

Preface

Analysis of biological networks is an important topic in various fields including bioinformatics, computational biology, complex networks, and systems biology. In order to perform computational analysis, mathematical models of biological networks are required and thus various models have been proposed and utilized. Among them, many studies have been done on the Boolean network (BN). The BN is a discrete model of biological networks, in which each node takes either 0 (inactive) or 1 (active) at each time step and the states of nodes are synchronously updated according to regulation rules assigned to nodes, where each regulation rule is given as a Boolean function. BNs have been mainly used as a model of genetic networks in which node corresponds to a gene. Although the BN is a simple and old model that was proposed about 50 years ago by Stuart Kauffman, BNs exhibit complex behavior and thus extensive studies have been done in order to understand their behavior.

While BNs are deterministic, biological systems contain intrinsic stochasticity and observed data also include noise. Therefore, various probabilistic extensions of the BN model have been proposed. Among them, extensive studies have been done on the probabilistic Boolean network (PBN). Although one Boolean function is assigned to one node in a BN, multiple Boolean functions can be assigned to one node in a PBN and one of them is randomly selected at each time step according to the prescribed probability distribution.

As mentioned above, many studies have been done on BNs and PBNs and many algorithms have also been proposed. However, not so much attention was paid on the computational complexity of these algorithms although many of them are practically useful. Since we often need to handle genome-scale models nowadays, it is important to analyze the

computational complexity of algorithms and problems. Therefore, this book focuses on the computational complexity of algorithms and problems on BNs and PBNs. In particular, this book mainly considers three fundamental problems: (i) finding a steady state in a given network, (ii) inference of a network structure from sample data, and (iii) finding a control strategy to drive a network from a given initial state to a given target state. In addition to explanations of algorithmic aspects on BNs and PBNs, this book gives a brief introduction to the semi-tensor product approach that was proposed and developed by Daizhan Cheng and his colleagues because many studies have recently been done based on this approach.

The main target readers of this book are graduate students and researchers studying bioinformatics and computational biology. This book might also be useful for graduate students and researchers in computer science who are interested in systems biology. This book is basically self-contained. Necessary background information on computer scientific aspects is given in the first chapter and theoretical proofs are given for most algorithms. Furthermore, figures and/or examples are often given for illustrating algorithms and problems. It is to be noted that although this book presents algorithms with theoretical guarantees, these algorithms are not necessarily practically better than existing algorithms. The purpose of this book is to theoretically analyze algorithms and problems on BNs and PBNs.

Many of the algorithms explained in this book were developed by the author and collaborators. Therefore, I would like to thank all the collaborators who worked on BNs/PBNs. Chelsea Chin, Kim Tan, and their colleagues at World Scientific have been very helpful in completing this book, for which I thank them. I would also like to thank my parents, wife, and daughter for their continuous support.

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November 2017