hidden-order transition are therefore vital. The photoemission data[4] should be seen in the context of a rising tide of activity, both experimental and theoretical, to explain the mysteries of this material. ❒

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COMPLEX NETWORKS

Structure comes to random graphs

Incorporating structural features into random-graph calculations should bring theoretical models describing the properties and behaviour of complex networks closer to real-world systems.

Raissa M. D'Souza

Many social, technological and biological systems are best described as a collection of interacting agents, parts or molecules. Insight into their behaviour can be gained through mathematical models of random networks, where we consider a collection of nodes with edges connecting them at random. Random networks — also called random graphs — show phase transitions[1,2], such as the sudden emergence of large-scale connectivity as a function of the density of connections. For real-world systems, such behaviour can have important consequences, from enhancing the reach of telecom and transportation networks to increasing the possible extent of a viral outbreak. Also, random-network formulations provide models for studying, for instance, percolation phenomena on networks with differing connectivity properties and the sudden formation of so-called dense *k*-cores (subgraphs of highly connected nodes)[1,2], and provide insights into how we might alter the onset of phase transitions[3]. These random constructions, however, typically assume that all connections between nodes are added independently of one another, thus missing key structural features found in real-world networks. Now, writing in *Physical Review Letters*[4], Mark Newman shows how to incorporate small-scale structural elements into calculations of random networks, bringing the structures studied mathematically closer to their real-world counterparts. In particular, the refined calculations of critical properties should enable better predictions for real systems.

The importance of structural elements in social networks has long been recognized, starting with the role of triangles, or triads, connecting together groups of three nodes[5]. Triads reflect transitivity, the property that individuals sharing a common friend are reasonably likely to be direct friends themselves. Consider a network of scientific collaboration in which nodes are scientists and edges connect coauthors. Over time, disconnected scientists sharing a common coauthor often meet, begin collaborating and become direct coauthors, thus gaining an edge. In a now seminal paper[6], Watts and Strogatz proposed that triangular patterns exist in many contexts, and demonstrated evidence for their presence in the neuronal network of the worm *Caenorhabditis elegans* and in a power-grid network. They defined a 'small world' network as one showing high 'clustering' (that is, many triangles) together with short paths connecting all pairs of nodes. Many more systems with small-world structures have been identified subsequently.

Watts and Strogatz also proposed a mathematical small-world model that accounts for clustering[6], but it places unrealistic restrictions on local patterns of connectivity. A more general starting point is the configuration-model approach[1] introduced by Bollobás in 1980 and Molloy and Reed[7] in 1995, which considers all possible networks that can be constructed such that each node has a specified number of edges. In 2001, Newman, Strogatz and

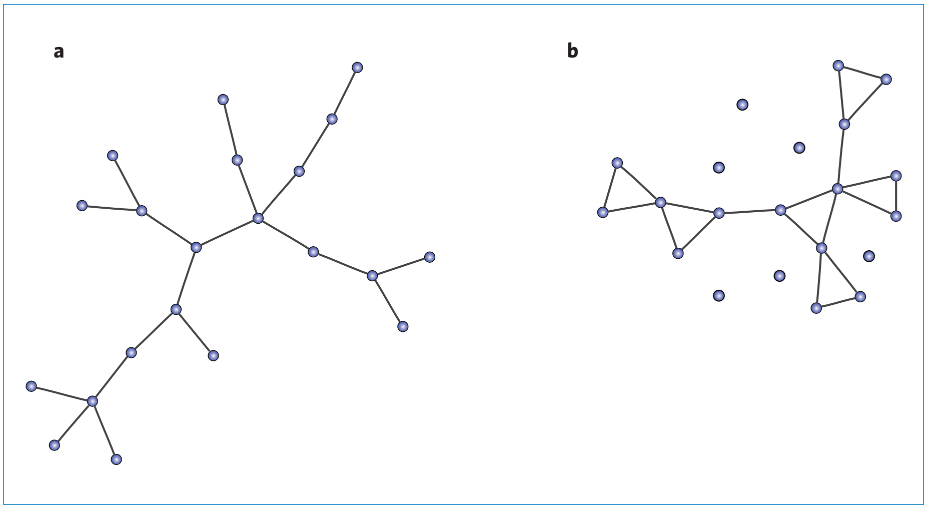

Figure 1 | Triangles limit the extent of connectivity achievable. **a**,**b**, Both networks consist of 21 nodes and 20 edges, but in **b** six nodes are disconnected. Triangles, however, aid the extent to which an infection can spread over the connected portion of the graph, owing to there being numerous alternative paths connecting nodes.

Watts[8] showed how so-called generating functions, commonly used in statistical physics, allow us to compactly enumerate over all configurations and to calculate properties of this ensemble of networks, opening up for mathematical analysis new types of systems, such as networks with directed edges, in which the relationships between nodes are not symmetric. To be valid, generating-function approaches have so far required that networks be tree-like, meaning there are no closed loops and, hence, no triangles. However, Newman[4] now introduces a combinatorial approach extending generating-function techniques to include small-scale structures. He explicitly incorporates triangles by considering two properties for each node, namely a specified number of both single edges and edges involved in triangles, and shows how to construct the expected joint distribution of single edges and triangles per node. This joint distribution can easily be measured in a real-world network and input into Newman's calculations, even if there are correlations between the two properties, as is often the case.

The 'tree-like assumptions' of previous approaches overestimate the probability of finding long chains of connected nodes. With clustering, many edges must go towards closing the third legs of triangles, reinforcing local connectivity (Fig. 1). Newman calculates a number of resulting consequences that could affect important network phenomena such as the spread of diseases or ideas, or the resilience of network connectivity (that is, whether a network maintains large-scale connectivity as its nodes fail or are deliberately removed). For example, the presence of triangles significantly lowers the disease virulence required for a large-scale outbreak of an infection to occur. Generating-function formulations with tree-like connectivity have previously been used to model the spread of real viruses over human contact networks[9]. The modifications introduced by Newman[4] should enable refined calculations with more relevant predictions.

Newman's framework extends, in principle, to enumerating over more complex structures, such as combinations of triangles, squares and hexagons, and also to accounting for directed edges. Hopefully, this is a step towards unifying mathematical formulations of random graphs with 'bottom up' numerical approaches, such as the identification of motifs in systems biology[10] and the exponential random-graph models used in social-network analysis and statistics[11], which allow us to numerically generate the ensemble of random graphs consistent with specified structural properties. (Note that as used in statistics, the term 'clustering' refers not to transitivity but to a method of dividing data into subgroups of similar elements.) One important issue remains: before acting on the predictions made using random-network models, we must still ask how the properties of an ensemble of networks relate to a particular individual realization of a real-world network. ❐

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ARROW OF TIME

Forward and back

Time as a concept has intrigued philosophers for, well, a long time. Is it intrinsic to the Universe, or is it a human construct that helps us to describe the world around us in terms of equations? To the question "what did God do before the beginning of time?", St Augustine is said to have quipped that He was preparing hell for those who dared to ask such questions. But ask such questions physicists must, no matter how dire the ever-lasting consequences. So here we go…

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The idea that time flows in one direction is intuitive: we get older, greyer, balder and, no matter how much we may wish it, we can never go back. Physicists define this forward direction in the language of the second law of thermodynamics: in a closed system entropy never decreases — the Universe moves forward in time towards disorder. The problem is that the fundamental equations that we use to describe our world are not sensitive to this direction; they work equally well with time going forwards or backwards. This is Loschmidt's paradox, named after the nineteenth-century Austrian physicist and chemist who said that irreversible processes should not emerge from time-symmetric dynamics.

Lorenzo Maccone now proposes a way to reconcile our everyday notion of time with quantum mechanics (*Phys. Rev. Lett.* (in the press); preprint at <http://arxiv.org/abs/0802.0438v2>, 2008). His basic idea is that changes that involve an increase or a decrease in entropy can both take place, but the decreasing cases do not leave any lasting trace: "the only physical evolutions we see in our past, and which can then be studied, are those where entropy has not decreased."

The caveat for the second law of thermodynamics is that all systems must be uncorrelated. However, correlations between us, as an observer, and other systems do exist even if we are not aware of them. A process that leads to a decrease in correlation would lead to a reduction in entropy; however, the observer would not be aware of them, as memories are correlations and would have been erased. Maccone notes that even a super-observer who can follow all correlations will not see an increase in entropy. St Augustine would not be impressed!

DAVID GEVAUX