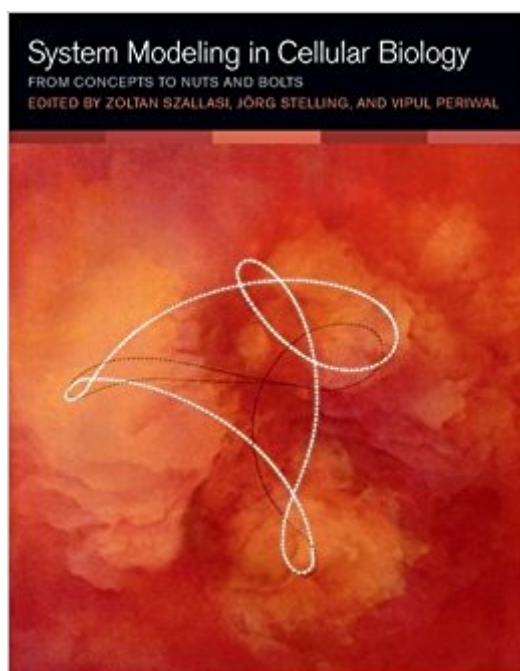


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System Modeling In Cellular Biology: From Concepts To Nuts And Bolts (MIT Press)



Synopsis

Research in systems biology requires the collaboration of researchers from diverse backgrounds, including biology, computer science, mathematics, statistics, physics, and biochemistry. These collaborations, necessary because of the enormous breadth of background needed for research in this field, can be hindered by differing understandings of the limitations and applicability of techniques and concerns from different disciplines. This comprehensive introduction and overview of system modeling in biology makes the relevant background material from all pertinent fields accessible to researchers with different backgrounds. The emerging area of systems level modeling in cellular biology has lacked a critical and thorough overview. This book fills that gap. It is the first to provide the necessary critical comparison of concepts and approaches, with an emphasis on their possible applications. It presents key concepts and their theoretical background, including the concepts of robustness and modularity and their exploitation to study biological systems; the best-known modeling approaches, and their advantages and disadvantages; lessons from the application of mathematical models to the study of cellular biology; and available modeling tools and datasets, along with their computational limitations.

Book Information

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Customer Reviews

Whether for graduate students or researchers, this book provides an excellent introduction to systems biology modeling. (Quarterly Review of Biology)

Zoltan Szallasi is Professor at the Center for Biological Sequence Analysis, Technical University of Denmark. Jörn Stelling is a faculty member of the Department of Biosystems Science and Engineering at ETH Zürich. Vipul Periwal is with the Mathematical Cell Modeling Section, NIDDK, National Institute of Health.

I'm torn between giving this book 3 or 4 stars. On one hand, it is enjoyable to read and a great value for its discounted price. On the other hand, the book tries to tackle many modeling techniques at once; I often found myself wishing for more complete descriptions than were provided. The first section introduces basic concepts of mathematical modeling and considers structures and behaviors characteristic of biological models: The text opens with a discussion of the compromise between model scope and informativeness. Trade-offs of biological robustness and complexity are discussed. Modularity is explored as a unifying property of biological systems. The next section discusses a range of mathematical modeling frameworks. Bayesian logic is introduced as a means to discriminate among competing models (hypotheses) of biological systems. Quasi-steady state stoichiometric methods, non-linear ODEs, PDEs, and stochastic methods are each given a chapter. Biological network topology is also discussed. While the topics are presented well (some better than others), many (especially the topology and PDE chapters) would benefit from more extensive coverage and mathematical background. The toy model examples are also very simplistic; I would have liked to see discussion of special considerations for higher-dimensional systems. The third section was the most useful for me and at the same time the most frustrating. It discusses practical issues: experimental data collection, model identification, parameter estimation, and control theory. There is a chapter on gene regulatory systems (think BioBricks or Uri Alon's work) and a brief discussion of multi-scale (cellular/tissue/organ) models. These practical issues - the 'nuts and bolts' of the title - were exactly what I hoped to learn about. However, the coverage is only superficial. I often found myself digging up references to clarify questions which (I felt) should have been addressed in the text. The final section addresses computing. Algorithm complexity and machine representation of models are informally described. I would have liked to see model identification and parameter estimation covered much more thoroughly - these can be computationally intensive for large models. Runge-Kutta ODE algorithms and stochastic algorithms (Gillespie, tau-leaping, and Langevin) are discussed and computational challenges (e.g., stiffness) are detailed. The book ends with a description of system biology markup language (SBML) and a list of current (as of 2006) open source modeling tools. I would recommend this book to biological modelers who wish to get a taste

of other modeling approaches outside their own specialty. Math students coming into biological projects might also benefit from the introduction to the field. However, the lack of a mathematical review section might leave pure-biology students confused unless they consult dedicated math or modeling texts. A complete table of contents may be found at The MIT Press website.

This text has been very helpful in understanding the theory behind systems biology. Although it's a pretty good text, some of the chapters are not very readable. I'm sure that's in part due to the fact that sys bio is new to me, but it's also due to some unclear writing. Nevertheless, I still recommend it for computer scientists and biologists that would like a better understanding of mathematical modeling of biological systems.

i love it , Nice and valuable. Great little business. Lovely, friendly follow-up. Awesome bread product. Go get yourself one. very useful. very fast, receive it next day.

A nicely written book for beginner-to-intermediate level system biologists. The math models are neat and helpful, and the price is certainly good enough for its value.

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