BioSystems 114 (2013) 125–148

Contents lists available at ScienceDirect

BioSystems

journal homepage: www.elsevier.com/locate/biosystems

Theory of interface: Category theory, directed networks and evolution of biological networks

Taichi Haruna*

Graduate School of Science, Kobe University, 1-1 Rokkodaicho, Nada, Kobe 657-8501, Japan

ARTICLE INFO

Article history:
Received 27 June 2013
Received in revised form 9 August 2013
Accepted 15 August 2013

Keywords:
Gene regulation network
Neuronal network
Ecological network
Category theory

ABSTRACT

Biological networks have two modes. The first mode is static: a network is a passage on which something flows. The second mode is dynamic: a network is a pattern constructed by gluing functions of entities constituting the network. In this paper, first we discuss that these two modes can be associated with the category theoretic duality (adjunction) and derive a natural network structure (a path notion) for each mode by appealing to the category theoretic universality. The path notion corresponding to the static mode is just the usual directed path. The path notion for the dynamic mode is called lateral path which is the alternating path considered on the set of arcs. Their general functionalities in a network are transport and coherence, respectively. Second, we introduce a betweenness centrality of arcs for each mode and see how the two modes are embedded in various real biological network data. We find that there is a trade-off relationship between the two centralities: if the value of one is large then the value of the other is small. This can be seen as a kind of division of labor in a network into transport on the network and coherence of the network. Finally, we propose an optimization model of networks based on a quality function involving intensities of the two modes in order to see how networks with the above trade-off relationship can emerge through evolution. We show that the trade-off relationship can be observed in the evolved networks only when the dynamic mode is dominant in the quality function by numerical simulations. We also show that the evolved networks have features qualitatively similar to real biological networks by standard complex network analysis.

1. Introduction

In this decade, large interaction network data on biological, social and technological systems have become available. Science of complex networks has attempted to reveal structures and functions underlying these network data by proposing various mathematical indices and models (Albert and Barabási, 2002; Newman, 2003; Boccaletti et al., 2006). For example, the notions of small-world property, scale-free property and modular organization have become important tools to understand complex systems. On the other hand, we are aware of the criticism for purely graph-theoretic analysis forgetting meanings of networks (Arita, 2004). However, it makes mathematical analysis difficult if we stick to a meaning of each individual network too much. We might need a mathematical language that makes discussion on meaning of networks in a large sense possible. This paper is an attempt to discuss a comprehensive meaning of nodes and arcs in directed biological networks by appealing to category theory (MacLane, 1998).

Applications of category theory to biology originates from papers by R. Rosen published in the late 1950s (Rosen, 1958a,b). In the beginning, Rosen proposed a model of the maintenance mechanism of metabolic networks in terms of category theory. However, it seems that the viewpoint of 'network' became implicit as his theory of the metabolism-repair system developed. There are several other attempts to describe functions of biological systems by category theory (for example, Ehresmann and Vanbremeersch, 1987; Wolkenhauer and Hofmeyr, 2007). Since these studies propose highly abstract models of biological systems, it is not so clear how they can be applied to real world data. In this paper, we theoretically extend the research direction which we have sought in recent years (Haruna and Gunji, 2007, 2009; Haruna, 2008, 2010, 2011) and try to make a bridge to real world data analysis.

Our starting point is two modes of biological networks. One is static and the other is dynamic. In the static mode, a network is a passage on which something flows. In the dynamic mode, a network is a pattern constructed by gluing functions of entities constituting the network. For example, let us consider a neuronal network: nodes are neurons and arcs are synaptic connections between neurons. In the static mode, the neuronal network is a passage on which electric or chemical signals flow. On the other hand, in the dynamic mode, each node (a neuron) is an information processing entity

* Tel.: +81 78 803 5739.
E-mail address: tharuna@penguin.kobe-u.ac.jp

0303-2647/$ – see front matter © 2013 Elsevier Ireland Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biosystems.2013.08.002

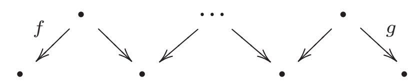
that receives signals from other nodes, modifies them and sends its response signals to other nodes. Similar pictures can hold for other biological networks such as ecological flow networks and gene regulation networks. Note that our dynamic mode does not consider change along the time parameter directly. Hence, it is different from both dynamics on networks such as percolation (Dorogovtsev et al., 2008), synchronization (Arenas et al., 2008) and games (Szabó and Fáth, 2007) and dynamic structural change in network structure as in temporal networks (Holme and Saramäki, 2012), although there may be conceptual links with them.

How can we extract information about the two mode from a given directed networks? In this paper, we argue that there is a natural pair of network transformations capturing features of the two modes. One can obtain information on the static mode by applying one network transformation to the given network and that on the dynamic mode by applying the other. For each network transformation, a natural network path notion is associated. For the static mode, it is simple and intuitive. If we assume that something flows along the direction of arcs, then the notion of directed path may be a natural network structure corresponding to the static mode. It arises from the network transformation transforming the given network to its line graph as shown below. For the dynamic mode, the corresponding network transformation and the path notion are derived via the category theoretic universality with respect to the idea that functions of entities constituting the network are glued on the interface among them. Once the network transformation for the dynamic mode is derived, that for the static mode is obtained as the unique dual transformation for it. Thus, the dynamic mode is primary in terms of the category theoretic universality.

Before closing this section, we sketch the story without using category theoretic terminology. The directed path corresponding to the static mode is generated by the network transformation R [1] defined below which sends arcs to nodes in the following sense: let $G=(A, N, \partial_0, \partial_1)$ be a directed network, where A is the set of arcs, N is the set of nodes and ∂_0, ∂_1 are maps from A to N sending each arc to its source or target, respectively. A directed network $R(G) = (A^*, N^*, \partial_0^*, \partial_1^*)$ is defined by putting $A^* = \{(f, g) \in A \times A | \partial_1(f) = \partial_0(g)\}$, $N^* = A$ and $\partial_0^*(f, g) = f$, $\partial_1^*(f, g) = g$ for $(f, g) \in A^*$. The set of arcs for $R(G)$ is the set of directed paths of length 2 in G. If we apply R to G twice, then we obtain the set of directed paths of length 3 in G as the set of arcs for $R^2(G)$. In general, the set of arcs for $R^n(G)$ is the set of directed paths of length $n+1$ in G for any $n \geq 0$.

For the network transformation R, we have the dual network transformation L (in category theoretic terminology, both R and L can be extended to endofunctors on the category of directed networks and L is the left adjoint functor to R). The network transformation L sends each node to an arc: for any directed network $G=(A, N, \partial_0, \partial_1)$, $L(G)=(A_*, N_*, \partial_{0*}, \partial_{1*})$ is defined by putting $A_* = N$, $N_* = N \times \{0, 1\}/\sim$ and $\partial_{0*}(x) = [(x, 0)]$, $\partial_{1*}(x) = [(x, 1)]$ for $x \in A_*$. Here, $\sim$ is the equivalence relation on the set $N \times \{0, 1\}$ generated by the relation r defined by $(x, 1)r(y, 0) :\Leftrightarrow$ there exists $f \in A$ such that $\partial_0(f) = x$ and $\partial_1(f) = y$. $[(x, i)]$ is the equivalence class containing (x, i). As we will discuss in Section 2, the network transformation L can be associated with the dynamic mode. From this, we can derive a path notion called lateral path that can be seen as the one dual to the directed path.

Let us consider the meaning of the network transformation L. When we apply L to a directed network G, each node is mapped to an arc. We regard this arc as representing *function* of the node, namely, the arc in $L(G)$ to which a node in G is mapped is thought of representing a process occurring on the node. On the other hand, we can regard each arc f in G as being sent to the node $[(\partial_0(f), 1)] (= [(\partial_1(f), 0)])$ connecting two arcs $\partial_0(f)$ and $\partial_1(f)$ in $L(G)$. Namely, *interaction is interface between functions*. This idea is materialized as a mathematical entity by the map $\varphi : A \to N_*$ defined by $f \mapsto [(\partial_0(f), 1)]$. For arcs f, g in G, a necessary and sufficient condition for the equality $\varphi(f) = \varphi(g)$ is the existence of an alternating sequence of arcs in G connecting f and g such as



Note that there are $2 \times 2 = 4$ possibilities for the situation at the two ends of the sequence. One of them is drawn above. We call such an alternating sequence of arcs **lateral path**. [2] Since the lateral path is associated with gluing of functions, we introduce the term *coherence* for its general functionality. On the other hand, the functionality of the directed path is considered as *transport* on a network here.

We claim that *the notion of lateral path is a natural network structure associated with the dynamic mode*. This claim is precisely formulated and proved in Section 2. In this rough sketch, it may be enough to give the following explanation: in the network transformation L, function of a node is represented by a single arc. However, we can represent function by a more complicated graph. It does not even need to be a graph. We can show that the representation of function corresponding to L occupies a special position among *all* representations of function of a node (in the language of category theory, it satisfies a certain universality): any representation of function gives rise to a map on the set of arcs that materializes the idea "interaction as interface between functions". This map in turn induces an equivalence relation on the set of arcs by its fibers. The claim is that the equivalence relation for the above map φ induced by L gives the finest partition of the set of arcs among all such equivalence relations.

This paper is organized as follows. In Section 2, we describe a mathematically precise formulation of the story sketched above. In Section 3, we introduce betweenness centralities of arcs for the static and dynamic modes based on directed path and lateral path, respectively. We see how these two modes are embedded in various real biological network data. As a result, we find that there is a trade-off relationship between the two centralities: if the value of one is large then the value of the other is small. In Section 4, we propose an optimization model of networks based on a quality function involving intensities of the static and dynamic modes. By numerical simulation, we see how networks with the above trade-off relationship can emerge. We show that the trade-off relationship emerges after the evolution only when the dynamic mode is dominant in the quality function. We also show that the evolved networks have features qualitatively similar to real biological networks by standard complex network analysis. In Section 5, we give conclusions and indicate some future directions. In Appendix, we present a generalization of the theory for directed networks described in Section 2. The aim of Appendix is twofold. One is to extend the theory in Section 2 to more general data structures. The other is to understand what features of directed networks are relevant to the main results in Section 2. We show that *self-duality* and *acyclicity* possessed by the type category for the category of directed networks are enough to reproduce the main results in Section 2 in more generalized situation.

[1] For a directed network G, $R(G)$ is so-called **line graph** of G. We use the two terms *network* and *graph* as synonymous words.

[2] Similar notion called **alternating walk** is considered in Crofts et al. (2010). However, it is defined on the set of nodes. In Crofts et al. (2010), it is used as an auxiliary means to obtain a bipartition of directed networks. On the other hand, lateral path in this paper is a central stuff associated with the dynamic mode of biological networks.