

MATHEMATICAL METHODS IN SYSTEMS BIOLOGY

The editors of this Special Issue of Mathematical Biosciences and Engineering were the organizers for the Third International Workshop “Mathematical Methods in System Biology” that took place on June 15-18, 2015 at the University College Dublin in Ireland. As stated in the workshop goals, we managed to attract a good mix of mathematicians and statisticians working on biological and medical applications with biologists and clinicians interested in presenting their challenging problems and looking to find mathematical and statistical tools for their solutions.

Following the kind invitation of Prof. Yang Kuang, we put together this volume as a Special Issue of the journal Mathematical Biosciences and Engineering. This volume is not intended as a comprehensive proceedings of the workshop. Only authors with original research results were invited to contribute, and only journal quality articles were accepted. All manuscripts underwent a rigorous review process. This was a challenging but also rewarding process as the joint efforts of the authors and referees led to significant improvements and enrichment of the papers.

Nine articles contained in this Special Issue represent a large spectrum of topics. Applications of mathematical, statistical, and computational tools to cancer modelling make up one of the main research directions in mathematical biosciences. Four papers included in the Special Issue are dedicated to the study of various cancer treatments. Among the topics presented in the Special Issue are the sensitivity analysis of a tumor growth model to radiotherapy (K. Fujarewicz and K. Lakomiec) and a model of the recently clinically approved post-surgery thermotherapy treatment of bladder cancer with an emphasis on its possible side-effects (C. Sadeé and E. Kashdan). Two papers consider different aspects of chemotherapy: minimization of chemotherapy drug resistance in models of micro-metastases (A. Shah, K. Rejniak and J. Gevertz) and optimal control in the mathematical model of chemotherapy under the assumption of tumor heterogeneity (S. Wang and H. Schättler).

However, cancer and related issues are by no means the only topic of our volume. Two papers are dedicated to the analysis of biochemical signaling networks. In their work, W. C. Young, A. Raftery and K. Y. Yeung use modern statistical techniques to reconstruct gene regulatory relationships from experimental data. Sensitivity of the mathematical models to experimental data is addressed in the paper by J. Smieja and M. Dolbniak who show what artifacts might appear due to experimental procedures and how to develop models to avoid them.

Another two papers discuss common diseases and methods for their modelling and diagnostics. Tachycardia is a very common heart condition caused by the disruption of electric circuitry of the heart. In their paper, B. Jackowska-Zduniak and U. Forys propose and analyze a mathematical model aimed to simulate the pathological behavior in the cardiovascular system. Alzheimer’s disease is a leading cause of dementia and is affecting tens of millions of people around the world. However, early diagnosis and treatment of this disease still remains elusive. In their paper, D. Duncan and T. Strohmmer present an automatic technique for the analysis of MRI data to identify Alzheimer’s patients in early stages of the disease.

One of the topics of the MMSB workshop was modelling and simulation of novel diagnostic techniques. In the Special Issue, this is represented by the paper of D. Mackey, E. Kelly, and R. Nooney, who developed a mathematical model of immunodiagnostic devices (also called immunoassays) used to detect biomarkers for a variety of diseases (such as cancer, HIV, or cardiovascular disease) and used it to optimize their performance.

All papers described above show the results obtained with the use of various mathematical methods and techniques, originated from the fields of dynamical systems, Bayesian statistics, kinetic theory, fluid mechanics, and many others. The variety of biological challenges and the wealth of mathematical tools that address them makes this volume an important contribution in biomathematics. We believe that this volume will find its place on the bookshelves of mathematicians who are active or interested in joining the growing field of mathematical biology as well as biologists looking for novel theoretical and computational approaches to advance their research.

We would like to thank all the authors for their valuable contributions and the referees for their tremendous work on reviewing the manuscripts. Special thanks go to Yang Kuang for making this publication possible.

Guest Editors:

Eugene Kashdan (University College Dublin, Ireland)
Dominique Duncan (University of Southern California, USA)
Andrew Parnell (University College Dublin, Ireland)
Heinz Schättler (Washington University, USA)