

Bioinformatics Managing Scientific Data The Morgan Kaufmann Series In Multimedia Information And Systems

This book presents thoroughly arranged tutorial papers corresponding to lectures given by leading researchers at the Second International Summer School on Reasoning Web in Lisbon, Portugal, in September 2006. Building on the predecessor school held in 2005 and published as LNCS 3564, the ten tutorial lectures presented provide competent coverage of current topics in semantic Web research and development.

Compared with data from general application domains, modern biological data has many unique characteristics. The goal of this book is to cover data and applications identifying new issues and directions for future research in biomedical domain. Thirty years ago, the most likely place to find a biologist was standing at a laboratory bench, peering down a microscope, surrounded by flasks of chemicals and petri dishes full of bacteria. Today, you are just as likely to find him or her in a room that looks more like an office, poring over lines of code on computer screens. The use of computers in biology has radically transformed who biologists are, what they do, and how they understand life. In Life Out of Sequence, Hallam Stevens looks inside this new landscape of digital scientific work. Stevens chronicles the emergence of bioinformatics—the mode of working across and between biology, computing, mathematics, and statistics—from the 1960s to the present, seeking to understand how knowledge about life is made in and through virtual spaces. He shows how scientific data moves from living organisms into DNA sequencing machines, through software, and into databases, images, and scientific publications. What he reveals is a biology very different from the one of predigital days: a biology that includes not only biologists but also highly interdisciplinary teams of managers and workers; a biology that is more centered on DNA sequencing, but one that understands sequence in terms of dynamic cascades and highly interconnected networks. Life Out of Sequence thus offers the computational biology community welcome context for their own work while also giving the public a frontline perspective of what is going on in this rapidly changing field. Although we can't usually see them, microbes are essential for every part of human life -- indeed all life on Earth. The emerging field of metagenomics offers a new way of exploring the microbial world that will transform modern microbiology and lead to practical applications in medicine, agriculture, alternative energy, environmental remediation, and many other areas. Metagenomics allows researchers to look at the genomes of all of the microbes in an environment at once, providing a "meta" view of the whole microbial community and the complex interactions within it. It's a quantum leap beyond traditional research techniques that rely on studying -- one at a time -- the few microbes that can be grown in the laboratory. At the request of the National Science Foundation, five Institutes of the National Institutes of Health, and the Department of Energy, the National Research Council organized a committee to address the current state of metagenomics and identify obstacles current researchers are facing in order to determine how to best support the field and encourage its success. The New Science of Metagenomics recommends the establishment of a "Global Metagenomics Initiative" comprising a small number of large-scale metagenomics projects as well as many medium- and small-scale projects to advance the technology and develop the standard practices needed to advance the field. The report also addresses database needs, methodological challenges, and the importance of interdisciplinary collaboration in supporting this new field.

Big Data Analytics In Bioinformatics and Healthcare
E-Science Meets Biomedical Informatics : Proceedings of HealthGrid 2008
Encyclopedia of Informatics and Technology, Fourth Edition
A Data-Driven History of Bioinformatics
Library and Information Services for Bioinformatics Education and Research
Advances in Database Technology - EDBT 2004
EDBT 2006 Workshop PhD, DataX, IIDB, IIBA, ICSSNW, QI,QP, PIM, PaMa, and Reactivity on the Web, Munich, Germany, March 26-31, 2006, Revised Selected Papers
Machine Learning techniques are increasingly being used to address problems in computational biology and bioinformatics. Novel machine learning computational techniques to analyze high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future drug discovery. Machine learning techniques such as Markov models, support vector machines, neural networks, and graphical models have been successful in analyzing life science data because of their capabilities in handling randomness and uncertainty of data noise and in generalization. Machine Learning in Bioinformatics compiles recent approaches in machine learning methods and their applications in addressing contemporary problems in bioinformatics approximating classification and prediction of disease, feature selection, dimensionality reduction, gene selection and classification of microarray data and many more.

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. About the Authors Kevin Byron is a PhD candidate in the Department of Computer Science at the New Jersey Institute of Technology. Katherine G. Herbert is Associate Professor of Computer Science at Montclair State University. Jason T.L. Wang is Professor of Bioinformatics and Computer Science at the New Jersey Institute of Technology.

This book constitutes the refereed proceedings of the 16th International Conference on Algorithmic Learning Theory, ALT 2005, held in Singapore in October 2005. The 30 revised full papers presented together with 5 invited papers and an introduction by the editors were carefully reviewed and selected from 98 submissions. The papers are organized in topical sections on kernel-based learning, Bayesian and statistical models, PaLearning, query-learning, inductive inference, language learning, learning and logic, learning from expert advice, online learning, defensive forecasting, and teaching.

HealthGrid 2008 is the sixth conference in this series of open forums for the integration of grid technologies and its applications in the biomedical, medical and biological domains to pave the path to an international research area in healthGrids. The main objective of the HealthGrid conference and the HealthGrid Association is the exchange and discussion of ideas, technologies, solutions and requirements that interest the grid and the life-sciences communities to foster the integration of grids into health. Subjects in this publication reflect the diversity of mature practice: Advancing Virtual Communities, offering a glimpse of the kind of communities that are brought together by means of collaboration grids; Public Health Informatics, exploring the diffusion of grid concepts and technologies in health informatics; Translational Bioinformatics, the contact point between medicine, healthcare and genomics; and Knowledge Management and Decision Support, one direction that is confidently expected to grow as the synergy of grids and 'evidence-based practice' in healthcare is exploited. Towards the Virtual Cell
A Machine Learning Perspective
Bioinformatics Technologies
International Provenance and Annotation Workshop, IPAW 2006, Chicago, IL, USA, May 3-5, 2006, Revised Selected Papers

Neuroinformatics
For Biomedical and Life Science Researchers
Provenance and Annotation of Data
The 9th International Conference on Extending Database Technology, EDBT 2004, was held in Heraklion, Crete, Greece, during March 14-18, 2004. The EDBT series of conferences is an established and prestigious forum for the exchange of the latest research results in data management. Held every two years in an attractive European location, the conference provides unique opportunities for database researchers, practitioners, developers, and users to explore new ideas, techniques, and tools, and to exchange experiences. The previous events were held in Venice, Vienna, Cambridge, Avignon, Valencia, Konstanz, and Prague. EDBT 2004 had the theme "new challenges for database technology," with the goal of encouraging researchers to take a greater interest in the current exciting technological and application advancements and to devise and address new research and development directions for database technology. From its early days, database technology has been challenged and advanced by new uses and applications, and it continues to evolve along with application requirements and hardware advances. Today's DBMS technology faces yet several new challenges. Technological trends and new computation paradigms, and applications such as pervasive and ubiquitous computing, grid computing, bioinformatics, trust management, virtual communities, and digital asset management, to name just a few, require database technology to be deployed in a variety of environments and for a number of different purposes. Such an extensive deployment will also require trustworthy, resilient database systems, as well as easy-to-manage and flexible ones, to which we can entrust our data in whatever form they are.

Citizen science enlists members of the public to make and record useful observations, such as counting birds in their backyards, watching for the first budding leaf in spring, or measuring local snowfall. The large numbers of volunteers who participate in projects such as Project FeederWatch or Project BudBurst collect valuable research data, which, when pooled together, create an enormous body of scientific data on a vast geographic scale. In return, such projects aim to increase participants' connections to science, place, and nature, while supporting science literacy and environmental stewardship. In Citizen Science, experts from a variety of disciplines—including scientists and environmentalists working at the Cornell Lab of Ornithology, where many large citizen science programs use birds as proxies for biodiversity—share their experiences of creating and implementing successful citizen science projects, primarily those that use massive data sets gathered by citizen scientists to better understand the impact of environmental change. This first and foundational book for this developing field of inquiry addresses basic aspects of how to conduct citizen science projects, including goal-setting, program design, and evaluation, as well as the nuances of creating a robust digital infrastructure and recruiting a large participant base through communications and marketing. An overview of the types of research approaches and techniques demonstrates how to make use of large data sets arising from citizen science projects. A final section focuses on citizen science's impacts and its broad connections to understanding the human dimensions and educational aspects of participation. Citizen Science teaches teams of program developers and researchers how to cross the bridge from success at public engagement to using citizen science data to understand patterns and trends or to test hypotheses about how ecological processes respond to change at large geographic scales. Intended as a resource for a broad audience of experts and practitioners in natural sciences, information science, and social sciences, this book can be used to better understand how to improve existing programs, develop new ones, and make better use of the data resources that have accumulated from citizen science efforts. Its focus on harnessing the impact of "crowdsourcing" for scientific and educational endeavors is applicable to a wide range of fields, especially those that touch on the importance of massive collaboration aimed at understanding and conserving what we can of the natural world.

This book constitutes the refereed proceedings of the 22 International Conference on Database and Expert Systems Applications, DEXA 2011, held in Toulouse, France, August 29 - September 2, 2011. The 52 revised full papers and 40 short papers presented were carefully reviewed and selected from 207 submissions. The papers are organized in topical sections on query processing; database semantics; skyline queries; security and privacy; spatial and temporal data; semantic web search; storage and search; web search; data integration, transactions and optimization; and web applications.

Approaches in Integrative Bioinformatics provides a basic introduction to biological information systems, as well as guidance for the computational analysis of systems biology. This book also covers a range of issues and methods that reveal the multitude of omics data integration types and the relevance that integrative bioinformatics has today. Topics include biological data integration and manipulation, modeling and simulation of metabolic networks, transcriptomics and phenomics, and virtual cell approaches, as well as a number of applications of network biology. It helps to illustrate the value of integrative bioinformatics approaches to the life sciences. This book is intended for researchers and graduate students in the field of Bioinformatics. Professor Ming Chen is the Director of the Bioinformatics Laboratory at the College of Life Sciences, Zhejiang University, Hangzhou, China. Professor Ralf Hofstad is the Chair of the Department of Bioinformatics and Medical Informatics, Bielefeld University, Germany.

Approaches in Integrative Bioinformatics
Basic Bioinformatics
Current Trends in Database Technology - EDBT 2006
23rd International Conference, SSDBM 2011, Portland, OR, USA, July 20-22, 2011. Proceedings
Bioinformatics-Managing Scientific Data
10 International Conference on Extending Database Technology, Munich, Germany, 26-31 March 2006, Proceedings
Managing Scientific Data

Bioinformatics is an interdisciplinary-assisted interface discipline dealing with acquisition, storage, management, access and processing of biological data. Bioinformatics is useful in identifying genes in DNA sequences, in the study of structure and function of genes and protein sequences in identifying families of related sequences, in aligning similar sequences and generating phylogenetic trees, in discovering drug targets, and in drug development. This book is designed to provide the newcomer with enough information to understand the principles of bioinformatics applications. As technology evolves and electronic data becomes more complex, digital medical record management and analysis becomes a challenge. In order to discover patterns and make relevant predictions based on large data sets, researchers and medical professionals must find new methods to analyze and extract relevant health information. Big Data Analytics in Bioinformatics and Healthcare merges the fields of biology, technology, and medicine in order to present a comprehensive study on the emerging information processing applications necessary in the field of electronic medical record management. Complete with interdisciplinary research resources, this publication is an essential reference source for researchers, practitioners, and students interested in the fields of biological computation, database management, and health information technology, with a special focus on the methodologies and tools to manage massive and complex electronic information.

The delivery and availability of information resources is a vital concern to professionals across multiple fields. This is particularly vital to data intensive professions, where easy accessibility to high-quality information is a crucial component of their research. Library and Information Services for Bioinformatics Education and Research is an authoritative reference source for the latest scholarly material on the role of libraries for the effective delivery of information resources to optimize the study of biological data. Highlighting innovative perspectives across a range of topics, such as user assessment, collection development, and information accessibility, this publication is ideally designed for professionals, managers, computer scientists, graduate students, and practitioners actively involved in the field of bioinformatics. Creative Environments follows up on the book Creative Space, by the same authors, who serve this time as editors. The first part further develops models of knowledge creation, in particular the Triple Helix of normal academic knowledge creation and a new, integrated model of normal academic and organizational knowledge creation, called Nanatsudaki (seven waterfalls) Model. Also presented are intelligence tools, statistics for support of creativity and more.

Reasoning Web
Keeping Found Things Found: The Study and Practice of Personal Information Management
Data Management in Bioinformatics
Text Book of Bioinformatics
9th International Conference on Extending Database Technology, Heraklion, Crete, Greece, March 14-18, 2004, Proceedings
Scientific and Statistical Database Management
International Conference on Scientific and Statistical Database Management

Due to its data handling and modeling capabilities as well as its flexibility, R is becoming the most widely used software in bioinformatics. R Programming for Bioinformatics explores the programming skills needed to use this software tool for the solution of bioinformatics and computational biology problems. Drawing on the author's first-hand experiences as an expert in R, the book begins with coverage on the general properties of the R language, several unique programming aspects of R, and object-oriented programming in R. It presents methods for data input and output as well as database interactions. The author also examines different facets of string handling and manipulations, discusses the interfacing of R with other languages, and describes how to write software packages. He concludes with a discussion on the debugging and profiling of R code. With numerous examples and exercises, this practical guide focuses on developing R programming skills in order to tackle problems encountered in bioinformatics and computational biology.

Over the last four decades computers and the internet have become an intrinsic part of all our lives, but this speed of development has left related philosophical enquiry behind. Featuring the work of computer scientists and philosophers, these essays provide an overview of an exciting new area of philosophy that is still taking shape.
This book constitutes the thoroughly refereed post-proceedings of the International Provenance and Annotation Workshops, IPAW 2006, held in Chicago, IL, USA in May 2006. The 26 revised full papers presented together with two keynote papers were carefully selected for presentation during two rounds of reviewing and improvement. The papers are organized in topical sections.

This book constitutes the thoroughly refereed joint post-proceedings of nine workshops held as part of the 10th International Conference on Extending Database Technology, EDBT 2006, held in Munich, Germany in March 2006. The 70 revised full papers presented were selected from numerous submissions during two rounds of reviewing and revision.

Bioinformatics Database Systems
Database and Expert Systems Applications
Biomedical Data and Applications
Revealing the Secrets of Our Microbial Planet
16th International Conference, ALT 2005, Singapore, October 8-11, 2005, Proceedings
Bioinformatics and Biomedical Engineering
The New Science of Metagenomics

Dealing with the volume, complexity, and diversity of data currently being generated by scientific experiments and simulations often causes scientists to waste productive time. Scientific Data Management: Challenges, Technology, and Deployment describes cutting-edge technologies and solutions for managing and analyzing vast amounts of data, helping scientists focus on their scientific goals. The book begins with coverage of efficient storage systems, discussing how to write and read large volumes of data without slowing the simulation, analysis, or visualization processes. It then focuses on the efficient data movement and management of storage spaces and explores emerging database systems for scientific data. The book also addresses how to best organize data for analysis purposes, how to effectively conduct searches over large datasets, how to successfully automate multi-step scientific process workflows, and how to automatically create metadata. This book provides a comprehensive understanding of the latest techniques for managing data during scientific exploration processes, from data generation to data analysis. Enhanced by numerous detailed color images, it includes real-world examples of applications drawn from biology, ecology, geology, climatology, and more. Check out Dr. Shoshani discuss the book during an interview with International Science Grid This Week (ISGTW): <http://www.isgtw.org/?pid=1002259>

BioinformaticsManaging Scientific DataElsevier
This book constitutes the thoroughly refereed post-proceedings of the First VLDB 2006 International Workshop on Data Mining and Bioinformatics, VDMB 2006, held in Seoul, Korea in September 2006 in conjunction with VLDB 2006. The 15 revised full papers cover various topics in the areas of microarray data analysis, bioinformatics system and text retrieval, application of gene expression data, and sequence analysis.

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 sequencing data, and microarray data. 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, MRM, SDCS, SRS, and Discoverylink.

Creative Environments
Bioinformatics Data Skills
R Programming for Bioinformatics
Life Out of Sequence
Scientific Data Management
Philosophy, Computing and Information Science

This two volume set LNBI 10208 and LNBI 10209 constitutes the proceedings of the 5th International Work-Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2017, held in Granada, Spain, in April 2017. The 122 papers presented were carefully reviewed and selected from 309 submissions. The scope of the conference spans advances in computational intelligence for critical care; bioinformatics for healthcare and diseases; biomedical engineering; biomedical image analysis; biomedical signal analysis; biomedicine: challenges representing large-scale biological data; computational genomics; computational proteomics; computational systems for modeling biological processes; biology - new tools, techniques and resources; eHealth: high-throughput bioinformatic tools for genomics; oncological big data and new mathematical tools; smart sensor and sensor-network architectures; time lapse experiments and multivariate biostatistics. Learn the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings. With this practical guide, you'll learn how to use freely available open source tools to extract meaning from large complex biological data sets. At no other point in human history has our ability to understand life's complexity and the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings. With this practical guide, you'll learn how to use freely available open source tools to extract meaning from large complex biological data sets. At no other point in human history has our ability to understand life's complexity and the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings. With this practical guide, you'll learn how to use freely available open source tools to extract meaning from large complex biological data sets. 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