

Dynamics of Complex Interconnected Systems: Networks and Bioprocesses

Edited by

Arne T. Skjeltorp and
Alexander V. Belushkin

NATO Science Series

Dynamics of Complex Interconnected Systems: Networks and Bioprocesses

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PREFACE

This volume comprises the proceedings of a NATO Advanced Study Institute (ASI) held at Geilo, Norway, 11-21 April 2005, the eighteenth ASI in a series held every two years since 1971. The objective of this ASI was to identify and discuss areas where synergism between modern physics and biology may be most fruitfully applied to the study of bioprocesses for molecular recognition, and of networks for converting molecular reactions into usable signals and appropriate responses.

Many fields of research are confronted with networks. Genetic and metabolic networks describe how proteins, substrates and genes interact in a cell; social networks quantify the interactions between people in the society; the Internet is a complex web of computers; ecological systems are best described as a web of species. In many cases, the interacting networks manifest so-called emergent properties that are not possessed by any of the individual components. This means that the detailed knowledge of the components is insufficient to describe the whole system. Recent work has indicated that networks in nature have so-called scale-free characteristics, and the associated dynamic network modelling shows unexpected results such as an amazing robustness against accidental failures, a property that is rooted in their inhomogeneous topology. Understanding these phenomena and turning them to use in chemical and biological threat detection and response will require exploring a wide range of network structures as well. Questions related to error and attack tolerance of complex networks and their robustness in particular, and the dynamics of networks in general also have to be addressed. Modelling the signal transduction networks in bioprocesses as in living cells is a challenging interdisciplinary research area. It is now realized that the many features of molecular interaction networks within a cell are shared to a large degree by the other complex systems mentioned above, such as the Internet, computer chips and society. Thus knowledge gained from the study of complex non-biological systems can be applied to the intricate braided relationships that govern cellular functions. Bio-inspired processes provide an attractive option for sensing chemical and biological (CB) agents because nature has solved many of the problems inherent to the sense-and-respond task. For example, many biological responses such as blood clotting, gene expression and the activation of enzymes require enormous amplification of signals carried by as few as a single molecule or ion. Adaptability to local environments, atomic level control of self-assembled structures, benign processing, combinatorial synthesis and complex computation are other features of

biological systems that are likely to prove useful in CB sensor development.

The starting point, and the underlying theme throughout the ASI, was a thorough discussion of general network theory. The next focus was on genetic networks and bioprocesses. Finally, focus was placed on the possible universality of network structures and how this knowledge can be combined to attack the urgent problem of rapid detection and diagnosis of CB agents.

The NATO ASI format in Geilo proved very efficient in getting researchers in different areas together and focus on the underlying theme that was common to all of them – that of networks and bioprocesses. In this manner a rapid communication was possible because a common vocabulary was developed during the ASI.

The scientific content of the school was timely and these proceedings should provide a useful definition of the current status. The Institute brought together many lecturers, students and active researchers in the field from a wide range of countries, both NATO and NATO Partner Countries. The lectures fulfilled the aim of the Study Institute in creating a learning environment and a forum for discussion on the topics stated above. They were supplemented by a few contributed seminars and a large number of poster presentations. These seminars and posters were collected in extended abstract form and issued as an open report available at the Institute for Energy Technology, Kjeller, Norway (Report IFE/KR/E-2005/005, ISBN 82-7017-535-8).

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December 2005

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STRUCTURE AND COMMUNICATION IN COMPLEX NETWORKS

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1. Introduction

Networks is tool to describe systems composed of many different units which each typically interact with a few of the other units. Networks thus used to quantify complex systems from the intricate interactions of proteins inside a living cell, to ecosystems, social systems and computer networks. In most cases the network quantify communication channels in the system. Thus directly connected nodes communicates easy, while more distant nodes only obtain exchange information through a number of intermediate steps. In fact already in 1982 a detailed study of social networks within university departments revealed that mutual information of one member about another one was decaying exponentially with their distance, and increased linearly with number of common friends (degenerate paths). We will take this viewpoint and consider a Network as a description of who get direct information from who, and which parts that has to resort to second hand or even more inaccurate information: networks quantify the extent to which complex systems operate under the constraints of a limited information horizon.

In the text we will first review a few facts about real world networks, including broad degree distributions and degree correlations and some simple models for how such broad degree distributions may self organize. Secondly we introduce a few measures to characterize the topology of network: Correlation profiles, network motifs, topological hierarchy, search information and a measure for order in topology of the networks. Thirdly we discuss self organization of networks under various degrees of limited information. Finally we discuss biological networks, with focuss on basic physics of gene regulation.

2. Basic Network Concepts

In Figure 1-4 we define a few basic quantities in graph theory. For a pair of nodes one define their distance as the length of the shortest path between them. For a connected graph we can define its diameter as the maximum distance between pairs. Examples of graphs include lattices in any dimension.

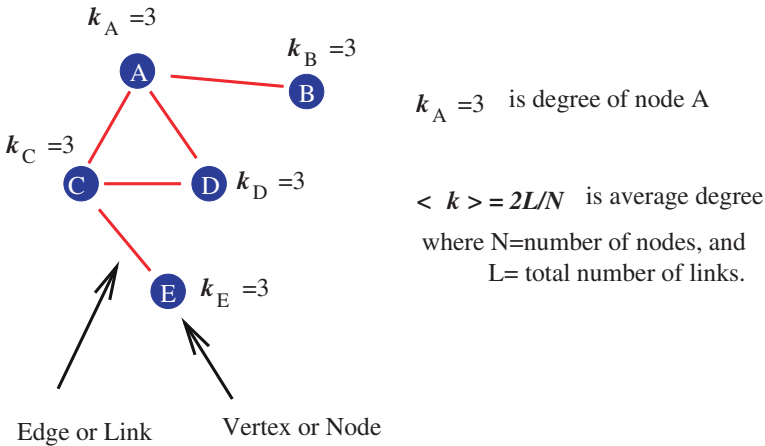


Figure 1. A graph, with nodes and edges.

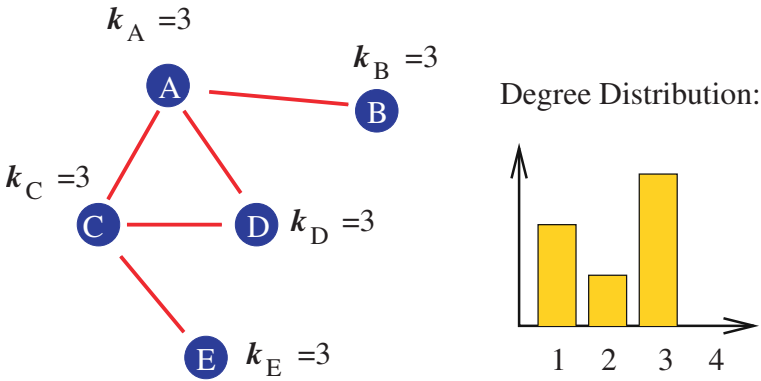


Figure 2. Degree distribution, here for undirected graph.

We now want to consider the simplest possible model for a random graph, the Erdos-Reynei Graph. In this type of graph one have N nodes, each pair connected to each other with probability p . The average (expected number of

edges would be $L = p \cdot N(N - 1)/2$. The degree distribution (probability that a given node have k links to the remaining $N-1$ nodes) will be

$$P(k) = C_{N-1}^k p^k (1 - p)^{N-1-k} \quad (1)$$

where $C_{N-1}^k = (N - 1)! / (k!(N - 1 - k)!)$. For a random graph one gain the neighborhood of any node increases by factor $\langle k \rangle$ for each step out in the graph (for large graphs, as long as there is essentially zero probability to reach same nodes through two different paths). Thus the network is traversed when

$$\sum_{i=0}^{diam} \langle k \rangle^i \approx N \quad (2)$$

that is when $diam = \log(N)/\log(\langle k \rangle)$, i.e. the distance between any two points in a random graph grows very slowly with its overall size.

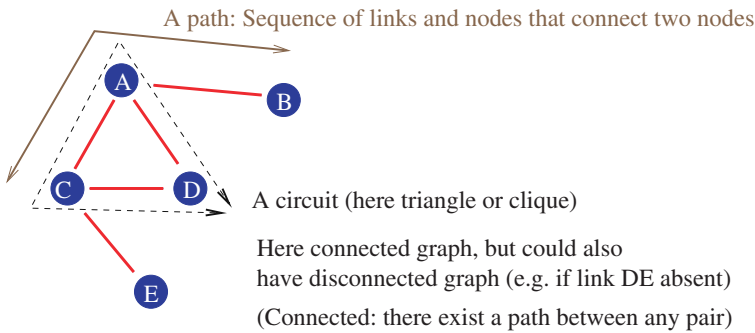


Figure 3. Path's in graphs.

Another quantity which often is used to characterize networks is their cliquishness. For each node this is defined as the fraction shown in Fig 4, meaning that a large cliquishness indicate large locality in the network everybody knows each other locally).

A network is defined as having small world property, when it is having a relatively large cliquishness, while still having a diameter of order $\log(N)/\log(k)$. Many networks are indeed found to have this interplay between global accessibility and local connectedness.

Finally we would like to stress that a network also have a unique matrix representation, A_{ij} where a link from node i to node j implies that $A_{ij} = 1$. A undirected network, even a symmetric matrix, $A_{ij} = A_{ji}$. The matrix representation opens for some simple manipulation where one for example can calculate the number of triangles in a network $= \text{trace} A^3 / 6$, where the factor $6 = 3 \cdot 2$ comes from going two ways around each triangle, and from starting the triangle a any of the three nodes.

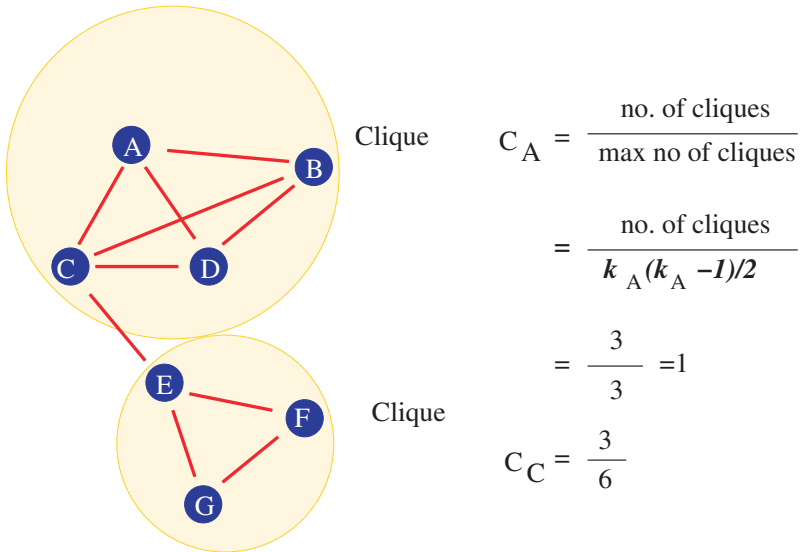


Figure 4. Cliquishness definition: the fraction of possible triangles that a node participate in, given its degree. If all its friends are friends, its cliquishness is 1.

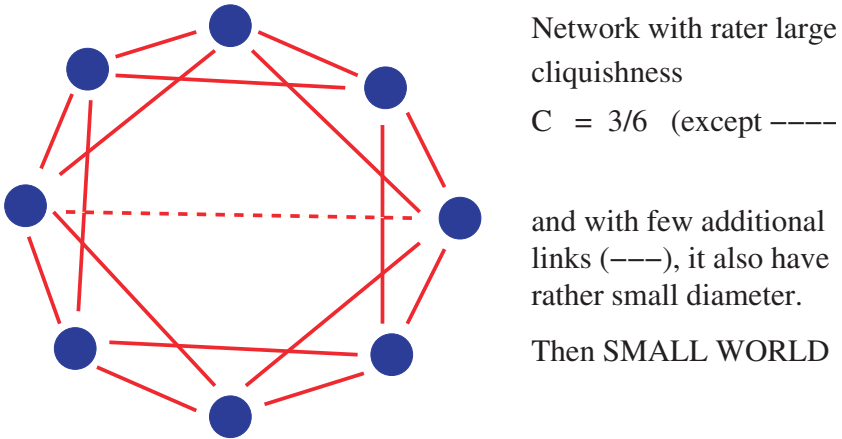
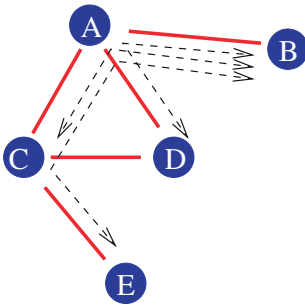


Figure 5. Small world network (Watts and Strogatz).

3. Real Networks

From the genetic blueprint in our DNA to the world-wide Internet, information and its dynamic counterpart communication sets the stage for further action. However, we live under the limited information horizon, in the sense that information is often imperfect and communication is always finite. Many complex systems are associated with information transfer. This includes neural networks with their synaptic rewiring, molecular networks



Betweenness:

The betweenness of a node is number of shortest paths that goes through the node

$$\beta_A = \text{no. path through A} = 3$$

similar definition of link betweenness

(Freeman, Sociometry 1977)

Figure 6. Betweenness (load) on a node, assuming that all transport goes through shortest paths.

evolved to modulate the protein activity in living cells, and social networks exemplified by the Internet. Below we show respectively the worldwide internet, a social network and some examples of molecular networks inside living cells. In all these cases the purpose of the network is to serve as a scaffold for information transfer.

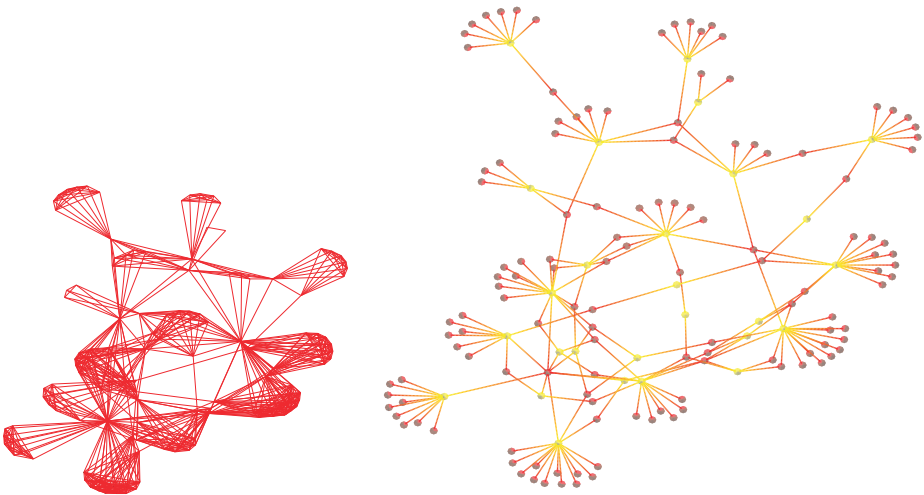


Figure 7. Directors in US: Left representation, connected by link if two nodes in same board. Right representation: Bipartite network representation consist of respective board nodes and member nodes, defining two distinct classes of nodes. In a bipartite graph there are only links from nodes in one class to a node in the other class. The shown network is a small sub-part of the full network of all CEO's in USA.

For many real world networks, the distribution of proteins with a given number of neighbors (connectivity) K may (very crudely) be approximated by a power law

$$N(K) \propto 1/K^\gamma \quad (3)$$

with exponent $\gamma \sim 2.5 \pm 0.5$ (Jeong et al. (2001)) for protein-protein binding networks, and exponent $\gamma \sim 1.5 \pm 0.5$ for “out-degree” distribution of transcription regulators. Notice that the distribution of the number of proteins a given protein regulate, the “out-degree”, differs from the much more narrow distribution of “in-degrees”. We would now like to discuss features and possible reasons for why life may have chosen to organize its signaling in this way.

One aspect of a wide distribution of connectivity, is the possible amplification of signals in the network. Consider a signal that enters a node, and assume that it is transmitted along all exit links (unspecific broadcasting). Thus it is amplified by a factor K_{out} . However, not all nodes has equal chance to amplify signals. The probability to enter a node is proportional to K_{in} . Thus one in average visit nodes with probability $\propto K_{in}$ and the weighted average amplification factor in a *directed* network (Newman et al. 2001):

$$\mathcal{A} = \frac{\langle K_{in} K_{out}(\text{given } K_{in}) \rangle}{\langle K_{in} \rangle} = \frac{\langle K_{in} K_{out} \rangle}{\langle K_{in} \rangle} \quad (4)$$

The first equality assumes that there is no correlations between degree of a node and the degree of its neighbors. The second equality assumes that there is no correlations between a given proteins “in” and “out” degree. For undirected random network the amplification would be:

$$\mathcal{A} = \frac{\langle K(K-1) \rangle}{\langle K \rangle} \quad (5)$$

If all nodes has close to the same connectivity we recover the simple result that when $\langle K \rangle = 2$ then $\mathcal{A} = 1$. Thus to have marginal transmission, one input signal in average should lead to one output signal through a new exit. When $\mathcal{A} > 1$ signals tends to be exponentially amplified, and thus most signals will influence signaling over the entire network. For broad connectivity distributions \mathcal{A} typically depend on the node with highest connectivity. To see this, assume that the number degree distribution is power law distributed (eq. 3). Then:

$$\mathcal{A} = \frac{\int_1^N \frac{K^2 dK}{K^\gamma}}{\int_1^N \frac{K dK}{K^\gamma}} - 1 \sim N^{3-\gamma} \quad (6)$$

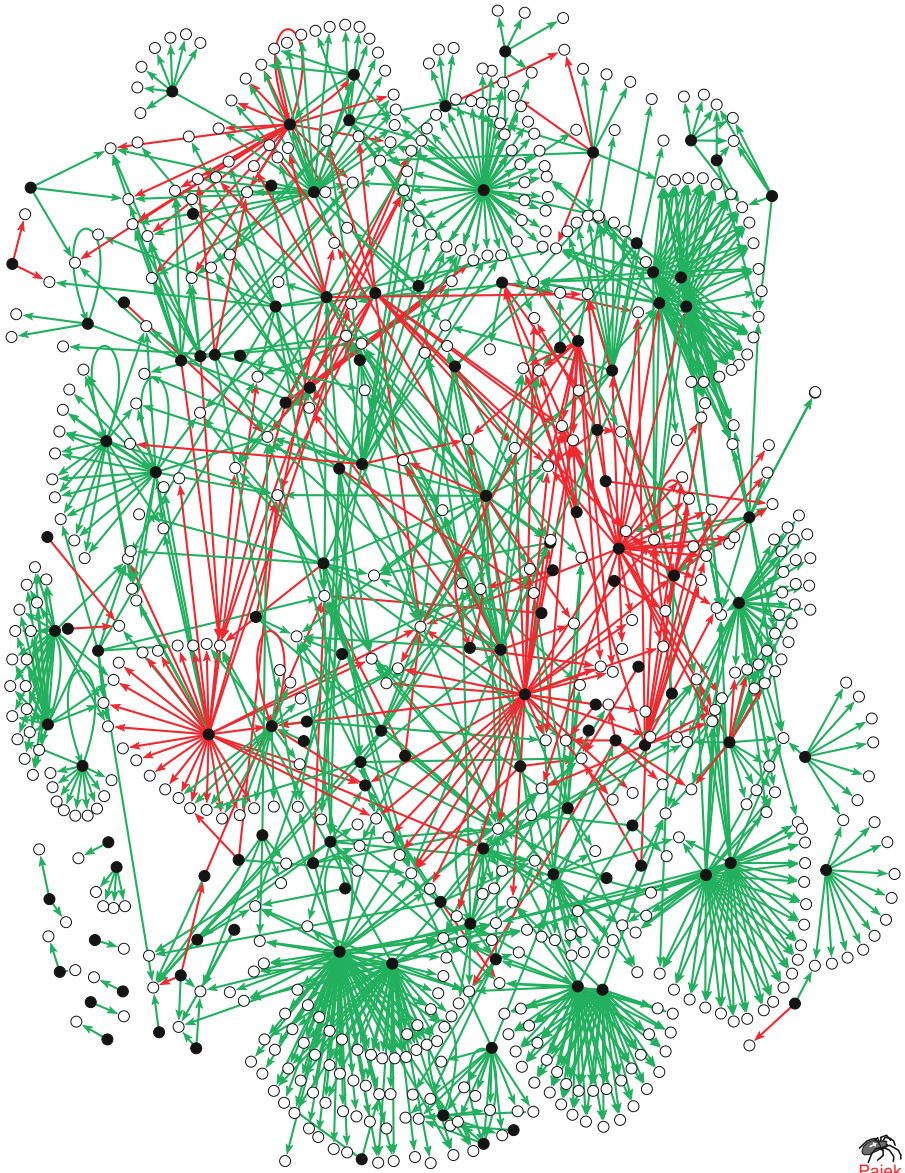


Figure 8. Presently known transcription regulations in Yeast (*Sacromyces Cerevisia*). Transcription regulation describes how one protein regulate the production of another protein. The network is directed, with both positive and negative regulations (see later for more detailed explanation).