

process, Haworth *et al.* now suggest a third, decidedly less complicated, approach — to isolate a pulse associated with a single half-cycle cutoff by spatial filtering⁶. The isolation results from careful phase matching so that only the single half-cycle cutoff produces on-axis emission, whereas the lower energy emissions occur on a ring.

In the longer term, the potential of such ability to measure and control the phase of single pulses goes beyond the study atoms to the manipulation of the processes taking

place within molecules. For example, it has been predicted that the phase can be used to break the left–right symmetry of a dissociating molecule and allow precise control over the dynamics and outcome of its dissociation¹⁰.

The development of techniques to measure and control the CEP of light pulses provides a new level of control in optics, bringing it closer to the level commonly achieved in the radiofrequency domain. Exploiting this control to achieve new

insight into the interaction of light and matter has only just begun.

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COMPLEX NETWORKS

Role model for modules

Traditionally, complex networks are classified on the basis of their global properties. But taking into account the modular structure of the network leads to a better understanding of how the underlying systems work.

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Statistical physics of complex systems strives for universality. The field is geared to discover common principles governing the organization and functioning of such diverse systems as living cells, the Internet or large social groups. Recent studies of these and other biological, technical and sociological networks have raised hopes; it was shown that networks underlying an extremely broad variety of complex systems do indeed share global properties. Many large real-world networks are scale-free¹ — that is, the distribution of

the numbers of immediate neighbours that a node in the network has (known as its ‘degree’) scales as a power law. The degree distribution is a very important topological property of a network, but it is just the first step towards the understanding of the overall connectivity pattern. Deeper insight follows by considering the fact that not every node has the same role within a network. In a real-world network, there will be always groups of some description — be it geo-political units of the Internet or of air-transportation networks, or functional clusters in biological networks. These groups are summarized as ‘modules’, subsets of nodes within which connections are dense; between modules, connections are sparser². Writing on page 63 of this issue, Roger Guimerà and colleagues³ provide a general framework to investigate

the role that modularity plays in shaping up complex networks.

The discovery of ubiquitous scale-free architecture¹ in a wide variety of real-world networks was quickly followed by the realization that in spite of similarities between them, networks in diverse complex systems differ in their higher-level topological properties. To give an example, the three networks in Fig. 1 have identical degree distributions, but distinctly different global architectures. Higher-level topological properties include the abundance of particular small subgraphs — known as network motifs⁴ — and degree–degree correlations, which are correlations between the degree of a node and the degree of the nearest neighbours^{5–7}. In social networks, high-degree nodes (hubs) preferentially

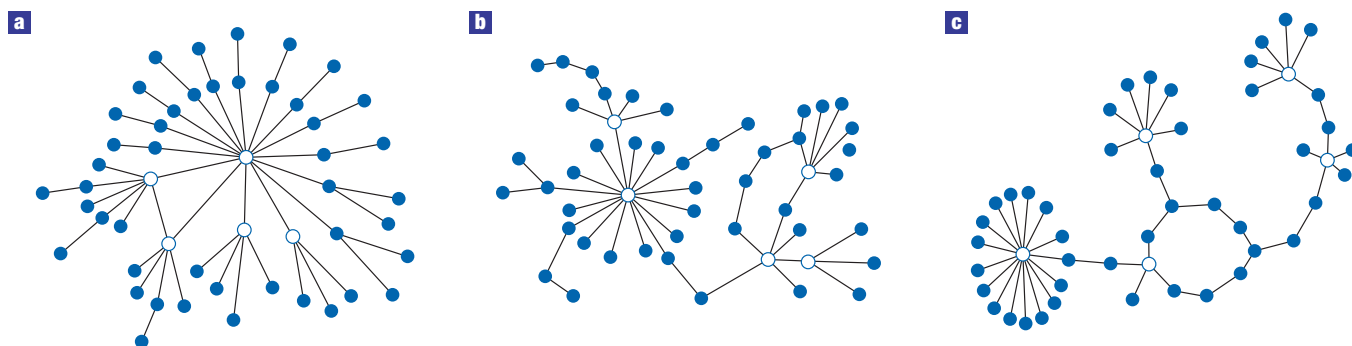


Figure 1 Equal, but very unlike. When looking at the global property known as degree distribution, these three networks are identical. The overall architectures, however, are very different. In **a**, highly connected nodes (or hubs), marked as open circles, tend to link to each other, in **b** they have no preference whatsoever, and in **c** they tend to avoid each other.

link to each other⁵ (similar to the situation depicted in Fig. 1a), whereas hubs in most biological networks avoid each other⁶ (see Fig. 1c). The correlation profile of the Internet is more complicated⁷ and reflects its hierarchical organization in which low-degree 'user' nodes connect to mid-level Internet Service Providers with intermediate degrees, which in turn are connected to highly-connected global hubs.

Guimerà *et al.*³ now extend our understanding of these connectivity patterns. They advocate that the classification of nodes should not be based exclusively on their degree but also on their position with respect to the modules present in the network. Both hubs and less-connected nodes can be classified either as being peripheral (or provincial) — that is, its neighbours tend to belong to the same module — or as connectors, nodes that efficiently link different modules. This classification scheme captures the intuitive notion that it is not just the quantity but also the quality of neighbours that matters.

For biological networks this approach is related to an earlier classification scheme⁸ dividing highly connected proteins in physical interaction networks into 'party' and 'date' hubs. Party hubs interact with most of their partners at once (that is,

they tend to belong to the same functional module), but date hubs prefer to meet their partners one at a time at different external or internal conditions. It is likely that party and date hubs in protein interaction networks⁸ roughly correspond to provincial and connector hubs in the more general definition of Guimerà and colleagues³.

The generalization of the classification scheme leads to important conclusions. First, in a whole series of real-world networks that Guimerà *et al.*¹ looked at, intermodular connectivity patterns fully account for the observed degree–degree correlations (with the notable exception of the network formed by physical protein–protein interactions). Second, Guimerà and colleagues³ find statistically significant patterns in how different categories of nodes connect to each other (they call these patterns 'role-to-role connectivity profiles'). This extends and refines an earlier concept of the correlation profile^{6,7} in that, for example, the 'repulsion' between hubs in protein interaction networks is shown to be limited to connector hubs and does not involve provincial hubs. Role-to-role connectivity profiles allow complex networks to be divided into two main classes. Intriguingly, the first class contains networks used for transport or flow of materials where conservation laws

apply — air-traffic and metabolic networks, for example — and the second class seems to be optimized for signalling and information transfer, such as in protein–protein interactions and the Internet.

Another important lesson learned from the work by Guimerà *et al.*³ is that to discover characteristic topological patterns in a complex network one needs to compare each case to a series of null-models of progressively increasing complexity. Whenever a higher-level topological property is studied, it makes sense to compare the real network with its randomized version⁷ preserving all known lower-level features such as the degree distribution or the extent of modularity. Only such a comparison ensures that overrepresentation of a higher-level pattern does indeed constitute a new result, and is not just a direct consequence of some previously reported property.

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BIOPHYSICS

Pushed to the limit

Viruses come in neat packages. The genetic material of a virus, which is passed into a host cell during infection, is bound up inside a shell of proteins, known as a capsid.

William S. Klug and colleagues have made both a theoretical and a practical study of the behaviour of a virus capsid under pressure (*Phys. Rev. Lett.* **97**, 228101; 2006). Their work underlines the importance of the Föppl–van Kármán (FvK) number — a dimensionless ratio of stretching to bending stiffness — in determining a capsid's resilience.

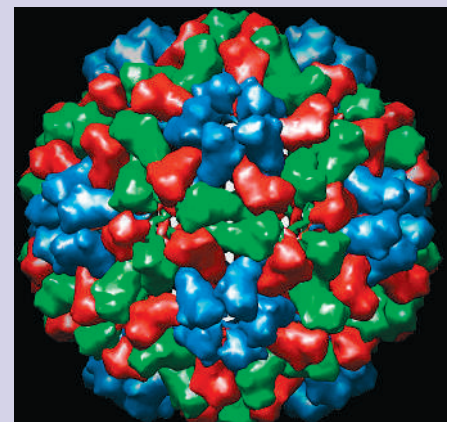
The FvK number is defined as YR^2/κ , where Y is the two-dimensional Young's modulus of the in-plane elasticity of the shell, R is the radius of the shell and κ is the out-of-plane bending modulus. The FvK number is already thought to be a factor in the morphology of capsids: if its value is lower than the so-called buckling threshold, the shell is almost spherical; if not, the shell is polyhedral.

According to Klug and colleagues' simulations, low FvK number (~100) also results in a linear force–indentation response, which breaks down only at

very deep indentations. But for higher FvK values (>400), the relationship becomes nonlinear at lower indentations and discontinuities appear.

That behaviour is borne out in their experimental tests on an empty capsid of cowpea chlorotic mottle virus (CCMV, pictured), prodded using the tip of an atomic force microscope. The CCMV capsid has an outer diameter of 24–28 nm, and a shell thickness of 2–4 nm. At pH 6, its force–indentation response is linear up to an indentation equivalent to 70% of the capsid diameter — suggesting a low FvK number. At that point, the capsid becomes incompressible (the two inner surfaces are in contact), but the process is reversible, and the authors report minimal hysteresis over repeated measurements.

Previous work at pH 5 told a different story: that nonlinearity kicks in at around 30% indentation, and a much higher FvK value is favoured. But the CCMV capsid is known to swell as the pH value of its surroundings is increased from 5 to 7, and that could be behind the seeming 'softening' of the capsid. Energetic considerations using



Ginzburg–Landau theory suggest a reduced effective Young's modulus comes into play, which in turn means a lower FvK value.

The change from high to low FvK value with the swelling doesn't, however, translate into a shape change, despite the earlier matching of FvK number to morphology. That, say Klug *et al.*, means the FvK number is more a general indicator of elastic response than had been thought.

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