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The Pacific Symposium on Biocomputing (PSB) 2016 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in problems of biological significance. Presentations are rigorously peer reviewed and are published in an archival proceedings volume.

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Papers and presentations were rigorously peer reviewed and were published in an archival proceedings volume. PSB 2016 was held January 4-8, 2016 at the Fairmont Orchid, Big Island of Hawaii. PSB 2016 brought together top researchers from the US, the Asian Pacific nations, and around the world to exchange research results and address open issues in all aspects of computational biology.

Pacific Symposium on Biocomputing 2016, PSB 2016

SUI '16: Proceedings of the 2016 Symposium on Spatial User Interaction. 2016. Previous Next. Abstract. It is our great pleasure to welcome you to the fourth ACM Symposium on Spatial User Interaction. This event focuses on the user interface challenges that appear when users interact in the space where the flat, two-dimensional, digital world ...

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Welcome to the Proceedings of the 2016 ACM Joint International Conference on Pervasive and Ubiquitous Computing (UbiComp 2016), held in Heidelberg, Germany from Sep. 12-16, co-located with the International Symposium on Wearable Computers (ISWC) 2016. This is the forth instance of the conference after the merger of the previous "Pervasive" and ...

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CHI 2016 is the premier world-wide conference for Human-Computer Interaction (HCI) and this year took place in the heart of Silicon Valley, San Jose, California. The Proceedings and Extended Abstracts represent today's most innovative, novel and creative work in HCI.

Proceedings of the 2016 CHI Conference on Human Factors in ...

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Biocomputing 2018 - World Scientific

Gil Speyer, Jeff Kiefer, Harshil Dhruv, Michael Berens, Seungchan Kim ; Pacific Symposium on Biocomputing 21:33-44 (2016) Integrating Genetic and Structural Data on Human Protein Kinome in Network-Based Modeling of Kinase Sensitivities and Resistance to Targeted and Personalized Anticancer Drugs

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This book highlights the latest research on practical applications of computational biology and bioinformatics, and addresses emerging experimental and sequencing techniques that are posing new challenges for bioinformatics and computational biology. Successfully applying these techniques calls for new algorithms and approaches from fields such as statistics, data mining, machine learning, optimization, computer science, and artificial intelligence. In response to these challenges, we have seen the rise of a new generation of interdisciplinary scientists with a strong background in the biological and computational sciences. These proceedings include 21 papers covering many different subfields of bioinformatics and computational biology. Focusing on interdisciplinary applications that combine e.g. bioinformatics, cheminformatics, and system biology, they are intended to promote the collaboration of scientists from different research groups and with different backgrounds (computer scientists, mathematicians, biologists) to reach breakthrough solutions and overcome the challenges outlined above.

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BIOINFORMATICS AND MEDICAL APPLICATIONS The main topics addressed in this book are big data analytics problems in bioinformatics research such as microarray data analysis, sequence analysis, genomics-based analytics, disease network analysis, techniques for big data analytics, and health information technology. *Bioinformatics and Medical Applications: Big Data Using Deep Learning Algorithms* analyses massive biological datasets using computational approaches and the latest cutting-edge technologies to capture and interpret biological data. The book delivers various bioinformatics computational methods used to identify diseases at an early stage by assembling cutting-edge resources into a single collection designed to enlighten the reader on topics focusing on computer science, mathematics, and biology. In modern biology and medicine, bioinformatics is critical for data management. This book explains the bioinformatician's important tools and examines how they are used to evaluate biological data and advance disease knowledge. The editors have curated a distinguished group of perceptive and concise chapters that presents the current state of medical treatments and systems and offers emerging solutions for a more personalized approach to healthcare. Applying deep learning techniques for data-driven solutions in health information allows automated analysis whose method can be more advantageous in supporting the problems arising from medical and health-related information. Audience The primary audience for the book includes specialists, researchers, postgraduates, designers, experts, and engineers, who are occupied with biometric research and security-related issues.

This book constitutes the proceedings of the 20th Annual Conference on Research in Computational Molecular Biology, RECOMB 2016, held in Santa Monica, CA, USA, in April 2016. The 15 regular papers presented in this volume were carefully reviewed and selected from 172 submissions. 20 short abstracts are included in the back matter of the volume. They report on original research in all areas of computational molecular biology and bioinformatics.

This book constitutes the refereed proceedings of the 4th International Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2016, held in Granada, Spain, in April 2016. The 69 papers presented were carefully reviewed and selected from 286 submissions. The scope of the conference spans the following areas: bioinformatics for healthcare and diseases; biomedical image analysis; biomedical signal analysis; computational systems for modeling biological processes; eHealth; tools for next generation sequencing data analysis; assistive technology for people with neuromotor disorders; fundamentals of biological dynamics and maximization of the information extraction from the experiments in the biological systems; high performance computing in bioinformatics, computational biology and computational chemistry; human behavior monitoring, analysis and understanding; pattern recognition and machine learning in the -omics sciences; and resources for bioinformatics.

This book constitutes the proceedings of the 6th International Conference on Analysis of Images, Social Networks and Texts, AIST 2017, held in Moscow, Russia, in July 2017. The 29 full papers and 8 short papers were carefully reviewed and selected from 127 submissions. The papers are organized in topical sections on natural language processing; general topics of data

analysis; analysis of images and video; optimization problems on graphs and network structures; analysis of dynamic behavior through event data; social network analysis.

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