



Nucleic Acid and Protein Sequence Analysis, a Practical Approach

Bishop, M. J.

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Nucleic Acid And Protein Sequence Analysis

**Richard Durbin, Sean R. Eddy, Anders
Krogh, Graeme Mitchison**



Nucleic Acid And Protein Sequence Analysis:

DNA and Protein Sequence Analysis Martin J. Bishop, Christopher J. Rawlings, 1997 DNA and Protein Sequence Analysis A Practical Approach is an essential manual for all researchers in molecular biology and a valuable guide for advanced undergraduates It will also be indispensable to computer scientists interested in bioinformatics

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

Biological Sequence Analysis Richard Durbin, 1998-04-23 Presents up to date computer methods for analysing DNA RNA and protein sequences

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 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

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

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

Suggested Readings in Nucleic Acid and Protein Sequence

Analysis Pittsburgh Supercomputing Center, University of Texas System. Center for High Performance Computing, 1970

Bioinformatics: From Nucleic Acids and Proteins to Cell Metabolism Dietmar Schomburg, Uta Lessel, 2008-09-26

Bioinformatics in this context the application of computer science to biological problems has become an indispensable part of any research in the biosciences. Rapid developments in gene sequencing, structure determination as well as rational protein engineering and design have made it necessary for biologists, chemists and computer scientists to channel their expertise into large scale collaborative projects. This GBF Monograph gives a general overview of the latest versatile activities in bioinformatics. Biological Data Bases, DNA and RNA, Protein Sequences and Structures, From Molecules to Cell Metabolism. The articles have been selected from contributions to a conference on Bioinformatics Computer Application in the Biosciences held in October 1995 in Braunschweig at the German National Research Center for Biotechnology.

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. 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, FRG, 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.

Methods in Protein Sequence Analysis Brigitte Wittmann-Liebold, 2012-12-06. Methods in Protein Sequence Analysis 1988 contains selected contributions on modern protein analytical techniques as presented by speakers at the Seventh International Conference on Methods in Protein Sequence Analysis held from July 3rd to July 8th, 1988 in Berlin. The book contains information on new methodologies for sensitive amino acid analysis, N and C terminal sequence analysis, and protein and peptide purification. In addition, recent mass spectrometric approaches are described as an alternative technique to the common stepwise degradative sequence analysis of polypeptides by the Edman method. The book presents new possibilities

in the design of sequencers and sophisticated equipment for the structural analysis of peptides and proteins It describes practical approaches for the investigation of protein domains and protein complexes and contains review chapters on the crystallization of cell organelles as well as on recent theoretical aspects of protein folding mechanisms The nature of protein folding is not yet understood but further advances in this area would greatly enhance our present knowledge of protein structure and function Further the book gives examples of the application of gene technology to protein characterization and to the design of new proteins This enables new studies on the structure and function of proteins to be made and opens up efficient approaches to the design of drugs

An Evaluation of Nucleic Acid and Protein Sequence Analysis Software Anne Soilleux,1988 **Molecular Databases for Protein Sequences and Structure Studies** John A.A. Sillince,Maria Sillince,2012-12-06 The amount of molecular information is too vast to be acquired without the use of computer bases systems The authors introduce students entering research in molecular biology and related fields into the efficient use of the numerous databases available They show the broad scientific context of these databases and their latest developments They also put the biological chemical and computational aspects of structural information on biomolecules into perspective The book is required reading for researchers and students who plan to use modern computer environment in their research

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 K. Imahori,F. Sakiyama,2013-06-29 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

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

Methods in Protein Sequence Analysis • 1986 Kenneth A. Walsh, 1987-06-17 Methods in Protein Sequence Analysis 1986 brings together reports of the most recent methodology available to protein chemists for studying the molecular detail of proteins The papers in this volume constitute the proceedings of the Sixth International Conference on Methods in Protein Sequence Analysis which was held at the University of Washington in Seattle Washington on August 17 21 1986 This series of conferences has taken place during a period when new techniques in protein chemistry and molecular biology have enabled not only exploration of the control of protein function but also deduction of the genetic origin of proteins and laboratory generation of rare protein molecules for therapeutic and commercial use The current reports are focused on the means by which experimental questions can be answered rather than on the biological implications in specific systems The scope of the meeting was quite broad emphasizing microanalytical techniques and the relative merits of DNA sequencing mass spectrometry and more traditional degradation techniques A highlight of the meeting was the growing awareness of the role of mass spectrometry In the analysis of proteins The complementarity of protein sequencing and DNA sequencing techniques was apparent throughout the discussions and several papers dealt with the strategy of obtaining sequence information from small amounts of protein in order that appropriate oligonucleotide probes could be constructed and the encoding nucleic acids sequenced and manipulated

Methods in Protein Sequence Analysis Jörnvall, Höög, 2013-11-21 Methods in protein sequence analysis constitute important fields in rapid progress We have experienced a continuous increase in analytical sensitivity coupled with decreases in time necessary for purification and

analysis Several generations of sequencers liquid solid gas phase have passed by and returned in other shapes during just over two decades Similarly the introduction of HPLC permitted an enormous leap forward in this as in other fields of biochemistry and we now start to see new major advances in purification analysis through capillary electrophoresis Furthermore progress in the field of mass spectrometry has matched that in chemical analysis and we witness continuous development now emphasizing ion spray and other mass spectrometric approaches In short protein analysis has progressed in line with other developments in modern science and constitutes an indispensable integral part of present day molecular biology Even the available molecular tools in the form of proteases with different specificities have increased in number although we still have far to go to reach an array of restriction proteases like the sets of nucleases available to the molecular geneticist Of course conferences have been devoted to protein sequence analysis in particular the MPSA Methods in Protein Sequence Analysis series of which the 8th conference took place in Kiruna Sweden July 1 6 1990 Again we witnessed much progress saw new instruments and experienced further interpretational insights into protein mechanisms and functions

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