Self-isolation vs frontiers closing: What prevents better of epidemic spread?

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We discuss combined effects of network clustering and adaptivity on epidemic spread. We address the question which mechanism is more effective for prohibiting disease propagation in a connected network: adaptive clustering, which mimics self-isolation (SI) in local communities, or sharp instant clustering, which looks like frontiers closing (FC) between cities and countries? Since in reality cross-community connections always survive, we can wonder how efficient is the excitation (illness) propagation through the entire clustered network which has some density of inter-cluster connections. Crucial difference between SI- and FC-networks is as follows: SI-networks are "adaptively grown" under condition of maximization of small cliques in the entire network, while FC-networks are "instantly created" by ad hoc imposed borders. We found that SI model has scale-free property for degree distribution \(P(k) \sim k^\eta\) with surprisingly small critical exponent \(-2 < \eta < -1\). Running standard SIR model on clustered SI- and FC-networks, we demonstrate that the adaptive network clustering caused by self-isolation in communities prohibits the epidemic spread better than the clustering due to instant boundaries closing.

I. INTRODUCTION

It is known \cite{1} that any epidemic spread is sensitive to two generic features: clustering and adaptivity. Both of them have a strong impact on epidemic threshold \cite{2,3,4,5}. Peak value and typical distribution time. Here we are focused on a specific mechanism of adaptive clustering, which has strong impact on the disease propagation. Our work is motivated by an observation made in \cite{6} concerning localization of one-body excitations on network clusters obtained in a specific evolutionary way. More recently similar results have been derived for networks with different patterns of dynamically induced clustering \cite{7,8}. In the current Letter we analyze and compare numerically the epidemic spread on adaptively and instantly clustered networks.

In \cite{6} we have considered spectral properties of two types of constrained random Erdős-Rényi networks in the clustered phase: (i) "e-networks" obtained by the evolutionary Metropolis maximization of small cliques, and (ii) "i-networks", instantly prepared clustered graphs having the same geometrical properties as "e-networks", but which are created without any evolutionary selection. In e-networks, which are non-ergodic, excitations are localized on clusters and do not propagate through the entire network, despite the entire graph is still connected and there is a small, though finite density of inter-cluster links. To the contrary, ergodic i-networks, which serve as a particular example of a "stochastic block model" \cite{10,11}, being geometrically very similar to e-networks, do not possess the localization property. In our work we report results of simulations of the standard SIR model on clustered e- and i-networks. The SIR model (described in Section IV) is the simplest and widely used model of diseases transmission from human to human.

The paper is structured as follows. In Section II we formulate the model of adaptive clustering. In Section III 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 \cite{14}. In Section IV we describe results of simulations of SIR model on Erdős-Rényi, e- and i-networks. In Discussion we speculate about possible interpretation of self-isolation (SI) in communities as formation of adaptively clustered e-networks, frontiers closing (FC) – as formation of i-networks, and demonstrate that SI prohibits the epidemic spread more efficient than FC.

II. DEFINITIONS AND NETWORKS GENERATION

The main object of our consideration is the dynamically evolving constrained Erdős-Rényi network. The N-vertex Erdős-Rényi (ER) network is a topological graph of N vertices constructed by random linking with probability \(p\) any pair of points from a set of N arbitrary points. The probability, \(P(k)\), to find a vertex in 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 \(\eta < 0\). The overwhelming majority of natural networks is scale-free, and the network of distribution of COVID-19 is not an exception \cite{12}.

Natural networks, being complex self-organized objects, evolve in time trying to adapt themselves to im-
posed 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 network rewiring). In unconstrained ER networks one can remove any link from one place and insert it in any other place. To the contrary, in constrained ER networks the realization of a rewiring is a bit more complex and involves simultaneous replacement at least two bonds. Speaking less abstract, consider a network of human social relations, where each graph vertex represents a particular individual. It seems reasonable to assume that the number of social connections of each individual (the particular vertex degree in a social network) is conserved. The number of connections may vary from one individual to another, however for each network (evolution) is conserved. The number of connections may not be assumed that the number of social connections of each individual (the particular vertex degree in a social network) is conserved. The number of connections may vary from one individual to another, 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 in time. Specifically, we proceed with the following rewiring setup which conserves 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, (i, j) (between vertices i and j) and (k, l) (between k and l), and reconnect them, getting new links (i, k) and (j, l). Such reconnections conserve the vertex degree, however allow for bonds redistribution and do not prohibit topological changes in the entire network.

The following question has been addressed in [14]. Suppose that we rewire links in the constrained Erdős-Rényi network under the condition that at each step of rewiring we try to maximize the number of small cliques (small complete subgraphs of few links). Which is 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 $n_\triangle$ the number of such triads in the network. The partition function of the network can be written as

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

where prime in $\{\text{states}\}$ means that the summation runs over all possible configurations of links ("states"), under the condition of fixed degrees $\{v_1, ..., v_N\}$ 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, ii) if the number of closed triads is decreasing by $\Delta n_\triangle$, or remains unchanged, a move is accepted with the probability $e^{-\mu \Delta n_\triangle}$. The Metropolis algorithm runs repeatedly for large set of randomly chosen pairs of links, until it converges. In [14] it was proven that such Metropolis algorithm converges to the Gibbs measure $e^{\mu N_\triangle}$ in the equilibrium ensemble of random undirected Erdős-Rényi networks with fixed vertex degree.

In [14] 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, $N_{\text{cl}}$:

$$N_{\text{cl}} = \left\lfloor \frac{N}{Np + 1} \right\rfloor \approx \left\lfloor \frac{1}{p} \right\rfloor,$$  

(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 $\sim [p^{-1}]$ at $N \to \infty$ in (2) is independent on the particular set of corresponding vertex degrees, $\{v_1, ..., v_N\}$.

It has been shown in [14] that clustering of evolving constrained Erdős-Rényi network under condition of triads maximization, occurs as a first order phase transition where $\mu$ is a control value. To have some insight about topological network structure in course of its evolution under condition of maximization of triadic motifs, we show in Fig.1 typical adjacency matrices at three sequential stages of a particular network rearrangement.

Figure 1: Few typical samples of intermediate stages of a network evolution at fixed vertex degree under condition of triads maximization.

To visualize the evolution, we enumerated 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 sequentially according to their belongings to clusters. Then we restore corresponding dynamic pathways back to the initial configuration – see [14] for details.

The evolutionary grown clustered "e-network", obtained by the maximization of triangles (triadic motifs) we compare with another mechanism of clustered "i-network" formation. The "i-network" is instantly formed being a particular example of a stochastic block random graph [10, 11]. The i-network is constructed by the following procedure. We detect clusters $\{J\}$ in the e-network, define the link probability, $p_{\text{in}}^J$, inside each cluster $J$, and between clusters, $p_{\text{out}}$. Firstly, we generate random subgraphs having the same numbers of nodes and the same probabilities $p_{\text{in}}^J$ as clusters in e-networks. Secondly, we randomly connect nodes belonging different subgraphs of i-network with the probability $p_{\text{out}}$ borrowed from the average connection probability between clusters in e-network. Such an "instantly created" i-network mimics in some sense e-network, since i-network
has the same degree distribution and community structure as the evolutionary grown e-network – see Fig. 2. However the i-network has no any pre-history, it knows nothing about the evolution, it has no dependence on $\mu$, and has no vertex degree conservation. Visual inspection of Fig. 2 does not allow us to distinguish adjacency matrices e- and i-networks. Besides, propagation of excitation on e- and i-networks behaves very differently.

Figure 2: Examples of typical adjacency matrices for random, e- and 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.

To summarize, we have in hands ensembles of two kinds of networks: (i) evolutionary grown (e-networks) which have memory about the history of its creation, and (ii) instantly formed (i-networks). Comparing mechanisms of construction of e- and i-networks, it seems plausible:

- To identify clustered e-networks, obtained by preferential arrangement of network vertices in small cliques with self-isolation (SI) of humans in small communities,
- To identify instantly created i-networks with splitting of entire human network into collection of weakly connected clusters obtained by frontiers (borders) closing (FC).

For comparison we also consider random Erdős-Rényi networks of the same vertex degree distribution, which are served for initial states of our evolutionary algorithm.

III. ADAPTIVE CLUSTERING AND SCALE-FREE DISTRIBUTION

In [14] we have pointed out some puzzling property of the spectral density (eigenvalue distribution) of adaptively clustered networks. The spectrum above clustering transition acquired two-band structure in which the first (main) band was naturally attributed with perturbative excitations inside clusters, while the second "non-perturbative" band emerged from eigenvalues tunneled from the first zone aside. It was found numerically that the spectral density in the perturbative band has triangular shape typical for scale-free networks [17, 18]. Such result looked surprising since the clustered network is originated from a standard Erdős-Rényi graph with a binomial degree distribution and since the vertex degree is conserved in the network evolution, naively thinking there is no place for a network to be scale-free.

The resolution of that puzzle turns out to be as follows: we have to consider separately distributions of internal (inside cluster) and external (between clusters) vertex degrees. Consider a vertex $i$, which belongs to the cluster $J$ of clustered e-network, and define the "outer degree" for a vertex $i$ as the number of links, connecting $i$ to vertices of clusters different from $J$. In Fig. 3 we plot the "outer vertex degree distribution", $\rho(k)$, of cluster nodes. The simulations show the power-law scaling with surprisingly small $\eta$

$$\rho(k) \sim k^{\eta}$$

The line of the best fit in Fig. 3 has the slope $\eta = -1.12$. The "inner vertex degree distribution" demonstrates the binomial distribution modified by the long tail at small degrees. Instantly constructed i-networks surely do not demonstrate such scale-free behavior for vertex degrees between clusters.

Figure 3: The outer cluster degree distribution $\rho(k)$ in log-log scale. Results were obtained for 100 realizations of e-networks with $N = 750$ nodes and the linking probability $p = 0.08$.

Thus, the dependence (3) is fully consistent with our investigations [6, 14] of spectral statistics of evolutionary grown clustered networks. It was shown in [14] that the enveloping shape of the main band in spectral density of the adjacency matrix is gradually changing from the semicircle (in the initial ER network) to the triangle (in the final clustered network). 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 the inter-cluster excitations.

The imposed constraint on vertex degree conservation is not exotic, being typical for chemical, biological and social networks. The adaptive clustering can be considered as the operational tool of network splitting into the optimal droplets of almost full subgraphs (cliques) for generic
random networks. Varying the constraints, the required design of the network state can be manufactured.

IV. 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 individual can be in one of three states (compartments): (a) susceptible (S) for healthy individuals having not yet contacted the pathogen, (b) infectious (I) for contagious individuals have contacted the pathogen and can infect others, (c) recovered (R) for recovered (or immune) individuals. The distribution of disease on some target space is considered in the frameworks of transformation between susceptible, infectious and recovered agents and is known as the SIR model [16]. We consider the SIR model, for which the dynamics can be written in form:

$$S + I \xrightarrow{\beta} I + I$$
$$I \xrightarrow{\gamma} R.$$

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 archetypes of graphs: random Erdős-Rényi (ER) network, e-network and i-network, the respective adjacency matrices are shown in Fig. 2. 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 developed networks from different classes with the identical set of parameters, namely with the number of nodes $N = 750$ and the link probability $p = 0.08$. Solid curves in Fig. 4 (black for random Erdős-Rényi (ER) network, red for e-network and blue for i-network) represent mean distributions, averaged over $n = 1000$ simulations on each network, while shadowed regions designate standard deviations. The parameters $\beta$ and $\gamma$ are set to $\beta = 0.05, \gamma = 0.03$. The numerical results are reproduced for different network realizations.

Analyzing distributions in Fig. 4 let us point out two important features of epidemic spread described by SIR model on different network archetypes. Apart from the maximal distribution on non-clustered ER network (black curve) 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 details are very sensitive to the way of clustered network construction. The evolutionary grown e-networks demonstrate better suppression of epidemic spread than the instantly created i-networks for the same parameters, however the peak of the distribution of infected agents on e-networks is shifted to later times compared to both random and i-networks.

V. RESULTS AND DISCUSSION

Here we speculate on a rather provocative title of our work in the context of selection between two different protocols of preventing virus distribution. Currently two main mechanisms of a human population clustering are exploited by different countries in order to prevent the uncontrolled distribution of COVID-19. Tentatively these mechanisms could be named a "self-isolation" (SI) and a "frontiers closing" (FC). In both cases the aim of clustering is to localize the illness in closed communities and prevent it from the propagation through the entire human network. Specifically, we are interested in the question which mechanism blocks better an epidemic spread: self-quarantine in local communities induced by adaptive clustering, or sharp clustering via closing of borders between cities and countries? In an ideal situation, when all self-isolated communities are absolutely disconnected and when the border crossings between cities and countries is 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 always is present.

We have demonstrated that the network evolutionary grown from a randomly generated Erdős-Rényi graph with fixed vertex degree under condition of maximization of small cliques (triadic motifs) gets clustered into
communities-clusters and the number of such communities depends on the linking probability $p$ in the initial graph (see [2]). We have also verified 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, however are memory-less), we see from Fig.4 that e-networks prevent better of epidemic spread than i-networks (the maximum of infected agents is lower for e-networks), while the maximum of infected agents is shifted to later times compared to i-networks.

Suggesting a superficial similarity between clustered e-networks with self-trapping of humans in small communities, we compare such self-isolation with human isolation in clustered i-networks constructed by instant closing of borders between districts, cities and countries. We claim better effectiveness of self-isolation of illness suppression. Readers are invited to make their own judgement whether such a speculation seems plausible and to which extent.

Importantly, we have found the scale-freeness of clustered e-network. That explains some previous numerical observation concerning spectral density of such adaptively grown networks. It means that small number of inter-cluster links has a very strong impact on the spectral properties of excitations inside clusters. The epidemic spread on scale-free network has some specific properties [19]. In particular, the epidemic threshold almost vanishes which means that scale-free network is bad for epidemic suppression at the beginning of its distribution. However once started, it can be operated on scale-free network more effectively than on other types of networks.

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