

Complex Networks: Small-World, Scale-Free and Beyond

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Abstract

In the past few years, the discovery of small-world and scale-free properties of many natural and artificial complex networks has stimulated a great deal of interest in studying the underlying organizing principles of various complex networks, which has led to dramatic advances in this emerging and active field of research. The present article reviews some basic concepts, important progress, and significant results in the current studies of various complex networks, with emphasis on the relationship between the topology and the dynamics of such complex networks. Some fundamental properties and typical complex network models are described; and, as an example, epidemic dynamics are analyzed and discussed in some detail. Finally, the important issue of robustness versus fragility of dynamical synchronization in complex networks is introduced and discussed.

Index terms—complex network, small-world network, scale-free network, synchronization, robustness

Introduction

Complex networks are currently being studied across many fields of science [1-3]. Undoubtedly, many systems in nature can be described by models of complex networks, which are structures consisting of nodes or vertices connected by links or edges. Examples are numerous. The Internet is a network of routers or domains. The World Wide Web (WWW) is a network of websites (Fig. 1). The brain is a network of neurons. An organization is a network of people. The global economy is a network of national economies, which are themselves networks of markets; and markets are themselves networks of interacting producers and consumers. Food webs and metabolic pathways can all be represented by networks, as can the relationships among words in a language, topics in a conversation, and even strategies for solving a mathematical problem. Moreover, diseases are transmitted through social networks; and computer viruses occasionally spread through the Internet. Energy is distributed through transportation networks, both in living organisms, man-made infrastructures, and in many physical systems such as the power grids. Figures 2-4 are artistic drawings that help visualize the complexities of some typical real-world networks.

The ubiquity of complex networks in science and technology has naturally led to a set of common and important research problems concerning how the network structure facilitates and constrains the network dynamical behaviors, which have largely been neglected in the studies of traditional disciplines. For example, how do social networks mediate the transmission of a disease? How do cascading failures propagate throughout a large power transmission grid or a global financial network? What is the most efficient and robust architecture for a particular organization or an artifact under a changing and uncertain environment? Problems of this kind are confronting us everyday, problems which demand answers and solutions.

For over a century, modeling of physical as well as non-physical systems and processes has been performed under an implicit assumption that the interaction patterns among the individuals of the underlying system or process can be embedded onto a regular and perhaps universal structure such as a Euclidean lattice. In late 1950s, two mathematicians, Erdős and Rényi (ER), made

a breakthrough in the classical mathematical graph theory. They described a network with complex topology by a random graph [4]. Their work had laid a foundation of the random network theory, followed by intensive studies in the next 40 years and even today. Although intuition clearly indicates that many real-life complex networks are neither completely regular nor completely random, the ER random graph model was the only sensible and rigor-

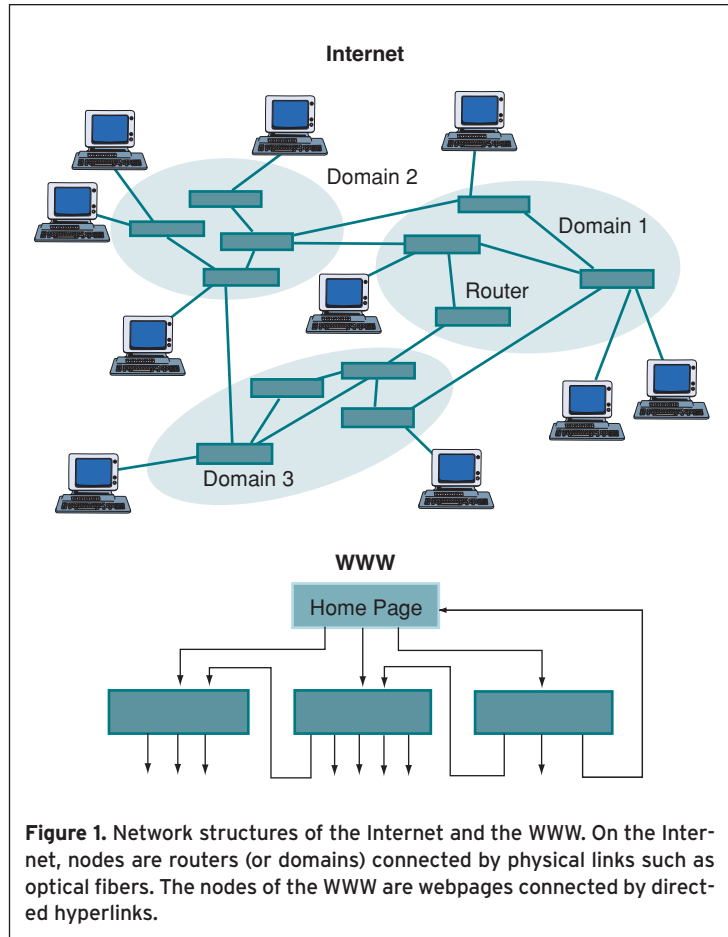


Figure 1. Network structures of the Internet and the WWW. On the Internet, nodes are routers (or domains) connected by physical links such as optical fibers. The nodes of the WWW are webpages connected by directed hyperlinks.

ous approach that dominated scientists' thinking about complex networks for nearly half of a century, due essentially to the absence of super-computational power and detailed topological information about very large-scale real-world networks.

In the past few years, the computerization of data acquisition and the availability of high computing power have led to the emergence of huge databases on various real networks of complex topology. The public access to the huge amount of real data has in turn stimulated great interest in trying to uncover the generic properties of different kinds of complex networks. In this endeavor, two

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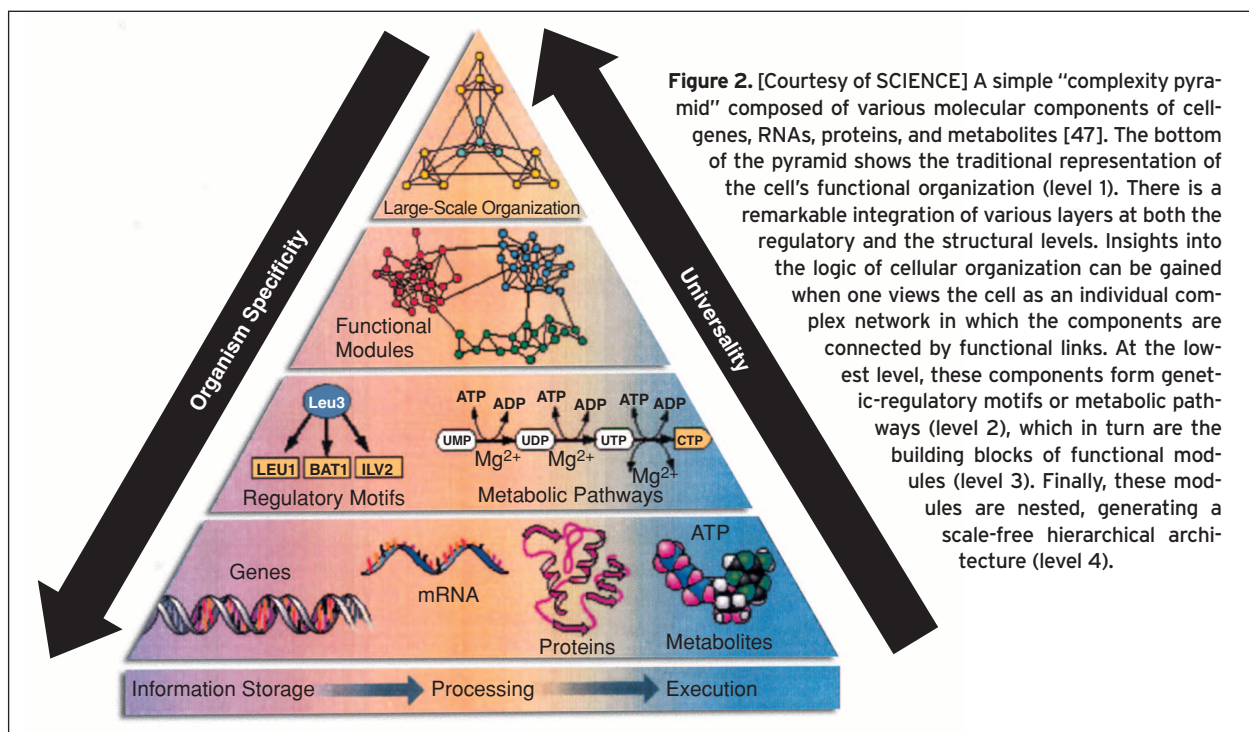


Figure 2. [Courtesy of SCIENCE] A simple “complexity pyramid” composed of various molecular components of cell—genes, RNAs, proteins, and metabolites [47]. The bottom of the pyramid shows the traditional representation of the cell’s functional organization (level 1). There is a remarkable integration of various layers at both the regulatory and the structural levels. Insights into the logic of cellular organization can be gained when one views the cell as an individual complex network in which the components are connected by functional links. At the lowest level, these components form genetic-regulatory motifs or metabolic pathways (level 2), which in turn are the building blocks of functional modules (level 3). Finally, these modules are nested, generating a scale-free hierarchical architecture (level 4).

significant recent discoveries are the small-world effect and the scale-free feature of most complex networks.

In 1998, in order to describe the transition from a regular lattice to a random graph, Watts and Strogatz (WS) introduced the concept of small-world network [5]. It is notable that the small-world phenomenon is indeed very common. An interesting experience is that, oftentimes, soon after meeting a stranger, one is surprised to find that they have a common friend in between; so they both cheer: “What a small world!” An even more interesting popular manifestation of the “small-world effect” is the so-called “six degrees of separation” principle, suggested by a social psychologist, Milgram, in the late 1960s [6]. Although this point remains controversial, the small-world pattern has been shown to be ubiquitous in many real networks. A prominent common feature of the ER random graph and the WS small-world model is that the connectivity distribution of a network peaks at an average value and decays exponentially. Such networks are called “exponential networks” or “homogeneous networks,” because each node has about the same number of link connections.

Another significant recent discovery in the field of complex networks is the observation that many large-scale complex networks are scale-free, that is, their connectivity distributions are in a power-law form that is independent of the network scale [7, 8]. Differing from an exponential network, a scale-free network is inhomogeneous in nature: most nodes have very few link connections and yet a few nodes have many connections.

The discovery of the small-world effect and scale-free

feature of complex networks has led to dramatic advances in the field of complex networks theory in the past few years. The main purpose of this article is to provide some introduction and insights into this emerging new discipline of complex networks, with emphasis on the relationship between the topology and dynamical behaviors of such complex networks.

Some Basic Concepts

Although many quantities and measures of complex networks have been proposed and investigated in the last decades, three spectacular concepts—the average path length, clustering coefficient, and degree distribution—play a key role in the recent study and development of complex networks theory. In fact, the original attempt of Watts and Strogatz in their work on small-world networks [5] was to construct a network model with small average path length as a random graph and relatively large clustering coefficient as a regular lattice, which evolved to become a new network model as it stands today. On the other hand, the discovery of scale-free networks was based on the observation that the degree distributions of many real networks have a power-law form, albeit power-law distributions have been investigated for a long time in physics for many other systems and processes. This section provides a brief review of these important concepts.

Average Path Length

In a network, the distance d_{ij} between two nodes, labeled i and j respectively, is defined as the number of edges

along the shortest path connecting them. The *diameter* D of a network, therefore, is defined to be the maximal distance among all distances between any pair of nodes in the network. The *average path length* L of the network, then, is defined as the mean distance between two nodes, averaged over all pairs of nodes. Here, L determines the effective “size” of a network, the most typical separation of one pair of nodes therein. In a friendship network, for instance, L is the average number of friends existing in the shortest chain connecting two persons in the network. It was an interesting discovery that the average path length of most real complex networks is relatively small, even in those cases where these kinds of networks have many fewer edges than a typical globally coupled network with a equal number of nodes. This smallness inferred the *small-world effect*, hence the name of small-world networks.

Clustering Coefficient

In your friendship network, it is quite possible that your friend’s friend is also your direct friend; or, to put it another way, two of your friends are quite possibly friends of each other. This property refers to the *clustering* of the network. More precisely, one can define a *clustering coefficient* C as the average fraction of pairs of neighbors of a node that are also neighbors of each other. Suppose that a node i in the network has k_i edges and they connect this node to k_i other nodes. These nodes are all neighbors of node i . Clearly, at most $k_i(k_i - 1)/2$ edges can exist among them, and this occurs when every neighbor of node i connected to every other neighbor of node i . The clustering coefficient C_i of node i is then defined as the ratio between the number E_i of edges that actually

exist among these k_i nodes and the total possible number $k_i(k_i - 1)/2$, namely, $C_i = 2E_i/(k_i(k_i - 1))$. The clustering coefficient C of the whole network is the average of C_i over all i . Clearly, $C \leq 1$; and $C = 1$ if and only if the network is

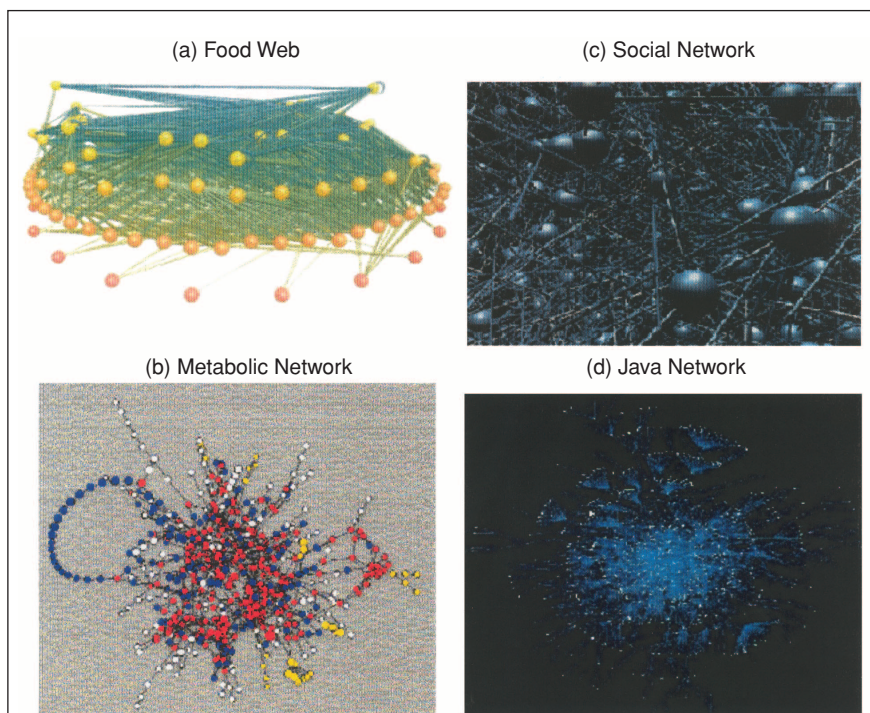


Figure 3. Wiring diagrams for several complex networks. (a) Food web of the Little Rock Lake shows “who eats whom” in the lake. The nodes are functionally distinct “trophic species”. (b) The metabolic network of the yeast cell is built up of nodes—the substrates that are connected to one another through links, which are the actual metabolic reactions. (c) A social network that visualizes the relationship among different groups of people in Canberra, Australia. (d) The software architecture for a large component of the Java Development Kit 1.2. The nodes represent different classes and a link is set if there is some relationship (use, inheritance, or composition) between two corresponding classes.

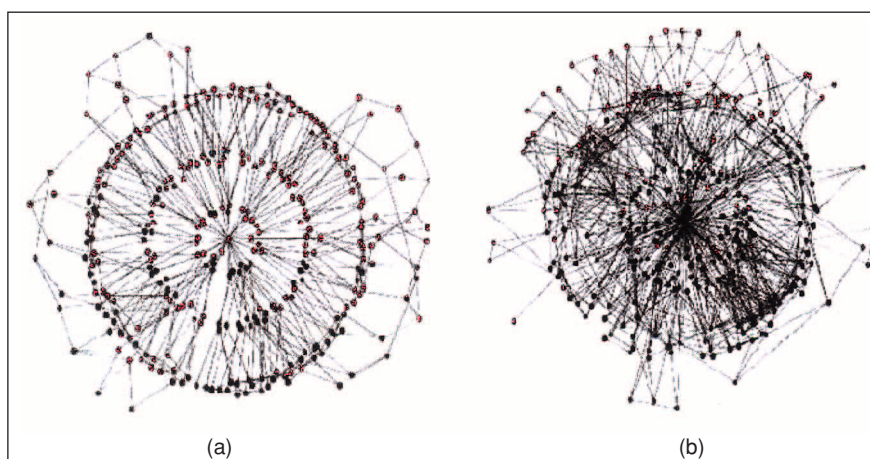


Figure 4. [Courtesy of Richard V. Sole] Wiring diagrams of a digital circuit (a), and an old television circuit (b). The dots correspond to components, and the lines, wiring. Concentric rings indicate a hierarchy due to the nested modular structure of the circuits.

Table 1.

Small-world pattern and scale-free property of several real networks. Each network has the number of nodes N , the clustering coefficient C , the average path length L and the degree exponent γ of the power-law degree distribution. The WWW and metabolic network are described by directed graphs.

Network	Size	Clustering coefficient	Average path length	Degree exponent
Internet, domain level [13]	32711	0.24	3.56	2.1
Internet, router level [13]	228298	0.03	9.51	2.1
WWW [14]	153127	0.11	3.1	$\gamma_{\text{in}} = 2.1 \quad \gamma_{\text{out}} = 2.45$
E-mail [15]	56969	0.03	4.95	1.81
Software [16]	1376	0.06	6.39	2.5
Electronic circuits [17]	329	0.34	3.17	2.5
Language [18]	460902	0.437	2.67	2.7
Movie actors [5, 7]	225226	0.79	3.65	2.3
Math. co-authorship [19]	70975	0.59	9.50	2.5
Food web [20, 21]	154	0.15	3.40	1.13
Metabolic system [22]	778	—	3.2	$\gamma_{\text{in}} = \gamma_{\text{out}} = 2.2$

is globally coupled, which means that every node in the network connects to every other node. In a completely random network consisting of N nodes, $C \sim 1/N$, which is very small as compared to most real networks. It has been found that most large-scale real networks have a tendency toward clustering, in the sense that their clustering coefficients are much greater than $O(1/N)$, although they are still significantly less than one (namely, far away from being globally connected). This, in turn, means that most real complex networks are not completely random. Therefore they should not be treated as completely random and fully coupled lattices alike.

Degree Distribution

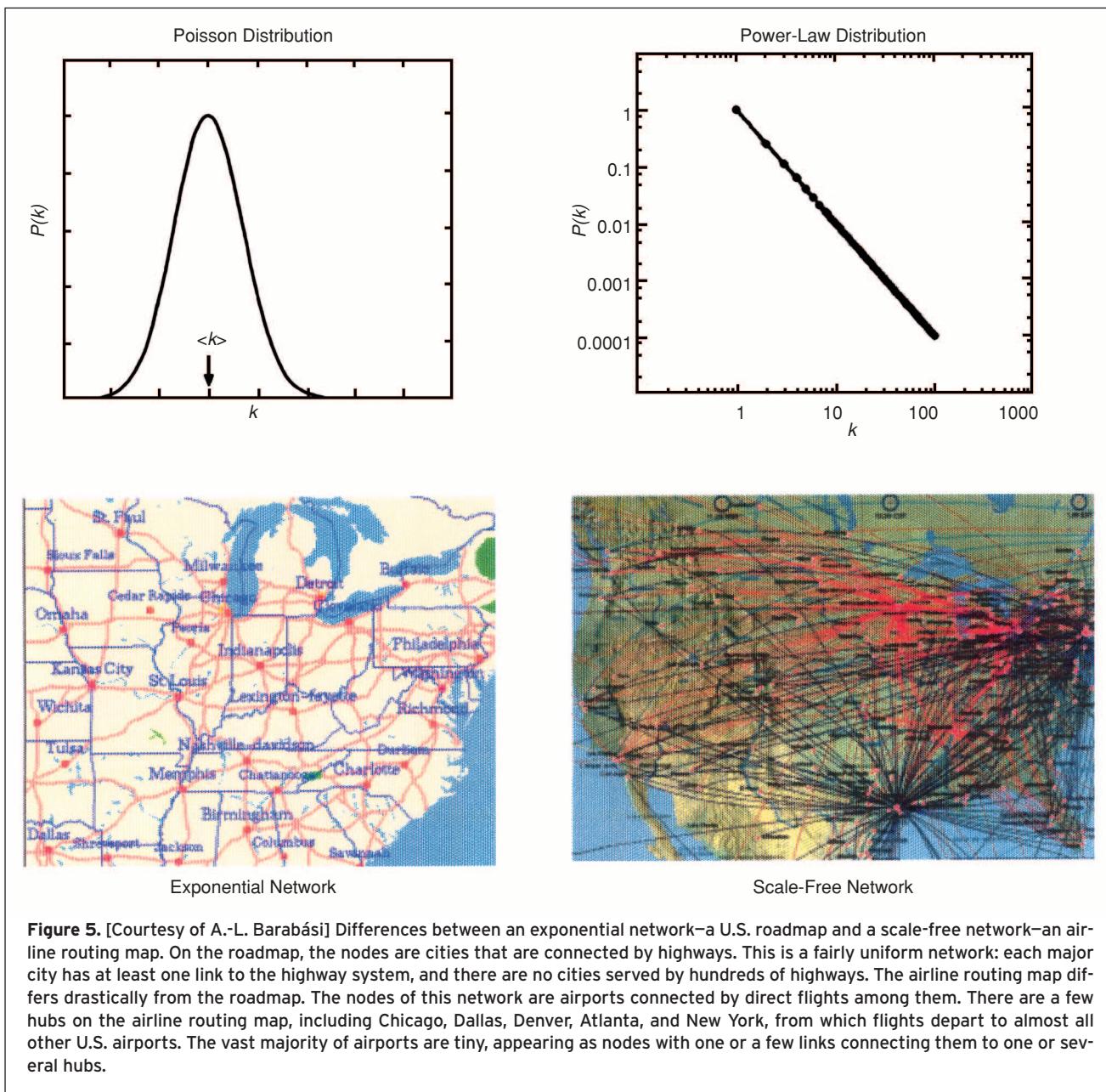
The simplest and perhaps also the most important characteristic of a single node is its *degree*. The degree k_i of a node i is usually defined to be the total number of its connections. Thus, the larger the degree, the “more important” the node is in a network. The average of k_i over all i is called the *average degree* of the network, and is denoted by $\langle k \rangle$. The spread of node degrees over a network is characterized by a distribution function $P(k)$, which is the probability that a randomly selected node has exactly k edges. A regular lattice has a simple degree sequence because all the nodes have the same number of edges; and so a plot of the degree distribution contains a single sharp spike (delta distribution). Any randomness in the network will broaden the shape of this peak. In the limiting case of a completely random network, the degree sequence obeys the familiar Poisson distribution; and the shape of the Poisson distribution falls off exponentially,

away from the peak value $\langle k \rangle$. Because of this exponential decline, the probability of finding a node with k edges becomes negligibly small for $k \gg \langle k \rangle$. In the past few years, many empirical results showed that for most large-scale real networks the degree distribution deviates significantly from the Poisson distribution. In particular, for a number of networks, the degree distribution can be better described by a power law of the form $P(k) \sim k^{-\gamma}$. This power-law distribution falls off more gradually than an exponential one, allowing for a few nodes of very large degree to exist. Because these power-laws are free of any characteristic scale, such a network with a power-law degree distribution is called a *scale-free network*. Some striking differences between an exponential network and a scale-free network can be seen by comparing a U.S. roadmap with an airline routing map, shown in Fig. 5.

The small-world and scale-free features are common to many real-world complex networks. Table 1 shows some examples that might interest the circuits and systems community (for example, the discovery of the scale-free feature of the Internet has motivated the development of a new brand of Internet topology generators [9-12]).

Complex Network Models

Measuring some basic properties of a complex network, such as the average path length L , the clustering coefficient C , and the degree distribution $P(k)$, is the first step toward understanding its structure. The next step, then, is to develop a mathematical model with a topology of similar statistical properties, thereby obtaining a platform on which mathematical analysis is possible.



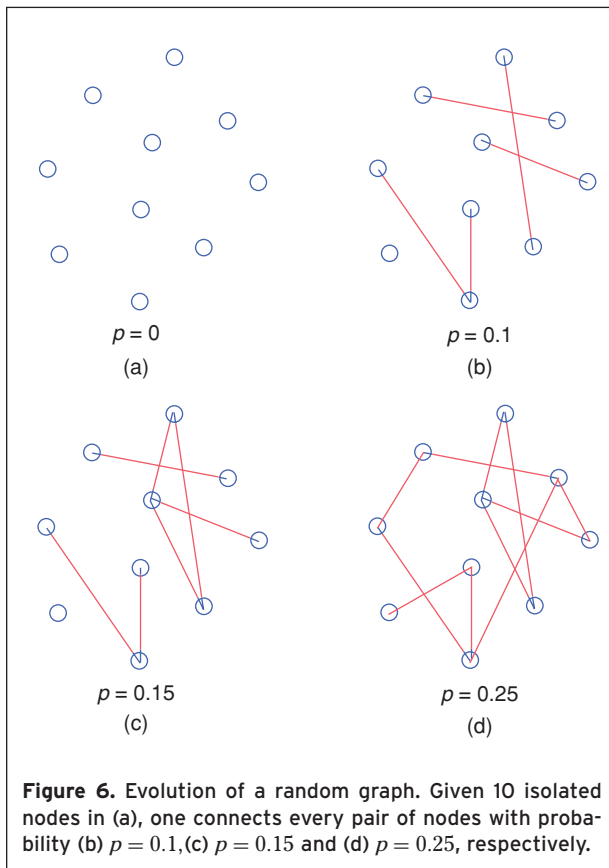
Regular Coupled Networks

Intuitively, a globally coupled network has the smallest average path length and the largest clustering coefficient. Although the globally coupled network model captures the small-world and large-clustering properties of many real networks, it is easy to notice its limitations: a globally coupled network with N nodes has $N(N-1)/2$ edges, while most large-scale real networks appear to be sparse, that is, most real networks are not fully connected and their number of edges is generally of order N rather than N^2 .

A widely studied, sparse, and regular network model is the nearest-neighbor coupled network (a lattice), which is a regular graph in which every node is joined only by a

few of its neighbors. The term “lattice” here may suggest a two-dimensional square grid, but actually it can have various geometries. A minimal lattice is a simple one-dimensional structure, like a row of people holding hands. A nearest-neighbor lattice with a periodic boundary condition consists of N nodes arranged in a ring, where each node i is adjacent to its neighboring nodes, $i = 1, 2, \dots, K/2$, with K being an even integer. For a large K , such a network is highly clustered; in fact, the clustering coefficient of the nearest-neighbor coupled network is approximately $C = 3/4$.

However, the nearest-neighbor coupled network is not a small-world network. On the contrary, its average path



length is quite large and tends to infinity as $N \rightarrow \infty$. This may help explain why it is difficult to achieve any dynamical process (e.g., synchronization) that requires global coordination in such a locally coupled network. Does there exist a regular network that is sparse and clustered, but has a small average path length? The answer is Yes. A simple example is a star-shaped coupled network, in which there is a center node and each of the other $N - 1$ nodes only connect to this center but not among themselves. For this kind of network, the average path length tends to 2 and its clustering coefficient tends to 1, as $N \rightarrow \infty$. The star-shaped network model captures the sparse, clustering, small-world, as well as some other interesting properties of many real-world networks. Therefore, in this sense, it is better than the regular lattice as a model of many well-known real networks. Clearly, though, most real networks do not have a precise star shape.

Random Graphs

At the opposite end of the spectrum from a completely regular network is a network with a completely random graph, which was studied first by Erdős and Rényi (ER) about 40 years ago [4].

Try to imagine that you have a large number ($N \gg 1$) of buttons scattered on the floor. With the same probability p , you tie every pair of buttons with a thread. The result

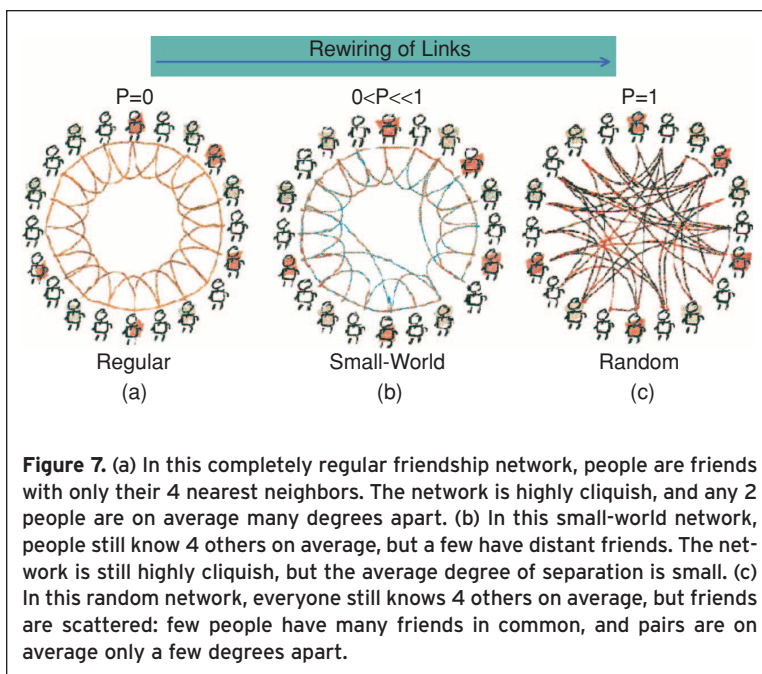
is a physical example of an ER random graph with N nodes and about $pN(N - 1)/2$ edges (Fig. 6). The main goal of the random graph theory is to determine at what connection probability p a particular property of a graph will most likely arise. A remarkable discovery of this type was that important properties of random graphs can appear quite suddenly. For example, if you lift up a button, how many other buttons will you pick up thereby? ER showed that, if the probability p is greater than a certain threshold $p_c \sim (\ln N)/N$, then almost every random graph is connected, which means that you will pick up all the buttons on the floor by randomly lifting up just one button.

The average degree of the random graph is $\langle k \rangle = p(N - 1) \cong pN$. Let L_{rand} be the average path length of a random network. Intuitively, about $\langle k \rangle^{L_{rand}}$ nodes of the random network are at a distance L_{rand} or very close to it. Hence, $N \sim \langle k \rangle^{L_{rand}}$, which means that $L_{rand} \sim \ln N / \langle k \rangle$. This logarithmic increase in average path length with the size of the network is a typical small-world effect. Because $\ln N$ increases slowly with N , it allows the average path length to be quite small even in a fairly large network. On the other hand, in a completely random network, for example in your friendship network (say it is completely random), the probability that two of your friends are friends themselves is no greater than the probability that two randomly chosen persons from your network happen to be friends. Hence, the clustering coefficient of the ER model is $C = p = \langle k \rangle / N \ll 1$. This means that a large-scale random network does not show clustering in general. In fact, for a large N , the ER algorithm generates a homogeneous network, where the connectivity approximately follows a Poisson distribution.

Small-World Models

As pointed out above, regular lattices are clustered, but do not exhibit the small-world effect in general. On the other hand, random graphs show the small-world effect, but do not show clustering. Thus, it is not surprising to see that the regular lattice model and the ER random model both fail to reproduce some important features of many real networks. After all, most of these real-world networks are neither entirely regular nor entirely random. The reality is that people usually know their neighbors, but their circle of acquaintances may not be confined to those who live right next door, as the lattice model would imply. On the other hand, cases like links among Web pages on the WWW were certainly not created at random, as the ER process would expect.

Aiming to describe a transition from a regular lattice to a random graph, Watts and Strogatz [5] introduced an interesting small-world network model, referred to as WS small-world model. The WS model can be generated as follows (Fig. 7).



WS Small-World Model Algorithm

1) **Start with order:** Begin with a nearest-neighbor coupled network consisting of N nodes arranged in a ring, where each node i is adjacent to its neighbor nodes, $i = 1, 2, \dots, K/2$, with K being even.

2) **Randomization:** Randomly rewire each edge of the network with probability p ; varying p in such a way that the transition between order ($p = 0$) and randomness ($p = 1$) can be closely monitored.

Rewiring within this context means shifting one end of the connection to a new node chosen at random from the whole network, with the constraints that any two different nodes cannot have more than one connection between them, and no node can have a connection with itself. This process introduces $pNK/2$ long-range edges, which connect nodes that otherwise would be part of different neighborhoods. Both the behaviors of the clustering coefficient $C(p)$ and of the average path length $L(p)$ in the WS small-world model can be considered as a function of the rewiring probability p . A regular ring lattice ($p = 0$) is highly clustered ($C(0) \cong 3/4$) but has a large average path length ($L(0) \cong \frac{N}{2K} \gg 1$). It is found that, for a small probability of rewiring, when the local properties of the network are still nearly the same as those for the original regular network, and when the clustering coefficient does not differ subsequently from its initial value ($C(p) \sim C(0)$), the average path length drops rapidly and is in the same order as the one for random networks ($L(p) \gg L(0)$) (Fig. 8). This result is actually quite natural. On the one hand, it is sufficient to make several random rewirings to decrease

the average path length significantly. On the other hand, several rewired links cannot crucially change the local clustering property of the network.

The small-world model can also be viewed as a homogeneous network, in which all nodes have approximately the same number of edges. In this regard, the WS small-world network model is similar to the ER random graph model. The work on WS small-world networks has started an avalanche of research on new models of complex networks, including some variants of the WS model. A typical variant was the one proposed by Newman and Watts [23], referred to as the NW small-world model lately. In the NW model, one does not break any connection between any two nearest neighbors, but instead, adds with probability p a connection between a pair of nodes.

Likewise, here one does not allow a node to be coupled to another node more than once, or to couple with itself. With $p = 0$, the NW model reduces to the original nearest-neighbor coupled network, and if $p = 1$ it becomes a globally coupled network. The NW model is somewhat easier to analyze than the original WS model because it does not lead to the formation of isolated clusters, whereas this can indeed happen in the WS model. For sufficiently small p and sufficiently large N , the NW model is essentially equivalent to the WS model. Today, these two models are together commonly termed small-world models for brevity.

The small-world models have their roots in social networks, where most people are friends with their immediate neighbors, for example neighbors on the same street

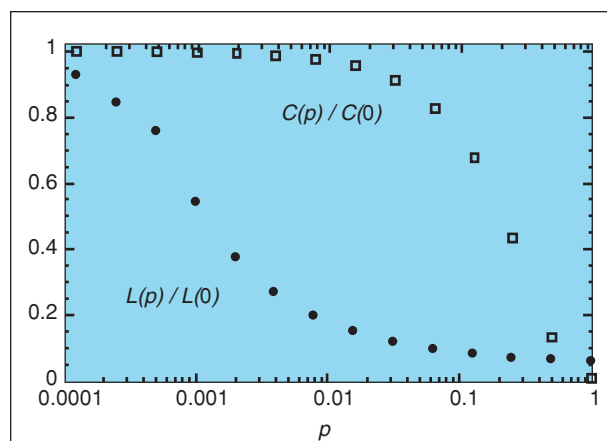


Figure 8. [Courtesy of NATURE] Average path length and clustering coefficient of the WS small-world model as a function of the rewiring probability p [5]. Both are normalized to their values for the original regular lattice ($p = 0$).

or colleagues in the same office. On the other hand, many people have a few friends who are far away in distance, such as friends in other countries, which are represented by the long-range edges created by the rewiring procedure in the WS model, or by the connection-adding procedure in the NW model.

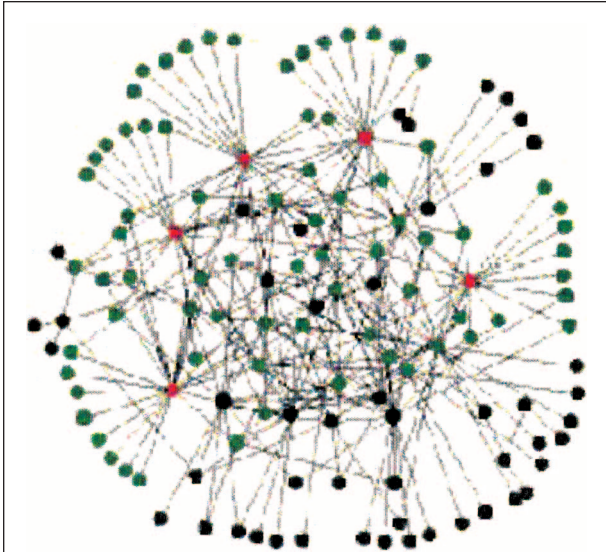


Figure 9. A scale-free network of 130 nodes, generated by the BA scale-free model. The five biggest nodes are shown in red, and they are in contact with 60% of other nodes (green).

Scale-Free Models

A common feature of the ER random graph and the WS small-world models is that the connectivity distribution of the network is homogenous, with peak at an average value and decay exponentially. Such networks are called *exponential networks*. A significant recent discovery in the field of complex networks is the observation that a number of large-scale complex networks, including the Internet, WWW, and metabolic networks, are scale-free and their connectivity distributions have a power-law form.

To explain the origin of power-law degree distribution, Barabási and Albert (BA) proposed another network model [7,8]. They argued that many existing models fail to take into account two important attributes of most real networks. First, real networks are open and they are dynamically formed by continuous addition of new nodes to the network; but the other models are static in the sense that although edges can be added or rearranged, the number of nodes is fixed throughout the forming process. For example, the WWW is continually sprouting new webpages, and the research literature constantly grows since new papers are continuously being published. Second, both the random graph and small-world models assume uniform probabilities when creating new edges, but this is not realistic either. Intuitively, webpages

that already have many links (such as the homepage of Yahoo or CNN) are more likely to acquire even more links; a new manuscript is more likely to cite a well-known and thus much-often-cited paper than many other less-known ones. This is the so-called “rich get richer” phenomenon, for which the other models do not account.

The BA model suggests that two main ingredients of self-organization of a network in a scale-free structure are growth and preferential attachment. These point to the facts that most networks continuously grow by the addition of new nodes, and new nodes are preferentially attached to existing nodes with large numbers of connections (again, “rich get richer”). The generation scheme of a BA scale-free model is as follows:

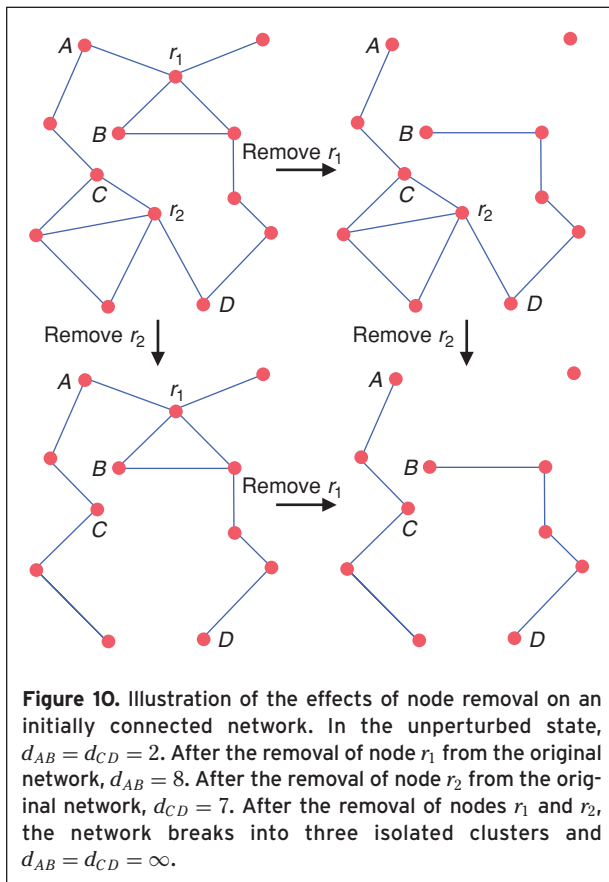
BA Scale-Free Model Algorithm

- 1) **Growth:** Start with a small number (m_0) of nodes; at every time step, a new node is introduced and is connected to $m \leq m_0$ already-existing nodes.
- 2) **Preferential Attachment:** The probability Π_i that a new node will be connected to node i (one of the m already-existing nodes) depends on the degree k_i of node i , in such a way that $\Pi_i = k_i / \sum_j k_j$.

After t time steps, this algorithm results in a network with $N = t + m_0$ nodes and mt edges (Fig. 9). Growing according to these two rules, the network evolves into a scale-invariant state: The shape of the degree distribution does not change over time, namely, does not change due to further increase of the network scale. The corresponding degree distribution is described by a power law with exponent -3 , that is, the probability of finding a node with k edges is proportional to k^{-3} .

Numerical results have indicated that, in comparison with a random graph having the same size and the same average degree, the average path length of the scale-free model is somewhat smaller, and yet the clustering coefficient is much higher. This implies that the existence of a few “big” nodes with very large degrees (i.e., with a very large number of connections) plays a key role in bringing the other nodes of the network close to each other. However, there is today no analytical prediction formula for the average path length and the clustering coefficient for the scale-free model. The BA model is a minimal model that captures the mechanisms responsible for the power-law degree distribution. This model has some evident limitations when compared with some real-world networks. This observation has in effect spurred more research on evolving networks, with the intention to overcome limitations such as those of the BA model. A summary of these models is given by Albert and Barabási [2].

Recently, Milo *et al.* [24] defined the so-called “network motifs” as patterns of interconnections occurring in

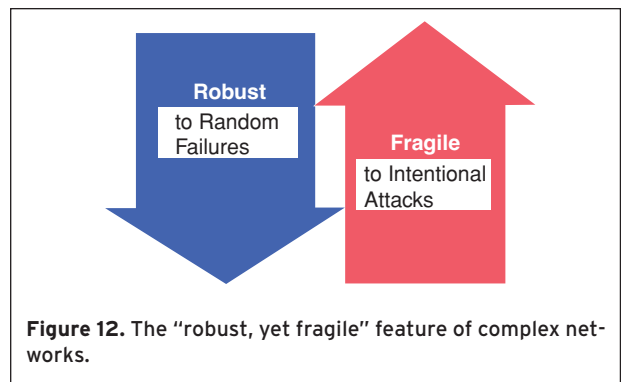
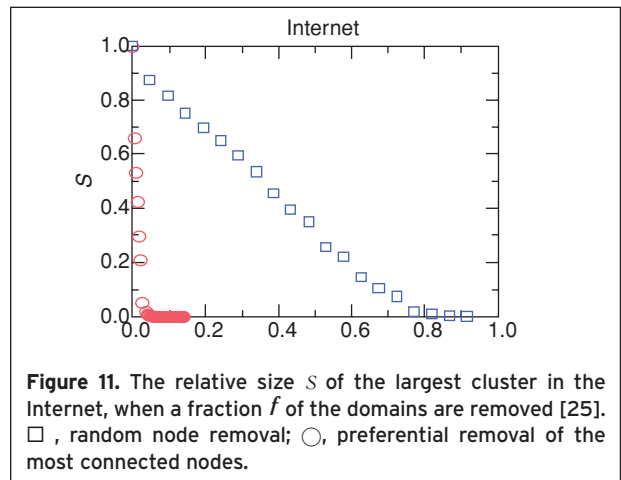


complex networks at numbers that are significantly higher than those in completely random networks. Such motifs have been found in networks ranging from biochemistry, neurobiology, ecology, to engineering. This research may uncover the basic building blocks pertaining to each class of networks.

Achilles' Heel of Complex Networks

An interesting phenomenon of complex networks is their "Achilles' heel"—robustness versus fragility. For illustration, let us start from a large and connected network. At each time step, remove a node (Fig. 10). The disappearance of the node implies the removal of all of its connections, disrupting some of the paths among the remaining nodes. If there were multiple paths between two nodes i and j , the disruption of one of them may mean that the distance d_{ij} between them will increase, which, in turn, may cause the increase of the average path length L of the entire network. In a more severe case, when initially there was a single path between i and j , the disruption of this particular path means that the two nodes become disconnected. The connectivity of a network is robust (or error tolerant) if it contains a giant cluster comprising many nodes, even after a removal of a fraction of nodes.

The predecessor of the Internet—the ARPANET—was



created by the US Department of Defense, by its Advanced Research Projects Agency (ARPA), in the late 1960s. The goal of the ARPANET was to enable continuous supply of communications services, even in the case that some subnetworks and gateways were failing. Today, the Internet has grown to be a huge network and has played a crucial role in virtually all aspects of the world. One may wonder if we can continue to maintain the functionality of the network under inevitable failures or frequent attacks from computer hackers. The good news is that by randomly removing certain portions of domains from the Internet, we have found that, even if more than 80% of the nodes fail, it might not cause the Internet to collapse. However, the bad news is that if a hacker targeted some key nodes with very high connections, then he could achieve the same effect by purposefully removing a very small fraction of the nodes (Fig. 11). It has been shown that such error tolerance and attack vulnerability are generic properties of scale-free networks (Fig. 12) [25-28]. These properties are rooted in the extremely inhomogeneous nature of degree distributions in scale-free networks. This attack vulnerability property is called an Achilles' heel of complex networks, because the mythological warrior Achilles had been magically protected in all but one small part of his body—his heel.

Epidemic Dynamics in Complex Networks

For one specific example, the AIDS propagation network is quite typical. When AIDS first emerged as a disease about twenty years ago, few people could have predicted how the epidemic would evolve, and even fewer could have been able to describe with certainty the best way of fighting it. Unfortunately, according to estimates from the Joint United Nations Programme on HIV/AIDS (UNAIDS) and the World Health Organization (WHO), 21.8 million people around the world had died of AIDS up to the end of 2000 and 36.1 million people were living with the human immunodeficiency virus (HIV) by the same time.

As another example, in spite of technological progress and great investments to ensure a secure supply of electric energy, blackouts of the electric transmission grid are not uncommon. Cascading failures in large-scale electric power transmission systems are an important cause of the catastrophic blackouts. Most well known is the cascading series of failures in power lines in August 1996, leading to blackouts in 11 US states and two Canadian provinces. This incident left about 7 million customers without power for up to 16 hours, and cost billions of dollars in total damage. There is an urgent need for developing innovative methodologies and conceptual breakthroughs for analysis, planning, operation, and protection of the complex and dynamical electric power networks. In yet another example, the ILOVEYOU computer virus spread over the Internet in May 2000 and caused a loss of nearly 7 billion dollars in facility damage and computer down-time.

How do diseases, jokes, and fashions spread out over the social networks? How do cascading failures propagate through large-scale power grids? How do computer viruses spread out through the Internet? Serious issues like these are attracting much attention these days. Clearly, the topology of a network has great influence on the overall behavior of an epidemic spreading in the network. Recently, some researchers have started to study such spreading phenomena, for example on small-world and scale-free networks [29-34].

A notable attempt of Pastor-Satorras and Vespignani [31-32] was to study both analytically and numerically a large-scale dynamical model on the spreading of epidemics in complex networks. The standard susceptible-infected-susceptible (SIS) epidemiological model was used for investigation. Each node of the network repre-

sents an individual, and each link is a connection along which the infection can spread from one individual to some others. It is natural to assume that each individual can only exist in one of two discrete states—susceptible and infected. At every time step, each susceptible node is infected with probability ν if it is connected to at least one infected node. At the same time, infected nodes are cured and become again susceptible with probability δ . They together define an effective spreading rate, $\lambda = \nu/\delta$. The updating can be performed with both parallel and sequential dynamics. The main prediction of the SIS model in homogeneous networks (including lattices, random graphs, and small-world models) is the presence of a nonzero epidemic threshold, $\lambda_c > 0$. If $\lambda \geq \lambda_c$, the infection spreads and becomes persistent in time; yet if $\lambda < \lambda_c$, the infection dies out exponentially fast (Fig. 13 (a)).

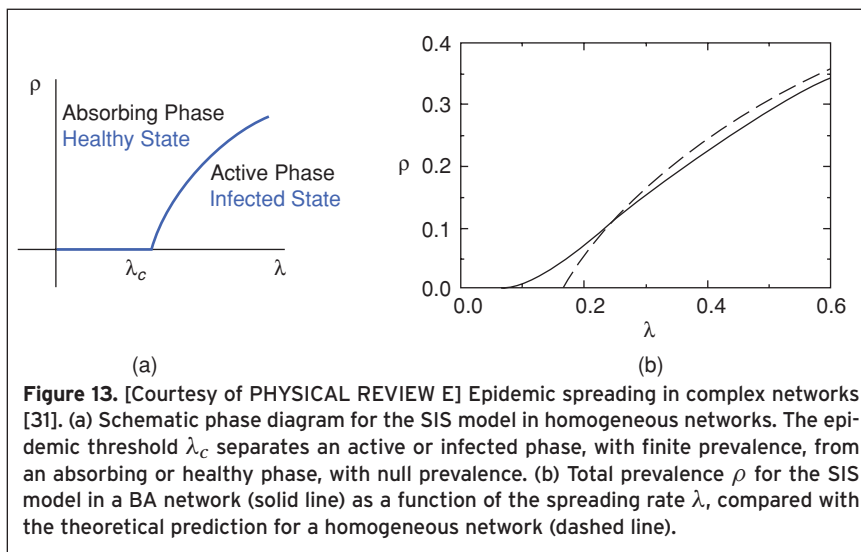


Figure 13. [Courtesy of PHYSICAL REVIEW E] Epidemic spreading in complex networks [31]. (a) Schematic phase diagram for the SIS model in homogeneous networks. The epidemic threshold λ_c separates an active or infected phase, with finite prevalence, from an absorbing or healthy phase, with null prevalence. (b) Total prevalence ρ for the SIS model in a BA network (solid line) as a function of the spreading rate λ , compared with the theoretical prediction for a homogeneous network (dashed line).

It was found [31-32] that, while for exponential networks the epidemic threshold is a positive constant, for a large class of scale-free networks the critical spreading rate tends to zero (Fig. 13(b)). In other words, scale-free networks are prone to the spreading and the persistence of infections, regardless of the spreading rate of the epidemic agents. It implies that computer viruses can spread far and wide on the Internet by infecting only a tiny fraction of the huge network. Fortunately, this is balanced by exponentially small prevalence and by the fact that it is true only for a range of very small spreading rates ($\lambda \ll 1$) that tend to zero.

Synchronization in Complex Dynamical Networks

A survey of recent literature reveals that networks of coupled dynamical systems have received a great deal of attention from the nonlinear dynamics community, mainly due to the fact that they can exhibit many complex and interesting dynamical phenomena, such as Turing patterns, auto-

waves, spiral waves, and spatiotemporal chaos. Also, these networks are important in modeling many large-scale real-world systems.

In the past decade, special attention has been focused on the synchronization of chaotic dynamical systems. For the same reason, many scientists have started to consider the synchronization phenomenon in large-scale networks of coupled chaotic oscillators. These networks are usually described by systems of coupled ordinary differential equations or maps, with completely regular topological structures such as chains, grids, lattices, and globally coupled graphs. Two typical settings are the discrete-time coupled map lattice (CML) [35] and the continuous-time cellular neural (or more generally, nonlinear) networks (CNN) [36]. The main advantage of these simple architectures is that it allows one to focus on the complexity caused by the nonlinear dynamics of the nodes without worrying about additional complexity in the network structure; and another appealing feature is the ease of their implementation by integrated circuits.

The topology of a network, on the other hand, often plays a crucial role in determining its dynamical behaviors. For example, although a strong enough diffusive coupling will result in synchronization within an array of identical nodes [37], it cannot explain why many real-world complex networks exhibit a strong tendency toward synchronization even with a relatively weak coupling. As an instance, it was observed that the apparently independent routing messages from different routers in the Internet can easily become synchronized, while the tendency for routers towards synchronization may depend heavily on the topology of the Internet [38]. One way to break up the unwanted synchronization is for each router to add a (sufficiently large) component randomly to the period between two routing messages. However, the tendency to synchronization in the Internet is so strong that changing one deterministic protocol to correct the synchronization is likely to generate another synchrony elsewhere at the same time. This suggests that a more efficient solution requires a better understanding of the nature

of the synchronization behavior in such complex networks as the Internet.

Recently, synchronization in different small-world and scale-free dynamical network models has been carefully studied [39–45]. These studies may shed new light on the synchronization phenomenon in various real-world complex networks.

A Typical Dynamical Network Model

Consider a typical dynamical network consisting of N identical linearly and diffusively coupled nodes, with each node being an n -dimensional dynamical system (e.g., a chaotic system). The state equations of this network are described by

$$\dot{\mathbf{x}}_i = f(\mathbf{x}_i) + c \sum_{j=1}^N a_{ij} \Gamma \mathbf{x}_j, \quad i = 1, 2, \dots, N. \quad (1)$$

In this model, $\mathbf{x}_i = (x_{i1}, x_{i2}, \dots, x_{in})^T \in \mathbb{R}^n$ are the state variables of node i , the constant $c > 0$ represents the cou-

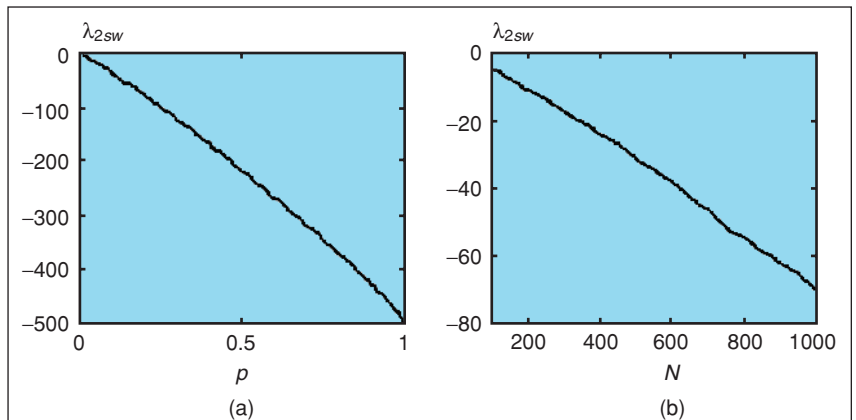


Figure 14. The second-largest eigenvalue λ_{2sw} of the coupling matrix of the small-world network (1) [41]. (a) λ_{2sw} as a function of the adding probability p with the network size $N = 500$. (b) λ_{2sw} as a function of the network size with adding probability $p = 0.1$.

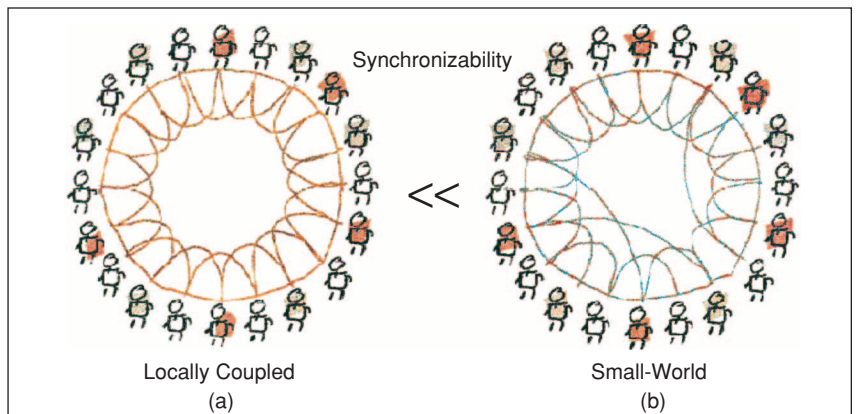


Figure 15. The ability to achieve synchronization in a locally coupled network can be greatly enhanced by just adding a tiny fraction of distant links, thereby making the network become a small-world network, which reveals an advantage of small-world networks for synchronization.

pling strength, and $\Gamma \in \mathbb{R}^{n \times n}$ is a constant 0 – 1 matrix linking coupled variables. If there is a connection between node i and node j ($i \neq j$), then $a_{ij} = a_{ji} = 1$; otherwise, $a_{ij} = a_{ji} = 0$ ($i \neq j$). Moreover, $a_{ii} = -k_i$, where k_i is the degree of node i . The coupling matrix $\mathbf{A} = (a_{ij}) \in \mathbb{R}^{N \times N}$ represents the coupling configuration of the network.

Dynamical network (1) is said to be (asymptotically) *synchronized* if

$$\mathbf{x}_1(t) = \mathbf{x}_2(t) = \cdots = \mathbf{x}_N(t) = \mathbf{s}(t), \text{ as } t \rightarrow \infty, \quad (2)$$

where $\mathbf{s}(t) \in \mathbb{R}^n$ is a solution of an isolated node, i.e., $\dot{\mathbf{s}}(t) = \mathbf{f}(\mathbf{s}(t))$. Here, $\mathbf{s}(t)$ can be an equilibrium point, a periodic orbit, or a chaotic attractor, depending on the interest of the study.

Consider the case that the network is connected in the sense that there are no isolated clusters. Then, the coupling matrix $\mathbf{A} = (a_{ij})_{N \times N}$ is a symmetric irreducible matrix. In this case, it can be shown that $\lambda_1 = 0$ is the largest eigenvalue of \mathbf{A} with multiplicity 1 but all the other eigenvalues of \mathbf{A} are strictly negative. Let $\lambda_2 < 0$ be the second-largest eigenvalue of \mathbf{A} . It has been proved [40, 41] that the synchronization state (2) is exponentially stable if

$$c \geq \left| \bar{d} / \lambda_2 \right|, \quad (3)$$

where $\bar{d} < 0$ is a constant determined by the dynamics of an isolated node and the inner linking structural matrix Γ . (In fact, \bar{d} can be more precisely characterized by the Lyapunov exponents of the network [46].)

Given the dynamics of an isolated node and the inner linking structural matrix Γ , the *synchronizability* of the dynamical network (1) with respect to a specific coupling configuration \mathbf{A} is said to be *strong* if the network can synchronize with a small value of the coupling strength c . The above result implies that the synchronizability of the dynamical network (1) can be characterized by the second-largest eigenvalue of its coupling matrix.

The second-largest eigenvalue of the coupling matrix of a globally coupled network is $-N$, which implies that for any given and fixed nonzero coupling strength c , a globally coupled network will synchronize as long as its size N is large enough. On the other hand, the second-largest eigenvalue of the coupling matrix of a nearest-neighbor coupled network tends to zero as $N \rightarrow \infty$, which implies that for any given and fixed nonzero coupling strength c , a nearest-neighbor coupled network cannot synchronize if its size N is sufficiently large.

Synchronization in Small-World Networks

Consider the dynamical network (1) with NW small-world connections [41]. Let λ_{2sw} be the second-largest eigenvalue of the network coupling matrix. Figures 14 (a) and (b)

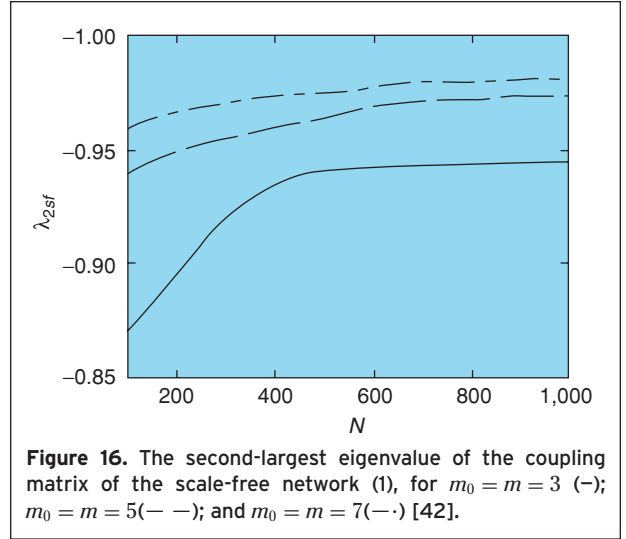


Figure 16. The second-largest eigenvalue of the coupling matrix of the scale-free network (1), for $m_0 = m = 3$ (---); $m_0 = m = 5$ (—); and $m_0 = m = 7$ (-·-) [42].

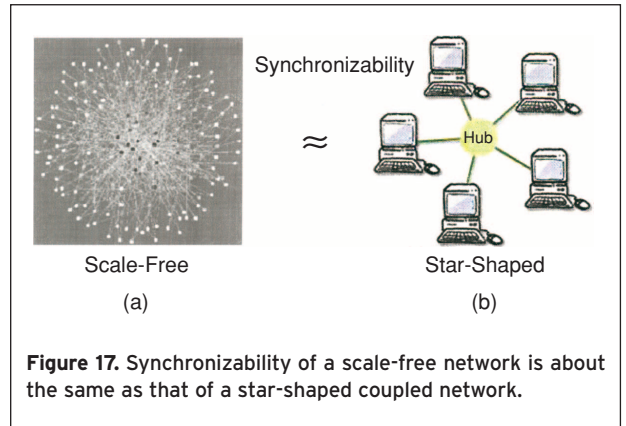


Figure 17. Synchronizability of a scale-free network is about the same as that of a star-shaped coupled network.

show the numerical values of λ_{2sw} as a function of the adding probability p and the network size N , respectively. It can be seen that, for any given coupling strength $c > 0$: (i) for any $N > |\bar{d}|/c$, there exists a critical value \bar{p} such that if $\bar{p} \leq p \leq 1$ then the small-world network will synchronize; (ii) for any given $p \in (0, 1]$, there exists a critical value \bar{N} such that if $N > \bar{N}$ then the small-world network will synchronize. These results imply that the ability to achieve synchronization in a large-size nearest-neighbor coupled network can be greatly enhanced by just adding a tiny fraction of distant links, thereby making the network become a small-world model. This reveals an advantage of small-world networks for achieving synchronization, if desired (Fig. 15).

Synchronization in Scale-Free Networks

Now consider the dynamical network (1) with BA scale-free connections instead [42]. Figure 16 shows that the second-largest eigenvalue of the corresponding coupling matrix is very close to -1 , which actually is the second-largest eigenvalue of the star-shaped coupled network. This implies that the synchronizability of a

scale-free network is about the same as that of a star-shaped coupled network (Fig. 17). It may be due to the extremely inhomogeneous connectivity distribution of such networks: a few “hubs” in a scale-free network play a similar (important) role as a single center in a star-shaped coupled network.

The robustness of synchronization in a scale-free dynamical network has also been investigated, against either random or specific removal of a small fraction f ($0 < f \ll 1$) of nodes in the network. Clearly, the removal of some nodes in network (1) can only change the coupling matrix. If the second-largest eigenvalue of the coupling matrix remains unchanged, then the synchronization stability of the network will remain unchanged after such a removal. It was found that even when as many as 5% of randomly chosen nodes are removed, the second-largest eigenvalue of the coupling matrix remains almost unchanged; therefore the ongoing synchronization is not altered. On the other hand, although the scale-free structure is particularly well-suited to tolerate random errors, it is also particularly vulnerable to deliberate attacks. In particular, it was found that the magnitude of the second-largest eigenvalue of the coupling matrix decreases rapidly, almost decreases to one half of its original value in magnitude, when only an $f \approx 1\%$ fraction of the highly connected nodes was removed. At a low critical threshold, e.g., $f \approx 1.6\%$, the eigenvalue abruptly changes to zero, implying that the whole network was broken into isolate clusters; therefore the ongoing synchronization will be completely destroyed. Similarly, it is believed that the error tolerance and attack vulnerability of synchronizability in scale-free networks are rooted in their extremely inhomogeneous connectivity patterns.

Conclusions

In the past few years, advances in complex networks have uncovered some amazing similarities among such diverse systems as the Internet, cellular neural networks, metabolic systems, and even the community of Hollywood movie stars. In particular, significant progress has been made on the effects of network topology on network dynamical behaviors. However, this has been seen as only the tip of a giant iceberg and there remain important problems and technical challenges with regard to modeling, analysis, control, and synchronization of complex dynamical networks.

Today, we are building increasingly integrated and interconnected networks for information, energy, transportation, commerce and the like. The critical nature of these networks raises concerns about the risk and impact of system failures, and makes it imperative for us to better understand the essence of such complex networks.

This calls for greater effort in the design and operation of all kinds of large-scale and complex dynamical networks, so as to provide better analysis and prediction of various potential issues. The ultimate goal is to maximize the net potentials that can better benefit our human society. Achieving this understanding requires intensive advanced research—the research that will develop a solid scientific foundation for further study of real-world complex dynamical networks and new methodologies for their construction and utilization. The complex issues that we are facing everyday, from cell biology to power systems to communication networks, demand breakthrough ideas and revolutionary techniques. It has become a great challenge and also provided a great opportunity for scientists and engineers at this very beginning of the twenty-first century.

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