

Editorial

Special Issue on “Biological Network Approaches and Applications”

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Biological phenomena comprise various interactions between genes and molecules. With the advent of high-throughput technologies, a single experiment can produce a vast amount of information concerning such interactions. Moreover, the knowledge of these interactions, and the databases in which an abundance of information regarding their study is stored and analyzed, have been growing exponentially; therefore, proper methods for the representation and analysis of these data have become necessary and indispensable. To analyze and extract information from these data more efficiently, network-based methodologies are being widely applied in the fields of genomics and bioinformatics [1,2]. Consequently, various biological networks have been proposed and proven to be advantageous for the comprehension of complex interactions in biology and medicine [3]. These biological networks include the results of network model-based analyses and biological knowledge, which are summarized and represented by networks.

The network model is widely used in the analysis of transcriptomics data. Gene co-expression networks are determined via the computation of the co-expression of gene pairs, and significant results are presented in the form of networks, which are frequently used in the inference of gene functions [4]. Multivariate network models—such as Bayesian networks, Markov networks, and structural equation models—have been applied to identify causal regulatory relationships between genes [5]. These methods identify the gene modules or regulatory relationships that will aid our understanding of gene-regulatory networks.

Protein–protein interactions (PPIs) constitute a representative biological knowledge base that is widely used for the inference of gene functions and regulatory relationships [6]. Yeast two-hybrid experiments can yield a complete network between the proteins in a cell, with the results of these analyses being deposited in several databases. In addition to experimental data, heterogeneous information is integrated to infer PPIs, with the results augmenting the PPI network [7].

Since network models are flexible and powerful tools for the representation of data and knowledge, network-based integrative analyses of heterogeneous data are being actively implemented in biomedical research. In particular, this approach was applied to the analysis of The Cancer Genome Atlas (TCGA) data, which comprise multi-omics data pertaining to sequences, epigenomics, and gene and protein expression [8]. Studies of TCGA data have adopted network methods to integrate these multi-omics data and have yielded many novel findings associated with cancer pathophysiology.

Network-based models can be developed using many statistical and machine learning methodologies. For the inference of biological networks from omics data and biological knowledge, pairwise measures or multivariate statistical models can be applied. The deep-learning-based identification of the structures of biological networks is an active research area [9]. It is expected that such models will provide more opportunities to discover novel findings.

This Special Issue presents articles concerning these issues. The recent progress in the research into biological networks and their applications in solving problems in the field of



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biomedical research will be introduced. Network models and methodologies, as well as the analytical results obtained using network models, will also be included.

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