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Advances in Structural Engineering was established in 1997 and has become one of the major peer-reviewed journals in the field of structural engineering. To better fulfil the mission of the journal, we have recently decided to launch two new features for the journal: (a) invited review papers providing an in-depth exposition of a topic of significant current interest; (b) short papers reporting truly new technologies in structural engineering.

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Advance in Structural Bioinformatics Dongqing Wei , Qin Xu , Tangzhen Zhao , Hao Dai (eds.) This text examines in detail mathematical and physical modeling, computational methods and systems for obtaining and analyzing biological structures, using pioneering research cases as examples.

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Advances in Civil Engineering publishes original research articles as well as review articles in all areas of civil engineering. The journal welcomes submissions across a range of disciplines, and publishes both theoretical and practical studies.

This text examines in detail mathematical and physical modeling, computational methods and systems for obtaining and analyzing biological structures, using pioneering research cases as examples. As such, it emphasizes programming and problem-solving skills. It provides information on structure bioinformatics at various levels, with individual chapters covering introductory to advanced aspects, from fundamental methods and guidelines on acquiring and analyzing genomics and proteomics sequences, the structures of protein, DNA and RNA, to the basics of physical simulations and methods for conformation searches. This book will be of immense value to researchers and students in the fields of bioinformatics, computational biology and chemistry. Dr. Dongqing Wei is a Professor at the Department of Bioinformatics and Biostatistics, College of Life Science and Biotechnology, Shanghai Jiaotong University, Shanghai, China. His research interest is in the general area of structural bioinformatics.

Structural Bioinformatics was the first major effort to show the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure, such as the prediction of protein structure and how proteins carry out cellular functions, and how the application of bioinformatics to these life science issues can improve healthcare by accelerating drug discovery and development. Designed primarily as a reference, the first edition nevertheless saw widespread use as a textbook in graduate and undergraduate university courses dealing with the theories and associated algorithms, resources, and tools used in the analysis, prediction, and theoretical underpinnings of DNA, RNA, and proteins. This new edition contains not only thorough updates of the advances in structural bioinformatics since publication of the first edition, but also features eleven new chapters dealing with frontier areas of high scientific impact, including: sampling and search techniques; use of mass spectrometry; genome functional annotation; and much more. Offering detailed coverage for practitioners while remaining accessible to the novice, Structural Bioinformatics, Second Edition is a valuable resource and an excellent textbook for a range of readers in the bioinformatics and advanced biology fields. Praise for the previous edition: "This book is a gold mine of fundamental and practical information in an area not previously well represented in book form." –Biochemistry and Molecular Education "...destined to become a classic reference work for workers at all levels in structural bioinformatics...recommended with great enthusiasm for educators, researchers, and graduate students." –BAMBED "...a useful and timely summary of a rapidly expanding field." –Nature Structural Biology "...a terrific job in this timely creation of a compilation of articles that appropriately addresses this issue." –Briefings in Bioinformatics

"This book compiles studies that demonstrate effective approaches to the structural analysis of genetic systems and bioinformatics"--Provided by publisher.

The advanced AI techniques are essential for resolving various problematic aspects emerging in the field of bioinformatics. This book covers the recent approaches in artificial intelligence and machine learning methods and their applications in Genome and Gene editing, cancer drug discovery classification, and the protein folding algorithms among others. Deep learning, which is widely used in image processing, is also applicable in bioinformatics as one of the most popular artificial intelligence approaches. The wide range of applications discussed in this book are an indispensable resource for computer scientists, engineers, biologists, mathematicians, physicians, and medical informaticists. Features: Focuses on the cross-disciplinary relation between computer science and biology and the role of machine learning methods in resolving complex problems in bioinformatics Provides a comprehensive and balanced blend of topics and applications using various advanced algorithms Presents cutting-edge research methodologies in the area of AI methods when applied to bioinformatics and innovative solutions Discusses the AI/ML techniques, their use, and their potential for use in common and future bioinformatics applications Includes recent achievements in AI and bioinformatics contributed by a global team of researchers

This book constitutes the refereed proceedings of the 12th International Conference entitled Beyond Databases, Architectures and Structures, BDAS 2016, held in Ustroń, Poland, in May/June 2016. It consists of 57 carefully reviewed papers selected from 152 submissions. The papers are organized in topical sections, namely artificial intelligence, data mining and knowledge discovery; architectures, structures and algorithms for efficient data processing; data warehousing and OLAP; natural language processing, ontologies and semantic Web; bioinformatics and biomedical data analysis; data processing tools; novel applications of database systems.

Advancements in medical and healthcare technologies pave the way to improving treatments and diagnoses while also streamlining processes to ensure the highest quality care is given to patients. In the last few decades, revolutionary technology has radically progressed the healthcare industry by increasing life expectancy and reducing human error. Advanced Methodologies and Technologies in Medicine and Healthcare provides emerging research on bioinformatics, medical ethics, and clinical science in modern applications and settings. While highlighting the challenges medical practitioners and healthcare professionals face when treating patients and striving to optimize their processes, the book shows how revolutionary technologies and methods are vastly improving how healthcare is implemented globally. This book is an important resource for medical researchers, healthcare administrators,

doctors, nurses, biomedical engineers, and students looking for comprehensive research on the advancements in healthcare technologies.

Recent Advancement in Prodrugs Drugs used as medicines have many limitations like low chemical stability, aqueous solubility, or oral absorption/bioavailability, rapid presystemic metabolism, toxicity, inadequate site specificity, or poor patient acceptance/compliance (unwanted adverse effects, unacceptable taste or odor, irritation or pain). Prodrugs design is an approach to overcome these limitations. Key features Covers recent advancements in development of prodrugs Presents balanced synthesis and applications of prodrug chemistry Discusses broad spectrum of prodrug categories and outlines industrial applications Reviews prodrugs in cancer nanomedicine, its therapy and treatment Elucidates mathematical models to study the kinetics of prodrugs This book covers recent advances in the design of prodrugs. It contains all the significant recent examples of prodrug chemistry developments and will aid academics and researchers seeking to generate new projects in the field.

The Advances in Protein Chemistry and Structural Biology series is an essential resource for protein chemists. Each volume brings forth new information about protocols and analysis of proteins, with each thematically organized volume guest edited by leading experts in a broad range of protein-related topics. Provides cutting-edge developments in protein chemistry and structural biology Chapters are written by authorities in their field Targeted to a wide audience of researchers, specialists, and students

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This book constitutes the refereed proceedings of the 6th International Conference on Intelligent Computing, ICIC 2010, held in Changsha, China, in August 2010. The 85 revised full papers presented were carefully reviewed and selected from a numerous submissions. The papers are organized in topical sections on neural networks, evolutionary learning & genetic algorithms, fuzzy theory and models, fuzzy systems and soft computing, particle swarm optimization and niche technology, supervised & semi-supervised learning, unsupervised & reinforcement learning, combinatorial & numerical optimization, systems biology and computational biology, neural computing and optimization, nature inspired computing and optimization, knowledge discovery and data mining, artificial life and artificial immune systems, intelligent computing in image processing, special session on new hand based biometric methods, special session on recent advances in image segmentation, special session on theories and applications in advanced intelligent computing, special session on search based software engineering, special session on bio-inspired computing and applications, special session on advance in dimensionality reduction methods and its applications, special session on protein and gene bioinformatics: methods and applications.

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