Bioinformatics In Cancer And Cancer Therapy Cancer Drug Discovery And Development

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Cancer Genomics for the Clinician   Ramaswamy Govindan 2019 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

Medical Physics   Anna Bajek 2021-08-02 Modern cancer research is a high-tech undertaking, overlapping with many fields in the physical sciences. These include nanotechnology, engineering, immunology, and bioinformatics. This book focuses on the science and technology underlying the diagnosis and treatment of cancer. The authors offer insights into technologies including radiotherapy, modelling, and drug encapsulation.

Modern Molecular Biology: Srinivasan Yegnasubramanian 2012-11-05 Molecular biology has rapidly advanced since the discovery of the basic flow of information in life, from DNA to RNA to proteins. While there are several important and interesting exceptions to this general flow of information, the importance of these biological macromolecules in dictating the phenotypic nature of living creatures in health and disease is paramount. In the last one and a half decades, and particularly after the completion of the Human Genome Project, there has been an explosion of technologies that allow the broad characterization of these macromolecules in physiology, and the perturbations to these macromolecules that occur in diseases such as cancer. In this volume, we will explore the modern approaches used to characterize these macromolecules in an unbiased, systematic way. Such technologies are rapidly advancing our knowledge of the coordinated and complicated changes that occur during carcinogenesis, and are providing vital information that, when correctly interpreted by biostatistical/bioinformatics analyses, can be exploited for the prevention, diagnosis, and treatment of human cancers. The purpose of this volume is to provide an overview of modern molecular biological approaches to unbiased discovery in cancer research. Advances in molecular biology allowing unbiased analysis of changes in cancer initiation and progression will be overviewed. These include the strategies employed in modern genomics, gene expression analysis, and proteomics.

Genomic Clinical Trials and Predictive Medicine   Richard M. Simon 2013-01-07 This book focuses on novel approaches that provide a reliable basis for identifying which patients are likely to benefit from each treatment. Aimed at both clinical investigators and statisticians, it covers the development and validation of prognostic and predictive biomarkers and their integration into clinical trials.

Cancer Bioinformatics   2022-09-28 This book discusses the application of bioinformatics in cancer disease management. It covers general aspects of cancer as a disease but also as a success story in the translation of omics data in clinical settings. It provides an overview of the specific applications of bioinformatics tools in cancer epidemiology, prevention, and screening and in the identification of novel genetic and molecular biomarkers involved in cancer development. This is accomplished through the inclusion of numerous examples of the use of bioinformatics in precision oncology.

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 promising 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 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 data 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.

Modern Molecular Biology: Srinivasan Yegnasubramanian 2010-09-02 Molecular biology has rapidly advanced since the discovery of the basic flow of information in life, from DNA to RNA to proteins. While there are several important and interesting exceptions to this general flow of information, the importance of these biological macromolecules in dictating the phenotypic nature of living creatures in health and disease is paramount. In the last one and a half decades, and particularly after the completion of the Human Genome Project, there has been an explosion of technologies that allow the broad characterization of these macromolecules in physiology, and the perturbations to these macromolecules that occur in diseases such as cancer. In this volume, we will explore the modern approaches used to characterize these macromolecules in an unbiased, systematic way. Such technologies are rapidly advancing our knowledge of the coordinated and complicated changes that occur during carcinogenesis, and are providing vital information that, when correctly interpreted by biostatistical/bioinformatics analyses, can be exploited for the prevention, diagnosis, and treatment of human cancers. The purpose of this volume is to provide an overview of modern molecular biological approaches to unbiased discovery in cancer research. Advances in molecular biology allowing unbiased analysis of changes in cancer initiation and progression will be overviewed. These include the strategies employed in modern genomics, gene expression analysis, and proteomics.

Computational Methods in Drug Discovery and Repurposing for Cancer Therapy   Ganji Purnachandra Nagaraju 2023-03-01 Computational Methods in Drug Discovery and Repurposing for Cancer Therapy provides knowledge about on-going research as well as computational approaches for drug discovery and repurposing for cancer therapy. It also provides detailed descriptions about target molecules, pathways and their inhibitors for easy understanding and applicability. The book discusses tools and techniques such as integrated bioinformatics approaches, systems biology tools, molecular docking, computational chemistry, artificial intelligence, machine learning, structure-based virtual screening, biomarkers, and transcriptome; those are discussed in the context of different cancer types, such as colon, glioblastoma, endometrial, retinoblastoma, among others. It is a valuable resource for researchers, students and member of the biomedical and medical fields who want to learn more about the use of computational modeling to better tailor the treatment for cancer patients.

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 refers to cancer. It is a genetic disease. The 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 targets for cancer therapies. It uses the techniques of transcriptomes, genome sequencing, bioinformatics, 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.

Cancer Drug Resistance   Jose Rueff 2019-03-20 This volume discusses the latest advancements and technologies used in cancer drug resistance research. Cancer Drug Resistance: Overviews and Methods contains chapters that cover topics such as: studying the mechanics of resistance to DNA damaging therapeutic drugs; studies to delineate the role of efflux transporters; expression of drug transporters; resistance to targeted therapies in breast cancer; the role of microRNAs in current pancreatic cancer treatment; and cancer exosomes as mediators of drug resistance or clinical and molecular methods in drug development and the use of bioinformatics in the management of cancer drug resistance data. Written in the highly successful Methods in Molecular Biology series format, chapters include overviews of the main issues in cancer drug resistance and the respective mechanisms, as well as introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Cancer Drug Resistance: Overviews and Methods, is a valuable resource to researchers, oncobiologists and clinical oncologists or anyone else who is interested in the study of cancer and its drug resistances.

Next Generation Sequencing in Cancer Research, Volume 2   Wei Wu 2015-05-06 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 can be 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.

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 must 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.

Genomic Medicine   Laura J. Tafe 2019-09-26 The field of Molecular Diagnostics is rapidly evolving and molecular characterization of neoplasms is becoming an increasingly important part of the pathologic work up and diagnosis of many tumor types. This work provides a high-yield reference book that compiles critical information related to molecular biomarkers for various solid tumor and hematologic malignancy subtypes. It is succinct yet comprehensive enough to be suitable for fellows in training and medical professionals with an interest in molecular pathology and biomarkers. The book covers many aspects of molecular diagnostics, from techniques to applications and comprehensive summaries of the current molecular biomarkers of critical importance in solid and liquid tumors. Attention is also specifically devoted to bioinformatics and next generation sequencing, as well as pre-analytical issues that must be considered for accurate interpretation of molecular results in the context of overall patient care. This text focuses on clinical utility and validity and serves as an "owner's manual" in Genomic Diagnostics for the practicing pathologist, pathology fellows and residents and other health care providers. Physicians will find this book invaluable as a quick reference for current molecular testing modalities and guidelines, tumor board preparation, deciding which test to order and interpreting genomic laboratory results. In addition, it is an accessible for trainees as a board review preparation reference.

Anticancer Plants: Mechanisms and Molecular Interactions   Mohd Sayeed Akhtar 2018-07-03 This book summarizes the application of plant derived anticancer compounds as chemopreventives to treat several cancer types, focusing on the molecular mechanisms of action of phytocompounds and providing an overview of the basic processes at the cellular and molecular level that are involved in the progression of the cancer and can be employed in targeted preventive therapies. In addition, it highlights the development of novel anticancer drugs from plant sources using bioinformatics approaches. The compiled chapter data aids readers understanding of issues related to bioavailability, toxic effects and mechanisms of action of phytocompounds, and helps them identify the leads and utilize them against various cancer types effectively. Furthermore, it promotes the use of bioinformatics tools in medicinal plants to expedite their use in plant breeding programs to develop molecular markers to distinguish disease subtypes and predicting mutation, which in turn improves cancer diagnosis and prognosis, and to develop new lead compounds computationally. The book provides scientific verifications of plant compounds mechanisms of action against various cancers and offers useful information for students, teachers, and healthcare professionals involved in drug discovery, and clinical and therapeutic research.

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 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 care. 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.

'Essentials of Cancer Genomic, Computational Approaches and Precision Medicine   Nosheen Masood 2020-04-04 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.

OMICS Debmalya Barh 2011-11-21 A reflection of the explosion of research and development in this field, OMICS: Biomedical Perspectives and Applications explores applications of omics in bioinformatics, cancer research and therapy, diabetes research, plant science, molecular biology, and neurosciences. A select editorial panel of experts discusses their cutting edge omics research and novel technologies, supplying a basic platform of methods and applications and a resource for enhanced cross-pollination in a multiomics approach to future endeavors in the fertile fields of omics research. After an introduction on the omics universe, the book presents modern omics and its applications in nanotechnology, genomics, proteomics, metagenomics, toxicogenomics, immunomics, nutrigenomics, diabetes, neurology, cardiology, and cancer to name just a few. The book begins with an overview of omics and omic technologies such as cellomics, glycomics, and lipidomics. It also discusses bioinformatics, demonstrating how it can be a tool in omics, and examines the various approaches of omics technology in toxicology research and applications in biomedical sciences. While there are a long list of omics books available, most focus narrowly on one area. Presenting a wide view of the current status of integrative omics, this resource contains complete coverage of omics in research and therapy, ranging from neuroscience to cardiology. It collates recent developments in the field into a state-of-the-art framework for this discipline.

Computational Intelligence in Oncology   Khalid Raza 2022 This book encapsulates recent applications of CI methods in the field of computational oncology, especially cancer diagnosis, prognosis, and its optimized therapeutics. The cancer has been known as a heterogeneous disease categorized in several different subtypes. According to WHOs recent report, cancer is a leading cause of death worldwide, accounting for over 10 million deaths in the year 2020. Therefore, its early diagnosis, prognosis, and classification to a subtype have become necessary as it facilitates the subsequent clinical management and therapeutics plan. Computational intelligence (CI) methods, including artificial neural networks (ANNs), fuzzy logic, evolutionary computations, various machine learning and deep learning, and nature-inspired algorithms, have been widely utilized in various aspects of oncology research, viz. diagnosis, prognosis, therapeutics, and optimized clinical management. Appreciable progress has been made toward the understanding the hallmarks of cancer development, progression, and its effective therapeutics. However, notwithstanding the extrinsic and intrinsic factors which lead to drastic increment in incidence cases, the detection, diagnosis, prognosis, and therapeutics remain an apex challenge for the medical fraternity. With the advent in CI-based approaches, including nature-inspired techniques, and availability of clinical data from various high-throughput experiments, medical consultants, researchers, and oncologists have seen a hope to devise and employ CI in various aspects of oncology. The main aim of the book is to occupy state-of-the-art applications of CI methods which have been derived from core computer sciences to back medical oncology. This edited book covers artificial neural networks, fuzzy logic and fuzzy inference systems, evolutionary algorithms, various nature-inspired algorithms, and hybrid intelligent systems which are widely appreciated for the diagnosis, prognosis, and optimization of therapeutics of various cancers. Besides, this book also covers multi-omics exploration, gene expression analysis, gene signature identification of cancers, genomic characterization of tumors, anti-cancer drug design and discovery, drug response prediction by means of CI, and applications of IoT, IoMT, and blockchain technology in cancer research.

Precision Cancer Medicine   Sameek 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.

Systems Biomedicine Approaches in Cancer Research   Shailza Singh 2022-08-12 This book presents the applications of systems biology and synthetic biology in cancer medicine. It highlights the use of computational and mathematical models to decipher the complexity of cancer heterogeneity. The book emphasizes the modeling approaches for predicting behavior of cancer cells, tissues in context of drug response, and angiogenesis. It introduces cell-based therapies for the treatment of various cancers and reviews the role of neural networks for drug response prediction. Further, it examines the system biology approaches for the identification of medicinal plants in cancer drug discovery. It explores the opportunities for metabolic engineering in the realm of cancer research towards development of new cancer therapies based on metabolically derived targets. Lastly, it discusses the applications of data mining techniques in cancer research. This book is an excellent guide for oncologists and researchers who are involved in the latest cancer research.

Prostate Cancer   Scott M. Dehm 2020-01-03 The purpose of this book is to provide a contemporary overview of the causes and consequences of prostate cancer from a cellular and genetic perspective. Written by experts in the fields of epidemiology, toxicology, cell biology, genetics, genomics, cell-cell interactions, cell signaling, hormone signaling, and transcriptional regulation, the text covers aspects of prostate cancer from disease initiation to metastasis. Chapters explore in depth the cells of origin for prostate cancer, its genomic subtypes, neural transcription factors in disease progression, epigenetic regulation of chromatin, and many other topics. This book distinguishes itself from other texts on prostate cancer by its focus on cellular and genetic mechanisms, as opposed to clinical diagnosis and management. As a result, this book will be of broad interest to basic and translational scientists with familiarity of these topics, as well as to trainees at earlier stages of their research careers.

Systems Biology of MicroRNAs in Cancer   Ulf Schmitz 2022-12-11 This book provides an update on the latest development in the field of microRNAs in cancer research with an emphasis on translational research. Since the early 2000s, microRNAs have been recognized as important and ubiquitous regulators of gene expression. Soon it became evident that their deregulation can cause human diseases including cancer. This book focuses on the emerging opportunities for the application of microRNA research in clinical practice. In this context, computer models are presented that can help to identify novel biomarkers, e.g. in circulating microRNAs, and tools that can help to design microRNA-based therapeutic interventions. Other chapters evaluate the role of microRNAs in immunotherapy, immune responses and drug resistance. Covering key topics on microRNAs in cancer research this book is a valuable resource for both emerging and established microRNA researchers who want to explore the potential of microRNAs as therapeutic targets or co-adjuvants in cancer therapies.

Holland-Frei Cancer Medicine   Robert C. Bast, Jr. 2017-03-13 Holland-Frei Cancer Medicine, Ninth Edition, offers a balanced view of the most current knowledge of cancer science and clinical oncology practice. This all-new edition is the consummate reference source for medical oncologists, radiation oncologists, internists, surgical oncologists, and others who treat cancer patients. A translational perspective throughout, integrating cancer biology with cancer management providing an in depth understanding of the disease An emphasis on multidisciplinary, research-driven patient care to improve outcomes and optimal use of all appropriate therapies Cutting-edge coverage of personalized cancer care, including molecular diagnostics and therapeutics Concise, readable, clinically relevant text with algorithms, guidelines and insight into the use of both conventional and novel drugs Includes free access to the Wiley Digital Edition providing search across the book, the full reference list with web links, illustrations and photographs, and post-publication updates

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

Tissue Phenomics: Profiling Cancer Patients for Treatment Decisions   Gerd Binnig 2018-01-29 In the age of digitization our society is transformed into a new state. In particular, machine intelligence dramatically elevates our capability to create and digest information. Naturally, healthcare is also impacted by this trend and will even be more transformed into a informatic driven discipline in the future. In the most important area of histo-pathology, the interpretation of tissue slices from cancer patients, informatics will have an early and huge impact on treatment decisions and probably will act as the leading discipline for this transformation in medicine. Tissue Phenomics provides a comprehensive methodology aiming at the discovery of the most accurate tissue-based decision support algorithm by close integration of assay development, image analysis and bioinformatics, and optimization feedback loops. In this book the methodology of Tissue Phenomics and its benefits and wealth's are described. The different components of Tissue Phenomics are explained in the different chapters. In the chapters 2 to 4 of this book different authors describe various approaches on how to convert the wealth of tissue slide pixel data into mineable information using knowledge-based and data-driven image analysis methods. Subsequently, the datafication of images and the bioinformatics part plays a crucial role in generating prognostic and predictive models for disease progression. The integration of other data sources such as genomics, radiomics and patient related information is also important and is described as well. As discussed in chapters 5 and 6, these models may classify patients in distinct groups such as those responding to a given therapy. Since Tissue Phenomics provides a huge set of potentially prognostic features (phenes), one focus of both chapters is robust feature selection methods by advanced Monte-Carlo cross validation algorithms. In chapter 7 we discuss multiple application examples of Tissue Phenomics in academic and commercial settings and its tremendous impact to advances in biomedical sciences. Building on the successes in research, chapters 8 and 9 discuss applications in clinical environments and provide a flavor to the future envision in chapter 10, where tissue datafication and subsequent patient profiling is part of every routine examination, with the goal to best match patients with the most successful therapy, as

predicted by tissue phenes.

Cancer Genomics Ulrich Pfeffer 2013-03-02 The combination of molecular biology, engineering and bioinformatics has revolutionized our understanding of cancer revealing a tight correlation of the molecular characteristics of the primary tumor in terms of gene expression, structural alterations of the genome, epigenetics and mutations with its propensity to metastasize and to respond to therapy. It is not just one or a few genes, it is the complex alteration of the genome that determines cancer development and progression. Future management of cancer patients will therefore rely on thorough molecular analyses of each single case. Through this book, students, researchers and oncologists will obtain a comprehensive picture of what the first ten years of cancer genomics have revealed. Experts in the field describe, cancer by cancer, the progress made and its implications for diagnosis, prognosis and treatment of cancer. The deep impact on the clinics and the challenge for future translational research become evident.

Molecular and Cell Biology of Cancer Rita Fior 2019-06-27 This textbook takes you on a journey to the basic concepts of cancer biology. It combines developmental, evolutionary and cell biology perspectives, to then wrap-up with an integrated clinical approach. The book starts with an introductory chapter, looking at cancer in a nut shell. The subsequent chapters are detailed and the idea of cancer as a mass of somatic cells undergoing a micro-evolutionary Darwinian process is explored. Further, the main Hanahan and Weinberg "Hallmarks of Cancer" are revisited. In most chapters, the fundamental experiments that led to key concepts, connecting basic biology and biomedicine are highlighted. In the book's closing section all of these concepts are integrated in clinical studies, where molecular diagnosis as well as the various classical and modern therapeutic strategies are addressed. The book is written in an easy-to-read language, like a one-on-one conversation between the writer and the reader, without compromising the scientific accuracy. Therefore, this book is suited not only for advanced undergraduates and master students but also for patients or curious lay people looking for a further understanding of this shattering disease

Handbook of Cancer Models with Applications W. Y. Tan 2008 Composed of contributions from an international team of leading researchers, this book pulls together the most recent research results in the field of cancer modeling to provide readers with the most advanced mathematical models of cancer and their applications.Topics included in the book cover oncogenetic trees, stochastic multistage models of carcinogenesis, effects of ionizing radiation on cell cycle and genomic instability, induction of DNA damage by ionizing radiation and its repair, epigenetic cancer models, bystander effects of radiation, multiple pathway models of human colon cancer, and stochastic models of metastasis. The book also provides some important applications of cancer models to the assessment of cancer risk associated with various hazardous environmental agents, to cancer screening by MRI, and to drug resistance in cancer chemotherapy. An updated statistical design and analysis of xenograft experiments as well as a statistical analysis of cancer occult clinical data are also provided.The book will serve as a useful source of reference for researchers in biomathematics, biostatistics and bioinformatics; for clinical investigators and medical doctors employing quantitative methods to develop procedures for cancer diagnosis, prevention, control and treatment; and for graduate students.

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, sharing data, and establishing partnerships within and across sectors of patient diagnosis and treatment.

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 regimens 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 professional, especially clinicians specializing in Clinical Oncology, and their patients who want to gain an understanding of cancer and available treatment options.

The Application of Sequencing Technologies and Bioinformatics Methods in Cancer Biology Geng Chen 2022-10-17

Cancer Cell Metabolism: A Potential Target for Cancer Therapy Dhruv Kumar 2020-02-13 This book illustrates various aspects of cancer cell metabolism, including metabolic regulation in solid tumours vs. non-solid tumours, the molecular pathways involved in its metabolism, and the role of the tumour microenvironment in the regulation of cancer cell metabolism. It summarizes the complexity of cancer cell metabolism in terms of the switch from anaerobic to aerobic glycolysis and how mitochondrial damage promotes aerobic glycolysis in cancer cells. The respective chapters provide the latest information on the metabolic remodelling of cancer cells and elucidate the important role of the signalling pathways in reprogramming of cancer cell metabolism. In addition, the book highlights the role of autophagy in cancer cell metabolism, and how metabolic crosstalk between cancer cells and cancer-associated fibroblasts promotes cancer cell progression. In closing, it summarizes recent advancements in drug development through targeting cancer metabolism.

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 various cancer-related processes, and to demonstrate how a bioinformatics approach is being used to bridge basic science and the clinical arena to positively impact patient care and management.

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.

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

Cancer Diagnostics with DNA Microarrays Steen Knudsen 2006-11-03 Authored by an international authority in the field,Cancer Diagnostics with DNA Microarrays is a complete reference work on the rapidly growing use of DNA microarray data in the diagnosis of and treatment planning for a large number of human cancers. Uniquely deals with direct clinical application of microarray data to oncology design, leading to more effective diagnosis and of clearer treatment regimens for a wide range of human cancers Offers clinicians summary presentation of state-of-the-art science of DNA microarrays Each chapter includes bibliographic and further reading suggestions Easily accessible, assuming no special training in statistics or bioinformatics Replete with examples and mini-cases, Cancer Diagnostics with DNA Microarrays offers cancer researchers in private, pharmacologic, and governmental institutions, biomedical statisticians, and practicing oncologists concise, thoughtfully authored guidance on the use of microarray data and analysis as clinical tools. The text carefully addresses the needs of end users – researchers and physicians – using microarrays as a tool to be applied in common clinical situations, and is of interest for students in medicine and biology and professionals in health care as well.

The Oncogenomics Handbook William J. LaRochelle 2005-04-15 "In The Oncogenomics Handbook, a panel of internationally recognized researchers and clinicians provides 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 that path, 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." --Résumé de l'éditeur.

Molecular Oncology Diagnostics, An Issue of the Clinics in Laboratory Medicine, E-Book Fei Dong 2022-09-23 In this issue of Clinics in Laboratory Medicine, guest editor Dr. Fei Dong brings his considerable expertise to the topic of Molecular Oncology Diagnostics. Top experts in the field review current practices in molecular oncology diagnostics, highlighting the rapid clinical adoption of next generation sequencing techniques. The articles address key laboratory considerations in the molecular testing of cancer specimens and the impact of advanced testing strategies on patient care. Contains 15 practice-oriented topics including utility of single gene testing in cancer specimens; analytical principles of cancer next generation sequencing; principles and validation of bioinformatics pipelines for next generation sequencing; panel sequencing for targeted therapy selection in solid tumors; and more. Provides in-depth clinical reviews on molecular oncology diagnostics, offering actionable insights for clinical practice. Presents the latest information on this timely, focused topic under the leadership of experienced editors in the field. Authors synthesize and distill the latest research and practice guidelines to create clinically significant, topic-based reviews.

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.

Correlation-based network analysis of cancer metabolism Emily G. Armitage 2014-05-12 With the rise of systems biology as an approach in biochemistry research, using high throughput techniques such as mass spectrometry to generate metabolic profiles of cancer metabolism is becoming increasingly popular. 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 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.