

Complexity of limit-cycle problems in Boolean networks

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Abstract

Boolean networks are a general model of interacting entities, with applications to biological phenomena such as gene regulation. Attractors play a central role, and the schedule of entities update is *a priori* unknown. This article presents results on the computational complexity of problems related to the existence of update schedules such that some limit-cycle lengths are possible or not. We first prove that given a Boolean network updated in parallel, knowing whether it has at least one limit-cycle of length k is **NP**-complete. Adding an existential quantification on the block-sequential update schedule does not change the complexity class of the problem, but the following alternation brings us one level above in the polynomial hierarchy: given a Boolean network, knowing whether there exists a block-sequential update schedule such that it has no limit-cycle of length k is **NP^{NP}**-complete.

1 Introduction

Boolean networks (BNs) were introduced by McCulloch and Pitts in the 1940s through the well known formal neural networks [17] that are specific BNs governed by a multi-dimensional threshold function. Informally, BNs are finite dynamical systems in which entities having Boolean states may interact with each other over discrete time. After their introduction, neural networks were studied in depth from the mathematical standpoint. Among the main works on them are the introduction by Kleene of finite automata and regular expression [16], first results on the dynamical behaviors of linear feedback shift register [13] and linear networks [8]. These researches led Kauffman and Thomas (independently) from the end of the 1960s to develop the use of BNs in the context of biological networks modeling [15, 27], which has paved the way to numerous applied works at the interface between molecular biology, computer science and discrete mathematics. In parallel, theoretical developments were done in the framework of linear algebra and numerical analysis by Robert [24], and in that of dynamical system theory and computational models, which constitutes the lens through which we look at BNs in this paper.

In this context, numerous studies have already been led and have brought very important results. Considering that a BN can be defined as a collection of local Boolean

The Complexity Of Boolean Networks

Michael Rajnik



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goal is to understand the emergence of physiological or functional properties Symbolic Approaches to Modeling and Analysis of Biological Systems presents contributions of formal methods from computer science for modeling the dynamics of biological systems It deals more specifically with symbolic methods i e methods that can establish the qualitative properties of models This book presents different approaches related to semantics language modeling and their link with data and allows us to examine the fundamental problems and challenges that biological systems are facing The first part of the book presents works that rely on various available data to build models while the second part gathers contributions surrounding issues of semantics and formal methods *Handbook of Research on Computational Methodologies in Gene Regulatory Networks* Das, Sanjoy, Caragea, Doina, Welch, Stephen, Hsu, William H., 2009-10-31 This book focuses on methods widely used in modeling gene networks including structure discovery learning and optimization Provided by publisher **Thinking About Biology** Wilfred Stein, Francisco J. Varela, 2018-03-08 This book discusses the emergence of life the development of the individual and the study of the interaction between individuals and species It gives the student of theoretical biology some idea of the flavor of current research in the field **SOFSEM 2021: Theory and Practice of Computer Science** Tomáš Bureš, Riccardo Dondi, Johann Gamper, Giovanna Guerrini, Tomasz Jurdziński, Claus Pahl, Florian Sikora, Prudence W.H. Wong, 2021-01-20 This book contains the invited and contributed papers selected for presentation at SOFSEM 2021 the 47th International Conference on Current Trends in Theory and Practice of Computer Science which was held online during January 25-28 2021 hosted by the Free University of Bozen Bolzano Italy The 33 full and 7 short papers included in the volume were carefully reviewed and selected from 100 submissions They were organized in topical sections on foundations of computer science foundations of software engineering foundations of data science and engineering and foundations of algorithmic computational biology The book also contains 5 invited papers **Proceedings of the Twenty-seventh Annual ACM Symposium on Theory of Computing**, 1995 *Logical Modeling of Cellular Processes: From Software Development to Network Dynamics* Matteo Barberis, Tomáš Helikar, 2019-08-16 Mathematical models have become invaluable tools for understanding the intricate dynamic behavior of complex biochemical and biological systems Among computational strategies logical modeling has been recently gaining interest as an alternative approach to address network dynamics Due to its advantages including scalability and independence of kinetic parameters the logical modeling framework is becoming increasingly popular to study the dynamics of highly interconnected systems such as cell cycle progression T cell differentiation and gene regulation Novel tools and standards have been developed to increase the interoperability of logical models which can now be employed to respond a variety of biological questions This Research Topic brings together the most recent and cutting edge approaches in the area of logical modeling including among others novel biological applications software development and model analysis techniques **Efficient Algorithms** Susanne Albers, Helmut Alt, Stefan Näher, 2009-09-01 This Festschrift volume published in honor of Kurt Mehlhorn on the occasion of his 60th birthday contains

28 papers that demonstrate how the field of algorithmics has developed and matured in the decades since Mehlhorn's first book on the subject in 1977 Complex Systems ,2007 **Size-time Complexity of Boolean Networks for Prefix Computations** Gianfranco Bilardi,Franco P. Preparata,1987 *Journal of the Association for Computing Machinery* JOURNAL OF THE ASSOCIATION FOR COMPUTING MACHINERY,1989 Mathematical Reviews ,1986 *Proceedings of the Fourth Israel Symposium on Theory of Computing and Systems* ,1996 This volume contains a selection of 29 papers presented at the Fourth Israeli Symposium on the theory of Computing and Systems held in Jerusalem in June of 1996 Topics include the Borowsky Gafni simulation algorithm arrangements of curves and surfaces in computational geometry advances in optical *Proceedings of the Twenty-sixth Annual ACM Symposium on the Theory of Computing* ,1994 **Size-time Complexity of Boolean Networks for Prefix Computation** Cornell University. Department of Computer Science,G. Bilardi,F. P. Preparata,1987 The prefix problem consists of computing all the products $x_0 x_1 \dots x_j$ $0 \leq j \leq N-1$ given a sequence $X = x_0 x_1 \dots x_{N-1}$ of elements in a semigroup In this paper we completely characterize the size time complexity of computing prefixes with boolean networks which are synchronized interconnections of boolean gates and one bit storage devices This complexity crucially depends upon a property of the underlying semigroup which we call cycle freedom no cycle of length greater than one in the Cayley graph of the semigroup Denoting by S and T size and computation time respectively we have $S = \Theta(N T \log N)$ for non cycle free semigroups and $S = \Theta(N T)$ for cycle free semigroups In both cases $T = \Omega(\log N)$ **Foundations of Software Technology and Theoretical Computer Science** ,1984 **International Congress of Mathematicians, Kyoto, Japan, August 21-29,1990: Plenary lectures, section lectures, ICMI lectures** ,1990 **SIAM Journal on Computing** Society for Industrial and Applied Mathematics,2001

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