

FROM THE GUEST EDITORS

The idea for this volume came from the session “Control and Dynamics of Biomedical Systems,” which we organized at the Fourth World Congress of Non-linear Analysts held in Orlando, Florida, on June 30–July 7, 2004. We invited a number of speakers, and although not all could attend and give a talk in person, many expressed interest in contributing a paper. Following an invitation from Yang Kuang to put together a volume on the topic as a special issue of *Mathematical Biosciences and Engineering*, some papers presented at the session were submitted immediately, and others were contributed after the Congress.

The seventeen articles contained in this special issue represent a large spectrum of topics in the area of biomathematics and biomedical systems. A number of papers address the modeling of tumor growth and various cancer treatments. Delays in formation of the necrotic core and the influence of the body-fluid motions in tumor cords on the growth of tumors are addressed by Bodnar, Forsys, and Bertuzzi et al. Then, on the topic of various cancer treatments, chemotherapy is discussed with an emphasis on evolving drug resistance (Swierniak and Smieja) and the role of pharmacokinetics (PK) and pharmacodynamics (PD) of drugs in designing optimal protocols (Ledzewicz and Schaettler). Using examples of cancer treatments, the more general issue of the role of mathematical modeling as a resource in clinical trials is presented by Afenya. Papers addressing various aspects of the cell cycle form another group of contributions. The analysis of a modular network coordinating the cell cycle and apoptosis is given by Craciun, Aguda and Friedman et al.; Presnov and Agur present the role of time delays, slow processes, and chaos in modulating the cell-cycle clock. More on cell-process modeling, such as analysis of cell signaling pathways or modeling of multicellular systems, is given by Swierniak, Fajarewicz, and Newman. The link between the growth of tumor cell clusters and the processes that occur on a cellular level is presented by Rejniak. New trends in cancer therapies, such as immunotherapy or angiogenesis, are addressed in papers by Fister and Forsys et al., respectively.

But modeling of cancer is not the only biomedical topic of the volume. Ganguli, Gammack and Kirschner present an interesting model of granuloma formation in the lungs during tuberculosis infection. Another topic of the volume is epidemiological models. The issue of the use of periodic vaccination strategies for these systems is discussed by Moneim and Greenhalgh. Finally, the volume contains two more statistically oriented papers. Milner deals with the effect of homosexuality on a population, and Cyran and Kimmel review the state-of-the-art knowledge concerning the relationship between Neanderthals and modern humans.

With this variety of biological challenges and the wealth of various mathematical approaches used to address them, we hope that this volume will appeal to a large number of readers. We are grateful to Kerri Flanagan and the “crew” of MBE for their diligent job and patience in putting the volume together.

Our separate thanks go to all the referees, who have done a superb job reviewing the papers. The number of valuable comments the authors took into account in their revisions created a great scientific atmosphere in which the referees also became, to some extent, anonymous contributors. Thank you very much for your time and efforts.

We hope all combined effort was worthwhile and that the readers will find our volume an interesting addition to the existing literature in biomathematics.

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