Book Review

A review on the book, *Network Biology: Theories, Methods and Applications*

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Abstract

The book, *Network Biology: Theories, Methods and Applications*, edited by WenJun Zhang and published by Nova Science Publishers, USA, was briefly reviewed in present report.

Keywords network biology; book; review.

1 Introduction

Biological network analysis is a fast moving science. Many core scientific issues, for example, ecological structure, coevolution, coextinction and biodiversity conservation in ecology, cancer development and metabolic regulation in health science, etc., are expected to be addressed by network analysis. Network analysis is becoming the core methodology to treat complex biological systems. With the quick development of this science, more and more papers on biological networks are published. This book includes such theories and methods of network biology as methodology of social network analyses, construction of statistic networks, phylogenetic networks, multi-stable and oscillatory biological networks, creation of real network with expected degree distribution, forest ecosystem model, etc. Chapters are contributed by about 20 scientists from USA, Canada, New Zealand, China, Sweden, Spain, Mexico, in the areas of computational science and life sciences. It will provide researchers with various aspects of the latest advances in network biology. It is a valuable reference for the scientists, university teachers and graduate students in biology, health science, ecology, social science, applied mathematics and computational science.

2 Contents

The main contents of the book are described as follows:

Chapter 1 (Weerasinghe, 2013). Existing relationships and connections among humans, animals and micro or macro organisms can be explored, analyzed and interpreted using "social" network methodologies. Though the term social implies the human (within societal) relationships, ties and interactions, the theory and applications of social networks can be extended to a wide spectrum disciplines, consisting of biology,

sociology, engineering, health, business and informatics. Emerging cyber space human communications through interactions on facebook, twitter and blog spaces, have added new dimensions, where dynamic information exchange and related text analytical methods have become prominent components in social network analytical frameworks. Within the scope of this chapter, the term social networking is applicable when the existing connections are dynamic, in the sense the network connectionsare used for exchangesand transactionssuch astransportation, information diffusion, disease transmissionsocial interactions.In the literature the term, social network is loosely defined to indicate static networks where there are no dynamic interactions among the actors. On the other hand dynamic networks are defined as those change over time or over geographical spaces (Kolaczyk, 2009). The analytical framework described in this chapter adopts the definition of social networks that do not change over time and geographical space. Scope of this chapter is to guide the reader through analytical frameworks that are common across disciplines. The chapter starts fromsimplesubject-to-subject data collection methods and then expands on to biological and health network data processing, organization and analyses. Albeit the focus is mainly on dynamic networks, applicable static network structures are also described in this chapter. The chapter ends with a description on methods of statistical analyses that enable meaningful inferences on samples of random network data. In keeping with the scope of this book, the attention is paid exclusively on health and biological networks.

Chapter 2 (Morrison, 2013). Complex networks are found in all parts of biology, but there are at least two distinct types of biological network. In the most common type the nodes and edges are empirically observed, and the network analysis involves summarizing the characteristics of the network. In the second type only the leaf nodes are observed, and the internal nodes and all of the edges must be inferred from information available about the leaf nodes. Perhaps the most widespread of this inferred type of network is the phylogenetic network, which illustrates the genealogical history connecting all of life. Evolution involves a series of unobservable historical events, each of which is unique, and we can neither make direct observations of them nor perform experiments to investigate them. This makes a phylogenetic study one of the hardest forms of data analysis known, as there is no mathematical algorithm for discovering unique historical accidents. This chapter summarizes the essential differences of this network type, and discusses the consequences of these differences. Due to the complexity of evolutionary history, two types of phylogenetic network have been developed, which have been actively used in parallel by biologists for 150 years: (1) rooted evolutionary networks, in which the internal nodes represent ancestors of the leaf nodes, and the directed edges represent historical pathways of transfer of genetic information between ancestors and their descendants; and (2) unrooted data-display networks, in which the internal nodes do not represent ancestors, and the undirected edges represent affinity (e.g. similarity) relationships among the leaf nodes. The latter type of network is the most commonly encountered in phylogenetics, because there is a wide range of available mathematical techniques that work well. They have been put to a number of uses by phylogeneticists, including exploratory data analysis, displaying similarity patterns, displaying data conflicts, summarizing analysis results, and testing phylogenetic hypotheses; and the author illustrates each of these with an empirical example. There are as yet few mathematical techniques available for evolutionary networks, and recent focus has therefore been on the development of practical and effective methods. There are, however, a wide range of methodological questions that need to be answered before this can happen; and the author raises a number of these here, along with a preliminary discussion of them. There are also issues related to the realism of the common mathematical constraints, the evolutionary units in a network, and the concept of a most recent common ancestor.

Chapter 3 (Zhang, 2013). The statistic network is a weighted and non-deterministic network. In the statistic network, a connection value (weight) represents connection strength and connection likelihood between two nodes and its absolute value falls in the interval (0, 1]. The connection value is expressed as a statistical

measure such as correlation coefficient, association coefficient, etc. Furthermore, all connections of the statistic network can be statistically tested for their validity. A connection is true if the connection value is statistically significant. If all connection values of a node are not statistically significant, it is an isolated node. An isolated node has not any connection to other nodes in the statistic network. Positive and negative connection values denote distinct connection types (positive or negative association or interaction). In the statistic network, two nodes with the greater connection value will show more similar trend in the change of their states. At any time we can obtain a sample network of the statistic network. A sample network is a non-weighted and deterministic network. The statistic network, in particular the plant association network that constructed from field sampling, is mostly an information network. Major conclusions have been drawn as follows: (1) in the plant association network, most connections are weak and positive interactions. The association network constructed from Spearman rank correlation has most connections and isolated taxa are fewer. From net linear correlation, linear correlation, to Spearman rank correlation, the practical number of connections and connectance in the constructed network increases. Network compactness also follows the trend. In addition, as the increase of network compactness and connectance, the portion and number of negative association declines dramatically. (2) In an association (interaction) network, only a few connections follow the linear relationship. Most connections follow the quasi-linear or non-linear relationships. (3) The association networks constructed from partial linear correlation and linear correlation measures are generally scale-free complex networks. The degree of these networks is power low distributed. (4) Isolated species (families, etc.) are likely important in the statistic network. They are the sink species for shaping new network after a community is seriously disturbed. (5) Beween-taxa connections at higher taxonomic level are generally weaker than that at lower taxonomic level.

Chapter 4 (Rager and Fry, 2013). Mounting evidence shows that the altered signaling of critical cellular pathways plays a major role in environmental toxicant exposure-induced disease. The current understanding of cellular perturbations caused by exposure to environmental toxicants at a systems biology level is continuing to grow. In an effort to summarize the literature relating systems-level responses to toxicants, in the present article the authors review critical studies that have evaluated six important toxicants: arsenic, benzene, cadmium, chromium, cigarette smoke, and formaldehyde. By integrating the data presented in the current review in a systems-level manner, the authors identify the "Environmental Toxicant Signalisome", a network containing pathways that are commonly responsive to varied environmental exposures. This chapter provides a novel overview of signaling pathways that are known to be modulated by environmental toxicants of relevance to human exposure and disease.

Chapter 5 (Zhang and Liu, 2013). In present study, an algorithm was developed to create real network with expected mean and variance of degree distribution. In this algorithm the normal distribution was used as the basic distribution. Given expected mean and variance and through the truncation of the negative interval $(-\infty, 0)$ of normal distribution, random distribution, exponential distribution and power law distribution can be approximated by normal distribution. It is a statistical simulation procedure in which a real network, with the least deviation of actual mean and variance to expected mean and variance of degree distribution, was created. The Java program was designed. It may produce adjacency matrix, connection details, and actual mean and variance of degree distribution.

Chapter 6 (Lo et al., 2013). Ecological networks link different ecosystem parts allowing the transfer of matter and energy. Among the ecosystem components, primary producers are vital for the rest of ecosystem components as they use solar energy to produce biomass that will be later processed by symbionts, parasites, herbivores, and their predators. In terrestrial ecosystems, plants are the dominant primary producers, with trees as the most important among them. Therefore, in a context of global change, it is necessary to understand how

changes in climate variables such as temperature and precipitation could affect the net primary production (NPP) of trees. In this chapter we introduce our research on how climate has affected the productivity of three conifer species in the Canadian Pacific Northwest. Data on annual tree ring growth was compared with predictions from a simple model of climate limitation on net primary production. The results showed that using a simple predictor of NPP based on temperature, precipitation and frost days, it is possible to capture a significant portion of annual variability in tree ring growth, although an appreciable variability remains unexplained. This research shows that simple ecological models of NPP in forest ecosystems could be a suitable first step to create more complex networks analyses for matter and energy fluxes in the ecosystem.

Chapter 7 (Wannige et al., 2013). Random nature of chemical reactions and low copy numbers of participating chemical species originate fluctuations in naturally open biological systems. These inevitable fluctuations drive these open biological systems even in the presence of perturbations to self-organised, dissipative structures far from thermodynamic equilibrium in the presence of inward and outward flows of material, energy and information. Far from equilibrium, biological systems exhibit much complex dynamical behaviour such as multi-stability, oscillations, chaos and fractals and this review focus on the important stochastic modelling issues and approaches relevant to modelling these complex systems with examples. For example, 2MA method provides a robust way to look at the evolution of first two moments and Keizer's theory provides a mechanistic, statistical framework for modelling fluctuations for large volume systems. Always analytical methods like Chemical Master Equation, Chemical Langevin Equation, Fokker-Plank equation provide more insights into system behaviour as they consider the effect of randomness and the real particle behaviour. Nevertheless, these modelling methods or experimental methods are not yet developed enough to see a meososcopic system's dynamic behaviour in all parameter ranges in one picture. More efficient, and accurate, modelling and simulation methods which consider the real thermodynamic and mechanistic behaviour of systems are necessarily needed for better understanding of dynamics in meososcopic complex bio-systems.

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