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| Edizione                | [1st ed. 2019.]  |
| Descrizione fisica      | 1 online resource (XI, 388 p. 487 illus., 87 illus. in color.)   |
| Collana                 | Lecture Notes in Bioinformatics, , 2366-6331 ; ; 11773   |
| Disciplina              | 572.8<br>570.285   |
| Soggetti                | Bioinformatics<br>Artificial intelligence<br>Algorithms<br>Machine theory<br>Computer science - Mathematics<br>Software engineering<br>Computational and Systems Biology<br>Artificial Intelligence<br>Formal Languages and Automata Theory<br>Mathematics of Computing<br>Software Engineering  |
| Lingua di pubblicazione | Inglese  |
| Formato                 | Materiale a stampa   |
| Livello bibliografico   | Monografia   |
| Note generali           | Includes index.  |
| Nota di contenuto       | Regular Papers -- Sequential Reprogramming of Boolean Networks Made Practical -- Sequential Reprogramming of Biological Network Fate -- Control Variates for Stochastic Simulation of Chemical Reaction Networks -- Effective computational methods for hybrid stochastic gene networks -- On Chemical Reaction Network Design by a Nested Evolution Algorithm -- Designing Distributed Cell Classifier Circuits using a Genetic Algorithm -- Investigating a Hodgkin-Huxley type model for Drosophila larval neuromuscular junctions via particle swarm fitting -- Cell volume distributions in exponentially growing |

populations -- Transient Memory in Gene Regulation -- A Logic-Based Learning Approach to Explore Diabetes Patient Behaviors -- Reachability design through Approximate Bayesian Computation -- Fast enumeration of non-isomorphic chemical reaction networks -- A large-scale assessment of exact model reduction in the BioModels repository -- Computing Difference Abstractions of Metabolic Networks Under Kinetic Constraints -- Tool Papers -- BRE:IN - A Backend for Reasoning about Interaction Networks with Temporal Logic -- The Kappa simulator made interactive -- Biochemical reaction networks with fuzzy kinetic parameters in Snoopy -- Compartmental Modeling Software: a fast, discrete stochastic framework for biochemical and epidemiological simulation -- Spike - reproducible simulation experiments with configuration file branching -- KAMIS studio: an environment for biocuration of cellular signalling knowledge -- A new version of DAISY to test structural identifiability of biological models -- Extended Abstracts (Posters and Highlight Talks) -- Semi-Quantitative Abstraction and Analysis of Chemical Reaction Networks -- Bayesian parameter estimation for stochastic reaction networks from steady-state observations -- Wasserstein Distances for Estimating Parameters in Stochastic Reaction Networks -- On Inferring Reactions from Data Time Series by a Statistical Learning Greedy Heuristics -- Barbaric Robustness Monitoring Revisited for STL\* in Parasim -- Symmetry breaking for GATA-1/PU.1 model -- Scalable Control of Asynchronous Boolean Networks -- Transcriptional response of SK-N-AS cells to methamidophos (Extended Abstract) -- Separators for polynomial dynamic systems with linear complexity -- Bounding First Passage Times in Chemical Reaction Networks -- Data-informed parameter synthesis for population Markov chains.

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#### Sommario/riassunto

This book constitutes the refereed proceedings of the 17th International Conference on Computational Methods in Systems Biology, CMSB 2019, held in Trieste, Italy, in September 2019. The 14 full papers, 7 tool papers and 11 posters were carefully reviewed and selected from 53 submissions. Topics of interest include formalisms for modeling biological processes; models and their biological applications; frameworks for model verification, validation, analysis, and simulation of biological systems; high-performance computational systems biology and parallel implementations; model inference from experimental data; model integration from biological databases; multi-scale modeling and analysis methods; computational approaches for synthetic biology; and case studies in systems and synthetic biology.

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