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Collana	Lecture Notes in Bioinformatics ; ; 7605
Disciplina	572.80285
Soggetti	Bioinformatics Computers Computer simulation Bioinformatics Computational biology Software engineering Computer science—Mathematics Computational Biology/Bioinformatics Computation by Abstract Devices Simulation and Modeling Computer Appl. in Life Sciences Software Engineering Symbolic and Algebraic Manipulation
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	International conference proceedings.
Nota di bibliografia	Includes bibliographical references and author index.
Nota di contenuto	Differential and Integral Views of Gene-Phenotype Relations -- Resolving the Three-Dimensional Histology of the Heart -- Bimodal Protein Distributions in Heterogeneous Oscillating Systems -- Expressive Statistical Model Checking of Genetic Networks with Delayed Stochastic Dynamics -- Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus -- Analysis of Modular Organization of Interaction Networks Based on Asymptotic Dynamics -- Concretizing the Process Hitting into Biological Regulatory

Networks -- Investigating Co-infection Dynamics through Evolution of Bio-PEPA Model Parameters: A Combined Process Algebra and Evolutionary Computing Approach -- Population Dynamics P Systems on CUDA -- Efficient Handling of Large Signaling-Regulatory Networks by Focusing on Their Core Control -- Simulating Insulin Infusion Pump Risks by In-Silico Modeling of the Insulin-Glucose Regulatory System -- Revisiting the Training of Logic Models of Protein Signaling Networks with a Formal Approach Based on Answer Set Programming.

Sommario/riassunto

This book constitutes the thoroughly refereed conference proceedings of the 10th International Conference on Computational Methods in Systems Biology, CMSB 2012, held in London, UK, during October 3-5, 2012. The 17 revised full papers and 8 flash posters presented together with the summaries of 3 invited papers were carefully reviewed and selected from 62 submissions. The papers cover the analysis of biological systems, networks, and data ranging from intercellular to multiscale. Topics included high-performance computing, and for the first time papers on synthetic biology.
