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THE “NEW” SCIENCE OF

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I then summarize related empirical studies and discuss some of the issues associated with interpreting empirical data. Finally, I review preliminary progress on applications of network models to dynamical processes like disease spreading and information exchange. Throughout the discussion, I focus on the motivation and interpretation of ideas and results, referring the reader elsewhere (Newman 2003c) for the mathematical details. And although I concentrate on developments that seem most relevant to social networks, it is worth bearing in mind that many of the same results have been applied to, or motivated by, problems in other disciplines.

MODELS OF NETWORK STRUCTURE

Small-World Networks

An early contribution to the new science of networks, and one that captures some of its major themes, was that by Watts & Strogatz (1998), in which the authors made several related but distinct points:

1. Real-world networks are neither completely ordered nor completely random, but rather exhibit important properties of both.
2. Some properties of these networks can be embodied by simple mathematical models that interpolate between order and randomness. In Watts & Strogatz's specific example, "order" was represented by a uniform one-dimensional lattice,[1] where each node was connected to its k nearest neighbors on the lattice, and "randomness" was characterized by a tunable parameter p that specified the fraction of randomly rewired links (see Figure 1*a*).
3. These properties can be quantified with simple statistics: for example, the clustering coefficient C of a network is a measure of local density, and the average shortest path length L is a global measure of separation. In the case of the proposed model, L and C can be measured as a function of p.
4. When $p = 0$ (completely ordered), the network is "large" [$L(0) \square N\ 2k$] and "highly clustered" [$C(0) \square 3\ 4$], and when $p = 1$ (completely random), it is "small" [$L(1) \square \ln(N)\ \ln(k)$] and "poorly clustered" [$C(1) \square k\ N$], suggesting that path lengths are short only when clustering is low.
5. However, the model exhibits a broad region of p values in which $C(p)$ is high relative to its random limit $C(1)$, yet $L(p)$ is, roughly speaking, as "small" as possible (see Figure 1*b*). Watts & Strogatz (1998) coined the term

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[1] Throughout this paper, the term "lattice" is used in the physicist's sense of a *crystal lattice* (roughly, a low-dimensional grid), not the mathematician's sense of a partial ordering on a set of elements [as in, for example, *Galois Lattices* that have been used to represent affiliation networks (Freeman & White 1993)].

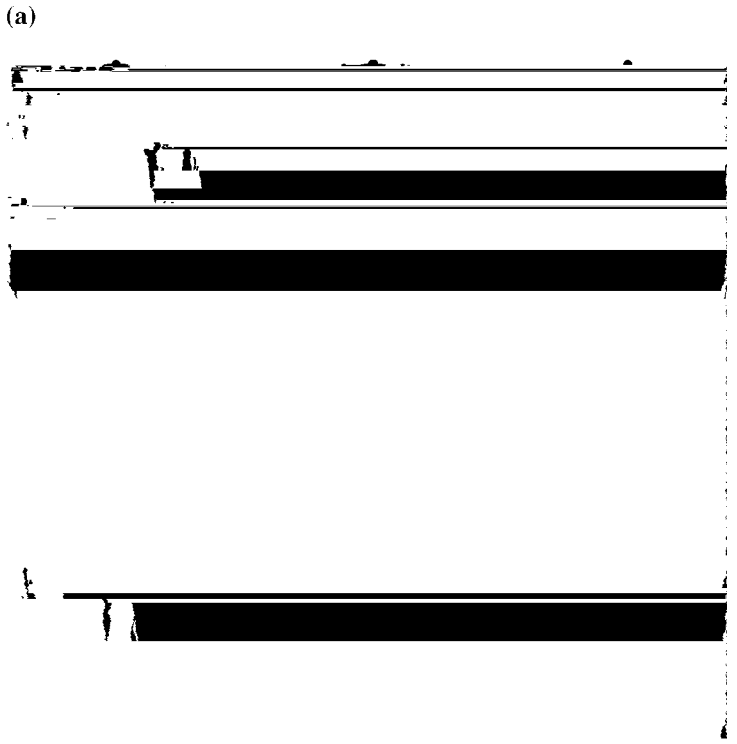

Figure 1 (*a*) Schematic of the Watts-Strogatz model. (*b*) Normalized average shortest path length L and clustering coefficient C as a function of the random rewiring parameter p for the Watts-Strogatz model with $N = 1000$, and $\langle k \rangle = 10$.

small-world networks[2] to refer to networks in this class, in reference to the early work of Pool & Kochen (1978), and subsequent experiments of Milgram and colleagues (Korte & Milgram 1970; Milgram 1967; Travers & Milgram 1969).

6. Because the conditions required for any network to belong to the small-world class (some nontrivial local order, combined with just a small fraction of long-range, random shortcuts) were relatively weak, Watts & Strogatz (1998) predicted that many real-world networks—whether social networks

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[2] Watts & Strogatz were not, in fact, the first to use the term small-world networks: that distinction belongs to Eugene Garfield (1979), who used it in a review article on the topic of small-world research. The term does not appear to have caught on, however, until Watts & Strogatz defined it to refer to networks with high local clustering and short global path lengths.

or otherwise—ought to be small-world networks. They then checked this prediction by considering three network datasets—the affiliation network of movie actors, the power transmission grid of the western United States, and the neural network of the nematode *Caenorhabditis elegans*—and found that all three examples satisfied the small-world criteria.

7. Finally, the authors claimed that the structure of a network can have dramatic implications for the collective dynamics of a system, whose connectivity

many of their individual details. This finding had two implications, both of which fit naturally into a physicist's worldview: (*a*) that at least some interesting features of even very complex networks could be captured by extremely simple models, and (*b*) that metrics and models devised to address social network problems might be usefully applied in other disciplines as well. Condensed matter physicists have subsequently analyzed what is now called the Watts-Strogatz model, or variants of it, in great detail (Barrat & Weigt 2000; Barthelemy & Amaral 1999; Dorogovtsev & Mendes 2000; Kulkarni et al. 2000; Newman & Watts 1999a,b; Newman et al. 2000). Specifically, it has been shown that whereas clustering C is a function of the fraction of random shortcuts p (Barrat & Weigt 2000), the average shortest path length L

and r_{ij} is the lattice distance from i to j. When $\gamma = 0$, random edges are formed with uniform probability (equivalent to the original Watts-Strogatz model), and when γ is sufficiently large, only local ties are possible. Clearly in neither limit is the network searchable—in the former case because short paths cannot be found (Kleinberg's earlier result), and in the latter case because no short paths exist. In fact, Kleinberg proved that only when $\gamma = d$, the dimension of the underlying lattice, would the network be searchable in the sense that the number of steps required to forward a message from a randomly chosen starter to a randomly chosen target is "short"[4] (Kleinberg 2000a). More generally, what Kleinberg showed is that network structure is important not only locally, i.e., because an individual's neighborhood provides him with information and resources, but also globally in that it enables him to navigate when searching for information or resources outside his neighborhood.

Affiliation Networks

Another problem with the Watts-Strogatz model, and also with Kleinberg's, is that both models rely on the presence of some underlying lattice substrate to (*a*) guarantee global connectivity and (*b*) provide a distance metric that is independent of the network distance. Clearly, social networks are not built on a lattice substrate, so the question arises whether one can account for clustering, short path lengths, and searchability in a less artificial manner. One alternative method of generating networks with small-world properties that uses more plausible assumptions, but is still parsimonious, is based on a bipartite (or "two mode") affiliation network (Wasserman & Faust 1994) comprising two classes of nodes: N actors each of whom belongs to one or more of M groups. As shown schematically in Figure 2, "single mode" (unipartite) networks can then be generated by projecting the bipartite network onto either the set of actors (the "actor affiliation network") or the set of groups (the "group interlock network"), where the standard projection assumes that actors/groups/F2/grour 1 Tf32.3(interlps)-24 Tf.2(netw)10(orks)d8.7s cy4 Tc/F2271s1

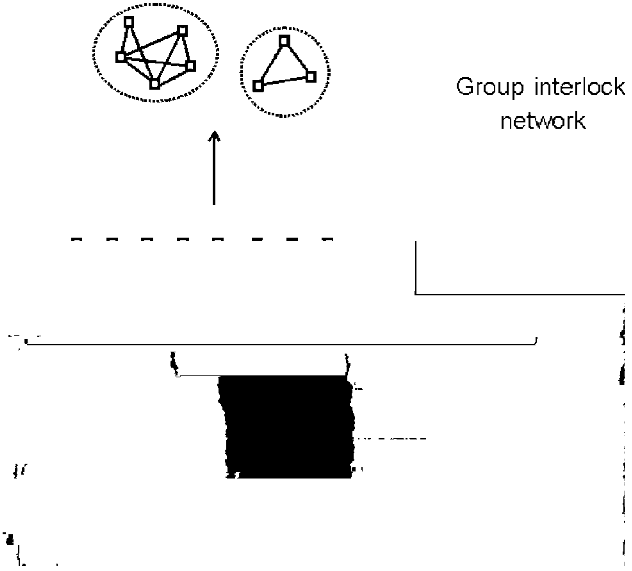

Figure 2 Bipartite (two mode) affiliation network (*center*), defined in terms of N actors belonging to M groups, along with unipartite (single mode) projections onto the set of groups (*top*) and actors (*bottom*). A connection in the single mode network occurs whenever two actors/groups share at least one group/actor respectively.

unipartite projection of a random bipartite network can account for much of the observed clustering in empirical affiliation network data. Because two actors are by definition connected whenever they share a group, the single mode projections exhibit many overlapping cliques that contribute to high local clustering, even when individuals choose groups at random. Furthermore, random bipartite networks almost always have short global path lengths; thus both actor affiliation and group interlock networks will inevitably fall in the small-world class.

Subsequently, the basic affiliation model has been generalized in two ways. First, Newman & Park (2003) have derived a number of results for random affiliation networks in which ties between actors in the single mode projection exist only with a probability that is proportional to the number of shared groups and inversely proportional to the size of each group. And second, Watts et al. (2002) have proposed a model of *generalized affiliation networks* in which distance between groups is defined according to some number of social dimensions (e.g., geography and occupation), and individuals are characterized by the coordinates of the groups to which they belong. Ties between individuals are then allowed to form with a probability that depends on the distance between the corresponding groups and a tunable homophily (Lazarsfeld & Merton 1954) parameter that biases interactions toward or away from similar nodes. They find that when groups are classified according to more than one social dimension and when interactions are homophilous

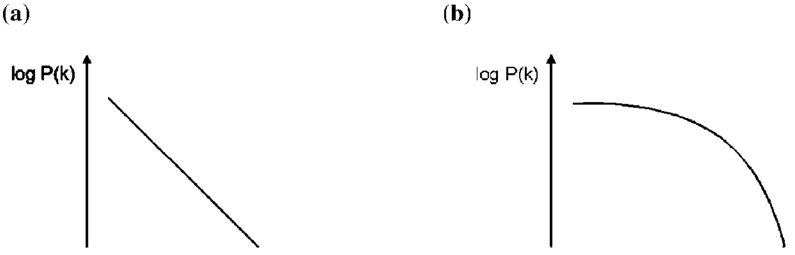

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Figure 3 (*a*) Power law with exponent α, when plotted on a double-logarithmic scale, appears as a straight line with negative slope α. (*b*) A normal-type distribution (i.e., with finite mean and variance) plotted on a double-logarithmic scale displays a well-defined cutoff, above which probabilities are effectively zero.

that all three exhibited power-law tails [a claim later shown to be incorrect in the case of the power grid (Amaral et al. 2000)], and coined the term *scale-free networks* to describe them.

Barabasi & Albert (1999) also proposed a simple mathematical model (known as the BA model) to account for their empirical observations. Their model—a special case of a much earlier model developed by Simon (1955) and later applied to citation networks by Price (1980)—embodied two mechanisms: population growth and preferential attachment. The intuition behind the first mechanism is straightforward: Real networks grow in time as new members join the population. The mechanism of preferential attachment then expressed the notion, analogous to Simon's "Gibrat principle" (Simon 1955), Merton's "Matthew Effect" (Merton 1968), and Price's "cumulative advantage" (Price 1980), that newly arriving nodes will tend to connect to already well-connected nodes rather than poorly connected nodes. Specifically, Barabasi & Albert defined the probability $p(k_i)$ of an existing node i with k_i links receiving a new link as $p(k_i) = ck_i$ (where c is a normalizing constant). Barabasi & Albert showed that over a sufficiently long time horizon, the degree distribution of a growing network exhibiting linear preferential attachment would converge to something in the form of Equation 2 with an exponent $\alpha = 3$.

A number of subsequent models have been proposed that expand on the basic theme of growth with preferential attachment.

1. When either the creation of additional ties (Amaral et al. 2000) or the process of searching for additional neighbors (Mossa et al. 2002) is costly, the power-law distribution of degree becomes truncated, yielding a scaling region with a characteristic cutoff ("broad-scale networks"), or even a narrow distribution

around a well-defined mean (“single-scale networks”), depending on the costs involved (Amaral et al. 2000).

2. When nodes are endowed with different intrinsic “attractiveness” (Bianconi & Barabasi 2001), or else are allowed to continue making

poorly connected nodes, representing them as isolates rather than as members of the groups with which they would naturally be associated. Recently, Girvan & Newman (2002) have introduced a new method for identifying community structure that departs from the standard approach in two ways: (*a*) instead of computing pairwise node similarity, they compute edge betweenness centrality [roughly speaking, Freeman's (1977) notion of betweenness centrality, but applied to edges instead of nodes]; and (*b*) instead of adding edges to an empty graph, they delete them from the original graph in order of highest betweenness first, recomputing the betweenness of all remaining edges after each deletion. Their results are a striking improvement over hierarchical clustering methods, which they compare directly with their own for a number of test networks. In addition, they identify plausible communities in previously untested networks, such as the NCAA football competition and the research community of the Santa Fe Institute. Subsequently, Newman & Girvan (2003) have extended their method to include different measures of edge centrality and also to optimize thmunity 1T(optimizere)-3909hm such that the ratio of in-group to out-of-group ties in the partitioned network is maximized.

Intrpreting Empirical Data

When interpreting the measured structural featureD[(them)-301.9(2s.6(struc-)]Tg273bkg8

recent empirical network findings suggest that care is required when claiming universal features of networks, particularly when the claims in question extend to the collective dynamics of networked systems—the topic to which we now turn.

NETWORKS AND COLLECTIVE DYNAMICS

Without doubt, the structure of real-world networks, and the evolution thereof, are legitimate scientific problems the general resolution of which presents us with substantial modeling and empirical challenges. It remains the case, however, that networks are interesting to sociologists (and to researchers in other disciplines as well) primarily because they are thought to influence individual (micro) and collective (macro) behavior, as well as the relationship between the two. At the individual level, network exchange theory (Cook et al. 1983, 1993; Walker et al. 2000; Willer 1999), for example, has demonstrated that the outcomes experienced by actors who engage in bilateral exchanges depend not only on their intrinsic preferences and perceived status differences, but also on the larger patterns of relations (i.e., the network) within which both actors are embedded. And at the collective level, sociologists since Solomonoff & Rapoport (1951) have been aware that the nature and arrangement of network ties may play an important role in fostering the global spread of information and disease (Boorman & Levitt 1980, Rapoport 1963), or facilitating collective action (Granovetter 1973). Unfortunately, although a rigorepidemiologists have preferred to develop modeling approaches that assume individuals within any given population mix randomly (Anderson & May 1991, Bailey 1975, Murray 1993).

The basic model of disease spread, introduced by Kermack & McKendrick (1927), is known as the SIR model representing the three basic classes—susceptible (S), infected (I), and removed (R)—that any given individual can inhabit at a particular time. The corresponding dynamics are as follows: (*a*) for each unit of time during which a susceptible is in contact with an infective, he or she may become infected with some probability β (the infectiousness of the disease); (*b*) infectives are removed from the population at some rate r (either by achieving immunity or by death); and (*c*) removed individuals are reinjected into the susceptible pool (through loss of immunity) at some other rate ρ. The populations $S(t)$, $I(t)$, and $R(t)$ [which necessarily sum to $N(t)$, the population size] therefore contain all current information about the state of the system. But because the infection stage requires contact between a susceptible and an infective, an additional assumption (or set of assumptions) is required to specify how individuals in different classes interact. In the basic model, the simplest assumption is made—that individuals interact randomly, in the manner of chemicals being stirred in a beaker. Thus the probability of a susceptible encountering an infective is proportional to the product of the S and I populations, where an interaction coefficient γ is usually introduced to specify the average rate of pairwise interactions. This assumption dramatically simplifies the subsequent analysis, yielding in the limit of large N a set of nonlinear differential equations, which can either be solved explicitly (in trivial cases) or else be used to determine the equilibrium states of the disease (typically the fraction of the population that becomes infected) for different parameter settings and initial conditions.

SIR Models on Networks

Although the bulk of the mathematical epidemiology literature comprises increasingly elaborate versions of the SIR model with random mixing, some progress has been made in analyzing the steady-state behavior of some simple SIR-type models in which interactions are described by a network. Most of this work to date has focused on a generalized class of random network models in which properties like the shape of the degree distribution and the tendency of high-degree nodes to associate with each other (assortativity) can be varied arbitrarily (as opposed to Bernoulli random graphs, in which they are fixed), but that do not exhibit any local or community structure.

Early work by Kretschmar & Morris (1996) focused on the effects of concurrent relations on the spread of sexually transmitted diseases. Individuals were allowed to choose partners at random but were constrained in how many partnerships could be maintained simultaneously. By fixing the average degree of the network at $\langle k \rangle = 1$, Kretschmar & Morris showed that when concurrent relations were forbidden, the network would necessarily disintegrate into N/2 isolated dyads, thus limiting any outbreak of disease. But when concurrency constraints were

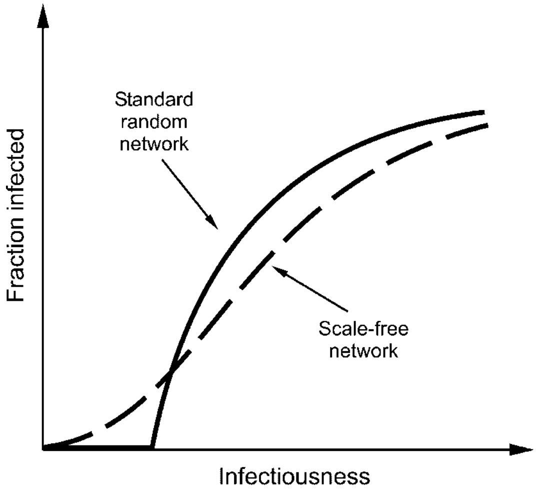

Figure 4 Comparison of disease spreading on Bernoulli (standard) and scale-free random networks. The steady-state fraction of infectives displays a distinct phase transition (i.e., an epidemic threshold) in the case of a Bernoulli random graph, but not for the scale-free network.

lifted, the resulting variance in degree caused the network to exhibit a giant connected component, thereby enabling most outbreaks to reach a finite fraction of the population. Pastor-Satorris & Vespignani (2001) have extended Kretschmar & Morris's notion of concurrency by investigating disease spreading on random networks with power-law distributions of degree. Their main finding has been that infinite random networks exhibiting power-law degree distributions with an exponent $\alpha < 3$ do not exhibit the epidemic threshold predicted by uniform mixing models. Rather, as indicated schematically in Figure 4, the fraction of the population infected in a standard SIR model is finite for all non-zero values of the infectiousness—a result that Lloyd & May (2001) subsequently pointed out had been derived earlier using different methods (Anderson & May 1988). The explanation is that in a scale-free network the presence of highly connected hubs (roughly equivalent to very high concurrency in the language of Kretschmar &

Watts 1999b). The correlation length regulates how far from its source a contagious influence must spread before it "feels" the effect of the shortcuts. Hence an outbreak

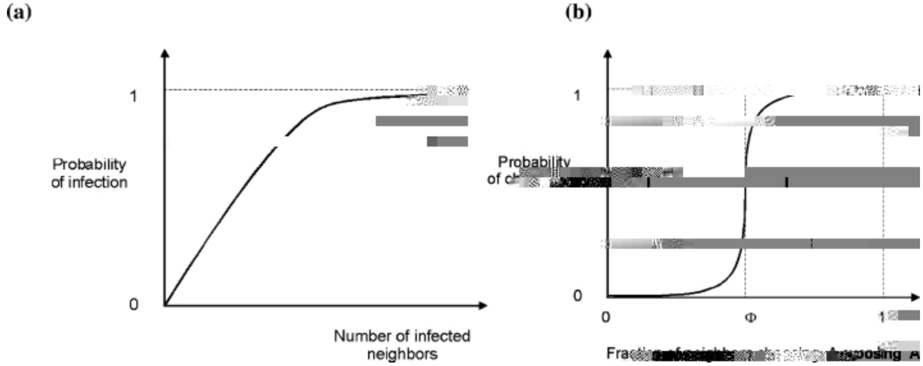

Figure 5 (*a*) The cumulative probability of infection for an SIR-type model increases approximately linearly with the number of exposures to infectives—a consequence of the assumed memory-free nature of biological infection. (*b*) In social contagion, decisions are costly and are affected by the memory of past interactions; hence, the cumulative probability of "infection" exhibits threshold-like behavior.

second or third (or subsequent) exposure, thus resembling Figure 5*b*, where the sudden jump occurs when the individual's "threshold" of belief is exceeded.

Threshold models of this kind arise widely (Boorman & Levitt 1980, Granovetter & Soong 1988, Schelling 1978, Watts 2003) and can display very different collective dynamics than the SIR-type models described above. When individuals are assumed to mix randomly, for example, SIR models admit the possibility that an epidemic can be triggered by an infinitesimal initial seed (even a single infective may suffice), whereas models that embody nontrivial thresholds require an initial critical mass—that is, a finite fraction of the population—before global infection is possible (Dodds & Watts 2004). And when social contagion takes place via a sparse network, epidemics—sometimes called global cascades—can only occur for social contagion when the connectivity of the network is neither too sparse nor too dense (Watts 2002). It is the latter condition that is surprising because in biological contagion greater connectivity always implies a greater possibility that a disease will spread. In social contagion, however, dense connectivity renders many individuals impervious to novel signals, thereby quashing cascades before they can even begin. Another consequence of increasing the connectivity routers in the Internet, airports in the air-transportation system, or individuals in a large organization, nodes in interactive networks are generally susceptible both to endogenous failure—the risk of which rises dramatically whenever a node's limited capacity to process information or material is exceeded by endogenously generated demand—and also to exogenous failure, driven for example by random component breakdown, sickness, accidents, environmental catastrophes, or even intentional attack. A robust network is one that resists one or both kinds of failure, ideally under a wide range of environmental conditions.

Assuming exogenous failures, Albert et al. (2000) demonstrated with computer simulations that scale-free random networks of the kind generated through growth and preferential attachment exhibit much greater resilience to random failures than Bernoulli random graphs, where they defined resilience as the size of the largest connected component remaining after a certain fraction of nodes in the network had been removed. When nodes were removed preferentially, however, in order from highest to lowest degree, the opposite result pertained. The explanation for both results is that the connectivity of a scale-free network is determined almost entirely by the small fraction of highly connected hubs that occupy the tail of the degree distribution. Because random failures are relatively unlikely to affect the hubs, the only nodes that are likely to become disconnected are those that fail. But when the hubs are deliberately targeted, each individual failure has the potential to impact the connectivity of the entire network. Subsequent work (Callaway et al. 2000; Cohen et al. 2000, 2001) has confirmed this basic feature of scale-free networks and extended the findings to more general classes of degree distributions (for example, power-law distributions with finite cutoffs), and also for link as well as node failure (Callaway et al. 2000).

More recently, endogenous failure—due, for example, to network congestion—has begun to be incorporated into models of network robustness (Arenas et al. 2001; Dodds et al. 2003b; Goh et al. 2001; Guimera et al. 2001, 2002). For example, Arenas et al. (2001) have shown that when randomly chosen pairs in a pure hierarchy pass messages to each other, where intermediate nodes incur a small cost for each message forwarded, then at a critical rate of message passing network congestion undergoes a phase transition (Newman & Barkema 1999), above which almost all messages are inhibited by the limited capacity of the small fraction of nodes at the top of the hierarchy. Thus both traditional (Williamson 1975) and also more recent (Bolton & Dewatripont 1994, Radner 1993) economic models of the internal architecture of firms, which typically propose pure hierarchies as the most efficient form of organization, can be seen as ignoring a critical aspect of distributed problem solving—namely the capacity constraints inherent in distributed communication.

Recently, Dodds et al. (2003b) have proposed a model of information exchange in organizational networks that combines the notion of efficiency (understood roughly as maximizing performance at minimum cost of adding network ties) and robustness, finding that a simple algorithm for adding horizontal and vertical ties to a pure hierarchical backbone yields what they call *ultrarobust networks*—networks that simultaneously minimize the likelihood of individual node failure (due to endogenously generated congestion), and also the impact on global connectivity that results from failures arising out of either endogenous or exogenous causes. The key to ultrarobustness, they find, is that organizational networks must exhibit nonhierarchical ties that extend across all scales of the underlying hierarchy—a quantitative result that stands in qualitative agreement with a longstanding body of work in organizational sociology (Burns & Stalker 1961, Granovetter 1985, Lawrence & Lorsch 1967), and is also consistent with recent accounts of firms surviving major disasters (Kelly & Stark 2002, Nishiguchi & Beaudet 2000).

CONCLUSION

As I hope this review has made clear, many of the ideas and metrics of the "new" science of networks have either been borrowed from, or else rediscovered independently of, a distinguished lineage of work in mathematics, economics, and sociology. For example, the intuition that a few random "shortcuts" in the midst of locally dense neighborhoods can generate the structure of small-world networks (Watts & Strogatz 1998) bears a remarkable similarity to Rapoport's (1963) analysis of random-biased nets, which inspired Granovetter's (1973) investigation of the strength of weak ties. Recent Internet-based social search experiments (Dodds et al. 2003) explicitly acknowledge their debt to Milgram's seminal studies (Korte & Milgram 1970, Milgram 1967, Travers & Milgram 1969). The finding that preferential attachment mechanisms in growing networks can lead to what are now called scale-free networks (Barabasi & Albert 1999) turns out to be a special case of Simon's (1955) implementation of the Gibrat principle, better known in sociol-

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