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Autore	Brown Thomas A (Thomas Andrew), <1972->
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ISBN	1-60795-252-1
Descrizione fisica	1 online resource (581 p.)
Disciplina	610.695
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Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	""Contents""; ""Contributors""; ""Preface""; ""Acknowledgments""; ""1""; ""2""; ""3""; ""4""; ""5""; ""6""; ""7""; ""8""; ""9""; ""10""; ""11""; ""12""; ""13""; ""14""; ""15""; ""16""; ""17""; ""18""; ""19""; ""20""; ""21""; ""22""; ""23""; ""24""; ""25""; ""26""; ""27""; ""28""; ""29""; ""30""; ""31""; ""32""; ""33""; ""34""; ""35""; ""36""; ""37""; ""38""; ""39""; ""40""; ""41""; ""42""; ""43""; ""44""; ""45""; ""46""; ""Index""

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Titolo	Computational methods in systems biology : 21st International Conference, CMSB 2023, Luxembourg City, Luxembourg, September 13-15, 2023, Proceedings / / edited by Jun Pang, Joachim Niehren
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Descrizione fisica	1 online resource (xviii, 270 pages) : illustrations (some color)
Collana	Lecture Notes in Bioinformatics, , 2366-6331
Altri autori (Persone)	PangJun (Computer scientist) NiehrenJoachim
Disciplina	570.285 570.113
Soggetti	Computational biology Systems biology
Lingua di pubblicazione	Inglese
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Note generali	Includes author index.
Nota di contenuto	A Formal Approach for Tuning Stochastic Oscillators -- Phenotype Control of Partially Specified Boolean Networks -- A More Expressive Spline Representation for SBML Models Improves Code Generation Performance in AMICI -- Intuitive Modelling and Formal Analysis of Collective Behaviour in Foraging Ants -- Cell-Level Pathway Scoring Comparison with a Bconstrained Variational Autoencoder -- On Estimating Derivatives of Input Signals in Biochemistry -- Harissa: Stochastic Simulation and Inference of Gene Regulatory Networks Based on Transcriptional Bursting -- Approximate Constrained Lumping of Polynomial Differential Equations -- Core SBML and its Formal Semantics -- Average Sensitivity of Canalizing Multivalued Functions -- Tackling Universal Properties of Minimal Trap Spaces of Boolean Networks -- SAF: SAT-Based Attractor Finder in Asynchronous Automata Networks -- Condition for Periodic Attractor in 4-Dimensional Repressilators -- Attractor Identification in Asynchronous Boolean Dynamics with Network Reduction -- 3D Hybrid Cellular Automata for Cardiac Electrophysiology: a Concept Study -- Fridge Compiler: Optimal Circuits from Molecular Inventories -- Joint Distribution of Protein Concentration and Cell Volume Coupled by Feedback in Dilution.

Sommario/riassunto

This book constitutes the refereed proceedings of the 21st International Conference on Computational Methods in Systems Biology, CMSB 2023, held in Luxembourg City, Luxembourg, during September 13–15, 2023. The 14 full papers and 3 tool papers presented in this book were carefully reviewed and selected from 28 submissions. CMSB focuses on modeling, simulation, analysis, design and control of biological systems and covers the broad field of computational methods and tools in systems and synthetic biology and their applications.
