

Ontologies in Bioinformatics

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Ontologies For Bioinformatics

Kenneth Baclawski & Tianhua Niu



Ontologies For Bioinformatics:

Anatomy Ontologies for Bioinformatics Albert Burger, Duncan Davidson, Richard Baldock, 2007-12-20 This book provides a timely and first of its kind collection of papers on anatomy ontologies It is interdisciplinary in its approach bringing together the relevant expertise from computing and biomedical studies The book aims to provide readers with a comprehensive understanding of the foundations of anatomical ontologies and the state of the art in terms of existing tools and applications It also highlights challenges that remain today **Introduction to Bio-Ontologies** Peter N.

Robinson, Sebastian Bauer, 2011-06-22 Introduction to Bio Ontologies explores the computational background of ontologies Emphasizing computational and algorithmic issues surrounding bio ontologies this self contained text helps readers understand ontological algorithms and their applications The first part of the book defines ontology and bio ontologies It also explains the importan

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Bioinformatics Albert G. Burger, Duncan Davidson, Richard Baldock, 2008 Provides a collection of papers on anatomy ontologies This book aims to provide readers with a comprehensive understanding of the foundations of anatomical ontologies and the state of the art in terms of tools and applications *Ontologies for Bioinformatics* Kenneth Baclawski, Tianhua Niu, 2006 Ontologies as a critical framework for the vast amounts of data in the postgenomic era an introduction to the basic concepts and applications of ontologies and ontology languages for the life sciences Recent advances in biotechnology spurred by the Human Genome Project have resulted in the accumulation of vast amounts of new data Ontologies computer readable precise formulations of concepts and the relationship among them in a given field are a critical framework for coping with the exponential growth of valuable biological data generated by high output technologies This book introduces the key concepts and applications of ontologies and ontology languages in bioinformatics and will be an essential guide for bioinformaticists computer scientists and life science researchers The three parts of Ontologies for Bioinformatics ask and answer three pivotal questions what ontologies are how ontologies are used and what ontologies could be which focuses on how ontologies could be used for reasoning with uncertainty The authors first introduce the notion of an ontology from hierarchically organized ontologies to more general network organizations and survey the best known ontologies in biology and medicine They show how to construct and use ontologies classifying uses into three categories querying viewing and transforming data to serve diverse purposes Contrasting deductive or Boolean logic with inductive reasoning they describe the goal of a synthesis that supports both styles of reasoning They discuss Bayesian networks as a

way of expressing uncertainty describe data fusion and propose that the World Wide Web can be extended to support reasoning with uncertainty They call this inductive reasoning web the Bayesian web **Handbook on Ontologies** Steffen Staab,Rudi Studer,2013-04-17 An ontology is a description like a formal specification of a program of concepts and relationships that can exist for an agent or a community of agents The concept is important for the purpose of enabling knowledge sharing and reuse The Handbook on Ontologies provides a comprehensive overview of the current status and future prospectives of the field of ontologies The handbook demonstrates standards that have been created recently it surveys methods that have been developed and it shows how to bring both into practice of ontology infrastructures and applications that are the best of their kind **Data Mining in Biomedicine Using Ontologies** Mihail Popescu,Dong Xu,2009 Presently a growing number of ontologies are being built and used for annotating data in biomedical research Thanks to the tremendous amount of data being generated ontologies are now being used in numerous ways including connecting different databases refining search capabilities interpreting experimental clinical data and inferring knowledge This cutting edge resource introduces you to latest developments in bio ontologies The book provides you with the theoretical foundations and examples of ontologies as well as applications of ontologies in biomedicine from molecular levels to clinical levels You also find details on technological infrastructure for bio ontologies This comprehensive one stop volume presents a wide range of practical bio ontology information offering you detailed guidance in the clustering of biological data protein classification gene and pathway prediction and text mining More than 160 illustrations support key topics throughout the book *Biological Ontologies and Semantic Biology* John Hancock,2014-10-03 As the amount of biological information and its diversity accumulates massively there is a critical need to facilitate the integration of this data to allow new and unexpected conclusions to be drawn from it The Semantic Web is a new wave of web based technologies that allows the linking of data between diverse data sets via standardised data formats big data Semantic Biology is the application of semantic web technology in the biological domain including medical and health informatics The Special Topic encompasses papers in this very broad area including not only ontologies development and applications but also text mining data integration and data analysis making use of the technologies of the Semantic Web Ontologies are a critical requirement for such integration as they allow conclusions drawn about biological experiments or descriptions of biological entities to be understandable and integratable despite being contained in different databases and analysed by different software systems Ontologies are the standard structures used in biology and more broadly in computer science to hold standardized terminologies for particular domains of knowledge Ontologies consist of sets of standard terms which are defined and may have synonyms for ease of searching and to accommodate different usages by different communities These terms are linked by standard relationships such as is_a an eye is_a sense organ or part_of an eye is part_of a head By linking terms in this way more detailed or granular terms can be linked to broader terms allowing computation to be carried out that takes these

relationships into account Artificial Intelligence in Bioinformatics Mario Cannataro,Pietro Hiram Guzzi,Giuseppe Agapito,Chiara Zucco,Marianna Milano,2022-05-12 Artificial Intelligence in Bioinformatics From Omics Analysis to Deep Learning and Network Mining reviews the main applications of the topic from omics analysis to deep learning and network mining The book includes a rigorous introduction on bioinformatics also reviewing how methods are incorporated in tasks and processes In addition it presents methods and theory including content for emergent fields such as Sentiment Analysis and Network Alignment Other sections survey how Artificial Intelligence is exploited in bioinformatics applications including sequence analysis structure analysis functional analysis protein classification omics analysis biomarker discovery integrative bioinformatics protein interaction analysis metabolic networks analysis and much more Bridges the gap between computer science and bioinformatics combining an introduction to Artificial Intelligence methods with a systematic review of its applications in the life sciences Brings readers up to speed on current trends and methods in a dynamic and growing field Provides academic teachers with a complete resource covering fundamental concepts as well as applications **Springer Handbook of Bio-/Neuro-Informatics** Nikola Kasabov,2013-11-30 The Springer Handbook of Bio Neuro Informatics is the first published book in one volume that explains together the basics and the state of the art of two major science disciplines in their interaction and mutual relationship namely information sciences bioinformatics and neuroinformatics Bioinformatics is the area of science which is concerned with the information processes in biology and the development and applications of methods tools and systems for storing and processing of biological information thus facilitating new knowledge discovery Neuroinformatics is the area of science which is concerned with the information processes in biology and the development and applications of methods tools and systems for storing and processing of biological information thus facilitating new knowledge discovery The text contains 62 chapters organized in 12 parts 6 of them covering topics from information science and bioinformatics and 6 cover topics from information science and neuroinformatics Each chapter consists of three main sections introduction to the subject area presentation of methods and advanced and future developments The Springer Handbook of Bio Neuroinformatics can be used as both a textbook and as a reference for postgraduate study and advanced research in these areas The target audience includes students scientists and practitioners from the areas of information biological and neurosciences With Forewords by Shun ichi Amari of the Brain Science Institute RIKEN Saitama and Karlheinz Meier of the University of Heidelberg Kirchhoff Institute of Physics and Co Director of the Human Brain Project

Bioinformatics Kenneth Baclawski & Tianhua Niu,2006-01-01 Recent advances in biotechnology spurred by the Human Genome Project have resulted in the accumulation of vast amounts of new data Ontologies computer readable precise formulations of concepts and the relationship among them in a given field are a critical framework for coping with the exponential growth of valuable biological data generated by high output technologies This book introduces the key concepts and applications of ontologies and ontology languages in bioinformatics and will be an essential guide for bioinformaticists

computer scientists and life science researchers The three parts of Ontologies for Bioinformatics ask and answer three pivotal questions what ontologies are how ontologies are used and what ontologies could be which focuses on how ontologies could be used for reasoning with uncertainty The authors first introduce the notion of an ontology from hierarchically organized ontologies to more general network organizations and survey the best known ontologies in biology and medicine They show how to construct and use ontologies classifying uses into three categories querying viewing and transforming data to serve diverse purposes Contrasting deductive or Boolean logic with inductive reasoning they describe the goal of a synthesis that supports both styles of reasoning They discuss Bayesian networks as a way of expressing uncertainty describe data fusion and propose that the World Wide Web can be extended to support reasoning with uncertainty They call this inductive reasoning web the Bayesian web

Artificial Intelligence Methods and Tools for Systems Biology W. Dubitzky, Francisco Azuaje, 2007-09-29 This book provides simultaneously a design blueprint user guide research agenda and communication platform for current and future developments in artificial intelligence AI approaches to systems biology It places an emphasis on the molecular dimension of life phenomena and in one chapter on anatomical and functional modeling of the brain As design blueprint the book is intended for scientists and other professionals tasked with developing and using AI technologies in the context of life sciences research As a user guide this volume addresses the requirements of researchers to gain a basic understanding of key AI methodologies for life sciences research Its emphasis is not on an intricate mathematical treatment of the presented AI methodologies Instead it aims at providing the users with a clear understanding and practical know how of the methods As a research agenda the book is intended for computer and life science students teachers researchers and managers who want to understand the state of the art of the presented methodologies and the areas in which gaps in our knowledge demand further research and development Our aim was to maintain the readability and accessibility of a textbook throughout the chapters rather than compiling a mere reference manual The book is also intended as a communication platform seeking to bridge the cultural and technological gap among key systems biology disciplines To support this function contributors have adopted a terminology and approach that appeal to audiences from different backgrounds

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

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based standards is the World Wide Web Consortium W3C <http://www.w3.org>

In Silico Technologies in Drug Target Identification and Validation Darryl Leon, Scott Markel, 2006-06-13 The pharmaceutical industry relies on numerous well designed experiments involving high throughput techniques and in silico approaches to analyze potential drug targets These in silico methods are often predictive yielding faster and less expensive analyses than traditional in vivo or in vitro procedures

In Silico Technologies in Drug Target Identification **Information-Theoretic Evaluation for Computational Biomedical Ontologies** Wyatt Travis Clark, 2014-01-09 The development of effective methods for the prediction of ontological annotations is an important goal in computational biology yet evaluating their performance is difficult due to problems caused by the structure of biomedical ontologies and incomplete annotations of genes This work proposes an information theoretic framework to evaluate the performance of computational protein function prediction A Bayesian network is used structured according to the underlying ontology to model the prior probability of a protein's function The concepts of misinformation and remaining uncertainty are then defined that can be seen as analogs of precision and recall Finally semantic distance is proposed as a single statistic for ranking classification models The approach is evaluated by analyzing three protein function predictors of gene ontology terms The work addresses several weaknesses of current metrics and provides valuable insights into the performance of protein function prediction tools

Databases and Information Systems Albertas Caplinskas, 2005 Modern databases and information systems essentially differ from their predecessors Ontology based and knowledge based approaches to system development UML based IS development methodologies XML databases and heterogeneous information models have come to the fore All these fundamental aspects are discussed in this book This publication contains a collection of 22 high quality papers written by 44 authors These articles present original results in modern database technologies database applications data warehousing data mining ontologies and modern information systems Special emphasis is put on multimedia database systems heterogeneous data integration methods view optimizations ontology engineering tools modeling and model transformations MDA Theoretical aspects as well as technical development issues are considered The intended audience for this book is researchers advanced students and practitioners who are interested in advanced topics on databases and information systems

Formal Ontology in Information Systems Carola Eschenbach, Michael Gruninger, 2008 Since its start ten years ago the International Conference in Formal Ontology on Information Systems FOIS has explored the multiple perspectives on the notion of ontology that have arisen from such diverse research communities as philosophy logic computer science cognitive science linguistics and various scientific domains As ontologies have been applied in new and exciting domains such as the World Wide Web bioinformatics and geographical information systems it has become evident that there is a need for ontologies that have been developed with solid theoretical foundations based on philosophical linguistic and logical analysis Similarly there is also a need for theoretical research that is driven by the issues that have been raised by recent work in the more applied domains

FOIS is intended to be a forum in which to explore this interplay between the theoretical insights of formal ontology and their application to information systems and emerging semantic technologies Themes emerging from this volume give a snapshot of current issues within the fields of formal ontology and ontological engineering as well providing a glimpse of future research directions Book Jacket **Formal Methods for the Analysis of Biomedical Ontologies** Guo-Qiang Zhang,Rashmie Abeysinghe,Licong Cui,2025-08-29 This book explores the application of formal methods rooted in mathematics and logic to the analysis and enhancement of biomedical ontologies The authors take a pragmatic approach focused on generating actionable insights to achieve high quality codified biomedical knowledge in the most active and impactful areas where ontologies have a direct real world impact The book first introduces simple yet formalized strategies for discovering undesired and incoherent patterns in ontologies before exploring the application of formal concept analysis for semantic completeness The authors then discuss formal concept analysis as an ontological engineering principle The book goes on to highlight the power and utility of uncovering non lattice structure for debugging ontologies This Second Edition includes a new chapter that covers recent research on leveraging logical definitions for identifying ontological defects The authors have also added a new chapter on the perspective of using large language models in the ontological analysis work

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