Bioinformatics For Diagnosis Prognosis And Treatment Of Complex Diseases Translational Bioinformatics

Cancer and Noncoding RNAs
Computer Modelling in Bioengineering
Essentials of Bioinformatics, Volume II
Omics Approaches in Breast Cancer
7th International Work-Conference, IWBBIO 2019, Granada, Spain, May 8-10, 2019, Proceedings, Part I
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BENJAMIN POWERS

Cancer and Noncoding RNAs Elsevier
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.

Computer Modelling in Bioengineering Springer Nature

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.

Essentials of Bioinformatics, Volume II Academic Press

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

Omics Approaches in Breast Cancer BoD – Books on Demand

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 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.

Springer

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 Tools for Detection and Clinical Interpretation of Genomic Variations Humana Press

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

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

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.

Genomics and Proteomics for Clinical Discovery and Development Springer

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.

Lessons Learned and the Path Forward Springer Nature

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

Single-Cell Omics Academic Press

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.

Computational Epigenetics and Diseases
Frontiers Media SA

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).

Computational Intelligence in Oncology
Springer

Molecular Diagnostics, Third Edition, focuses on the technologies and applications that professionals need to work in, develop, and manage a clinical diagnostic laboratory. Each chapter contains an expert introduction to each subject that is next to technical details and many applications for molecular genetic testing that can be found in comprehensive reference lists at the end of each chapter. Contents are divided into three parts, technologies, application of those technologies, and related issues. The first part is dedicated to the battery of the most widely used molecular pathology techniques. New chapters have been added, including the various new technologies involved in next-generation sequencing (mutation detection, gene expression, etc.), mass spectrometry, and protein-specific methodologies. All revised chapters have been completely updated, to include not only technology innovations, but also novel diagnostic applications. As with previous editions, each of the chapters in this section includes a brief description of the technique followed by examples from the area of expertise from the selected contributor. The second part of the book attempts to integrate previously analyzed technologies into the different aspects of molecular diagnostics, such as identification of genetically modified organisms, stem cells,

pharmacogenomics, modern forensic science, molecular microbiology, and genetic diagnosis. Part three focuses on various everyday issues in a diagnostic laboratory, from genetic counseling and related ethical and psychological issues, to safety and quality management. Presents a comprehensive account of all new technologies and applications used in clinical diagnostic laboratories Explores a wide range of molecular-based tests that are available to assess DNA variation and changes in gene expression Offers clear translational presentations by the top molecular pathologists, clinical chemists, and molecular geneticists in the field

Encyclopedia of Bioinformatics and Computational Biology

John Wiley & Sons

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.

A Nature Inspired Algorithm for Biclustering Microarray Data Analysis

Springer Science & Business Media

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 for Diagnosis, Prognosis and Treatment of Complex Diseases Springer Nature

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.

Towards Next-Generation Diagnosis, Prognosis and Therapy Springer

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.

Biomedical Data Mining for Information Retrieval

Springer Science & Business Media

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.

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development

Academic 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.

Computational and Statistical Epigenomics

CRC Press

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

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