Chapter IX
Measuring Information Propagation and Processing in Biological Systems

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ABSTRACT

In this chapter the authors study the propagation and processing of information in dynamical systems. Various information management systems can be represented as dynamical systems of interconnected information processing units. Here they focus mostly on genetic regulatory networks that are information processing systems that process and propagate information stored in genome. Boolean networks are used as a dynamical model of regulation, and different ways of parameterizing the dynamical behavior are studied. What are called critical networks are in particular under study, since they have been hypothesized as being the most effective under evolutionary pressure. Critical networks are also present in man-made systems, such as the Internet, and provide a candidate application area for findings on the theory of dynamical networks in this chapter. The authors present approaches of annealed approximation and find that avalanche size distribution data supports criticality of regulatory networks. Based on Shannon information, they then find that a mutual information measure quantifying the coordination of pairwise element activity is maximized at criticality. An approach of algorithmic complexity, the normalized compression distance (NCD), is shown to be applicable to both dynamical and topological features of regulatory networks. NCD can also be seen to enable further utilization of measurement data to estimate information propagation and processing in biological networks.

INTRODUCTION

Information propagation and flow are key aspects in understanding how systems interact and function. Various information management systems can be represented as dynamical systems where information processing units (nodes) are connected with links (edges) that represent information transfer. Here we present recent results that provide insight into the general properties of this kind of systems. We focus our discussion on the context of important class of systems, namely the **genetic regulatory networks** that can, at very high level, be modeled as **Boolean network**s (Kauffman, 1993). **Genetic regulatory networks** process and propagate digital information stored in genome and orchestrate a specific response to various external stimuli (inputs) (Hood & Galas, 2003). What makes this class of systems the most interesting is that regulatory networks have evolved over millions of years. Thus, it can be argued that through natural selection and self organization only the most robust and evolvable network structures remain today. Understanding the information processing principles that are present in **genetic regulatory networks** can help us to engineer man made information processing systems that are extremely robust and take advantage of the insights that biological systems have gained over the years of evolution.

The dynamical behavior of large, complex networks of interacting elements is generally difficult to understand in detail. The existence of multiple influences on each element can give rise to exceedingly complicated dynamics even in deterministic systems. A paradigmatic case is the network of genes within a cell, where the interactions correspond to transcriptional and post-transcriptional regulatory mechanisms. The expression of a single gene may be subject to regulation by itself and up to 20 proteins expressed by other genes, and the network of such interactions has a complicated structure, including positive and negative feedback loops and nontrivial combinatorial logic.

The **genetic regulatory networks** may be compared with e.g. Internet traffic, which has been seen to exhibit critical dynamics (Fukuda et al., 2000; Valverde & Sole, 2002). This suggests that Internet as a self-organizing system may optimize information transfer. Internet provides an example of a man-made system of information management and processing, and thus, any insights into information processing in critical networks may have consequences in terms of information management as well. A large part of what we present in this book chapter may be seen as general in the sense that many of the precise characteristics of the network can be abstracted away, and the principles of dynamical behavior still hold.

The structure of this chapter is as follows. First, we present some background of information in **genetic regulatory networks**, our main object of study. In addition, the **Boolean network** model utilized as a simple approximation of **genetic networks** is presented. Our main aim in this chapter is to uncover general features of information processing in cells, and for this purpose, different measures related to global dynamics of the system are suggested. Each of the measures is able to capture an aspect of dynamical information processing in the cells. **Criticality** of cellular dynamics is taken to be the main focus of attention and each of the measures utilized is, in turn, shown to shed some light on this question.

After the background information, we begin by outlining the principles of basic **annealed approximation**. This is a technique that can be used as a first-order approximation of global dynamics. Its main drawback is that the analysis cannot take into account topological details of the networks under study. The findings presented utilizing branching process models give some support to the hypothesis that cells might have critical dynamics. Next, we discuss an application of Shannon's information theory to **genetic regulatory network** models. **Pairwise mutual information** between states of network nodes is utilized as a dynamical measure of coordination between nodes. It is observed that critical networks

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