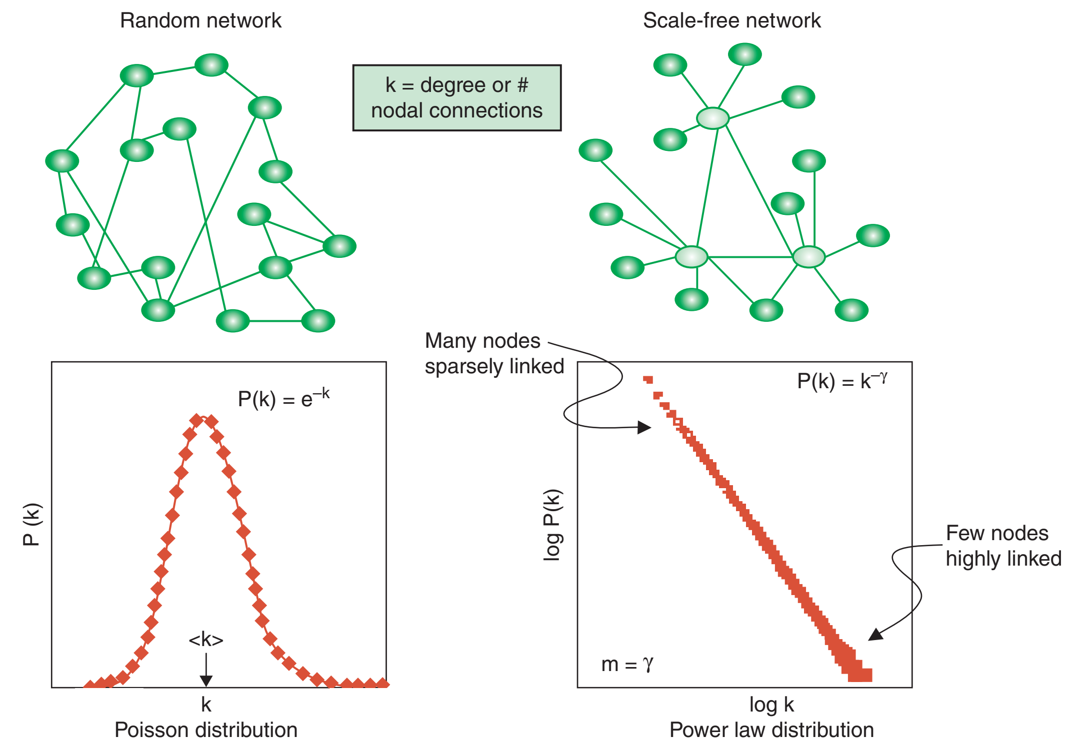

FIGURE 87e-1 Network representations and their distributions. A random network is depicted on the left, and its Poisson distribution of the number of nodal connections (k) is shown in the graph below it. A scale-free network is depicted on the right, and its power law distribution of the number of nodal connections (k) is shown in the graph below it. Highly connected nodes (hubs) are lightly shaded.

links per node ($P[k] = k^{-[\gamma]}$, where k is the number of links per node and γ is the slope of the log P[k] versus log[k] plot); this unique property of most biologic networks is a reflection of their self-similarity or fractal nature (Fig. 87e-1).

There are unique properties of scale-free biologic systems that reflect their evolution and promote their adaptability and survival. Biologic networks likely evolved one node at a time in a process in which new nodes are more likely to link to a highly connected node than to a sparsely connected node. Furthermore, scale-free networks can become sparsely linked to one another, yielding more complex, *modular scale-free topologies*. This evolutionary growth of biologic networks has three important properties that affect system function and survival. First, this scale-free addition of new nodes promotes *system redundancy*, which minimizes the consequences of errors and accommodates adverse perturbations to the system robustly with minimal effects on critical functions (unless the highly connected nodes are the focus of the perturbation). Second, this resulting network redundancy provides a survival advantage to the system. In complex gene networks, for example, mutations or polymorphisms in weakly linked genes account for biodiversity and biologic variability without disrupting the critical functions of the system; only mutations in highly linked (*essential*) genes (hubs) can shut down the system and cause embryonic lethality. Third, scale-free biologic systems facilitate the flow of information (e.g., metabolite flux) across the system compared with randomly organized biologic systems; this so-called "small-world" property of the system (in which the clustered nature of the highly linked hubs defines a local neighborhood within the network that communicates through weaker, less frequent links to other clusters) minimizes the energy cost for the dynamic action of the system (e.g., minimizes the transition time between states in a metabolic network).

These basic organizing principles of complex biologic systems lead to three unique properties that require emphasis. First, biologic systems are *robust*, which means that they are quite stable in response to most changes in external conditions or internal modification. Second, a corollary to the property of robustness is that complex biologic systems are *sloppy*, which means that they are insensitive to changes in external conditions or internal modification except under certain uncommon conditions (i.e., when a hub is involved in the change). Third, complex biologic systems exhibit *emergent properties*, which means that they manifest behaviors that cannot be predicted from the reductionist principles used to characterize their component parts. Examples of emergent behavior in biologic systems include spontaneous, self-sustained oscillations in glycolysis; spiral and scroll waves of depolarization in cardiac tissue that cause reentrant arrhythmias; and self-organizing patterns in biochemical systems governed by diffusion and chemical reaction.

APPLICATIONS OF SYSTEMS BIOLOGY TO PATHOBIOLOGY

The principles of systems biology have been applied to complex pathologic processes with some early successes. The key to these applications is the identification of emergent properties of the system under study in order to define novel, otherwise unpredictable (i.e., from the reductionist perspective) methods for regulating the system's response. Systems biology approaches have been used to characterize epidemics and ways to control them, taking advantage of the scale-free properties of the network of infected individuals that constitute the epidemic. Through the use of a systems analysis of a neural protein-protein interaction network, unique disease-modifying proteins have been identified that are common to a wide range of cerebellar neurodegenerative disorders causing inherited ataxias. Systems analysis and disease network construction of a pulmonary arterial hypertension network led to the identification of a unique disease module involving a pathway governed by microRNA21. Systems biology models have been used to dissect the dynamics of the inflammatory response using oscillatory changes in the transcription factor nuclear factor (NF) κB as the system output. Systems biology principles also have been used to predict the development of an idiotypy–anti-idiotypy antibody network, describe the dynamics of species growth in microbial biofilms, and analyze the innate immune response. In each of these examples, a systems (patho)biology approach provided insights into the behavior of these complex systems that could not have been recognized with conventional scientific reductionism.

A unique application of systems biology to biomedicine is in the area of drug development. Conventional drug development involves