Nonequilibrium phase transition due to isolation of communities

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We introduce a simple model of a growing system with m competing communities. The model corresponds to the phenomenon of defeats suffered by social groups living in isolation. A nonequilibrium phase transition is observed when at critical time t_c the first isolated cluster occurs. In the one-dimensional system the volume of the new phase, i.e., the number of the isolated individuals, increases with time as $Z \sim t^3$. For a large number of possible communities, the critical density of filled space is equal to $\rho_c = (m/N)^{1/3}$, where N is the system size. A similar transition is observed for Erdős-Rényi random graphs and Barabási-Albert scale-free networks. Analytical results are in agreement with numerical simulations.

Recently, physicists working on modeling of social phenomena are frequently touching the idea of *dissemination* and *competition*—especially in the case of language [1], culture [2], and opinions [3]. The key subject can be posed as follows: how does the node internal variable change when it is influenced by others? The issue has occurred especially in the Axelrod model of culture dissemination [2] or many sociophysics systems such as Sznajd model [4], voter model [5], majority rule voting [6], social impact model [7], or bounded confidence models [8]. At this moment one should stress that the above-mentioned models are bound to explore social effects of diffusion or adoption of node states. Such processes are usually running in accordance with the following scheme: one takes the state of its neighbor, provided that a set of rules is fulfilled.

There is however also another qualitatively different phenomenon—*isolation* of surrounded social groups and resulted extinction of their members due to lack of communication with other groups of the same specie. In fact this issue should be regarded as equally important as the previously mentioned dissemination or migration effects. The isolation and consequently the lack of communication among the groups belonging to the same community (and vice versa, no communication causing the isolation) might lead to severe disturbances in the society. One of them can be racial isolation (segregation) that can cause serious social problems [9]. In fact the phenomenon of residential segregation has been studied in several physical papers [10] that in part follow the famous work of Schelling [11] or other Ising-like approaches. In other situations the lack of social contact results in an increased mortality of seriously ill patients as compared to those that are not isolated [12]. Finally, recent research [13] shows that Americans suffer from social isolation due to a dramatic decrease in the number of discussion partners even with those whom they share the closest relationship with. Given the fact that such social phenomena as elections [14] or war [15] are currently being examined using methods of statistical physics, a quantitative model of social isolation could be a useful tool to predict blocking of voting districts or trapping of hostile troops during wartime.

In this paper we propose an evolving model to investigate the question of the critical density that has to be reached in order for a certain phenomenon to happen. In fact when such

a system as the Roman empire did not collapse in a single Barbarian struck, it was rather transformed during a slow decline of culture and knowledge that happened in the course of migration period and resulting separation of various parts of west and east empires [16]. One needs to stress that in many cases an isolated specie does not belong anymore to either of the community present in the system. The described situation can be spotted in such problems as urbanization, spanning of the suburbs (i.e., suburbanization) [17], or currently vital problems of immigrant offspring identity [18]. Our model is aimed to give some general descriptions of the critical phenomena that can occur in such circumstances.

The key idea of our work can be presented in form of two questions: (i) what happens if instead of species spreading the interaction results in species isolation and *extinction*? (ii) What are the consequences of the fact that sometimes a small group is capable to surround and defeat a larger one? The first point comes as a result of the observation that a group of people that are suddenly surrounded by people from opposite groups is often defeated by enemies or opponents. It occurs because the surrounded group is isolated and is not able to communicate with other group members who could support them, e.g., to provide a military backup (it was a common case during many wars). To justify the second question, one can think of the Chinese game Go where, in some condition, one player can block the opponent using the amount of stones, which is less than those that are just being surrounded.

In this paper we impose these dynamical rules onto various regular and random networks. We start with a simple chain where sites are being filled with individuals belonging to two different species. Then, we extend the model to a case of m different species and finally we consider the Erdős-Rényi (ER) graphs and Barabási-Albert (BA) scale-free networks.

Let us consider a chain of N initially unoccupied nodes. In each time step one empty node is chosen randomly. Then, an internal variable ($\uparrow$) or ($\downarrow$) for this node is randomly selected. Both possibilities correspond to different species or communities and are drawn with the same probability. If a cluster of n identical filled nodes (e.g., $\uparrow\uparrow\uparrow\uparrow$) is surrounded by individuals belonging to other community (e.g., $\downarrow\uparrow\uparrow\uparrow\uparrow\downarrow$), the nodes in the surrounded cluster are treated as
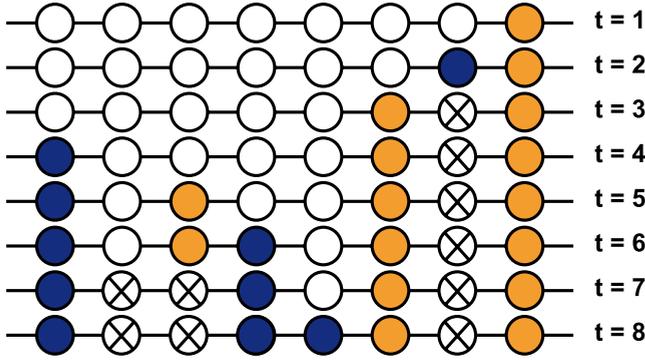
FIG. 1. (Color online) An example of evolution in the chain consisting of eight nodes. Open circles are empty sites; black and gray circles correspond to different communities. Isolated nodes are marked with a cross.
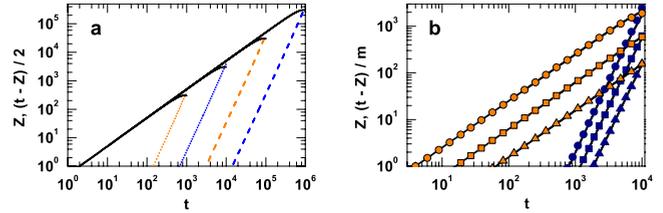

FIG. 2. (Color online) (a) Number of isolated nodes (Z, dotted and dashed lines) and not isolated nodes of each specie [$(t-Z)/2$, solid lines] versus time for different chain sizes N (gray dotted line, 10^3; black dotted line, 10^4; gray dashed line, 10^5; and black dashed line, 10^6). (b) Number of isolated nodes (Z, filled symbols) and not isolated nodes of each specie [$(t-Z)/m$, open symbols] versus time for different number of species m (circles, $m=4$; squares, $m=16$; and triangles, $m=64$). All simulations are for $N=10^4$ and the lines come form the solution of Eq. (5).

extinct and can no longer interact with the rest of the chain, i.e., they will not be able to surround other clusters. The procedure is held until the chain is full, which happens in the Nth time step. An example of the complete evolution of the system is presented in Fig. 1. Our main points of interest are (i) the critical time t_c when the first isolated cluster appears and (ii) the number of isolated nodes for $t > t_c$.

Figure 2(a) shows the number of isolated nodes Z and the number of nonisolated nodes of both species $(t-Z)/2$ as functions of time for four different chain sizes: 10^3, 10^4, 10^5, and 10^6. In each case the number of isolated sites follows a power law $Z \sim t^\alpha$ with α exponent close to 3.0 ($\alpha = 3.09$ for $N = 10^3$, $\alpha = 3.06$ for $N = 10^4$, $\alpha = 3.05$ for $N = 10^5$, and $\alpha = 3.04$ for $N = 10^6$). Each simulation was repeated 10 000 times and the results were averaged—this procedure applies to all plots presented in this paper.

The plots indicate that in this system we observe a nonequilibrium phase transition—after reaching a certain time of the evolution (after filling a specific number of nodes), a new phase emerges due to the occurrence of the first isolated cluster. The volume of this phase can be treated as the system order parameter. It grows up when one runs above the critical time t_c. Moreover, it can be seen in Fig. 3(a) that data for different chain sizes collapse onto one curve after rescaling both the Z and the t axes by the system size N. Figure 3(b) shows that the critical time t_c of the first isolated node appearance grows with system size as $t_c \sim N^\beta$, where $\beta = 0.664 \pm 0.001$.

In order to obtain the average number of isolated nodes, we have to sum all different possibilities of a cluster to become isolated. A single isolated site emerges either as a result of a combination $\uparrow\downarrow\uparrow$ or $\downarrow\uparrow\downarrow$ in which the middle node is turned into the isolated one. To express the total number of such nodes in the system (Z_1), we need to multiply the probability of the sum of those combinations by the number of such possibilities, that is, $N-2$. Similarly, the number of isolated sites coming from isolated clusters of size n is

$$Z_n = n(N-n-1)$$
$$\times \left[\text{Prob}^2(\uparrow) \prod_{i=1}^{i=n} \text{Prob}(\downarrow) + \text{Prob}^2(\downarrow) \prod_{i=1}^{i=n} \text{Prob}(\uparrow) \right], \tag{1}$$

where $n = 1, 2, \ldots$. As the examined system is symmetric [i.e., $\text{Prob}(\uparrow) = \text{Prob}(\downarrow)$], taking into account that at time t there are already Z isolated nodes, the average probability of finding a certain specie at time t is $(t-Z)/(2N)$. Since $Z = \sum_{i=1}^{i=n} Z_i$, we obtain after short algebra

$$Z = 2 \sum_{n=3}^{n=\infty} (n-2)(N-n+1) \left(\frac{t-Z}{2N} \right)^n \tag{2}$$

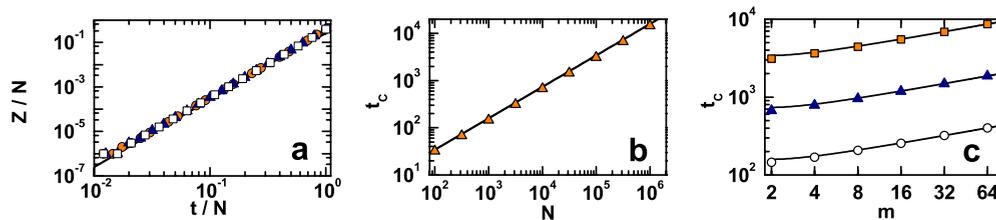or $Z = (t-Z)^3/(2N-t+Z)^2$. Solving this equation leads to

FIG. 3. (Color online) (a) Data collapse for rescaled number of isolated nodes (Z/N) versus the rescaled time (t/N) observed for three different data sets: $N=10^4$ (circles), $N=10^5$ (triangles), and $N=10^6$ (squares). The curve (hardly visible) is obtained from Eq. (3). (b) The critical value of time t_c for $m=2$ versus the chain size N. The line is Eq. (4) while triangles are numerical simulations. (c) The critical value of time t_c versus the number of species m for different chain sizes $N=10^3$ (circles), $N=10^4$ (triangles), and $N=10^5$ (squares). Lines come from Eq. (6).

$$Z_r = \tfrac{1}{6}[5t_r - 4 + (8 + 16t_r - t_r^2)u_r^{-1} - u_r] \qquad (3)$$

with $u_r = [\sqrt{3(16 - 24t_r + 39t_r^2 - 2t_r^3)} - 80 + 84t_r - 24t_r^2]^{1/3}$, where $t_r = t/N$ and $Z_r = Z/N$. The formula is universal for any value of chain size—all data should collapse on this curve, as can be seen in Fig. 3(a). If $Z \ll t \ll N$, which is acceptable for the most part of the evolution, then Eq. (2) leads to $Z \approx t^3/(4N^2)$, i.e., the number of isolated nodes should increase as t^3. This fact is in agreement with the numerical experiment. This approximated formula can be also used to calculate the critical time t_c at which the first isolated node appears in the chain. Putting $Z = 1$ we get a simple expression for the critical time

$$t_c = (2N)^{2/3}. \qquad (4)$$

This result is consistent with the value of the β parameter observed in the numerical data.

We can easily extend the previously described model of two competing species onto a case where the number of species is $m \geq 2$. Similarly to the two-species case, in each time step a type of specie is drawn from the uniform distribution $\langle 1, m \rangle$ and placed in a random unoccupied place in the chain. The isolated nodes are formed from a cluster of identical species surrounded by other *identical* species.

An example of the evolution of the extended model is presented in Fig. 2(b). Like in the case of $m = 2$, the number of isolated nodes follows a power law $Z \sim t^\gamma$ with γ exponent close to 3 ($\gamma = 3.05$ for $m = 4$, $\gamma = 3.00$ for $m = 16$, and $\gamma = 3.01$ for $m = 64$).

The analytical approach in the case $m > 2$ is identical to the case $m = 2$ except for two things. First, there are m different species which can be isolated. Each of those m species can be isolated in $m - 1$ ways; therefore, instead of the factor 2 we should put $m(m - 1)$ in front of each equation in the set of equations (1). Second, larger number of species results in the change in probability of finding a specific specie—in the extended model, it is equal to $(t - Z)/(mN)$. Thus Eq. (1) has now the form

$$Z_n = nm(m - 1)(N - n - 1)\left(\frac{t - Z}{mN}\right)^{n+2}, \qquad (5)$$

where $n = 1, 2, \ldots$. Following an identical algebra as in the case of the two-species model, we arrive at a self-consistent equation for the number of isolated nodes $Z = (m - 1)(t - Z)^3/(mN - t + Z)^2$, which is exactly algebraically solvable. The solution fits to the numerical data quite well [see Fig. 2(b)] and as before one can approximate it with $Z \approx [(m - 1)t^3]/(m^2N^2)$. This proves that the increase in isolated nodes follows the same rule as in the two-specie case, i.e., t^3. The critical time t_c at which the first isolated node appears is

$$t_c = \left(\frac{m^2}{m - 1}\right)^{1/3} N^{2/3}, \qquad (6)$$

which, once again, is consistent with the numerical data [see Fig. 3(c)].

The form of Eq. (6) gives us the opportunity to spot the interplay between the only two parameters of the model: the
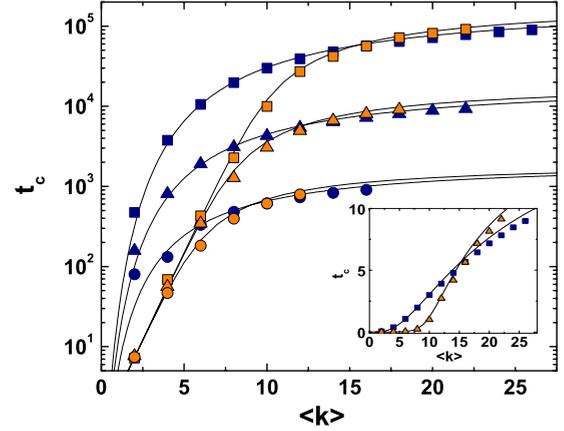

FIG. 4. (Color online) Logarithmic plot of the critical time t_c for Erdős-Rényi graphs (empty symbols) and Barabási-Albert networks (full symbols) for different networks sizes: $N = 10^3$ (circles), $N = 10^4$ (triangles), and $N = 10^5$ (squares). Symbols are numerical simulations and lines come from Eqs. (8) and (9). The inset shows t_c in linear scale for $N = 10^5$ in case of ER graph (triangles) and BA network (squares); t_c is rescaled by a factor of 10 000.

length of the chain N and the number of species m. If $m \gg 1$, Eq. (6) can be rewritten in a form of $t_c = (mN^2)^{1/3}$, which leads to the critical density of filled nodes $\rho_c = (m/N)^{1/3}$. The obvious conclusion from this relation is that when the chain becomes larger the critical density gets smaller and in the thermodynamical limit vanishes completely. Then, if we would like to maintain a constant value of ρ_c we should require $m/N = \text{const}$. In other words, it is possible to prevent the convergence of the critical density to zero by making the number of species proportional to the chain's length.

The critical time t_c for $m = 2$ can be also found in the cases of two- and three-dimensional cubic lattices and, what is more important, for any random network characterized with a specific degree probability distribution $p(k)$ (k is the number of links of a given node). The general formula for the number of single isolated nodes is

$$Z_1 = 2N\sum_{k=0}^{k=\infty} p(k)x^{k+1}, \qquad (7)$$

where $x = t/(2N)$. In order to obtain the critical time, we require that $Z_1 = 1$ and solve this equation for t. In case of regular lattices we have $t_c = (2N)^{z/(z+1)}$, where z is the number of neighbors. We have calculated the critical time for the two most popular types of complex networks: Erdős-Rényi random graphs [19] and Barabási-Albert scale-free networks [20]. In case of ER graphs characterized by the degree distribution $p(k) = e^{-\langle k \rangle}\langle k \rangle^k/k!$, the critical time t_{ER} can be expressed as

$$t_{ER} = \frac{2N}{\langle k \rangle}W\left(\frac{e^{\langle k \rangle}\langle k \rangle}{2N}\right), \qquad (8)$$

where $W(x)$ is the Lambert W function. For BA network [degree distribution $p(k) = \tfrac{1}{2}\langle k \rangle^2 k^{-3}$], we get

$$t_{BA} \approx \left(\frac{\langle k \rangle}{4} \right)^{2/(\langle k \rangle + 2)} (2N)^{\langle k \rangle / (\langle k \rangle + 2)}. \qquad (9)$$

The obvious condition for avoiding an isolated node in the system is $t_c > N$. It leads to the following inequalities for different networks: $N > 2^z$ for regular lattices, $N > 2^{(\langle k \rangle - 4)/2} \langle k \rangle$ for BA networks, and $N > e^{\langle k \rangle / 2}$ for ER graphs. The above described results are shown in Fig. 4.

In this work we proposed a simple approach to model community isolations in growing societies. The numerical simulations fully supported by the analytical approach show that at a critical time t_c a nonequilibrium phase transition takes place and a new phase consisting of surrounded clusters emerges. In the case of one-dimensional system, the number of isolated nodes rises with time as a power law with exponent $\gamma = 3$. The scaling is universal, i.e., it depends neither on the chain's length N nor on the number m of possible species. An analytical form for the critical time t_c is found and for large m this time scales as $t_c = (mN^2)^{1/3}$. The phenomenon has been also observed for higher-dimensional systems as well as for Erdős-Rényi random graphs and Barabási-Albert scale-free networks.

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