Integrating Sequence and Structure Data for Annotating Functional Sites on Protein Structures

Mike Liang Stanford University

Structural genomics initiatives are developing high-throughput methods for large-scale determination of all protein structures. The biological roles for many of these proteins are still unknown, and high-throughput computational methods for determining their function are necessary. Understanding the function of these proteins will have profound impact in drug development and protein engineering.

Current methods for functional annotation of these protein structures are based on sequence only or structure only analysis. Although sequence based methods have been quite powerful, they often have limited use when sequence similarity is low. Structure base methods are less sensitive to sequence similarity, but many of the structure based methods require manual creation of models and are thus limited by the number of available functional models. Methods for function annotation at a structural-genomics scale will require both greater sensitivity than what sequence only methods provide and more functional models than what the structural models offer.

To address the requirements for structural-genomics scale function annotation, we have developed a method, SegFEATURE, for automatically constructing a three-dimensional (3D) model of the functional site by integrating sequence and structure data. The 3D models describe the physicochemical environment around sequence motifs and identify the significant properties that are statistically conserved or absent in the functional site. These 3D models have better sensitivity than one-dimensional (1D) sequence motifs in function annotation. By automatically creating these 3D models from sequence motifs, we have developed a method for building a library of models that can be used in context of a structural genomics pipeline for functional annotation of protein structures.

SegFeature is available on the web at http://feature.stanford.edu/webfeature. Biologists can rapidly annotate their structure with the currently available library of functional models.

Frontiers Of Bioinformatics Unsolved Problems And Challenges

Samuel Karlin, David Eisenberg, Russ
Altman, National Academy of Sciences

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Frontiers of Bioinformatics ,2005 (Sackler NAS Colloquium) Frontiers of Bioinformatics Samuel Karlin, David Eisenberg, Russ Altman, National Academy of Sciences, 2005-09-28 Ethical Issues in AI for Bioinformatics and Chemoinformatics Yashwant V. Pathak, Surovi Saikia, Sarvadaman Pathak, Jayvadan K. Patel, Jigna Bhupendra Prajapati, 2023-11-14 This unique volume presents AI in relation to ethical points of view in handling big data sets Issues such as algorithmic biases discrimination for specific patterns and privacy breaches may sometimes be skewed to affect research results so that certain fields to appear more appealing to funding agencies The discussion on the ethics of AI is highly complex due to the involvement of many international stakeholders such as the UN OECD parliaments industry groups professional bodies and individual companies The issue of reliability is addressed including the emergence of synthetic life 5G networks intermingling of human artificial intelligence nano robots and cyber security tools Features Discusses artificial intelligence and ethics the challenges and opportunities Presents the issue of reliability in the emergence of synthetic life 5G networks intermingling of human artificial intelligence nano robots and cyber security tools Ethical responsibility and reasoning for using AI in Big Data Addresses practicing medicine and ethical issues when applying artificial intelligence

A Journey Through Nonlinear Functional Analysis and Its Applications Pasquale De Genome Research .2007 Marco, In the realm of mathematics nonlinear functional analysis stands as a beacon of innovation illuminating the complexities of nonlinear operators and their far reaching applications This comprehensive volume A Journey Through Nonlinear Functional Analysis and Its Applications invites readers to embark on an enlightening odyssey into this captivating mathematical landscape With meticulous explanations insightful examples and a captivating narrative this book unveils the elegance and practical significance of nonlinear functional analysis Its meticulously crafted chapters guide readers through the fundamental concepts and techniques of nonlinear functional analysis laying a solid foundation for understanding its diverse applications Delving into a myriad of fields this book showcases the transformative power of nonlinear functional analysis in addressing intricate problems in mathematical physics engineering economics finance and beyond Readers will discover how nonlinear functional analysis empowers researchers and practitioners to gain deeper insights into complex phenomena leading to groundbreaking advancements in various disciplines Written with both clarity and rigor this book caters to a broad audience encompassing students researchers and practitioners seeking to expand their knowledge and expertise in nonlinear functional analysis Its comprehensive coverage engaging writing style and abundance of illustrative examples make it an invaluable resource for anyone seeking to master this powerful mathematical tool Throughout this intellectual journey readers will gain a comprehensive grasp of nonlinear functional analysis and its far reaching applications empowering them to tackle intricate problems with renewed confidence and ingenuity A Journey Through Nonlinear Functional Analysis and Its Applications is an essential guide for anyone seeking to delve into the depths of this captivating

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molecular genetics is facilitating the rapid evaluation of the essentiality of these targets on a genomic scale In 2015 a group of researchers established the International Conference on Antibiotic Resistance IC2AR The primary objective of this meeting is to bring together scientists involved in antibiotic resistance prevention and control The IC2AR conducted its inaugural world congress in January 2015 at Caparica Portugal Antimicrobial resistance presents a significant challenge to scientists in the field of infectious diseases The full knowledge of how antibiotics resistance is evolving and being transmitted between hosts in different ecosystems is taking on great importance Necessary action includes research to define the scope of the problem including its various sources This eBook comprises a series of original research and review articles dealing with the epidemiology of resistance in animal and zoonotic pathogens mobile elements containing resistance genes the omics of antimicrobial resistance emerging antimicrobial resistance mechanisms control of resistant infections establishing antimicrobial use and resistance surveillance systems and alternatives strategies to overcome the problem of antimicrobial resistance worldwide Gilberto Igrejas Jos Luis Capelo and Patr cia Poeta Scientific Committee of IC2AR February 20th 2017

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