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| Nota di contenuto | Background and Scope of the Book -- Part I Treatment of Cancer with Small Molecule Inhibitors -- An Introduction to Small Molecule Inhibitors and Chronic Myeloid Leukemia -- Basic Dynamics of Chronic Myeloid Leukemia During Imatinib Treatment -- Stochastic Modeling of Cellular Growth, Treatment, and Resistance Generation -- Evolutionary Dynamics of Drug Resistant Mutants in Targeted Treatment of CML -- Effect of Cellular Quiescence on the Evolution of Drug Resistance in CML -- Combination Therapies: Short term versus Long term Strategies -- Cross Resistance: Treatment and Modeling -- Mathematical Modeling of Cyclic Cancer Treatments -- Part II Treatment of Cancer with Oncolytic Viruses -- Introduction to Oncolytic Viruses -- Basic |

Dynamics of Oncolytic Viruses -- Mitotic Virus Transmission and Immune Responses -- Axiomatic Approaches to Oncolytic Virus Modeling -- Spatial Oncolytic Virus Dynamics -- Oncolytic Viruses and the Eradication of Drug-resistant Tumor Cells.

Sommario/riassunto

This monograph provides the first in-depth study of how mathematical and computational approaches can be used to advance our understanding of cancer therapies and to improve treatment design and outcome. Over the past century, the search for a cancer cure has been a primary occupation of medical researchers. So far, it has led to a wide range of treatment techniques, including surgery, chemo- and radiotherapy, antiangiogenic drugs, and most recently, small molecule inhibitors and oncolytic viruses. Each treatment tends to have a certain effectiveness in a specific class of patients, but it is often unclear what exactly causes it to succeed or fail. Recent technological advances have given rise to an ever increasing pool of data and information that highlight the complexity underlying the cancers and their response to treatment. Next to experimental and clinical research, mathematical and computational approaches are becoming an indispensible tool to understand this complexity. Targeted Cancer Treatment in Silico is organized into two parts, corresponding to two types of targeted cancer treatment: small molecule inhibitors and oncolytic viruses. In each part, the authors provide a brief overview of the treatment's biological basis and present the mathematical methods most suitable for modeling it. Additionally, they discuss how these methods can be applied to answer relevant questions about treatment mechanisms and propose modifications to treatment approaches that may potentially increase success rates. The book is intended for both the applied mathematics and experimental oncology communities, as mathematical models are becoming an increasingly important supplement to laboratory biology in the fight against cancer. Written at a level that generally requires little technical background, it will be a valuable resource for scientists and graduate students alike, and can also serve as an upper-division undergraduate or graduate textbook.