Greenberg-Hastings dynamics on a small-world network: the effect of disorder on the collective extinct-active transition

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Abstract

We present a numerical study of a reaction-diffusion model on a small-world network. We characterize the model’s average activity $F_T$ after $T$ time steps and the transition from a collective (global) extinct state to an active state in parameter space. We provide an explicit relation between the parameters of our model at the frontier between these states. A collective active state can be associated to a global epidemic spread, or to a persistent neuronal activity. We found that $F_T$ does not depend on disorder in the network if the transmission rate $r$ or the average coordination number $K$ are large enough. The collective extinct-active transition can be induced by changing two parameters associated to the network: $K$ and the disorder parameter $p$ (which controls the variance of $K$). We can also induce the transition by changing $r$, which controls the threshold size in the dynamics. In order to operate at the transition the parameters of the model must satisfy the relation $rK = a_p$, where $a_p$ as a function of $p/(1 - p)$ is a stretched exponential function. Our results are relevant for systems that operate at the transition in order to increase its dynamic range and/or to operate under optimal information-processing conditions. We discuss how glassy behaviour appears within our model.

Keywords: Complex systems, Cellular automata, Phase transitions

Many problems in Science can be cast in terms of dynamics on networks: social phenomena [1,2,3], epidemic spread [4], food webs [5] and ecosystem’s diversity [6], brain activity [7,8,9,10,11,12], granular materials [13,14,15] and, in general, complex systems [16]. Among the most studied models, the small-world network model of Watts and Strogatz (WS) [17,18] can be tuned to interpolate between a regular and a random network, a very attractive property that allows us to explore the consequences of network disorder on dynamics. In this work we consider a stochastic reaction-diffusion cellular automata model on a small-world network and study its average activity after $T$ time steps and its collective extinct-active transition. For the first time, we provide a explicit relation between the parameters of the model for the system to operate at the transition, and disorder enters in this relation as a stretched exponential function.

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In the WS model we start from an ordered ring in which each node is connected to its $K$ nearest neighbours, and then we randomly rewire each connection with probability $p$. Since we only rewire and we don’t create new connections, the average coordination number is still $K$, but the distribution of $K$ gets broader as we increase $p$ [18]. Two quantities typically used to characterize a network are the mean minimal distance between two nodes $L$ and the clustering coefficient $C$. For each node, we can measure how many of its neighbours are connected between them. $C$ is defined as the actual number of connections between a node’s neighbours over the maximum number of possible connections between neighbours, averaged over all nodes. Hence, in a social network $C$ could measure up to what extent someone’s friends are friends between them. In the WS network there is a range of values of $p$ for which $C$ is still high and $L$ is small, a signature of a small-world scenario. The case $p = 0$ corresponds to an ordered network, with high $C$ and $L$. The case $p = 1$ corresponds to a random network, with small $C$ and $L$ [13, 17].

A very generic reaction-diffusion model is the Greenberg-Hastings model (GH). This model has been used to model the Belousov chemical reaction, biological systems, epidemic spread, collective behaviour of heart cells and neuronal activity [19, 20, 21, 22, 23, 24, 25, 7]. Our stochastic version of this three state model is as follows:

- If a cell is in the excited state at time $t$ then it is in the passive state at time $t + 1$.
- If a cell is in the passive state at time $t$ then it is in the susceptible state at time $t + 1$.
- If a given cell is in the susceptible state at time $t$, and at least one of its neighbours is in the excited state at time $t$, then the given cell is in the excited state at time $t + 1$ with probability $r$, otherwise the given cell remains in the susceptible state.

The GH is a model for excitable media [20, see fig. 1 in 32] whose threshold is controlled by the parameter $r$. We call the parameter $r$ the transmission (or infection) probability. If excited means no-healthy, then I become infected if at least one of my neighbours is infected, but with probability $r$. In this context $r$ would be a measure of the average state of the immune system of the population, with a smaller $r$ implying more resistance to become ill. If we are in a social context, $r$ could be associated to the confidence of the social agents on an specific action, with greater $r$ implying more confidence. For neuronal activity or chemical reactions, $r$ can be associated to a potential barrier, with a smaller $r$ implying a greater potential barrier (a greater threshold). In a raw model for dense granular flows, the states of the GH model could be associated to fluid or solid type of contacts between grains [27], with the excited state associated to fluid contacts, the passive state associated to contacts with static friction and with a large time of contact [27] or with a small mobilization of friction [12], and the susceptible state associated to contacts with static friction and with a short time of contact or with a large mobilization of friction. Versions of the GH model have been implemented on regular networks [28, 22, 24], scale free networks [25], on a small-world network to study spiral waves [22] and on the human connectome [7].

It is of particular interest under what conditions the system, for a given initial condition, evolves towards a global active state, in which a finite fraction of the nodes remains active [22]. A collective active state can be associated to a global epidemic spread, or to a persistent neuronal activity. For random initial conditions, we have found transitions
Figure 1: Average activity $F_T$ as a function of the average coordination number $K$, for several values of $p$ and $r$. In the inset is shown the plateau of $F_T$, obtained for large $K$, as a function of $1/r$. For $r = 0.05$ and $p = 0.1$, for example, we have a collective active state for $K > 32$. If $r \to 1$ or if $K$ is large enough $F_T$ becomes independent of the disorder parameter $p$. The number of nodes is $N = 1000$ and we show the average result for 100 realizations for each set of parameters. For this figure, we looked for activity in the system after $T = 1000$ time steps.
to a collective active state as we vary any of the three parameters in the GHWS model: the transition can be induced by increasing the average coordination number $K$, by increasing the disorder in the network $p$ or by increasing the transmission probability $r$. Based on our numerical results, we provide for the first time an explicit relation between the parameters of the model for the system to operate at the transition, and disorder enters this relation as a stretched exponential function. Stretched exponentials are usually found in glasses and disordered systems \[33, 34, 35\]. As far as we know, for this model (GHWS) \[29\] we are presenting a novel way to consider the influence of disorder on the extinct-active frontier. In reference \[7\] the network was the human connectome and only a threshold was varied in order to tune the transition.

Our system consists of $N = 1000$ nodes. Initially, each node is randomly assigned, with equal probability, to one of the three states of the model. We call $F$ the average number of nodes in the excited state. The behavior of the GHWS model is summarized in figure 1 on which we show the average activity after $T = 1000$ time steps $F_T(K, p, r)$. We have a collective active state if after $T$ time steps (see below) $F_T > 0$. We have a collective extinct state if after $T$ time steps $F_T = 0$. For $K > K_c$ we have a collective active state, and from this figure we see that $K_c = K_c(r, p)$. It can be observed that for $r \to 1$ $F_T$ becomes independent of the disorder parameter $p$. Also, for any given transmission probability $r$, $F_T$ becomes independent of $p$ if $K$ is large enough: it tends to a plateau whose dependence on $1/r$ is shown in the inset.

For $r = 0.05$, we show in figure 2a zones of global active states in parameter space. We have found, as previously reported \[30\], that for $K < K_c$ the relaxation time of decay to zero activity increases largely as we approach a transition to a collective active state. Because of this, we looked for activity after $T$ time steps, and by a time step we mean an update of the whole network. Thus, we are characterizing the evolution in time of the frontier, and the limit $T \to \infty$ corresponds to the usual meaning of the frontier. For a given $r$, we can induce a transition to a collective active state by increasing the disorder parameter $p$ or by increasing the average coordination number $K$.

In order to characterize the frontier between active and extinct global states in parameter space we show in figures 2b and 2c the critical transmission probability $r_c$ as a function of $1/K$, for disorder spanning four orders of magnitude in $p$. Our results can be summarized in the following simple relation:

$$r_c = \frac{a_p}{K}. \tag{1}$$

This scaling of $r_c$ with $K$ was obtained by Berry and Fates \[22\] in a mean field approximation of a similar GH model, where the crucial ingredient was to obtain an approximation to the conditional probability that in the neighborhood of a given node there is at least one node in the excited state, given that the considered node is in the susceptible state. The scaling $r_c \sim K^{-1}$ was verified by numerical simulations on a regular network by considering different types of neighborhoods, obtaining $a_p \approx 2$ (the exact mean field result was $a_p = 1$) \[22\]; this result was robust against the inclusion of defects in the regular network. In figure 2l we show $a_p$ as a function of $p$, and we conclude from this figure that disorder in the network reduces $r_c$. Since we have a collective active state for $r > r_c$, within the GHWS model disorder favors a collective active state.

In figure 3 we see a detailed version of figure 2l. Our numerical results for $a_p$ are
Figure 2: a) Zones of collective active states for $r = 0.05$ after $T$ time steps. b) Critical transmission probability $r_c$ as a function of $1/K$, estimated after $T = 100$ time steps for different $p$. c) Same as in b) but with $T = 1000$. As in b), the dashed lines corresponds to the relations $r_c = 1/K$ and $r_c = 2/K$. Our system is a network with $N = 1000$ nodes and we averaged over $m = 100$ realizations. Dotted lines, here and in b), are best fits to the relation $r_c = a_p/K$. We don’t considered the case $r = 1$ (the deterministic GH model) for which we have a collective active state for $K = 2$, for any $p$. d) The slope $a_p$ as a function of the disorder parameter $p$, obtained from c) and b).
Figure 3: This figure is a detailed version of figure 2d. In order to obtain each point in this graph we considered for each $p$ five values of $K$: $K = 4, 8, 16, 32, 64$, with $m$ realizations for each $K$. We then adjusted the best line to equation (1). For $T = 50$ and $T = 100$, we used $m = 1000$; for $T = 1000$ we used $m = 100$; for $T = 10000$ we used $m = 30$. Dashed lines are best fits to stretched exponentials of the form given by equation (2). In the inset we show the four parameters of eq. 2 as a function of $T$. The dot-dashed line is equation (4) for $T = 1000$. We show, in stars, the results for $N = 10000$ and $T = 100$, with no major differences with the case $N = 1000$; certainly $L$ depends on $N$ [18] but $L$ appears to affect only the time required to propagate the activity to the whole system [17]. The dotted line is the mean field result $a_p = 1$ [22]. Recently (v6), I have been aware that if we average in a different way we do have a $N$ dependence: if we do only one realization for each value of $K$ (see the beginning of this caption), obtaining $a_p$ and then average several realizations we do have a $N$ dependende in the results. This fact will be considered elsewhere. For $N = 1000$, the results presented here do not change qualitatively.
consistent with a stretched exponential of the form:

$$a_p = \Delta \exp\left[-\left(\frac{x}{\tau}\right)^\beta\right] + a_1$$

(2)

with \(x = p/(1-p)\). Stretched exponentials are usually found in relaxation of glasses and disordered systems [33, 34, 35, 36, 37]. In the inset of figure 3 we show the evolution of the four parameters of equation 2.

In terms of \(z \equiv \ln(1/x)\), there is a maximum in the quantity \(\chi(z) \equiv \partial a_p/\partial z\) at \(z_c = \ln(1/\tau)\), with the maximum given by \(\chi_m \equiv \chi(z_c)\):

$$\chi_m = \frac{\Delta \beta}{e}$$

(3)

The quantity \(\chi\) measures the sensitivity of the extinct-active frontier to changes in disorder (through the variable \(z\)), going to zero for very ordered or very disordered networks. In terms of \(\mu \equiv e^{-z}/\tau\), the order parameter \(w \equiv (a_p - a_1)/\Delta = \exp(-\mu^\beta)\) and \(\chi(z) = \Delta \partial w/\partial z\), we have: \(\chi(z)/\chi_m = e\mu \nu\) (see figure 4). If we operate at \(z_c\) we can communicate more easily through collective states when considering, for example, a network of networks in which each unit is a GHWS one: at the frontier and at \(z_c\) small changes in disorder can allow the system to switch between an extinct and an active collective state more easily.

If we expand around \(z_c\), we obtain the approximate relation:

$$a_p - a_{pc} \approx \chi_m(z - z_c)$$

(4)

with \(a_{pc} = \Delta/e + a_1\). In figure 3 we show eq. 4 for \(T = 1000\).

By monitoring the activity \(F\) as a function of \(T\) we have found that \(a_p\) is well described by a stretched exponential function in the variable \(x = p/(1-p)\), for all \(T\). Since at the extinct-active frontier \(rK = a_p\) (eq. 1), we can interpret \(a_p\) as the average minimal number of effective neighbours to become active. In eq. 2 we have defined \(\Delta\) as the
difference between $a_0\ (a_p\text{ when } p \to 0)$ and $a_1\ (a_p\text{ when } p \to 1)$, see the inset of figure 3. What happens, for example, if we consider an ensemble of systems such that $rK \approx 1.63$, in which each member of the ensemble can have any value of $p$. We see in figure 3 that $a_0 \approx 1.63$ for $T = 100$. Thus, up to $T = 100$ we’ll have ordered and disordered members of the ensemble that are still active, but in the long run only the more disordered members of the ensemble ($x > 0.2$, approx., see fig. 3) will stay active. If we consider an ensemble of systems with $rK < a_1$, then in the long run all the members of the ensemble will go extinct. On the other hand, if we consider an ensemble of systems with $rK > a_0$ then all the members of the ensemble will stay active in the long run.

In figure 4a we can see that the frontier no longer changes its shape for $T > 10^4$, only $a_1$ keeps increasing with time, as can be seen in figure 4. With the relation $a_1 = 1.18 + 0.015 \ln(T)$ being satisfied for $T > 2000$ (see fig. 4a), we have that for an ensemble with $rK \approx 2.4$, at $T_0 = 10^5$ the more ordered members of the ensemble starts to go extinct (see fig. 4b). For this ensemble, if we denote $T_1$ as the time when the more disordered members of the ensemble will go extinct we have that $T_1/T_0 = e^{\Delta/0.015} \approx e^{67} \approx 10^{29}$. This is reminiscent of glassy behaviour.

Several generalizations can be introduced in the model implemented here. One of them would be to consider a weighted network, with weights that can be correlated or not to the local coordination number \cite{3}. In order to consider different passive time scales, a possible generalization of our GH model would be to introduce $M$ time steps in the passive (refractory) state before becoming susceptible. Regarding this possibility, in reference \cite{22} was found that, for a regular network, the critical transmission probability depends weakly on $M$, and that at the active-extinct transition the decay in time of the average activity $F$ follows a power law, with an exponent that does not depends on $M$: its universality class remains directed percolation.

We have characterized the activity of a GHWS model, and we found that the average activity does not depends on disorder in the network if the transmission rate $r$ or the average coordination number $K$ are large enough. We have found that a collective extinct-active transition in a GHWS model can be induced by increasing $r$, a parameter that controls the threshold size in the system’s dynamics. Also, the transition can be induced by increasing the disorder parameter $p$ and by increasing $K$. Our results are relevant to systems that need to operate at the extinct-active transition, in order to increase its dynamic range and/or to operate under optimal information-processing conditions \cite{31}. Remarkably, in reference \cite{7} it was found that in order to reproduce the patterns of neuronal activity observed in experiments, the threshold of a stochastic GH model implemented on the human connectome has to be tuned for the system to operate at the transition. Within the GHWS model studied here, in order to operate at the transition the parameters of the model must satisfy the relation $rK = a_p$, where $a_p$ as a function of $p/(1 - p)$ is a stretched exponential function.

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