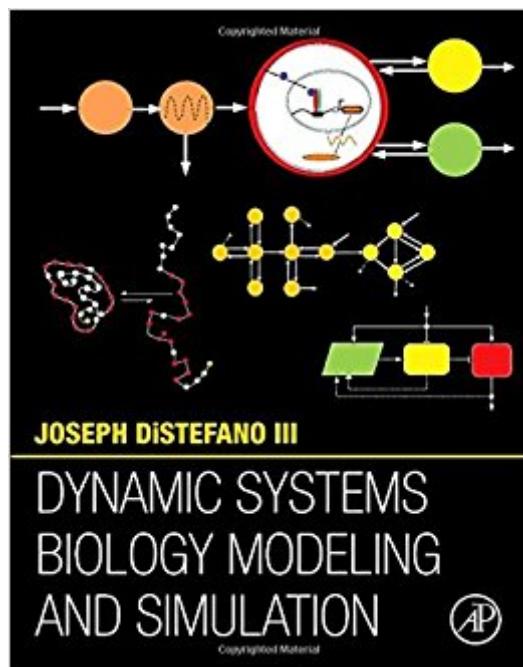The book was found

# Dynamic Systems Biology Modeling And Simulation

# Synopsis

Dynamic Systems Biology Modeling and Simuation consolidates and unifies classical and contemporary multiscale methodologies for mathematical modeling and computer simulation of dynamic biological systems â€" from molecular/cellular, organ-system, on up to population levels.Â Â The book pedagogy is developed as a well-annotated, systematic tutorial â€" with clearly spelled-out and unified nomenclature â€" derived from the authorâ€™s own modeling efforts, publications and teaching over half a century.Â Â Ambiguities in some concepts and tools are clarified and others are rendered more accessible and practical.Â Â The latter include novel qualitative theory and methodologies for recognizing dynamical signatures in data using structural (multicompartmental and network) models and graph theory; and analyzing structural and measurement (data) models for quantification feasibility.Â Â The level is basic-to-intermediate, with much emphasis on biomodeling from real biodata, for use in real applications.Introductory coverage of core mathematical concepts such as linear and nonlinear differential and difference equations, Laplace transforms, linear algebra, probability, statistics and stochastics topics; PLUS â€¦â€¦.The pertinent biology, biochemistry, biophysics or pharmacology for modeling are provided, to support understanding the amalgam of â€œmath modeling&#x94; with life sciences.Strong emphasis on quantifying as well as building and analyzing biomodels: includes methodology and computational tools for parameter identifiability and sensitivity analysis; parameter estimation from real data; model distinguishability and simplification; and practical bioexperiment design and optimization.Companion website provides solutions and program code for examples and exercises using Matlab, Simulink, VisSim, SimBiology, SAAMII, AMIGO, Copasi and SBML-coded models.A full set of PowerPoint slides are available from the author for teaching from his textbook.Â Â He uses them to teach a 10 week quarter upper division course at UCLA, which meets twice a week, so there are 20 lectures. They can easily be augmented or stretched for a 15 week semester course.  Importantly, the slides are editable, so they can be readily adapted to a lecturerâ€™s personal style and course content needs.Â Â The lectures are based on excerpts from 12 of the first 13 chapters of DSBMS. They are designed to highlight the key course material, as a study guide and structure for students following the full text content. The complete PowerPoint slide package (~25 MB) can be obtained by instructors (or prospective instructors) by emailing the author directly, at: joed@cs.ucla.edu

# Book Information

Hardcover: 884 pages

Average Customer Review: 5.0 out of 5 stars 3 customer reviews

Best Sellers Rank: #337,800 in Books (See Top 100 in Books) #174 inÃ Â Books > Computers & Technology > Databases & Big Data > Data Modeling & Design #239 inÃ Â Books > Engineering & Transportation > Engineering > Bioengineering > Biotechnology #268 inÃ Â Books > Textbooks > Science & Mathematics > Biology & Life Sciences > Ecology

## Customer Reviews

"This very satisfying book has multiple strengths. The text has marvelous clarity, as do the mathematical demonstrations. All are synoptic, while simultaneously explaining the underlying, fine details. The useful organization is enhanced by superb graphics. Although the author has many technical capabilities, with both range and depth, below IÃ¢â¬â„¢ll give just one illustrative example of the excellent result. Major themes of modern computation and modeling, as applied to biology, include issues of nonlinearities, chaotic dynamics, emergent properties, and instabilities. For example, consider the problems attendant on complex dynamic systems with multiple scales of time and space so typical of living systems.Ã Â The scientific literature in this domain is rich and immense. When I looked into DiStefanoÃ¢â¬â„¢s book for entries dealing with these topics, I found as early as Chapter One a heading: &#x94;Multiscale Modeling&#x94;. Elsewhere were other treatments of these aspects of complexity and modeling difficulties such as the famous problem of Ã¢â¬Å"stiff ODEs&#x94;, here brilliantly examined and explained, with remedies. The many authoritative tutorials by DiStefano amazed me for so effectively distilling the technical essences. They confirm that DiStefano is a great teacher and guide through various profound, classical difficulties. This book is a masterwork."--F. Eugene Yates "This book provides a systematic review of the concepts of mathematical modeling in various fields. With its simple language, varied practical examples, quick references, appendixes, and clear basic concepts, it provides a thorough explanation of the subject. The well-organized chapters, along with the use of different notations and typescripts, make it a user-friendly book." Rating: 5 Stars--Doody.com, March 7, 2014

"DiStefano presents this interdisciplinary text merging mathematics, modeling, systems science,

and biology. The first chapter introduces the philosophy and nomenclature of modeling and simulation. Chapter two covers mathematics including algebraic models, differential equations, linear and nonlinear modeling, and chapter three describes the use of Taylor series and algorithmic treatment of differential equations in computer simulation methods."--ProtoView.com, February 2014 Ã¢â ¬Å"I am just in awe of your ability to start with simple ideas and use them to explain sophisticated concepts and methodologies in modeling biochemical and cellular systems (Chapters 6 and 7).Ã Â This is a great new contribution to the textbook offerings in systems biology.&#x94;--Alex Hoffmann, Director of the San Diego Center for Systems Biology and the UCSD Graduate Program in Bioinformatics and Systems Biology Ã¢â ¬Å"I found Chapter 1 to be a marvel of heavy-lifting, done so smoothly there was no detectable sweat.Ã Â Heavy-lifting because you laid out the big load of essential vocabulary and concepts a reader has to have to enter the world of biomodeling confidently.Ã Â In that chapter you generously acknowledge some us who tried to accomplish this earlier but, compared to your Chapter 1, we were clumsy and boring.Ã Â For me, now, Chapter 1 was a "page-turner" to be enjoyed straight through.Ã Â You have the gift of a master athlete who does impossible performances and makes them seem easy. Ã¢â ¬Å"Your Chapter 9 Ã¢â ¬â œ on oscillations and stability Ã¢â ¬â œ is a true jewel.Ã Â I have a shelf full of books etc on nonlinear mechanics and system analyses and modeling, but nothing to match the clarity and deep understanding you offer the reader. You are a great explainer and teacher.&#x94;--F. Eugene Yates, Emeritus Professor of Medicine, Chemical Engineering and Ralph and Marjorie Crump Professor of Biomedical Engineering, UCLA Ã¢â ¬Å"Chapter 4 covers many aspects of the notion of compartmentalization in the structural modeling of biomedical and biological models Ã¢â ¬â œ both linear and nonlinear.Ã Â Developments are biophysically motivated throughout; and compartments are taken to represent entities with the same dynamic characteristics (dynamic signatures). A very positive feature of this text is the numerous worked examples in the text, which greatly help readers follow the material.Ã Â At the end of the chapter, there are further well thought out analytical and simulation exercises that will help readers check that they have understood what has been presented. Ã Â Ã¢â ¬Å"Chapter 5 looks at many important aspects of multicompartmental modeling, examining in more detail how output data limit what can be learnt about model structure, even when such data are perfect. Among the many features explained are how to establish the size and complexity of a model; how to select between several candidate models; and whether it is possible to simplify a model. All of this is done with respect to the dynamic signatures in the model. As in Chapter 4, readers are helped to understand the often challenging material by means of numerous worked examples in the text, and there are

further examples given at the end.^--Professor Keith Godfrey, University of Warwick, Coventry, U.K.

“Professor Joe^ - as he is called by his students - is a Distinguished Professor of Computer Science and Medicine and Chair of the Computational & Systems Biology Interdepartmental Program at UCLA - an undergraduate research-oriented program he nurtured and honed over several decades. As an active full-time member of the UCLA faculty for nearly half a century, he also developed and led innovative graduate PhD programs, including Computational Systems Biology in Computer Science, and Biosystem Science and Engineering in Biomedical Engineering. He has mentored students from these programs since 1968, as Director of the UCLA Biocybernetics Laboratory, and was awarded the prestigious UCLA Distinguished Teaching Award and Eby Award for Creative Teaching in 2003, and the Lockeed-Martin Award for Teaching Excellence in 2004. Professor Joe also is a Fellow of the Biomedical Engineering Society. Visiting professorships included stints at universities in Canada, Italy, Sweden and the UK and he was a Senior Fulbright-Hays Scholar in Italy in 1979. Professor Joe has been very active in the publishing world. As an editor, he founded and was Editor-in-Chief of the Modeling Methodology Forum - a department in seven of the American Journals of Physiology - from 1984 thru 1991. As a writer, he authored or coauthored both editions of Feedback and Control Systems (Schaum-McGraw-Hill 1967 and 1990), more than 200 research articles, and recently published his opus textbook: Dynamic Systems Biology Modeling and Simulation (Academic Press/Elsevier November 2013 and February 2014). Much of his research has been based on integrating experimental neuroendocrine and metabolism studies in mammals and fishes with data-driven mathematical modeling methodology - strongly motivated by his experiences in “wet-lab^. His seminal contributions to modeling theory and practice are in structural identifiability (parameter ambiguity) analysis, driven by experimental encumbrances. He introduced the notions of interval and quasi-identifiablity of unidentifiable dynamic system models, and his lab has developed symbolic algorithmic approaches and new internet software (web app COMBOS) for computing identifiable parameter combinations. These are the aggregate parts of otherwise unidentifiable models that can be quantified - with broad application in model reduction (simplification) and experiment design. His long-term contributions to quantitative understanding of thyroid hormone production and metabolism in mammals and fishes have recently been crystallized into web app THYROSIM - for internet-based research and teaching about thyroid hormone dynamics in humans. Last but not least, Professor Joe is a passionate straight-ahead jazz saxophone player (alto and tenor), an alternate career begun in the 1950s in

NYC at Stuyvesant High School - temporarily suspended when he started undergrad school, and resumed again in middle-age. He recently added flute to his practice schedule and he and his band - Acoustically Speaking -can be found occasionally gigging in Los Angeles or Honolulu haunts.

I had this book for a mathematical physiology course for my PhD in Biomedical Engineering. I loved this book even though some of the questions at the end had some grammatical errors. The professor that taught this course was familiar with the author of the book and actually got be interested in this area of research. I honestly wish I went further with this stuff!

verygood

Your book has enriched the course on modeling and physiology that I teach to our juniors. Last year we were able to cover the first 8 chapters in a semester plagued by ice-days and closings. The treatment is coherent and blends biology, engineering and mathematics in a sound way.

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