Multiscale Modeling Of Cancer An Integrated Experimental And Mathematical Modeling Approach 1st Edition By Cristini Vittorio Lowengrub John 2010 Hardcover

A modern quantitative study of lung mechanics, relating mathematical modeling and engineering principles to lung function, structure, mechanics, and disease. This book presents and discusses the state of the art and future perspectives in mathematical modeling and homogenization techniques with the focus on addressing key physiological issues in the context of multiphase healthy and malignant biological materials. The highly interdisciplinary content brings together contributions from scientists with complementary areas of expertise, such as pure and applied mathematicians, engineers, and biophysicists. The book also features the lecture notes from a half-day introductory course on asymptotic homogenization. These notes are suitable for undergraduate mathematics or physics students, while the other chapters are aimed at graduate students and researchers.

Presenting a state-of-the-art overview of theoretical and computational models that link characteristic biomechanical phenomena, this book provides guidelines and examples for creating multiscale models in representative systems and organisms. It develops the reader's understanding of and intuition for multiscale phenomena in biomechanics and mechanobiology, and introduces a mathematical framework and computational techniques paramount to creating predictive multiscale models. Biomechanics involves the study of the interactions of physical forces with biological systems at all scales – including molecular, cellular, tissue and organ scales. The emerging field of mechanobiology focuses on the way that cells produce and respond to mechanical forces – bridging the science of mechanics with the disciplines of genetics and molecular biology. Linking disparate spatial and temporal scales using computational techniques is emerging as a key concept in investigating some of the complex problems underlying these disciplines. Providing an invaluable field manual for graduate students and researchers of theoretical and computational modelling in biology, this book is also intended for readers interested in biomedical engineering, applied mechanics and mathematical biology.

This collection of selected chapters offers a comprehensive overview of state-of-the-art mathematical methods and tools for modeling and analyzing cancer phenomena. Topics covered include stochastic evolutionary models of cancer initiation and progression, tumor cords and their response to anticancer agents, and immune competition in tumor progression and prevention. The complexity of modeling living matter requires the development of new mathematical methods and ideas. This volume, written by first-rate researchers in the field of mathematical biology, is one of the first steps in that direction.

The Encyclopedia of Cell Biology offers a broad overview of cell biology, offering reputable, foundational content for researchers and students across the biological and medical sciences. This important work includes 285 articles from domain experts covering every aspect of cell biology, with fully annotated figures, abundant illustrations, videos, and references for further reading. Each entry is built with a layered approach to the content, providing basic information for those new to the area and more detailed material for the more experienced researcher. With authored contributions by experts in the field, the Encyclopedia of Cell Biology provides a fully cross-referenced, one-stop resource for students, researchers, and teaching faculty across the biological and medical sciences. Fully annotated color images and videos for full comprehension of concepts, with layered content for readers from different levels of experience Includes information on cytokinesis, cell biology, cell mechanics, cytoskeleton dynamics, stem cells, prokaryotic cell biology, RNA biology, aging, cell growth, cell Injury, and more In-depth linking to Academic Press/Elsevier content and additional links to outside websites and resources for further reading A one-stop resource for students, researchers, and teaching faculty across the biological and medical sciences

The study of complex systems and their related phenomena has become a major research venue in the recent years and it is commonly regarded as an important part of the scientific revolution developing through the 21st century. The science of complexity is concerned with the laws of operation and evolution of systems formed by many locally interacting elements that produce collective order at spatiotemporal scales larger than that of the single constitutive elements. This new thinking, that explores formally the emergence of spontaneous higher order and feedback hierarchies, has been particularly successful in the biological sciences. One particular life-threatening disease in humans, overwhelmingly common in the modern world is cancer. It is regarded as a collection of phenomena involving anomalous cell growth caused by an underlying genetic instability with the potential to spread to other parts of the human body. In the present book, a group of well recognised specialists discuss new ideas about the disease. These authors coming from solid backgrounds in physics, mathematics, medicine, molecular and cell biology, genetics and anthropology have dedicated their time to write an authoritative free-available text published under the open access philosophy that hopefully would be in the front-line struggle against cancer, a complex disease.

Recent advances witness the potential to employ nanomedicine and game-changing methods to deliver drug molecules directly to diseased sites. To optimize and then enhance the efficacy and specificity, the control and guidance of drug carriers in vasculature has become crucial. Current bottlenecks in the optimal design of drug carrying particles are the lack of knowledge about the transport of particles, adhesion on endothelium wall and subsequent internalization into diseased cells. To study the transport and adhesion of particle

in vasculature, the authors have made great efforts to numerically investigate the dynamic and adhesive motions of particles in the blood flow. This book discusses the recent achievements from the establishment of fundamental physical problem to development of multiscale model, and finally large scale simulations for understanding transport of particle-based drug carriers in blood flow.

Cancer is a complex disease process that spans multiple scales in space and time. Driven by cutting-edge mathematical and computational techniques, in silico biology provides powerful tools to investigate the mechanistic relationships of genes, cells, and tissues. It enables the creation of experimentally testable hypotheses, the integration of data across scales, and the prediction of tumor progression and treatment outcome (in silico oncology). Drawing on an interdisciplinary group of distinguished international experts, Multiscale Cancer Modeling discusses the scientific and technical expertise necessary to conduct innovative cancer modeling research across scales. It presents contributions from some of the top in silico modeling groups in the United States and Europe. The ultimate goal of multiscale modeling and simulation approaches is their use in clinical practice, such as supporting patient-specific treatment optimization. This volume covers state-of-the-art methods of multiscale cancer modeling and addresses the field's potential as well as future challenges. It encourages collaborations among researchers in various disciplines to achieve breakthroughs in cancer modeling.

This volume – for pharmacologists, systems biologists, philosophers and historians of medicine – points to investigate new avenues in pharmacology research, by providing a full assessment of the premises underlying a radical shift in the pharmacology paradigm. The pharmaceutical industry is currently facing unparalleled challenges in developing innovative drugs. While drug-developing scientists in the 1990s mostly welcomed the transformation into a target-based approach, two decades of experience shows that this model is failing to boost both drug discovery and efficiency. Selected targets were often not druggable and with poor disease linkage, leading to either high toxicity or poor efficacy. Therefore, a profound rethinking of the current paradigm is needed. Advances in systems biology are revealing a phenotypic robustness and a network structure that strongly suggest that exquisitely selective compounds, compared with multitarget drugs, may exhibit lower than desired clinical efficacy. This appreciation of the role of polypharmacology has significant implications for tackling the two major sources of attrition in drug development, efficacy and toxicity. Integrating network biology and polypharmacology holds the promise of expanding the current opportunity space for druggable targets.

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

computational chemistry and high-performance computing. As such, it is a valuable resource for researchers, medical and bioengineering students, and medical device and software experts

Discover how the latest computational tools are building our understanding of particle interactions and leading to new applications With this book as their guide, readers will gain a new appreciation of the critical role that particle interactions play in advancing research and developing new applications in the biological sciences, chemical engineering, toxicology, medicine, and manufacturing technology The book explores particles ranging in size from cations to whole cells to tissues and processed materials. A focus on recreating complex, real-world dynamical systems helps readers gain a deeper understanding of cell and tissue mechanics, theoretical aspects of multiscale modeling, and the latest applications in biology and nanotechnology. Following an introductory chapter, Multiscale Modeling of Particle Interactions is divided into two parts: Part I, Applications in Nanotechnology, covers: Multiscale modeling of nanoscale aggregation phenomena: applications in semiconductor materials processing Multiscale modeling of rare events in self-assembled systems Continuum description of atomic sheets Coulombic dragging and mechanical propelling of molecules in nanofluidic systems Molecular dynamics modeling of nanodroplets and nanoparticles Modeling the interactions between compliant microcapsules and patterned surfaces Part II, Applications in Biology, covers: Coarse-grained and multiscale simulations of lipid bilayers Stochastic approach to biochemical kinetics In silico modeling of angiogenesis at multiple scales Large-scale simulation of blood flow in microvessels Molecular to multicellular deformation during adhesion of immune cells under flow Each article was contributed by one or more leading experts and pioneers in the field. All readers, from chemists and biologists to engineers and students, will gain new insights into how the latest tools in computational science can improve our understanding of particle interactions and support the development of novel applications across the broad spectrum of disciplines in biology and nanotechnology.

To profoundly understand biology and harness its intricacies for human benefit and the mitigation of human harm requires cross-disciplinary approaches that incorporate sophisticated computational and mathematical modeling techniques. These integrative strategies are essential to achieve rapid and significant progress in issues, in health and disease, which span molecular, cellular and tissue levels. The use of mathematical models to describe various aspects of tumor growth has a very long history, dating back over six decades. Recently, however, experimental and computational advances have improved our in the understanding of how processes act at multiple scales to mediate the development of tumor vasculature and drive the advancement of cancer. This book will showcase the development and utilization of new computational and mathematical approaches to address multiscale challenges associated with tumor vascular development. In Part I: Cell Signaling and Molecular Aspects of Tumor Blood Vessel Formation, it will be come clear that mathematical modeling can help to biochemically and biomechanically phenotype one of the most important cell types involved in cancer progression: vascular endothelial cells. When subverted by the tumor modulated environment, vascular endothelial cells form a new vascular supply capable of nourishing and translocating cancer cells to other tissues. The models in Part I illustrate the importance of quantitative approaches for gaining a deeper understanding of how

normal and abnormal aspects of signal integration culminate in the cell proliferation, migration, and survival decisions that result in pathological tumor angiogenesis. The focus of Part II is the angiogenesis cascade and all of its complexities. Successful angiogenesis is mediated by the intricate interplay between biochemical and biomechanical mechanisms, including cell-cell and cell-matrix interactions, cell surface receptor binding, and intracellular signal transduction. A major challenge facing the cancer research community is to integrate known information in a way that improves our understanding of the principal underpinnings driving tumor angiogenesis and that will advance efforts aimed at the development of new therapies for treating cancer. The chapters in Part II will highlight several mathematical and computational approaches for that can potentially address this challenge. While the first two thirds of the book's chapters demonstrate how important insights can be gained by studying cell signaling and vascular morphology and function, the series of chapters in Part III: Whole Organ Modeling of Tumor Growth and Vasculature, will integrate vasculature development with tumor growth dynamics. These two processes strongly depend on one another in ways that can only be theoretically investigated by biophysical approaches that cut across several levels of biological organization and describe both the tumor and the developing vasculature as they co-evolve. The purpose of this edited volume is not to provide a comprehensive review of all modeling efforts that address tumor vascular modeling; instead, a variety of interesting and innovative mathematical modeling approaches for understanding the development and effects of tumor vasculature are highlighted in order to illustrate some of the emerging trends in the field.

Arguably the first book of its kind, Computational Bioengineering explores the power of multidisciplinary computer modeling in bioengineering. Written by experts, the book examines the interplay of multiple governing principles underlying common biomedical devices and problems, bolstered by case studies. It shows you how to take advantage of the la

Mathematical modeling, analysis and simulation are set to play crucial roles in explaining tumor behavior, and the uncontrolled growth of cancer cells over multiple time and spatial scales. This book, the first to integrate state-of-the-art numerical techniques with experimental data, provides an in-depth assessment of tumor cell modeling at multiple scales. The first part of the text presents a detailed biological background with an examination of single-phase and multi-phase continuum tumor modeling, discrete cell modeling, and hybrid continuum-discrete modeling. In the final two chapters, the authors guide the reader through problem-based illustrations and case studies of brain and breast cancer, to demonstrate the future potential of modeling in cancer research. This book has wide interdisciplinary appeal and is a valuable resource for mathematical biologists, biomedical engineers and clinical cancer research communities wishing to understand this emerging field.

An overview of the current systems biology-based knowledge and the experimental approaches for deciphering the biological basis of cancer.

Understanding how cancer tumours develop and spread is vital for finding treatments and cures. Cancer Modelling and Simulation demonstrates how mathematical modelling and computer simulation techniques are used to discover and gain insight into the dynamics of tumour development and growth. It highlights the benefits of tumour modelling, such as discovering optimal tumour therapy schedules, identifying

the most promising candidates for further clinical investigation, and reducing the number of animal experiments. By examining the analytical, mathematical, and biological aspects of tumour growth and modelling, the book provides a common language and knowledge for professionals in several disciplines.

This article collection reviews key developments in the new science of mathematical oncology and includes 20 open access research papers by various authors. Topics include: The evolutionary impact of androgen levels on prostate cancer in a multi-scale mathematical model; Cancer as a metabolic disease; Using mathematical models to understand metabolism, genes, and disease; Plausibility of stromal initiation of epithelial cancers without a mutation in the epithelium: a computer simulation of morphostats; Mathematical models for translational and clinical oncology; The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells; A 3D multiscale model of cancer stem cell in tumor development; Immunoediting: evidence of the multifaceted role of the immune system in self-metastatic tumor growth; Theoretical aspects and modelling of cellular decision making, cell killing and information processing in photodynamic therapy of cancer; Non-stem cancer cell kinetics modulate solid tumor progression; Set theoretical and algebraic model for redundancies in the genetic code; Natural resistance to cancers: a Darwinian hypothesis to explain Peto's paradox; Mathematical and computational modeling in biology at multiple scales; A theoretical quantitative model for evolution of cancer chemotherapy resistance; Proton dynamics in cancer; A multiscale systems perspective on cancer, immunotherapy, and Interleukin-12; Cancer progression modeling using static sample data; Organoid modeling for cancer precision medicine; Multi-scale agent-based brain cancer modeling and prediction of TKI treatment response: Incorporating EGFR signaling pathway and angiogenesis; Prediction of signaling cross-talks contributing to acquired drug resistance in breast cancer cells by Bayesian statistical modeling.

This monograph has the ambitious aim of developing a mathematical theory of complex biological systems with special attention to the phenomena of ageing, degeneration and repair of biological tissues under individual self-repair actions that may have good potential in medical therapy. The approach to mathematically modeling biological systems needs to tackle the additional difficulties generated by the peculiarities of living matter. These include the lack of invariance principles, abilities to express strategies for individual fitness, heterogeneous behaviors, competition up to proliferative and/or destructive actions, mutations, learning ability, evolution and many others. Applied mathematicians in the field of living systems, especially biological systems, will appreciate the special class of integro-differential equations offered here for modeling at the molecular, cellular and tissue scales. A unique perspective is also presented with a number of case studies in biological modeling.

A flexible, cell-level, and lattice-based technique, the cellular Potts model accurately describes the phenomenological mechanisms involved in many biological processes. Cellular Potts Models: Multiscale Extensions and Biological Applications gives an interdisciplinary, accessible treatment of these models, from the original methodologies to the latest developments. The book first explains the biophysical bases, main merits, and limitations of the cellular Potts model. It then proposes several innovative extensions, focusing on ways to integrate and interface the basic cellular Potts model at

the mesoscopic scale with approaches that accurately model microscopic dynamics. These extensions are designed to create a nested and hybrid environment, where the evolution of a biological system is realistically driven by the constant interplay and flux of information between the different levels of description. Through several biological examples, the authors demonstrate a qualitative and quantitative agreement with the relative experimental data. The cellular Potts model is increasingly being used for the mathematical modeling of a wide range of biological phenomena, including wound healing, tumor growth, and cancer cell migration. This book shows how the cellular Potts model can be used as a framework for model building and how extended models can achieve even better biological practicality, accuracy, and predictive power. Genomic signal processing (GSP) can be defined as the analysis, processing, and use of genomic signals to gain biological knowledge, and the translation of that knowledge into systems-based applications that can be used to diagnose and treat genetic diseases. Situated at the crossroads of engineering, biology, mathematics, statistics, and computer science, GSP requires the development of both nonlinear dynamical models that adequately represent genomic regulation, and diagnostic and therapeutic tools based on these models. This book facilitates these developments by providing rigorous mathematical definitions and propositions for the main elements of GSP and by paying attention to the validity of models relative to the data. Ilya Shmulevich and Edward Dougherty cover real-world situations and explain their mathematical modeling in relation to systems biology and systems medicine. Genomic Signal Processing makes a major contribution to computational biology, systems biology, and translational genomics by providing a self-contained explanation of the fundamental mathematical issues facing researchers in four areas: classification, clustering, network modeling, and network intervention.

This book explores outcome modeling in cancer from a data-centric perspective to enable a better understanding of complex treatment response, to guide the design of advanced clinical trials, and to aid personalized patient care and improve their quality of life. It contains coverage of the relevant data sources available for model construction (panomics), ranging from clinical or preclinical resources to basic patient and treatment characteristics, medical imaging (radiomics), and molecular biological markers such as those involved in genomics, proteomics and metabolomics. It also includes discussions on the varying methodologies for predictive model building with analytical and data-driven approaches. This book is primarily intended to act as a tutorial for newcomers to the field of outcome modeling, as it includes in-depth how-to recipes on modeling artistry while providing sufficient instruction on how such models can approximate the physical and biological realities of clinical treatment. The book will also be of value to seasoned practitioners as a reference on the varying aspects of outcome modeling and their current applications. Features: Covers top-down approaches applying statistical, machine learning, and big data analytics and bottom-up approaches using first principles and multi-scale techniques, including numerical simulations based on Monte Carlo and automata techniques Provides an overview of the available software tools and resources for outcome model development and evaluation, and includes hands-on detailed examples throughout Presents a diverse selection of the common applications of outcome modeling in a wide variety of areas: treatment planning in radiotherapy, chemotherapy and immunotherapy, utility-based and biomarker applications, particle

therapy modeling, oncological surgery, and the design of adaptive and SMART clinical trials

This book reviews the state-of-the-art in multiscale computer modeling, in terms of both accomplishments and challenges. The information in the book is particularly useful for biomedical engineers, medical physicists and researchers in systems biology, mathematical biology, micro-biomechanics and biomaterials who are interested in how to bridge between traditional biomedical engineering work at the organ and tissue scales, and the newer arenas of cellular and molecular bioengineering.

Martin Oliver Steinhauser deals with several aspects of multiscale materials modeling and simulation in applied materials research and fundamental science. He covers various multiscale modeling approaches for high-performance ceramics, biological bilayer membranes, semi-flexible polymers, and human cancer cells. He demonstrates that the physics of shock waves, i.e., the investigation of material behavior at high strain rates and of material failure, has grown to become an important interdisciplinary field of research on its own. At the same time, progress in computer hardware and software development has boosted new ideas in multiscale modeling and simulation. Hence, bridging the length and time scales in a theoretical-numerical description of materials has become a prime challenge in science and technology.

Ubiquitous and fundamental in cell mechanics, multiscale problems can arise in the growth of tumors, embryogenesis, tissue engineering, and more. Cell Mechanics: From Single Scale-Based Models to Multiscale Modeling brings together new insight and research on mechanical, mathematical, physical, and biological approaches for simulating the behavior of cells, specifically tumor cells. In the first part of the text, the book discusses the powerful tool of microrheology for investigating cell mechanical properties, multiphysics and multiscale approaches for studying intracellular mechanisms in cell motility, and the role of subcellular effects involving certain genes for inducing cell motility in cancer. Focusing on models based on physical, mathematical, and computational approaches, the second section develops tools for describing the complex interplay of cell adhesion molecules and the dynamic evolution of the cell cytoskeleton. The third part explores cell interactions with the environment, particularly the role of external mechanical forces and their effects on cell behavior. The final part presents innovative models of multicellular systems for developmental biology, cancer, and embryogenesis. This book collects novel methods to apply to cells and tissues through a multiscale approach. It presents numerous existing tools while stimulating the discovery of new approaches that can lead to more effective and accurate predictions of pathologies.

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Physical oncology has the potential to revolutionize cancer research and treatment. The fundamental rationale behind this approach is that physical processes, such as transport mechanisms for drug molecules within tissue and forces exchanged by cancer cells with tissue, may play an equally important role as biological processes in influencing progression and treatment outcome. This book introduces the emerging field of physical oncology to a general audience, with a focus on recent breakthroughs that help in the design and discovery of more effective cancer treatments. It describes how novel mathematical models of physical transport processes incorporate patient tissue and imaging data routinely produced in the clinic to predict the efficacy of many cancer treatment approaches, including chemotherapy and radiation therapy. By helping to identify which therapies would be most beneficial for an individual patient, and quantifying their effects prior to actual implementation in the clinic, physical oncology allows doctors to design treatment regimens customized to each patient's clinical needs, significantly altering the current clinical approach to cancer treatment and improving the outcomes for patients.

The combination of readily available computing power and progress in numerical techniques has made nonlinear systems - the kind that only a few years ago were ignored as too complex - open to analysis for the first time. Now realistic models of living systems incorporating the nonlinear variation and anisotropic nature of physical properties can be solved numerically on modern computers to give realistically usable results. This has opened up new and exciting possibilities for the fusing of ideas from physiology and engineering in the burgeoning new field that is biomechanics. Computational Biomechanics presents pioneering work focusing on the areas of orthopedic and circulatory mechanics, using experimental results to confirm or improve the relevant mathematical models and parameters. Together with two companion volumes, Biomechanics: Functional Adaptation and Remodeling and the Data Book on Mechanical Properties of Living Cells, Tissues, and Organs, this monograph will prove invaluable to those working in fields ranging from medical science and clinical medicine to biomedical engineering and applied mechanics.

Cancer is a major life threatening disease in the world. With the advancement of computational mathematics, big data science and unprecedented computational power, it becomes possible to investigate the complex multiscale growth

phenomenon of the tumor for cancer prognosis to provide pre-operative treatment planning and predict treatment outcome using mathematical modeling and computer simulation. The growth of biological tissue is a complex process because it involves various biophysically- and biochemically-induced events at different spatial and temporal scales. Multiscale modeling techniques allow us to incorporate important features at multiple scales to examine the tissue growth mechanism and determine the major factors affecting the growth process. The primary objective of this doctoral research is to develop a multiscale modeling framework for the growth of biological tissue and apply to tumor growth and cancer prognosis. Another objective of this study is to understand the effect of anticancer drugs on cancer cell growth, cell proliferation, and overall tumor size. The multiscale framework consists of a tissue scale model, a cellular activity and growth model and a subcellular signaling pathway model. To predict the tissue growth in the macroscopic (tissue) scale, a continuum model is constructed where the biological tissue is represented as a mixture of multiple constituents. Each of such constituents, in their solid, liquid or gas phase, are represented by either a volume fraction or concentration. The constituents interact with each other through mass and momentum exchange. The governing equations are developed based on both mass and momentum conservation laws. The constitutive equations account for tissue anisotropy, nonlinear behavior, and thermodynamic consistency. The system of partial differential equations are solved using finite element techniques. To bridge the spatial scales, each finite element is further discretized into finer cell clusters of different kinds to represent various biological cellular states at the microscopic scale to model cellular growth and proliferation by using an agent-based model to determine various activities at the cellular scale such as the cell division, cell death, phenotypical alteration, etc. The cellular scale events are also broken down and discretized temporally to model the effects of a subcellular signaling pathway (e.g. PI3K/AKT/mTOR pathway, also known as mTOR pathway) on the cellular and tissue scales. In many cancers, mTOR pathway becomes hyperactive and promotes abnormal cell proliferation. The mechanism and effects of an mTOR inhibiting drug known as rapamycin (e.g., eRapa) are tested using in silico methods. These subcellular activities are modeled using a set of ordinary differential equations. A statistical inverse algorithm is used for model calibration and validation. The Bayesian inference method accounts for the uncertainties of the model parameters, which are calibrated with the experimental observations. Generally speaking, the multiscale modeling framework presented in this dissertation may provide better understanding of the tissue growth process by providing insight on the effects of various factors at different spatiotemporal scales. It can also be potentially used to construct patient-specific tissue growth models for in silico drug testing, treatment planning, and prognosis.

This edited volume discusses the complexity of tumor microenvironments during cancer development, progression and treatment. Each chapter presents a

different mathematical model designed to investigate the interactions between tumor cells and the surrounding stroma and stromal cells. The topics covered in this book include the quantitative image analysis of a tumor microenvironment, the microenvironmental barriers in oxygen and drug delivery to tumors, the development of tumor microenvironmental niches and sanctuaries, intravenous transport of the circulating tumor cells, the role of the tumor microenvironment in chemotherapeutic interventions, the interactions between tumor cells, the extracellular matrix, the interstitial fluid, and the immune and stromal cells. Mathematical models discussed here embrace both continuous and agent-based approaches, as well as mathematical frameworks of solid mechanics, fluid dynamics and optimal control theory. The topics in each chapter will be of interest to a biological community wishing to apply the mathematical methods to interpret their experimental data, and to a biomathematical audience interested in exploring how mathematical models can be used to address complex questions in cancer biology.

This book presents a theoretical multiscale modeling framework for the integration of processes spanning from molecular signaling to individual and collective cellular behavior to complex spatiotemporal dynamics at the tissue and organ levels. It then gives a detailed discussion on how to incorporate experimental and patient data into the modeling framework. The book also illustrates multiscale modeling approaches through several applications, including breast cancer and mammary gland development, lymphoma and leukemia growth, the investigation of biobarriers to chemotherapeutic drugs, and nanoparticle-based delivering strategies.

With chapters on free boundaries, constitutive equations, stochastic dynamics, nonlinear diffusion–consumption, structured populations, and applications of optimal control theory, this volume presents the most significant recent results in the field of mathematical oncology. It highlights the work of world-class research teams, and explores how different researchers approach the same problem in various ways. Tumors are complex entities that present numerous challenges to the mathematical modeler. First and foremost, they grow. Thus their spatial mean field description involves a free boundary problem. Second, their interiors should be modeled as nontrivial porous media using constitutive equations. Third, at the end of anti-cancer therapy, a small number of malignant cells remain, making the post-treatment dynamics inherently stochastic. Fourth, the growth parameters of macroscopic tumors are non-constant, as are the parameters of anti-tumor therapies. Changes in these parameters may induce phenomena that are mathematically equivalent to phase transitions. Fifth, tumor vascular growth is random and self-similar. Finally, the drugs used in chemotherapy diffuse and are taken up by the cells in nonlinear ways. Mathematical Oncology 2013 will appeal to graduate students and researchers in biomathematics, computational and theoretical biology, biophysics, and bioengineering.

The aim of this volume that presents lectures given at a joint CIME and Banach

Center Summer School, is to offer a broad presentation of a class of updated methods providing a mathematical framework for the development of a hierarchy of models of complex systems in the natural sciences, with a special attention to biology and medicine. Mastering complexity implies sharing different tools requiring much higher level of communication between different mathematical and scientific schools, for solving classes of problems of the same nature. Today more than ever, one of the most important challenges derives from the need to bridge parts of a system evolving at different time and space scales, especially with respect to computational affordability. As a result the content has a rather general character; the main role is played by stochastic processes, positive semigroups, asymptotic analysis, kinetic theory, continuum theory, and game theory.

This book constitutes the refereed proceedings of the First International on Bioinformatics and Computational Biology, BICoB 2007, held in New Orleans, LA, USA, in April 2007. The 30 revised full papers presented together with 10 invited lectures were carefully reviewed and selected from 72 initial submissions. The papers address current research in the area of bioinformatics and computational biology fostering the advancement of computing techniques and their application to life sciences in topics such as genome analysis sequence analysis, phylogenetics, structural bioinformatics, analysis of high-throughput biological data, genetics and population analysis, as well as systems biology. This book contains a collection of original research articles and review articles that describe novel mathematical modeling techniques and the application of those techniques to models of cell motility in a variety of contexts. The aim is to highlight some of the recent mathematical work geared at understanding the coordination of intracellular processes involved in the movement of cells. This collection will benefit researchers interested in cell motility as well graduate students taking a topics course in this area.