Networks: Structure and Dynamics

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Article Outline

Glossary and Notation

- **Simple graph or network:** a group of N nodes (vertices) among which there exist L undirected connections (links, edges), identical in strength.

- **Directed graph:** a group of nodes among which connections are directed.

- **Weighted network:** a group of nodes among which connections are not identical in strength, but carry a weight.

- **Bipartite network:** a network with more than one type of node, in which connections only exist between different node types (the definition can be relaxed to a network were most, but not all links run between vertices of different types).

- **Adjacency matrix A:** an $N \times N$ matrix representing the network, whose elements a_{ij} are equal to 1 when there is a link from node i to j, zero otherwise.

- **Degree distribution $P(k)$:** the probability that a node of a network, chosen uniformly at random, has degree k.

- **Scale-free network:** a network in which the tail of the degree distribution follows a power law (strictly speaking, the term scale-free implies $P(k) \sim k^{-\gamma}$, however, it is often used for networks where the tail of the distribution follows a power-law).

- **Degree exponent γ:** the power law exponent of the (tail of the) degree distribution

- **Scale-free model:** a growing network model proposed by Barabási and Albert [1]. The model builds a simple graph starting from a small connected group of nodes, to which new nodes are added one by one. These new nodes connect to m old nodes with probabilites that increase linearly with the degree of the old nodes.

- **Shortest path (geodesic path):** the smallest collection of links that form a path through the network from one vertex to another.

- **Diameter D:** the length of the largest geodesic path in a network.

- **Small-world network:** a network in which the average shortest path length grows logarithmically (or slower) with N.

- **Node betweennes (betweenness centrality or load):** the number of shortest paths between nodes of the network that run through a given node [2–4].

- **Edge betweennes:** the number of shortest paths between nodes of the network that run through a given edge.

- **Clustering coefficient C:** the fraction of connections that are realized between the neighbours of a node:
$$C_i = \frac{2\, n_i}{k_i\, (k_i - 1)},$$
where n_i denotes the number of links connecting the k_i neighbors of node i. (The average clustering coefficient is given by $\langle C \rangle = \frac{1}{N} \sum_i C_i$. An alternative global measure of clustering, also called *transitivity*, is the fraction of node triples that are linked into triangles.)

- **Assortativity coefficient:** a measure of the tendency of links to run among nodes that are similar in some respect. If the similarity is described by a scalar quantity (most often the node's degree), then the assortativity coefficient is given by
$$r = \frac{\sum_{x,y} xy\, (e_{x,y} - a_x b_y)}{\sigma_a\, \sigma_b},$$
where x (y) is the scalar at the origin (end) of a link, $e_{x,y}$ denotes the fraction of all edges in the network that go from nodes with value x to ones with value y, a_x (b_y) is the fraction of edges that start (end) at a link vith values x (y), and σ_a (σ_b) is the standard deviations of the distributions of a_x (b_y) values [5].

- **Modularity Q:** the number of links between nodes within the same community minus the number expected by chance:

$$Q = \frac{1}{2L} \sum_{i=1}^{N} \sum_{j=1}^{N} (A_{ij} - P_{ij})\, \delta_{g_i, g_j},$$

where node i (j) belongs to the community g_i (g_j). P_{ij} gives the expected number of links between two nodes if the network is random with respect to communities [6].

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In the simplest case, in which the null model is a random network, $P_{ij} = 2L/N^2$. A more suitable assumption is $P_{ij} = k_i\,k_j/2L$, which preserves the degree distribution of the network in question (the expected degree of node i is $\sum_j P_{ij} = k_i$) [7].

1 Definition & Relevance

Scientific research has had a long history of bottom-up approaches, which break the system into small or elementary constituents and map out interactions between these components. The Standard Model describing elementary particles and the four types of interactions governing our world is perhaps the most successful example. Biology has developed a very detailed description of cellular components such as the DNA molecule or the various proteins and metabolites. Furthermore, many of the interactions that govern a cells life have been investigated in great detail, including transcription of DNA, protein assembly and enzyme function. The first attempts to understand complexity, at least in physics, were focused on small, simple system with complex dynamics: chaos theory. Nonetheless, large natural or social systems, like a cell, an ecosystem or the Internet are much more intuitive examples of complex systems. A meaningful description of these systems requires more than a mere account of the constituent parts: one does not understand the way the Internet works by detailing the physical characteristics of computers. Nor is the sequence of a cell's genome the final tool for understanding its behavior.

Complex systems display characteristics that are fundamentally determined by their organization, emergent phenomena created by all the interacting constituents. In many cases, if one takes a step back, avoiding the details of the interactions, a complex system as a whole is made up of an assemblage of generic elements and connections; in other words, it looks like a network. For example, a cells metabolism is maintained by a biochemical network, whose nodes are substrates and links chemical reactions [8–12]. Equally complex webs describe human societies, whose nodes are individuals and links represent social interactions [2, 13], the World Wide Web (WWW) [14–17], where nodes are Web documents connected by URL links, the scientific literature, whose nodes are publications and links citations [18–20], or language, made of words and linked by various syntactic or grammatical relationships between them [21–23]. Due to the diversity and large number of the nodes and interactions, the system-level characteristics of these networks remained largely unknown and unexplored prior to the last decade. At the same time, the inability of contemporary science to address the properties of complex networks limited advances in many disciplines, including molecular biology, computer science, ecology and the social sciences. The recent availability of system-level data

on the network of interactions in large numbers of systems has opened the door for interdisciplinary research in fields where the behavior of the system as a whole is a central question. Recognizing generic organizational principles and order behind diversity and apparent randomness in these different systems has certainly been a surprise along the way.

2   Introduction

The explosion of available data describing interaction of hundreds to millions of components in systems like the Internet or the protein interaction network is a recent development for the study of complex systems. Nonetheless, networks are not new to mathematics or the social sciences. Graph theory was born from the famous Königsberg bridge problem and its even more famous solution by Euler in 1736 [24]. The problem was simple: find a closed walk that visits each of Königsberg's seven bridges once, but only once. The trouble was, nobody could find such a walk. Euler drew a four-node graph of the pieces of land connected by the bridges and showed that graphs that have nodes with odd degrees cannot have closed self-avoiding paths. (All four pieces of land in Königsberg are connected via an odd number of bridges). Euler's emphasis on the topology of the bridge problem as key to the solution marks the starting point of two prolific subfields of mathematics: topology and graph theory.

The early 1920's witnessed the birth of social network analysis, a subfield of sociology trying to understand how social interactions organize. Data gathering methods limited the size of the networks studied, nonetheless many network measures important today were defined: degree distribution, betweenness, clustering and the small world effect.

In the 1950's two prolific hungarian mathematicians, Erdős and Rényi, took the challenge of describing the structure of large social networks from social science to mathematics and formulated their famous random graph model [25–28]. Their key innovation was a statistical approach to graph theory: their theorems were proved on the set of all networks generated by the rules of their model. They found that above a certain threshold probability of connecting any two nodes, the ensemble of random graphs undergoes a percolation-type phase transition from a graph made of small disjoint subgraphs to one with a giant component comparable with the system size. Random graphs have a Poissonian degree distribution: they are homogeneous network with a well-defined average degree. Erdős and Rényi pointed out that random networks are "small worlds": their diameter scales with the logarithm of system size (node number), quite different from the power-law relationship that holds for regular lattices.

The Erdős–Rényi model guided our thinking about complex networks until the end

of the 1990's, when two seminal papers triggered a very rapid growth of the field which today is called complex networks research. The first paper, published by Watts and Strogatz in 1998 [29], showed that natural systems such as the neural network of the *C. Elegans* worm, the power grid and the network of movie actors connected by feature films have a topology somewhere between regular lattices and random graphs. These networks have large clustering coefficients, but also the small world property. The small-world model presented in the paper is the first important step away from the random world of the Erdős–Rényi graph. The second paper, published one year later by Barabási and Albert, showed that the degree distributions of the movie actor network, the WWW and the power grid are not Poissonian: they have a power-law tail, inspiring the term scale-free networks [1]. The list of power-law tailed degree distributions measured on natural and man-made systems is still growing, with degree exponents that rarely fall outside the $(2, 3)$ interval. Power law degree distributions tell us that most real networks are highly heterogeneous: the majority of nodes have very small degree, but a few hubs with degrees orders of magnitude larger than the average also exist, along with nodes with degrees of all scales in between. A good example is the US airport network connected by direct flights: Chicago and Atlanta at the high end of the degree scale, the numerous regional airports at the low end.

Naturally, the sudden explosion of data and tools to explore them brought us closer to the heart of questions fundamental to understanding complex systems: what drives their organization, what defines their emergent properties. What do these networks do, what is their function? This question is natural to biology. A metabolic network has a well-defined job in the living cell: it fuels the cell with energy, nutrients and building blocks, and it does so adaptively and robustly. Man-made complex networks, such as the Internet or WWW, the power grid or the network of synonyms in a language also perform well-defined functions. In contrast with the delicate and well-thought-out internal structure of a computer, these systems were not designed from scratch with their function in mind: they evolved and emerged naturally. Also in contrast with the fragility of a computer (pull out a random element and it stops working), complex systems in biology and technology have a remarkable resilience to random node failure: the internet does not die when a few routers go down, in fact this probably is its normal mode of operation.

Questions about the characteristics mandated by function and thus common to all these systems, along with questions about the selection principles that shape these structures, are at the heart of our quest to understand complex function. These questions are typically formulated in terms of the dynamics that are natural to the nodes of the network: metabolic flux driven by enzymes, packet traffic on the internet, web browsing, electric current flow on the power grid, the spread of HIV on the sexual contact network,

etc. Understanding how structure affects dynamics and vice versa is in the spotligh of complex networks research today.

3 Structural Properties of Complex Networks

Let us look at the metabolism of a cell as an example that highlights the increasingly detailed ways one can pose the question: what is the large-scale structure of cellular metabolism? At first glance, the metabolic network is a *simple graph* in which metabolites (the nodes) are connected by chemical reactions. This representation tells us whether the network is homogeneous in degree or has hubs, whether it is a "small world", whether it has a community structure. A more detailed description of the system takes into account the direction of chemical reactions, since a large number of them are not reversible in a living cell. This leads to a *directed network* in which the in- and -out-degree distributions can be different and paths are directed. The next step is a *weighted network*: metabolites are characterized by their concentrations in the cell, edges are weighted by fluxes carried by reactions. A different way of adding complexity to the representation is by constructing a *bipartite grapgh*, where metabolites on one side connect to reactions on the other.

The above example suggests a natural organization for this section: presentation of simple graphs and their characteristics followed by more detailed networks, in parallel with specific real-world examples and models.

3.1 Simple Graphs

3.1.1 Degree Distributon

The Königsberg bridge network had only four nodes; the network examples we cite nowadays have from hundreds to millions. Most of them show a degree heterogeneity best captured by the degree distribution, which carries more information than the average degree, as pointed out by Barabási and Albert [1]. Examples of scale-free networks today include networks of metabolic reactions [11, 30], genetic regulatory interactions [31–33], earthquake event correlations [34], word co-occurence and synonyms [21–23, 35–39], power lines [29, 40], air routes [41, 42], the Internet [43–46], the World Wide Web [14, 16, 47–49], software systems [50], Wikipedia links [51], phone calls [52, 53], e-mails [54, 55], co-authorsip [56, 57], scientific citations [18], World trade [58], innovation flow [59], sexual partnership [60] and the list goes on.

Barabási and Albert had a much shorter list of examples to work with in 1999. Nonetheless, they saw three very different networks, the actor network, power grid and

World Wide Web had similar degree distributions, different from that of a random network. They argued that the Erdős–Rényi random network lacks two important features present in real-world systems. First, it is a static model, while most real-world networks constantly evolve and grow. Second, the random network model is too democratic: the probability of linking any two nodes is constant. Barabási and Albert proposed that in real networks the nodes that already have a large degree are more likely to receive new links as the network grows (think of Google in the WWW network). Preferential attachment accompanied by network growth was the first mechanism ever reported to reproduce the scale-free (power-law) degree distribution seen in real networks. Interestingly, though, Barabási and Albert were not the first to report it. A sociologist named Price reported the first example of a scale-free network back in 1965, that of citations linking scientific papers [19]. Building on the "the rich get richer" idea proposed to explain wealth distributions [61], Price constructed a network model for citations in which the more citations a paper has, the more likely it is to acquire further citations [62].

The scale-free model, simple and analytically solvable, propelled scale-free networks and preferential attachment to the forefront of the expanding field of complex networks research. Barabási and Albert showed that both growth and preferential attachment are essential for obtaining a scale-free network. Growth along with uniform attachment leads to an exponential degree distribution, while no growth with preferential attachment leads to a Gaussian distribution (although the system does start out with a transient power law) [63]. They also considered the effects of random rewiring and internal link formation, showing that internal link dynamics cause deviation from the power-law at low degrees, observed in real-world networks [64]. A variety of models and analytical methods were developed in the wake of these papers, addressing the effects of further changes in rules of growth or attachment on the degree distribution [65, 66]. The exact solution for the degree distribution of the Barabási–Albert model was worked out by graph theorists Bollobás and Riordan [67].

One of the most important generalizations of the original scale-free model was the study of nonlinear preferential attachment by Krapivsky and Redner [66, 68]. They found that power-law scaling is destroyed by nonlinearity: sublinear attachment leads to a power law multiplied by a stretched exponential, while faster than linear attachment causes the network to "condense": a the fraction of nodes connected to a single superhub is finite in the thermodynamic limit. Indeed, the simple linear attachment rule of the scale-free model was later verified in real systems: citation networks, the Internet, the actor and scientific collaboration networks [69, 70].

Variations on the scale-free model include linear preferential attachment offset by a constant [68, 71], internal edge creation and removal [72, 73] , growing average degree [74] (seen in the WWW and co-authorship networks [56]), and edge rewiring [64, 75, 76].

One of the challenges of modeling the WWW with the original scale-free model was spotted by Adamic and Huberman: while the oldest nodes are the ones with the highest degree in the model, the WWW does not show this correlation [48]. Bianconi and Barabási proposed a multiplicative fitness model [77–81] in which the attachment rule is influenced by the degree as well as the "worth" of a node. This model generates both scale-free networks and "winner takes all" scenarios, where the transition between the two outcomes maps beautifully onto a Bose-Einstein condensation [78].

The presence of preferential attachment can be justified in many real systems such as the WWW, citation, collaboration or airport networks through the larger visibility of high-degree nodes and the advantage nodes gain by linking to them. There are, however, scale-free networks where a different mechanism leading to preferential attachment is necessary. Biological networks offer intriguing examples: the metabolic and the protein-protein interaction networks are scale-free, even though their connections are governed by biochemistry and not choice. Protein interaction networks have inspired a class of models based on gene duplication (duplication of a node and all it's links) and subsequent mutation (addition and/or deletion of some of the copy's links) [82–85]. Preferential attachment in these models is a consequence of the evolutionary dynamics: nodes with a higher degree have more duplicating neighbors, thus receiving more links. Vertex (node) copying has been proposed as a possible mechanism for the growth of the WWW [16, 86] and auto-catalytic networks [87, 88].

In the spirit of the Erdős–Rényi model, Bender and Canfield proposed an ensemble model for scale-free networks. The configuration model describes the group of all networks with a prescribed degree sequence [89–91]. If the sequence is chosen from a power-law distribution, the resulting networks are naturally scale-free. However, the average properties of the ensemble carry no other characteristics intrinsic to evolving models (such as degree correlations or clustering). Moreover, the simple definition of the model makes it ideal for analytical approaches. Newman et al. used probability generating functions to calculate exact expressions for average path length and clustering in configuration networks[1] [92]. Many analytical results for scale-free networks were proven using the configuration model: they have asymptotically vanishing clustering coefficients [93] and they are ultra-small for the degree exponents measured on most real-world networks ($\gamma \in (2, 3)$): their average path length scales as $\mathcal{O}(\log \log N)$ [94, 95].

Real networks are sometimes embedded in physical space and have physical connections: brain networks [96], the power grid, the Internet, airport networks, streets [97], public transportation systems [98], highways [99] and rivers [100]. Some of the above

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[1]They used a generalized definition: the ensemble of all networks with an ensemble of degree sequences drawn from the same distribution.

examples (brain networks, streets, rivers) are missing from the list of scale-free networks: spatial constraints can be forbidding to the formation of hubs. Several studies with both preferential attachment and bias towards shorter links show that large length costs can destroy the scale-free nature of spatial networks [101–107]. Systems with fixed maximum link length, such as wireless networks in which the range of a particular device is much smaller than the physical size of the system are not scale-free. Conformation networks made of all physically allowed conformations of a system (a polymer or bead chain) are also homogeneous structures naturally embedded in an n-dimensional configuration space defined by the system's degrees of freedom [108, 109].

The distribution of nodes in space can also have great influence on network topology, as shown in a detailed study of the Internet by Yook et al. [110]. They found that the router density distribution is a fractal with the same dimension $D = 1.5$ as the population density distribution. They were able to mimic the topology of the Internet using a simple evolving model in which nodes are distributed according to a fractal distribution and incoming nodes connect to old ones using preferential attachment divided by some power of their distance. Interestingly, the only model parameters able to reproduce the internet's topology were the ones actually measured for the real system: fractal dimension $D = 1.5$, linear preferential attachment and a probability of connecting two nodes that is inversely proportional to the distance between them. A similar model was also successful in describing the topology of the world-wide airport network [111, 112].

3.1.2 Paths on Networks, Small Worlds and Betweenness

A networks' most basic function always requires some type of communication along its edges. Thus it is natural that average shortest paths, network diameter and local betweenness measures are of great interest to networks research. Erdős and Rényi proved that the diameter of their random network model scales as the logarithm of node number. Watts and Strogatz called such networks small worlds [29], in tribute to the "small world phenomenon" in sociology: the idea that one can connect any two people on Earth by about six handshakes between mutual acquaintances. In 1967, an ingenious experiment by Milgram proved the existence of short paths of an average six hops between random people in the US, known as "six degrees of separation" [113]. The small word nature and searchability of small-world networks allow movie lovers to find short chains of movies connecting their favorite actor to Kevin Bacon. Mathematicians (and networks researchers) play the same game on the co-autorship network: one's shortest path to Pál Erdős is called the Erdős number.

The small world model introduced by Watts and Strogatz is based on the idea that real networks are in between random graphs and regular lattices: they are highly clus-

tered (as a regular lattice), but they also have shortcuts. The model is built starting with a regular low-dimentional lattice to which one adds (or rewires) a certain number of edges, shortcuts between distant parts of the lattice [29]. Watts and Strogatz showed that increasing the number of shortcuts turns regular lattices into random networks, moreover, a small number of shortcuts is sufficient for the small-world effect without destroying the high clustering coefficient of the original lattice[2]. Most real networks display both characteristics of the small world model: short average path lengths and high clustering. However, the small world model has a peaked degree distribution, thus the topology of real networks with scale-free degree distribution is fundamentally different from the ones generated by the model. The Barabási–Albert scale-free model, on the other hand, fails to account for the high clustering of most real networks.

Logarithmic or slower increase of the average path length was proved for a variety of network models [94, 116–119]. Bollobás and Riordan showed that the average shortest path length in scale-free networks grows no faster than $\log N / \log(\log N)$ [117, 119]. Cohen and Havlin used the configuration model to show that random scale-free networks with $\gamma \in (2,3)$ are ultra-small: their average shortest path length grows as $\log(\log N)$ [95].

The structure of shortest paths is crucial to any communication or flow between nodes of a network. Naturally, betweenness was found to be the relevant quantity when one deals with congestion or disruption of flow in networks. Goh et al. measured the distribution of node betweenness values for a variety of real networks as well as models, and showed that it follows a power-law with only two distinct exponents [120].

3.1.3   Clustering and Network Motifs

Clustering is a rediscovery of "network density" [4], a quantity widely used in sociological network analysis: it provides a measure of how well one's acquaintances know each other. High values have been observed in social networks, but also in most other real-world networks, motivating the development of clustered scale-free models. The Holme-Kim model, aimed at creating scale-free networks that also have high clustering coefficients, is a straightforward generalization of the scale-free model, with triangle-forming steps complementing preferential attachment [121]. Klemm and Eguíluz introduced a citation network model based on the idea that papers are only cited for a limited stretch of time before they are forgotten [122]. The model is built by the constant addition of nodes that connect to all "active" nodes and join their ranks. Then, one of the active nodes is deactivated with a probability inversely proportional to its in-degree (offset by

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[2]For various definitions of the model see [29, 114, 115].

a constant). This model leads to scale-free networks with high clustering coefficient, but fails to capture their small-world nature: visualized, the networks look like tubes. Gene duplication models, while motivated by evolutionary arguments, also lead to clustered scale-free networks [82–85].

An interesting generalization of the clustering coefficient was introduced by Uri Alon's group: network motifs are significantly over- or underrepresented patters of connections between n vertices (compared to the randomly rewired network). Distinct characteristic motifs were found in regulatory networks, food webs, neural networks and WWW, corresponding to local functions performed by the network [32, 33, 123]. For example, different types of feed-forward loops (FFLS, directed motifs of 3 nodes: $A \to B$, $B \to C$ and $A \to C$) in genetic regulatory networks perform distinct signal processing roles as shown by both simulation and experiments with living cells [124–133]. FFLs made of activating iterations only (abundant in the regulatory network) can filter out transient changes in the concentration of the input node, while also delaying the turn-on or turn-off of the output node. On the other hand, FFLs where the $B \to C$ link is a repressing one (also abundant) act as a pulse generators.

3.1.4 Degree Correlations and Mixing Patterns

In social networks, links between people who are alike are more common; popular people are connected with popular people. Assortative mixing means that degrees at two ends of an edge are correlated, as measured by the conditional probability, $P(k'|k)$, that a node with k links is connected to another one with k' links. Measurements on the Internet and protein interaction networks show that in these system, as opposed to their social counterparts, small degrees are more likely to connect to high degree nodes [134, 135]. The conditional probability is difficult to measure in most real networks due to poor statistics, although it is convenient in analytical work. A more compact representation of degree correlations was defined by Pastor-Satorras et al. [136, 137]: the average degree of neighbors as a function of degree, $k_{nn}(k)$, which decreases with k for disassortative systems. One can further simplify the measure of assortativity by calculating the Pearson correlation coefficient of degrees at the ends of a network's edges: the assortativity coefficient [5, 138]. Intriguingly, most social systems are assortative (actor network,company directors, coauthorship networks, phone calls, email address books), while most technological and biological systems prefer disassortative mixing (WWW, Internet, train routes, software packages, software classes, electronic circuits, peer-to-peer networks, metabolic networks, food webs, neural networks).

Degree is not the only property of a network that can show assortative or disassortative mixing. In networks where nodes can be classified in types of some kind, mixing

between types can also be characterized by the assortativity coefficient (see definition). Maslov et al. showed that there are three main types of nodes in the Internet: high level providers who manage the backbone and trunk lines, Internet Service Providers who bring the network out to end-users and the end-users themselves. These three types show strong disassortativity: few end-user to end-user or ISP to ISP links in the network. In social networks, mixing by race, age or income has been observed [5].

3.1.5 Communities, Hierarchy and Fractality

Community structure is an intuitive feature of complex networks: one expects them in social systems (circles of friends), biological networks (functional units), the WWW (websites related to a topic or organizations), co-authorship networks (scientific fields and sub-fields), etc. Communities within networks are structural features related to the function of the network as a whole, and are thus expected to have a strong influence on their dynamics. Defining and finding network communities has its history in both sociology and computer science, and has been revisited many times. The methods developed along the way paint a rich picture of the structural diversity of complex networks.

Non-Overlapping Community Structure

Hierarchical clustering or cluster analysis is widely used in the study of social networks [139]. The first step in hierarchical clustering is the construction of a similarity measure between network nodes. Next, each node is assigned to a separate cluster (the leaves of the dentogram). The two most similar clusters are joined to form junctions of the dentogram, until all clusters have been united, forming the root. Many similarity measures have been defined and used successfully. Structural equivalence, a concept introduced by Lorrain and White [140], gives two nodes the highest similarity score if they have the same pattern of relationships. It can be measured using Euclidean distance [141] or Pearson correlation coefficient [2] between rows of the adjacency matrix, as well as topological overlap, defined as the number of overlapping neighbors divided by the smaller of the two degrees[3] [142]. Other definitions of vertex similarity are based on measures of flow in the network such as edge betweenness [55, 143, 144] or random walks [145, 146], as well as spectral methods [147, 148].

Girvan and Newman introduced a famous community detection algorithm that is similar to hierarchical clustering, but works divisively [143]. It is based on the idea that the edges most likely to run between communities are the ones that have the highest

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[3]The precise definition takes into account the existence of a direct link between the two nodes.

edge betweenness centrality. They first remove the edge with the highest betweenness, then recompute edge betweenness and keep removing edges until the network falls apart into non-connected nodes. As the network falls appart, they draw a dentogram where each joint is a splitting event.

Hierarchical clustering works with varying success for different systems, but it cannot determine how many communities there are in the network. Newman et al. introduced an elegant measure for the "quality" of any given partitioning into communities, called modularity, which compares a community partitioning to a null model that can be appropriately chosen for the system at hand [7]. The Girvan–Newman algorithm, together with the dentogram cut that maximizes modularity, has been successfully used for many different social and biological networks [6, 55, 144, 149–153]. The main drawback of the method is computation time ($\mathcal{O}(N^3)$ on a sparse graph): it is not feasible for networks with more than a few housand nodes.

In a quest to develop a faster community detection method closely tied to the definition of communities, Newman used direct optimization of the modularity measure [154]. Since finding the best partitioning is an NP-hard problem, his first approach was a greedy optimization. All nodes start out as separate communities, which are then repeatedly joined such that the increase in modularity is maximal (or decrease is minimal). Newman showed that the method works well both in tests and real networks, and it works quite fast: $\mathcal{O}(N^2)$ time for sparse graphs. Still not fast enough? A collaboration with Clauset and Moore resulted in an algorithm that performed the same optimization in $\mathcal{O}(N \log^2 N)$ for sparse graphs with many levels of communities[4] [155], solving the problem of partitioning networks with billions of nodes.

Interested in the theoretical foundations of community structure detection and its relationship to matrix spectra, Newman argued that community detection requires the use of the modularity matrix [7] in place of the Laplacian matrix[5], as done by traditional spectral methods of graph partitioning [156, 157]. The modularity matrix is defined as $B_{ij} = A_{ij} - P_{ij}$ (see modularity definition). He showed that the eigenvalues and eigenvectors of the modularity matrix encode the networks's community structure. Methods based on this relationship perform as well, if not better, than previous ones, but more importantly, they are also able to detect "anti-modular", or bipartite structure [7].

Hierarchical Community Structure and Fractal Networks

Ravasz et al. argued that in many real networks with interesting modular structure

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[4]The general result for runtime is $\mathcal{O}(KD \log N)$, where K is the total number of links and D is the depth of the generated dentogram.

[5]The Laplacian matrix of a graph, L, is the real symmetric matrix with elements $L_{ij} = k_i \, \delta_{ij} - A_{ij}$ (A is the adjacency matrix)

there is no ideal partitioning into distinct modules: the network is built of small, very cohesive communities, hierarchically embedded in larger, less cohesive ones [142, 158]. Their hierarchical model is a deterministic construction of a scale-free network with hierarchically embedded modules. They showed that hubs on all scales unite communities on all scales: small nodes are part of small, very cohesive clusters (thus have large clustering coefficients), larger nodes serve as connectors of these clusters, while the largest hubs span modules at the highest level or organization (and have low clustering coefficients). Indeed, they found that the clustering coefficient $C(k)$ decreases with increasing k in a variety of real networks, such as the metabolic network, synonyms, movie actors, the WWW and the Internet represented at Autonomous System level (each node is a domain, not just a computer), and it often scales as $1/k$ [158]. This scaling was found in a variety other networks: software systems [50], the World Trade network [58], the world-wide airport network, the co-authorship network of `http://arxiv.org/archive/cond-mat` [42, 57] and protein folding networks [159]. Not all networks are hierarchical: the power grid and the Internet at router level show no scaling of the clustering coefficient [158]. Ravasz et al. suggested that spatial embedding of both systems, where length costs are significant, works against hierarchical modularity. Both networks distribute something to a physical area. Thus, the formation of tight communities is not required for these networks to function.

Hierarchical organization in metabolic networks was found to reflect biological function on different scales of organization: the branches of the dentogram obtained by hierarchical clustering (using topological overlap as similarity measure) correspond to known functional classes of the metabolism on two different levels of organization [142].

The question of self-similarity or fractal nature has been on the mind of network researchers since the scale-free degree distribution was observed. Are networks like fractals, self-similar on all scales? Hierarchical organization strengthens this image: most networks not only have degrees in a broad range of scales, they are also made of modules of different scales embedded into each-other. The problem with complex networks as fractals was, of course, that most networks of interest to us are also small-world [29]. In a small-world network the number nodes at a distance l from any given node increases exponentially. One expects this number to grow as a power law in the case of a fractal object: measuring the "mass" within distance l from a point on the object, called the cluster growing method, is one way of measuring fractal dimension [160].

While some deterministic models have been constructed with the idea of fractality in mind [161, 162], the breakthrough in understanding topological self-similarity in complex networks was brought forth by Song, Havlin and Makse [163, 164]. They generalized the standard box counting method for measuring fractal dimension of a physical object to complex networks. How does one cover a network with boxes of different size? Divide all

nodes in groups such that the shortest path between any two nodes in a group is at most l_B long: these are the boxes. Use the smallest number of groups necessary to do this (or a decent approximation) and repeat it for $l_B \in [2, D]$. The results of this procedure were quite surprising: many scale-free real-world networks, such as the WWW, actor network and various metabolic networks show a neat fractal scaling between the number of boxes and their size. Thus these networks are self-similar, fractal structures. To prove their point further, the authors used a renormalization procedure where they collapsed each box into a node and linked these new nodes to each other if any member of the original boxes had a connection. The networks renormalized this way were also a scale-free, with the same degree distribution exponent, independent of the box size used for renormalization [163].

The question of how these networks are small world and self similar at the same time has also been resolved: the two methods of determining the fractal dimension of an object, box counting and cluster growing are not equivalent on complex networks with broad degree distribution. While box counting covers all the hubs only once (they are assigned to one box only), cluster growing finds the hubs for almost any choice of seed node, thus bringing a large part of the network into the cluster with them. This explains the exponential increase in the number of nodes within a distance l, and shows the small-world property of the system. Box counting, on the other hand, can reveal the fractal nature of the network, if present [163].

Song et al. uncover some of the requirements of fractality via proposing a network growth model based on reverse renormalization. Starting from one point, the network grows by nodes transforming into small clusters in each iteration. The conversion from a node to a small cluster mimics the renormalization process in reverse: the degree of a node grows by multiplication with a scaling factor (thus nodes of previous iterations become the hubs). The newly formed clusters have a diameter of b_B (the box size). They showed that the key feature that influences fractality in the emerging networks is how the clusters connect: if the link always runs between the hubs (leading to assortative mixing), the result is small-world network that is not a fractal. The internet at router level, found to be non-hierarchical, is a good example of such an assortative, non-fractal network. On the other hand, if the clusters only connect to each other via the non-hub (newly created) nodes, the resulting network is a fractal, but it loses it's small-world character. Many real-world networks, however, seem to be both fractal and small-world (WWW, actor network, protein interaction networks, metabolic networks); indeed a very small number of hub-to-hub connections in their model can restore the small-world property of the network while preserving its fractal nature.

Overlapping Community Structure

The community detection methods presented thus far assign each node to only one community. Palla et al. argued that many nodes in real networks belong to more than one community [165]: proteins can simultaneously be part of several complexes, people have disjoint groups of acquaintances from friends to work to extended family. They proposed a community definition that allows them to capture overlap between communities. Their method is based on "k-clique rolling": a k-clique community is the union of all k-cliques (complete subgraphs of size k) that can be connected through a series of k-cliques that share $k - 1$ nodes. Increasing values of k lead to smaller, denser, but more disjoint communities. They find that k-clique communities in real networks (co-authorship, word association and protein interaction networks) have a power-law size distribution, and there are significant overlaps: the size distributions of overlap as well as node membership have fat tails.

3.2   Directed networks

Directionality of a link is often important in real networks: scientific citations, url links, genetic regulatory interactions are only a few examples of inherently asymmetric connections. Directed links require the separate measurement of in- and out-degree distributions. In case of the WWW both are power-laws, but the degree exponents differ: $P_{in}^{WWW}(k) \sim k^{-2.1}$ and $P_{out}^{WWW}(k) \sim k^{-2.45}$ [14]. Genetic regulatory networks show an even stronger difference. Their out-degree distributions are power laws, however, the in-degree ones are scaled: genes cannot receive input from hundreds of transcription factors.

Another interesting consequence of directed links is the rich structure of directed paths. They were found to partition the WWW as well as metabolic networks into parts resembling a bow-tie [17, 166, 167]: a strongly connected component, in which there is a directed path in both directions between any pair of nodes, an IN-component, the nodes of which can reach the strongly connected component bot cannot themselves be reached, and an OUT-component that can be reached from, but has no directed paths leading into the strongly connected component. Not all directed networks have bow-tie structure: some of them are entirely acyclic, with no directed loops. Citation networks are a natural example: one can only cite papers already published. However, genetic regulatory networks are also acyclic (not considering auto-regulatory loops), even though the cause of this is now yet understood [31, 168].

Gradient networks are directed graphs that generalize the concept of gradients from continuous scalar fields to networks. They capture the backbone of a gradient-induced flow on complex networks: given a substrate graph with a scalar value associated to every node, its gradient network is formed by the collection of all directed links that

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lead from every node to its neighbor with the highest scalar value [169–171]. These directed links form collections of trees. For an independent, identically distributed association of random variables to the nodes of an Erdős–Rényi graph, the generated gradient network has been shown to be scale-free, with a connectivity exponent of $\gamma = -1$. This finding can be proved for any substrate graph with no loops shorter than 5 [170, 172]. Moreover, the gradient networks' scale-free nature seems to be universal: it was numerically observed for a wide variety of substrate networks (including ones with short loops): regular and random trees, Erdős-Rényi and small-world networks, high dimensional regular lattices and n-tori, random geometric networks [173], the scale-free and the configuration model [109, 170, 172].

3.3   Weighted networks

Real world networks display significant heterogeneity in the strength of their connections. The distribution of link weights has been found to have a heavy tail in metabolic networks: the steady-state flux distribution follows $\Theta(w) \sim (w_0 + w)^{-1.5}$ ($w_0 = 3 \cdot 10^{-4}$) [174]. Moreover, the average link strength scales with the connectivity of the nodes at the two ends as $\langle w_{ij} \rangle \sim (k_i \, k_j)^{0.5}$ in both metabolic networks and the Worldwide Airport Network, indicating correlations between node degree and links weights [42, 174]. Scientific collaboration networks, on the other hand, have a weight distribution that is not correlated with degree.

The existence of weighted links requires a generalization of most network measures:

- **Node strength and strength distribution.** Node strength, s_i is a natural generalization of the node degree, k_i:

$$s_i = \sum_{j=1}^{N} w_{ij} \, A_{ij},$$

the sum of weights over the links of node i. The strength distribution, $P(s)$, is typically also heavy tailed [42].

Weights are often dependent upon topology (see metabolic and airport networks), expressed by a non-linear relationship between node strength and degree: $s \sim k^\beta$ (in the airport network $\beta = 1.5$). Heterogeneity in the weights around a node can be measured using

$$Y_i = \sum_{j=1}^{N} \left(\frac{w_{ij}}{s_i} \right)^2 A_{ij}.$$

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If all edges have the same weight, $Y(k)$ scales as $1/k$, while if one weigth is significantly larger than the others, $Y(k) \simeq 1$. In metabolic networks $Y(k)$ was found to scale as $k^{-0.27}$, indicating that metabolites used in a large number of reactions are more likely to have one high-flux reaction dominating their production (consumption) [174].

- **Weighted clustering coefficient.** Defined by Barrat et al. as

$$C_i^W = \frac{1}{s_i\,(k_i - 1)} \sum_{j=1}^{N} \sum_{m=1}^{N} \frac{w_{ij} + w_{im}}{2}\, A_{jm}\, A_{ij}\, A_{im},$$

the weighted clustering coefficient is often compared to the standard one: $C^W > C$ means that the triangles of the network are preferentially formed by high-weight links. This is indeed the case in the co-authorship network, for nodes with $k > 10$: more established investigators form stable, high-weight cliques (research groups) from which the main volume of their publications originate. A similar phenomenon can be seen in the world-wide airport network: larger airports form high passenger-flux triangles, so called "rich-clubs" [42].

- **Degree Correlations.** The weighted average degree of neighbours is defined as:

$$k_{nn,i}^W = \frac{1}{s_i} \sum_{j=1}^{N} w_{ij}\, k_j\, A_{ij},$$

a sensitive probe into the structure of weighted networks. The behavior of $k_{nn}(k)$ in the airport network shows a plateau for airports with more than 10 direct fights, indicating no degree preference. However, $k_{nn}^W(k)$ increases in a wider range and is in general larger $k_{nn}(k)$, showing that while large airports do not preferentially connect to large airports, the high traffic links run among members of the "rich-clubs" [42].

4 Dynamics on Complex Networks

The main theme of this section is: how does the structure of a network influence its dynamics? Most lessons of statistical mechanics are worth revisiting when the underlying space is a network: does an inhomogeneous topology change the dynamics? The answer, as we will see, is yes, in interesting ways.

4.1 Robustness and Vulnerability of Complex Networks

Perhaps the most intriguing feature of complex systems is their robustness. Close to 75% of the genes in *E. coli* are non-essential: the organism can survive without them (under one set of growth conditions) [12, 175]. If the webpage of a company or university goes down, the WWW as a whole is still perfectly functional, the effect of the failure is local. On the other hand, an intentional "attack", similar to the denial-of-servise attacks that crippled Yahoo, Amazon, eBay, CNN and a few other very popular websites in February of 2000, can substantially cripple the function of a complex system. Vulnerability and robustness go hand in hand in most complex systems: bad weather in Atlanta (although usually not labeled an "attack") has very different consequences for air traffic than problems at a regional airport. Opinions expressed in the New York Times are much more likely to spread and influence events than opinions in a small town local newspaper. These trivial examples hint at interesting consequences of inhomogeneous network topology, brought to light in a 2000 Nature paper by Albert, Jeong and Barabási [176]: while scale-free networks are largely unaffected by random failure, they are very sensitive to change in their highly connected, central nodes, rendering them vulnerable (responsive) to planned, targeted interventions.

4.1.1 Resilience

One of the simplest indicators of robustness under the damage done by node or link removal is a structural one: the size of the largest connected component. Numerical studies performed by Albert et al. show that the giant connected component of Erdős–Rényi random networks falls apart at a much lower fraction of randomly removed nodes that of a scale-free network [176]. A fraction of nodes the removal of which causes a random network to falls into pieces, only slightly shrinks the giant component of a scale-free network, while small fragments of the system become isolated. An attack, on the other hand, where the most connected nodes are the first to be removed, shows a different picture. While the Erdős–Rényi random network falls appart somewhat faster but in essentially the same way, a scale-free network is blasted appart by the removal of a much lower fraction of nodes. The results hold for simulations using the actual network topologies of the Internet and WWW [17, 176].

The topological aspects of random node or edge removal can be calculated by mapping random failures to percolation problems. Cohen et al. have shown that uncorrelated random networks with a diverging second moment of their degree distribution (scale-free networks with degree exponents between 2 and 3) have zero percolation thresholds [177, 178]. Vázques and Moreno used an approach that allowed them to investigate

the percolation properties of correlated networks, showing that assortative mixing is beneficial for resilience: it can push the percolation threshold down to zero, even for networks with a finite second moment [179]. The opposite effect is also true: scale-free networks with diverging second moments but dissasortative degree correlations are less rezilient to node failure [180]. A general analytical approach based on generating function formalism not only reproduced the previous results, but also allowed Callaway and Newmann to investigate degree-dependent node removal scenarios, such as attacks [181]. Interestingly, assortative mixing does not help in case of an attack: Song et al. have found that non-fractal networks created via a mechanism that favours hub to hub connections on all scales are more vulnerable to intentional attack than their fractal (and also dissasortative) counterparts [164].

4.1.2   Cascading Failures

The function of a variety of complex networks involves the transmission or flow of some conserved quantity. Removal or failure of a node in such a network has consequence that ripple through the rest of the system far beyond the effects on connectivity: the node suddenly sheds the load or flux that it carried before, thus its neighbours suddenly experience higher loads: some of these overload and fail. A cascading failure can follow, as often seen on the power grid, perhaps the most quoted example of the phenomenon. Unlike the fragmentation of a network, a cascading failure can be triggered by a relatively small number of node failures, often a single one [182–185].

Using a model of overload in which the load-bearing capacity of a node is proportional to its load (betweenness) in the full network, Motter and Lai showed that scale-free networks are more vulnerable to randomly seeded cascading failures than random networks [182]. The vulnerability becomes especially pronounced under targeted attack: overload of the largest node can cause cascades that propagate through the whole system. They find that the most dangerous targets are not the most highly connected, but the most load-baring (highest betweenness centrality) nodes. Betweennes is usually correlated with degree. The US powergrid, however, is vulnerable under attack targeting its most central nodes, but not its highest degree ones.

In a followup paper Motter introduced a fast defense strategy against targeted cascading failures [186]. He argued that the only defence strategy which is fast enough is further removal of nodes: counterintuitive, but effective, if the nodes are carefully chosen. The reason this is possible, he argued, is because nodes that carry small amounts of load (thus are less central to the network) actually generate much more load than they carry. Their shortest paths to the rest of the system are larger, thus all the communication (traffic, power) they receive or generate affects a larger number of intermediary

nodes, increasing the total network load. Generated and handled load are anticorrelated, thus removal of nodes in ascending order of loads significantly reduces the size of cascading failures in the rest of the network, as verified by numerical simulations.

4.1.3 Congestion

Cascading failures and congestion of traffic carried by networks are similar problems. As opposed to the node-removing effect of a failure, congestion does not disconnect a node, nonetheless, it can brings the traffic-bearing capability of a system to a halt [187, 188]. Most congestion models show a transition from free flow to congestion as the load is increased, regardless of the network type.

Ohira and Sawatari showed the occurrence of a jamming transition on a simple traffic model in which packets travel along the shortest paths of a two dimensional lattice between randomly chosen boundary nodes [189]. On a regular lattice shortest paths are highly degenerate, thus the authors considered two strategies: one is deterministic in picking it's route, the other is random, preferring shortest paths but occasionally picking longer than optimal ones. They found that the jamming transition occurred at larger packet creation rates if the routing was probabilistic, with an optimal randomness that does not considerably lengthen the travel paths, but relieves the network from always choosing congested paths. Guimerá et al. considered a different formulation of the congestion problem on lattices and Cayley trees where all nodes generate packets to random destinations and send them along shortest paths, but the probability for a packet to hop between two nodes along the path depends on the queues accumulated by these two nodes [188, 190]. Thus, there is some congestion-awareness built into the model. If the processing speed of nodes decreases with an increased number of packets, the system shows a discontinuous transition from free flow to congested state: the ratio of undelivered packets (the order parameter) jumps from 0 to 1. The positive feedback between congestion and slower processing leads to the formation of congestion nuclei that spread through the network. On the other hand, no transition is observed in networks in which the processing speed of nodes increases with queue lengths, only a crossover from low-density flow to high density flow accompanied by a change in fluctuation statistics. The critical case in between is queue-independent processing, which shows a continuous transition between free flow and congestion.

Solé and Valverde proposed a generalization of the Ohira–Sawatari model [191] and showed that the system at transition point exhibits self-similar time-series dynamics with an $1/f$ power spectrum, as observed in measurements of packet transmission times on the Internet [192, 193]. Latency times and queue lengths also showed heavy tails with similar queue length distributions to jam size distribution in highway traffic models.

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Interestingly, the systems reaches its highest efficiency and information transfer regime right at the critical point, before entering the congested state [191]. Building on the observation that the time series dynamics of the model close to the critical point matches the real data, the authors introduced a self-organizing version of the model [194]. They argued that packet generation (thus user behavior) is linked to dynamics: each user tries to increase its rate until congestion of neighboring nodes is detected, at which point it starts to decrease it, dropping its rate to 0 if all it's neighbors are congested [195]. This model generates highly heterogeneous dynamics in space and time, with a power-law congestion length distribution. Moreover, this model points to internal network dynamics being responsible for fluctuations, supported by an analysis of fluctuations by de Menezes and Barabási. They observed a power-law scaling of flux fluctuations as a function of total flux values, with two distinct scaling exponents. $\alpha = 1/2$ scaling is generated by fluctuations internal to the system (as seen in the Internet and on a microchip), while $\alpha = 1$ corresponds to external noise (seen in the WWW, river networks and the highway system) [196]. Solé and Valverde have further extended their model to study complex topologies similar to the Internet (using the model by Yook et al. [110]), with a routing strategy that can be tuned from random routing to global shortest path routing. Each node is assumed to know its neighborhood to m hops. If the destination of a packet is within a node's search horizon it uses shortest path routing, otherwise it passes the packet to a random neighbor [197] (local routing strategies with a fixed search horizon were also investigated by Tadić et al. [198–200]). They found that the routing was optimal when the search horizon equaled the average path length of the network. Further push toward global shortest paths actually decreased the efficiency by over-specifying paths and thus exacerbating congestion. The dynamics observed with optimal search depth reproduced the 1/2 scaling between fluctuations and mean flow observed in [196], as well as the power-law exponent of the average latency time distribution measured on the Internet [201].

Zhao et al. investigated the effect of network topology on congestion in a model in which the packet processing speed of nodes is determined by their degree or their betweenness. They found that if the capacity of nodes was proportional to their degree, random networks as well as scale-free ones were less prone to congestion than regular lattices or Cayley trees. However, systems in which the node capacities were proportional to their betweenness had the same critical packet generation rate regardless of topology, suggesting that selectively increasing the capacity of high-betweenness nodes is a good way of increasing the carrying capacity of the system as a whole [202].

A different approach for investigating the effect of network topology on congestion was proposed by Toroczkai and Bassler [169]. They measured the congestion factor of the Erdős–Rényi and Barabási–Albert models, defined as the average fraction of

nodes that do not receive and thus process incoming traffic. Instead of an explicit choice of routing or packet generation behavior, they assumed that packets on average follow the steepest gradients towards the neighbor with the highest "potential", thus the gradient links determine the congestion factor (they assume a random distribution of node potentials). They found that the congestion factor of Erdős–Rényi random graphs increases with the size of the network, asymptotically growing to 1, while for scale-free networks it quickly reaches a value of ~ 0.7 and does not increase with system size. A followup study by Danila et al. proposed a traffic model based on the idea of congestion-gradient driven flows [203].

The recognition that congestion occurs when the average number of packets processed by the busiest node reaches 1 (time-step) highlighted the importance of betweenness in the study of congestion. Routing protocols can influence the experienced betweenness of a node (the number of packets that actually go through it on average), several methods of reducing the largest betweenness value have been investigated: optimization of link weights such that the shortest weighted paths give rise to a small maximum betweennes [204], hub avoiding global routing schemes [205] or traffic-aware routing [206, 207]. Sreenivasan et al. proved that for any network topology there always exist an absolute upper bound for the communication threshold, determined by network topology, above which no routing algorithm can increase the critical congestion threshold [205].

4.2   Spreading Processes & Social Dynamics

4.2.1   Epidemic Models

Epidemiological modeling jumped to the forefront of networks research with a landmark paper by Pastor–Satorras and Vespignani which revealed the striking difference between virus spreading on scale-free networks and homogeneous systems [208, 209]. They studied the "susceptible–infected–susceptible" (SIS) epidemic model [210, 211], suited to describe diseases that confer no immunity, such as tuberculosis, gonorrhea as well as computer viruses on systems that do not update their virus protection software. Each susceptible node can be infected with rate ν if it is connected to one or more infected nodes, while infected nodes are cured with rate δ and become susceptible again. The SIS model was known to show a non-equilibrium phase transition at a critical spreading rate λ_c ($\lambda = \nu/\delta$): if the spreading rate is higher than this threshold, the disease is endemic: a finite faction of nodes is persistently infected. Below the threshold the disease dies out completely after an initial breakout. As Pastor–Satorras and Vespignani pointed out, these results were obtained on lattices and failed to explain the very low but

sustained prevalence of computer viruses. The authors report the absence of a critical point on scale-free networks with $2 < \gamma \leq 3$: there is no non-zero spreading rate for which the disease dies out. As λ approaches 0, the prevalence of the disease decreases exponentially, but only reaches 0 when $\lambda = 0$.

In a followup study together with Moreno they showed that the lack of an epidemic threshold holds for the "susceptible–infected–recovered" (SIR) model as well [210–212]. This model, applicable for diseases that result in immunity or death, has a radically different overall behavior from the SIS model Recovered individuals cannot get infected again, thus the disease always dies out. Nonetheless, for homogeneous networks it shows a phase transition at a critical spreading rate λ_c, reflected in the total fraction of the population to ever get the disease. Below λ_c this fraction is vanishing as the system size goes to infinity, above λ_c there is a finite infected fraction. Moreno et al. have found that the critical spreading rate for uncorrelated complex networks is $\lambda_c = \langle k \rangle / \langle k^2 \rangle$. Thus, networks with diverging connectivity fluctuations (such as scale-free graphs with $2 < \gamma \leq 3$) have no non-zero epidemic threshold. Although real and thus finite-size networks cannot have infinite $\langle k^2 \rangle$, the epidemic threshold is very small for large systems, much smaller than that of a similar homogeneous network, and it decreases with systems size [213, 214]. The SIR model has been mapped onto a bond percolation problem by Grassberger [215]. This mapping was exploited by Newman, who used the generating function formalism [92, 181] to obtain the exact solution of the model in the infinite time limit for simple graphs with arbitrary degree distribution as well as bipartite graphs, as a model of sexually transmitted diseases spreading between men and women [216].

The absence of an epidemic threshold has profound implications on immunization policies effective in scale-free networks. Dezső and Barabási [217] as well as Pastor–Satorras and Vespignani [218] have shown that scale-free networks do not respond to random immunization: such a strategy cannot restore the epidemic threshold, or bring the effective spreading rate below it, even for an unrealistically high number of administered vaccines. On the other hand, immunization preferentially targeting the hubs of the network successfully reintroduces an epidemic threshold at very low vaccination rates, even if the strategy is imperfect in identifying the hubs. These results have important and controversial consequences for public policy of vaccination in the context of sexually transmitted diseases. This is partly because a policy that gives priority vaccination to prostitutes is controversial even if the public benefits are substantial, but also because it is generally difficult to identify the hubs of sexual networks. Cohen et al. proposed an immunization policy that overcomes this problem without relying on any global knowledge of the system: immunize a randomly chosen friend of a random person [219, 220]. They showed that this strategy preferentially targets the hubs, thus restoring the epidemic threshold.

Epidemic spreading on networks with degree correlations show that degree correlations do not affect the lack of epidemic threshold in scale-free networks [221, 222]. However, the epidemic incidence is smaller in these networks, while diseases are longer lived [221].

The influence of link weights on epidemic spreading has been investigated in the context of diseases such as Severe Acute Respiratory Syndrome (SARS), spreading on the world-wide airline network [223–225]. Colizza et al. developed a detailed multi-scale model of global epidemic spreading and found that the degree heterogeneity of the airport network accounts for most of the observed behavior of the epidemics, the heterogeneity of its weights has a much smalled influence on the spread of the disease [224]. They found that epidemics are fairly predictable, except at the very beginning of an outbreak originating from a hub, as well as the end of epidemics [224].

4.2.2   Information Spreading

The similarity between rumor spreading and epidemic spreading was recognized as early as 1964, when Goffman and Newill used the SIR model to describe the spread of ideas instead of diseases [226]. The authors pointed out an important difference between the two processes: while one studies epidemic models with an effective immunization strategy in mind, information spread is in general favored; moreover, the process can be engineered in a way that facilitates high reliability of the spread. Later in the same year, Daley and Kendall published a spreading model that is specific to rumor (or information) spreading: instead of the random recovery rate of the SIR model (which assumes spontaneous forgetting of the news), they assumed that nodes loose their interest in spreading the news upon encounter with another node that knows it [227]. Thus the "recovery" process of the Daley–Kendall model is very different that that of SIR, leading to a significant difference in the outcome of spreading. Assuming homogeneous mixing (each infected individual, or spreader can randomly contact any node in the system), the final fraction of nodes who have heard the news is $\sim 80\%$.

A decentralized spontaneous and robust method of spreading information was welcome by the computer science community; it allowed them to overcome the scalability problems of data disseminating protocols in large-scale distributed computing [228] and peer-to-peer networks [229] It was also used in update management of databases duplicated at many sites [230].

In the context of complex networks, the Daley–Kendall model was first investigated on the small-world model by Zanette, who found that below a density of shortcuts the rumor dies out without reaching a finite fraction of nodes [231]. Moreover, this threshold is finite for infinite systems ($p_c = 0.2$ for $K = 2$), even though the network is turned

into a small-world by a vanishingly small number of shortcuts. Moreno et al. studied the same model on homogeneous versus scale-free networks and found that as opposed to epidemic spreading, rumors spread to a higher fraction of nodes in homogeneous networks [232, 233]. Hubs in scale-free networks have a conflicting effect on rumor spreading: while they are highly likely and quick to hear the information, they also facilitate the formation of stifler nodes who do not spread the rumor.

4.3 Searching on Complex Networks

Milgram's famous experiment showing six degrees of separation between two random people not only showed the existence of short paths on social networks, it also highlighted the fact that finding a destination node with local information is not very difficult [113]. Motivated by these findings, Kleinberg showed that the performance of a simple greedy search critically depends on the topology of the underlying network. He used a small-world type model in which nodes sit on a two-dimensional lattice (connected to their four neighbours) to which a few long-range connections are added. Unlike in the small-world model, these connections are not added entirely randomly: the probability of a shortcut is proportional to $r^{-\alpha}$, where r is the Manhattan distance between two nodes. In this model the best-case performance of a decentralized algorithm (the expected delivery time) scales as $(\log N)^2$ for $\alpha = 2$. However, both larger and smaller values of α result in expected times that scale as polynomials in N, highlighting that not all networks with short average path lengths allow the use of efficient decentralized searches [234, 235].

Adamic et al. proposed to exploit the heterogeneous nature of scale-free networks to significantly speed up breath-first type searches (also called burning algorithms) which typically run in $\mathcal{O}(N)$ time [236, 237]. Instead of broadcasting a query to all neighbours who in turn broadcast it further, their algorithm checks whether the target is among its first neighbours, and if not, it passes the query along to the neighbour with the highest degree. This neighbour continues the search in a similar way, and if a dead end is reached, the message is recursively back-tracked until there are no neighbours left to explore. This strategy can improve the performance to $\mathcal{O}(N^{1/2})$ for $\gamma = 3$, and $\mathcal{O}(\log N)$ for $\gamma = 2$ scale-free networks. The method was tested by the authors on the GNUTELLA peer-to-peer network, as well as by Kim et al. on scale-free networks generated by the configuration model and the Barabási–Albert model [237][6].

Searchability of social networks has been revisited several times since Milgram's experiment. Killworth and Bernard found that the choice of neighbor to pass the letter on

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[6]Kim, Yoon, Han and Jeong proposed the strategy independently a few months after Adamic et al. submitted their paper.

was most often based on common characteristics with the target, such as geographical location and profession [238]. An electronic version of the experiment carried out by Dodds et al. concluded that the search on the e-mail network is also guided by reliance on common "social identities", and the chosen routes do not favor social hubs [239]. Motivated by these results, Watts et al. and Kleingerg independetly proposed a searchable social network model in which nodes are grouped in a nested hierarchy of social categories. A link between two nodes is exponentially less likely if their social distance (length of the path along the hierarchical tree of social groups) is large [240, 241]. In a simulated Milgram–type experiment, the letter would be passed from a node to a neighbor with the smallest social distance to the target. Such a search performs well for a range of the model parameters, with it's best performance scaling as $\mathcal{O}(\log N)$ [241].

5 Future Directions

The short account of research advances into dynamics on complex networks presented here is by no means exhaustive. Several fairly large and lively research areas, synchronization, boolean networks, random walks on complex networks, brain networks, models of adaptive or dynamical wiring among them, have all been omitted here.

Future directions in networks research are hard to account for in a few paragraphs. It is believed that further understanding of dynamics on complex networks is the general direction of the field. Along with a shift from pure structural studies to dynamics, there has also been a shift from studies of networks in general and features that are common to most of them to more application-driven studies of increasingly narrow classes of networks. This is not to say that important lessons learned this way do not often carry over from one system to the other, but it shows that enough is known about network characteristics now to tell them apart, to look for distinguishing features as well as universal ones.

A fairly standard toolkit for the assessment of the structural properties of a network has already emerged, making the notion of networks and knowledge about them a useful toolkit in studying the architecture of complex systems. Our hope is that dynamical studies will further extend the toolkit to cover general aspects of the type of events occurring on complex networks, and perhaps lead the way in understanding how function emerges in complex systems.

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