PREFACE

In the past 15 years, molecular biologists and geneticists have uncovered some of the most basic mechanisms by means of which normal stem cells in a certain organ or tissue develop into cancerous tumors. This biological knowledge serves as a basis for various models of carcinogenesis. Furthermore, in order for biological findings to be tested quantitatively against human epidemiological data and animal experimental data and in order to develop efficient diagnostic, controlling, curative and preventive strategies for cancer, it is essential that these biological theories be transformed into adequate mathematical models supported by relevant methods of statistical data analysis. With this in mind, the goal of this book is to present review papers on most recent and advanced cancer models and their applications from world experts in cancer modelling.

The book contains 18 chapters and is organized into two parts. Part I consists of 11 chapters giving detailed treatment of an assortment of cancer models whereas Part II consists of 7 chapters dealing with applications of various cancer models. In Part I, oncogenetic trees, stochastic multi-stage models of carcinogenesis, models of cancer metastasis, cell cycle regulation by radiation, genomic instability, DNA damage and repair, bystander effects of radiation as well as epigenetic hypotheses and multiple pathways of colon cancer are extensively discussed. Also, Part I reviews the most recent discoveries in cancer biology and the ways they are transformed into stochastic models of carcinogenesis. Among topics dealt with in Part II the reader will find bladder cancer screening by MRI (Magnetic Resonance Imaging), models of drug resistance in cancer chemotherapy, and applications of stochastic and state space models to the assessment of cancer risks associated with environmental agents. Part II of the book also contains chapters on applications of wavelets to proteomics, design and analysis of tumor xenograft experiments, and analysis of occult tumor trial data.

Cancer models presented in the book include deterministic, stochastic, statistical, and state space models. They provide the reader with a state-of-the-art overview of the rapidly evolving field of cancer modelling. Our aspiration when putting together this volume was to bring the best of modern science to bear on biomedical problems related to the study of cancer. We hope that the book will be a useful source of information and references for scientists working in cancer research, biomathematics, biostatistics and bioinformatics as well as for biologists, cancer epidemiologists, clinical investigators and medical doctors at various stages of their career. We also hope that graduate students and their instructors will find it beneficial to their learning and teaching. The chapters of the book should not be viewed as a fixed compendium of methods and results but rather as a source of ideas inspiring further research by those who use (or wish to learn how to use) quantitative methods in cancer studies.

We are well aware that selection of topics for the book reflected our research interests and that our desire to cover a broad range of cancer models and their applications made the book to a certain degree heterogeneous. Through reviewing and editing process we encouraged clarity of exposition; however, it is up to the reader to judge the measure of our success. Finally, the reader should be advised that several chapters require some proficiency in mathematics and statistics.

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