crucial for understanding these applications. The book features a free download of the R software statistics package and the text provides great crossover material that is interesting and accessible to students in biology, mathematics, statistics and computer science. More than 100 illustrations and diagrams reinforce concepts and present key results from the primary literature. Exercises are given at the end of chapters.

An Introduction to Bioinformatics Algorithms - Neil C. Jones - 2004-08-06

An introductory text that emphasizes the underlying algorithmic ideas that are driving advances in bioinformatics. Accessible to students in both biology and computer science, it strikes a unique balance between rigorous mathematics and practical techniques, emphasizing the ideas underlying algorithms rather than offering a collection of apparently unrelated problems. The book introduces biological and algorithmic ideas together, linking issues in computer science to biology and thus capturing the interest of students in both subjects. It demonstrates that relatively few design techniques can be used to solve a large number of practical problems in biology, and presents this material intuitively. An Introduction to Bioinformatics Algorithms is one of the first books on bioinformatics that can be used by students at an undergraduate level. It includes a dual table of contents, algorithmic ideas and biological problems, discussions of biologically relevant algorithms, including a detailed problem formulation and one or more solutions for each; and brief biographical sketches of leading figures in the field. These interesting vignettes offer students a glimpse of the inspirations and motivations for real work in bioinformatics, making the concepts presented in the text more concrete and the techniques more approachable. PowerPoint presentations, practical bioinformatics problems, sample code, diagrams, demonstrations, and other materials can be found at the Author’s website.

Bioinformatics, second edition - Pierre Baldi - 2001-07-20

A guide to machine learning approaches and their application to the analysis of biological data. An unprecedented wealth of data is being generated by genome sequencing projects and other experimental efforts to determine the structure and function of biological molecules. The demands and opportunities for interpreting these data are...
High-throughput sequencing has revolutionised the field of biological sequence analysis. Its application has enabled researchers to address important biological questions, often for the first time. This book provides an integrated presentation of the fundamental algorithms and data structures that power modern sequence analysis workflows. The topics covered range from the foundations of biological sequence analysis (alignments and hidden Markov models), to classical index structures (k-mer indexes, suffix arrays and suffix trees), Burrows-Wheeler indexes, graph algorithms and a number of advanced omics applications. The chapters feature numerous examples, algorithm visualisations, exercises and problems, each chosen to reflect the steps of large-scale sequencing projects, including read alignment, variant calling, haplotyping, fragment assembly, alignment-free genome comparison, transcript prediction and analysis of metagenomic samples. Each biological problem is accompanied by precise formulations, providing graduate students and researchers in bioinformatics and computer science with a powerful toolkit for the emerging applications of high-throughput sequencing.

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Understanding Bioinformatics - Marketa J. Zvelebil - 2008
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BLAST - Ian Korf - 2003-07-29
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Bioinformatics and Functional Genomics - Jonathan Pevsner - 2005-03-04
Wiley is proud to announce the publication of the first ever broad-based textbook introduction to Bioinformatics and Functional Genomics by a trained biologist, experienced researcher, and award-winning instructor. In this new text, author Jonathan Pevsner, winner of the 2001 Johns Hopkins University “Teacher of the Year” award, explains problem-solving using bioinformatic approaches using real examples such as breast cancer, HIV-1, and retinal-binding protein throughout. His book includes 375 figures and over 170 tables. Each chapter includes: Problems, discussion of Pitfalls, Boxes explaining key techniques and math/stats principles, Summary, Recommended Reading list, and URLs for freely available software. The text is suitable for professionals and students at every level, including those with little to no background in computer science.

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Probabilistic Models for DNA Sequence Evolution - Rick Durrett - 2013-03-09
"What underlying forces are responsible for the observed patterns of variability, given a collection of DNA sequences?" In approaching this question a number of probability models are introduced and analyzed. Throughout the book, the theory is developed in close connection with data from more than 60 experimental studies that illustrate the use of these results.

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Practical Applications of Computational Biology and Bioinformatics, 12th International Conference - Florentino Fdez-Riverola - 2018-08-16
This book introduces the latest international research in the fields of bioinformatics and computational biology. It includes various studies in the area of machine learning in bioinformatics, systems biology, omics data analysis and mining, biomedical applications and sequences, which were selected by an international committee and
This book offers comprehensive coverage of all the core topics of bioinformatics, and includes practical examples completed using the MATLAB bioinformatics toolboxTM. It is primarily intended as a textbook for engineering and computer science students attending advanced undergraduate and graduate courses in bioinformatics and computational biology. The book develops bioinformatics concepts from the ground up, starting with an introductory chapter on molecular biology and genetics. This chapter will enable physical science students to fully understand and appreciate the ultimate goals of applying the principles of information technology to challenges in biological data management, sequence analysis, and systems biology. The first part of this book also includes a survey of existing biological databases, tools that have become essential in today’s biotechnology research. The second part of the book covers methodologies for retrieving biological information, including fundamental algorithms for sequence comparison, scoring, and determining evolutionary distance. The main focus of the third part is on modeling biological sequences and patterns as Markov chains. It presents key principles for analyzing and searching for sequences of significant motifs and biomarkers. The last part of the book includes practical applications—both elementary tutorials as well as more advanced applications in case studies.

Probabilistic Modeling in Bioinformatics and Medical Informatics - Dirk Husmeier - 2006-03-30

Probabilistic Modeling in Bioinformatics and Medical Informatics has been written for researchers and students in statistics, machine learning, and the biological sciences. The first part of this book provides a self-contained introduction to the methodology of Bayesian networks. The following parts demonstrate how these methods are applied in bioinformatics and medical informatics. All three fields—the methodology of probabilistic modeling, bioinformatics, and medical informatics—are evolving very quickly. The text should therefore be seen as an introduction, offering both elementary tutorials as well as more advanced applications and case studies.

Computational Molecular Biology - S. Istrail - 2003-04-16

This volume contains papers demonstrating the variety and richness of computational problems motivated by molecular biology. The application areas within biology that give rise to the problems studied in these papers include solid molecular modeling, sequence comparison, phylogeny, evolution, mapping, DNA chips, protein folding and 2D gel technology. The mathematical techniques used are algorithmics, combinatorics, optimization, probability, graph theory, complexity and applied mathematics. This is the fourth volume in the Discrete Applied Mathematics series on computational molecular biology, which is devoted to combinatorial and algorithmic techniques in computational molecular biology. This series publishes novel research results on the mathematical and algorithmic foundations of the inherently discrete aspects of computational biology. Key features: protein folding, phylogenetic inference, 2-dimensional gel analysis, graphical models for sequencing by hybridisation, dynamic visualization of molecular surfaces, problems and algorithms in sequence alignment. This book is a reprint of Discrete Applied Mathematics Volume 127, Number 1.

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Bioinformatics Algorithms: Design and Implementation in Python provides a comprehensive book on many of the most important bioinformatics problems, putting forward the best algorithms and showing how to implement them. The book focuses on the use of the Python programming language and its algorithms, which is quickly becoming the most popular language in the bioinformatics field. Readers will find the tools they need to improve their knowledge and skills with regard to algorithm development and implementation, and will also uncover prototypes of bioinformatics applications that demonstrate the main principles underlying real-world applications. Presents an ideal text for bioinformatics students with little to no knowledge of computer programming. Based on over 12 years of pedagogical materials used by the authors in their own classrooms Features a companion website with downloadable codes and runnable examples (such as using Jupyter Notebooks) and exercises relating to the book.

Bioinformatics Technologies - Yi-Ping Phoebe Chen - 2005-01-18

Algorithms in Bioinformatics - Raffaele Giancarlo - 2007-08-22
The refereed proceedings from the 7th International Workshop on Algorithms in Bioinformatics are provided in this volume. Papers address current issues in algorithms in bioinformatics, ranging from mathematical tools to experimental studies of approximation algorithms to significant computational analyses. Biological problems examined include genetic mapping, sequence alignment and analysis, phylogeny, comparative genomics, and protein structure.

Essential Bioinformatics - Jin Xiong - 2006-03-13
Essential Bioinformatics is a concise yet comprehensive textbook of bioinformatics, which provides a broad introduction to the entire field. Written specifically for a life science audience, the basics of bioinformatics are explained, followed by discussions of the state-of-the-art computational tools available to solve biological research problems. All key areas of bioinformatics are covered including biological databases, sequence alignment, genes and promoter prediction, molecular phylogenetics, structural bioinformatics, genomics and proteomics. The book emphasizes how computational methods work and compares the strengths and weaknesses of different methods. This balanced yet easily accessible text will be invaluable to students who do not have sophisticated computational backgrounds. Technical details of computational algorithms are explained with a minimum use of mathematical formulae; graphical illustrations are used in their place to aid understanding. The effective synthesis of existing literature as well as in-depth and up-to-date coverage of all key topics in bioinformatics make this an ideal textbook for all bioinformatics courses taken by life science students and for researchers wishing to develop their knowledge of bioinformatics to facilitate their own research.

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Bioinformatics Algorithms - Philip Compeau - 1986-06

Bioinformatics Algorithms: an Active Learning Approach is one of the first textbooks to emerge from the recent Massive Online Open Course (MOOC) revolution. A light-hearted and analogy-filled companion to the authors' acclaimed online course (http://coursera.org/course/bioinformatics), this book presents students with a dynamic approach to learning bioinformatics. It strikes a unique balance between practical challenges in modern biology and fundamental algorithmic ideas, thus capturing the interest of students of biology and computer science alike. Each chapter begins with a central biological question, such as "Are There Fragile Regions in the Human Genome?" or "Which DNA Patterns Play the Role of Molecular Clocks?" and then steadily develops the algorithmic sophistication required to answer this question. Hundreds of exercises are incorporated directly into the text as soon as they are needed; readers can test their knowledge through automated coding challenges on Rosalind (http://rosalind.info), an online platform for learning bioinformatics. The textbook website (http://bioinformaticsalgorithms.org) directs readers toward additional educational materials, including video lectures and PowerPoint slides.


This book looks at the mathematical foundations of the models currently in use. All existing books on bioinformatics are software-oriented and they concentrate on computer implementations of mathematical models of biology. This book is unique in the sense that it looks at the mathematical foundations of the models, which are crucial for correct interpretation of the outputs of the models.


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Parallel Computational Fluid Dynamics - Kenli Li - 2014-03-08

This book constitutes the refereed proceedings of the 25th International Conference on Parallel Computational Fluid Dynamics, ParCFD 2013, held in Changsha, China, in May 2013. The 35 revised full papers presented were carefully reviewed and selected from more than 240 submissions. The papers address issues such as parallel algorithms, developments in software tools and environments, unstructured adaptive mesh applications, industrial applications, atmospheric and oceanic global simulation, interdisciplinary applications and evaluation of computer architectures and software environments.
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