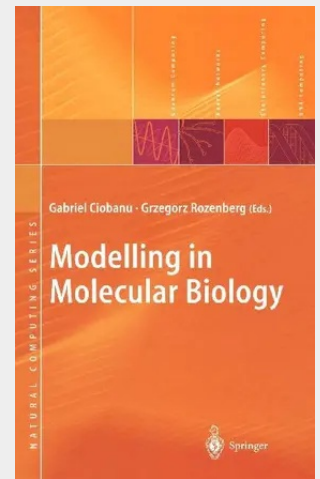


Modelling in Molecular Biology

The key idea underlying this book is the notion that molecules and cells, which constitute the basic building blocks of all living systems, are too complex to be fully understood by the human mind without the aid of a good model and a computer. Therefore, the modeling of living systems and processes is mandatory in order to gain a complete description and understanding. The authors present new mathematical and computational models as well as statistical methods for the solution of fundamental problems in the biosciences.

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 reactions 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.



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