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	Nota di contenuto	Modelling and Analysis -- Rate Equations For Graphs -- Stationary Distributions and Metastable Behaviour for Self-Regulating Proteins with General Lifetime Distributions -- Accelerating Reactions at the DNA Can Slow Down Transient Gene Expression -- Graphical Conditions for Rate Independence in Chemical Reaction Networks -- Interval Constraint Satisfaction and Optimization for Biological Homeostasis and Multistationarity -- Growth Dependent Computation of Chokepoints in Metabolic Networks -- On the Complexity of Quadratization for Polynomial Differential Equations -- Comparing Probabilistic and Logic Programming Approaches to Predict the Effects of Enzymes in a Neurogenerative Disease Model -- Boolean Networks -- Control Strategy Identification via Trap Spaces in Boolean Networks -- Qualitative Analysis of Mammalian Circadian Oscillations: Cycle Dynamics and Robustness -- Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision -- Classifier Construction in Boolean Networks Using Algebraic Methods -- Sequential Temporary and Permanent Control of Boolean Networks -- Inference and Identification -- ABC(SMC)^2: Simultaneous Inference and Model Checking of Chemical Reaction Networks -- Parameter Synthesis for Hybrid Systems from Hybrid CTL Specifications -- Core Models of Receptor Reactions Evaluate Basic Pathway Designs Enabling Heterogeneous Commitments to Apoptosis -- Drawing the Line: Basin

Boundaries in Safe Petri Nets -- Tools -- ModRev - Model Revision Tool for Boolean Logical Models of Biological Regulatory Networks -- fnyzer: a Python Package for the Analysis of Flexible Nets -- eBCSgen: A Software Tool for Biochemical Space Language -- What is a Cell Cycle Checkpoint ? The TotemBioNet Answer -- Kaemika App, Integrating Protocols and Chemical Simulation -- Tutorials -- Tutorial: The CoLoMoTo Interactive Notebook, Accessible and Reproducible Computational Analyses for Qualitative Biological Networks -- Integrating Experimental Pharmacology and Systems Biology for GPCR Drug Discovery.

Sommario/riassunto

This book constitutes the refereed proceedings of the 18th International Conference on Computational Methods in Systems Biology, CMSB 2020, held in Konstanz, Germany, in September 2020.* The 17 full papers and 5 tool papers were carefully reviewed and selected from 30 submissions. In addition 3 abstracts of invited talks and 2 tutorials have been included in this volume. Topics of interest include formalisms for modeling biological processes; models and their biological applications; frameworks for model verification, validation, analysis, and simulation of biological systems; high-performance computational systems biology and parallel implementations; model inference from experimental data; model integration from biological databases; multi-scale modeling and analysis methods; computational approaches for synthetic biology; and case studies in systems and synthetic biology. * The conference was held virtually due to the COVID-19 pandemic.