

Generalized contact process on random environments

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Spreading from a seed is studied by Monte Carlo simulation on a square lattice with two types of sites affecting the rates of birth and death. These systems exhibit a critical transition between survival and extinction. For time-dependent background, this transition is equivalent to those found in homogeneous systems (i.e., to directed percolation). For frozen backgrounds, the appearance of the Griffiths phase prevents the accurate analysis of this transition. For long times in the subcritical region, the spreading remains localized in compact (rather than ramified) patches, and the average number of occupied sites increases logarithmically in the surviving trials.

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I. INTRODUCTION

The contact process (CP) was introduced by Harris [1] to describe competition between the death and birth events for a spatially distributed species. In this model, the organisms localized at the sites of a lattice can die with a death rate or can create additional offspring in one of their (empty) neighboring sites. When increasing the ratio of birth to death rates, this system exhibits a critical phase transition from the empty to the active state as the system size approaches infinity. This transition belongs to the so-called directed percolation (DP) universality class [2,3]. Similar transitions have been observed for some other, related models (for recent reviews see Refs. [4,5]).

The above-mentioned CPs applied homogeneous backgrounds. The effects of random environment on the CP were carefully analyzed in one-dimensional systems [6,7]. Numerical investigations on the two-dimensional random environments have been restricted to diluted lattices [8–12]. Noest [8] has shown that, although the transition remains continuous, the extinction process is modified drastically on the randomly diluted lattice above the percolation threshold. Recently Dickman and Moreira [11] have reported that scaling (a fundamental feature of critical transitions) is violated in this case. According to a field-theoretic analysis, a similar result is predicted by Janssen [13].

Below the percolation threshold on a diluted lattice, the available sites form isolated (finite) clusters. In any particular cluster the species is expected to die out within finite time and the cluster remains empty afterwards. A simple mathematical description suggested by Noest [9] indicates that the average concentration of species vanishes algebraically with time and this phenomenon is analogous to the relaxation observed for the “Griffiths phase” in disordered spin models [14].

Field-theoretic arguments [5] support that the temporally quenched disorder itself, as well as the spatially quenched disorder, disturbs crucially the DP transition. However, the DP transition is expected on large scales for those random environments where the spatiotemporal disorder is uncorrelated. For two-dimensional systems this expectation is supported only by a small number of numerical evidences. For

example, in an evolutionary game, the extinction of one of the three competing strategies represents a DP transition on a background whose time dependence is maintained by the competition of the remaining two strategies [15].

In the present paper, we study a generalized CP on a square lattice with two types of sites that provide different conditions for the survival and reproduction for a hypothetical species. Our analysis is not restricted to the frozen backgrounds. We give numerical evidence that the extinction process becomes analogous to the DP transition if the random environment involves uncorrelated time dependence. Using numerical simulations, we investigate the main characteristics of spreading when initially there is only a single individual in the system. This method was suggested by Grassberger and de la Torre [16] to study the DP transition (for homogeneous background) in the close vicinity of the critical point. Moreira and Dickman [10] have demonstrated that this technique is also efficient for the investigation of inhomogeneous systems. Now we have adopted this method to study the above-mentioned generalized CP in random environments. The results confirm the theoretical expectations [4,5,13,17] as well as the previous observations based on Monte Carlo (MC) simulations [8–12]. We have also studied some geometrical features of the patches formed by occupied sites in the subcritical region.

II. THE MODEL

Each site of a square lattice, $\mathbf{r}=(x,y)$ (x and y are integers), is assumed to represent a microhabitat for one individual of a species. The quality of a site $g(\mathbf{r})$ determines the probabilities of the survival and reproduction of the inhabitant individual. We assume two microhabitat types: good and bad [where $g(\mathbf{r})=1$ or 0 , respectively]. The site qualities are distributed randomly in space. Initially, each site is chosen to be good (bad) with a probability $P(1-P)$. Distribution of individuals over this random background is described by a state variable $\sigma(\mathbf{r})$ that is 1 for occupied and 0 for empty state. Time evolution of the system is governed by three elementary processes affecting the values of $\sigma(\mathbf{r})$ and $g(\mathbf{r})$. For an occupied site, extinction (death) can occur with a death rate $d[g(\mathbf{r})]$. For an empty site, colonization (birth)

can take place with a birth rate $b[g(\mathbf{r})]$, provided that a randomly chosen nearest-neighbor site is occupied. It is supposed that the good sites provide better conditions for living, that is $b(1) > b(0)$ and $d(1) < d(0)$. Furthermore, redrawing the value of $g(\mathbf{r})$ we change the environment with a rate f . The new state is independent of the actual values of $g(\mathbf{r})$ and $\sigma(\mathbf{r})$. This occasional modification results in stationary distribution of the good or bad sites over time, with probabilities P and $1 - P$, respectively, and leaves their distribution uncorrelated.

In the special case when every site is good ($P = 1$), the present model is equivalent to the well investigated contact process on homogeneous background [4,5]. Previous studies have shown that in this case, the species dies out if $\lambda = b(1)/d(1) < \lambda_c = 1.6488(1)$. The concentration of population vanishes algebraically in the active stationary state, that is $c \propto (\lambda - \lambda_c)^\beta$ where $\beta = 0.575(3)$ if $\lambda \rightarrow \lambda_c$ [4,5,18,19]. This critical transition is accompanied with diverging fluctuations and correlation length.

The conditions of the CP on diluted lattice can be reproduced by allowing the species to stay only in good sites [$b(0) = 0$ and $d(0) = \infty$] for $P < 1$ and $f = 0$.

III. SIMULATION OF SPREADING

The MC simulations are performed on a lattice with $L \times L$ sites under periodic boundary conditions. Following the method suggested by Grassberger and de la Torre [16] the spreading is investigated by averaging over many trials M when the initial state is close to the absorbing state. More precisely, each run is started with a single individual [at position $\mathbf{r} = (0,0)$] on a new, random, uncorrelated background. We have determined the survival probability

$$S(t) = \langle \theta(n(t)) \rangle, \quad (1)$$

where the number of individuals at a given time t is defined as

$$n(t) = \sum_{\mathbf{r}} \sigma(\mathbf{r}), \quad (2)$$

$\langle \dots \rangle$ means the average over M trials, and $\theta(z) = 1(0)$ for $z > 0 (z \leq 0)$. We have also evaluated the average number of surviving individuals,

$$N(t) = \langle n(t) \rangle, \quad (3)$$

and the mean-square distance of individuals from the origin,

$$R^2(t) = \frac{1}{N(t)} \left\langle \sum_{\mathbf{r}} r^2 \sigma(\mathbf{r}) \right\rangle. \quad (4)$$

M is varied from 10^4 to 10^8 in the systematic investigations. The system size L is adjusted to exceed significantly the average radius of occupied sites, namely, $L \geq 15R(t_{max})$, where t_{max} indicates the time limit. As usual, time is measured in Monte Carlo steps. During one time unit, each site has a chance to modify the value of $\sigma(\mathbf{r})$ (approximately once on average).

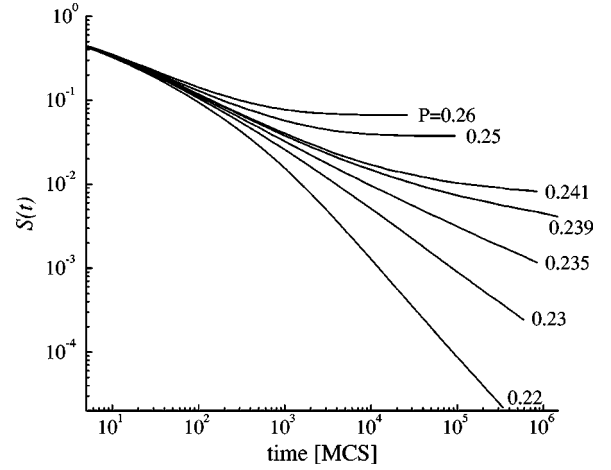


FIG. 1. Survival probabilities as functions of time at different P values (indicated by labels) for $b(1) = 1$, $b(0) = 0.5$, $d(1) = 0.25$, and $d(0) = 0.5$.

The efficiency of these simulations can be greatly improved by labeling the individuals, recording their coordinates, and picking up one individual randomly for updating the state of occupancy [4]. In the present case, the chosen individual residing at site \mathbf{r} dies with a probability $d(g(\mathbf{r}))/[b(1) + d(0)]$ or creates an offspring on one of its nearest-neighboring sites \mathbf{r}' with a probability $b(g(\mathbf{r}'))/[b(1) + d(0)]$. These attempted events take time $\Delta t = 1/n$ on average, therefore, the time is increased by Δt . The variation of the background can be handled in the same way within a smaller ($l \times l$) region whose sites affect the CP at the given time. Namely, the values of $g(\mathbf{r})$ are redrawn at randomly chosen $\Delta t f l^2$ sites.

The average values defined above [see Eqs. (1)–(4)] are determined for discrete time values chosen equidistantly on a logarithmic scale.

IV. RESULTS FOR FROZEN BACKGROUND

First we concentrate on a system where the random background is frozen, i.e., $f = 0$. Varying the proportion of good sites (P), we have made a systematic MC analysis for fixed death and birth rates. For the present parameters (see Fig. 1) the good sites form isolated clusters [having $P < P_{perc} = 0.5926$ (percolation threshold)] and infinite spreading is possible across the bad sites. The results summarized in the subsequent figures agree quantitatively with those found by Moreira and Dickman [10] on a diluted lattice for $P > P_{perc}$.

Figure 1 shows some typical time-dependence functions of survival in a log-log plot. The statistical errors are comparable to the linewidth due to the large number of trials (e.g., $M = 10^8$ for $P = 0.22$). In the active region ($P > P_c$), $S(t)$ tends to a constant value as expected [16]. In the subcritical region, $S(t)$ can be well approximated by a power law. Unfortunately, the convergency toward the limit value becomes extremely slow in the vicinity of the critical point, and this prevents the accurate determination of P_c . The division between the active and inactive regions becomes more

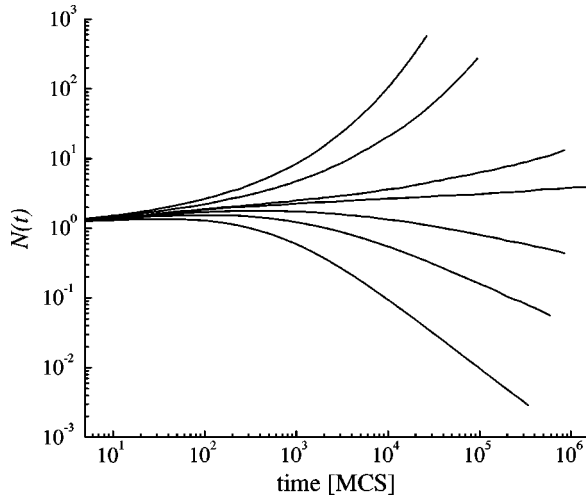


FIG. 2. Average number of individuals vs time for the same simulations as in Fig. 1.

visible when considering the function $N(t)$ (see Fig. 2).

In the active region, the surviving individuals occupy a compact patch whose radius increases linearly with time. Consequently, $N(t)$ becomes proportional to t^2 for sufficiently long times as indicated in Fig. 2. By contrast, when $P < P_c$, then $N(t)$ tends to a power law decay with an exponent depending on P .

Figure 3 shows the time evolution of the mean-square distance of surviving individuals as defined by Eq. (4). In agreement with the expectations $R^2(t) \propto t^2$ for sufficiently long times if $P > P_c$. In the subcritical region, the increase of $R^2(t)$ becomes significantly slower than that found for the homogeneous system. In the homogeneous system, the surviving individuals perform random walks independently of each other, therefore, $R^2(t) \propto t$ in the subcritical region. In the present case, however, our data indicate a power law increase: $R^2(t) \propto t^\lambda$, where the exponent $\lambda(P) < 1$. This indicates the localization of spreading as it will be explained in Sec. VI.

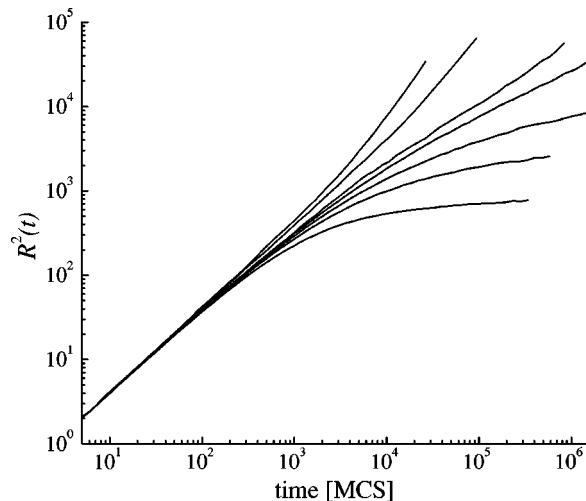


FIG. 3. Log-log plot of the mean-square distance of individuals from the origin as a function of time. Parameter values are the same as in Fig. 1.

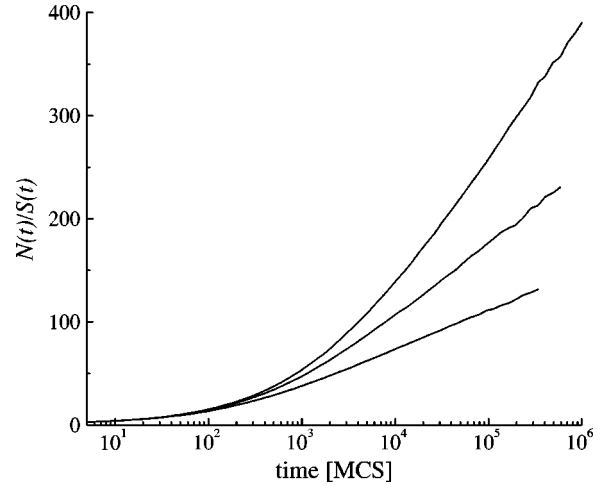


FIG. 4. Time dependence of the average number of individuals in the surviving trials at $P=0.22, 0.23$, and 0.235 .

Evaluation of $N(t)$ involves those (stopped) trials that have reached the empty state before the given time t . Consequently, the ratio $N(t)/S(t)$ expresses the average number of individuals in the surviving trials. In the subcritical region, the time dependence of this quantity tends to logarithmic increase as shown in a lin-log plot (see Fig. 4).

In the classical theory of percolation (reviewed in Refs. [20,21]), a geometrical feature of the clusters of size s is characterized by an average cluster radius $R_{\text{perc}}(s)$. Below the percolation threshold $R_{\text{perc}}(s) \propto s^\rho$ for the large s limit. According to MC simulations [20,22,23], $\rho \approx 2/3$, while the “self-avoiding walk” prediction [24] gives $\rho \approx 3/4$. In general, $\rho > 1/2$ values are characteristic for ramified clusters [20]. On the contrary, above the percolation threshold the finite size clusters are compact, that yields $\rho = 1/2$.

Following this analogy, we examine the relation between $N(t)/S(t)$, the actual size of population in the surviving trials, and the average radius of the area they occupy at a given time in the subcritical region. Figure 5 shows this relation on a log-log plot. In the close vicinity of the critical point (at

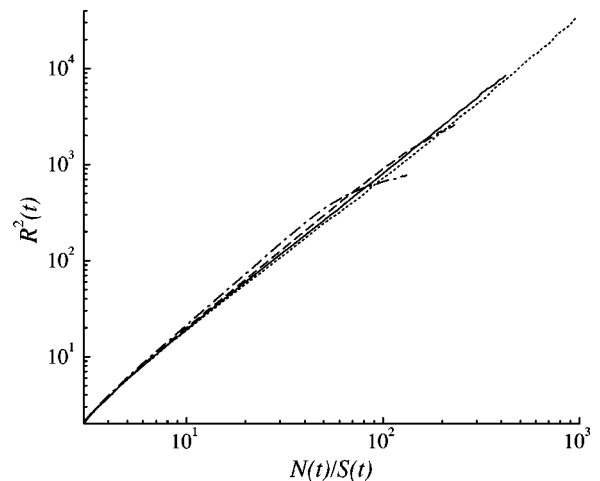


FIG. 5. $R^2(t)$ vs $N(t)/S(t)$ for $P=0.22$ (dashed dotted), 0.23 (dashed), 0.235 (solid), and 0.239 (dotted line).

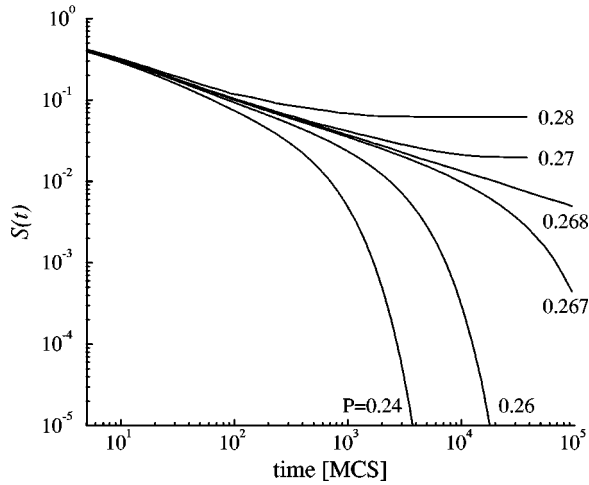


FIG. 6. Log-log plot of survival probabilities vs time at different P values (as indicated by labels) for $b(1)=1$, $b(0)=0.5$, $d(1)=0.25$, $d(0)=0.5$, and $f=0.01$.

$P=0.239$) we find power law behavior with an exponent $1.66(6)$. This behavior indicates that if the species spreads over a ramified cluster in the whole time interval we could study the system.

In the subcritical region, however, we can observe two different types of behavior. In the transient (short-time) region, the increase of $R^2(t)$ is faster than at the critical point. This indicates that the offspring move away from the origin along preferred paths formed by good sites. Conversely, the long-time behavior is dominated by those trials where the individuals stay on a compact patch.

In the following section we show that these features fundamentally change when we allow the background change over time.

V. RESULTS FOR TIME-DEPENDENT BACKGROUND

Applying time-dependent backgrounds, we determined the same quantities [$S(t)$, $N(t)$, and $R^2(t)$] as before. We use the same birth and death rates when varying the value of P for a fixed rate (f) of background change. Our results estimate the critical value for the ratio of good sites at $P_c = 0.2680(1)$. Figure 6 shows that the survival probability $S(t)$ vanishes exponentially when $P < P_c$. In the active region ($P > P_c$), however, $S(t)$ tends to a constant value. Notice that the convergence is significantly faster here than at the frozen background (see Fig. 1).

Data for $P = 0.268$ represent the behavior of the system at the critical point. The numerical analysis confirms that the survival probabilities can be well approximated by a power law, $S(t) \propto t^{-\delta}$ for sufficiently long times. Numerical fitting gives $\delta = 0.45(2)$ in agreement with the exponent found in DP transitions in homogeneous systems [4,5].

When considering $N(t)$, we can also distinguish between three different behaviors (see Fig. 7). Above the critical point ($P > P_c$), $N(t)$ tends towards quadratic time dependence. Below the critical point, $N(t)$ decreases exponentially. At the critical point, however, our MC data indicate power law behavior, i.e., $N(t) \propto t^\eta$ with $\eta = 0.23(1)$. This numerical value

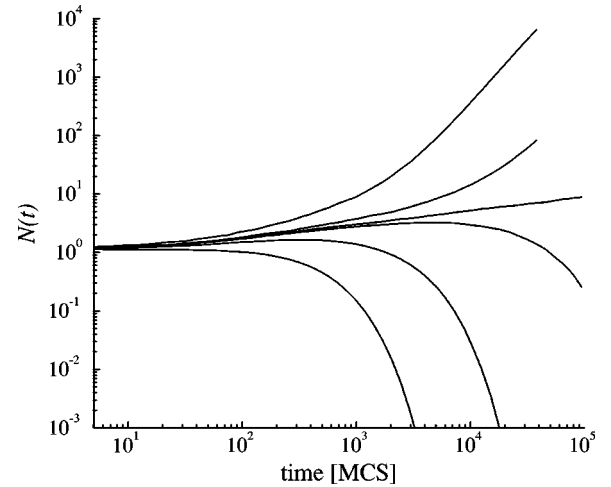


FIG. 7. Average number of individuals vs time for the same simulations as in Fig. 6.

of η agrees with the characteristic exponent of DP transitions [4,5].

In summary, all the above-mentioned numerical results support that contact process exhibits the same features in time-dependent random environments as in homogeneous background. Similarly to $S(t)$ and $N(t)$, $R^2(t)$ also supports this conclusion (data not shown).

These results have been gained at a fixed rate of changes ($f=0.01$). Preliminary results suggest, however, that the same conclusions hold for other values of f as well. General features of spreading remain unchanged due to the robustness of DP transition.

Here it is worth mentioning that we have also studied the concentration of individuals (as well as its fluctuation) in the stationary state for some parameter values. These analyses support that the variation of both quantities is consistent with the expectations, i.e., the species concentration and its fluctuation exhibit power law behavior with exponents characteristic for the two-dimensional DP systems [4,5,18,19].

VI. CONCLUSIONS AND SUMMARY

We have studied a generalized version of contact process on a square lattice. The background in the present model provides a continuous transition from a homogeneous system to a randomly fluctuating environment, including (frozen) diluted lattices. The environment is inhomogeneous, consisting of two types of sites (good and bad) that affect the rates of birth and death of the species. In this model, the spreading from a cluster of good sites to another one is permitted across the bad sites and/or bridges (of good sites) created occasionally by background fluctuations.

Our analyses have been restricted to the consideration of some typical features because the simulations are rather time consuming. The results confirm the theoretical expectations as well as the general picture drawn by previous authors [8–11] who considered CP on diluted lattices.

Obviously, an inhomogeneous environment contains areas that provide better (or worse) conditions for the survival relative to the average quality of the habitat. This variation be-

comes particularly important in the vicinity of the transition point that separates the active and inactive regions for long-time behavior. In the subcritical region, the surviving individuals are constrained to remain within isolated patches. Conversely, in the active region, favorable areas can form a percolating cluster, that has infinite extension, and sustains infinite survival.

To explain the main results, we briefly remind the reader of a simple calculation suggested by Noest [9]. In this description we characterize the favorable patches by size s and assume that their probability decreases exponentially, i.e., $n_s \propto e^{-As}$. Furthermore, it is also assumed that the average over many trials (or patches of size s) yields an exponentially decreasing number of individuals over time, that is, $m_s(t) \propto e^{-t/\tau_s}$ where the average survival time can be approximated as $\tau_s \propto e^{Bs}$ if initially all sites are occupied. Noest has shown that the long-time behavior can be well approximated in this case by a power law decrease, that is, $m(t) = \sum_s s n_s m_s(t) \propto t^{-A/B}$. This prediction is derived from a maximum likelihood estimation that implies the existence of a typical cluster size giving the dominant contribution to $m(t)$. According to this approach, the size of dominant clusters increases logarithmically with time t .

The adoption of this approach is not straightforward to the present situation where we consider the spreading from a single seed. In our case, the species can die out before achieving homogeneous distribution, while homogeneous initial state is assumed in the former calculation. We can assume, however, that the species spreads over the whole cluster or dies out within a transient time, and the probabilities of these outcomes are independent of cluster size. If this hypothesis holds, than the approach of Noest can be applied for the analysis of long-time behavior.

Some predictions of this rough method have been con-

firmed by our MC simulations. Namely, $S(t)$ and $N(t)$ exhibit a dominant power law decrease in the subcritical region, while $N(t)/S(t)$ (in proportion to the dominant cluster size) increases logarithmically. Furthermore, in the active region, the algebraically decaying contribution of $S(t)$ comes from extinction on (compact) finite size clusters whose probability distribution satisfies the above assumption [21,23].

Noest's approach is focused on compact clusters where $s \propto R^2$. Consequently, $N(t)/S(t) \propto R^2(t)$ is expected when the system behavior is dominated by a typical cluster size. This behavior can be observed for long times far below the critical point. Figure 5 indicates, however, that these predictions (and assumptions) fail in the close vicinity of the critical point. In other words, the ramified clusters give relevant contribution to $S(t)$ and $N(t)$ during a transient time that increases when approaching the critical point. In this case, we need a more sophisticated description allowing the emergence of ramified clusters and the shape dependence of τ_s .

Numerical analysis of the extinction process is difficult (in a quenched environment) because decrease of $S(t)$ and $N(t)$ slows down in the vicinity of the critical point. In practice this implies persistence over long-time periods before extinction. The slow extinction process, however, requires rather specific environmental conditions. Even a small degree of temporal fluctuation results in an extinction process that is analogous to DP transition on large scales. Our preliminary simulations have indicated that the transition point is strongly affected by the rate f of background change. Further analyses are required to quantify this phenomenon for different birth and death rates.

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