

1. Record Nr.	UNINA9910484573603321
Titolo	Transactions on computational systems biology XI : computational models for cell processes / / Corrado Priami, Ralph-Johan Back, Ion Petre (eds.)
Pubbl/distr/stampa	Berlin ; ; New York, : Springer, c2009
ISBN	3-642-04186-8
Edizione	[1st ed. 2009.]
Descrizione fisica	1 online resource (VIII, 335 p.)
Collana	Lecture notes in computer science. Lecture notes in bioinformatics ; ; 5750
Altri autori (Persone)	PriamiCorrado BackRalph-Johan Petrelon
Disciplina	572/.6
Soggetti	Computational biology Bioinformatics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Computational Models for Cell Processes -- Process Algebra Modelling Styles for Biomolecular Processes -- Simple, Enhanced and Mutual Mobile Membranes -- Bio-PEPA with Events -- In Silico Modelling and Analysis of Ribosome Kinetics and aa-tRNA Competition -- Qualitative and Quantitative Analysis of a Bio-PEPA Model of the Gp130/JAK/STAT Signalling Pathway -- Rule-Based Modelling and Model Perturbation -- Extended Stochastic Petri Nets for Model-Based Design of Wetlab Experiments -- A Projective Brane Calculus with Activate, Bud and Mate as Primitive Actions -- Accepting Networks of Non-inserting Evolutionary Processors -- Discrete Modeling of Biochemical Signaling with Memory Enhancement -- Dynamical Systems and Stochastic Programming: To Ordinary Differential Equations and Back -- Computing Equilibrium Points of Genetic Regulatory Networks -- Code, Context, and Epigenetic Catalysis in Gene Expression.
Sommario/riassunto	The LNCS journal Transactions on Computational Systems Biology is devoted to inter- and multidisciplinary research in the fields of computer science and life sciences and supports a paradigmatic shift in the techniques from computer and information science to cope with the new challenges arising from the systems oriented point of view of

biological phenomena. This special issue on Computational Models for Cell Processes is based on a workshop with the same name that took place in Turku, Finland, on May 27, 2008. The accepted papers, which have passed through a separate peer-review process, span an interesting mix of approaches to systems biology, ranging from quantitative to qualitative techniques, from continuous to discrete mathematics, from deterministic to stochastic methods, and from computational models for biology to computing paradigms inspired by biology. Also included in this issue are three regular submissions dealing with the relationship between ODEs and stochastic concurrent constraint programming, with the equilibrium points of genetic regulatory networks, and with probability models describing how epigenetic context affects gene expression and organismal development.

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