



**Self-isolation or borders closing: What prevents the spread of the epidemic better?**O. Valba <sup>1,2</sup>, V. Avetisov <sup>2</sup>, A. Gorsky,<sup>3,4</sup> and S. Nechaev<sup>5,6</sup><sup>1</sup>*Department of Applied Mathematics, National Research University Higher School of Economics, 101000 Moscow, Russia*<sup>2</sup>*Federal Research Center of Chemical Physics RAS, 119991 Moscow, Russia*<sup>3</sup>*Institute of Information Transmission Problems RAS, 127051 Moscow, Russia*<sup>4</sup>*Moscow Institute of Physics and Technology, Dolgoprudny 141700, Russia*<sup>5</sup>*Interdisciplinary Scientific Center Poncelet, CNRS UMI 2615, 119002 Moscow, Russia*<sup>6</sup>*P.N. Lebedev Physical Institute RAS, 119991 Moscow, Russia*

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Pandemic propagation of COVID-19 motivated us to discuss the impact of the human network clustering on epidemic spreading. Today, there are two clustering mechanisms which prevent of uncontrolled disease propagation in a connected network: an “internal” clustering, which mimics self-isolation (SI) in local naturally arranged communities, and an “external” clustering, which looks like a sharp frontiers closing (FC) between cities and countries, and which does not care about the natural connections of network agents. SI networks are “evolutionarily grown” under the condition of maximization of small cliques in the entire network, while FC networks are instantly created. Running the standard SIR model on clustered SI and FC networks, we demonstrate that the evolutionary grown clustered network prevents the spread of an epidemic better than the instantly clustered network with similar parameters. We find that SI networks have the scale-free property for the degree distribution  $P(k) \sim k^\eta$ , with a small critical exponent  $-2 < \eta < -1$ . We argue that the scale-free behavior emerges as a result of the randomness in the initial degree distributions.

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**Introduction.** It is known [1] that the spread of an epidemic on a network is sensitive to two generic features: clustering and adaptivity [2–5], where under adaptivity typically it is understood that the self-consistent network rewiring minimizes the impact of the disease on the human population. Both the clustering and the adaptivity have a strong effect on epidemic threshold, peak value, and typical distribution time. Our work is inspired by the pandemic distribution of COVID-19 and we are focused on some mechanisms of network clustering which have an essential influence on the disease propagation. Specifically, we discuss effects of adaptive network rewiring.

We are encouraged by an observation made in Ref. [6] concerning the localization of one-body excitations on network clusters obtained in a specific evolutionary way. More recently, similar results have been derived for networks with various patterns of dynamically induced clustering [7–9]. In this Rapid Communication, we analyze and compare numerically the spread of an epidemic on adaptively rewired and instantly clustered connected networks.

In Ref. [6], we have considered spectral properties of two types of constrained random Erdős-Rényi networks in the clustered phase: (i) so-called e-networks, obtained by the evolutionary Metropolis maximization of small cliques of connected nodes, and (ii) so-called i-networks, instantly prepared clustered graphs having the same geometrical properties as e-networks but which are created *ad hoc* without any evolutionary selection.

In e-networks, which are nonergodic, excitations are mostly localized on clusters and weakly spread through the entire network. However, the entire network is connected and there is a small, though finite, density of intercluster links

which prevents complete localization. In contrast, i-networks are ergodic and they serve as a particular example of a stochastic block model [10,11]. Being geometrically very similar to e-networks, i-networks nevertheless are less effective in blocking the spreading of excitations. As we show below, the distinction between e- and i-networks deals with different statistics of intercluster links. In our work, we report results of simulations of the standard SIR model on clustered e- and i-networks. The SIR model (described in Sec. IV) is the simplest and widely used model of disease transmission from human to human.

The paper is organized as follows: First, we formulate the model of adaptive clustering. Second, we argue that our model has a scale-free degree distribution providing explanation of a very specific triangular shape of the spectral density of clustered e-networks observed in Ref. [12]. Then, we describe results of simulations of the SIR model on Erdős-Rényi (ER) e- and i-networks. Finally, we speculate about the possible interpretation of self-isolation (SI) in communities as a formation of adaptively clustered e-networks and frontiers closing (FC) as a formation of i-networks, and we demonstrate that SI prevents the spread of the epidemic more efficiently than FC.

**Definitions and networks generation.** The main object of our consideration is the dynamically evolving constrained Erdős-Rényi network. The  $N$ -node Erdős-Rényi network is a topological graph of  $N$  vertices constructed by random linking with the probability  $p$  any pair of points from a set of  $N$  arbitrary points. The probability,  $P(k)$ , to find a vertex in the ER network, linked with other  $k$  vertices, is Poissonian with the mean value  $\langle k \rangle = Np$ . Another well-studied class of random networks are the so-called scale-free networks, for

which the vertex degree distribution,  $P(k) \sim k^\eta$ , has a power-law tail with a critical exponent  $\eta < 0$  (typically  $\eta < -2$ ). The overwhelming majority of natural networks are scale-free, and the network of distribution of COVID-19 is not an exception [13].

Natural networks, being complex self-organized objects, evolve in time, trying to adapt to imposed external conditions. We distinguish two classes of dynamic Erdős-Rényi networks: “unconstrained” (without the vertex degree conservation during the network evolution) and “constrained” (with preservation of vertex degrees in all nodes under the network rewiring). In unconstrained ER networks, one can remove any link from one place of the graph and insert it into any other place. In contrast, in constrained ER networks, the realization of a rewiring is more complex and involves simultaneous replacement of at least two bonds.

Speaking more practically, consider a network of human social relations, where each graph vertex represents a particular agent. It seems reasonable to assume that for each agent, the number of social connections (the particular vertex degree in a social network) is conserved. The number of connections may vary from one agent to the other one; however, for each human, it is supposed to be fixed and unchanged during the social network evolution. Such a supposition seems rather natural since the number of relations per one individual rapidly increases, saturates, and then remains approximately conserved during the lifetime, being a typical social habit of a human.

Returning to the network, we proceed with the following rewiring setup which conserves all vertex degrees. We take a random Erdős-Rényi  $N$ -vertex graph without double connections as an initial state of a network. Then, we randomly select a pair of arbitrary links, say,  $(ij)$  between vertices  $i$  and  $j$  and  $(kl)$  between  $k$  and  $l$ , and reconnect them, getting new links  $(ik)$  and  $(jl)$ . Such reconnections conserve the vertex degree [14] but allow for bond redistribution and do not prohibit topological changes in the entire network. In the context of phase transitions in social networks, such a dynamic model has been discussed in Ref. [15].

The following question has been addressed in Ref. [12]. Suppose that we rewire links in the constrained Erdős-Rényi network (CERN) under the condition that at each step of rewiring we try to maximize the number of small cliques (small complete subgraphs of few links). What would be the equilibrium structure of the entire network? In mathematical terms, this question reads as follows. We assign the energy,  $\mu$ , to each simplest clique (closed triad of bonds) and denote by  $n_\Delta$  the number of such triads in the network. The partition function of the network can be written as

$$Z(\mu) = \sum_{\{\text{states}\}} e^{-\mu n_\Delta}, \quad (1)$$

where prime in (1) means that the summation runs over all possible configurations of links (“states”), under the condition of fixed degrees  $\{v_1, \dots, v_N\}$  in all network vertices.

To simulate the rewiring process, one applies the standard Metropolis algorithm with the following rules: (i) If under the reconnection the number of closed triads is increasing, a move (rewiring) is accepted, and (ii) if the number of closed triads is decreasing by  $\Delta n_\Delta$ , or remains unchanged, a

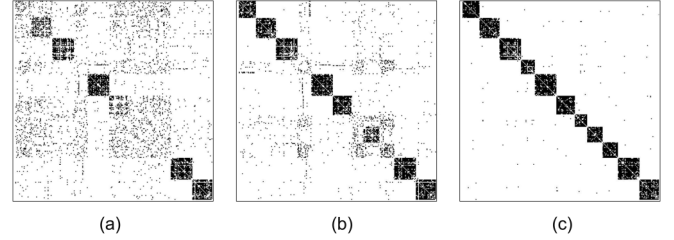


FIG. 1. A few typical samples of intermediate stages of a network evolution at fixed vertex degree upon the maximization of triads. Network has  $N = 750$  vertices and the connection probability at the preparation is  $p = 0.08$ .

move is accepted with the probability  $e^{-\mu \Delta n_\Delta}$ . The Metropolis algorithm runs repeatedly for a large set of randomly chosen pairs of links, until it converges. In Ref. [16], it was proven that the algorithm converges to the Gibbs measure  $e^{\mu n_\Delta}$  in the equilibrium ensemble of random undirected Erdős-Rényi networks with fixed vertex degrees.

In Ref. [12], it has been shown that given the bond formation probability,  $p$ , in the initial graph, the evolving network splits into the maximally possible number of clusters,  $N_{cl}$ :

$$N_{cl} = \left\lfloor \frac{N}{Np + 1} \right\rfloor_{N \gg 1} \approx \left\lfloor \frac{1}{p} \right\rfloor, \quad (2)$$

where  $\lfloor x \rfloor$  means the integer part of  $x$  and the denominator  $Np + 1$  defines the minimal size of formed cliques. The asymptotic limit  $\sim \lfloor p^{-1} \rfloor$  at  $N \rightarrow \infty$  in (2) is independent of the particular set of vertex degrees,  $\{v_1, \dots, v_N\}$ .

According to Ref. [17], clustering of evolving constrained Erdős-Rényi network occurs upon the triad maximization, as a first-order phase transition with increase of the control parameter,  $\mu$ , the chemical potential of the triads. To have some insight about topological network structure in course of the evolution, we reproduce in Fig. 1 typical adjacency matrices at three sequential stages of a particular network rearrangement: The initial adjacency matrix of the CERN is shown in Fig. 1(a), its snapshot at the intermediate stage of rewiring upon triad maximization is depicted in Fig. 1(b), while the final stage of the network adjacency matrix after the first-order clustering transition is represented in Fig. 1(c); see Ref. [12] for details.

To visualize the evolution, we enumerate vertices at the preparation condition in arbitrary order and run the Metropolis stochastic dynamics. When the system is equilibrated and clusters are formed, we re-enumerate vertices according to their belongings to clusters. Then we restore corresponding dynamic pathways back to the initial configuration.

We compare the evolutionary grown clustered e-network, obtained by the maximization of triangles (triadic motifs), with another mechanism of clustered i-network formation. The i-network is instantly formed and is a particular example of a stochastic block random graph [10,11]. To be precise, the i-network is constructed by the following procedure. First, we construct the  $N$ -vertex clustered e-network, in which we detect all clusters  $\{J\}$  and define the average link probabilities as  $p_{in}^J$  inside each cluster  $J$  and  $p_{out}$  between clusters. Then, we take a set of  $N$  points, split the set in groups as in

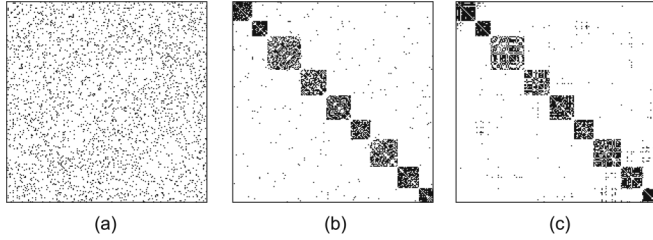


FIG. 2. Examples of typical adjacency matrices for (a) Erdős-Rényi random network, (b) e-networks evolutionary grown by triangle maximization from the network in panel (a), and (c) i-networks, which have  $N = 750$  vertices and are created with the link probability  $p = 0.08$ . By visual inspection, it is almost impossible to distinguish the adjacency matrices of e- and i-networks.

the e-network, and connect points in these groups with the probability  $p'_{in}$ . In such a way, we generate a set  $\{J'\}$  of new clusters which mimic clusters of e-networks. Finally, we randomly connect vertices belonging to different clusters from the set  $\{J'\}$  with the probability  $p_{out}$  borrowed from the average connection probability between clusters in the e-network. Such an instantly created i-network mimics the e-network, since the i-network has the same linking probability and community structure as the evolutionary grown e-network. In Fig. 2(a), we have shown the initial Erdős-Rényi random network, from which the e-network, shown in Fig. 2(b), and i-network, shown in Fig. 2(c), are constructed according to the procedure described above. Let us emphasize that the i-network has no history, knows nothing about the evolution, has no dependence on  $\mu$ , and has no vertex degree conservation. However, the visual inspection of Figs. 2(a) and 2(c) does not allow us to distinguish adjacency matrices e- and i-networks. Besides, the propagation of excitation on e- and i-networks behaves very differently.

To summarize, we have ensembles of two kinds of networks: (i) evolutionary grown e-networks which have memory about the history of their creation and (ii) instantly *ad hoc* formed i-networks. Projecting mechanisms of construction of e- and i-networks onto the human society, it seems plausible (1) to identify clustered e-networks obtained by a preferential arrangement of network vertices in small cliques with the self-isolation (SI) of humans in small communities and (2) to identify instantly created i-networks with the splitting of entire human network into the collection of weakly connected clusters obtained by frontier (border) closing (FC). For comparison, we also consider random Erdős-Rényi networks with the same vertex degree distribution, which are the source of our evolutionary algorithm.

*Evolutionary clustering and scale-free distribution in e-networks.* In Ref. [12], we have pointed out some puzzling property of the spectral density (eigenvalue distribution) of evolutionary clustered networks. The spectrum above clustering transition has demonstrated the two-band structure in which the first (main) band was naturally attributed to the perturbative excitations inside clusters, while the second non-perturbative<sup>1</sup> band emerged from the eigenvalues tunneling from the first zone aside. It was found numerically that the spectral density in the perturbative band has a triangular shape typical of the scale-free networks [18,19]. Such a result looks

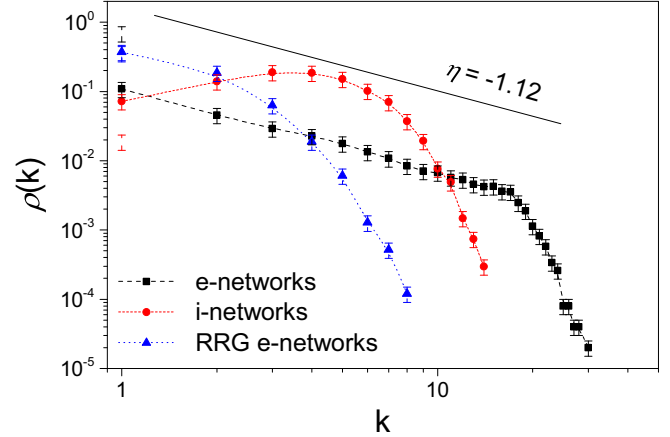


FIG. 3. The outer cluster degree distribution  $\rho(k)$  in log-log scale for e-networks (black squares), i-networks (red circles), and random regular graphs (blue triangles). Results are obtained for 100 realizations of networks with  $N = 750$  nodes and the linking probability  $p = 0.08$ . The solid line shows the slope  $\eta = -1.12$  for the power law  $\rho(k) = k^{-\eta}$ .

surprising since a clustered network has emerged from an Erdős-Rényi graph with a binomial degree distribution in which the vertex degree is conserved during the network evolution (rewiring), naively thinking there is no place for a clustered network to be scale-free.

The resolution of that puzzle turns out to be as follows: In the evolutionarily grown clustered network, we have to consider separately the distributions of internal (inside cluster) and external (between clusters) vertex degrees. Let us consider a vertex  $i$  belonging to the cluster  $J$  of a clustered e-network, and define the “outer degree” for a vertex  $i$  as the number of links, connecting  $i$  to vertices of clusters other than  $J$ . In Fig. 3, we have plotted the outer vertex degree distribution,  $\rho(k)$ , of cluster nodes for three types of networks: e-networks (black squares), i-networks (red circles), and RRG e-networks (blue triangles). The simulations show that the e-networks demonstrate the power-law scaling

$$\rho(k) \sim k^\eta \quad (3)$$

with a surprisingly small value of  $\eta$ . The line of the best fit in Fig. 3 for the outer vertex degree distribution of e-networks has the slope  $\eta = -1.12$ . In contrast, the inner vertex degree demonstrates the binomial distribution modified by the long tail at small degrees.<sup>1</sup> Instantly created i-networks (red circles) do not possess such a scale-free behavior for outer vertex degrees.

It is eligible to ask which property of an e-network is responsible for the scale-free distribution. To this aim, we consider the e-networks constructed on the basis of random regular graphs (RRG), which possess similar cluster structures. The outer vertex degree distribution of RRG e-networks,

<sup>1</sup>Outer vertices we understand as nodes connected by cross-cluster (outer) links, while inner vertices are nodes connected by in-cluster (inner) links. These notations should not be confused with outer and inner links in directed networks.

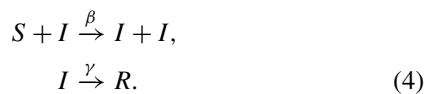


shown by blue triangles in Fig. 3, does not demonstrate the scale-free behavior; however, the distribution itself seems to be closer to the one of e-networks rather than of i-networks. Thus, we have solid arguments to believe that the scale-free behavior of e-networks is induced by the disorder in the vertex degree distribution of the parent constrained Erdős-Rényi network.

The scale-free dependence (3) is fully consistent with our former investigations [6,12] of spectral statistics of evolutionary grown clustered networks. It has been shown in Ref. [12] that the enveloping shape of the main band in the spectral density of the adjacency matrix is changing with increasing of  $\mu$  from the semicircle (in the initial ER network below  $\mu_{cr}$ ) to the triangle (in the clustered network above  $\mu_{cr}$ ), where  $\mu_c$  is the first-order transition point. According to our observation, the triangular shape of the spectral density in the main band should be attributed mainly to the scale-free property of intercluster excitations of e-networks.

The critical exponent  $\eta$  is small ( $-2 < \eta < -1$ ), meaning that the average vertex degree distribution diverges. General conditions to have  $\eta > -2$  in the scale-free networks with fixed number of nodes is discussed in Refs. [20,21]. A nontrivial rewiring procedure for generating networks with  $\eta > -2$  has been proposed in Ref. [20]. Although the algorithm of Ref. [20] looks sophisticated, the ideas behind its construction are in good agreement with our simple generation procedure of the scale-free network with  $-2 < \eta < -1$ . Namely, to get  $\eta > -2$  one should carefully tune the combination of local and global constraints. One more rewiring procedure was suggested in Ref. [21] for getting  $\eta = -1$ . Fortunately, our simple algorithm dealing with maximization of triads in constrained Erdős-Rényi network brings the system automatically in the regime where the generation of a scale-free subnetwork with  $-2 < \eta < -1$  occurs. To summarize, the main result of this section consists in providing a simple rewiring mechanism for the fabrication of scale-free distribution in constrained Erdős-Rényi networks.

*Numerical simulation of SIR model.* Epidemic models classify individual agents (humans) based on the stage of disease affecting them. The simplest classification scheme assumes that an agent can be in one of three states (compartments): (a) susceptible (S) for healthy agents having not yet contacted the pathogen, (b) infectious (I) for contagious agents who have contacted the pathogen and can infect others, and (c) recovered (R) for recovered (or immune) agents. The distribution of disease on some target space is considered in the frameworks of transformations among susceptible, infectious, and recovered agents and is known as the SIR model [22]. The standard dynamics of the SIR model reads as follows:



The model has two adjustable parameters,  $(\beta, \gamma)$ . These parameters set transition rates  $\beta$  for susceptible nodes to become infected from infected neighbors and  $\gamma$  for infected nodes to recover.

We have run the SIR model on three types of graphs: random Erdős-Rényi (ER) network, e-network, and i-network, and the respective adjacency matrices are shown in

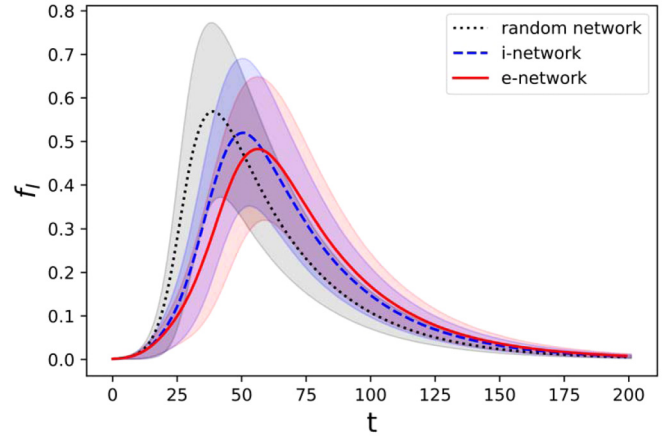


FIG. 4. The fraction of infected nodes in time for Erdős-Rényi networks, i-networks, and e-networks. Results are obtained for the SIR dynamics with transmission rate  $\beta = 0.05$  and recovery rate  $\gamma = 0.03$  for  $n = 1000$  simulation runs on each networks. Shaded regions designate the confidence range of the dependence  $f_i(t)$  for a network type.

Figs. 2(a)–2(c). The results of our simulations are depicted in Fig. 4, where we have plotted the density of infected agents,  $f_i$ , versus time,  $t$ . To be able to compare distributions, we took networks from different classes (random ER, e-networks, and i-networks) with the identical sets of parameters, namely with the number of nodes  $N = 750$  and the link probability  $p = 0.08$ . The black dotted, blue dashed, and red solid lines in Fig. 4 show the dependencies  $f_i(t)$  for random Erdős-Rényi (ER) networks, i-networks, and e-networks, respectively. The shadowed regions represent the standard deviations from the curves, averaged over  $n = 1000$  simulations for each type of network. The parameters  $\beta$  and  $\gamma$  are chosen as follows:  $\beta = 0.05$  and  $\gamma = 0.03$ .

Analyzing distributions in Fig. 4, we see two important features of the epidemic spread described by the SIR model on different network types. Apart from the maximal distribution on the nonclustered ER network (which is our reference state), the interesting features demonstrate e-networks and i-networks. It turns out that clustering actually weakens the epidemic spread, but the details are very sensitive to the way the clustered network is created. The evolutionary grown e-networks demonstrate better suppression of the epidemic spread than instantly created i-networks for the same set of parameters. Meanwhile, the peak of the distribution of infected agents on e-networks is shifted to later times compared to both ER and i-networks.

*Results and discussion.* Here we briefly speculate about the provocative title of our work in the context of selecting between two different protocols of suppressing the epidemic proliferation. Currently, two main mechanisms of human population network clustering are used by different countries to prevent the uncontrolled spreading of COVID-19. Tentatively, these mechanisms could be named self-isolation (SI) and frontiers closing (FC). In both cases, the aim of clustering is to localize the illness propagation in a closed community and prevent it from spread through the entire human network. Specifically, we are interested in the question of which mechanism better blocks the spread of the epidemic:

self-quarantine in local communities induced by increasing the weights of small cliques in the human network or sharp clustering via closing of borders between arbitrary parts of the human network. In an ideal situation, when all self-isolated communities are absolutely disconnected from each other, and when the border crossings between cities and countries are totally prohibited, both protocols are equally efficient and definitely inhibit disease expansion. However, in reality, it is impossible to isolate communities completely and some fraction of cross-community connections is always present. In that case, we claim that the human network clustering obtained by self-isolation better prevents the spread of the epidemic than the instant separation of the network into the clusters. Readers are invited to make their own judgment of whether this speculation seems plausible in the context of the human society and to what extent.

We have demonstrated that a network which is evolutionarily grown from a randomly generated Erdős-Rényi graph with the fixed vertex degree under the condition of maximizing small cliques (triadic motifs) gets clustered into community clusters and the number of such communities depends on the linking probability  $p$  in the initial graph [see Eq. (2)]. We have also verified numerically that similar adaptive clustering occurs when triadic motifs are replaced by complete 4-cliques. Running SIR model on e-networks and in parallel on i-networks (which mimic clustered structure of e-networks but are memoryless), we see from Fig. 4 that e-networks prevent better spread of the epidemic than i-networks (the

maximum of infected agents is lower for e-networks), while the maximum of infected agents (peak of the epidemic spread) on e-networks is shifted to later times compared to i-networks.

Importantly, we have found that the clustered e-networks are scale-free, which explains some previously obtained numerical observations concerning spectral density of the adaptively grown networks. Thus, by maximizing the number of triadic motifs in the constrained Erdős-Rényi networks, we have proposed a simple mechanism of generating scale-free graphs via the rewiring process.

The epidemic spreading on the scale-free networks has some specific peculiarities [23]. In particular, the epidemic threshold almost vanishes, which means that the scale-free network is bad for epidemic suppression at the beginning of its distribution. However, once started, the epidemic can be operated on a scale-free network more effectively than on other types of networks. This rewiring mechanism for getting scale-free behavior can be useful for these purposes.

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