mathematical modeling in systems biology

mathematical modeling in systems biology represents a critical interdisciplinary approach that combines mathematics, biology, and computer science to understand complex biological systems. This field leverages quantitative models to simulate, analyze, and predict the behavior of biological components and their interactions at various scales, from molecular pathways to entire organisms. By constructing mathematical representations of biological processes, researchers can uncover underlying mechanisms, test hypotheses, and guide experimental design. The integration of computational techniques and experimental data enhances the accuracy and utility of these models, making them indispensable tools in fields such as drug development, disease modeling, and synthetic biology. This article explores the fundamental concepts, methodologies, applications, and challenges associated with mathematical modeling in systems biology, providing a comprehensive overview of the topic.

Fundamentals of Mathematical Modeling in Systems Biology

Mathematical modeling in systems biology involves creating formal mathematical representations of biological systems to capture their structure, dynamics, and interactions. These models serve as abstractions that help researchers interpret complex biological phenomena and generate predictive insights. The primary goal is to describe how components such as genes, proteins, metabolites, and cells interact within networks and pathways to produce observable behaviors.

Biological Systems as Dynamic Networks

Biological systems can be conceptualized as dynamic networks where nodes represent biological entities and edges represent interactions or relationships. This network perspective allows the use of graph theory and systems analysis to study the flow of information and regulation within the system. Mathematical models can encode these networks using differential equations, stochastic processes, or logical frameworks, depending on the nature of the system and available data.

Types of Mathematical Models

Various types of mathematical models are utilized in systems biology, each suited to different scales and complexities of biological phenomena:

- **Deterministic models:** Often based on ordinary differential equations (ODEs), these models describe the continuous change of system components over time with fixed parameters.
- **Stochastic models:** Incorporate randomness and noise inherent in biological processes, typically using stochastic differential equations or Gillespie algorithms.
- **Boolean models:** Use binary states to represent gene or protein activity, effective for qualitative analysis of regulatory networks.
- **Agent-based models:** Simulate individual entities and their interactions to capture emergent behaviors at higher organizational levels.

Key Methodologies and Techniques

Mathematical modeling in systems biology employs a range of methodologies and computational techniques to build, analyze, and validate models. These approaches facilitate the translation of biological data into actionable mathematical forms and allow the exploration of system dynamics under various conditions.

Model Construction and Parameter Estimation

Constructing a mathematical model starts with defining the system boundaries, identifying components, and specifying interactions based on biological knowledge. Parameter estimation is critical and involves determining numerical values for model parameters such as reaction rates or binding affinities. This is often achieved through optimization techniques that fit models to experimental data, including methods like least squares, maximum likelihood estimation, or Bayesian inference.

Simulation and Analysis Techniques

Once constructed, mathematical models undergo simulation to predict system behavior over time or under different perturbations. Numerical methods such as Euler's method, Runge-Kutta algorithms, or stochastic simulation algorithms are used depending on the model type. Analytical techniques, including stability analysis, sensitivity analysis, and bifurcation analysis, help understand system robustness, parameter influence, and potential dynamic regimes like oscillations or multistability.

Integration with Experimental Data

High-throughput technologies such as genomics, proteomics, and metabolomics provide vast amounts of quantitative data. Integrating these datasets with mathematical models enables refinement and validation, ensuring that models accurately reflect biological reality. Data-driven modeling approaches, including machine learning and statistical inference, complement traditional modeling techniques to enhance predictive power.

Applications of Mathematical Modeling in Systems Biology

Mathematical modeling in systems biology has broad and impactful applications across biomedical research and biotechnology. These applications demonstrate how computational models can drive discovery and innovation in understanding biological systems and developing therapeutic strategies.

Understanding Cellular Processes

Models help elucidate complex cellular processes such as signal transduction, gene regulatory networks, and metabolic pathways. By simulating the dynamic behavior of these processes, mathematical models reveal critical control points and interactions that govern cellular function and adaptation.

Disease Modeling and Drug Development

Mathematical models are instrumental in studying the progression of diseases at molecular, cellular, and tissue levels. They enable the prediction of disease outcomes and the identification of potential drug targets. In pharmaceutical research, models assist in optimizing drug dosing regimens and understanding drug resistance mechanisms.

Synthetic Biology and Bioengineering

In synthetic biology, mathematical modeling guides the design and construction of artificial biological systems with desired functions. Models predict how engineered genetic circuits will behave, facilitating the rational design of biosensors, therapeutic agents, and metabolic engineering strategies.

- Elucidation of metabolic fluxes and pathway optimization
- Design of gene circuits with predictable dynamics

- Simulation of population dynamics in microbial consortia

Challenges and Future Directions

Despite significant advances, mathematical modeling in systems biology faces several challenges related to model complexity, data limitations, and computational demands. Addressing these challenges will enhance the accuracy and applicability of models in biological research and medicine.

Model Complexity and Scalability

Biological systems often exhibit enormous complexity with thousands of interacting components and nonlinear feedback loops. Developing models that capture this complexity without becoming computationally intractable remains a major challenge. Techniques for model reduction and modular modeling are being explored to improve scalability.

Data Quality and Integration

Reliable model construction and validation depend on high-quality experimental data. However, biological data can be noisy, incomplete, or heterogeneous. Integrating multi-omics datasets and developing standardized data formats are crucial for building comprehensive and robust models.

Advancements in Computational Tools

Future progress will rely on the development of sophisticated computational tools that facilitate model building, simulation, and analysis. Machine learning and artificial intelligence are increasingly integrated with traditional modeling to handle large datasets and uncover hidden patterns. Cloud computing and high-performance computing resources also enable the simulation of complex systems at unprecedented scales.

- Enhanced algorithms for parameter inference and model selection
- Improved visualization techniques for complex model outputs
- Collaborative platforms for model sharing and reproducibility

Frequently Asked Questions

What is mathematical modeling in systems biology?

Mathematical modeling in systems biology involves using mathematical frameworks and computational techniques to represent and analyze complex biological systems and their dynamic behaviors.

Why is mathematical modeling important in systems biology?

It helps in understanding complex biological processes, predicting system behavior, testing hypotheses, and designing experiments by providing a quantitative framework for integrating diverse biological data.

What are common types of mathematical models used in systems biology?

Common types include deterministic models (e.g., ordinary differential equations), stochastic models, Boolean network models, agent-based models, and hybrid models combining multiple approaches.

How do ordinary differential equations (ODEs) apply to systems biology modeling?

ODEs describe the continuous change of biological variables over time, such as concentrations of molecules in biochemical pathways, allowing the study of dynamic system behavior.

What role does parameter estimation play in mathematical modeling of biological systems?

Parameter estimation involves determining model parameters from experimental data to ensure the model accurately reflects biological reality and can make reliable predictions.

How can mathematical models aid in drug discovery and development?

Models can simulate drug effects on biological pathways, predict outcomes, optimize dosing strategies, and identify potential targets, thereby reducing time and cost in drug development.

What challenges are faced in mathematical modeling of systems biology?

Challenges include model complexity, incomplete or noisy data, parameter identifiability, computational cost, and integrating multi-scale biological information effectively.

How is machine learning integrated with mathematical modeling in systems biology?

Machine learning can be used to infer model structure, estimate parameters, analyze large datasets, and complement traditional modeling to improve system understanding and predictive power.

What software tools are commonly used for mathematical modeling in systems biology?

Popular tools include COPASI, CellDesigner, MATLAB, SBML (Systems Biology Markup Language) compatible platforms, BioNetGen, and Python libraries like PySB and Tellurium.

How does mathematical modeling contribute to personalized medicine in systems biology?

By modeling individual-specific biological data, mathematical models can predict personalized responses to treatments, enabling tailored therapeutic strategies for improved efficacy and reduced side effects.

Additional Resources

1. *Mathematical Modeling in Systems Biology: An Introduction*
This book offers a comprehensive introduction to the principles and techniques used in mathematical modeling within systems biology. It covers fundamental concepts such as differential equations, stochastic processes, and network analysis, tailored for biological applications. The text is accessible for beginners and provides numerous examples from cellular and molecular biology to illustrate modeling approaches.

2. *Systems Biology: Mathematical Modeling and Model Analysis*
Focusing on the development and analysis of mathematical models, this book explores both deterministic and stochastic frameworks used in systems biology. It discusses methods for model construction, parameter estimation, and sensitivity analysis. The book also includes case studies on gene regulatory networks and metabolic pathways, emphasizing practical model validation.

3. *Dynamic Models in Biology*
This title emphasizes the use of dynamic models to understand biological processes over time. It introduces ordinary differential equations and their application to modeling population dynamics, enzyme kinetics, and cellular signaling pathways. Readers gain insight into how temporal changes in biological systems can be quantitatively described and analyzed.

4. *Mathematical Systems Biology: An Introduction*
Aimed at bridging biology and mathematics, this book introduces core mathematical tools such as linear algebra, dynamical systems, and probability theory in the context of systems biology. It provides a variety of biological examples to demonstrate how mathematical models can simulate complex biological behavior and predict system responses.

5. *Computational Systems Biology*
This book covers computational techniques for building and simulating mathematical models of

biological systems. Topics include algorithmic approaches, software tools, and data integration methods essential for large-scale biological modeling. It is particularly useful for researchers interested in combining computational power with theoretical modeling.

6. *Modeling Biological Systems: Principles and Applications*
Focusing on the practical aspects of modeling, this book discusses how to translate biological hypotheses into mathematical formulations. It covers a range of modeling approaches including discrete, continuous, and hybrid models. The text also addresses challenges like model identifiability and experimental design for model testing.

7. *Systems Biology: Mathematical Modeling and Model Analysis*
This book delves into advanced topics like bifurcation theory, stability analysis, and nonlinear dynamics in biological systems. It emphasizes the interpretation of complex biological phenomena through mathematical insights. Detailed examples from developmental biology and neuroscience illustrate theoretical concepts in practice.

8. *Stochastic Modelling for Systems Biology*
Highlighting the role of randomness in biological systems, this book introduces stochastic modeling techniques such as Markov processes and Gillespie algorithms. It explains how noise and variability impact cellular functions and how these effects can be captured mathematically. The book is suited for readers interested in probabilistic approaches to biological modeling.

9. *Mathematical Modeling of Biological Systems*
This comprehensive text covers a broad spectrum of biological modeling topics, from molecular interactions to ecological systems. It integrates mathematical theory with biological insights to provide a holistic view of modeling strategies. The book also discusses computational tools and experimental data analysis to support model development and validation.

Mathematical Modeling In Systems Biology

mathematical modeling in systems biology: Mathematical Modeling in Systems Biology Brian P. Ingalls, 2013-07-05 An introduction to the mathematical concepts and techniques needed for the construction and analysis of models in molecular systems biology. Systems techniques are integral to current research in molecular cell biology, and system-level investigations are often accompanied by mathematical models. These models serve as working hypotheses: they help us to understand and predict the behavior of complex systems. This book offers an introduction to mathematical concepts and techniques needed for the construction and interpretation of models in molecular systems biology. It is accessible to upper-level undergraduate or graduate students in life science or engineering who have some familiarity with calculus, and will be a useful reference for researchers at all levels. The first four chapters cover the basics of mathematical modeling in molecular systems biology. The last four chapters address specific biological domains, treating modeling of metabolic networks, of signal transduction pathways, of gene regulatory networks, and of electrophysiology and neuronal action potentials. Chapters 3–8 end with optional sections that address more specialized modeling topics. Exercises, solvable with pen-and-paper calculations, appear throughout the text to encourage interaction with the mathematical techniques. More involved end-of-chapter problem sets require computational software. Appendixes provide a review of basic concepts of molecular biology, additional mathematical background material, and tutorials for two computational software packages (XPPAUT and MATLAB) that can be used for model simulation and analysis.

mathematical modeling in systems biology: Systems Biology Andreas Kremling, 2013-11-12 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 sy

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mathematical modeling in systems biology: Dynamic Systems Biology Modeling and Simulation Joseph DiStefano III, 2015-01-10 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 - 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

mathematical modeling in systems biology: Mathematical Modeling of Biological Systems, Volume II Andreas Deutsch, Rafael Bravo de la Parra, Rob J. de Boer, Odo Diekmann, Peter Jagers, Eva Kisdi, Mirjam Kretzschmar, Petr Lansky, Hans Metz, 2007-10-12 Volume II of this two-volume, interdisciplinary work is a unified presentation of a broad range of state-of-the-art topics in the rapidly growing field of mathematical modeling in the biological sciences. Highlighted throughout are mathematical and computational apporaches to examine central problems in the life sciences, ranging from the organization principles of individual cells to the dynamics of large populations. The chapters are thematically organized into the following main areas: epidemiology, evolution and ecology, immunology, neural systems and the brain, and innovative mathematical methods and education. The work will be an excellent reference text for a broad audience of researchers, practitioners, and advanced students in this rapidly growing field at the intersection of applied mathematics, experimental biology and medicine, computational biology, biochemistry, computer science, and physics.

mathematical modeling in systems biology: A Guide to Numerical Modelling in Systems Biology Peter Deuflhard, Susanna Röblitz, 2015-07-06 This book is intended for students of computational systems biology with only a limited background in mathematics. Typical books on systems biology merely mention algorithmic approaches, but without offering a deeper understanding. On the other hand, mathematical books are typically unreadable for computational biologists. The authors of the present book have worked hard to fill this gap. The result is not a book on systems biology, but on computational methods in systems biology. This book originated from courses taught by the authors at Freie Universität Berlin. The guiding idea of the courses was to convey those mathematical insights that are indispensable for systems biology, teaching the necessary mathematical prerequisites by means of many illustrative examples and without any theorems. The three chapters cover the mathematical modelling of biochemical and physiological processes, numerical simulation of the dynamics of biological networks and identification of model parameters by means of comparisons with real data. Throughout the text, the strengths and weaknesses of numerical algorithms with respect to various systems biological issues are discussed. Web addresses for downloading the corresponding software are also included.

mathematical modeling in systems biology: Systems Biology: Mathematical Modeling and Model Analysis Lynda Feidan, 2019-06-05 Systems biology is the mathematical and computational modeling of complex biological systems. It is an interdisciplinary field of study concerned with complex interactions within biological systems. One of the primary objectives of systems biology is to discover and model emergent properties and explore the properties of cells, tissues and organisms functioning as a system. The foundations of systems biology are control theory and cybernetics, quantitative modeling of enzyme kinetics, synergetics, simulations for the study of neurophysiology and the mathematical modeling of population dynamics. The topics covered in this extensive book deal with the core aspects of mathematical modeling and model analysis in the discipline of systems biology. For all readers who are interested in this field, the case studies included in this book will serve as an excellent guide to develop a comprehensive understanding. It aims to equip students and experts with the advanced topics and upcoming concepts in this area of study.

mathematical modeling in systems biology: Kinetic Modelling in Systems Biology Oleg Demin, Igor Goryanin, 2008-10-24 With more and more interest in how components of biological systems interact, it is important to understand the various aspects of systems biology. Kinetic Modelling in Systems Biology focuses on one of the main pillars in the future development of systems biology. It explores both the methods and applications of kinetic modeling in this emerging field. The book introduces the basic biological cellular network concepts in the context of cellular functioning, explains the main aspects of the Edinburgh Pathway Editor (EPE) software package, and discusses the process of constructing and verifying kinetic models. It presents the features, user interface, and examples of DBSolve as well as the principles of modeling individual enzymes and transporters. The authors describe how to construct kinetic models of intracellular systems on the basis of models of individual enzymes. They also illustrate how to apply the principles of kinetic modeling to collect all available information on the energy metabolism of whole organelles, construct a kinetic model, and predict the response of the organelle to changes in external conditions. The final chapter focuses on applications of kinetic modeling in biotechnology and biomedicine. Encouraging readers to think about future challenges, this book will help them understand the kinetic modeling approach and how to apply it to solve real-life problems. Downloadable Resources FeaturesExtensively used throughout the text for pathway visualization and illustration, the EPE software is available on the accompanying downloadable resources. The downloadable resources also include pathway diagrams in several graphical formats, DBSolve installation with examples, and all models from the book with dynamic visualization of simulation results, allowing readers to perform in silico simulations and use the models as templates for further applications.

mathematical modeling in systems biology: Stochastic Modelling for Systems Biology, Third Edition Darren J. Wilkinson, 2018-12-07 Since the first edition of Stochastic Modelling for Systems Biology, there have been many interesting developments in the use of likelihood-free methods of Bayesian inference for complex stochastic models. Having been thoroughly updated to reflect this, this third edition covers everything necessary for a good appreciation of stochastic kinetic modelling of biological networks in the systems biology context. New methods and applications are included in the book, and the use of R for practical illustration of the algorithms has been greatly extended. There is a brand new chapter on spatially extended systems, and the statistical inference chapter has also been extended with new methods, including approximate Bayesian computation (ABC). Stochastic Modelling for Systems Biology, Third Edition is now supplemented by an additional software library, written in Scala, described in a new appendix to the book. New in the Third Edition New chapter on spatially extended systems, covering the spatial Gillespie algorithm for reaction diffusion master equation models in 1- and 2-d, along with fast approximations based on the spatial chemical Langevin equation Significantly expanded chapter on inference for stochastic kinetic models from data, covering ABC, including ABC-SMC Updated R package, including code relating to all of the new material New R package for parsing SBML models into simulatable stochastic Petri net models New open-source software library, written in Scala, replicating most of the functionality of the R packages in a fast, compiled, strongly typed, functional language Keeping with the spirit of earlier editions, all of the new theory is presented in a very informal and intuitive manner, keeping the text as accessible as possible to the widest possible readership. An effective introduction to the area of stochastic modelling in computational systems biology, this new edition adds additional detail and computational methods that will provide a stronger foundation for the development of more advanced courses in stochastic biological modelling.

mathematical modeling in systems biology: *Model-Based Hypothesis Testing in Biomedicine* Rikard Johansson, 2017-10-03 The utilization of mathematical tools within biology and medicine has traditionally been less widespread compared to other hard sciences, such as physics and chemistry. However, an increased need for tools such as data processing, bioinformatics, statistics, and mathematical modeling, have emerged due to advancements during the last decades. These advancements are partly due to the development of high-throughput experimental procedures and techniques, which produce ever increasing amounts of data. For all aspects of biology and medicine, these data reveal a high level of inter-connectivity between components, which operate on many levels of control, and with multiple feedbacks both between and within each level of control. However, the availability of these large-scale data is not synonymous to a detailed mechanistic understanding of the underlying system. Rather, a mechanistic understanding is gained first when we construct a hypothesis, and test its predictions experimentally. Identifying interesting predictions that are quantitative in nature, generally requires mathematical modeling. This, in turn, requires that the studied system can be formulated into a mathematical model, such as a series of ordinary differential equations, where different hypotheses can be expressed as precise mathematical expressions that influence the output of the model. Within specific sub-domains of biology, the utilization of mathematical models have had a long tradition, such as the modeling done on electrophysiology by Hodgkin and Huxley in the 1950s. However, it is only in recent years, with the arrival of the field known as systems biology that mathematical modeling has become more commonplace. The somewhat slow adaptation of mathematical modeling in biology is partly due to historical differences in training and terminology, as well as in a lack of awareness of showcases illustrating how modeling can make a difference, or even be required, for a correct analysis of the experimental data. In this work, I provide such showcases by demonstrating the universality and applicability of mathematical modeling and hypothesis testing in three disparate biological systems. In Paper II, we demonstrate how mathematical modeling is necessary for the correct interpretation and analysis of dominant negative inhibition data in insulin signaling in primary human adipocytes. In Paper III, we use modeling to determine transport rates across the nuclear membrane in yeast cells, and we show how this technique is superior to traditional curve-fitting methods. We also demonstrate the issue of population heterogeneity and the need to account for individual differences between cells and the population at large. In Paper IV, we use mathematical modeling to reject three hypotheses concerning the phenomenon of facilitation in pyramidal nerve cells in rats and mice. We also show how one surviving hypothesis can explain all data and adequately describe independent validation data. Finally, in Paper I, we develop a method for model selection and discrimination using parametric bootstrapping and the combination of several different empirical distributions of traditional statistical tests. We show how the empirical log-likelihood ratio test is the best combination of two tests and how this can be used, not only for model selection, but also for model discrimination. In conclusion, mathematical modeling is a valuable tool for analyzing data and testing biological hypotheses, regardless of the underlying biological system. Further development of modeling methods and applications are therefore important since these will in all likelihood play a crucial role in all future aspects of biology and medicine, especially in dealing with the burden of increasing amounts of data that is made available with new experimental techniques. Användandet av matematiska verktyg har inom biologi och medicin traditionellt sett varit mindre utbredd jämfört med andra ämnen inom naturvetenskapen, såsom fysik och kemi. Ett ökat behov av verktyg som databehandling, bioinformatik, statistik och matematisk modellering har trätt fram tack vare framsteg under de senaste decennierna. Dessa framsteg är delvis ett resultat av utvecklingen av storskaliga datainsamlingstekniker. Inom alla områden av biologi och medicin så har dessa data avslöjat en hög nivå av interkonnektivitet mellan komponenter, verksamma på många kontrollnivåer och med flera återkopplingar både mellan och inom varje nivå av kontroll. Tillgång till storskaliga data är emellertid inte synonymt med en detaljerad mekanistisk förståelse för det underliggande systemet. Snarare uppnås en mekanisk förståelse först när vi bygger en hypotes vars prediktioner vi kan testa experimentellt. Att identifiera intressanta prediktioner som är av kvantitativ natur, kräver generellt sett matematisk modellering. Detta kräver i sin tur att det studerade systemet kan formuleras till en matematisk modell, såsom en serie ordinära differentialekvationer, där olika hypoteser kan uttryckas som precisa matematiska uttryck som påverkar modellens output. Inom vissa delområden av biologin har utnyttjandet av matematiska modeller haft en lång tradition, såsom den modellering gjord inom elektrofysiologi av Hodgkin och Huxley på 1950-talet. Det är emellertid just på senare år, med ankomsten av fältet systembiologi, som matematisk modellering har blivit ett vanligt inslag. Den något långsamma adapteringen av matematisk modellering inom biologi är bl.a. grundad i historiska skillnader i träning och terminologi, samt brist på medvetenhet om exempel som illustrerar hur modellering kan göra skillnad och faktiskt ofta är ett krav för en korrekt analys av experimentella data. I detta arbete tillhandahåller jag sådana exempel och demonstrerar den matematiska modelleringens och hypotestestningens allmängiltighet och tillämpbarhet i tre olika biologiska system. I Arbete II visar vi hur matematisk modellering är nödvändig för en korrekt tolkning och analys av dominant-negativ-inhiberingsdata vid insulinsignalering i primära humana adipocyter. I Arbete III använder vi modellering för att bestämma transporthastigheter över cellkärnmembranet i jästceller, och vi visar hur denna teknik är överlägsen traditionella kurvpassningsmetoder. Vi demonstrerar också frågan om populationsheterogenitet och behovet av att ta hänsyn till individuella skillnader mellan celler och befolkningen som helhet. I Arbete IV använder vi matematisk modellering för att förkasta tre hypoteser om hur fenomenet facilitering uppstår i pyramidala nervceller hos råttor och möss. Vi visar också hur en överlevande hypotes kan beskriva all data, inklusive oberoende valideringsdata. Slutligen utvecklar vi i Arbete I en metod för modellselektion och modelldiskriminering med hjälp av parametrisk ”bootstrapping” samt kombinationen av olika empiriska fördelningar av traditionella statistiska tester. Vi visar hur det empiriska ”log-likelihood-ratio-testet” är den bästa kombinationen av två tester och hur testet är applicerbart, inte bara för modellselektion, utan också för modelldiskriminering. Sammanfattningsvis är matematisk modellering ett värdefullt verktyg för att analysera data och testa biologiska hypoteser, oavsett underliggande biologiskt system. Vidare utveckling av modelleringsmetoder och tillämpningar är därför viktigt eftersom dessa sannolikt kommer att spela en avgörande roll i framtiden för biologi och medicin, särskilt när det gäller att hantera belastningen från ökande datamängder som blir tillgänglig med nya experimentella tekniker.

mathematical modeling in systems biology: *Stochastic Modelling for Systems Biology* Darren J. Wilkinson, 2011-11-09 Since the first edition of Stochastic Modelling for Systems Biology, there have been many interesting developments in the use of likelihood-free methods of Bayesian inference for complex stochastic models. Re-written to reflect this modern perspective, this second edition covers everything necessary for a good appreciation of stochastic kinetic modelling of biological networks in the systems biology context. Keeping with the spirit of the first edition, all of the new theory is presented in a very informal and intuitive manner, keeping the text as accessible as possible to the widest possible readership. New in the Second Edition All examples have been updated to Systems Biology Markup Language Level 3 All code relating to simulation, analysis, and inference for stochastic kinetic models has been re-written and re-structured in a more modular way An ancillary website provides links, resources, errata, and up-to-date information on installation and use of the associated R package More background material on the theory of Markov processes and stochastic differential equations, providing more substance for mathematically inclined readers Discussion of some of the more advanced concepts relating to stochastic kinetic models, such as random time change representations, Kolmogorov equations, Fokker-Planck equations and the linear noise approximation Simple modelling of extrinsic and intrinsic noise An effective introduction to the area of stochastic modelling in computational systems biology, this new edition adds additional mathematical detail and computational methods that will provide a stronger foundation for the development of more advanced courses in stochastic biological modelling.

mathematical modeling in systems biology: *Systems Biology* Marvin Cassman, Adam Arkin, Frank Doyle, Fumiaki Katagiri, Douglas Lauffenburger, Cynthia Stokes, 2007-05-16 Systems biology is defined for the purpose of this study as the understanding of biological network behaviors, and in particular their dynamic aspects, which requires the utilization of mathematical modeling tightly linked to experiment. This involves a variety of approaches, such as the identification and validation of networks, the creation of appropriate datasets, the development of tools for data acquisition and software development, and the use of modeling and simulation software in close linkage with experiment. All of these are discussed in this volume. Of course, the definition becomes ambiguous at the margins, but at the core is the focus on networks, which makes it clear that the goal is to understand the operation of the systems, rather than the component parts. It was concluded that the U.S. is currently ahead of the rest of the world in systems biology, largely because of earlier investment by funding organizations and research institutions. This is reflected in a large number of active research groups, and educational programs, and a diverse and growing funding base. However, there is evidence of rapid development outside the U.S., much of it begun in the last two to three years. Overall, however, the picture is of an active field in the early stages of explosive growth. This volume is aimed at academic researchers, government research agency representatives and graduate students.

mathematical modeling in systems biology: *Studyguide for Mathematical Modeling in Systems Biology* Cram101 Textbook Reviews, 2013-08-29 Never HIGHLIGHT a Book Again! Includes all testable terms, concepts, persons, places, and events. Cram101 Just the FACTS101 studyguides gives all of the outlines, highlights, and quizzes for your textbook with optional online comprehensive practice tests. Only Cram101 is Textbook Specific. Accompanies: 9780262018883. This item is printed on demand.

mathematical modeling in systems biology: *Mathematical Modelling in Plant Biology* Richard J. Morris, 2018-11-05 Progress in plant biology relies on the quantification, analysis and mathematical modeling of data over different time and length scales. This book describes common mathematical and computational approaches as well as some carefully chosen case studies that demonstrate the use of these techniques to solve problems at the forefront of plant biology. Each chapter is written by an expert in field with the goal of conveying concepts whilst at the same time providing sufficient background and links to available software for readers to rapidly build their own models and run their own simulations. This book is aimed at postgraduate students and researchers working the field of plant systems biology and synthetic biology, but will also be a useful reference for anyone wanting to get into quantitative plant biology.

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