Bioinformatics For Diagnosis Prognosis And Treatment Of Complex Diseases Translational Bioinformatics

"Chapter 1 An introduction to next-generation biological platforms Virginia Mohlere, Wenting Wang, and Ganiraju Manyam The University of Texas. MD Anderson Cancer Center 1.1 Introduction When Sanger and Coulson first described a reliable, efficient method for DNA sequencing in 1975 (Sanger and Coulson, 1975), they made possible the full sequencing of both genes and entire genomes. Although the method was resource-intensive, many institutions invested in the necessary equipment, and Sanger sequencing remained the standard for the next 30 years. Refinement of the process increased read lengths from around 25 to 2 Mohlere, Wang, and Manyam almost 750 base pairs (Schadt et al., 2010, fig. 1). While this greatly increased efficiency and reliability, the Sanger method still required not only large equipment but significant human investment, as the process requires the work of several people. This prompted researchers and companies such as Applied Biosystems to seek improved sequencing techniques and instruments. Starting in the late 2000s, new instruments came on the market that, although they actually decreased read length, lessened run time and could be operated more easily with fewer human resources (Schadt et al., 2010). Despite discoveries that have illuminated new therapeutic targets, clarified the role of specific mutations in clinical response, and yielded new methods for diagnosis and predicting prognosis (Chin et al., 2011), the initial promise of genomic data has largely remained so far unfulfilled. The difficulties are numerous"--

Single-cell Omics: Technological Advances and Applications provides the latest technological developments and the applications of single-cell technologies in the field of biomedicine. The advent of omics technologies have enable us to identify the differences between cell types and subpopulations at the level of the genome, proteome, transcriptome, epigenome, and in several other fields of omics. In the current era of precision medicine, the single-cell omics technology is highly promising due to its potential in diagnosis, prognosis, and therapeutics. The book is divided in five parts: the first one brings an overview of single-cell omics researches and applications; the second deals with the diverse technologies applied in the topic, such as pangenomics, metabolomics, and multi-omics of single cells; the third is dedicated to data analysis; the forth one discusses the several applications of single-cell omics within biomedical field, for example in cancer, metabolic and neuro diseases, immunology, pharmacogenomics, personalized medicine and reproductive health; and a final discussion on future perspectives. This book is a valuable source for bioinformaticians, molecular diagnostic researchers, clinicians and several members of biomedical field interested in understanding more about single-cell omics and its potential for research and diagnosis. Covers not only the technological aspects, but also the diverse applications of single cell omics in the biomedical field Summarizes the latest progress in single cell omics and discusses potential future developments for research and diagnosis Written by experts across the world, bringing different points-of-view and case studies to give a comprehensive overview on the topic

Computational Epigenetics and Diseases, written by leading scientists in this evolving field, provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases. In particular, the major computational tools, databases, and strategies for computational epigenetics analysis, for example, DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA, are summarized, in the context of human diseases. This book discusses bioinformatics methods for epigenetic analysis specifically applied to human conditions such as aging, atherosclerosis, diabetes mellitus, schizophrenia, bipolar disorder, Alzheimer disease, Parkinson disease, liver and autoimmune disorders, and reproductive and respiratory diseases. Additionally, different organ cancers, such as breast, lung, and colon, are discussed. This book is a valuable source for graduate students and researchers in genetics and bioinformatics, and several biomedical field members interested in applying computational epigenetics in their research. Provides a comprehensive and cutting-edge knowledge of computational epigenetics in human diseases Summarizes the major computational tools, databases, and strategies for computational epigenetics analysis, such as DNA methylation, histone modifications, microRNA, noncoding RNA, and ceRNA Covers the major milestones and future directions of computational epigenetics in various kinds of human diseases such as aging, atherosclerosis, diabetes, heart disease, neurological disorders, cancers, blood disorders, liver diseases, reproductive diseases, respiratory diseases, autoimmune diseases, human imprinting disorders, and infectious diseases

The state of the science of bioinformatics - that is, application of computer processes to solving biological problems - and its potential for assisting early cancer detection, risk assessment, and risk reduction form the focus of this volume.

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development, Volume II

Genomics and Proteomics for Clinical Discovery and Development

Outcome Prediction in Cancer

Single-cell Omics

Functional Coherence of Molecular Networks in Bioinformatics

Kernel Methods in Computational Biology

Molecular networks provide descriptions of the organization of various biological processes, including cellular signaling, metabolism, and genetic regulation. Knowledge on molecular networks is commonly used for systems level analysis of biological function; research and method development in this area has grown tremendously in the past few years. This book will provide a detailed review of existing knowledge on the functional characterization of biological networks. In 15 chapters authored by an international group of prolific systems biology and bioinformatics researchers, it will organize, conceptualize, and summarize the existing core of research results and computational methods on understanding biological function from a network perspective.

This book is organized into 4 sections, each looking at the question of outcome prediction in cancer from a different angle. The first section describes the clinical problem and some of the predicaments that clinicians face in dealing with cancer. Amongst issues discussed in this section are the TNM staging, accepted methods for survival analysis and competing risks. The second section describes the biological and genetic markers and the rôle of bioinformatics. Understanding of the genetic and environmental basis of cancers will help in identifying high-risk populations and developing effective prevention and early detection strategies. The third section provides technical details of mathematical analysis behind survival prediction backed up by examples from various types of cancers. The fourth section describes a number of machine learning methods which have been applied to decision support in cancer. The final section describes how information is shared within the scientific and medical communities and with the general population using information technology and the World Wide Web. * Applications cover 8 types of cancer including brain, eye, mouth, head and neck, breast, lungs, colon and prostate * Include contributions from authors in 5 different disciplines * Provides a valuable educational tool for medical informatics

Bioinformatics is an integrative field of computer science, genetics, genomics, proteomics, and statistics, which has undoubtedly revolutionized the study of biology and medicine in past decades. It mainly assists in modeling, predicting and interpreting large multidimensional biological data by utilizing advanced computational methods. Despite its enormous potential, bioinformatics is not widely integrated into the academic curriculum as most life science students and researchers are still not equipped with the necessary knowledge to take advantage of this powerful tool. Hence, the primary purpose of our book is to supplement this unmet need by providing an easily accessible platform for students and researchers starting their career in life sciences. This book aims to avoid sophisticated computational algorithms and programming. Instead, it focuses on simple DIY analysis and interpretation of biological data with personal computers. Our belief is that once the beginners acquire these basic skillsets, they will be able to handle most of the bioinformatics tools for their research work and to better understand their experimental outcomes. Our second title of this volume set In Silico Life Sciences: Medicine provides hands-on experience in analyzing high throughput molecular data for the diagnosis, prognosis, and treatment of monogenic or polygenic human diseases. The key concepts in this volume include risk factor assessment, genetic tests and result interpretation, personalized medicine, and drug discovery. This volume is expected to train readers in both single and multi-dimensional biological analysis using open data sets, and provides a unique learning experience through clinical scenarios and case studies.

This book introduces the reader to modern computational and statistical tools for translational epigenomics research. Over the last decade, epigenomics has emerged as a key area of molecular biology, epidemiology and genome medicine. Epigenomics not only offers us a deeper understanding of fundamental cellular biology, but also provides us with the basis for an improved understanding and management of complex diseases. From novel biomarkers for risk prediction, early detection, diagnosis and prognosis of common diseases, to novel therapeutic strategies, epigenomics is set to play a key role in the personalized medicine of the future. In this book we introduce the reader to some of the most important computational and statistical methods for analyzing epigenomic data, with a special focus on DNA methylation. Topics include normalization, correction for cellular heterogeneity, batch effects, clustering, supervised analysis and integrative methods for systems epigenomics. This book will be of interest to students and researchers in bioinformatics, biostatistics, biologists and clinicians alike. Dr. Andrew E. Teschendorff is Head of the Computational Systems Genomics Lab at the CAS-MPG Partner Institute for Computational Biology, Shanghai, China, as well as an Honorary Research Fellow at the UCL Cancer Institute, University College London, UK.

Bioinformatics Tools for Detection and Clinical Interpretation of Genomic Variations

Bioinformatics Approaches to Cancer Biomarker Discovery and Characterization

Bioinformatics for Diagnosis, Prognosis and Treatment of Complex Diseases

Computational Epigenetics and Diseases

Cancer Genomics

Cancer and Noncoding RNAs

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.

This book constitutes the thoroughly refereed post-proceedings of the 7th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics, CIBB 2010, held in Palermo, Italy, in September 2010. The 19 papers, presented together with 2 keynote speeches and 1 tutorial, were carefully reviewed and selected from 24 submissions. The papers are organized in topical sections on sequence analysis, promoter analysis and identification of transcription factor binding sites; methods for the unsupervised analysis, validation and visualization of structures discovered in bio-molecular data -- prediction of secondary and tertiary protein structures; gene expression data analysis; bio-medical text mining and imaging -- methods for diagnosis and prognosis; mathematical modelling and simulation of biological systems; and intelligent clinical decision support systems (i-CDSS).

Integrated bioinformatics solutions have become increasingly valuable in past years, as technological advances have allowed researchers to consider the potential of omics for clinical diagnosis, prognosis, and therapeutic purposes, and as the costs of such techniques have begun to lessen. In Bioinformatics Methods in Clinical Research, experts examine the latest developments impacting clinical omics, and describe in great detail the algorithms that are currently used in publicly available software tools. Chapters discuss statistics, algorithms, automated methods of data retrieval, and experimental consideration in genomics, transcriptomics, proteomics, and metabolomics. Composed in the highly successful Methods in Molecular BiologyTM series format, each chapter contains a brief introduction, provides practical examples illustrating methods, results, and conclusions from data mining strategies wherever possible, and includes a Notes section which shares tips on troubleshooting and avoiding known pitfalls. Informative and ground-breaking, Bioinformatics Methods in Clinical Research establishes a much-needed bridge between theory and practice, making it an indispensable resource for bioinformatics researchers.

This book constitutes the proceedings of the 17th International Symposium on Bioinformatics Research and Applications, ISBRA 2021, held in Shenzhen, China, in November 2021. The 51 full papers presented in this book were carefully reviewed and selected from 135 submissions. They were organized in topical sections named: AI and disease; computational proteomics; biomedical imaging; drug screening and drug-drug interaction prediction; Biomedical data; sequencing data analysis.

Models and Integrative Inference for High-Throughput Data

The Applications of Bioinformatics in Cancer Detection

Technological Advances and Applications

7th International Work-Conference, IWBBIO 2019, Granada, Spain, May 8-10, 2019, Proceedings, Part I

Bioinformatics Research and Applications

Computer Modelling in Bioengineering

Recently, high-throughput profiling techniques such as microarray and next generation sequencing have revolutionized modern biology and enabled disease understanding at a genome scale. Due to the large volume of data from these technologies, enormous amount of scientific efforts are needed for identifying key biological insights. To achieve this goal, it is urgent to develop novel computational methodologies and tools that integrate different types of data for augmenting system level understanding of disease and improving personalize treatment to the next level. From this perspective we address three critical challenges of computational biology and bioinformatics in this dissertation: (1) to identify key genes/biomarkers related to disease, (2) to design better classifiers to identify disease status for improving overall treatment process, and (3) to design better model for predicting drug efficacy in early drug development stage. This dissertation has made significant contributions to improve disease classification, prognosis and treatment for the above mentioned challenges. First, we developed a graph theoretical approach to combine microarray gene expression profiles and protein-protein interaction (PPI) network for biomarker discovery for different cancers. Identifying key genes (biomarkers) involved in different disease is a central problem in system biology and an important step towards constructing better models for disease prognosis and treatment. Using PPI network to capture pathway-level gene-gene relationships, our method have the potential to identify true biomarkers that are reproducible across different patient cohorts and can increase the accuracy of disease diagnosis / prognosis. Next, we designed a personalized committee based approach to predict metastatic status for cancer patients based on their gene expression profiles. The key idea of our method is to construct personalized models that address both the heterogeneity of disease, which is normally overlooked by existing methods, and the ambiguous as well as stereotypical cancer subtypes defined in previous studies. Results showed that our method can significantly improve cancer metastasis prediction compared to other popular methods. Finally, we developed an ensemble classification method to combine multiple types of data for better prediction of drug side-effects. The data were obtained from different public domains that include drug chemical structural information and drug side-effect information. Applying our method on large scale characterized and un-characterized small molecule drugs in drug-bank database, we find that our method can significantly increase accuracy for drug side-effect prediction compared to other methods and showed better performance for `hard to predict' rare side-effects cases. Taken together, the results achieved from the sub-problems demonstrates in this dissertation shows the feasibility of applying and enhancing machine learning and graph based approaches to solve complex biological problems.

Cancers are a heterogeneous set of diseases that are defined by uncontrolled cellular growth with the potential to invade or spread to adjacent and distant tissues. While sharing certain biological capabilities that define the development and behavior of all human malignancies, cancers are governed by complex molecular changes that are often tumor-specific. As a result, even tumors arising from the same cell-type can exhibit highly divergent prognoses and treatment responses depending upon the underlying molecular mechanisms that are dysregulated and that drive its abnormal growth and cellular processes. New data collection methods grant researchers unprecedented capability to investigate and characterize cancers on a systems level. Rather than being restricted in measurement to a specific target molecule or set of molecules, "-omics" approaches allow experiments to identify and measure thousands of molecules at a time. These "-omics" approaches can therefore characterize significant proportions of the genetic, transcript, protein, and post-translational modification landscapes that underlie and drive human malignancies. Because cancers represent such a diverse set of diseases, clinicians and researchers rely on biomarkers for a variety of uses in cancer, ranging from diagnosis to prognosis and prediction of treatment response. A good cancer biomarker is a molecular signal that is capable of distinguishing, for example, disease from normal, high-risk from low risk disease, or disease cases that may be particularly susceptible to targeted treatments.In this dissertation, I demonstrate the use of multiple bioinformatics tools for cancer biomarker discovery and characterization. Models of epigenetic age, termed epigenetic clocks, are investigated in gliomas and are shown to be associated with previously defined prognostic molecular subtypes and are independently predictive of survival. I introduce a novel method for phosphoproteomics analysis, termed pKSEA, which uses in silico kinase-substrate predictions to infer changes in kinase activity. pKSEA is described, benchmarked against previously published data, and compared to existing methods. Three examples are provided of pKSEA analysis in cancer-related data, identifying kinase activity signals that may be useful as biomarkers in identifying and targeting high risk glioblastomas, as well as identifying treatment-related phosphorylation signaling changes in response to kinase inhibition and phosphatase activation in cancer cells.

Single-cell Omics, Volume 2: Advances in Applications provides the latest single-cell omics applications in the field of biomedicine. The advent of omics technologies have enabled us to identify the differences between cell types and subpopulations at the level of the genome, proteome, transcriptome, epigenome, and in several other fields of omics. The book is divided into two sections: the first is dedicated to biomedical applications, such as cell diagnostics, non-invasive prenatal testing (NIPT), circulating tumor cells, breast cancer, gliomas, nervous systems and autoimmune disorders, and more. The second focuses on cell omics in plants, discussing micro algal and single cell omics, and more. This book is a valuable source for bioinformaticians, molecular diagnostic researchers, clinicians and several members of biomedical field interested in understanding more about single-cell omics and its potential for research and diagnosis. Covers the diverse single cell omics applications in the biomedical field Summarizes the latest progress in single cell omics and discusses potential future developments for research and diagnosis Written by experts across the world, it brings different points-of-view and study cases to fully give a comprehensive overview of the topic

Bioinformatics for Diagnosis, Prognosis and Treatment of Complex DiseasesSpringer Science & Business Media

Single Cell Sequencing and Systems Immunology

Clustering, Classification and Function Estimation for High Dimensional Data Arising from Bioinformatics and Related Domains

Advances in Statistical Bioinformatics

Volume 1: Technological Advances and Applications

ABC of Bioinformatics

Computational Intelligence in Oncology

A Primer on Molecular Biology. A Primer on Kernel Methods. Support Vector Machine Applications in Computational Biology. Inexact Matching String Kernels for Protein Classification. Fast Kernels for String and Tree Matching. Local Alignment Kernels for Biological Sequences. Kernels for Graphs. Diffusion Kernels. A Kernel for Protein Secondary Structure Prediction. Heterogeneous Data Comparsion and Gene Selection with Kernel Canonical Correlation Analysis. Kernel-Based Integration of Genomic Data Using Semdefinite Programming. Protein Classification via Kernel Matrix Completion. Accurate Splice Site Detection for Caenorhabditid elegans. Gene Espression Analysis: Joint Feature Selection and Classifier Design. Gene Selection for Microarray Data.

Epigenetic Biomarkers and Diagnostics comprises 31 chapters contributed by leading active researchers in basic and clinical epigenetics. The book begins with the basis of epigenetic mechanisms and descriptions of epigenetic biomarkers that can be used in clinical diagnostics and prognostics. It goes on to discuss classical methods and next generation sequencing-based technologies to discover and analyze epigenetic biomarkers. The book concludes with an account of DNA methylation, post-translational modifications and noncoding RNAs as the most promising biomarkers for cancer (i.e. breast, lung, colon, etc.), metabolic disorders (i.e. diabetes and obesity), autoimmune diseases, infertility, allergy, infectious diseases, and neurological disorders. The book describes the challenging aspects of research in epigenetics, and current findings regarding new epigenetic elements and modifiers, providing guidance for researchers interested in the most advanced technologies and tested biomarkers to be used in the clinical diagnosis or prognosis of disease. Focuses on recent progress in several areas of epigenetics, general concepts regarding epigenetics, and the future prospects of this discipline in clinical diagnostics and prognostics Describes the importance of the quality of samples and clinical associated data, and also the ethical issues for epigenetic diagnostics Discusses the advances in epigenomics technologies, including next-generation sequencing based tools and applications Expounds on the utility of epigenetic biomarkers for diagnosis and prognosis of several diseases, highlighting the study of these biomarkers in cancer, cardiovascular and metabolic diseases, infertility, and infectious diseases Includes a special section that discusses the relevance of biobanks in the maintenance of high quality biosamples and clinical-associated data, and the relevance of the ethical aspects in epigenetic studies

The book introduces the bioinformatics resources and tools available for the study of allergenicity. Allergy symptoms affect more than 25% of the population in industrialized countries. At the same time, biotechnology is a rapidly developing field, which often involves the introduction of potentially allergenic novel proteins into drugs or foods. It is essential to avoid transferring a gene that encodes a major allergenic protein (from any source) into a drug/food crop that did not previously contain that protein. Accurately distinguishing candidate genes from allergens before transferring them into a drug or food would aid preventive efforts to curb the rising incidence of allergies. Several public databases have been created in response to increasing allergen data. The resources provided by these databases have paved the way for the creation of specialized bioinformatics tools that allow allergenicity to be predicted. The book is a useful resource for biologists and biomedical informatics scientists, as well as clinicians. Dr. Ailin Tao is the chief of Guangdong Province Key Laboratory of Allergy & Clinical Immunology, Principal Investigator of the State Key Laboratory of Respiratory Disease, the Second Affiliated Hospital of Guangzhou Medical University; Dr. Prof. Eyal Raz is a Professor of Medicine at University of California, San Diego, La Jolla, California, USA. They collaborate very well on allergy research and this book editi ng.

Single-Cell Omics: Volume 1: Technological Advances and Applications provides the latest technological developments and applications of single-cell technologies in the field of biomedicine. In the current era of precision medicine, the single-cell omics technology is highly promising due to its potential in diagnosis, prognosis and therapeutics. Sections in the book cover single-cell omics research and applications, diverse technologies applied in the topic, such as pangenomics, metabolomics, and multi-omics of single cells, data analysis, and several applications of single-cell omics within the biomedical field, for example in cancer, metabolic and neuro diseases, immunology, pharmacogenomics, personalized medicine and reproductive health. This book is a valuable source for bioinformaticians, molecular diagnostic researchers, clinicians and members of the biomedical field who are interested in understanding more about single-cell omics and its potential for research and diagnosis. Covers not only the technological aspects, but also the diverse applications of single cell omics in the biomedical field Summarizes the latest progress in single cell omics and discusses potential future developments for research and diagnosis Written by experts across the world, bringing different points-of-view and case studies to give a comprehensive overview on the topic

Encyclopedia of Bioinformatics and Computational Biology

Cancer Bioinformatics: Bioinformatic Methods, Network Biomarkers and Precision Medicine

Single-Cell Omics

Bioinformatics Analysis of 'Omics' Data Towards Cancer Diagnosis and Prognosis

Molecular Classification, Prognosis and Response Prediction

Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics 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, professionals in research institutes, and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries. Brings together information from computer science, information technology, mathematics, statistics and biotechnology Written and reviewed by leading experts in the field, providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images, multimedia tools and crosslinking to further resources and databases

Research Paper (undergraduate) from the year 2015 in the subject Computer Science - Bioinformatics, grade: 1, Bannari Amman Institute of Technology, language: English, abstract: Extracting meaningful information from gene expression data poses a great challenge to the community of researchers in the field of computation as well as to biologists. It is possible to determine the behavioral patterns of genes such as nature of their interaction, similarity of their behavior and so on, through the analysis of gene expression data. If two different genes show similar expression patterns across the samples, this suggests a common pattern of regulation or relationship between their functions. These patterns have huge significance and application in bioinformatics and clinical research such as drug discovery, treatment planning, accurate diagnosis, prognosis, protein network analysis and so on. In order to identify various patterns from gene expression data, data mining techniques are essential. Major data mining techniques which can be applied for the analysis of gene expression data include clustering, classification, association rule mining etc. Clustering is an important data mining technique for the analysis of gene expression data. However clustering has some disadvantages. To overcome the problems associated with clustering, biclustering is introduced. Clustering is a global model where as biclustering is a local model. Discovering such local expression patterns is essential for identifying many genetic pathways that are not apparent otherwise. It is therefore necessary to move beyond the clustering paradigm towards developing approaches which are capable of discovering local patterns in gene expression data. Biclustering is a two dimensional clustering problem where we group the genes and samples simultaneously. It has a great potential in detecting marker genes that are associated with certain tissues or diseases. However, since the problem is NP-hard, there has been a lot of research in biclustering involving statistical and graph-theoretic. The proposed Cuckoo Search (CS) method finds the significant biclusters in large expression data. The experiment results are demonstrated on benchmark datasets. Also, this work determines the biological relevance of the biclusters with Gene Ontology in terms of function.

Cancer and Noncoding RNAs offers an in-depth exploration of noncoding RNAs and their role in epigenetic regulation of complex human disease, most notably cancer. In addition to examining microRNAs, this volume provides a unique evaluation of more recently profiled noncoding RNAs now implicated in carcinogenesis, including lncRNAs, piRNAs, circRNAs, and tRNAs, identifying differences in function between these noncoding RNAs and how they interact with the rest of the epigenome. A broad range of chapters from experts in the field detail epigenetic regulation of various cancer types, along with recent next generation sequencing technologies, genome-wide association studies (GWAS) and bioinformatics approaches. This book will help researchers in genomic medicine and cancer biology better understand the role of noncoding RNAs in epigenetics, aiding in the development of useful biomarkers for diagnosis, prognosis and new RNA-based disease therapies. Provides a comprehensive analysis of noncoding RNAs implicated in epigenetic regulation of gene expression and chromatin dynamics Educates researchers and graduate students by highlighting, in addition to miRNAs, a range of noncoding RNAs newly associated with carcinogenesis Applies current knowledge of noncoding RNAs and epigenomics towards developing cancer and RNA-based disease therapies Features contributions by leading experts in the field

The combination of molecular biology, engineering and bioinformatics has revolutionized our understanding of cancer revealing a tight correlation of the molecular characteristics of the primary tumor in terms of gene expression, structural alterations of the genome, epigenetics and mutations with its propensity to metastasize and to respond to therapy. It is not just one or a few genes, it is the complex alteration of the genome that determines cancer development and progression. Future management of cancer patients will therefore rely on thorough molecular analyses of each single case. Through this book, students, researchers and oncologists will obtain a comprehensive picture of what the first ten years of cancer genomics have revealed. Experts in the field describe, cancer by cancer, the progress made and its implications for diagnosis, prognosis and treatment of cancer. The deep impact on the clinics and the challenge for future translational research become evident.

Springer Handbook of Bio-/Neuro-Informatics

Applications in Diagnosis, Prognosis and Therapeutics of Cancers

7th International Meeting, CIBIB 2010, Palermo, Italy, September 16-18, 2010, Revised Selected Papers

Computational Bioengineering and Bioinformatics

Essentials of Bioinformatics, Volume II

Machine Learning and Graph Theoretical Approaches Toward Precise Disease Classification, Prognosis and Treatment

The volume focuses on the genomics, proteomics, metabolomics, and bioinformatics of a single cell, especially lymphocytes and on understanding the molecular mechanisms of systems immunology. Based on the author's personal experience, it provides revealing insights into the potential applications, significance, workflow, comparison, future perspectives and challenges of single-cell sequencing for identifying and developing disease-specific biomarkers in order to understand the biological function, activation and dysfunction of single cells and lymphocytes and to explore their functional roles and responses to therapies. It also provides detailed information on individual subgroups of lymphocytes, including cell characters, function, surface markers, receptor function, intracellular signals and pathways, production of inflammatory mediators, nuclear receptors and factors, omics, sequencing, disease-specific biomarkers, bioinformatics, networks and dynamic networks, their role in disease and future prospects. Dr. Xiangdong Wang is a Professor of Medicine, Director of Shanghai Institute of Clinical Bioinformatics, Director of Fudan University Center for Clinical Bioinformatics, Director of the Biomedical Research Center of Zhongshan Hospital, Deputy Director of Shanghai Respiratory Research Institute, Shanghai, China.

The book introduces the bioinformatics tools, databases and strategies for the translational research, focuses on the biomarker discovery based on integrative data analysis and systems biological network reconstruction. With the coming of personal genomics era, the biomedical data will be accumulated fast and then it will become reality for the personalized and accurate diagnosis, prognosis and treatment of complex diseases. The book covers both state of the art of bioinformatics methodologies and the examples for the identification of simple or network biomarkers. In addition, bioinformatics software tools and scripts are provided to the practical application in the study of complex diseases. The present state, the future challenges and perspectives were discussed. The book is written for biologists, biomedical informatics scientists and clinicians, etc. Dr. Bairong Shen is Professor and Director of Center for Systems Biology, Soochow University; he is also Director of Taicang Center for Translational Bioinformatics.

Breast cancer is the most common cancer in females that accounts for highest cancer specific deaths worldwide. In the last few decades research has proven that breast cancer can be treated if diagnosed at early stages and proper therapeutic strategy is adopted. Omics-based recent approaches have unveiled the molecular mechanism behind the breast tumorigenesis and aid in identification of next-generation molecular markers for early diagnosis, prognosis and even the effective targeted therapy. Significant development has taken place in the field of omics in breast cancer in the last decade. The most promising omics approaches and their outcomes in breast cancer have been presented in this book for the first time. The book covers omics technologies and budding fields such as breast cancer miRNA, lipidomics, epigenomics, proteomics, nutrigenomics, stem cell, pharmacogenomics and personalized medicine and many more along with conventional topics such as breast cancer management etc. It is a research-based reference book useful for clinician-scientists, researchers, geneticists and health care industries involved in various aspects of breast cancer. The book will also be useful for students of biomedicine, pathology and pharmacy.

Genomic variations and phenotypic diversity are closely linked and form the underlying mechanism for development of many human diseases. This book addresses the methods of detection, analysis, and interpretation of genomic variations in clinically relevant scenarios. If your research or clinical practice involves handling of genomic sequencing data, this book is for you. Topics covered include: methods for identifying genetic diversity, the workflow for analyzing whole exome and whole genome sequencing data, local ancestry deconvolution models, the value of molecular patterns and pattern biomarkers in cancer diagnosis and prognosis, and genotyping and profiling resistance-associated variants of hepatitis C. If your research or clinical practice involves handling of genomic sequencing data, this book is for you.

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development

Computational and Statistical Epigenomics

Methodologies, Techniques, and Applications

Allergy Bioinformatics

Epigenetic Biomarkers and Diagnostics

In Silico Life Sciences: Medicine

This book comprehensively covers the topic of mining biomedical text, images and visual features towards information retrieval. Biomedical and Health Informatics is an emerging field of research at the intersection of information science, computer science, and health care and brings tremendous opportunities and challenges due to easily available and abundant biomedical data for further analysis. The aim of healthcare informatics is to ensure the high-quality, efficient healthcare, better treatment and quality of life by analyzing biomedical and healthcare data including patient's data, electronic health records (EHRs) and lifestyle. Previously it was a common requirement to have a domain expert to develop a model for biomedical or healthcare; however, recent advancements in representation learning algorithms allows us to automatically to develop the model. Biomedical Image Mining, a novel research area, due to its large amount of biomedical images increasingly generates and stores digitally. These images are mainly in the form of computed tomography (CT), X-ray, nuclear medicine imaging (PET, SPECT), magnetic resonance imaging (MRI) and ultrasound. Patients' biomedical images can be digitized using data mining techniques and may help in answering several important and critical questions related to health care. Image mining in medicine can help to uncover new relationships between data and reveal new useful information that can be helpful for doctors in treating their patients.

The "Cancer bioinformatics" thematic series focuses on the latest developments in the emerging field of systems clinical medicine in cancer which integrates systems biology, clinical science, omics-based technology, bioinformatics and computational science to improve diagnosis, therapies and prognosis of cancer. Topics include: Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation; Cascaded discrimination of normal, abnormal, and confounder classes in histopathology: Gleason grading of prostate cancer; A molecular computational model improves the preoperative diagnosis of thyroid nodules; A systems biology approach to the global analysis of transcription factors in colorectal cancer; Cancer bioinformatics: A new approach to systems clinical medicine; A unified computational model for revealing and predicting subtle subtypes of cancers; Prognostic gene signatures for patient stratification in breast cancer - accuracy, stability and interpretability of gene selection approaches using prior knowledge on protein-protein interactions; A new analysis approach of epidermal growth factor receptor pathway activation patterns provides insights into cetuximab resistance mechanisms in head and neck cancer; Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets; Gene expression signatures modulated by epidermal growth factor receptor activation and their relationship to cetuximab resistance in head and neck squamous cell carcinoma; A dynamic model for tumour growth and metastasis formation; Synthetic Lethal Screen Identifies NF-kappaB as a Target for Combination Therapy with Topotecan for patients with Neuroblastoma.

This book explores the latest and most relevant topics in the field of computational bioengineering and bioinformatics, with a particular focus on patient-specific, disease-progression modeling. It covers computational methods for cardiovascular disease prediction, with an emphasis on biomechanics, biomedical decision support systems, data mining, personalized diagnostics, bio-signal processing, protein structure prediction, biomedical image processing, analysis and visualization, and high-performance computing. It also discusses state-of-the-art tools for disease characterization, and recent advances in areas such as biomechanics, cardiovascular engineering, patient-specific modeling, population-based modeling, multiscale modeling, image processing, data mining, biomedical decision-support systems, signal processing, biomaterials and dental biomechanics, tissue and cell engineering, computational chemistry and high-performance computing. As such, it is a valuable resource for researchers, medical and bioengineering students, and medical device and software experts

The book is intended to be a resource for students as well as scientists in education and for the general public to learn about proteomics and genomics. Chromosomes form the basis for our genetic heritage and are the code for protein synthesis. The Human Genome Map came out in 2002, and the Proteome Sequence Map is under currently being created by a global consortia initiative. Proteome and genome building blocks already form the basis of scientific research areas as well as large parts of the pharmaceutical and biomedical industry. The book initiative will provide the background to and our current understanding of these gene and protein areas, as well as describe how cutting-edge science is using these resources to develop new medicines and new diagnostics for patient care and treatment. The book will be useful for undergraduate students as well as university students and researchers who need a good understanding of genomics and proteomics within the clinical field. The book will also be targeted at a broad public as well as readers not specialized within this field. Dr. Marko-Varga is the head of the Head of Div. Clinical Protein Science & Imaging at the Biomedical Center, Dept. of Measurement Technology and Industrial Electrical Engineering, Lund University, and Professor at the 1st Department of Surgery, Tokyo Medical University, Tokyo, Japan.

A Nature Inspired Algorithm for Biclustering Microarray Data Analysis

Towards Next-Generation Diagnosis, Prognosis and Therapy

Computational Intelligence Methods for Bioinformatics and Biostatistics

Bioinformatics and Biomedical Engineering

17th International Symposium, ISBRA 2021, Shenzhen, China, November 26-28, 2021, Proceedings

Bioinformatics Approaches to Biomarker and Drug Discovery in Aging and Disease

The two-volume set LNBI 11465 and LNBI 11466 constitutes the proceedings of the 7th International Work-Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2019, held in Granada, Spain, in May 2019. The total of 97 papers presented in the proceedings, was carefully reviewed and selected from 301 submissions. The papers are organized in topical sections as follows: Part I: High-throughput genomics: bioinformatics tools and medical applications; omics data acquisition, processing, and analysis; bioinformatics approaches for analyzing cancer sequencing data; next generation sequencing and sequence analysis; structural bioinformatics and function; telemedicine for smart homes and remote monitoring; clustering and analysis of biological sequences with optimization algorithms; and computational approaches for drug repurposing and personalized medicine. Part II: Bioinformatics for healthcare and diseases; computational genomics/proteomics; computational systems for modelling biological processes; biomedical engineering; biomedical image analysis; and biomedicine and e-health.

This collection of 25 research papers comprised of 22 original articles and 3 reviews is brought together from international leaders in bioinformatics and biostatistics. The collection highlights recent computational advances that improve the ability to analyze highly complex data sets to identify factors critical to cancer biology. Novel deep learning algorithms represent an emerging and highly valuable approach for collecting, characterizing and predicting clinical outcomes data. The collection highlights several of these approaches that are likely to become the foundation of research and clinical practice in the future. In fact, many of these technologies reveal new insights about basic cancer mechanisms by integrating data sets and structures that were previously immiscible. Accordingly, the series presented here bring forward a wide range of artificial intelligence approaches and statistical methods that can be applied to imaging and genomics data sets to identify previously unrecognized features that are critical for cancer. Our hope is that these articles will serve as a foundation for future research as the field of cancer biology transitions to integrating electronic health record, imaging, genomics and other complex datasets in order to develop new strategies that improve the overall health of individual patients.

Application of Bioinformatics in Cancers

Bioinformatics Methods in Clinical Research

Biomedical Data Mining for Information Retrieval

Volume 2: Applications in Biomedicine and Agriculture

Omics Approaches in Breast Cancer