

Figure 2 The dual nature of liquid crystals. a, In a bottle the liquid-crystal material looks turbid, owing to the imperfect alignment of the liquid crystal. b, Like a solid, liquid crystals can also show surprising amounts of order. Perfect alignment of individual liquid crystal molecules (an alkylated cyanobiphenyl) on a graphite surface, as observed with a scanning tunnelling microscope (J. Gerritsen, Univ. Nijmegen, The Netherlands; see also ref. 8).

debris, making it incompatible with a clean room environment. Rubbing can also leave streaks and produce electrostatic charge, which degrade image quality. Manufacturers go to great lengths and expense to avoid any sort of contamination, so a contact-free process would be a better long-term solution.

Chaudhari and co-workers¹ have developed a cleaner and more reliable process for aligning liquid crystals. They have replaced the polymer film with a thin, transparent inorganic material, known as diamond-like carbon. Exposing materials like diamond-like carbon or amorphous silicon to a low-energy beam of ions causes a rearrangement of the atoms on the surface. Placing these atoms in contact with a layer of liquid-crystal material causes the liquid crystals to align in one direction. By changing the energy and the angle of incidence of the ion beam, Chaudhari and colleagues are able to vary the tilt angle of the liquid crystal between 0° and 10°.

The IBM team have previously used ion beams to align polymer films without rubbing⁴, but now they can do away with the polymer entirely. They show that light transmission through LCDs containing diamond-like carbon films was typically 97% of that of polymer-based displays. They have also manufactured a laptop with an LCD using the diamond-like carbon film as the alignment layer. Chaudhari and his team have also shown that ion-beam alignment can be used to make monitor displays that have good image quality under different viewing angles. They use a metal mask to selectively overwrite parts of a prealigned film with the ion beam, thereby creating a two-domain display with better contrast at oblique viewing angles.

Other manufacturers are likely to follow up the IBM work with their own studies. Replacing rubbing by ion-beam alignment is an attractive idea, but the costs of this new

technology in terms of processing time and equipment need to be studied. Processing reliability, product durability and image quality will need to be investigated. Chaudhari and co-workers have paid attention to this in their prototype displays, but an industrial release of the technology is a separate and significant task. An alternative to rubbing that has not yet made it into factories is using light to align the polymer films^{5,6}. Another option developed by Fujitsu⁷ uses a type of liquid crystal that is aligned perpendicular to the substrate, rather than tilted. This configuration is radically different from conventional LCDs and leads to new issues in manufacturing and display operation.

Monitors with LCDs are currently more expensive than those with bulky cathode-ray-tubes. New manufacturing methods could bring down the costs, opening up the huge but highly price-competitive television market to LCDs. The main efficiency

improvements in the past decade have come from LCD production on larger and larger glass substrates (Fig. 1) and from changes in factory layouts. A rubbing machine for even larger substrates will be a nightmare for engineers to build and operate. Contact-free alignment, whether using ion beams or another technique, is a way to avoid the rubbing process on this scale. ■

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1. Chaudhari, P. *et al. Nature* **411**, 56–59 (2001).
2. Zocher, H. *Naturwissenschaften* **13**, 1015–1021 (1925).
3. van Aarle, N. J. A. M. & Tol, A. J. W. *Macromolecules* **27**, 6520–6526 (1994).
4. Chaudhari, P. *et al. Jpn J. Appl. Phys.* **37**, L55–L56 (1998).
5. Gibbons, W. *Nature* **352**, 49–50 (1991).
6. Schadt, M. H., Seiberle, H. & Schuster, A. *Nature* **381**, 212–215 (1996).
7. Ohmura, K., Kataoka, S., Sasaki, T. & Koike, Y. *SID Int. Symp. Digest of Technical Papers XXVIII* 845–848 (Society of Information Display, San Jose, CA, 1997).
8. Rastegar, A., Škarabot, M., Blij, B. & Rasing, Th. *J. Appl. Phys.* **89**, 960–964 (2001).

Protein interactions

Unspinning the web

Jeff Hasty and James J. Collins

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 issue¹, 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^{2,3}, 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 Internet⁴ and metabolic networks⁵, should be both error-tolerant and vulnerable to attack⁶. Jeong and colleagues demonstrate that these properties do indeed exist by using protein-deletion data⁷ to show 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 out⁸ 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^{6,4,9}. 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.

Modelling work¹⁰ has shown how power-law networks can arise from simple dynamical rules on the basis of evolutionary principles. This latter study demonstrates that power-law connectivity is a property of networks that are in a state of transitory expansion, suggesting that the connectivity properties of a network are a signature of its particular evolutionary state. If this is correct, it implies the existence of networks that do not follow power laws. For example, the modelling work indicates that newly developed networks are, by nature, sparsely connected and are best described by exponential distributions. Moreover, models of this type may also be relevant to the observed power-law distributions of protein family sizes¹¹, in which a 'family' consists of proteins that share sequence similarity and have similar biological functions. In this context, a power-law distribution implies the existence of 'mega-families' composed of a large number of proteins that are both structurally and functionally similar.

From a biomedical standpoint, Jeong and colleagues' findings¹ suggest that it may be unwise to select a highly connected protein as a drug target, given that inactivation of the protein could prove to be fatal or highly disruptive to the cell. Accordingly, a better strategy may be to target a less well connected protein that has a similar function. In this regard, understanding the connectivity of the network could provide likely candidates through the principle of 'guilt by association' — that is, if two proteins interact with one another, they are probably involved in similar cellular functions^{2,12}.

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1. Jeong, H., Mason, S. P., Barabási, A.-L. & Oltvai, Z. N. *Nature* **411**, 41–42 (2001).
2. Uetz, P. *et al.* *Nature* **403**, 623–627 (2000).
3. Xenarios, I. *et al.* *Nucleic Acids Res.* **28**, 289–291 (2000).
4. Barabási, A.-L. & Albert, R. *Science* **286**, 509–512 (1999).

5. Jeong, H., Tombor, B., Albert, R., Oltvai, Z. N. & Barabási, A.-L. *Nature* **407**, 651–654 (2000).
6. Albert, R., Jeong, H. & Barabási, A.-L. *Nature* **401**, 130–131 (1999).
7. Costanzo, M. C. *et al.* *Nucleic Acids Res.* **28**, 73–76 (2000).
8. Vogelstein, B., Lane, D. & Levine, A. J. *Nature* **408**, 307–310 (2000).
9. Simon, H. A. *Models of Man* 145 (Wiley, New York, 1957).
10. Slanina, F. & Kotrla, M. *Phys. Rev. E* **62**, 6170–6177 (2000).
11. Bader, J. S. <http://xxx.lanl.gov/abs/physics/9908032>
12. Oliver, S. *Nature* **403**, 601–603 (2000).

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 supernova¹. 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

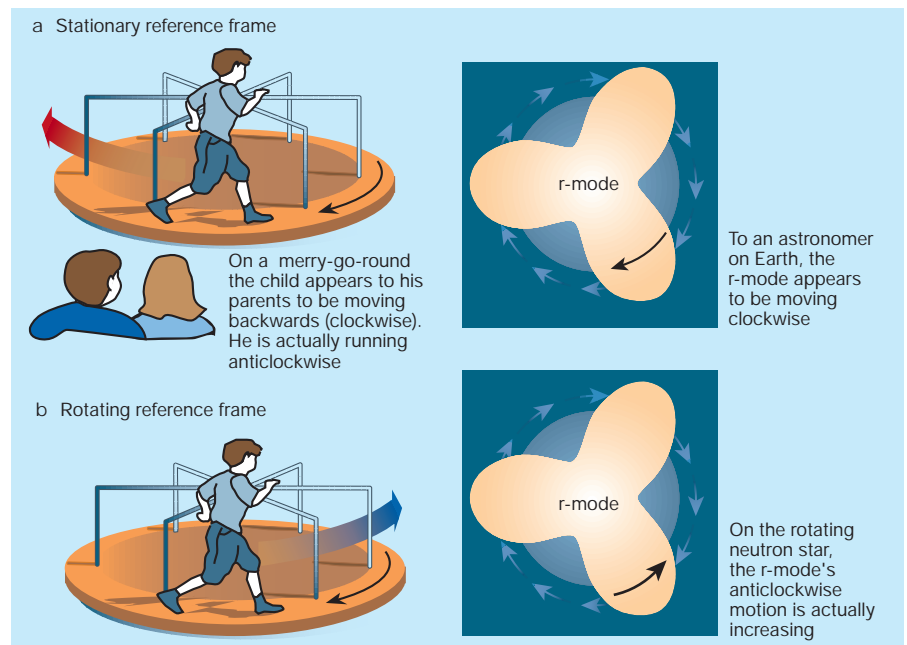


Figure 1 Rotating neutron stars and gravity waves. The growth of r-modes can be understood through an analogy with a child running anticlockwise on a clockwise-spinning merry-go-round. a, If the child is running slower than the merry-go-round is spinning, he appears to his parents sitting on a nearby bench to be moving clockwise (although slower than the merry-go-round). In the case of a spinning neutron star, an r-mode moving slowly in the opposite direction to the spinning neutron star will appear to an observer on Earth in the 'stationary reference frame' to be moving with the spin of the neutron star. The gravitational waves created by the current variations of the r-mode carry away angular momentum, causing the r-mode to slow down in the observer's stationary frame. b, In the rotating reference frame of the merry-go-round, the child is running in the opposite direction to that of the spinning merry-go-round. When the child runs faster in this frame, he appears to slow down in the stationary reference frame of his parents. Similarly, when the r-mode emits gravitational waves and slows down in the stationary reference frame of the observer, the r-mode velocity in the rotating reference frame of the neutron star is actually accelerating, causing the r-mode amplitude to grow. As the amplitude grows, more gravitational waves are emitted, leading to a runaway process. New calculations^{2,3} show that this process may be responsible for slowing down rapidly spinning neutron stars.