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Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 12881
Disciplina	570.285
Soggetti	Bioinformatics Artificial intelligence Software engineering Database management Computer science Computer networks Computational and Systems Biology Artificial Intelligence Software Engineering Database Management System Theory of Computation Computer Communication Networks
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Reducing Boolean Networks with Backward Boolean Equivalence -- Abstraction of Markov Population Dynamics via Generative Adversarial Nets -- Greening R. Thomas’ Framework with Environment Variables: a Divide and Conquer Approach -- Automated inference of production rules for glycans -- Compiling Elementary Mathematical Functions into Finite Chemical Reaction Networks via a Polynomialization Algorithm for ODEs -- Interpretable exact linear reductions via positivity -- Explainable artificial neural network for recurrent venous thromboembolism based on plasma proteomics -- Neural networks to

	predict survival from RNA-seq data in oncology -- Microbial Community Decision Making Models in Batchand Chemostat Cultures.- Learning Boolean controls in regulated metabolic networks: a case-study -- Population design for synthetic gene circuits -- Nonlinear pattern matching in rule-based modeling languages -- Protein noise and distribution in a two-stage gene-expression model extended by an mRNA inactivation loop -- Aeon 2021: Bifurcation Decision Trees in Boolean Networks -- LNetReduce: tool for reducing linear dynamic networks with separated time scales -- ppsim: A software package for efficiently simulating and visualizing population protocols -- Web-based Structural Identifiability Analyzer BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems.
Sommario/riassunto	This book constitutes the refereed proceedings of the 19th International Conference on Computational Methods in Systems Biology, CMSB 2021, held in Bordeaux, France, September 22–24, 2021. * The 13 full papers and 5 tool papers were carefully reviewed and selected from 32 submissions. The topics of interest include biological process modelling; biological system model verification, validation, analysis, and simulation; high-performance computational systems biology; model inference from experimental data; multi-scale modeling and analysis methods; computational approaches for synthetic biology; machine learning and data-driven approaches; microbial ecology modelling and analysis; methods and protocols for populations and their variability; models, applications, and case studies in systems and synthetic biology. The chapters "Microbial Community Decision Making Models in Batch", "Population design for synthetic gene circuits", "BioFVM-X: An MPI+OpenMP 3-D Simulator for Biological Systems" are published open access under a CC BY license (Creative Commons Attribution 4.0 International License). * The conference was held in a hybrid mode due to the COVID-19 pandemic.