

Preface

Computational systems biology, a term coined by Kitano in 2002, is a field that aims at a system-level understanding by analyzing biological data using computational techniques. The explosive progress of genome sequencing projects and the massive amounts of data generated by high-throughput experiments in DNA microarrays, proteomics, and metabolomics advances this field in a bidirectional but dependent fashion. As the need for a complete quantitative part list in biology is recognized, the understanding develops that living systems cannot be understood by studying just individual parts. Under the guiding vision of systems biology, sophisticated computational methods are currently being developed to analyze the data generated by this new technology in a systematic fashion, unraveling complex and networked biological phenomena, and modeling processes that take place in cells, tissues, and organisms. With recent advances in information technology, fast and inexpensive computer power, global networking infrastructure, and comprehensive databases, mathematical modeling and simulation of complex biological processes have become increasingly important and feasible. Modeling and simulation methods involve the use of different system analysis tools such as discrete mathematics and stochastics, differential equations, complex system simulation, as well as model-database integration architectures. The construction and testing of quantitative representations and models will be possible through the collaborative input of experimental and theoretical biologists working together with system analysts, computer scientists, mathematicians, engineers, physicists, and physicians to contend creatively with the hierarchical and nonlinear nature of cellular systems, while bioengineers will maintain a focus on directing the research results toward developing and improving cell-based, biotechnological processes.

This book has a distinct focus on computational issues related to systems biology. As such, it presents a timely, multi-authored compendium representing state-of-the-art computational technologies and methods developed in this area. This includes a review of enabling information and data integration technologies that have not been covered elsewhere in this depth. Modeling of gene, signaling and metabolic networks, being the main thrust in current computational efforts, is comprehensively covered. Contributions have been selected and compiled to introduce the different methods, including methods of abstraction, modeling of dynamical properties, and biological perspectives. A comprehensive coverage of computer representations of the multiple scales within a cell in relation to emergent properties in biological systems is also provided.

Beside the 17 primary authors and their respective teams who have dedicated their time to contribute to this book, there are many other individuals whose support was instrumental in making book a reality. We would like to in particular

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It is often mentioned that biological systems in its entirety present more than a sum of its parts. To this extent, we hope that the chapters in this book, not only give a contemporary and comprehensive overview about recent developments, but that this volume advances the field and encourages new strategies, interdisciplinary cooperation, and research activities.

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