

Tentative Outline

Special Thematic Issue for CNS & Neurological Disorders - Drug Targets

Thematic issue title: **Recent Advances in Modeling Genetic Networks and Biological Systems**

Guest Editors: *Yang Liu, Jianquan Lu, Caiyun Fu, Wei Lin*

Aims & Scope:

It is a central focus of modern biology to understand the intrinsic complex functions of a neuron, a cell or/and an organism, the complex manners on how a neuron, a cell or/and an organism executes its or/and their potency, and the undiscovered patterns which render those genetic or cellular systems into the states of sickness or diseases.

Neural networks, which are a kind of simplification, simulation and abstraction of human brain neural structures, are composed of a large number of interconnected neurons, combination optimization, etc. In general, neural networks include input, output and computation functions, which are analogous to the dendrites of a neuron, the axon of a neuron and the nucleus, respectively. Every neuron can be regarded as a computing unit and storage. Specifically, the computation unit is essentially the function of a neuron which can be used to compute its input. The storage represents that the neuron will temporarily the computation result, and then pass to the next layer. The training algorithm of a neural network is to adjust the weight value make the prediction effect of the whole network the best. Neural networks have extraordinary expressiveness and broad application prospects including but not limited to image procession, deep learning, signal processing, pattern recognition.

Due to the rapid developments of biotechnology in systems biology, genetic regulatory networks and the topics of controlling human signaling networks such as interventions on neurological disorders and drug targets have become a developing and vital research topic in recent decades. Generally speaking, a genetic regulatory network is an assembly of mRNA, DNA elements, molecular regulators that are directly or indirectly interconnected with other substances like protein products in the cell, which governs the gene expression levels of mRNAs and proteins. Based on network modeling, it would be better to disclose the internal and interactive genetic regulatory networks. Additionally, the information of signaling pathway extracted from a large number of biological experiments can be translated into a graph (network) by representing mRNAs, DNAs, proteins, transcripts and molecules as network nodes and the interactions between genes as network edges. Thus, genetic regulatory networks are of great importance in bio-medical processes and the control problem has a crucial impact on interventions of neurological disorders and drug target identification and diagnosis.

Sparked by massive practical applications, a variety of genetic regulatory networks have been proposed, such as Bayesian networks, Markov-type gene networks, chemical master equations, chemical reaction-diffusion equations, and Boolean networks, etc. Among these models, each of them has its specific advantages and limitations in the context of some specific considerations: the feasibility of models with regard to practical genetic regulatory networks, the errors among state evolutions of models and behaviors of real biological systems, the fidelity of network restored by real experiments, and the computational complexity of models sampled from the available data. As a powerful logical model of biological systems, Boolean network was originally proposed by Kauffman with an aim of discovering the internal behaviors of genes in genetic regulatory networks. For example, selecting appropriate drug treatments in order to force the system to reach a steady state can be modeled by the problem of controllability of logical networks. Thus, using logical models, identifying and regulating control gene nodes will be useful for controlling cellular state, or identifying neurological disorders of abnormal gene manners. During the past a few decades, the investigations on Boolean networks have tremendously promoted by a novel tool, the semi-tensor product (STP) of matrices. Based on the bijective equivalence between the logical functions and the corresponding algebraic forms using the STP, numerous results of analytical or/and practical significance have been established on controllability, observability, stability, optimal control, synchronization, robustness, and so on. However, due to the high computational complexity of Boolean networks using the STP, the applications are limited to certain networks of lower dimensions and smaller scales. Therefore, it is of great importance to revisit the topics on analysis and synthesis in gene networks and biological systems modelled by logical network\Boolean networks, especially focusing on addressing the issue of computational complexity, developing certain efficient methods so as to reduce the computational complexity significantly.

Keywords: Biological systems; Logical networks; Signal pathways networks; Neural networks; Analysis and synthesis.

Subtopics:

Such a special issue is anticipated to meet practical challenges with the most recent theoretical and practical advances in related research topics. We focus on publishing Original Research and Review Articles on some urgent research questions of interests included, but not limited to the following questions:

- modeling of biological systems and gene networks;
- analysis of neural networks and gene networks: stability/ robustness/complexity analysis/observability;

- synthesis of neural networks and gene networks: stabilization/ disturbances decoupling / perturbations / optimal control;
- modeling, analysis and control of Boolean (control) networks;
- state space analysis of logical (control) networks: controllability/observability/stability/optimal control;
- applications of biological systems and gene networks: neural networks/ feedback shift registers/ compressed sensing/traffic networks/social networks, and
- experimental research related to signal pathways/networks in disease treatments and their evaluations.

Schedule:

- ✧ Manuscript submission deadline: 31 Sep. 2020
- ✧ Announcement of acceptance by the Guest Editors: 28 Feb. 2021
- ✧ Final manuscripts due: early 2021

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