

Computational Biology

K. Erciyes

Distributed and Sequential Algorithms for Bioinformatics



 Springer

Nice Book Distributed Sequential Algorithms Bioinformatics Computational

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Distributed and Sequential Algorithms for Bioinformatics Kayhan Erciyes, 2015-10-31 This unique textbook reference presents unified coverage of bioinformatics topics relating to both biological sequences and biological networks providing an in depth analysis of cutting edge distributed algorithms as well as of relevant sequential algorithms In addition to introducing the latest algorithms in this area more than fifteen new distributed algorithms are also proposed Topics and features reviews a range of open challenges in biological sequences and networks describes in detail both sequential and parallel distributed algorithms for each problem suggests approaches for distributed algorithms as possible extensions to sequential algorithms when the distributed algorithms for the topic are scarce proposes a number of new distributed algorithms in each chapter to serve as potential starting points for further research concludes each chapter with self test exercises a summary of the key points a comparison of the algorithms described and a literature review

Bioinformatics of the Brain Kayhan Erciyes, Tuba Sevimoglu, 2024-09-25 The brain consisting of billions of neurons is probably the most complex and mysterious organ of the body Understanding the functioning of the brain in its health and disease states has baffled the researchers working in this area for many years The diversity of brain diseases and disorders makes the analysis of brain functions an even more challenging area of research In vitro and in vivo studies regarding the brain may be laborious however bioinformatics using in silico approaches may take the burden off the experimental studies and give us a clearer perspective on disease and healthy states of the brain its functions and disease mechanisms Recent advancements in neuroimaging technologies the development of high performance computers and the development of software algorithms and methods to analyze data obtained from various neuroimaging processes have opened new frontiers in neuroscience enabling unprecedented finer analysis of the brain functions This relatively new approach of brain analysis which may be termed Bioinformatics of the Brain is the main subject of this volume aiming to provide a thorough review of various bioinformatics approaches for analyzing the functioning of the brain and understanding brain diseases such as neurodegenerative diseases brain tumors and neuropsychiatric disorders Authors from various disciplines in this volume each focus on a different aspect aiming to expand our understanding of this area of research Topics included are Brain diseases and disorders Stem cell therapy of neurodegenerative diseases Tissue engineering applications of gliomas Brain tumor detection and modeling Brain tumor growth simulation Brain computer interface Bioinformatics of brain diseases Graph theoretical analysis of complex brain networks Brain proteomics This book is intended to aid scientists researchers and graduate students in carrying out interdisciplinary research in the areas of bioinformatics bioengineering computer engineering software engineering mathematics molecular biology genetics and biotechnology

Recent Progress in Parallel and Distributed Computing Wen-Jyi Hwang, 2017-07-19 Parallel and distributed computing has been one of the most active areas of research in recent years The techniques involved have found significant applications in areas as diverse as engineering management natural

sciences and social sciences This book reports state of the art topics and advances in this emerging field Completely up to date aspects it examines include the following 1 Social networks 2 Smart grids 3 Graphic processing unit computation 4 Distributed software development tools 5 Analytic hierarchy process and the analytic network process **Parallel Computing for Bioinformatics and Computational Biology** Albert Y. Zomaya, 2006-05-24 Discover how to streamline complex bioinformatics applications with parallel computing This publication enables readers to handle more complex bioinformatics applications and larger and richer data sets As the editor clearly shows using powerful parallel computing tools can lead to significant breakthroughs in deciphering genomes understanding genetic disease designing customized drug therapies and understanding evolution A broad range of bioinformatics applications is covered with demonstrations on how each one can be parallelized to improve performance and gain faster rates of computation Current parallel computing techniques and technologies are examined including distributed computing and grid computing Readers are provided with a mixture of algorithms experiments and simulations that provide not only qualitative but also quantitative insights into the dynamic field of bioinformatics Parallel Computing for Bioinformatics and Computational Biology is a contributed work that serves as a repository of case studies collectively demonstrating how parallel computing streamlines difficult problems in bioinformatics and produces better results Each of the chapters is authored by an established expert in the field and carefully edited to ensure a consistent approach and high standard throughout the publication The work is organized into five parts Algorithms and models Sequence analysis and microarrays Phylogenetics Protein folding Platforms and enabling technologies Researchers educators and students in the field of bioinformatics will discover how high performance computing can enable them to handle more complex data sets gain deeper insights and make new discoveries

Distributed Computing -- IWDC 2004 Nabanita Das, 2004-12-16 This book constitutes the refereed proceedings of the 6th International Workshop on Distributed Computing IWDC 2004 held in Kolkata India in December 2004 The 27 revised full papers and 27 revised short papers presented together with 3 invited contributions and abstracts of 11 reviewed workshop papers were carefully reviewed and selected from 157 submissions The papers are organized in topical sections on distributed algorithms high performance computing distributed systems wireless networks information security network protocols reliability and testing network topology and routing mobile computing ad hoc networks and sensor networks

Parallel and Distributed Computing Alberto Ros, 2010-01-01 The 14 chapters presented in this book cover a wide variety of representative works ranging from hardware design to application development Particularly the topics that are addressed are programmable and reconfigurable devices and systems dependability of GPUs General Purpose Units network topologies cache coherence protocols resource allocation scheduling algorithms peertopeer networks largescale network simulation and parallel routines and algorithms In this way the articles included in this book constitute an excellent reference for engineers and researchers who have particular interests in each of these topics in parallel and distributed computing

Genome-Scale Algorithm Design Veli Mäkinen,Djamal Belazzougui,Fabio Cunial,Alexandru I. Tomescu,2023-10-12

Presenting the fundamental algorithms and data structures that power bioinformatics workflows this book covers a range of topics from the foundations of sequence analysis alignments and hidden Markov models to classical index structures k mer indexes suffix arrays and suffix trees Burrows Wheeler indexes graph algorithms network flows and a number of advanced omics applications The chapters feature numerous examples algorithm visualizations and exercises providing graduate students researchers and practitioners with a powerful algorithmic toolkit for the applications of high throughput sequencing An accompanying website www.genome-scale.info offers supporting teaching material The second edition strengthens the toolkit by covering minimizers and other advanced data structures and their use in emerging pangenomics approaches

Systems and Computational Biology Ning-Sun Yang,2011-09-12 Whereas some microarray or bioinformatics scientists among us may have been criticized as doing cataloging research the majority of us believe that we are sincerely exploring new scientific and technological systems to benefit human health human food and animal feed production and environmental protections Indeed we are humbled by the complexity extent and beauty of cross talks in various biological systems on the other hand we are becoming more educated and are able to start addressing honestly and skillfully the various important issues concerning translational medicine global agriculture and the environment The two volumes of this book present a series of high quality research or review articles in a timely fashion to this emerging research field of our scientific community

Computational Biology and Applied Bioinformatics Heitor Lopes,Leonardo Magalhães Cruz,2011-09-02 Nowadays it is difficult to imagine an area of knowledge that can continue developing without the use of computers and informatics It is not different with biology that has seen an unpredictable growth in recent decades with the rise of a new discipline bioinformatics bringing together molecular biology biotechnology and information technology More recently the development of high throughput techniques such as microarray mass spectrometry and DNA sequencing has increased the need of computational support to collect store retrieve analyze and correlate huge data sets of complex information On the other hand the growth of the computational power for processing and storage has also increased the necessity for deeper knowledge in the field The development of bioinformatics has allowed now the emergence of systems biology the study of the interactions between the components of a biological system and how these interactions give rise to the function and behavior of a living being This book presents some theoretical issues reviews and a variety of bioinformatics applications For better understanding the chapters were grouped in two parts In Part I the chapters are more oriented towards literature review and theoretical issues Part II consists of application oriented chapters that report case studies in which a specific biological problem is treated with bioinformatics tools

Multiple Biological Sequence Alignment Ken Nguyen,Xuan Guo,Yi Pan,2016-07-18 Covers the fundamentals and techniques of multiple biological sequence alignment and analysis and shows readers how to choose the appropriate sequence analysis tools for their tasks This book describes the traditional and modern

approaches in biological sequence alignment and homology search This book contains 11 chapters with Chapter 1 providing basic information on biological sequences Next Chapter 2 contains fundamentals in pair wise sequence alignment while Chapters 3 and 4 examine popular existing quantitative models and practical clustering techniques that have been used in multiple sequence alignment Chapter 5 describes characterizes and relates many multiple sequence alignment models Chapter 6 describes how traditionally phylogenetic trees have been constructed and available sequence knowledge bases can be used to improve the accuracy of reconstructing phylogeny trees Chapter 7 covers the latest methods developed to improve the run time efficiency of multiple sequence alignment Next Chapter 8 covers several popular existing multiple sequence alignment server and services and Chapter 9 examines several multiple sequence alignment techniques that have been developed to handle short sequences reads produced by the Next Generation Sequencing technique NSG Chapter 10 describes a Bioinformatics application using multiple sequence alignment of short reads or whole genomes as input Lastly Chapter 11 provides a review of RNA and protein secondary structure prediction using the evolution information inferred from multiple sequence alignments Covers the full spectrum of the field from alignment algorithms to scoring methods practical techniques and alignment tools and their evaluations Describes theories and developments of scoring functions and scoring matrices Examines phylogeny estimation and large scale homology search Multiple Biological Sequence Alignment Scoring Functions Algorithms and Applications is a reference for researchers engineers graduate and post graduate students in bioinformatics and system biology and molecular biologists Ken Nguyen PhD is an associate professor at Clayton State University GA USA He received his PhD MSc and BSc degrees in computer science all from Georgia State University His research interests are in databases parallel and distribute computing and bioinformatics He was a Molecular Basis of Disease fellow at Georgia State and is the recipient of the highest graduate honor at Georgia State the William M Suttles Graduate Fellowship Xuan Guo PhD is a postdoctoral associate at Oak Ridge National Lab USA He received his PhD degree in computer science from Georgia State University in 2015 His research interests are in bioinformatics machine leaning and cloud computing He is an editorial assistant of International Journal of Bioinformatics Research and Applications Yi Pan PhD is a Regents Professor of Computer Science and an Interim Associate Dean and Chair of Biology at Georgia State University He received his BE and ME in computer engineering from Tsinghua University in China and his PhD in computer science from the University of Pittsburgh Dr Pan s research interests include parallel and distributed computing optical networks wireless networks and bioinformatics He has published more than 180 journal papers with about 60 papers published in various IEEE ACM journals He is co editor along with Albert Y Zomaya of the Wiley Series in Bioinformatics

Distributed Computing, Artificial Intelligence, Bioinformatics, Soft Computing, and Ambient Assisted Living Sigeru Omatu,Miguel P. Rocha,Jose Bravo,Florentino Fdez Riverola,Emilio Corchado,Andrés Bustillo,Juan Manuel Corchado Rodríguez,2009-06-06 This volume II contains all publications accepted for the symposiums and workshops held in parallel

with the 10th International Work Conference on Artificial Neural Networks IWANN 2009 covering a wide spectrum of technological areas such as distributed computing artificial intelligence bioinformatics soft computing and ambient assisted living DCAI 2009 International Symposium on Distributed Computing and Artificial Intelligence covering artificial intelligence and its applications in distributed environments such as the Internet electronic commerce mobile communications wireless devices distributed computing and so on This event accepted a total of 96 submissions selected from a submission pool of 157 papers from 12 different countries IWAAL 2009 International Workshop of Ambient Assisted Living covering solutions aimed at increasing the quality of life safety and health problems of elderly and disabled people by means of technology This event accepted a total of 42 submissions selected from a submission pool of 78 papers from 9 different countries IWPACBB 2009 Third International Workshop on Practical Applications of Computational Biology and Bioinformatics covering computational biology and bioinformatics as a possibility for knowledge discovery modelling and optimization tasks aiming at the development of computational models so that the response of biological complex systems to any perturbation can be predicted This event accepted a total of 39 submissions selected from a submission pool of 75 papers from 6 different countries

Bioinformatics for Beginners Supratim Choudhuri, 2014-05-09 Bioinformatics for Beginners Genes Genomes Molecular Evolution Databases and Analytical Tools provides a coherent and friendly treatment of bioinformatics for any student or scientist within biology who has not routinely performed bioinformatic analysis The book discusses the relevant principles needed to understand the theoretical underpinnings of bioinformatic analysis and demonstrates with examples targeted analysis using freely available web based software and publicly available databases Eschewing non essential information the work focuses on principles and hands on analysis also pointing to further study options Avoids non essential coverage yet fully describes the field for beginners Explains the molecular basis of evolution to place bioinformatic analysis in biological context Provides useful links to the vast resource of publicly available bioinformatic databases and analysis tools Contains over 100 figures that aid in concept discovery and illustration

Software Tools and Algorithms for Biological Systems Hamid Arabnia, Quoc-Nam Tran, 2011-03-23 Software Tools and Algorithms for Biological Systems is composed of a collection of papers received in response to an announcement that was widely distributed to academicians and practitioners in the broad area of computational biology and software tools Also selected authors of accepted papers of BIOCOMP 09 proceedings International Conference on Bioinformatics and Computational Biology July 13-16 2009 Las Vegas Nevada USA were invited to submit the extended versions of their papers for evaluation

Recent Advances in Evolutionary Computation for Combinatorial Optimization Carlos Cotta, Jano van Hemert, 2008-09-08 Combinatorial optimisation is a ubiquitous discipline whose usefulness spans vast applications domains The intrinsic complexity of most combinatorial optimisation problems makes classical methods unaffordable in many cases To acquire practical solutions to these problems requires the use of metaheuristic approaches that trade completeness for

pragmatic effectiveness Such approaches are able to provide optimal or quasi optimal solutions to a plethora of difficult combinatorial optimisation problems The application of metaheuristics to combinatorial optimisation is an active field in which new theoretical developments new algorithmic models and new application areas are continuously emerging This volume presents recent advances in the area of metaheuristic combinatorial optimisation with a special focus on evolutionary computation methods Moreover it addresses local search methods and hybrid approaches In this sense the book includes cutting edge theoretical methodological algorithmic and applied developments in the field from respected experts and with a sound perspective

Encyclopedia of Bioinformatics and Computational Biology, 2018-08-21 Encyclopedia of Bioinformatics and Computational Biology ABC of Bioinformatics Three Volume Set combines elements of computer science information technology mathematics statistics and biotechnology providing the methodology and in silico solutions to mine biological data and processes The book covers Theory Topics and Applications with a special focus on Integrative omics and Systems Biology The theoretical methodological underpinnings of BCB including phylogeny are covered as are more current areas of focus such as translational bioinformatics cheminformatics and environmental informatics Finally Applications provide guidance for commonly asked questions This major reference work spans basic and cutting edge methodologies authored by leaders in the field providing an invaluable resource for students scientists professionals in research institutes and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries Brings together information from computer science information technology mathematics statistics and biotechnology Written and reviewed by leading experts in the field providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images multimedia tools and crosslinking to further resources and databases

Bioinformatics Horacio Pérez-Sánchez, 2012-11-28 This book is divided into different research areas relevant in Bioinformatics such as biological networks next generation sequencing high performance computing molecular modeling structural bioinformatics molecular modeling and intelligent data analysis Each book section introduces the basic concepts and then explains its application to problems of great relevance so both novice and expert readers can benefit from the information and research works presented here

Research in Computational Molecular Biology Satoru Miyano, Jill Mesirov, Simon Kasif, Sorin Istrail, Pavel Pevzner, Michael Waterman, 2005-04-28 This volume contains the papers presented at the 9th Annual International Conference on Research in Computational Molecular Biology RECOMB 2005 which was held in Cambridge Massachusetts on May 14 18 2005 The RECOMB conference series was started in 1997 by Sorin Istrail Pavel Pevzner and Michael Waterman The list of previous meetings is shown below in the section Previous RECOMB Meetings RECOMB 2005 was hosted by the Broad Institute of MIT and Harvard and Boston University's Center for Advanced genomic Technology and was excellently organized by the Organizing Committee Co chairs Jill Mesirov and Simon Kasif This year 217 papers were submitted of which the Program Committee lected 39 for

presentation at the meeting and inclusion in this proceedings Each submission was refereed by at least three members of the Program Committee After the completion of the referees reports an extensive Web based discussion took place for making decisions From RECOMB 2005 the Steering Committee decided to publish the proceedings as a volume of Lecture Notes in Bioinformatics LNBI for which the founders of RECOMB are also the editors The prominent volume number LNBI 3500 was assigned to this proceedings The RECOMB conference series is closely associated with the Journal of Computational Biology which traditionally publishes special issues devoted to presenting full versions of selected conference papers The RECOMB Program Committee consisted of 42 members as listed on a separate page I would like to thank the RECOMB 2005 Program Committee members for their dedication and hard work

Hidden Markov Models for Bioinformatics T.

Koski, 2001-11-30 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

Bioinformatics in Agriculture Pradeep Sharma, Dinesh Yadav, R.K.

Gaur, 2022-04-28 Bioinformatics in Agriculture Next Generation Sequencing Era is a comprehensive volume presenting an integrated research and development approach to the practical application of genomics to improve agricultural crops Exploring both the theoretical and applied aspects of computational biology and focusing on the innovation processes the book highlights the increased productivity of a translational approach Presented in four sections and including insights from experts from around the world the book includes Section I Bioinformatics and Next Generation Sequencing Technologies Section II Omics Application Section III Data mining and Markers Discovery Section IV Artificial Intelligence and Agribots Bioinformatics in Agriculture Next Generation Sequencing Era explores deep sequencing NGS genomic transcriptome analysis and multiplexing highlighting practices for reducing time cost and effort for the analysis of gene as they are pooled and sequenced Readers will gain real world information on computational biology genomics applied data mining machine learning and artificial intelligence This book serves as a complete package for advanced undergraduate students researchers and scientists with an interest in bioinformatics Discusses integral aspects of molecular biology and pivotal tools for molecular breeding Enables breeders to design cost effective and efficient breeding strategies Provides examples of innovative genome wide marker SSR SNP discovery Explores both the theoretical and practical aspects of computational biology with focus on innovation processes Covers recent trends of bioinformatics and different tools and techniques

A Textbook of Biotechnology, 6e RC Dubey, A Textbook of Biotechnology is a comprehensive and student friendly resource

designed specifically for undergraduate students pursuing biotechnology and related life science disciplines This textbook offers a clear systematic introduction to the core concepts and modern techniques that define the field today This textbook explains the core principles of biotechnology and its real world applications ranging from genetic engineering tools like DNA cutting joining and cloning vectors to advanced techniques such as gene cloning DNA analysis and fingerprinting Students will explore key areas like genomics proteomics and bioinformatics learning how computational tools manage complex biological data The book provides in depth coverage of topics such as molecular biology tissue culture agricultural biotechnology gene therapy drug design probiotics and genetic engineering in plants animals and microorganisms It also introduces lab based techniques like cryopreservation and cell culture molecular mapping for genetic traits and the industrial use of microbes to produce antibiotics vitamins acids and single cell proteins

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