Preface

The future of oncology has a name: Molecular Medicine (MM). Molecular Medicine is a new science based on three pillars. Two of them are well known and evident in its very name: medical science and molecular biology. However, there is a general unawareness that MM is firmly based on a third but equally important pillar: Systems Biomedicine. Currently this term mainly evokes Bioinformatics and modern Applied Statistics, but increasingly it shall have to include (as in part it already does) the interacting complex of scientific fields such as Mathematical Biology, Systems Biology, Theoretical Biophysics.

The data from MM of tumors are complex and heterogeneous (e.g. clinical data paired with -omics data) but – and this is their most important feature - are unified by their dynamical nature. Indeed, cancers are a family of dynamic diseases, endowed by multiple temporal and spatial scales, and their polymorphic macroscopic instances are emergent properties originating from a wide number of microscopic interplays at intracellular and intercellular level. The complexity of these multiscale data cannot be deciphered by natural language reasoning, or by classical data analysis based on static data mining and model-unrelated time series analysis. These classical tools no longer suffice to cope with MM data in order to understand them and to produce meaningful and useful predictions.

As a consequence, it is mandatory to build mechanistic mathematical models of biomedical phenomena with complex outputs. These models could allow a deeper understanding of the "internal dynamics" of single patients or classes of patients, hopefully opening the road for tailored therapies. This is a huge challenge at the frontier of contemporary mathematical modeling, since dynamic modeling in MM is what allows to bridge the bench to the bedside, and in perspective it will be increasingly instrumental in aiding the cure of patients. By no means this implies that future medical doctors will be like electronic engineers, skilfully using special software to cure patients. Nevertheless, in a realistic perspective, future generation of oncologists will be more similar to cardiologists that rely on basic knowledge of the physics of heart and circulation, and use devices from bioengineering in their everyday clinical work.

Strict collaboration between biomedical researchers and Systems Biomedicine scientists is mandatory to make these hypotheses true in the future. What is the current state of this collaboration? A small number of outstanding experimental groups are seriously collaborating with biomathematicians, physicists and computer scientists, still maintaining separate competences. This is an important phenomenon. However, what is happening mainly in Systems Biology is even more interesting. An increasing number of inter-disciplinary groups are forming thanks to a new generation of group-leaders whose undergraduate background is in biomedical sciences. This trend leads to a far closer contact between two worlds quite separate in the past, and to the use of a common language. Many life scientists then become – in different degrees – confident and aware of the Systems Biomedicine potential. As an example of this potential, we can mention the possible role of mathematical modeling in drug development. Post-genomic drug discovery is indeed revealing serious shortcomings in the current way of performing clinical trials, which appears inadequate to face the age of personalized medicine. Systems Biomedicine, in the future generation of clinical trials, could thus play a fundamental role in shaping cancer treatments for single patients or groups of patients.

Many are the challenges that Systems Biomedicine of cancer must face. We have the responsibility of showing to the Life Sciences community that the potential of this discipline may become reality.

The present book has been inspired by the ideas underlying the Workshop Mathematical Oncology: New Challenges for Systems Biomedicine, held at the Ettore Majorana Centre for Scientific Culture in Erice (Italy), September 26–30, 2011.

The aim of this book is not only to illustrate the state of the art of tumor systems biomedicine, but also (and especially) to explicitly capture and collect results of the above-mentioned collaborative trends. Indeed, this volume is characterized by a well-structured presence of a large number of life scientists working directly in Systems Biomedicine, and a number of mathematical biology researchers working in biomedical institutions. With this book we wish to provide a coherent view of tumor modeling, based on the concept that mathematical modeling is the third pillar of molecular medicine. We hope that these features give to this work an unprecedented tone, providing an original interdisciplinary insight into the biomedical applications. We also hope the book may foster and encourage new fruitful communications and cooperations.

The present volume covers five basic topics of interest in oncology: comprehensive theories of cancer growth, systems biology of cancer, basic mechanisms of tumor progression, tumor-immune system interplay and immunotherapy, computational methods for improving chemotherapies. All the scales are so addressed, from the intracellular molecular networks to the therapy of patients. Moreover, relevance is given to recent mathematical methodologies such as nonlinear analysis, control and optimization theory, cellular automata and cellular-Potts modeling, agent-based modeling, and formal methods of computer science.

We wish to thank Professor Nicola Bellomo for the kind invitation to edit this book as part of the new SIMAI-Springer Series, and for his constant encouragement. We also wish to thank Professor Zvia Agur for her effort as co-organizer in setting the scientific shape of the Erice Workshop, and for the help in defining the project of this book.

Milan, Pisa, Rome, May 2012

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http://www.springer.com/978-88-470-2570-7

New Challenges for Cancer Systems Biomedicine

D'Onofrio, A.; Cerrai, P.; Gandolfi, A. (Eds.)
2012, XII, 400 p., Hardcover
ISBN: 978-88-470-2570-7