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The sequencing of actions, input/output and message flow, and state changes, are often difficult to understand solely by reviewing static representations. Animating various diagrams during the execution of a dynamic system model representing the system behavior can significantly enhance user understanding. A simple simulation can either rely on execution of pre-scripted scenarios, or it can react to specific user interaction (e.g., 'toggle this input and see what happens').

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Dynamic Systems Biology Modeling and Simuation consolidates and unifies classical and contemporary multiscale methodologies for mathematical modeling and computer simulation of dynamic biological systems - from molecular/cellular, organ-system, on up to population levels. The book pedagogy is developed as a well-annotated, systematic tutorial - with clearly spelled-out and unified nomenclature - derived from the author's own modeling efforts, publications and teaching over half a century. Ambiguities in some concepts and tools are clarified and others are rendered more accessible and practical. 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. 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 ... the pertinent biology, biochemistry, biophysics or pharmacology for modeling are provided, to support understanding the amalgam of "math modeling" 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.

Biophysical models have been used in biology for decades, but they have been limited in scope and size. In this book, Bernhard Ø. Palsson shows how network reconstructions that are based on genomic and bibliomic data, and take the form of established stoichiometric matrices, can be converted into dynamic models using metabolomic and fluxomic data. The Mass Action Stoichiometric Simulation (MASS) procedure can be used for any cellular process for which data is available and allows a scalable step-by-step approach to the practical construction of network models. Specifically, it can treat integrated processes that need explicit accounting of small molecules and protein, which allows simulation at the molecular level. The material has been class-tested by the author at both the undergraduate and graduate level. All computations in the text are available online in MATLAB and MATHEMATICA® workbooks, allowing hands-on practice with the material.

Dynamic Systems Biology Modeling and Simuation consolidates and unifies classical and contemporary multiscale methodologies for mathematical modeling and computer simulation of dynamic biological systems – from molecular/cellular, organ-system, on up to population levels. The book pedagogy is developed as a well-annotated, systematic tutorial – with clearly spelled-out and unified nomenclature – derived from the author's own modeling efforts, publications and teaching over half a century. Ambiguities in some concepts and tools are clarified and others are rendered more accessible and practical. 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. 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 .... The pertinent biology, biochemistry, biophysics or pharmacology for modeling are provided, to support understanding the amalgam of 'math modeling' 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. 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 lecturer's personal style and course content needs. 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

Master the process of building MASS models with real examples and hands-on practice.

This book explores the dynamic processes in economic systems, concentrating on the extraction and use of the natural resources required to meet economic needs. Sections cover methods for dynamic modeling in economics, microeconomic models of firms, modeling optimal use of both nonrenewable and renewable resources, and chaos in economic models. This book does not require a substantial background in mathematics or computer science.

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Many biologists and ecologists have developed models that find widespread use in theoretical investigations and in applications to organism behavior, disease control, population and metapopulation theory, ecosystem dynamics, and environmental management. This book captures and extends the process of model development by concentrating on the dynamic aspects of these processes and by providing the tools such that virtually anyone with basic knowledge in the Life Sciences can develop meaningful dynamic models. Examples of the systems modeled in the book range from models of cell development, the beating heart, the growth and spread of insects, spatial competition and extinction, to the spread and control of epidemics, including the conditions for the development of chaos. Key features: - easy-to-learn and easy-to-use software - examples from many subdisciplines of biology, covering models of cells, organisms, populations, and metapopulations - no prior computer or programming experience required Key benefits: - learn how to develop modeling skills and system thinking on your own rather than use models developed by others - be able to easily run models under alternative assumptions and investigate the implications of these assumptions for the dynamics of the biological system being modeled - develop skills to assess the dynamics of biological systems

Drawing on the latest research in the field, Systems Biology: Mathematical Modeling and Model Analysis presents many methods for modeling and analyzing biological systems, in particular cellular systems. It shows how to use predictive mathematical models to acquire and analyze knowledge about cellular systems. It also explores how the models are systematically applied in biotechnology. The first part of the book introduces biological basics, such as metabolism, signaling, gene expression, and control as well as mathematical modeling fundamentals, including deterministic models and thermodynamics. The text also discusses linear regression methods, explains the differences between linear and nonlinear regression, and illustrates how to determine input variables to improve estimation accuracy during experimental design. The second part covers intracellular processes, including enzymatic reactions, polymerization processes, and signal transduction. The author highlights the process function sequence in cells and shows how modeling and analysis of signal transduction units play a mediating role between process and function. The third part presents theoretical methods that address the dynamics of subsystems and the behavior near a steady state. It covers techniques for determining different time scales, sensitivity analysis, structural kinetic modeling, and theoretical control engineering aspects, including a method for robust control. It also explores frequent patterns (motifs) in biochemical networks, such as the feed-forward loop in the transcriptional network of E. coli. Moving on to models that describe a large number of individual reactions, the last part looks at how these cellular models are used in biotechnology. The book also explains how graphs can illustrate the link between two components in large networks with several interactions.

From controlling disease outbreaks to predicting heart attacks, dynamic models are increasingly crucial for understanding biological processes. Many universities are starting undergraduate programs in computational biology to introduce students to this rapidly growing field. In Dynamic Models in Biology, the first text on dynamic models specifically written for undergraduate students in the biological sciences, ecologist Stephen Ellner and mathematician John Guckenheimer teach students how to understand, build, and use dynamic models in biology. Developed from a course taught by Ellner and Guckenheimer at Cornell University, the book is organized around biological applications, with mathematics and computing developed through case studies at the molecular, cellular, and population levels. The authors cover both simple analytic models--the sort usually found in mathematical biology texts--and the complex computational models now used by both biologists and mathematicians. Linked to a Web site with computer-lab materials and exercises, Dynamic Models in Biology is a major new introduction to dynamic models for students in the biological sciences, mathematics, and engineering.