

| | |
|-------------------------|--|
| 1. Record Nr. | UNISA996464396403316 |
| Titolo | Computational methods in systems biology : 9th international conference, CMSB 2021, Bordeaux, France, September 22-24, 2021, proceedings // edited by Eugenio Cinquemani and Loic Pauleve |
| Pubbl/distr/stampa | Cham, Switzerland : , : Springer, , [2021] ©2021 |
| ISBN | 3-030-85633-X |
| Descrizione fisica | 1 online resource (292 pages) |
| Collana | Lecture Notes in Computer Science ; ; v.12881 |
| Disciplina | 570.285 |
| Soggetti | Software engineering Bioinformatics |
| Lingua di pubblicazione | Inglese |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
| Nota di bibliografia | Includes bibliographical references and index. |
| Nota di contenuto | Intro -- Preface -- Organization -- Contents -- Reducing Boolean Networks with Backward Boolean Equivalence -- 1 Introduction -- 2 Preliminaries -- 3 Backward Boolean Equivalence -- 3.1 Backward Boolean Equivalence and BN Reduction -- 3.2 Computation of the Maximal BBE -- 3.3 Relating Dynamics of Original and Reduced BNs -- 4 Application to BNs from the Literature -- 4.1 Large Scale Validation of BBE on BNs -- 4.2 Attractor Analysis of Selected Case Studies -- 4.3 Comparison with ODE-Based Approach From ch1cardelli2017maximal -- 5 Related Work -- 6 Conclusion -- References -- Abstraction of Markov Population Dynamics via Generative Adversarial Nets -- 1 Introduction -- 2 Background -- 2.1 Chemical Reaction Networks -- 2.2 Generative Adversarial Nets -- 3 GAN-Based Abstraction -- 3.1 Model Abstraction -- 3.2 Dataset Generation -- 3.3 cWCGAN-GP Architecture -- 3.4 Model Training -- 4 Experimental Results -- 4.1 cWCGAN-GP Architecture -- 4.2 Results -- 4.3 Discussion -- 5 Conclusions -- References -- Greening R. Thomas' Framework with Environment Variables: A Divide and Conquer Approach -- 1 Introduction -- 2 Adding Environment Variables to Thomas' Framework -- 2.1 Regulatory Network with Multiplexes -- 2.2 Formulas of Biological Properties and Their Models -- 2.3 Environmental Regulatory Networks -- 3 All Environments' Coexistence in Thomas' Framework -- |

3.1 Regulatory Network -- 3.2 Formula Summing Up all Behavioural Properties -- 3.3 Application to *Pseudomonas aeruginosa* -- 4 Divide with Environments, Combine with Intersection -- 4.1 Regulatory Networks with Environments -- 4.2 Formulas and Abstraction of Models -- 4.3 Application to *Pseudomonas aeruginosa* -- 5 Comparing the Two Approaches -- 5.1 Theoretical Point of View -- 5.2 Practical Results -- 6 Case Study: Cell Metabolism -- 6.1 Metabolism Regulations According to Environments. 6.2 All Environments Coexistence in Thomas' Framework -- 6.3 Divide with Environments, Combine with Intersection -- 7 Conclusion -- References -- Automated Inference of Production Rules for Glycans -- 1 Introduction -- 2 Production of Glycans -- 3 Motivating Example -- 4 Modelling of the Synthesis Problem -- 5 Method for the Synthesis Problem -- 5.1 SugarSynth in Detail -- 5.2 EncodeProduce in Detail -- 6 Experiments -- 7 Conclusion and Future Work -- References -- Compiling Elementary Mathematical Functions into Finite Chemical Reaction Networks via a Polynomialization Algorithm for ODEs -- 1 Introduction -- 2 Input Language of Elementary Functions -- 2.1 Example -- 2.2 Elementary Functions as Compilation Pipeline Input Language -- 3 Polynomialization Algorithm for Elementary ODEs -- 3.1 Polynomialization Algorithm -- 3.2 Interval of Definition -- 3.3 Termination -- 3.4 Complexity -- 3.5 Remark on the Compilation of the Exponentiation -- 4 CRN Compilation Pipeline for Elementary Functions -- 4.1 Detailed Example -- 4.2 Implementation -- 5 Evaluation -- 6 Conclusion and Perspectives -- References -- Interpretable Exact Linear Reductions via Positivity -- 1 Introduction -- 2 Methods -- 2.1 Preliminaries on Lumping -- 2.2 The Nonuniqueness/Interpretability Issue -- 2.3 Our Approach via Nonnegativity -- 2.4 Algorithmic Details -- 3 Case Studies -- 3.1 Multisite Protein Phosphorylation -- 3.2 Fc-RI Signaling Pathways -- 3.3 Jak-Family Protein Tyrosine Kinase Activation -- 4 Conclusion -- References -- Explainable Artificial Neural Network for Recurrent Venous Thromboembolism Based on Plasma Proteomics -- 1 Introduction -- 2 Materials and Methods -- 2.1 MARTHA Study -- 2.2 Proposed Workflow -- 3 Results -- 3.1 MARTHA Study -- 3.2 Constructing and Validation of the ANN -- 3.3 Post-hoc Explainability of ANN -- 4 Conclusion -- References. Neural Networks to Predict Survival from RNA-seq Data in Oncology -- 1 Introduction -- 2 Models -- 2.1 The Cox Model -- 2.2 Neural Networks -- 3 Simulations -- 3.1 Generation of Survival Times -- 3.2 Simulation with the Cox - Weibull Model -- 3.3 Simulation with the AH - Log-Normal Model -- 3.4 Metrics -- 4 Results -- 4.1 Simulation Study -- 4.2 Application on Real Datasets -- 5 Discussions -- A Appendix: Supplementary Results -- A.1 Simulation from the AFT - Log-Normal Model -- A.2 Simulation Study -- References -- Microbial Community Decision Making Models in Batch and Chemostat Cultures -- 1 Introduction -- 2 Concepts -- 2.1 Chemostat vs Batch Environment -- 2.2 Implications for Coexistence -- 2.3 Implications for Decision Making -- 3 Community Models -- 3.1 General Consortium Models -- 3.2 Rational Agents -- 3.3 Rational Community -- 4 Applications -- 4.1 Prisoners Dilemma -- 4.2 Coexistence Microbial Consortium -- 5 Discussion -- References -- Learning Boolean Controls in Regulated Metabolic Networks: A Case-Study -- 1 Introduction -- 2 Background: Regulated Metabolic Networks -- 2.1 Coupling Metabolic and Regulatory Networks -- 2.2 Dynamic rFBA -- 3 Boolean Abstraction of Dynamic rFBA -- 3.1 Boolean Metabolic Steady States -- 3.2 Boolean Dynamics -- 4 Inference of Regulations from rFBA Time Series -- 4.1 Approximation as a Boolean Satisfiability

Problem -- 4.2 Implementation in Answer-Set Programming -- 5 Case Study -- 6 Discussion -- A Binarized Metabolic Steady State -- B Experiments and Simulations -- References -- Population Design for Synthetic Gene Circuits -- 1 Introduction -- 2 Population Design Framework -- 3 Case Study: Design of a Transcriptional Controller -- 3.1 Overview -- 3.2 Individual Model -- 3.3 Population Model -- 3.4 Design Problem -- 3.5 Sampling the Individual Parameters -- 3.6 Sampling the Population Parameters.

4 Discussion -- 5 Conclusion -- References -- Nonlinear Pattern Matching in Rule-Based Modeling Languages -- 1 Introduction -- 2 Rule-Based Modeling -- 3 Nonlinear Patterns in the Wild -- 4 Linear Pattern Matching -- 4.1 Abstract Syntax -- 4.2 Pattern Matching Semantics -- 4.3 Algorithm -- 5 Nonlinear Pattern Matching with Expressions -- 5.1 Abstract Syntax -- 5.2 Pattern Matching Semantics -- 6 Benchmarks -- 7 Discussion and Conclusion -- References -- Protein Noise and Distribution in a Two-Stage Gene-Expression Model Extended by an mRNA Inactivation Loop -- 1 Introduction -- 2 Model Formulation -- 3 Factorial Cumulant Generating Function -- 4 Protein Variability -- 5 Special-Function Representation -- 6 Marginal Distributions -- 7 Conclusion -- References -- Aeon 2021: Bifurcation Decision Trees in Boolean Networks -- 1 Introduction -- 2 Methods -- 3 Case Study -- 4 Conclusion -- References -- LNetReduce: Tool for Reducing Linear Dynamic Networks with Separated Timescales -- 1 Introduction -- 2 Model -- 3 Reduction Algorithm -- 4 Applications -- 4.1 Connection Between Topology and Dynamics -- 4.2 Design of Slow Transients -- 5 Conclusion -- References -- Ppsim: A Software Package for Efficiently Simulating and Visualizing Population Protocols -- 1 Introduction -- 2 Usage of the Ppsim Tool -- 3 Speed Comparison with Other CRN Simulators -- 4 Issues with Other Speedup Methods -- 5 Conclusion -- References -- Web-Based Structural Identifiability Analyzer -- 1 Introduction and Related Work -- 2 Input-Output Specification -- 3 Use Cases for Structural Identifiability Toolbox -- 3.1 Globally Identifiable Example (Two-Species Competition Model) -- 3.2 Locally Identifiable Model (SIRS Model with Forcing) -- 3.3 Identifiable Combination of Non-identifiable Parameters (Tumor Targeting) -- 3.4 System with a Non-identifiable Parameter (Lotka-Volterra Model). 3.5 Refining Multi-experiment Identifiability Bound (Slow-Fast Ambiguity in a Chemical Reaction Network) -- A Details on the Underlying Algorithms -- B Systems in Structural Identifiability Toolbox Input Form -- B.1 Example from Sect.3.2 -- B.2 Example from Sect.3.3 -- B.3 Example from Sect.3.4 -- B.4 Example from Sect. 3.5 -- B.5 Example of Speedup with Bypasses -- References -- BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems -- 1 Introduction -- 2 Related Work -- 3 Internal Design and Domain Partitioning -- 4 Experiments -- 5 Conclusion and Future Work -- A 1-D Pure x-Domain Decomposition -- B Mapping Basic Agents to a Voxel -- C Extended Results -- D Correctness Checking -- References -- Author Index.

| | |
|-------------------------|---|
| 2. Record Nr. | UNICASRML0234387 |
| Autore | Walras, Léon |
| Titolo | Elementi di economia politica pura / Leön Walras ; trad. di Anna Bagiotti |
| Pubbl/distr/stampa | Torino, : UTET, 1974 |
| Descrizione fisica | 656 p. : tav. ; 24 cm |
| Lingua di pubblicazione | Italiano |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |