

Revisiting “scale-free” networks

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Summary

Recent observations of power-law distributions in the connectivity of complex networks came as a big surprise to researchers steeped in the tradition of random networks. Even more surprising was the discovery that power-law distributions also characterize many biological and social networks. Many attributed a deep significance to this fact, inferring a “universal architecture” of complex systems. Closer examination, however, challenges the assumptions that (1) such distributions are special and (2) they signify a common architecture, independent of the system’s specifics. The real surprise, if any, is that power-law distributions are easy to generate, and by a variety of mechanisms. The architecture that results is not universal, but particular; it is determined by the actual constraints on the system in question.

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Introduction

In 1999, a pair of papers appeared in the leading scientific journals of our day: the first in *Nature*, written by Albert-László Barabási, Hawoong Jong (a post-doc), and Barabási’s then graduate student, Réka Albert, and the second in *Science*, by Barabási and Albert.^(1,2) The papers were crucial for the status of network theory in the sciences at large, for the careers of the authors, and for expectations in the larger scientific community of the possibility of understanding complex systems. In the first paper, Barabási and his colleagues reported the apparently startling discovery (independently reported twice that year)^(3,4) that the distribution of nodal connections (or hyperlinks) in the World Wide Web seems to follow a power law (that is, the frequency of nodes [web pages] with connectivity k falls off as $k^{-\alpha}$, indicating high variability in the number of connections, with the number of large hubs being small and that of weakly connected nodes, large). In the second paper, he and Albert presented a model that could computer-generate such a distribution, while also giving a new name to power law distributions (dubbing them “scale-free”), and with that name, a new meaning (see BOX 1). Implicitly invoking a reference to the physics of phase transitions that Barabási

later makes explicit (the term “scale-free”, he explains, is “a name that is rooted in statistical physics literature”),⁽⁵⁾ they argue that the finding of a power law distribution “indicates that large networks self-organize into a scale-free state”.⁽²⁾ The basic hypothesis of their model was that, as new connections form, they attach to a node with a probability proportional to the existing number of connections (growth and preferential attachment). In other words, the rich get richer, a process otherwise known as the “Matthew effect”.⁽⁶⁾ In addition to generating distributions resembling those observed for the Web, Barabási and Albert also suggested that “Growth and preferential attachment are mechanisms common to a number of complex systems, including business networks, social networks (describing individuals or organizations), transportation networks, and so on. Consequently, we expect that the scale-invariant state observed in all systems for which detailed data has been available to us is a generic property of many complex networks, with applicability reaching far beyond the quoted examples.”

Within a year, Barabási and his colleagues produced six more papers on “scale-free” networks, two of which appeared in *Nature*, creating an even bigger stir.^(7,8) The first, “Error and attack tolerance of complex networks”, made the cover of the July 27 issue of *Nature*, and the story was immediately picked up by BBC news and CNN. The second, “The large-scale organization of metabolic networks”, appeared in October, and opened the floodgates for the application of network theory in biology. Just weeks later, in a *News and Views* on the complexities of the network in which the p53 tumor suppressing gene is embedded, Bert Vogelstein, David Lane and Arnold J. Levine suggested “One way to understand the p53 network is to compare it to the Internet. The cell, like the Internet, appears to be a ‘scale-free network’: a small subset of proteins are highly connected (linked) and control the activity of a large number of other proteins, whereas most proteins interact with only a few others. The proteins in this network serve as the ‘nodes’, and the most highly connected nodes are ‘hubs’.”⁽⁹⁾

Reports of the generality of scale-free networks soon appeared everywhere—in genetics, neuroscience, proteomics, signal transduction studies, research on power grids, transportation systems, food-webs, sexual networking, epidemiology, economics, etc. George Johnson, writing on “scale-free” networks for *The New York Times* quotes Ricard V. Solé: “These results suggest that nature has some universal

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BOX 1. What does “scale-free” mean?

Barabási and Albert introduced the term in 1999⁽²⁾ as a descriptor of graphs and networks and it has since become a generic label for any graph or network in which vertex connectivities follow a power-law distribution. Unfortunately, however, the term has acquired a number of associations over the intervening years that are often, albeit erroneously, taken to follow from this definition and have accordingly led to considerable confusion. One obvious association that the term invites is with self-similarity and, indeed, power-law distributions are trivially self-similar in the sense that they are invariant under rescaling. But there are many other uses of the concept of self-similarity relevant to graphs that are not inherent in power-law degree distributions.⁽⁴⁵⁾ Other associations, encouraged by Barabási’s remark that the term “is rooted in statistical physics literature”, mistakenly link the structure of such networks with properties of phase transitions. Many authors link the term with the particular model of growth and preferential attachment proposed by Barabási and Albert to explain the evolution of such networks, and still others with an architecture dominated by a few central hubs. But the mere fact that a nodal degree distribution follows a power law actually implies nothing either about the mechanism giving rise to it or about its particular architecture.

organizational principles that might finally allow us to formulate a general theory of complex systems.”⁽¹⁰⁾ By the end of 2000, the study of “scale-free” networks was well on its way to becoming an industry, and expectations for the understanding of complex systems began to soar. Since then, claims for the power of “scale-free” network models have only escalated, and general enthusiasm only grown. *Science* (September 2003), *New Scientist* (April, 2002), *Complexity* (September/October, 2002) and *The European Physical Journal B* (March, 2004) have all published special issues on the subject. Indeed, references to a new “law of nature” and a “universal architecture” linking complex systems across the natural, social, and engineering sciences have become commonplace.

Of particular interest is the wide-spread influence of this work on recent studies of complex biological networks, and findings of scale-free properties have been reported for many kinds of networks in a wide range of organisms (e.g. metabolic,⁽¹¹⁾ protein-protein interaction,^(12–14) transcription regulation,⁽¹⁵⁾ protein domain networks,⁽¹⁶⁾ etc). Although some exceptions have been noted (e.g. Giot⁽¹²⁾

BOX 2. Random networks, Poisson and Gaussian distributions, and Power laws

The term *random* is conventionally used in two senses: in one sense of the term (as in, e.g. a random network) the term implies unweighted probabilities; in the other, it implies unpredictability but allows for weighting of the probabilities. Using the term in its first sense, a random network is understood to be constructed from n nodes by choosing m links with equal probability. In such a network, the degree distribution p_k follows a Poisson law: $p_k \sim \lambda^k e^{-\lambda}/k!$, where λ is the average degree. (Note that, if z is large, the distribution approaches a Gaussian.) Intuitively, such a distribution means that most nodes have a degree close to the average, and that the number of nodes with a given degree decays exponentially fast away from the mean degree. Other network architectures are characterized by degree distributions that are Gaussian (which may be achieved through growth without preferential attachment), that decay exponentially: $p_k \sim ce^{-ak}$ (achievable, e.g. through preferential attachment without growth), or, perhaps most commonly, that follow a power-law: $p_k \sim ck^{-\alpha}$ as $k \rightarrow \infty$, where $0 < \alpha < 2$. One of the most important features of power-law degree distributions is that, unlike Poisson, Gaussian and exponential distributions, they are characterized by high variability in the number of links, with a small number of nodes having many links, and a much larger number of nodes having few links. But a network following a power-law degree distribution can be constructed in many different ways, ranging from a biased but, using the term in its second sense, still random distribution of links (e.g. as in the Barabási-Albert model of growth with preferential attachment) to a completely non-random distribution of links designed to optimize performance (e.g. the HOT structure discussed in Li et al.⁽³⁴⁾ and illustrated in Fig. 1).

et al report that “the distribution of interactions per protein decays faster than the power law predicted by a ‘rich-get-richer’ model of scale-free networks”), the majority of papers support the claim of the virtual ubiquity of “scale-free characteristics”.⁽¹⁵⁾ Wolff et al. infer large philosophical implications from these findings: “the power-law connectivity distribution seen in scale-free networks seems to emerge as one of the very few universal mathematical laws of life”.⁽¹⁷⁾

The basic assumptions underlying the claims (and astonishing success) of Barabási and his colleagues are that power law distributions run counter to traditional expectations and, perhaps for this reason, their occurrence implies some deep meaning. “For more than 40 years”, Barabási and Bonabeau

write, “science treated all complex networks as being completely random”.⁽¹⁸⁾ Accordingly, when first discovering that the connectivity of the Web follows a power-law distribution, Barabási was astonished. The networks that he was looking at were clearly not entirely random.¹ The data showed him “that millions of Web-page creators work together in some magic way to generate a complex Web that defines the random universe. Their collective action forces the degree distribution to evade the Bell curve. . . and to turn the Web into a very peculiar network”.⁽¹⁹⁾ The question was, could the mystery (or magic) behind this extraordinary phenomenon be explained? Might there even be some “simple laws” underlying most complex networks? Barabási is a physicist, and physicists are trained to look for simple explanations. Furthermore, he had been trained in the methods of statistical mechanics, and was abundantly familiar with another area in which power-law distributions had surfaced, namely in the distribution of fluctuations in macroscopic properties (e.g. density, magnetization, specific heat, etc.) of systems in a phase transition. There, in the recent dramatic successes of physicists like Ken Wilson, Leo Kadanoff, Michael Fischer (and others) unlocking the mysteries of phase transitions, power laws did indeed appear to acquire deep significance. As Barabási explains,

Nature’s normal abhorrence of power laws is suspended when the system is forced to undergo a phase transition. Then power laws emerge—nature’s unmistakable sign that chaos is departing in favor of order. The theory of phase transitions told us loud and clear that the road from disorder to order is maintained by the powerful forces of self-organization and is paved by power laws. It told us that power laws are the patent signatures of self-organization in complex systems. This unique and deep meaning of power laws perhaps explains our excitement when we first spotted them on the Web. Gazing at the power laws our little search engine carried home from its journey, we caught a glimpse of a new and unsuspected order within networks, one that displayed an uncommon beauty and coherence.⁽¹⁹⁾

Such a glimpse may also help explain the excitement of his colleagues and readers, as well as their receptivity to the idea of “a new and unsuspected order”. The question arises however, *are* power law distributions so new and unsuspected? Also, what in fact do they signify?

A brief history

In claiming that science has “treated all complex networks as being completely random”, Barabási’s primary reference is clearly the mathematics of random networks, pioneered by

Paul Erdős and his collaborator Alfred Renyi. Looking at science through a somewhat wider window, however, one discovers a considerable history to discussions of power law distributions, and even of networks that give rise to such distributions. As Barabási acknowledges, the 19th century Italian economist, Vilfredo Pareto, was well aware of the fact that the distribution of many variables around us departs from the familiar Gaussian distribution. Observing that 80% of Italian land was owned by 20% of the population (his “80:20 rule”), he sought to establish a similar pattern in the distribution of incomes throughout history, and in all societies.⁽²⁰⁾ The first model (based on a variant of preferential attachment) attempting to explain such observations was published by G. Udny Yule in 1925.⁽²¹⁾ By the middle of the century, examples of similar power-law distributions (sometimes referred to as skewed, heavy-, fat-, or long-tailed distributions) were everywhere—e.g. distributions of scientists by number of papers published,⁽²²⁾ of word frequency in prose texts,^(23,24) and of cities by size.⁽²⁵⁾ In 1955, Herbert A. Simon produced a general (analytic) derivation of such distributions with a model virtually identical to that of Barabási and Albert.⁽²⁶⁾ But Simon was cautious, and he concluded his paper by noting that “the frequency with which the Yule distribution occurs in nature . . . should occasion no surprise”.

Simon was not surprised, first, because “The probability assumptions we need for the derivation are relatively weak, and of the same order of generality as those employed in the derivation of other distribution functions—the normal, Poisson, geometric and negative binomial”. But he also reminded his readers that “not all occurrences of this empirical distribution are to be explained by the process discussed here. To the extent that other mechanisms can be shown also to lead to the same distribution its common occurrence is the less surprising. Conversely, the mere fact that particular data conform to the Yule distribution and can be given a plausible interpretation in terms of the stochastic model proposed here tells little about the underlying phenomena beyond what is contained in [our] assumptions. . . .”⁽²⁶⁾

Simon’s paper had a noticeable influence in a number of fields—e.g. economics, management science, urban studies, and scientometrics—but it never made anything like the splash that Barabási and Albert’s paper did. Nor was he writing about networks as such. Thus, when D. J. de Solla Price demonstrated a power-law distribution of links in a network of scientists linked by citation in 1965,⁽²⁷⁾ no reference to Simon appears. Eleven years later, however, when Price derives his observed distribution with yet another version of the preferential attachment model, the omission is corrected.⁽²⁸⁾ In short, as Michael Mitzenmacher concludes from his excellent overview of the history of this literature, “[M]uch of what [computer scientists] have begun to understand and utilize about power law . . . distributions has long been known in other fields.”⁽²⁹⁾

¹The departure from randomness in their preferential attachment model is of great significance to Barabási,^(1,2) but it should not be forgotten that that model is still statistical, generating connections that are still random, albeit under the constraint of preferential attachment [See Box 2].

Finally, to further complicate the history of power law distributions, one more developmental thread needs to be added, one that runs parallel to both the early empirical observations and the attempts to account for them. This is a chapter—launched in the 1930s by the work of French mathematician Paul Lévy on distributions with infinite variance (variously called ‘L-stable’, ‘Lévy’, or ‘Pareto Lévy’ distributions)—belonging to the history of probability theory. Among other contributions, Lévy extended the “Central Limit Theorem” to such distributions, except that, asymptotically, their sum takes the form of a power law function rather than the more familiar Gaussian function. These technical issues are covered in the second volume of William Feller’s canonical text on probability theory⁽³⁰⁾ as well as other subsequent texts, and need not be further considered here. Three general points are however worth noting:

- (1) The essence of Lévy distributions is the presence of extreme high variability in the size of events, and this is just the property found in many naturally occurring or engineered complex systems. That fact is certainly of interest, but to some, it is far from obvious why it requires special explanation, any more than do Gaussian distributions.⁽³¹⁾ Indeed, given existing mathematical, statistical, and data-analytic arguments for the ease with which such distributions can be generated, Walter Willinger and his colleagues suggest that such distributions should be viewed as “more normal than Normal”.⁽³²⁾
- (2) By 1971, the attempt to fit empirical phenomena to such distributions was already so widespread that Feller felt obliged to warn his readers against their overuse by drawing attention to an earlier episode in the history of science exhibiting a similar excess of enthusiasm: in efforts to elevate the principle of ‘logistic growth’ to the status of a ‘transcendental law’. The trouble, Feller explained, “is that not only the logistic distribution but also the normal, the Cauchy, and other distributions can be fitted to the *same material with the same or better goodness of fit*. In this competition the logistic distribution plays no distinguished role whatever; most contradictory theoretical models can be supported by the same observational material.”⁽³⁰⁾
- (3) High variability does not necessarily imply power-law distributions, and current assessments of the commonality of power-laws are probably overestimates.⁽³²⁾ The problem is that power-law behavior is often inferred from plots of relative frequency of occurrence ($f(x)$) of events against size (x) on a log-log scale, but many different kinds of data can be easily approximated by straight lines on such plots. A more discriminating, and hence far better, way to plot the data is to plot the complementary cumulative distribution function ($\bar{F}(x)$) _{∞} against size (x) on a log-log scale, where $\bar{F}(x) = \int_x^{\infty} f(\mu) d\mu$. The difference between these

two methods is clearly illustrated in Figure 2. The left plot shows a wide range of data that can be fitted to a power law of the form $f(x) = Cx^{-(1+\alpha)}$ with values of α ranging from 0 to 1, while the right plot sharply distinguishes between $\alpha = 0$ and $\alpha = 1$.

From data to model:

What do power law distributions in fact signify? To Simon, they seemed common, and their occurrence unsurprising. In his view, their commonality was explained partly by the weakness of the assumptions that his derivation required, but also by the possibility that other mechanisms could be shown to lead to the same distribution. One needs to ask, therefore, just how strong *is* the relation between the occurrence of such distributions and the model of preferential attachment that Barabási and his colleagues—like Simon and Price—used to derive them. Mathematical modeling generally begins with the attempt to formulate a model that reproduces a set of data, but the risks of inferring inversely—from data back to model—are notorious, and for the obvious reason that Simon indicates: there may be other models that give rise to the same data and, if there are, one would need to know which model best describes the systems that actually exist in the real world. In fact, Feller’s emphasis on the logistic curve as “an explicit example of how misleading a mere goodness of fit can be” was motivated precisely by the persistence of such “naïve reasoning”. Historically, biologists especially have been suspicious of mathematical models and on just these grounds, often regarding the invention of models to fit an empirical curve as of little more value than curve fitting with arbitrary many free parameters.

To illustrate the problem, several researchers have recently shown that a given “scale-free” Internet topology can be generated by a number of different models, that of preferential attachment being only one.^(33,34) Lun Li and her co-authors begin by asking (in what they call a “first principles approach”), “What really matters when it comes to topology construction? . . . [M]inimally one needs to consider the role of router technology and network economics in the network design process.” Accordingly, they compare five different ways of generating the same node degree distribution: (1) growth and preferential attachment, (2) the general random graph method (GRG)⁽³⁵⁾ in which each node is assigned its expected degree and edges are inserted probabilistically, according to a probability proportional to the product of the degrees of the two endpoints, (3) heuristically optimal topology (HOT) explicitly designed to optimize performance under existing technological and economic constraints (and resulting in a high speed mesh-like core supported by a hierarchical tree-like architecture with its high degree nodes at the edges; its aim is to aggregate traffic through high connectivity), (4) a topology inspired by the Abilene Network (the national Internet backbone network for higher education currently in use in the US),

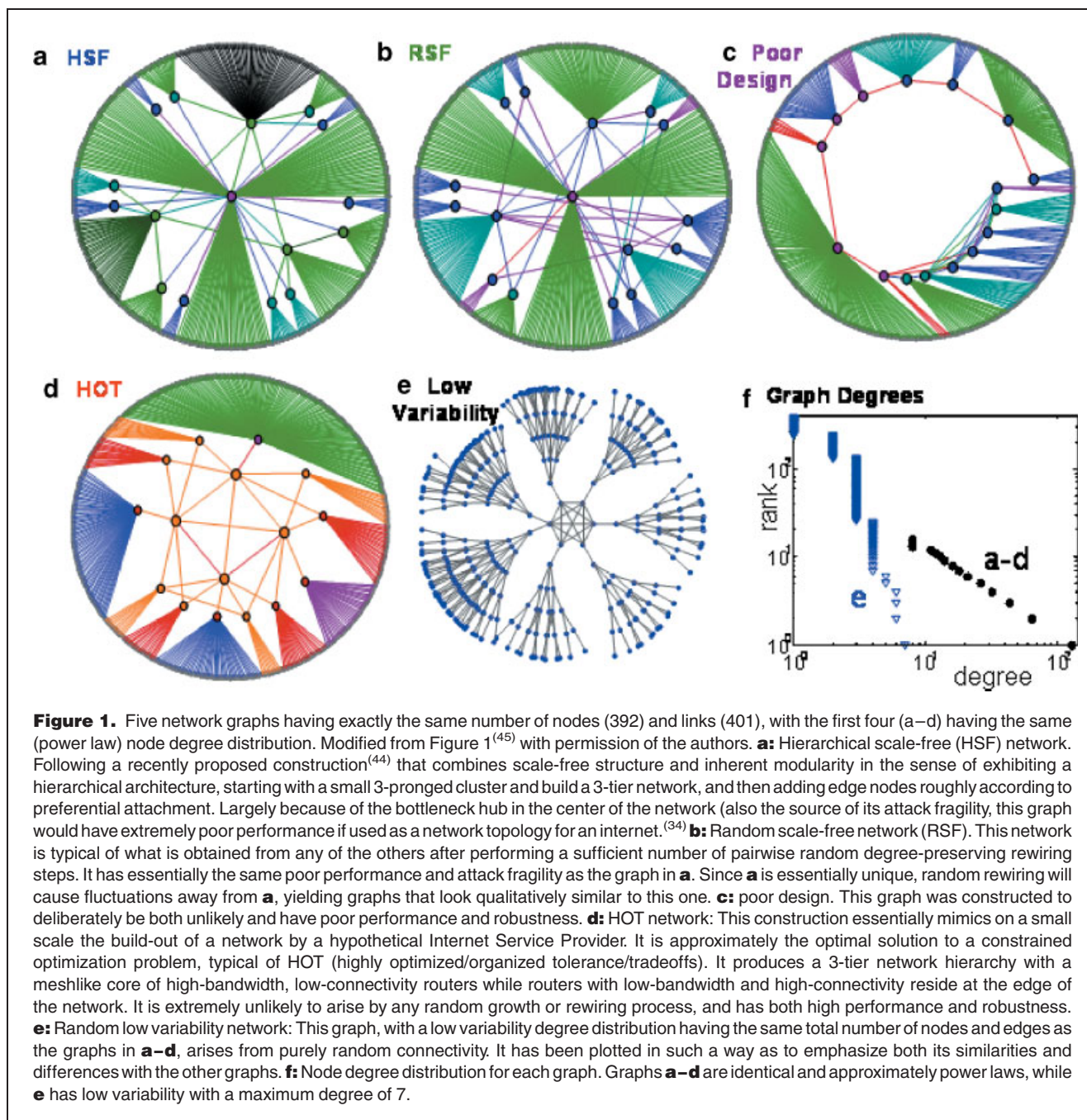
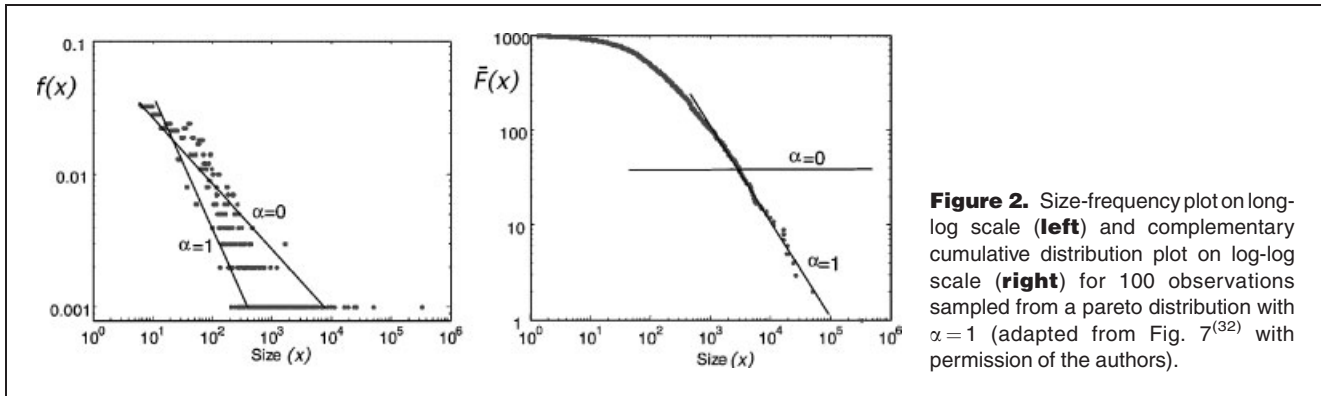


Figure 1. Five network graphs having exactly the same number of nodes (392) and links (401), with the first four (a–d) having the same (power law) node degree distribution. Modified from Figure 1⁽⁴⁵⁾ with permission of the authors. **a:** Hierarchical scale-free (HSF) network. Following a recently proposed construction⁽⁴⁴⁾ that combines scale-free structure and inherent modularity in the sense of exhibiting a hierarchical architecture, starting with a small 3-pronged cluster and build a 3-tier network, and then adding edge nodes roughly according to preferential attachment. Largely because of the bottleneck hub in the center of the network (also the source of its attack fragility, this graph would have extremely poor performance if used as a network topology for an internet.⁽³⁴⁾ **b:** Random scale-free network (RSF). This network is typical of what is obtained from any of the others after performing a sufficient number of pairwise random degree-preserving rewiring steps. It has essentially the same poor performance and attack fragility as the graph in **a**. Since **a** is essentially unique, random rewiring will cause fluctuations away from **a**, yielding graphs that look qualitatively similar to this one. **c:** poor design. This graph was constructed to deliberately be both unlikely and have poor performance and robustness. **d:** HOT network: This construction essentially mimics on a small scale the build-out of a network by a hypothetical Internet Service Provider. It is approximately the optimal solution to a constrained optimization problem, typical of HOT (highly optimized/organized tolerance/tradeoffs). It produces a 3-tier network hierarchy with a meshlike core of high-bandwidth, low-connectivity routers while routers with low-bandwidth and high-connectivity reside at the edge of the network. It is extremely unlikely to arise by any random growth or rewiring process, and has both high performance and robustness. **e:** Random low variability network: This graph, with a low variability degree distribution having the same total number of nodes and edges as the graphs in **a–d**, arises from purely random connectivity. It has been plotted in such a way as to emphasize both its similarities and differences with the other graphs. **f:** Node degree distribution for each graph. Graphs **a–d** are identical and approximately power laws, while **e** has low variability with a maximum degree of 7.

and (5) an additional topology, explicitly designed to be suboptimal, and added purely for purposes of comparison. [See Fig. 1 for similar but more easily visualized graphs that make essentially the same point.]

Comparing the five models according to performance criteria on the one hand (throughput, router utilization, and bandwidth distribution), and the likelihood of occurrence in a random world on the other hand, they find (perhaps not

surprisingly) that the first two topologies (preferential attachment and random graph method) score relatively high in likelihood, but low in performance, while both Abilene and HOT score low in likelihood and high in performance. (As predicted, the designed suboptimal topology scores low in both). In short, topologies designed to optimize performance under existing constraints are effective but improbable. The authors go so far as to conclude that the “likely” topologies “have such bad



performance as to make it completely unrealistic that they could reasonably represent a highly engineered system". Finally, they point out that designed systems also have different kinds of fragilities. They lack the attack vulnerability of "scale-free" networks with high degree hubs at their center through which almost all traffic must flow (their "Achilles heel"), but they are fragile in other ways, ways that are in fact direct by-products of the kinds of robustness for which they were designed:

"[E]ven a small amount of random rewiring destroys their highly designed features and results in poor performance and loss in efficiency. Clearly, this is not surprising—one should not expect to be able to randomly rewire the Internet's router-level connectivity graph and maintain a high performance network!"⁽³⁴⁾

Indeed, in a closely related paper, they conclude, "the recently popular 'scale-free' network models... are in almost every theoretical and practical aspect completely opposite from the real Internet".⁽³⁶⁾

Similar analyses, leading to similar conclusions, have also been undertaken for the metabolic networks in bacteria,⁽³⁷⁾ and there is ample reason to believe that the cautionary warnings presented here about engineering designed systems ought to apply quite generally to systems designed by biological evolution. Biologists have learned that evolution, although it makes critical use of randomly generated variations, leaves remarkably little to chance in the operation of the mechanisms that it finally leads to. Thus it would be quite surprising to find gene, metabolic or protein networks that could continue to function, and in the same ways, after a random rewiring process constrained only by the requirement that the mean number of connections at each node be maintained. Indeed, such insensitivity to the specific details of network topology would probably be as surprising to biologists as they are to engineers. Of course, biological systems are not engineering systems, and notions of *design* in biology are infamously fraught. For the most part, biologists have

contented themselves with strictly metaphorical uses of the term. Nevertheless—and this may well be the important point—they have not been able to do without it. Biological systems have not been designed by any hand—either of man or of God—yet the dependence of their functioning on the precise and coordinated arrangement of their component parts is nowhere in question.

The architectures of social systems introduce still other differences. Duncan Watts and Steven Strogatz⁽³⁸⁾ have made wonderful use of simple mathematical models applied to social networks, but I take the principle moral of their work to be that, however powerful simplifying assumptions can be, however enticing the lure of universality, the specificities of the system can nonetheless prove essential. To take just one example, some of their most interesting results emerged only after they took into account the property that sociologists well recognize as fundamental to social dynamics: social identity. The inspiring work of physicists on criticality taught us that some properties of material systems can be understood without attending to the particular details of the system. But how many properties can be so understood, and which ones? As Watts writes about social systems: "In some respects the behavior of the system is independent of the particulars, but some details still matter. For any complex system, there are many simple models we can invent to understand its behavior. The trick is to pick the right one. And that requires us to think carefully—to *know something*—about the essence of the real thing."⁽³⁸⁾

Is there a moral?

The cover of the 13 April 2002 issue of the *New Scientist* asks, "How can a single law govern our sex lives, the proteins in our bodies, movie stars and supercool atoms?", and continues, "Nature is telling us something..." But the question I have been leading up to is—*Can* a single law govern connectivity in all these disparate realms? And why would we expect that it might?

The search for unifying laws, for universal principles that can bypass the specificity of particular systems to capture the

underlying unity of the world, is a deeply established tradition in physics, and the discovery of such laws has long represented the highest possible achievement of that discipline. Yearnings of this sort are not absent in biology—witness the search for unifying laws in the neo-Darwinian theory of evolution by natural selection, or in the Central Dogma of molecular biology—but in the history of the life sciences such aspirations have long been countered by a very different tradition, one rooted in respect for and even veneration of diversity. Indeed, philosophers of biology now debate the question, Are there laws of biology?^(39,40) Physicists, however, rarely have such misgivings. It is Barabási's experience in the statistical mechanics of critical phenomena that imprints his faith in, as he says, "the unique and deep meaning of power laws". As he himself reminds us, it is the fact that, in the theory of phase transitions, power laws signal self-organization and the emergence of order from disorder, that underlies his excitement at finding these same laws show up in completely different contexts. Here too, he cannot but believe, they must be "nature's unmistakable sign that chaos is departing in favor of order".⁽¹⁹⁾

But what in fact do network structures actually have to do with phase transitions, with criticality, or for that matter, with self-organization? And what do Barabási and his colleagues *mean* by the term "scale-free"? These are all terms that have acquired considerable fluidity as their use becomes widespread; indeed, their very fluidity contributes to their popularity. But my own take is that, while their original technical meanings may play a substantial role in the reception of the arguments that have been put forth, the role that these terms have played in the actual construction of arguments has been primarily evocative.

Let me start with the suggestion of a link to "criticality" and "phase transitions". There is little question that a number of techniques developed to analyze phase transitions in statistical mechanics have proven extremely useful in the development of models for the analysis of complex systems. But these techniques were developed to deal with the abrupt changes of state observed in real systems (gases, fluids, solids), and the obvious question to ask is, do real networks (say, e.g. the internet) exhibit any phenomena analogous to such abrupt changes of state? And if not, is it reasonable to assume that they have critical points? Willinger et al.⁽⁴¹⁾ think not, and even Barabási has come to the conclusion that "Networks are not en route from a random to an ordered state. Neither are they at the edge of randomness and chaos. Rather, the scale-free topology is evidence of organizing principles acting at each stage of the network formation process".⁽¹⁹⁾ Similarly, just how would the concept of self-organization (attractive as that concept undoubtedly is) actually apply to the construction of an internet? Or to the construction of a metabolic network? Notions of criticality and self-organization certainly have meaning in some of the mathematical models used to gain insight about networks, but it is far from evident what relevance

they might have for the real networks arising in the worlds of engineering, biology or social interactions.

All this is not to deny that the science of networks is substantially indebted to the physics of phase transitions; it is. But the source of that debt is a set of analytic tools, developed in statistical mechanics and applied to networks, and not either a new level of explanation or a fundamental principle capable of unifying the structure of complex systems as disparate as "our sex lives, the proteins in our bodies, movie stars and supercool atoms".

Conclusion

Networks of the kind that Barabási and Albert theorized—interconnected complexes that grow according to a principle of preferential attachment (or Matthew effect) and stabilize in a power-law distribution—certainly do exist. Indeed, the industry that their 1999 paper helped to launch might itself serve as a prime example. Among other phenomena, preferential attachment characterizes the growth of fashions or enthusiasms. And, like all other areas of human activity, science too is subject to enthusiasms. But there is a particular requirement in science that a new strategy in scientific research must satisfy if it is to capture the interest of the community: it must generate research. Furthermore, to persist over time, it must be productive in ways that allow the new research to build on itself. Sometimes such enthusiasms can last for a very long time, continuing to fuel the research engine over many generations. More often, however, they are short lived. Whither the current zeal for scale-free networks? So far, it shows no sign of abating: the technical literature continues to explode with reports of still more findings of power-law distributions, cropping up in ever different contexts, and with yet additional applications of the model of preferential attachment. Needless to say, only time will tell, but in the meantime—judging by generally accepted scientific criteria—even this long a run seems surprising. First, power law distributions are neither new nor rare; second, fitting available data to such distributions is suspiciously easy; third, even when the fit is robust, it adds little if anything to our knowledge either of the actual architecture of the network, or of the processes giving rise to a given architecture (many different architectures can give rise to the same power laws, and many different processes can give rise to the same architecture). Finally, even though power laws do show up in the physics of phase transitions, the hope that the resemblance would lead to a "new and unsuspected order" in complex systems of the kind that physicists had found in their analysis of critical phenomena appears, upon closer examination, to lack basis. How then are we to understand its enthusiastic embrace by so many highly respected scientists (perhaps especially surprising, by so many biologists with their traditional skepticism toward mathematical models, particularly when those models offer no more than "mere goodness

of fit”), and by so many of our leading scientific journals (e.g. *Science*, *Nature*, *PNAS*)?

Some possible answers seem obvious: One is the rapid growth of the sector of the publishing industry aimed at the dissemination of scientific achievements in recent years, coupled with the rhetoric of dramatic discovery that has arisen in response to the demands of that market. Another might be found in the remarkably effective uses of language employed in presenting these ideas to scientific readers (of the sort that I have only briefly touched upon here). But there are also other factors as well. At least part of the explanation must surely lie in the rapid changes that have been taking place in biology over the last few years, and in the dramatic reconfiguration that we are beginning to see in relations between the life and the physical sciences. For the most part, these changes have been driven by the explosion of data coming from contemporary genomics, from the complexity that these data reveal, and from the inability of convention models to account for them. Genes, like proteins and metabolites, do not operate as isolated units but rather, as parts of networks that are often extremely complex. And to understand the patterns of gene expression, it is necessary to unpack the immensely tangled webs of signal transduction and gene regulation. Thus, for the first time in recent history, biologists now have strong incentives to welcome the cooperation of physical and mathematical scientists and the application of the kinds of modeling techniques that are the bread and butter of these sciences to their problems. Physicists, engineers and computer scientists have responded in droves, seeing irresistible opportunities in the challenges posed by recent findings in molecular biology.

Inevitably though, the integration of workers from disciplines with such widely different traditions brings challenges of its own. Elsewhere,^(42,43) I’ve written about the important differences in epistemological culture that can be seen between the mathematical and the life sciences in the 20th century, and discussed at length the often acute tensions that such differences have generated. Successful collaboration between scientists coming from these two very different traditions has seemed to me to require critical shifts in perspectives and values on both sides, perhaps more than either side has yet to appreciate. On the one hand, biologists need not only to overcome their traditional antipathies, but also to acquire new skills in mathematical and computational analysis; on the other hand, physicists need to shed many of their most basic assumptions about the nature of theory. In particular, I have argued that the new mathematical biology that is now emerging requires, if it is to be successful, rethinking the meanings of words like *deep* and *fundamental*: what is fundamental in biology, I suggested, is far more likely to be found in the accidental particularities of biological structure arising early in evolution (like, for example, that of DNA) than in any abstract or simple laws. They are fundamental in the sense of having been built in on the ground floor, and hence having

become most deeply entrenched, and not in the sense most familiar to physicists.

Obviously, there are competing views of the best ways for physicists to contribute to biology, and the developments discussed in this paper represent one such alternative approach. The strategy employed in the story of scale-free networks is one that makes full use of the traditional prestige of physics and its achievements. I suspect that few biologists would have responded so positively even as recently as ten years ago, but now that the ice has broken, and the number of physicists, mathematicians, and computer scientists working in biology has grown so large, perhaps a certain amount of competition between different epistemological traditions has become inevitable. How such competition will resolve itself remains to be seen, but it does seem clear that straightforward accommodation was simply too much to hope for.

References

1. Albert R, Jeong H, Barabási AL. 1999. Diameter of the World Wide Web. *Nature* 401:130–131.
2. Barabási AL, Albert R. 1999. Emergence of scaling in random networks. *Science* 286:509–512.
3. Faloutsos M, Faloutsos P, Faloutsos C. 1999. On power-law relationships of the Internet topology. *Comput Commun Rev* 29:251–262.
4. Kumar R, Raghavan P, Rajalopagan S, Tomkins A. 1999. Extracting large-scale knowledge basis from the Web. Proceedings of the 9th ACM Symposium on Principles of Database Systems 1.
5. Barabási AL, Oltvai ZN. 2004. Network biology: Understanding the cell’s functional organization. *Nat Rev Genet* 5:101–114.
6. Merton RK. 1968. The Matthew effect in science. *Science* 159:56–63.
7. Albert R, Jeong H, Barabási AL. 2000. Error and attack tolerance of complex networks. *Nature* 406:378–382.
8. Jeong H, Tombor B, Albert R, Oltvai ZN, Barabási AL. 2000. The large-scale organization of metabolic networks. *Nature* 407:651–654.
9. Vogelstein B, Lane D, Levine AJ. 2000. Surfing the p53 network. *Nature* 408:307–310.
10. Johnson G, NY Times, December 26, 2000. First cells, then species, now the Web. p F–1.
11. Hatzimanikatis V, Li C, Ionita JA, Broadbelt LJ. 2004. Metabolic networks: enzyme function and metabolite structure. *Current Opinion in Structural Biology* 14:300–306.
12. Giot L, et al. 2003. A Protein Interaction Map of *Drosophila melanogaster*. *Science* 302:1727–1736.
13. Li S, et al. 2004. A Map of the Interactome Network of the Metazoan *C. elegans*. *Science* 23 January 303:540–543.
14. Peer B, Jensen LJ, von Mering C, Ramani AK, Lee I, et al. 2004. Protein interaction networks from yeast to human. *Current Opinion in Structural Biology* 14:292–299.
15. Nicholas M, Luscombe M, Babu M, Yu H, Snyder M, et al. 2004. Genomic analysis of regulatory network dynamics reveals large topological changes. *Nature* 431:308–312.
16. Wuchty S. 2001. Scale-free behavior in protein domain networks. *Mol Biol Evol* 18:1694–1702.
17. Wolf YI, Karev G, Koonin EV. 2002. Scale-Free Networks In Biology: New Insights Into The Fundamentals Of Evolution? *Bioessays* 24:105–109.
18. Barabási AL, Bonabeau E. 2003. Scale-free networks. *Sci Am* 288(5): 50–59.
19. Barabási AL. 2002. *Linked: The new science of networks*. Cambridge: Perseus Publishing.
20. Pareto V. 1896. *Cours d’économie politique*. Geneva, Switzerland: Droz.
21. Yule GU. 1925. A mathematical theory of evolution, based on the conclusions of Dr JC Willis, FRS. *Phil Trans Roy Soc Lond Series B* 213:21–87.
22. Lotka AJ. 1926. The Frequency Distribution of Scientific Productivity. *Journal Wash Acad Sci* 16:317–323.

23. Estoup JB. 1916. *Gammes Stenographique*. Paris: Institut Stenographique de France.
24. Yule GU. 1925. A mathematical theory of evolution, based on the conclusions of Dr JC Willis, FRS. *Phil Trans Roy Soc Lond Series B* 213:21–87.
25. Zipf GK. 1949. *Human behavior and the principle of least effort*. Cambridge: Addison-Wesley.
26. Simon HA. 1955. On a class of skew distribution functions. *Biometrika* 42:425–440; Reprinted in Ijiri Y, Simon HA. 1977. *Skew distributions and the sizes of business firms*. New York: Elsevier/North Holland.
27. de Solla Price DJ. 1965. Networks of scientific papers. *Science* 149:510–515.
28. de Solla Price DJ. 1976. A general theory of bibliometrics and other cumulative advantage processes. *J Am Soc Inform Sci* 27:292–306.
29. Mitzenmacher M. 2003. A brief history of generative models for power law and lognormal distributions. *Internet Math* 12:226–251.
30. Feller W. 1971. *An introduction to probability theory and its applications*. Volume 2. New York: John Wiley & Sons.
31. Mandelbrot BB. 1997. *Fractals and scaling in finance: Discontinuity, concentration, risk*. New York: Springer-Verlag.
32. Willinger W, Alderson D, Doyle JC, Li L. 2004. More “normal” than normal: Scaling distributions and complex systems. In: Ingalls RG, Rossetti MD, Smith JS, Peters BA, editors. Piscataway, NJ: IEEE. Proceedings of the 2004 Winter Simulation Conference.
33. Kumar R, Raghavan P, Rajagopalan S, Sivakumar D. 2000. Stochastic models for the web graph. FOCS: IEEE Symposium on Foundations of Computer Science.
34. Li L, Alderson D, Doyle JC, Willinger W. 2004. A first-principles approach to understanding the Internet’s router-level topology. *Proc ACM SIGCOMM*, Portland, Oregon, Aug 30–Sept 2.
35. Chung F, Lu L. 2003. The average distance in a random graph with given expected degrees. *Internet Mathematics* 1:91–113.
36. Willinger W, Alderson D, Doyle JC, Li L. 2004. A pragmatic approach to dealing with high variability measurements. *Proc ACM SIGCOMM Internet Measurement Conference 2004*, Taormina, Sicily, Italy. October 25–27.
37. Csete M, Doyle JC. 2004. Bow ties, metabolism and disease. *Trends in Biotechnology* 22:446–450.
38. Watts DJ. 2003. *Six degrees: The science of a connected age*. New York: WW Norton & Company.
39. Beatty J. 1995. The evolutionary contingency thesis. In: Lennox JG, Wolters G, editors. *Concepts, theories and rationality in the biological sciences*. Pittsburgh: University of Pittsburgh Press. 45–81.
40. Brandon RN. 1997. Does biology have laws? The experimental evidence. *Philos Sci* 64:s444–s457.
41. Willinger W, Govindan R, Jamin S, Paxson V, Shenker S. 2002. Scaling phenomena in the Internet: Critically examining criticality. *Proc Nat Acad Sci* 99(1):2573–2580.
42. Keller EF. 2002. *Making sense of life: Explaining biological development with models, metaphors, and machines*. Cambridge: Harvard University Press.
43. Keller EF. 2004. From nucleotide sequences to living systems. *J Biosci* 30, February 2005.
44. Ravasz E, Somera AL, Mongru DA, Oltvai ZN, Barabási AL. 2002. Hierarchical Organization of Modularity in Metabolic Networks. *Science* 297:1551–1555.
45. Li L, Alderson D, Tanaka R, Doyle JC, Walter Willinger W. 2005. Towards a Theory of Scale-Free Graphs: Definition, Properties, and Implications. http://xxx.lanl.gov/PS_cache/cond-mat/pdf/0501/0501169.pdf