A large-scale study of the protein network in yeast cells demonstrates the merit of taking an integrated approach to cellular dynamics, and shows the value of databases.

In the climactic scene of the movie Independence Day, a massive alien spacecraft, hovering just above the Earth, appears to be immune to the petty assaults mounted by the earthlings. In a last-ditch effort, the character played by Randy Quaid decides to fly his jet fighter on a kamikaze mission into the spacecraft’s primary weapon. It turns out that the primary weapon is a highly connected node in the spacecraft’s defence architecture. So although Quaid’s attack constitutes only a pinprick, it induces an avalanche effect through the defence network, leading to the ultimate annihilation of the spacecraft.

On page 41 of this issue, Jeong et al. show that protein networks in yeast cells have wiring characteristics that are analogous to those of the alien spacecraft. These characteristics include both high resistance to random assaults, or mutations, and vulnerability to targeted attacks on specific, highly connected nodes in the network. Their data support the idea that tolerance to mutations, which has been linked to genetic redundancy, is also derived from the organization of interactions and topological position of individual proteins.

Jeong et al. derive their results by cleverly combining information from several different databases. First, by using data on protein-protein interactions in yeast, they show that the associated network follows a power-law distribution; that is, the system contains a large number of proteins with a small number of connections and a small number of proteins with many connections. This type of network architecture, which is common to other complex systems including the Internet and metabolic networks, should be both error-tolerant and vulnerable to attack. Jeong and colleagues demonstrate that these properties do indeed exist, and Figure 3 shows that the connectivity of a protein in the network is directly correlated with the likelihood that its removal will be lethal to the cell. For instance, they show that roughly two-thirds of proteins that have more than 15 connections are essential, in the sense that deleting them is lethal, whereas only one-fifth of proteins with five or fewer connections are essential.

These findings are, in many ways, intuitive. One would expect, for example, that the removal of a highly connected node in a complex network would be especially disruptive to network function. Likewise, it has been pointed out that the protein product of the p53 tumour-suppressor gene is one of the most highly connected proteins in human cells and that mutations of p53 can have severe consequences on basic cellular functions. Jeong et al. quantify this effect on a larger scale, and show how the topology of a cellular network can be related to biologi-
cal function. Their work demonstrates the value of taking an integrated approach to cellular dynamics, and shows that even though the cell is a complex, hierarchical system, it is possible to gain insight into its functional organization using relatively simple analyses.

The stage is set for further investigation of these types of protein network. How, for example, did they evolve? Possible clues can be found in related work on the emergence of power-law distributions. Such distributions will emerge if the probability that a particular node makes future connections is proportional to the number of current connections. Put another way, highly connected nodes tend to become even more connected as time goes by. What, therefore, is happening at the level of protein interactions? Certain highly connected proteins could have a special structure that enables them to bind to many different types of protein, including new ones that arise through mutation. So it may be that the proteins that make up the highly connected nodes in cellular networks share common structural features.

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Astronomy

A new twist on neutron stars

Chris Fryer and Stan Woosley

Theory suggests that neutron stars should be born rotating rapidly, but in reality they spin more slowly. New calculations suggest that they may be slowed by the emission of exotic gravity waves.

A neutron star is like a gigantic atomic nucleus, packing more than a solar mass of neutrons inside a ball just 20 kilometres across. Neutron stars are born when the iron core of a massive star collapses violently inside a supernova. Before they collapse, the inner cores of massive stars can have high angular momentum. Indeed theory suggests that neutron stars could be born rotating at near the maximum value they can endure without flying apart, 1,000 times per second. This is much faster than the spin rates...