Bioinformatics Database Systems

Kevin Byron Katherine G. Herbert Jason T. L. Wang



Online Bioinformatics Database Systems Jason T L

Sarah Cohen-Boulakia, Val Tannen

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Bioinformatics Database Systems Kevin Byron, Katherine G. Herbert, Jason T. L. Wang, 2016-12-19 Modern biological databases comprise not only data but also sophisticated query facilities and bioinformatics data analysis tools This book provides an exploration through the world of Bioinformatics Database Systems The book summarizes the popular and innovative bioinformatics repositories currently available including popular primary genetic and protein sequence databases phylogenetic databases structure and pathway databases microarray databases and boutique databases It also explores the data quality and information integration issues currently involved with managing bioinformatics databases including data quality issues that have been observed and efforts in the data cleaning field Biological data integration issues are also covered in depth and the book demonstrates how data integration can create new repositories to address the needs of the biological communities It also presents typical data integration architectures employed in current bioinformatics databases The latter part of the book covers biological data mining and biological data processing approaches using cloud based technologies General data mining approaches are discussed as well as specific data mining methodologies that have been successfully deployed in biological data mining applications Two biological data mining case studies are also included to illustrate how data query and analysis methods are integrated into user friendly systems Aimed at researchers and developers of bioinformatics database systems the book is also useful as a supplementary textbook for a one semester upper level undergraduate course or an introductory graduate bioinformatics course **Advances in Applied Self-organizing Systems** Mikhail Prokopenko, 2007-11-24 This book presents the state of the art in successfully engineered self organizing systems It goes further too to examine ways to balance design and self organization in the context of applications As demonstrated throughout finding this balance helps to deal with diverse practical challenges. The case studies described illustrate the richness of the topic and provide guidance on its more intricate areas **Hydroinformatics Praveen** Kumar, Mike Folk, Momcilo Markus, Jay C. Alameda, 2005-11-02 Modern hydrology is more interdisciplinary than ever Staggering amounts and varieties of information pour in from GIS and remote sensing systems every day and this information must be collected interpreted and shared efficiently Hydroinformatics Data Integrative Approaches in Computation Analysis and Modeling introduces the tools approache Big Data Min Chen, Shiwen Mao, Yin Zhang, Victor C.M. Leung, 2014-05-05 This Springer Brief provides a comprehensive overview of the background and recent developments of big data The value chain of big data is divided into four phases data generation data acquisition data storage and data analysis For each phase the book introduces the general background discusses technical challenges and reviews the latest advances Technologies under discussion include cloud computing Internet of Things data centers Hadoop and more The authors also explore several representative applications of big data such as enterprise management online social networks healthcare and medical applications collective intelligence and smart grids This book concludes with a thoughtful discussion of possible research

directions and development trends in the field Big Data Related Technologies Challenges and Future Prospects is a concise yet thorough examination of this exciting area It is designed for researchers and professionals interested in big data or related research Advanced level students in computer science and electrical engineering will also find this book useful

Data Integration in the Life Sciences Sarah Cohen-Boulakia, Val Tannen, 2007-06-30 This book constitutes the refereed proceedings of the 4th International Workshop on Data Integration in the Life Sciences DILS 2007 held in Philadelphia PA USA in July 2007 It covers new architectures and experience on using systems managing and designing scientific workflows mapping and matching techniques modeling of life science data and annotation in data integration **SIGKDD** IBM Systems Journal International Business Machines Corporation, 2001 Explorations ,2000 A Handbook of Information Technology C. T. Bhunia, 2007 Information technology IT can be collectively described as that used by man to gather store and retrieve manipulate and communicate data and information Today in the Information Age this takes place over and across vast geographical demographical socio political and economic scopes and the ceasing of it will choke society as know it today to a pre historic standstill It is understandably implemented through various aspects of computing and Electronic Technology With the growing complexity of the information processing needs throughout fields as diverse as business science technology exploration and entertainment several issues involving data security time complexity Bandwidth and thought put parallel and alternative computing technology and the technology used in an ever increasing band of newer types of devices are posing the most crucial questions to the future of society in general and IT in particular The book is a collection of articles written by professors industry persons and researchers if international repute and comprises the latest breakthrough sin the fields of Information Theory and Coding Information Security Next Generation Internet technology Data Mining and Knowledge Management Mobile Computing and Communication Bioinformatics Soft Computing Multimedia Systems and Communication Quantum Computing Image Processing and other areas which together comprise IT This book is a must read for those seeking to expand their knowledge about various aspects of Information Technology The Construction and Usage of a Microarray Data Warehousing System Allen Jason Day, 2008 *Bioinformatics Database* Systems Kevin Byron, Katherine G. Herbert, Jason T. L. Wang, 2016-12-19 Modern biological databases comprise not only data but also sophisticated guery facilities and bioinformatics data analysis tools This book provides an exploration through the world of Bioinformatics Database Systems The book summarizes the popular and innovative bioinformatics repositories currently available including popular primary genetic and protein sequence databases phylogenetic databases structure and pathway databases microarray databases and boutique databases It also explores the data quality and information integration issues currently involved with managing bioinformatics databases including data quality issues that have been observed and efforts in the data cleaning field Biological data integration issues are also covered in depth and the book demonstrates how data integration can create new repositories to address the needs of the biological communities It also

presents typical data integration architectures employed in current bioinformatics databases The latter part of the book covers biological data mining and biological data processing approaches using cloud based technologies General data mining approaches are discussed as well as specific data mining methodologies that have been successfully deployed in biological data mining applications Two biological data mining case studies are also included to illustrate how data query and analysis methods are integrated into user friendly systems Aimed at researchers and developers of bioinformatics database systems the book is also useful as a supplementary textbook for a one semester upper level undergraduate course or an introductory graduate bioinformatics course Genome Research ,2002 Dissertation Abstracts International ,2006 Proceedings of the National Academy of Sciences of the United States of America National Academy of Sciences (U.S.).,2006

Standard & Poor's Stock Reports ,2004 Bioinformatics David Edwards, Jason Stajich, David Hansen, 2009-09-03 Bioinformatics is a relatively new field of research It evolved from the requirement to process characterize and apply the information being produced by DNA sequencing technology The production of DNA sequence data continues to grow exponentially At the same time improved bioinformatics such as faster DNA sequence search methods have been combined with increasingly powerful computer systems to process this information Methods are being developed for the ever more detailed quantification of gene expression providing an insight into the function of the newly discovered genes while molecular genetic tools provide a link between these genes and heritable traits Genetic tests are now available to determine the likelihood of suffering specific ailments and can predict how plant cultivars may respond to the environment The steps in the translation of the genetic blueprint to the observed phenotype is being increasingly understood through proteome metabolome and phenome analysis all underpinned by advances in bioinformatics Bioinformatics is becoming increasingly central to the study of biology and a day at a computer can often save a year or more in the laboratory The volume is intended for graduate level biology students as well as researchers who wish to gain a better understanding of applied bioinformatics and who wish to use bioinformatics technologies to assist in their research The volume would also be of value to bioinformatics developers particularly those from a computing background who would like to understand the application of computational tools for biological research Each chapter would include a comprehensive introduction giving an overview of the fundamentals aimed at introducing graduate students and researchers from diverse backgrounds to the field and bring them up to date on the current state of knowledge To accommodate the broad range of topics in applied bioinformatics chapters have been grouped into themes gene and genome analysis molecular genetic analysis gene expression analysis protein and proteome analysis metabolome analysis phenome data analysis literature mining and bioinformatics tool development Each chapter and theme provides an introduction to the biology behind the data describes the requirements for data processing and details some of the methods applied to the data to enhance biological understanding **Bioinformatics** Stanley I. Letovsky, 2006-06-01 Bioinformatics brings computational methods to the analysis and processing of genomic data

Bioinformatics Databases and Systems focuses on the issues of system building and data curation that dominate the day to day concerns of bioinformatics practitioners Included are chapters by many of today s leading bioinformatics practitioners describing most of the current paradigms of system building and curation including both their strengths and weaknesses Biological topics covered include sequence databases metabolic pathways phenotypes variety collections gene expression atlases and neuroinformatics Species range from bacteria to mammals to plants Software systems and technologies covered include OPM CORBA SRS KLEISLI ACEDB Web based integration and laboratory workflow Bioinformatics Databases and Systems provides a valuable introduction for newcomers to the field and a useful reference for veterans David Edwards, Jason Stajich, David Hansen, 2010-04-29 Bioinformatics is a relatively new field of research It evolved from the requirement to process characterize and apply the information being produced by DNA sequencing technology The production of DNA sequence data continues to grow exponentially At the same time improved bioinformatics such as faster DNA sequence search methods have been combined with increasingly powerful computer systems to process this information Methods are being developed for the ever more detailed quantification of gene expression providing an insight into the function of the newly discovered genes while molecular genetic tools provide a link between these genes and heritable traits Genetic tests are now available to determine the likelihood of suffering specific ailments and can predict how plant cultivars may respond to the environment The steps in the translation of the genetic blueprint to the observed phenotype is being increasingly understood through proteome metabolome and phenome analysis all underpinned by advances in bioinformatics Bioinformatics is becoming increasingly central to the study of biology and a day at a computer can often save a year or more in the laboratory The volume is intended for graduate level biology students as well as researchers who wish to gain a better understanding of applied bioinformatics and who wish to use bioinformatics technologies to assist in their research The volume would also be of value to bioinformatics developers particularly those from a computing background who would like to understand the application of computational tools for biological research Each chapter would include a comprehensive introduction giving an overview of the fundamentals aimed at introducing graduate students and researchers from diverse backgrounds to the field and bring them up to date on the current state of knowledge To accommodate the broad range of topics in applied bioinformatics chapters have been grouped into themes gene and genome analysis molecular genetic analysis gene expression analysis protein and proteome analysis metabolome analysis phenome data analysis literature mining and bioinformatics tool development Each chapter and theme provides an introduction to the biology behind the data describes the requirements for data processing and details some of the methods applied to the data to enhance biological understanding Data Mining in Bioinformatics Jason T. L. Wang, Mohammed J. Zaki, Hannu Toivonen, Dennis Shasha, 2005-09-02 8 1 1 Protein Subcellular Location The life sciences have entered the post genome era where the focus of biological research has shifted from genome sequences to protein functionality. With whole genome drafts of mouse and human in hand

scientistsareputting more and more e ort into obtaining information about the entire proteome in a given cell type The properties of a protein include its amino acid sequences its expression levels under various developmental stages and in di erenttissues its3Dstructureandactivesites itsfunctionalandstructural binding partners and its subcellular location Protein subcellular location is important for understanding protein function inside the cell For example the observation that the product of a gene is localized in mitochondria will support the hypothesis that this protein or gene is involved in energy metabolism Proteins localized in the cytoskeleton are probably involved in intracellular tracking and support The context of protein functionality is well represented by protein subcellular location Proteins have various subcellular location patterns 250 One major category of proteins is synthesized on free ribosomes in the cytoplasm Soluble proteins remain in the cytoplasm after their synthesis and function as small factories catalyzing cellular metabolites Other proteins that have a target signal in their sequences are directed to their target organelle such as mitochondria via posttranslational transport through the organelle membrane Nuclear proteins are transferred through pores on the nuclear envelope to the nucleus and mostly function as regulators The second major category of proteins is synthesized on endoplasmic reticulum ER associated ribosomes and passes through the reticuloendothelial system consisting of the ERand the Golgi apparatus

Bioinformatics Zoé Lacroix, Terence Critchlow, 2003-09-08 Life science data integration and interoperability is one of the most challenging problems facing bioinformatics today In the current age of the life sciences investigators have to interpret many types of information from a variety of sources lab instruments public databases gene expression profiles raw sequence traces single nucleotide polymorphisms chemical screening data proteomic data putative metabolic pathway models and many others Unfortunately scientists are not currently able to easily identify and access this information because of the variety of semantics interfaces and data formats used by the underlying data sources Bioinformatics Managing Scientific Data tackles this challenge head on by discussing the current approaches and variety of systems available to help bioinformaticians with this increasingly complex issue The heart of the book lies in the collaboration efforts of eight distinct bioinformatics teams that describe their own unique approaches to data integration and interoperability Each system receives its own chapter where the lead contributors provide precious insight into the specific problems being addressed by the system why the particular architecture was chosen and details on the system's strengths and weaknesses In closing the editors provide important criteria for evaluating these systems that bioinformatics professionals will find valuable Provides a clear overview of the state of the art in data integration and interoperability in genomics highlighting a variety of systems and giving insight into the strengths and weaknesses of their different approaches Discusses shared vocabulary design issues complexity of use cases and the difficulties of transferring existing data management approaches to bioinformatics systems which serves to connect computer and life scientists Written by the primary contributors of eight reputable bioinformatics systems in academia and industry including BioKris TAMBIS K2 GeneExpress P FDM MBM SDSC SRS and DiscoveryLink

Integrative Bioinformatics for Biomedical Big Data Xiuzhen Huang, Jason H. Moore, Yu Zhang, 2023-09-28 Explains the value of no boundary thinking NBT in biological and biomedical research in helping to define impactful research questions

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