Biological Sequence Analysis Using The Seqan C Library Chapman Hallcrc Mathematical And Computational Biology

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HUNTER WISE

Invitation to Protein Sequence Analysis Through Probability and Information Humana
An Easy-to-Use Research Tool for Algorithm Testing and Development Before the SeqAn project, there was clearly a lack of available implementations in sequence analysis, even for standard tasks. Implementations of needed algorithmic components were either unavailable or hard to access in third-party monolithic software products. Addressing these concerns, the developers of SeqAn created a comprehensive, easy-to-use, open source C++ library of efficient algorithms and data structures for the analysis of biological sequences. Written by the founders of this project, Biological Sequence Analysis Using the SeqAn C++ Library covers the SeqAn library, its documentation, and the supporting infrastructure. The first part of the book describes the general library design. It introduces biological sequence analysis problems, discusses the benefit of using software libraries, summarizes the design principles and goals of SeqAn, details the main programming techniques used in SeqAn, and demonstrates the application of these techniques in various examples. Focusing on the components provided by SeqAn, the second part explores basic functionality, sequence data structures, alignments, pattern and motif searching, string indices, and graphs. The last part illustrates applications of SeqAn to genome alignment, consensus sequence in assembly projects, suffix array construction, and more. This handy book describes a user-friendly library of efficient data types and algorithms for sequence analysis in computational biology. SeqAn enables not only the implementation of new algorithms, but also the sound analysis and comparison of existing algorithms. Visit SeqAn for more information.
Bioinformatics For Dummies Springer Science & Business Media
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.
Sequence Analysis in Molecular Biology Springer Science & Business Media
Master's Thesis from the year 2014 in the subject Computer Science - Bioinformatics, grade: N, language: English, abstract: The data from next generation sequencing technologies has led to an explosion in genome sequence data available in public databases. This data provides unique opportunities to study the molecular mechanisms of gene evolution: how new genes and proteins originate and how they diversify. A major challenge is retracing origin of extant genes or proteins, by searching existing databases for related sequences and identifying evolutionary similarities. Therefore, enhanced and faster search algorithms are being developed, e.g. on accelerators such as GPU, in order to cope with the huge size of today's DNA or protein sequence databases. Gene-Tracer is a tool was developed to localize the common sub-sequences between two ancestors and its offspring. Besides, compute percentages of ancestors' contributions in offspring. Gene-Tracer was developed to find the origin of unknown shuffling/offspring sequence. A database is scanned and the similarity between offspring sequence and each one in the database is computed using pairwise local sequence alignment algorithm. Based on similarity score, 100 sequences that have the highest score is re-aligned with shuffling sequence to determine length of common sub-sequences between them using local alignment algorithm. The two sequences that have longest sub-sequences with shuffling are the nearest origin to offspring. Swiss-port database contains around 400,000 proteins is used in the test. The execution time around hours. So, GPU is to accelerate the tool. Speedup is 84x using single-GPU Tesla C2075 versus Intel(c) Core i3 multiprocessor. Finally, the main contribution of work is developing fast tool that re-trace origins of unknown gene/protein sequences."
Comparative Gene Finding Oxford University Press
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, by Durbin et al. (Cambridge, 1998), widely adopted as a required text for bioinformatics courses at leading universities worldwide. Although many of the problems included in Biological Sequence Analysis 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 Biological Sequence Analysis 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 MSc degree program in Bioinformatics was held.
Analysis of Biological Data Springer Science & Business Media
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 expanding rapidly. Bioinformatics is the development and application of computer methods for management, analysis, interpretation, and prediction, as well as for the design of experiments. Machine learning approaches (e.g., neural networks, hidden Markov models, and belief networks) are ideally suited for areas where there is a lot of data but little theory, which is the situation in molecular biology. The goal in machine learning is to extract useful information from a body of data by building good probabilistic models—and to automate the process as much as possible. In this book Pierre Baldi and Søren Brunak present the key machine learning approaches and apply them to the computational problems encountered in the analysis of biological data. The book is aimed both at biologists and biochemists who need to understand new data-driven algorithms and at those with a primary background in physics, mathematics, statistics, or computer science who need to know more about applications in molecular biology. This new second edition contains expanded coverage of probabilistic graphical models and of the applications of neural networks, as well as a new chapter on microarrays and gene expression. The entire text has been extensively revised.
Mathematical Approaches to Polymer Sequence Analysis and Related Problems John Wiley & Sons
Comparative genomics is a new and emerging ?eld, and with the explosion of ava- able biological sequences the requests for faster, more ef?cient and more robust algorithms to analyze all this data are immense. This book is meant to serve as a self-contained instruction of the state-of-the-art of computational gene ?nding in general and of comparative approaches in particular. It is meant as an overview of the various methods that have been applied in the ?eld, and a quick introduction into how computational gene ?nders are built in general. A beginner to the ?eld could use this book as a guide through to the main points to think about when constructing a gene ?nder, and the main

algorithms that are in use. On the other hand, the more experienced gene ?nder should be able to use this book as a reference to different methods and to the main components incorporated in these methods. I have focused on the main uses of the covered methods and avoided much of the technical details and general extensions of the models. In exchange I have tried to supply references to more detailed accounts of the different research areas touched upon. The book, however, makes no claim on being comprehensive.

Sequence Analysis Primer Springer Science & Business Media

Geneticists wish to pairwise align protein sequences in order to determine if the two sequences have a similar function. This thesis explains the use of hidden Markov models (HMM's) in the pairwise alignment of protein sequences. The pairwise alignment HMM allows geneticists to align and assign a likelihood that the two sequences being compared have similar biological functions. In the thesis, an HMM is defined as a model for pairwise alignment. A method for using this HMM to score alignments is described, and a method for testing these scores for statistical significance is explained. We elaborate on the role that extreme value theory plays in this testing. Keywords; Hidden Markov Model, Pairwise Alignment, Biological Sequence Analysis, Protein Function, Extreme Value Theory

Discriminative Structured Models for Biological Sequence Analysis World Scientific

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 CRC Press

The recent accumulation of information from genomes, including their sequences, has resultednotonlyinnewattemptstoansweroldquestionsandsolvelongstandingissues inbiology,butalsointheformulationofnovelhypothesesthatarisepreciselyfromthis wealth of data. The storage, processing, description, transmission, connection, and analysis of these data has prompted bioinformatics to become one the most relevant applied sciences for this new century, walking hand-in-hand with modern molecular biology and clearly impacting areas like biotechnology and biomedicine. Bioinformatics skills have now become essential for many scientists working with DNA sequences. With this idea in mind, this book aims to provide practical guidance andtroubleshootingadviceforthecomputationalanalysisofDNAsequences,covering a range of issues and methods that unveil the multitude of applications and relevance that Bioinformatics has today. The analysis of protein sequences has been purposely excludedtogainfocus.Individualbookchaptersareorientedtowardthedescriptionof theuseofspecificbioinformaticstools,accompaniedbypracticalexamples,adiscussion on the interpretation of results, and specific comments on strengths and limitations of the methods and tools. In a sense, chapters could be seen as enriched task-oriented manuals that will direct the reader in completing specific bioinformatics analyses. The target audience for this book is biochemists, and molecular and evolutionary biologiststhatwanttolearnhowtoanalyzeDNAsequencesinasimplebutmeaningful fashion. Readers do not need a special background in statistics, mathematics, or computer science, just a basic knowledge of molecular biology and genetics. All the tools described in the book are free and all of them can be downloaded or accessed throughtheweb.Mostchapterscouldbeusedforpracticaladvancedundergraduateor graduate-level courses in bioinformatics and molecular evolution.

Hidden Markov Models in Biological Sequence Analysis Biological Sequence Analysis

Sequence Analysis in Molecular Biology ...

Genome-Scale Algorithm Design John Wiley & Sons

Computerized sequence analysis is an integral part of biotechnological research, yet many biologists have received no formal training in this important technology. Sequence Analysis Primer offers the beginner the necessary background to enter this vital field and helps more seasoned researchers to fine-tune their approach. It covers basic data manipulation such as homology searches, stem-loop identification, and protein secondary structure prediction, and is compatible with most sequence analysis programs. A detailed example giving steps for characterizing a new gene sequence provides users with hands-on experience when combined with their current software. The book will be invaluable to researchers and students in molecular biology, genetics, biochemistry, microbiology, and biotechnology.

Biological Sequence Analysis Springer Science & Business Media

This second edition provides updated and expanded chapters covering a broad sampling of useful and current methods in the rapidly developing and expanding field of bioinformatics. Bioinformatics, Volume I: Data, Sequence Analysis, and Evolution, Second Edition is comprised of three sections: Data and Databases, Sequence Analysis, and Phylogenetics and Evolution. The first section details bioinformatics methodologies in the generation of sequence and structural data and its organization into conceptual categories, and databases to facilitate further analyses. The Sequence Analysis section describes the fundamental methodologies for processing the sequences of biological molecules: techniques that are used in almost every pipeline of bioinformatics analysis, particularly in the preliminary stages of such pipelines. Last but not least, the phylogenetics and evolution section deals with methodologies that compare biological sequences for the purpose of understanding how they evolved. As a volume in the highly successful Methods in Molecular Biology series, chapters feature the kind of detail and expert implementation advice to ensure positive results. Comprehensive and practical, Bioinformatics, Volume I: Data, Sequence Analysis, and Evolution, Second Edition is an essential resource for graduate students, early career researchers, and others who are in the process of integrating new bioinformatics methods into their research.

Fundamentals of Bioinformatics and Computational Biology John Wiley & Sons

The Ninth International Conference on Methods in Protein Sequence Analysis was held for the first time in Asia from September 20 to September 24, 1992 in Otsu (a city near Kyoto), Japan. Approximately 400 delegates attended the meeting. Forty papers were presented orally and 147 poster presentations were discussed. Academic sessions were held from early in the morning until late in the evening. We are confident that the Conference was successful in providing up-to-date information about methods in protein sequence analysis to all participants. Moreover, with the knowledge and understanding of the present standard of various methods of analysis that are being used and will be used, we were able to clarify areas that need to be evaluated, to be improved and be explored further. Major topics in the Conference mostly covered areas in the methodology of protein sequence analysis, such as: micropreparation and microsequencing of proteins, mass spectrometry, post-translational modification, prediction and database analysis, and analysis of protein structures of special interests. The evolution of genetic engineering in molecular biology has greatly accelerated the accumulation of knowledge on the amino acid sequence of novel proteins regardless of whether they are expressed or not expressed in living organisms. In the early stage of accumulation of structural information, the amino acid sequence itself is worthy of notice.

Bioinformatics, second edition Humana Press

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. This book gives an up-to-date account with a Bayesian slant.

Biological Sequence Analysis Cambridge University Press

Bioinformatics, the application of computers in biological sciences and especially analysis of biological sequence data, is becoming an essential tool in molecular biology as genome projects generate vast quantities of data. This text provides an introduction to the subject for undergraduates (final year), focussing on two key areas, genojmics and protein sequence analysis. It provides an overview of primary, composite and secondary databases, and gives a brief introduction to the Internet and the World Wide Web.

Biological Sequence Analysis Cambridge University Press

Bioinformatics, a field devoted to the interpretation and analysis of biological data using computational techniques, has evolved tremendously in recent years due to the explosive growth of biological information generated by the scientific community. Soft computing is a consortium of methodologies that work synergistically and provides, in one form or another, flexible information processing capabilities for handling real-life ambiguous situations. Several research articles dealing with the application of soft computing tools to bioinformatics have been published in the recent past; however, they are scattered in different journals, conference proceedings and technical reports, thus causing inconvenience to readers, students and researchers. This book, unique in its nature, is aimed at providing a treatise in a unified framework, with both theoretical and experimental results, describing the basic principles of soft computing and demonstrating the various ways in which they can be used for analyzing biological data in an efficient manner. Interesting research articles from eminent scientists around the world are brought together in a systematic way such that the reader will be able to understand the issues and challenges in this domain, the existing ways of tackling them, recent trends, and future directions. This book is the first of its kind to bring together two important research areas, soft computing and bioinformatics, in order to demonstrate how the tools and techniques in the former can be used for efficiently solving several problems in the latter. Sample Chapter(s). Chapter 1: Bioinformatics: Mining the Massive Data from High Throughput Genomics Experiments (160 KB). Contents: Overview: Bioinformatics: Mining the Massive Data from High Throughput Genomics Experiments (H Tang & S Kim); An Introduction to Soft Computing (A Konar & S Das); Biological Sequence and Structure Analysis: Reconstructing Phylogenies with Memetic Algorithms and Branch-and-Bound (J E Gallardo et al.); Classification of RNA Sequences with Support Vector Machines (J T L Wang & X Wu); Beyond String Algorithms: Protein Sequence Analysis Using Wavelet Transforms (A Krishnan & K-B Li); Filtering Protein Surface Motifs Using Negative Instances of Active Sites Candidates (N L Shrestha & T Ohkawa); Distill: A Machine Learning Approach to Ab Initio Protein Structure Prediction (G Pollastri et al.); In Silico Design of Ligands Using Properties of Target Active Sites (S Bandyopadhyay et al.); Gene Expression and Microarray Data Analysis: Inferring Regulations in a Genomic Network from Gene Expression Profiles (N Noman & H Iba); A Reliable Classification of Gene Clusters for Cancer Samples Using a Hybrid Multi-Objective Evolutionary Procedure (K Deb et al.); Feature Selection for Cancer Classification Using Ant Colony Optimization and Support Vector Machines (A Gupta et al.); Sophisticated Methods for Cancer Classification Using Microarray Data (S-B Cho & H-S Park); Multiobjective Evolutionary Approach to Fuzzy Clustering of Microarray Data (A Mukhopadhyay et al.). Readership: Graduate students and researchers in computer science, bioinformatics, computational and molecular biology, artificial intelligence, data mining, machine learning, electrical engineering, system science; researchers in pharmaceutical industries.

Bioinformatics MIT Press

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.

Bioinformatics for DNA Sequence Analysis "O'Reilly Media, Inc."

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 Frontiers Media SA

This work pulls together all of the vital information about the most commonly used databases, analytical tools, and tables used in sequence analysis.

BLAST Prentice Hall

"In this book, Andy Baxevanis and Francis Ouellette . . . haveundertaken the difficult task of organizing the knowledge in thisfield in a logical progression and presenting it in a digestibleform. And they have done an excellent job. This fine text will makea major impact on biological research and, in turn, on progress inbiomedicine. We are all in their debt." —Eric Lander from the Foreword Reviews from the First Edition "...provides a broad overview of the basic tools for sequenceanalysis ... For biologists approaching this subject for the firsttime, it will be a very useful handbook to keep on the shelf afterthe first reading, close to the computer." —Nature Structural Biology "...should be in the personal library of any biologist who usesthe Internet for the analysis of DNA and protein sequencedata." —Science "...a wonderful primer designed to navigate the novice throughthe intricacies of in scripto analysis ... The accomplished genesearcher will also find this book a useful addition to theirlibrary ... an excellent reference to the principles ofbioinformatics." —Trends in Biochemical Sciences This new edition of the highly successful Bioinformatics:A Practical Guide to the Analysis of Genes and Proteinsprovides a sound foundation of basic concepts, with

practicaldiscussions and comparisons of both computational tools anddatabases relevant to biological research. Equipping biologists with the modern tools necessary to solvepractical problems in sequence data analysis, the Second Editioncovers the broad spectrum of topics in bioinformatics, ranging fromInternet concepts to predictive algorithms used on sequence,structure, and expression data. With chapters written by experts inthe field, this up-to-date reference thoroughly covers vitalconcepts and is appropriate for both the novice and the experiencedpractitioner. Written in clear, simple language, the book isaccessible to users without an advanced mathematical or computerscience background. This new edition includes: All new end-of-chapter Web resources, bibliographies, andproblem sets Accompanying Web site containing the answers to the problems,as well as links to relevant Web resources New coverage of comparative genomics, large-scale genomeanalysis, sequence assembly, and expressed sequence tags A glossary of commonly used terms in bioinformatics andgenomics Bioinformatics: A Practical Guide to the Analysis of Genesand Proteins, Second Edition is essential reading forresearchers, instructors, and students of all levels in molecularbiology and bioinformatics, as well as for investigators involvedin genomics, positional cloning, clinical research, andcomputational biology.

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