Preface

This volume is based on the workshop "Modelling in Molecular Biology" that took place in 2002 in Singapore. The main goal of the workshop was to present models/methods used in solving some fundamental problems in biosciences. The volume consists of a selection of papers presented at the workshop as well as of some other papers that are included so that the presentation of the theme of the workshop is broader and more balanced. As a matter of fact we feel that the collection of papers comprising this volume represents a wide spectrum of quite diverse ideas and trends.

The paper by D.A. Beard et al. explores the common thesis that understanding the behaviour of large interacting systems of many enzymes and reactants underlies the modelling and simulation of whole-cell systems. Moreover, the models need to represent the basic stoichiometry, with balanced chemical reactions and the conservation of mass, energy and charge. The authors discuss the stoichiometric and then kinetic details of approaches to modelling and simulation of biochemical systems. P.R.A. Campos et al. are concerned with models of evolution and adaptation (which is essential for precise understanding of molecular phylogeny). In particular, their paper is concerned with the rate of adaptation of asexual organisms (which is important because it influences the speed of the assumed molecular clock). It is known that for such organisms the rate of adaptation does not steadily increase with the increasing rate of advantageous mutations, and this paper studies the mutual interference of two advantageous mutants that are each initially present in only a single organism. The authors derive a phenomenological description of the mutants' fixation probabilities in the interference regime. G. Ciobanu exploits the potential of π-calculus (a process algebra invented for the purpose of studying concurrent systems) for modelling and simulation of biological systems. More specifically, he is using π-calculus to describe the kinetics of the sodium-potassium exchange pump, emphasizing the software verification of some properties of the pump. The paper by O. Demin et al. describes a new approach for constructing large-scale kinetic network models. Then, in the framework of this approach, it suggests a novel way to collect and mine

large-scale experimental data, and a way of using these data to build and verify kinetic models. The paper shows how to apply these models for various practical problems of biotechnology, bioengineering and biomedicine.

The paper by A. Ehrenfeucht et al. is concerned with modelling of the gene assembly process that takes place in ciliates (which are single-cell organisms). Gene assembly is the most involved DNA processing in living organisms (that we know of), and authors discuss three models of this process, all three on different abstraction levels. In particular, the paper demonstrates that all three abstraction levels are equivalent as far as the operational modelling of gene assembly is concerned. M. Hagiya reviews major research trends presented at the DNA Based Computers Meeting (DNA8) in Sapporo, Japan in 2002 to illustrate the main areas of molecular programming – the term used by the author for the research concerned with establishing systematic design principles for molecules and molecular systems with information processing capabilities. S. Ji argues that in order to really understand the functioning of the living cell one needs a computer model of it, and that such a model should be based *not* on a traditional physics approach utilizing differential equations but rather on a fuzzy logic-based approach employing fuzzy if-then rules. The paper by N. Kam et al. presents a novel approach to modelling biological phenomena. It is using the methodology consisting of the language of live sequence charts with the play-in/play-out process (that was developed by computer scientists for the purpose of designing and analysing reactive systems) to model the well-characterized process of cell fat acquisition during *C. elegans* vulval development.

C. Martín-Vide and G. Păun are concerned with membrane systems (also called P systems) – a model of computation inspired by the role that biological membranes play in the functioning of the living cell. In particular, they discuss the class of membrane systems with symport/antiport rules which is motivated by the symport and antiport mechanisms of transport of ions and molecules through membranes. S. Motta and V. Brusic discuss the immune system considered here as a network of cells, molecules, and organs whose primary tasks are to defend the organism from pathogens and maintain its integrity. They give a brief introduction to the biology of the immune system and describes several approaches used in the mathematical modelling of the immune system. It is hoped that huge experimental data sets produced by genomics, proteomics, and molecular biology efforts will ultimately be integrated with mathematical models of the immune system at the organism level to produce models of the whole organism. The paper by A. Regev and E. Shapiro begins with the general problem of abstraction for biomolecular systems, which must be relevant, computable, understandable and extensible. The paper argues for the "molecule-as-computation" paradigm that satisfies these properties, and it presents an extensive and in-depth study of π-calculus as an abstraction for biomolecular systems. B.M.R. Stadler and P.F. Stadler explore the idea that central notions in evolutionary biology are intrinsically topological. They discuss a mathematical framework that derives the concept

of phenotypic characters and homology from the topological structure of the phenotype space. This structure in turn is determined by the genetic operators and their interplay with the properties of the genotype-phenotype map. Finally, the paper by Y. Zhou and B. Mishra centers around the proposition that the theory of "evolution by duplication" is likely to be a central ("and most elegant") among the fundamental dogmas of biological sciences. Based on this theory the paper explores and surveys various connections between biology, mathematics and computer science in order to reveal simple, and yet deep models of life itself.

The research area of modelling in molecular biology is genuinely interdisciplinary, and (as seen from the above) this volume reflects this feature very well – the main trends and ideas are coming from mathematics, computer science, statistics, chemistry, and biology.

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