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Nota di contenuto	Prediction of Protein-Protein Interacting Sites: How to Bridge Molecular Events to Large Scale Protein Interaction Networks -- The Equivalence between Biology and Computation -- BlenX4Bio – BlenX for Biologists -- Modelling Biological Clocks with Bio-PEPA: Stochasticity and Robustness for the Neurospora crassa Circadian Network -- Quantitative Pathway Logic for Computational Biology -- A Prize-Collecting Steiner Tree Approach for Transduction Network Inference -- Formal Analysis of the Genetic Toggle -- Control Strategies for the Regulation of the Eukaryotic Heat Shock Response -- Computing Reachable States for Nonlinear Biological Models -- On Coupling Models Using Model-Checking: Effects of Irinotecan Injections on the Mammalian Cell Cycle -- The τ -Lattice: Decidability Boundaries for Qualitative Analysis in Biological Languages -- Approximation of Event Probabilities in Noisy Cellular Processes -- Equivalence and Discretisation in Bio-PEPA -- Improved Parameter Estimation for Completely Observed Ordinary Differential Equations with Application to Biological Systems -- A Bayesian Approach to Model Checking Biological Systems -- Dynamic Compartments in the Imperative τ -Calculus -- Probabilistic Approximations of Signaling Pathway Dynamics -- A Reduction of Logical Regulatory Graphs Preserving Essential Dynamical Properties -- On the Use of Stochastic Petri Nets in

the Analysis of Signal Transduction Pathways for Angiogenesis Process
-- CSL Model Checking of Biochemical Networks with Interval Decision
Diagrams -- Qualitative Transition Systems for the Abstraction and
Comparison of Transient Behavior in Parametrized Dynamic Models.

Sommario/riassunto

This book constitutes the refereed proceedings of the 7th International Conference on Computational Methods in Systems Biology, CMSB 2009, held in Bologna, Italy, August 31 - September 1, 2009. The 18 revised full papers presented together with the summaries of 3 invited papers were carefully reviewed and selected from more than 45 submissions. The papers cover theoretical or applied contributions that are motivated by a biological question focusing on modeling approaches, including process algebra, simulation approaches, analysis methods, in particular model checking and flux analysis, and case studies.
