Record Nr.	UNINA9910349412803321
Titolo	Computational Methods in Systems Biology : 16th International Conference, CMSB 2018, Brno, Czech Republic, September 12-14, 2018, Proceedings / / edited by Milan eška, David Šafránek
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2018
ISBN	3-319-99429-8
Edizione	[1st ed. 2018.]
Descrizione fisica	1 online resource (XXIII, 326 p. 88 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 11095
Disciplina	570.285
Soggetti	Bioinformatics Artificial intelligence Software engineering
	Mathematical logic Computer logic
	Computational Biology/Bioinformatics
	Artificial Intelligence
	Software Engineering
	Mathematical Logic and Formal Languages Logics and Meanings of Programs
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Modeling and Engineering Promoters with Pre-defined RNA Production Dynamics in Escherichia coli Deep Abstractions of Chemical Reaction Networks Derivation of A Biomass Proxy for Dynamic Analysis of Whole Genome Metabolic Models Computing Diverse Boolean Networks from Phosphoproteomic Time Series Data Characterization of the Experimentally Observed Clustering of VEGF Receptors Synthesis for Vesicle Traffic Systems Formal Analysis of Network Motifs Buffering Gene Expression Noise by microRNA Based Feed Forward Regulation Stochastic Rate Parameter Inference Using the Cross-Entropy Method Experimental Biological Protocols with Formal Semantics Robust Data-Driven Control of Artificial Pancreas Systems Using Neural Networks Programming Substrate-Independent Kinetic

1.

	Barriers with Thermodynamic Binding Networks A Trace Query Language for Rule-based Models Inferring Mechanism of Action of an Unknown Compound from Time Series Omics Data Composable Rate-Independent Computation in Continuous Chemical Reaction Networks ASSA-PBN 3.0: Analysing Context-sensitive Probabilistic Boolean Networks KaSa: A Static Analyzer for Kappa On Robustness Computation and Optimization in BIOCHAM-4 LNA++: Linear Noise Approximation with First and Second Order Sensitivities Reparametrizing the Sigmoid Model of Gene Regulation for Bayesian Inference On the Full Control of Boolean Networks Systems Metagenomics: Applying Systems Biology Thinking to Human Microbiome Analysis.
Sommario/riassunto	Chapters 3, 9 and 10 are available open access under a Creative Commons Attribution 4.0 International License via link.springer.com.