

## Self-Configuration of Dynamical Networks Based on an Information Theoretic Criterion

Jian-Qin Liu

National Institute of Information and Communications Technology (NICT),  
Kobe Advanced ICT Research Center (KARC), Biological ICT Group,  
588-2, Iwaoka, Iwaoka-cho, Nishi-ku, Kobe, Hyogo, 651-2492 Japan

### 情報理論基準に基づくダイナミクス・ネットワークの自己構造化

劉 健勤

独立行政法人 情報通信研究機構 未来 ICT 研究センター バイオ ICT グループ  
〒651-2492 兵庫県神戸市西区岩岡町岩岡 588-2

**Abstract** A self-configuration algorithm for dynamical networks, in which a criterion based on mutual information is used for node generation, is proposed in terms of mathematics.

**概要** 数学の手法によるダイナミクス・ネットワークのための自己構造化を提案する。ここで、相互情報量の基準に基づいてノードを生成する。

#### 1. Introduction

The dynamics features and the network structure are tightly connected in dynamical networks, which include the aspects of nonlinear dynamics and graph theory. The dynamics features of the dynamical networks help us to understand their behavior. The methods in graph theory are helpful for us to analyze the network structure of dynamical networks.

In this paper, the algorithmic study on dynamical networks is presented in terms of mathematics. As an example of dynamical networks, the inspiration from cellular signaling pathway networks is briefly discussed, from which new ideas are expected to be emerged to help us to explore the information processing mechanism for future communication networks.

#### 2. Self-Configuration of Dynamical Networks

The self-configuration of dynamical networks is an important way to adaptively sustain the function of dynamical networks in an un-expected environment. It is pointed

out in [1] that "... the aspect of *self-configuration* is crucial – the network is expected to work without manual management or configuration". The self-configuration method have been applied in sensor networks [2,3]. Here the concept of self-configuration refers to the process that change the network structure, that is, changing the nodes and links of a network (vertexes and edges of a graph that corresponds to the network) in a dynamical network according to a criterion (e.g., generating new nodes from existing nodes in a dynamical network).

In a dynamical network, the characteristics of generated nodes describe the basic behavior of operations on the dynamical network when the dynamical network is constructed or reconstructed by certain rules. The dynamical mechanism for cellular signaling process is often described by the Michaelis-Menten equation<sup>1</sup>. Based on the signaling processes calculated by the

<sup>1</sup> [http://en.wikipedia.org/wiki/Michaelis-Menten\\_kinetics](http://en.wikipedia.org/wiki/Michaelis-Menten_kinetics)

Michaelis-Menten equation, the dynamical feature of the input and output signals of a node is studied for node generation in a self-configuration algorithm.

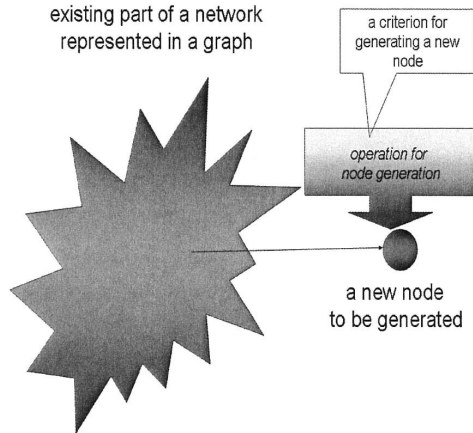


Figure 1 Schematic description of node generation

Based on the behavior of the nonlinear dynamics of the nodes in dynamical networks, the method for node generation can be studied (Cf. Fig.1). The condition for node generation is summarized as follows:

From node  $x$  in the graph that corresponds to the network, within the neighborhood of node  $x$ , the node set  $\{y\}$  will be generated and will be selected.

Node  $y_{selected}$  will be generated according to the criterion

$$\max I(x; y),$$

where  $I(x; y)$  refers to the mutual information in information theory.

Within the neighborhood, the set of nodes is generated and the quantity (measure) of mutual information from  $x$  to each node in the neighborhood is calculated. The criterion based on mutual information in information theory provides us the quantity of the

information flow in the signaling process. The steps of node generation are iteratively carried out until a constraint is satisfied.

### The Self-configuration Algorithm

The self-configuration algorithm for construction of a network based on the node generation mode presented is given in mathematics as follows:

- Step 0:  $i=0$ ;  
 Step 1: *node* ( $i$ ) is generated;  
 The concentration of *node* ( $i$ ) is set as a random value by the Monte Carlo method.  
 Step 2:  
 for ( $j=0$  to *the-threshold-for-j*,  $j++$ )  
 {  
 for ( $k=0$  to *the-maximum-number-of-sample*,  $k++$ )  
 {  
 (2.1): to set *node* ( $i$ ) as the enzyme (*enzyme0* in the Michaelis-Menten equation), which is regarded as the input to the pathway in concept;  
 (2.2): to encode *node* ( $i$ ) by a binary code indexed by  $k$  denoted as  $X(k)$ ;  
 (2.3): to generate *node* ( $j$ );  
 (2.4): to set the parameters of the Michaelis-Menten equation  $\{k_1, k_2, k_3\}$  and *substrate*, where  $k_m$  is calculated;  
 (2.5): to calculate the concentration of *node* ( $j$ ) by Michaelis-Menten equation;  
 (2.6): to encode *node* ( $j$ ) by a binary code indexed by  $k$  denoted as  $Y(k)$ , which is regarded as the output of the pathway in concept;  
 }  
 (2.7): to calculate *mutual information*  $I(\text{node}(i), \text{node}(j))$ ;  
 }  
 (2.8): *selected-node-number*  $\leq$  *the value j* with the *max I(node(i), node(j))*;  
 Step 3:  $i=j$ ;  
 Step 4:  $i$ =*the-new-value-of-i*;  
 $j$ =*the-new-value-of-j*;  
 Step 5:  
 IF  $i <$  *the-maximum-step-allowed*  
 THEN goto step 2;  
 ELSE goto step 6.  
 Step 6: end.

Here let us define the notations that

$$X = \{X(k)\}$$

and

$$Y = \{Y(k)\}.$$

Two ways described by pseudo-language are proposed in terms of mathematics. In the above-mentioned algorithm, feedback is not embedded. The feedback  $z$  is defined as

$$z(k) = \delta Y(k),$$

where  $\delta$  refers to the coefficient for the feedback and its values show a positive or negative feedback.

If the operation

$$X(k+1) = X(k) - z(k),$$

where  $X(k)$  and  $X(k+1)$  are encoded as a binary code  $X(k)$ ,

is inserted into (2.6), the algorithm will become a feedback-embedded dynamical networking algorithm.

On the calculation of the biochemical reaction processes, not only steady states but also non-steady states need to be taken into consideration. The related information processing mechanism can be formulated in terms of certain quantitative measurement for the biochemical signals.

### 3 Discussion

#### 3.1 Communication Capacity of Cellular Signaling Processes

The communication capacity<sup>2</sup> can be

<sup>2</sup> Jian-Qin Liu, On Communication Capacity of Cellular Signal Transduction Networks, Oral presentation at 第11回シンポジウム 代数、言語と計算 (Algebra, Languages and Computation, ALC), Feb.23, 2008, Kyoto Sangyo University, Kyoto, Japan.

calculated in terms of coding and information theory. The input and output of signaling pathway is coded into binary code by setting a threshold. The time series of the input and output are calculated by the Michaelis-Menten equation so that the probability in the formula of the definition of the mutual information is calculated. This is useful for quantitative description of the cellular communication processes based on signaling pathway networks.

#### 3.2 Inspiration from Cellular Signaling Pathway Networks

From the biochemistry concepts in cellular pathway networks [4,5], the hints can be found from the following major aspects:

(1) The robustness of cellular pathway networks:

The robustness [6] is also an important goal for new generation networks and future communications. Here the concept of robustness refers to the ability and the mechanism of a network that can adaptively adjust itself (parameter and/or structure) to sustain the certain states (e.g., the reachability of stable steady states of the pathway network reported in [7]. The nonlinear features of the signaling mechanism (input/output relation) of the pathway networks can be calculated by using (based on) the Hill equation/coefficient [7] and the Michaelis-Menten equation.

(2) The topological structure of cellular pathway networks:

The data structure of graph is proper to describe the topological structure of networks. In cellular pathway network, the pathways are formulated in terms of graph theory. The nodes correspond to the signaling molecules. The related links among the nodes correspond to the logical relation of pathways. In order to describe the dynamical characteristics of dynamical networks, the graph rewriting operators can be introduced. The operators of graph rewriting may include the ones for adding

new edge, deleting edges, adding vertexes, deleting vertexes and others (if possible). These operators can be designed according to the conditions that describe the dynamics aspect (of the features) of the dynamical networks.

(3) The metaphor from cellular signaling and networks:

The concentration implies the quantity of information flow in networks. The enzyme activation for ultrasensitivity implies the adaptive control of the characteristics of the information processing units of networks. The informatics or information- theoretical measurement of the networks shows certain kinds of objective-function-like measure for networking. The spatial and temporal dynamics of networks is expected to be compared with the logical description of the communication processes corresponding to the related networks.

### 3.3. Perspectives on Future Networks

Oriented to 4G communications and cognitive networks, it is expected to develop biologically-inspired [8] networking algorithms to provide the self-aware ability to (dynamical) networks, which can be studied in terms of autonomic computing as well.

On molecular sensor networks for future communications, one of the challenging topics could be olfactory information processing for future communications by nanobioICT<sup>3</sup>.

## 4. Conclusion

A self-configuration algorithm is proposed in mathematics, from which the experiment on its parallel implementation is expected.

---

<sup>3</sup> Jian-Qin Liu and Shinro Mashiko, Nanobiotechnology for mechatronics: biomolecular information processing and moleware control for nanobio-mechatronics, *A Tutorial at 2007 IEEE/ASME International Conference on Advanced Intelligent Mechatronics (September 4, 2007, ETH Zürich, Switzerland)*.

## References

- [1] Holger Karl, Andreas Willig, *Protocols and Architectures for Wireless Sensor Networks*, Chichester: John Wiley & Sons, Ltd, 2007, p.10.
- [2] Michael Breza, Richard Anthony, Julie McCann, Scalable and Efficient Sensor Network Self-Configuration in BioANS, First International Conference on Self-Adaptive and Self-Organizing Systems, 2007 (SASO '07), 9-11 July 2007, pp. 351-354.
- [3] Alberto Cerpa, Deborah Estrin, ASCENT: Adaptive Self-Configuring sEnsor Networks Topologies, *IEEE Transactions on Mobile Computing*, Vol.3, No.3, July-September 2004, pp. 272- 285.
- [4] B. D. Gomperts, IJ. M. Kramer, P. E. R. Tatham, *Signal Transduction*, San Diego: Academic Press, 2002.
- [5] Jian-Qin Liu and Katsunori Shimohara, *Biomolecular Computation for Bionanotechnology*, Boston/London: Artech House, 2007.
- [6] Behrooz Parhami and Mikhail A. Rakov, Performance, Algorithmic, and Robustness Attributes of Perfect Difference Networks, *IEEE Transactions on Parallel and Distributed Systems*, Vol. 16, No. 8, August 2005, pp. 725-736.
- [7] James E. Ferrell Jr. and Eric M. Machleder, The Biochemical Basis of an All-to-None Cell Fate Switch in *Xenopus* Oocytes, *Science*, 280, 1998, 895-898.
- [8] Kenji Leibnitz, Naoki Wakamiya, Masayuki Murata, Biologically-Inspired Self-Adaptive Multi-Path Routing in Overlay Networks, *Communications of the ACM*, vol. 49, no.3, March 2006, pp. 62-67.