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	Nota di contenuto	On the Use of the Moment Equations for Parameter Inference, Control and Experimental Design in Stochastic Biochemical Reaction Networks -- Numerical Approximation of Rare Event Probabilities in Biochemically Reacting Systems -- An Approximate Execution of Rule-Based Multi-level Models -- Computing Cumulative Rewards Using Fast Adaptive Uniformisation -- Linking Discrete and Stochastic Models: The Chemical Master Equation as a Bridge between Process Hitting and Proper Generalized Decomposition -- Coarse-Grained Brownian Dynamics Simulation of Rule-Based Models -- Modelling and Analysis of Phase Variation in Bacterial Colony Growth -- Using Probabilistic Strategies to Formalize and Compare -Synuclein Aggregation and Propagation under Different Scenarios -- Dynamic Image-Based

Modelling of Kidney Branching Morphogenesis -- Statistical Model Checking Based Calibration and Analysis of Bio-pathway Models -- Constraint Programming in Community-Based Gene Regulatory Network Inference -- ABC–Fun: A Probabilistic Programming Language for Biology -- A Temporal Logic Approach to Modular Design of Synthetic Biological Circuits -- A Lattice-Theoretic Framework for Metabolic Pathway Analysis -- On the Hybrid Composition and Simulation of Heterogeneous Biochemical Models -- On the Verification and Correction of Large-Scale Kinetic Models in Systems Biology -- Context-Sensitive Flow Analyses: A Hierarchy of Model Reductions -- Posters   Backmatter) -- ARNI: Abductive Inference of Complex Regulatory Network Structures -- A Systems Biology and Ecology Framework for POPs Bioaccumulation in Marine Ecosystems -- A Symbolic Approach Based on Model Checking and Constraint Solving Techniques for Reverse Engineering of Thomas Networks Parameters -- Compositionality Results for Cardiac Cell Dynamics -- Quantification of Biological Network Perturbations: Impact Assessment Using Causal Biological Networks -- Deciphering the Transcriptional Landscape of Caulobacter crescentus at Base Pair Resolution -- Identifiablity Analysis and Improved Parameter Estimation of a Human Blood Glucose Control System Model -- RNA Interference in Cancer and Cell Cycle Networks: A Case Study of E2F Proteins -- A Balancing Act: Parameter Estimation for Biological Models with Steady-State Measurements -- A Fusion Approach Linking Signaling Logic and Metabolic Mass-Flow Kinetics in Hepatocytes -- Esther: Introducing an Online Platform for Parameter Identification of Boolean Networks -- Identifying Latent Dynamic Components in Biological Systems -- Next-Newtomics: The Next Generation Repository for Bioinformatical Interpreted Omics Datasets from the Newt Notophthalmus viridescens -- MiRNA Expression Analysis during Heart Regeneration of N. viridescens -- Algorithm to Predict G-Quadruplex Folding through Score Computing -- Optimization Based Inference of Metabolic Networks from Metabolome Data -- PHISTO: A New Web Platform for Pathogen-Human Interactions -- Frameshift Correction in De Novo Assembled Transcriptome Data Using Peptide Data, Blast Sequence Alignments and Hidden Markov Models -- From Prokaryote Genome Sequencing to Pan-Genomic Modeling -- A Simulation Approach to Detect Oscillating Behaviour in Stochastic Population Models -- On Bistability Causing Structures in Escherichia Coli's Metabolism -- Mathematical Modelling of the Function of Ubiquitylation in TNFR1-MediatedNF-B Signalling -- Organizing SIV Gene Network Modules into Graph Database.

Sommario/riassunto	This book constitutes the proceedings of the 11th International Conference on Computational Methods in Systems Biology, CMSB 2013, held in Klosterneuburg, Austria, in September 2013. The 15 regular papers included in this volume were carefully reviewed and selected from 27 submissions. They deal with computational models for all levels, from molecular and cellular, to organs and entire organisms.