



Nucleic Acid Sequence Analysis

Michael Gribskov, John Devereux



Nucleic Acid Sequence Analysis:

Computer Analysis of Sequence Data, Part I Annette M. Griffin, Hugh G. Griffin, 2008-02-02 DNA sequencing has become increasingly efficient over the years resulting in an enormous increase in the amount of data generated. In recent years the focus of sequencing has shifted from being the endpoint of a project to being a starting point. This is especially true for such major initiatives as the human genome project where vast tracts of DNA of unknown function are sequenced. This sheer volume of available data makes advanced computer methods essential to analysis and a familiarity with computers and sequence analysis software a vital requirement for the researcher involved with DNA sequencing. Even for nonsequencers a familiarity with sequence analysis software can be important. For instance, gene sequences already present in the databases can be extremely useful in the design of cloning and genetic manipulation experiments. This two-part work on Analysis of Data is designed to be a practical aid to the researcher who uses computers for the acquisition, storage, or analysis of nucleic acid and/or protein sequences. Each chapter is written such that a competent scientist with basic computer literacy can carry out the procedure successfully at the first attempt by simply following the detailed practical instructions that have been described by the author. A Notes section, which is included at the end of each chapter, provides advice on overcoming the common problems and pitfalls sometimes encountered by users of the sequence analysis software. Software packages for both the mainframe and personal computers are described. DNA and Protein Sequence Analysis Martin J. Bishop, Christopher J. Rawlings, 1997 Sequence data, either lists of nucleotides or of amino acids, are now easily gathered using automated equipment; the real effort is involved in interpreting the data to produce predictions of protein structure or function. With the advent of worldwide computer networks, a plethora of software is now available for sequence analysis. This book describes the techniques for computer analysis of sequence data with the emphasis on general issues rather than specific algorithms. Unlike many books on these topics which focus on the how-to aspects of software packages, this one places more emphasis on the science behind the packages and on interpretation of the results. Computer Analysis of Sequence Data Annette M. Griffin, Hugh G. Griffin, 1994-02-08 DNA sequencing has become increasingly efficient over the years, resulting in an enormous increase in the amount of data generated. In recent years the focus of sequencing has shifted from being the endpoint of a project to being a starting point. This is especially true for such major initiatives as the human genome project where vast tracts of DNA of unknown function are sequenced. This sheer volume of available data makes advanced computer methods essential to analysis and a familiarity with computers and sequence analysis software a vital requirement for the researcher involved with DNA sequencing. Even for nonsequencers a familiarity with sequence analysis software can be important. For instance, gene sequences already present in the databases can be extremely useful in the design of cloning and genetic manipulation experiments. This two-part work on Computer Analysis of Sequence Data is designed to be a practical aid to the researcher who uses computers for the acquisition, storage, or analysis of nucleic acid and/or protein sequences.

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Nucleic Acid and Protein Sequence Analysis Martin J. Bishop, Christopher J. Rawlings, 1987

Sequence Analysis in Molecular Biology Gunnar Von Heijne, 2012-12-02

Sequence Analysis in Molecular Biology Treasure Trove or Trivial Pursuit presents the methods for sequence analysis of DNA and proteins. This book contains eight chapters that consider the sequence analysis either directly on a microcomputer or using one of the main sequence programs/data banks. This book starts with a description of the main nucleic acid and protein sequence data banks followed by a short section on the housekeeping aids that the computer can provide during a sequencing project. Chapters 4 and 5 deal with nucleic acid and protein sequence analysis. Chapter 6 treats algorithms for homology searching and sequence alignments. Chapter 7 presents some selected examples of how computer modeling can help decide whether an observed sequence pattern is significant or not and how computer simulation is sometimes used to get a feeling for the behavior of intrinsically complex sequence dependent processes. Chapter 8 contains some comments on the role of theoretical sequence analysis in molecular biology. This book is directed toward molecular biologists.

Sequence Analysis Primer Michael Gribskov, John Devereux, 1993-09-23

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.

Computer Analysis of Sequence Data Annette M. Griffin, Hugh G. Griffin, 1994-02-23

These comprehensive up to date handbooks are designed for those scientists engaged in the computer analysis of sequence data who want hands on help in using the most important commercial software available but simply do not have the time to become computer experts. The expert authors guide you through the programs with easy to follow step by step instructions. The topics covered include translations of sequences, sequence alignment, phylogenetic trees, analysis of RNA secondary structure, database searching, submission of data to EMBL, GenBank, DDBJ, etc., maintaining sequence projects and using patterns to analyze protein sequences. Many chapters have been written by world class authorities in the field among them R. Staden, M. Gribskov, D. Higgins, W. Pearson, M. Zuker and G. Barton. Each volume shares five essential chapters concerning the analysis of sequence data: the FASTA program, converting between sequence formats, obtaining software via INTERNET and

the submission of nucleotide sequence data Part I covers GCG MicroGenie PC GENE and FASTA programs Part II covers Staden and Staden Plus DNA Strider FASTA and MacVector programs

Nucleic Acid Sequence Analysis Stanley Mandel, 1972 Choice of a method The overlap method Stepwise enzymatic procedures Stepwise chemical degradation End label methods Sequence analysis Physical methods Isolation of purified nucleic acid Basic sequence analysis procedures Summary of nucleic acid sequences and structure index

Computer Analysis of Sequence Data Annette M. Griffin, Hugh G. Griffin, 1994-02-08 These comprehensive up to date handbooks are designed for those scientists engaged in the computer analysis of sequence data who want hands on help in using the most important commercial software available but simply do not have the time to become computer experts The expert authors guide you through the programs with easy to follow step by step instructions The topics covered include translations of sequences sequence alignment phylogenetic trees analysis of RNA secondary structure database searching submission of data to EMBL GenBank DDBJ etc maintaining sequence projects and using patterns to analyze protein sequences Many chapters have been written by world class authorities in the field among them R Staden M Gribskov D Higgins W Pearson M Zuker and G Barton Each volume shares five essential chapters concerning the analysis of sequence data the FASTA program converting between sequence formats obtaining software via INTERNET and the submission of nucleotide sequence data Part I covers GCG MicroGenie PC GENE and FASTA programs Part II covers Staden and Staden Plus DNA Strider FASTA and MacVector programs

Methods in Protein Sequence Analysis Marshall Elzinga, 2012-12-06 Methods in Protein Sequence Analysis contains an intensely practical account of all the new methodology available to scientists carrying out protein and peptide sequencing studies Many of the striking advances in fields as diverse as immunology cell motility and neurochemistry have in fact been fueled by our ever more powerful ability to determine the sequences and structures of key proteins and peptides It is our hope that the rich array of techniques and methods for sequencing proteins discussed in this volume methods that generate much of the information crucial to progress in modern biology will now become accessible to all who can benefit from them The papers of the present volume constitute the Proceedings of the IVth International Conference on Methods in Protein Sequence Analysis which was held at Brookhaven National Laboratory Upton NY September 21-25 1981 It was the most recent in a series of biennial conferences the previous one having been held in Heidelberg GFR in 1979 The series was originated by Richard Laursen and initially dealt with one aspect of the field solid phase sequencing The scope of the meeting was very broad and among the many aspects of protein sequencing discussed were instrumentation strategy chemicals mass spectrometry cleavage of proteins and separation of peptides and solid liquid manual and even gas phase sequencing

A Novel Method of Nucleic Acid Sequence Analysis Uwe Maskos, 1991

Bioinformatics David W. Mount, 2004 As more species genomes are sequenced computational analysis of these data has become increasingly important The second entirely updated edition of this widely praised textbook provides a comprehensive and critical examination of the computational methods needed for

analyzing DNA RNA and protein data as well as genomes The book has been rewritten to make it more accessible to a wider audience including advanced undergraduate and graduate students New features include chapter guides and explanatory information panels and glossary terms New chapters in this second edition cover statistical analysis of sequence alignments computer programming for bioinformatics and data management and mining Practically oriented problems at the ends of chapters enhance the value of the book as a teaching resource The book also serves as an essential reference for professionals in molecular biology pharmaceutical and genome laboratories

Biological Sequence Analysis Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison, 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

Automated DNA Sequencing and Analysis Mark D. Adams, Chris Fields, J. Craig Venter, 1994-06-29 A timely book for DNA researchers Automated DNA Sequencing and Analysis reviews and assesses the state of the art of automated DNA sequence analysis from the construction of clone libraries to the development of laboratory and community databases It presents the methodologies and strategies of automated DNA sequence analysis in a way that allows them to be compared and contrasted By taking a broad view of the process of automated sequence analysis the present volume bridges the gap between the protocols supplied with instrument and reaction kits and the finalized data presented in the research literature It will be an invaluable aid to both small laboratories that are interested in taking maximum advantage of automated sequence resources and to groups pursuing large scale cDNA and genomic sequencing projects The field of automation in DNA sequencing and analysis is rapidly moving this book fulfils those needs reviews the history of the art and provides pointers to future development

Computational Molecular Biology Arthur M. Lesk, 1988 An overview of the field of computing with protein and nucleic acid sequences aimed at investigators determining sequences those who analyze them to identify unknown proteins and interpret their function and those interested in the three dimensional structures of biological molecules

[Analysis of Amino Acid Sequences](#), 2000-05-23 Amino acid sequence analysis is useful for the study of problems ranging from modifications of single molecules to complex networks and interactions of species Many available amino acid sequences are providing the basis for various studies at the proteome level The dynamics of protein expression and the simulation of complex biological systems in which proteins interact with certain kinetics and in their respective compartments are just about to be tackled

Amino acid sequences will be crucial reference points for such studies Mass spectrometric analysis of proteins Protein sequence databases Amino acid substitution matrices Amino acid based phylogeny and alignment Individual variation in protein coding sequences of the human genome Identifying nature's protein Lego set **Bioinformatics** Andreas D. Baxevanis, B. F. Francis Ouellette, 1998 A reference that should be in the personal library of any biologist who uses the Internet for the analysis of DNA and protein sequence data Science **DNA Sequencing Protocols** Annette M. Griffin, Hugh G. Griffin, 2008-02-02 The purpose of DNA Sequencing Protocols is to provide detailed practical procedures for the widest range of DNA sequencing methods and we believe that all the vanguard techniques now being applied in this fast evolving field are comprehensively covered Sequencing technology has advanced at a phenomenal rate since the original methods were first described in the late 1970s and there is now a huge variety of strategies and methods that can be employed to determine the sequence of any DNA of interest More recently a large number of new and innovative sequencing techniques have been developed including the use of such novel polymerases as Tag polymerase and Sequenase the harnessing of PCR technology for linear amplification cycle sequencing and the advent of automated DNA sequencers DNA sequencing is surely one of the most important techniques in the molecular biology laboratory Sequence analysis is providing an increasingly useful approach to the characterization of biological systems and major multinational projects are already underway to map and sequence the entire genome of organisms such as *Escherichia coli* *Saccharomyces cerevisiae* *Caenorhabditis elegans* and *Homo sapiens* Most scientists recognize the importance of DNA sequence data and perceive DNA sequencing as a valuable and indispensable aspect of their work Recent technological advances especially in the area of automated sequencing have removed much of the drudgery that was formerly associated with the technique whereas innovative computer software has greatly simplified the analysis and manipulation of sequence data Image Processing in Nucleic Acid Sequence Analysis John Kenneth Elder, 1993 *Permuted Medical Subject Headings* National Library of Medicine (U.S.), 1994

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