Bioinformatics In Cancer And Cancer Therapy Cancer Drug Discovery And Development

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Cancer Systems Biology, Bioinformatics and Medicine 2011-08-25

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development Xiangqian Guo 2020-12-23

Cancer Systems Biology, Bioinformatics and Medicine Alfredo Cesario 2011-08-21 This teaching monograph on systems approaches to cancer research and clinical applications provides a unique synthesis, by world-class scientists and doctors, of laboratory, computational, and clinical methods, thereby establishing the foundations for major advances not possible with current methods. Specifically, the book: 1) Sets the stage by describing the basis of systems biology and bioinformatics approaches, and the clinical background of cancer in a systems context; 2) Summarizes the laboratory, clinical, data systems analysis and bioinformatics tools, along with infrastructure and resources required; 3) Demonstrates the application of these tools to cancer research; 4) Extends these tools and methods to clinical diagnosis, drug development and treatment applications; and 5) Finishes by exploring longer term perspectives and providing conclusions. This book reviews the state-of-the-art, and goes beyond into new applications. It is written and highly referenced as a textbook and practical guide aimed at students, academics, doctors, clinicians, industrialists and managers in cancer research and therapeutic applications. Ideally, it will set the stage for integration of available knowledge to optimize communication between basic and clinical researchers involved in the ultimate fight against cancer, whatever the field of specific interest, whatever the area of activity within translational research.

Cancer Genomics for the Clinician Ramaswamy Govindan, MD 2019-01-28 Cancer Genomics for the Clinician is a practical guide to cancer genomics and its application to cancer diagnosis and care. The book begins with a brief overview of the various types of genetic alterations that are encountered in cancer, followed by accessible and applicable information on next generation sequencing technology and bioinformatics; tumor heterogeneity; whole genome, exome, and transcriptome sequencing; epigenomics; and data analysis and interpretation. Each chapter provides essential explanations of concepts, terminology, and methods. Also included are tips for interpreting and analyzing molecular data, as well as a discussion of molecular predictors for targeted therapies covering hematologic malignancies and solid tumors. The final chapter explains the use of FDA-approved genomic-based targeted therapies for breast cancer, lung cancer, sarcomas, gastrointestinal cancers, urologic cancers, head and neck cancer, thyroid cancer, and many more. Assembled in an accessible format specifically designed for the non-expert, this book provides the clinical oncologist, early career practitioner, and trainee with an essential understanding of the molecular and genetic basis of cancer and the clinical aspects that have led to advancements in diagnosis and treatment. With this resource, physicians and trainees will increase their breadth of knowledge and be better equipped to educate patients and families who want to know more about their genetic predispositions to cancer and the targeted therapies that could be considered and prescribed. Key Features: Describes how cancer genomics and next generation sequencing informs cancer screening, risk factors, therapeutic options, and clinical management across cancer types Explains what mutations are, what tests are needed, and how to interpret the results Provides information on FDA-approved targeted therapies that are being used in the clinic Covers different sequencing platforms and technologies and how they perform in research settings Includes access to the fully searchable eBook

Biomedical Data Mining for Information Retrieval Sujata Dash 2021-08-24 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 engagement 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.

Systems Biology in Cancer Research and Drug Discovery Asfar S Azmi 2012-09-29 Systems Biology in Cancer Research and Drug Discovery provides a unique collection of chapters, by world-class researchers, describing the use of integrated systems biology and network modeling in the cancer field where traditional tools have failed to deliver expected promise. This book touches four applications/aspects of systems biology (i) in understanding aberrant signaling in cancer (ii) in identifying biomarkers and prognostic markers especially focused on angiogenesis pathways (iii) in unwinding microRNAs complexity and (iv) in anticancer drug discovery and in clinical trial design. This book reviews the state-of-the-art knowledge and touches upon cutting edge newer and improved applications especially in the area of network modeling. It is aimed at an audience ranging from students, academics, basic researcher and clinicians in cancer research. This book is expected to benefit the field of translational cancer medicine by bridging the gap between basic researchers, computational biologists and clinicians who have one ultimate goal and that is to defeat cancer.

Cancer Chemotherapy Gary S. Goldberg 2020-04-13 Provides a clear and accessible summary of all stages and aspects of the discovery, design, development, validation and clinical use of anticancer drugs This new edition provides an update on the current state of the art of cancer chemotherapy and clinical practice and presents new pipeline anticancer agents and promising therapeutic strategies that are emerging alongside new breakthroughs in cancer biology. Its unique approach enables students to gain an understanding of the pathological, physiological, and molecular processes governing malignancy, while also introducing the role of health professionals and scientists in the research and treatment of cancer. Invaluable for its clarity and accessibility, Cancer Chemotherapy: Basic Science to the Clinic, 2nd Edition offers complete coverage of the scientific and clinical aspects of the creation, development, and administration of drugs or drug delivery systems used in the treatment of the disease. Chapters look at: cancer epidemiology and histopathology; carcinogenesis; current research; tumor hypoxia; antiangiogenic and antivascular agents; protein kinase and Ras blockers; new targets associated with development such as Hedgehog and Wnt signaling; stem cells; immunotherapy and oncolytic viruses; and more. Presents a clear, accessible, and comprehensive approach to cancer chemotherapy from basic science to clinical practice Offers a major update that reflects the latest developments in personalized chemotherapy Provides in-depth coverage of advances in biomarker diagnostics Includes new chapters/sections on bioinformatics and the 'omic sciences'; pharmaceutical strategies used to achieve tumor-selective drug delivery; and cancer cell autophagy Combines descriptions of both clinical protocol and explanations of the drug design process in one self-contained book Features numerous diagrams and illustrations to enhance reader understanding Aimed at upper undergraduate, graduate, and medical students, Cancer Chemotherapy: Basic Science to the Clinic, 2nd Edition is also an excellent reference for health professionals, especially clinicians specializing in Clinical Oncology, and their patients who want to gain an understanding of cancer and available treatment options.

The Oncogenomics Handbook William J. LaRochelle 2007-11-09 An integrated overview of cancer drug discovery and development from the bench to the clinic, showing with broad strokes and representative examples the drug development process as a network of linked components leading from the discovered target to the ultimate therapeutic product. Following a systems biology approach, the authors explain genomic databases and how to discover oncological targets from them, how then to advance from the gene and transcript to the level of protein biochemistry, how next to move from the chemical realm to that of the living cell, and, ultimately, pursue animal modeling and clinical development. Emerging cancer therapeutics including Rituxan, Erbitux, Gleevec Herceptin, Avastin, ABX-EGF, Velcade, Kepivance, Iressa, Tarceva, and Zevalin are addressed. Highlights include cancer genomics, pharmacogenomics, transcriptomics, gene expression analysis, proteomic and enzymatic cancer profiling technologies, and cellular and animal approaches to cancer target validation.

Biomedical Informatics for Cancer Research Michael F. Ochs 2010-04-06 view, showing that multiple molecular pathways must be affected for cancer to develop, but with different specific proteins in each pathway mutated or differentially expressed in a given tumor (The Cancer Genome Atlas Research Network 2008; Parsons et al. 2008). Different studies demonstrated that while widespread mutations exist in cancer, not all mutations drive cancer development (Lin et al. 2007). This suggests a need to target only a deleterious subset of aberrant proteins, since any tre- ment must aim to improve health to justify its potential side effects. Treatment for cancer most become highly individualized, focusing on the specific aberrant driver proteins in an individual. This drives a need for informatics in cancer far beyond the need in other diseases. For instance, routine treatment with statins has become widespread for minimizing heart disease, with most patients responding to standard doses (Wilt et al. 2004). In contrast, standard treatment for cancer must become tailored to the molecular phenotype of an individual tumor, with each patient receiving a different combination of therapeutics aimed at the specific aberrant proteins driving the cancer. Tracking the aberrations that drive cancers, identifying biomarkers unique to each individual for molecular-level di- nosis and treatment response, monitoring adverse events and complex dosing schedules, and providing annotated molecular data for ongoing research to improve treatments comprise a major biomedical informatics need.

Prostate Cancer Leland W. K. Chung 2007-11-10 Prostate Cancer: Biology, Genetics, and the New Therapeutics, Second Edition, reviews new, valuable approaches to the treatment of prostate cancer in men. The latest edition contains new material on molecular imaging, new treatments for prostate cancer, molecular targets, cell signaling pathways, bioinformatics, and pathogenomics. The book details the latest innovations and advances in prostate cancer and may be used as a rapid reference text for readers. The volume profiles the latest advances in cancer research and treatment and includes profound studies in prostate stem cells, cancer-host interactions, hedgehog signaling in development and cancer, cholesterol and cell signaling, gene therapy for advanced prostate cancer, and noninvasive strategies such as molecular imaging to visualize gene expression. This new edition also investigates expression profiling and somatic alterations in prostate cancer progression and linkage studies of prostate cancer families to identify susceptibility genes. The issues of racial differences in prostate cancer mortality, radiotherapy for the treatment of locally advanced prostate cancer, recombinant antibody candidates for treatment, taxane-based chemotherapy, lethal phenotypes, and novel and efficient translation clinical trials are also presented in great depth. Prostate Cancer: Biology, Genetics, and the New Therapeutics, Second Edition, provides readers with a general reference for prostate cancer from prevention to therapy and will be of value to clinicians, scientists, and administrators who strive to solve the cancer problem.

Precision Cancer Medicine Samir Roychowdhury 2020-01-02 Genomic sequencing technologies have augmented the classification of cancer beyond tissue of origin and towards a molecular taxonomy of cancer. This has created opportunities to guide treatment decisions for individual patients with cancer based on their cancer's unique molecular characteristics, also known as precision cancer medicine. The purpose of this text will be to describe the contribution and need for multiple disciplines working together to deliver precision cancer medicine. This entails a multi-disciplinary approach across fields including molecular pathology, computational biology, clinical oncology, cancer biology, drug development, genetics, immunology, and bioethics. Thus, we have outlined a current text on each of these fields as they work together to overcome various challenges and create opportunities to deliver precision cancer medicine. As trainees and junior faculty enter their respective fields, this text will provide a framework for understanding the role and responsibility for each specialist to contribute to this team science approach.

Essentials of Cancer Genomic, Computational Approaches and Precision Medicine Nosheen Masood 2020-03-20 This book concisely describes the role of omics in precision medicine for cancer therapies. It outlines our current understanding of cancer genomics, shares insights into the process of oncogenesis, and discusses emerging technologies and clinical applications of cancer genomics in prognosis and precision-medicine treatment strategies. It then elaborates on recent advances concerning transcriptomics and translational genomics in cancer diagnosis, clinical applications, and personalized medicine in oncology. Importantly, it also explains the importance of high-performance analytics, predictive modeling, and system biology in cancer research. Lastly, the book discusses current and potential future applications of pharmacogenomics in clinical cancer therapy and cancer drug development.

Cancer Bioinformatics Sylvia Nagl 2006-03-06 "The development and application of bioinformatics tools to basic and translational cancer research is, in fact, a rapidly expanding field that deserves a timely review. Therefore, a publication of this type is needed. The editors have done an excellent job in recruiting well-established scientists to author the various chapters of the book." —Dieter Naf, Jackson Laboratory, USA Cancer bioinformatics is now emerging as a new interdisciplinary field, which is facilitating an unprecedented synthesis of knowledge arising from the life and clinical sciences. This groundbreaking title provides a comprehensive and up-to-date account of the enormous range of bioinformatics for cancer therapy development from the laboratory to clinical trials. It functions as a guide to integrated data exploitation and synergistic knowledge discovery, and support the consolidation of the interdisciplinary research community involved.

Cancer Diagnostics: New Insights for the Healthcare Professional: 2011 Edition 2012-01-09 Cancer Diagnostics: New Insights for the Healthcare Professional: 2011 Edition is a ScholarlyPaper™ that delivers timely, authoritative, and intensively focused information about Cancer Diagnostics in a compact format. The editors have built Cancer Diagnostics: New Insights for the Healthcare Professional: 2011 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Cancer Diagnostics in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Cancer Diagnostics: New Insights for the Healthcare Professional: 2011 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.

Next Generation Sequencing Based Diagnostic Approaches in Clinical Oncology Anton A. Buzdin 2021-03-09 Dr. Anton Buzdin (AB) is employed by Omicsway Corp. (USA). AB received grants from Amazon and Microsoft Azure to support cloud computations. Dr. Xinmin Li is director of JCCC Shared Genomics Resource, the University of California, Los Angeles, CA Dr. Ye Wang is Director of Gene Testing Department (Core Lab) of Qingdao Central Hospital, the Second Affiliated Hospital of Qingdao University

Cancer Informatics in the Post Genomic Era Igor Jurisica 2007-05-04 Cancer Informatics in Post-Genomic Era provides both the necessary methodology and practical information tools for analyzing data in the field of medical information science. This, of course, requires analytic tools. Those tools are garnered by developing and assessing methods and systems for the acquisition, processing, and interpretation of patient data, aided by scientific discovery. Key challenges in this field include integrating research and clinical care, and establishing partnerships within and across sectors of patient diagnosis and treatment.

Gene Expression Profiling in Cancer Dimitrios Vlachakis 2019-06-19 The contribution of modern-day genetics in designing efficient gene expression profiles for cancer is immense. The progress of technology and science in recent years provides the opportunity for application of new techniques for treating various diseases that affect humanity. Methods for finding and analyzing the profile of gene expression of infected cells give scientists the ability to develop more targeted and effective treatments, especially for diseases such as cancer. The development of gene expression profiling is one of the most important achievements in cancer genetics in our time. It is essentially the driving force behind personalized and modern medicine. This book highlights recent developments, applications, and breakthroughs in the field of gene expression profiling in cancer.

Computational Biology of Cancer Dominik Wodarz 2005-01-24 ' The book shows how mathematical and computational models can be used to study cancer biology. It introduces the concept of mathematical modeling and then applies it to a variety of topics in cancer biology. These include aspects of cancer initiation and progression, such as the somatic evolution of cells, genetic instability, and angiogenesis. The book also discusses the use of mathematical models for the analysis of therapeutic approaches such as chemotherapy, immunotherapy, and the use of oncolytic viruses. Contents:Cancer and Somatic Evolution:Mathematical Modeling of Tumorigenesis:Cancer Initiation: One-Hit and Two-Hit Stochastic Models;Microsatellite and Chromosomal Stability in Sporadic and Familial CancersCellular Origins of Cancer:Costs and Benefits of Chromosomal InstabilityDNA Damage and Genetic InstabilityTissue Aging and the Development of CancerBasic Models of Tumor Inhibition and PromotionMechanisms of Tumor NeovascularizationCancer and Immune ResponsesTherapeutic Approaches: Viruses as Anti-Tumor Weapons Readership: Researchers and academics in bioinformatics, biocomputing, biomathematics, cell/molecular biology and cancer biology, as well as clinicians. Keywords:Mathematics Models;Computational Biology;Cancer Initiation;Cancer Progression;Somatic Evolution;Genetic Instability;Therapy;Oncolytic VirusesKey Features:Provides an introduction to computational methods in cancer biologyFollows a multi-disciplinary approachAuthoritative'"This book adds aspects not covered by other books and, therefore, represents a valuable addition to the literature about mathematical models in cancer biology."Zentralblatt MATH '

Bioinformatics Tools (and Web Server) for Cancer Biomarker Development, Volume II Xiangqian Guo 2022-06-16

Application of Bioinformatics in Cancers Chad Brenner 2019-11-20 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 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 invisible. 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 roadmap 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.

Correlation-based network analysis of cancer metabolism Emily G. Armitage 2014-05-12 With the rise of systems biology as an approach in bioinformatics research, using high throughput techniques such as mass spectrometry to understand the metabolic profiles of cancer metabolism is becoming increasingly important. There are examples of cancer metabolic profiling studies in the academic literature; however they are often only in journals specific to the metabolomics community. This book will be particularly useful for post-graduate students and post-doctoral researchers using this pioneering technique of network-based correlation analysis. The approach can be adapted to the

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analysis of any large scale metabolic profiling experiment to answer a range of biological questions in a range of species or for a range of diseases.

Bioinformatics Approaches to Cancer Biomarker Discovery and Characterization Peter Lee Ming Liao 2018 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 this 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.

Computational Systems Biology of Cancer Emmanuel Barillot 2012-08-25 The future of cancer research and the development of new therapeutic strategies rely on our ability to convert biological and clinical questions into mathematical models—integrating our knowledge of tumour progression mechanisms with the tsunami of information brought by high-throughput technologies such as microarrays and next-generation sequencing. Offering engrossing insights on how to defeat cancer, the emerging field of systems biology captures the complexity of biological phenomena using mathematical and computational tools. Novel Approaches to Fighting Cancer Drawn from the authors' decade-long work in the cancer computational systems biology laboratory at Institut Curie (Paris, France), Computational Systems Biology of Cancer explains how to apply computational systems biology approaches to cancer research. The authors provide proven techniques and tools for cancer bioinformatics and systems biology research. Effectively Use Algorithmic Methods and Bioinformatics Tools in Real Biological Applications Suitable for readers in both the computational and life sciences, this self-contained guide assumes very limited background in biology, mathematics, and computer science. It explores how computational systems biology can help fight cancer in three essential aspects: Categorising tumours and finding new targets Designing improved and tailored therapeutic strategies Each chapter introduces a problem, presents applicable concepts and state-of-the-art methods, describes existing tools, illustrates applications using real cases, lists publically available software and software, and includes references to further reading. Some chapters also contain exercises. Figures from the text and scripts/data for reproducing a breast cancer data analysis are available at www.cancer-systems-biology.net.

Cancer Bioinformatics: Bioinformatic Methods, Network Biomarkers and Precision Medicine Applied Research Press 2015-11-05 The "Cancer bioinformatics" thematic series focuses on the latest developments in the emerging field of cancer bioinformatics. Cancer bioinformatics is an interdisciplinary approach in 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 cancer bioinformatics; 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.

Bioinformatics in the Diagnostics, Prognosis and Treatment of Complex Diseases Bairong Shen 2013-11-25 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 resources used for 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.

Next Generation Sequencing in Cancer Research, Volume 2 Wei Wu 2015-04-25 Latest generation sequencing revolutionizes the fields of cancer research and oncology. This follow-up volume focuses more extensively on single cell sequencing of cancer and trials in drug resistance. Another exciting feature is the bioinformatics tools given, that are used on cancer genome studies. Scientists around the world are attempting to find the root cause of cancer. A reasonable cancer treatment plan and potential cure is more optimistic now with the unfolding of the cancer genome. The collective knowledge of how to leverage next generation sequencing in cancer research is paving the way. The important information provided in this volume will move the field forward in developing novel, targeted cancer therapies.

Omics Technologies in Cancer Biomarker Discovery Xuewu Zhang 2011-03-10 The early detection of human cancer is still one of the great challenges in the battle against this disease. Single biomarkers are not likely to provide sufficient diagnostic power and multibiomarker assays should be developed in order to reach high diagnostic accuracy for cancer screening at the population level. Omics technologies are emerging ne

Cancer Amita Kashyap 2014-09-08 Cancer is initiated by activation of oncogenes or inactivation of tumor suppressor genes. Mutations in the K-ras proto-oncogene are responsible for 10-30% of adenocarcinomas. Clinical Findings point to a wide variety of other cancers contributing to lung cancer incidence. Such a scenario makes identification of lung cancer difficult and thus identifying its mechanisms can contribute to the society. Identifying using conserved patterns common to contributing proto-oncogenes may further be a boon to Pharmacogenomics and pharmacoinformatics. This calls for ab initio/de novo drug discovery that in turn will require a comprehensive in silico approach of Sequence, Domain, Phylogenetic and Structural analysis of the receptors, ligand screening and optimization and detailed Docking studies. This brief reviews current bioinformatics techniques to study the K-ras RAS subfamily that includes a set of proteins, which cause an over expression of cancer-causing genes like M-ras and initiate tumor formation in lungs. SNP Studies and Structure based drug discovery will also be undertaken.

Bioinformatics S. Balamurugan 2021-12-14 Bioinformatics is a platform between the biology and information technology. The book covers a broad spectrum of the bioinformatics fields starting from the basic principles, concepts, and multidisciplinary application areas. It comprises a collection of chapters describing the role of bioinformatics in drug discovery and discovery including the molecular modeling aspects; chapters detailing topics such as silico design, protein modeling, DNA Microarray Analysis, DNA-RNA barcoding, gene sequencing; specialized topics such as bioinformatics in cancer detection, genomics, proteomics, machine learning, covalent approaches in drug design

A Concise Review of Molecular Pathology of Breast Cancer Mehmet Gunduz 2015-03-25 Cancer is one of the leading causes of death in most countries and its consequences result in huge economic, social and psychological burden. Breast cancer is the most frequently diagnosed cancer type and the leading cause of cancer death among females. In this book, we discussed gene expression and DNA abnormalities including methylation in breast cancer. A recent important topic, roles of miRNAs and their potential use in cancer therapy have been discussed in the cancer type as well. Bioinformatics is very important part of recent human genome developments and data mining and thus this topic has also been added for the readers. It is hoped that this book will contribute to development of novel diagnostic as well as therapeutic approaches, which lead to cure of breast cancer.

A Computational Systems Biology Approach to Predictive Oncology Sandeep Sanga 2009 Technological advances in the recent decades have enabled cancer researchers to probe the disease at multiple resolutions. This wealth of experimental data combined with computational systems biology methods is now leading to predictive models of cancer progression and response to therapy. We present the macroscale group's multiscale model of tumor growth, whose core is a tissue-scale computational model capable of tracking the progression of tumors from a diffusion-limited avascular phase through angiogenesis, and into invasive lesions with realistic, complex morphologies. We adapt this core model to consider the delivery of systemically-administered anticancer agents and their effect on lesions once they reach their intended nuclear target. We calibrate the model parameters using in vitro data from the literature, and demonstrate through simulation that transport limitations affecting drug and oxygen distributions play a significant role in hampering the efficacy of chemotherapy; a result that has since been validated by in vitro experimentation. While this study demonstrates the capability of our adapted core model to predict distributions (e.g., cell density, pressure, oxygen, nutrient, drug) within lesions and consequent tumor morphology, nevertheless, the underlying factors driving tumor-scale behavior occur at finer scales. What is needed in our multi-scale approach is to parallel reality, where molecular signaling models predict cellular behavior, and ultimately drive what is seen at the tumor level. Models of signaling pathways linked to cell models are already beginning to surface in the literature. We next transition our research to the molecular level, where we employ data mining and bioinformatics methods to infer signaling relationships underlying a subset of breast cancer that might benefit from targeted therapy of Androgen Receptor and associated pathways. Defining the architecture of signaling pathways is a critical first step towards development of pathways models underlying tumor models, while also providing valuable insight for drug discovery. Finally, we develop an agent-based, cell-scale model focused on predicting motility in response to chemical signals in the microenvironment, generally accepted to be a necessary feature of cancer invasion and metastasis. This research demonstrates the use of signaling models to predict emergent cell behavior, such as motility. The research studies presented in this dissertation, if performed in a more collaborative setting and integrated with richer models, form our prognosis and response to therapy. Our Laboratory for Computational, & Predictive Oncology, in collaboration with research groups throughout in the United States and Europe are following a computational systems biology paradigm where model development is fueled by biological knowledge, and model predictions are refining experimental focus.

Pharmacogenomics in Cancer therapy CTI Reviews 2016-10-16 Facts101 is your complete guide to Pharmacogenomics in Cancer therapy. In this book, you will learn topics such as as those in your book plus much more. With key features such as key terms, people and places, Facts101 gives you all the information you need to prepare for your next exam. Our practice tests are specific to the textbook so you will get the exact results you need for your test.

Targeting Autophagy in Cancer Therapy Jin-Ming Yang 2016-09-02 This volume will detail the current state and perspectives of autophagy cancer therapy. Covering a wide range of topics, it will include an overview of autophagy as a therapeutic target in cancer, autophagy modulators as cancer therapeutic agents, implications of micro-RNA-regulated autophagy in cancer therapy, modulation of autophagy through targeting PI3 kinase in cancer therapy, targeting autophagy in cancer stem cells, and roles of autophagy in cancer immunotherapy. In addition, the volume will review applications of system biology and bioinformatics approaches to discovering cancer therapeutic targets in the autophagy regulatory network. The volume will be beneficial for a variety of basic and clinical scientists, including cancer biologists, autophagy researchers, pharmacologists, and clinical oncologists who wish to delve more deeply into the field of cancer research. This volume will be the first book to focus solely on autophagy as a target in cancer therapy. As well, it will comprehensively discuss the roles of autophagy in most currently available cancer treatments.

Lung Cancer Karen L. Reckamp 2016-08-17 This book describes the molecular mechanisms of lung cancer development and progression that determine therapeutic interventions in the era of genomics, when the rapid evolution in lung cancer diagnosis and treatment necessitates critical review of new results to integrate advances into practice. The text opens with background and emerging information regarding the molecular biology of lung cancer pathogenesis. Updated results regarding lung cancer prevention and screening are discussed, followed by chapters on diagnostic techniques and pathological evaluation. This leads on to a detailed presentation of treatment modalities, from surgery and radiation therapy to standard chemotherapy and targeted agents. The coverage includes resistance to therapy and the emergence of immunotherapy for lung cancer; in addition, the current evidence in respect of small cell lung cancer is summarized. The book presents insights from experts across disciplines to emphasize the importance of collaborative care. Advances in our understanding of issues in geriatric oncology and palliative care complete the comprehensive discussion of lung cancer.

Computational Intelligence in Oncology Khalid Raza

Bioinformatics in Cancer and Cancer Therapy Gavin J. Gordon 2008-10-25 Bioinformatics can be loosely defined as the collection, classification, storage, and analysis of biochemical and biological information using computers and mathematical algorithms. Bioinformatics represents a marriage of biology, medicine, computer science, physics, and mathematics, fields of study that have historically existed as mutually exclusive disciplines. Edited by Gavin Gordon, Bioinformatics in Cancer and Cancer Therapy, the focus of this book is to provide a historical and technical perspective on the analytical techniques, methodologies, and platforms used in bioinformatics experiments, to show how a bioinformatics approach has been used to characterize the state of cancer biology research on a molecular level and to demonstrate how a bioinformatics approach can be applied to bridge basic science and the clinical arena to positively impact patient care and management.

Da Yong Liu 2014-12-05 Personalized Cancer Chemotherapy separately describes and addresses "individualized cancer chemotherapy" (ICC) strategies new and old, to provide readers with new insights into their characteristics and techniques, as well as key debates and future trends in this area. The book devotes chapters to drug sensitivity testing, cancer biomarkers and bioinformatics detection, pharmacogenetics, individualized antimetastatic therapy, drug combinations, assistant chemotherapy, and cost-effectiveness considerations. A major obstacle to controlling cancer growth and metastases in patients is the inappropriate use of anticancer and antimetastatic drugs. Researchers and clinicians are now beginning to focus on ICC also called "personalized cancer chemotherapy" (PCC), to improve therapeutic quality and outcomes by selecting and prescribing the most appropriate and effective drugs. Using genetic, molecular, and bioinformatics tools and modern experimental techniques, known tumor genes can be detected more easily than ever before; the average speed of genetic sequencing has increased 15,000 to 50,000 times since the Human Genome Project was completed. This book will help readers understand the pros and cons of each individualized cancer chemotherapy strategy from different angles so as to make good judgments and predictions of drug responses and clinical outcomes. Explores the central components of cancer treatment Investigates new developments in cancer treatment Discusses the many strategies of individualized cancer chemotherapy

Handbook of Oncogenomics Zena Murray 2021-11-16 The accumulation of DNA mutations and epigenetic variations that leads to uncontrolled cell proliferation and formation of neoplasm defects in cancer. It is a genetic disease. This sub branch of genomics that deals with the study of cancer related genes is known as oncogenomics. The primary goal of the discipline is to recognize new tumor suppressor genes and oncogenes that may lead to new insights in the diagnosis of cancer, help predict the clinical outcome of different cancers and identify new targeted for cancer therapies. It uses the techniques of comparative genomics, functional analysis of oncogenes, etc. The field is also concerned with personalizing cancer treatment by identifying and targeting mutations in an individual patient. The book elucidates the concepts and innovative models around the prospective developments with respect to oncogenomics. The various studies that are constantly contributing towards advancing technologies and evolution of this field are examined in detail. This book, with its detailed analyses and data, will prove immensely beneficial to professionals and students involved in this area at various levels.

An Omics Perspective on Cancer Research William C.S. Cho 2010-04-07 Omics is an emerging and exciting area in the field of science and medicine. Numerous promising developments have been elucidated using omics (including genomics, transcriptomics, epigenomics, proteomics, metabolomics, interactomics, cytomics and bioinformatics) in cancer research. The development of high-throughput technologies that permit the solution of deciphering cancer from higher dimensionality will provide a knowledge base which changes the face of cancer understanding and therapeutics. This is the first book to provide such a comprehensive coverage of a rapidly evolving area written by leading experts in the field of omics. It compiles and details cutting-edge cancer research that covers the broad advances in the field and its application in cancer-associated gene discovery to drug target validation. It also highlights the potential of using integration approach in cancer research. This unique and timely book provides a thorough overview of developing omics, which will appeal to anyone involved in cancer research. It will be a valuable reference book for graduate students of different subjects (medicine, biology, engineering, etc) and senior scientists interested in the fascinating area of advanced technologies in cancer research. Readership: This is a precious book for all types of readers – cancer researchers, oncologists, pathologists, biologists, clinical chemists, pharmaceutical specialists, biostatisticians, and bioinformaticists who want to expand their knowledge in cancer research.

Cancer Genomics Ulrich Pfeffer 2013-02-12 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 future translational research become evident. The deep impact on the clinics and the challenge for future translational research become evident.

Molecular Biology, Pharmacogenomics and Bioinformatics of Natural Products and Synthetic Compounds for Cancer Therapy Tolga Eichhorn 2011