Romanesque networks

Steven H. Strogatz

Newly won evidence shows that many real-world network systems obey a power-law scaling, just as if they were fractal shapes. Could this be the harbinger of a new architectural law for complex systems?

At lunch a few weeks ago, a colleague abruptly pulled a massive vegetable from his briefcase and passed it around the table. He was offering the rest of us a head of Romanesque broccoli — to ponder, not to eat.

The surface of a Romanesque is exquisitely symmetrical, sporting dozens of knobbly florets, each a miniature version of the entire structure, and each built from even smaller copies of the whole (Fig. 1). On page 392 of this issue, Song, Havlin and Makse[1] show that this same kind of symmetry, called self-similarity, is shared by a wide array of networked systems, from the hyperlinked pages of the World Wide Web to the biochemical reactions underlying cellular metabolism.

The pervasiveness of this symmetry hints at a new architectural law for complex systems. Roughly speaking, many large, interconnected systems are tied together in the same way across increasing levels in their hierarchical organization. The links between clusters of nodes, and between clusters of clusters, and so on, obey the same statistical trends as the links between individual nodes themselves.

To quantify these ideas, Song et al.[1] borrow tools from fractal geometry and statistical physics. Fractals are self-similar shapes[2]. They have been studied for decades, first in pure mathematics (where they were initially derided as monsters), and later in the natural sciences, to help researchers analyse such erratic phenomena as the 'burstiness' of Internet traffic and the shapes of cities as they grow.

A fractal geometer might characterize the roughness of Romanesque broccoli by computing its 'box dimension', as follows. Represent the broccoli's surface as an enormous collection of points, and divide the space around the surface into a fine lattice of cubic boxes, a three-dimensional analogue of graph paper. The boxes that intersect the broccoli's surface contain points; the others remain empty. The key is that if you make the boxes bigger, you need fewer of them to cover the same set of points. Specifically, the number of occupied boxes N decreases with ℓ, the side length of the cubes, according to a power law: $N(\ell) \propto \ell^{-d}$. The exponent d is the box dimension. For classical, non-fractal shapes, d reduces to the usual dimension: $d = 1$ for a line or a smooth curve, and $d = 2$ for a

Figure 1 **Fractal vegetable. Fractals are intricately repeated shapes, like the surface of this Romanesque broccoli, in which the parts resemble the whole across several levels of resolution. The work of Song et al.[1] indicates that many complex networks, from protein–protein interaction maps to the collaboration graph of Hollywood film actors, are 'self-similar' in much the same way.**

plane or a smooth surface. But for the wildly corrugated surface of the Romanesque, it turns out that $2 < d < 3$, a result that strikes the uninitiated as bizarre.

To generalize this box-counting method to networks, Song et al.[1] had to define a suitable collection of non-overlapping boxes of size ℓ. The difficulty is that for most social or biological networks, there is no natural euclidean space surrounding the network, so ℓ has to be defined intrinsically, using the network itself. The solution is to define the distance between two nodes as the number of links in the shortest chain between them. For instance, in a friendship network your immediate friends are one step away from you, friends of a friend are two steps away, and so on. Next, Song et al. enumerated all the ways to partition the network into distinct boxes of size ℓ. The rules are that two nodes can be in the same box if the distance between them is less than ℓ; each node must be in some box; and no node is allowed to be in two or more boxes.

For a large network, there are a tremendous number of such partitions. By exhaustive searching, Song et al. found the partition requiring the fewest boxes, and then examined how this minimal number N depends

on the resolution ℓ. They found that many (but not all) real-world networks obey a power-law scaling, $N(\ell) \propto \ell^{-d}$, just as if they were fractal shapes.

More evidence of self-similarity came when Song et al. 'renormalized' their networks. Adopting a standard technique in condensed-matter physics, the authors now ignored the microscopic details of how the nodes were connected within a given box, and focused instead on how the boxes were connected to each other. (Two boxes are defined as being connected if any of their constituent nodes are linked.) In effect, renormalizing the network coarsens it, with boxes now playing the role of super-nodes. The coarsened networks satisfy the same power-law scaling, with the same value of d, suggesting that boxes are wired together in the same way as individual nodes.

These results raise some puzzles of interpretation. First, what do the boxes really mean? Although it's tempting to think of them as something like modules[3], communities[4] or network motifs[5], the boxes have no known functional significance, raising the possibility that the observed self-similarity might contain an element of numerology. On the other hand, some real networks

(for example, the Internet backbone) and some standard models (such as random graphs[6] and preferential attachment models of scale-free networks[7]) lack the self-similarity reported by Song et al., indicating that such scaling is not automatic and, consequently, that it can used as a benchmark for testing models of network structure. Second, it's odd that networks should find themselves configured as fractals. In statistical physics, power laws and self-similarity are associated with phase transitions — with systems teetering on the brink between order and chaos. Why do so many of nature's networks live on a razor's edge? Have they self-organized to reach this critical state[8], perhaps to optimize some aspect of their performance, or have they merely followed one of the

manifold paths to power-law scaling[9], full of sound and fury, signifying nothing? ∎

Steven H. Strogatz is at the Center for Applied Mathematics and the Department of Theoretical and Applied Mechanics, 212 Kimball Hall, Cornell University, Ithaca, New York 14853-1503, USA.
e-mail: strogatz@cornell.edu

1. Song, C., Havlin, S. & Makse, H. A. *Nature* **433**, 392–395 (2005).
2. Falconer, K. *Fractal Geometry: Mathematical Foundations and Applications* (Wiley, Chichester, 1990).
3. Hartwell, L. H., Hopfield, J. J., Leibler, S. & Murray, A. W. *Nature* **402**, C47–C52 (1999).
4. Girvan, M. & Newman, M. E. J. *Proc. Natl Acad. Sci. USA* **99**, 7821–7826 (2002).
5. Milo, R. *et al. Science* **298**, 824–827 (2002).
6. Erdös, P. & Rényi, A. *Publ. Math. Inst. Hung. Acad. Sci.* **5**, 17–61 (1960).
7. Barabási, A.-L. & Albert, R. *Science* **286**, 509–512 (1999).
8. Bak, P., Tang, C. & Wiesenfeld, K. *Phys. Rev. Lett.* **59**, 381–384 (1987).
9. Newman, M. *Nature* **405**, 412–413 (2000).

Sexually transmitted diseases

Epidemic cycling and immunity

Bryan Grenfell and Ottar Bjørnstad

Are syphilis epidemics caused by external factors such as human sexual behaviour, or are factors intrinsic to the pathogen more important? Comparing the dynamics of syphilis and gonorrhoea provides some clues.

The great Renaissance physician and scholar Girolamo Fracastoro achieved lasting fame for his early observations on the contagion theory of the transmisssion of infectious disease[1]. In 1530, he also coined the name for syphilis — which was then spreading rapidly through Europe — in an extended allegory written in Latin hexameter (epidemiologists were more culturally rounded in those days). In Fracastoro's poem, the god Apollo is angered by a shepherd, Syphilus, and afflicts him with the new disease. On page 417 of this issue, Grassly

et al.[2] provide a more down-to-earth explanation of the dynamic processes underlying the incidence of syphilis.

Whether fluctuations in epidemics are governed by external drivers (such as behaviour, climate — or the gods), or by intrinsic processes that arise from the dynamic feedback between host and pathogen populations, has been debated since the early 1900s. This controversy parallels long-standing ecological arguments about the relative role of extrinsic (environmental) forces and intrinsic, nonlinear dynamics in driving

population fluctuations[3]. Arguably, ecologists are more familiar than epidemiologists with the potential of nonlinear dynamics to drive cycles. This is ironic, because many infectious diseases have excellent historical records of incidence and a simple natural history — an ideal combination for exploring the underpinnings of dynamic fluctuations[4,5].

Comparative approaches, where differences in the dynamics of various infections can be related to biological differences in the underlying host–pathogen interactions, are particularly powerful in studying this problem[6]. Grassly et al.[2] use this approach to explore the dynamics of syphilis and gonorrhoea. They base their analysis on disease notification statistics from the United States, where these two sexually transmitted diseases are endemic. The authors use time series of annual disease reports for 68 US cities to demonstrate marked 8–11-year cycles in syphilis incidence from the 1960s to the 1980s. These cycles had previously been attributed to changes in factors extrinsic to the host–pathogen interaction, particularly to changes in human sexual behaviour. If this were the case, however, there should be correlated fluctuations in gonorrhoea because of its similar transmission route and infectious period. Grassly et al. demonstrate that there is no such correlation: gonorrhoea shows slow trends rather than cycles during the same period.

The authors use mathematical models to reveal that the distinct behaviours of syphilis and gonorrhoea arise from their different interactions with the human immune system. Thus, the simplest explanation for the periodicity in syphilis incidence is that it results from nonlinear interactions that are fundamental to the host–pathogen transmission process.

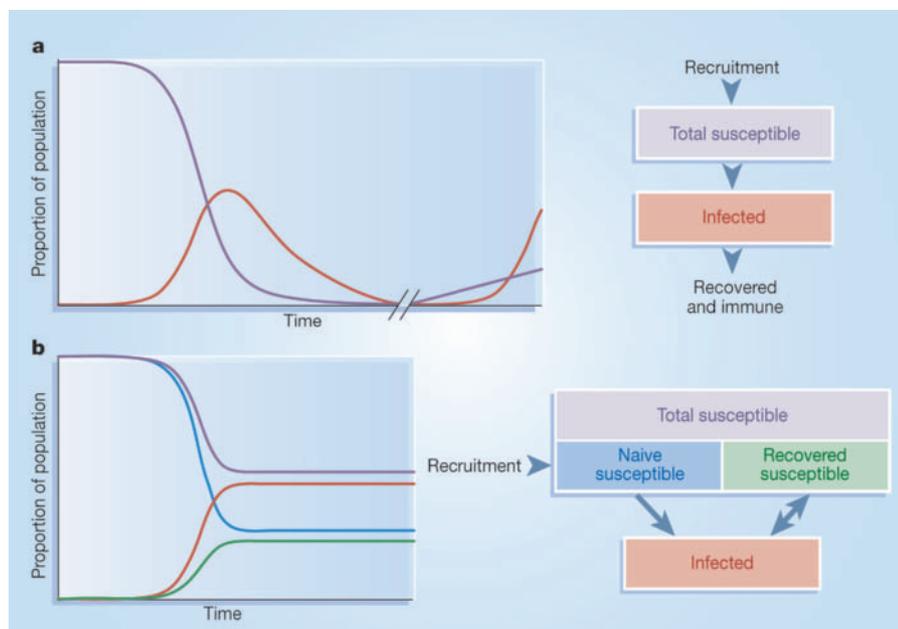Syphilis stimulates significant — albeit

Figure 1 **The impact of immunity on the dynamics of epidemics. a, Dynamics of the basic susceptible–infected–recovered (SIR) model, assuming that the infection attacks a naive susceptible population. Because of prolonged immunity following recovery, the supply of susceptible individuals becomes exhausted and the epidemic extinguishes itself. After the epidemic, new recruits augment the susceptible class until a further epidemic is possible (shown schematically here). This is the basis of syphilis dynamics, as shown by Grassly et al.[1]. b, The susceptible–infected–susceptible (SIS) model, where there is no immunity to reinfection (as with gonorrhoea). Unlike the SIR model, total susceptible numbers are replenished by a flow of previously infected individuals, so that the epidemic moves smoothly to an equilibrium level (analogous to the carrying capacity of logistic models in ecology[8]), rather than declining.**