1. Record Nr. UNISA996465406403316 Algebraic Biology [[electronic resource]]: Second International **Titolo** Conference, AB 2007, Castle of Hagenberg, Austria, July 2-4, 2007. Proceedings / / edited by Hirokazu Anai, Katsuhisa Horimoto, Temur Kutsia Pubbl/distr/stampa Berlin, Heidelberg:,: Springer Berlin Heidelberg:,: Imprint: Springer, 2007 **ISBN** 3-540-73433-3 Edizione [1st ed. 2007.] Descrizione fisica 1 online resource (XIII, 379 p.) Theoretical Computer Science and General Issues, , 2512-2029;; 4545 Collana Disciplina 574.0151 Soggetti Computer science Machine theory Computer science—Mathematics **Bioinformatics** Software engineering Computer Science Logic and Foundations of Programming Formal Languages and Automata Theory Symbolic and Algebraic Manipulation Computational and Systems Biology Software Engineering Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Note generali Bibliographic Level Mode of Issuance: Monograph Nota di bibliografia Includes bibliographical references and index. Nota di contenuto Algebraic Systems Biology: Theses and Hypotheses -- Discrete Models of Biochemical Networks: The Toric Variety of Nested Canalyzing Functions -- Membrane Computing as a Framework for Bio-modeling (An Informal Glimpse) -- Relating Attractors and Singular Steady States in the Logical Analysis of Bioregulatory Networks -- Translating Time-Course Gene Expression Profiles into Semi-algebraic Hybrid Automata Via Dimensionality Reduction -- On Proving the Absence of Oscillations in Models of Genetic Circuits -- Attenuation Regulation as a Term Rewriting System -- Glucose-Insulin Control of Type1 Diabetic Patients

in H2/H??? Space Via Computer Algebra -- Exact Parameter

Determination for Parkinson's Disease Diagnosis with PET Using an

Algebraic Approach -- Efficient Haplotype Inference with Pseudoboolean Optimization -- An Algebraic Algorithm for the Identification of Glass Networks with Periodic Orbits Along Cyclic Attractors --Analyzing Pathways Using SAT-Based Approaches -- Algorithmic Algebraic Model Checking IV: Characterization of Metabolic Networks -- Cascaded Games -- On Differential Algebraic Decision Methods for the Estimation of Anaerobic Digestion Models -- Protein Structure Prediction Using Residual Dipolar Couplings -- A Stochastic Pi Calculus for Concurrent Objects -- Modeling Static Biological Compartments with Beta-binders -- Deducing Interactions in Partially Unspecified Biological Systems -- Reduction of Algebraic Parametric Systems by Rectification of Their Affine Expanded Lie Symmetries -- Prefix Reversals on Binary and Ternary Strings -- Toric Ideals of Phylogenetic Invariants for the General Group-Based Model on Claw Trees K 1,n --Inference of Protein-Protein Interactions by Using Co-evolutionary Information -- A Short Survey of Automated Reasoning -- Inference of Complex Regulatory Network for the Cell Cycle System in Saccharomyces Cerevisiae -- Manifestation and Exploitation of Invariants in Bioinformatics.