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Single-Cell Omics John Wiley & Sons
Technologies collectively called omics enable simultaneous measurement of an enormous number of biomolecules; for example, genomics investigates thousands of DNA sequences, and proteomics examines large numbers of proteins. Scientists are using these technologies to develop innovative tests to detect disease and to predict a patient's likelihood of responding to specific drugs. Following a recent case involving premature use of omics-based tests in cancer clinical trials at Duke University, the NCI requested that the IOM establish a committee to recommend ways to strengthen omics-based test development and evaluation. This report identifies best practices to enhance development, evaluation, and translation of omics-based tests while simultaneously reinforcing steps to ensure that these tests are appropriately assessed for scientific validity before they are used to guide patient treatment in clinical trials.
Computer Modelling in Bioengineering Springer Nature

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.

Volume 1: Technological Advances and Applications Frontiers Media SA

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

Technological Advances and Applications Academic Press

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.

The Applications of Bioinformatics in Cancer Detection Academic Press

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.

A Computational Approach Academic Press

One of the main applications of machine learning in bioinformatics is the construction of classication models which can accurately classify new instances using information gained from previous instances. With the help of machine learning algorithms (such as supervised classication and gene selection) new meaningful knowledge can be extracted from bioinformatics datasets that can help in disease diagnosis and prognosis as well as in prescribing the right treatment for a disease. One particular challenge encountered when analyzing bioinformatics datasets is data noise, which refers to incorrect or missing values in datasets. Noise can be introduced as a result of experimental errors (e.g. faulty microarray chips, insucient resolution, image corruption, and incorrect laboratory procedures), as well as other errors (errors during data processing, transfer, and/or mining). A special type of data noise called class noise, which occurs when an instance/example is mislabeled. Previous research showed that class noise has a detrimental impact on machine learning algorithms (e.g. worsened classication performance and unstable feature selection). In addition to data noise, gene expression datasets can suffer from the problems of high dimensionality (a very large feature space) and class imbalance (unequal distribution of instances between classes). As a result of these inherent problems, constructing accurate classication models becomes more challenging. To provide guidance to researchers and practitioners in deciding which machine learning algorithms

to apply for their analysis, this dissertation performs thorough empirical investigations of machine learning algorithms on bioinformatics data of varying data quality. Comprehensive experiments are performed to assess the robustness of machine learning techniques to class noise. First, we provide a detailed experimental analysis of feature selection techniques as well as classication algorithms in the context of data quality. We then investigate the effectiveness of three forms of ensemble classication techniques when learning from balanced bioinformatics datasets in the context of data quality. We also investigate the importance of alleviating class imbalance for classication problems on bioinformatics datasets. Finally, we address the combined problem of high dimensionality and class imbalance in the context of data quality.

Bioinformatics Approaches to Cancer Biomarker Discovery and Characterization GRIN Verlag

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.

Essentials of Bioinformatics, Volume II Springer Science & Business Media

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.

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

Bioinformatics for Diagnosis, Prognosis and Treatment of Complex Diseases

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

Functional Coherence of Molecular Networks in Bioinformatics Springer Nature

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.

Systems Biology and Bioinformatics Springer

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

Bioinformatics Tools for Detection and Clinical Interpretation of Genomic Variations Elsevier

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

Biomedical Data Mining for Information Retrieval Academic Press

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.

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development Academic Press

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.

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

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

Cancer and Noncoding RNAs CRC Press

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.

Cancer Bioinformatics: Bioinformatic Methods, Network Biomarkers and Precision Medicine Academic Press

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.

Bioinformatics Research and Applications Springer

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).

Cancer Genomics Springer Science & Business Media

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.
Computational and Statistical Epigenomics Humana Press
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.