

Ergodic theorems for a sexual reproduction contact process including genotypes

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Abstract We introduce a multitype version of the contact process with sexual reproduction on the d -dimensional integer lattice \mathbb{Z}^d in which a genotype is attached to each occupied site. Individuals are produced by pairs of occupied sites and their genotype determined from the genotypes of the parent pair according to the Mendel's laws of inheritance. Relying on a number of new techniques, we prove that the genes may coexist in $d \geq 3$ whereas the system clusters in $d \leq 2$. The analogous result has already been proved for two simpler models, namely the voter model and the multitype contact process.

1. Introduction

Since its introduction, the contact process [8] has been intensively studied by mathematicians and widely employed by biologists. The contact process is a continuous-time Markov process whose state at time t is a function ζ_t that maps the d -dimensional lattice \mathbb{Z}^d into $\{0, 1\}$. In the demographic context, one shall think of sites $x \in \mathbb{Z}^d$ in state 0 as being empty, and sites in state 1 as being occupied by an individual. Independently of each other, individuals produce offspring at rate λ and die at rate 1. An offspring produced at site x is sent to a site y chosen at random according to a transition probability $p(x, y)$ on \mathbb{Z}^d which is translation invariant and symmetric. When the target site y is already occupied, the offspring produced at x and the individual at y coalesce, or equivalently the birth at site x is suppressed. The dynamics at site $x \in \mathbb{Z}^d$ are thus formally described by the transition rates

$$c_{0 \rightarrow 1}(x, \zeta) = \lambda \sum_y p(x, y) \zeta(y) \quad \text{and} \quad c_{1 \rightarrow 0}(x, \zeta) = 1,$$

where $c_{i \rightarrow j}(x, \zeta)$ denotes the rate at which the state of site x flips from i to j . One of the most important properties of the contact process is the existence of a critical value $\lambda_c \in (0, \infty)$ such that the process starting with a single individual always dies out when $\lambda \leq \lambda_c$ while there is a positive probability that it survives when $\lambda > \lambda_c$.

The sexual reproduction contact process is a closely related process in which offspring are produced by pairs of occupied sites rather than single occupied sites, i.e., individuals have exactly two parents instead of one. The dynamics at site $x \in \mathbb{Z}^d$ are described by the transition rates

$$c_{0 \rightarrow 1}(x, \eta) = \lambda \sum_{y_1 \neq y_2} p(x, y_1) p(x, y_2) \eta(y_1) \eta(y_2) \quad \text{and} \quad c_{1 \rightarrow 0}(x, \eta) = 1 \quad (1)$$

where, as previously, $p(x, y)$ is a transition probability on \mathbb{Z}^d which is translation invariant and symmetric. We have taken the sum over the set of $y_1, y_2 \in \mathbb{Z}^d$ such that $y_1 \neq y_2$ to have a

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biologically meaningful birth mechanism in which individuals have two (distinct) parents. The first transition rate indicates that if site x is empty then, at rate λ , two sites y_1 and y_2 are chosen independently and at random with probability $p(x, y_1)$ and $p(x, y_2)$, respectively. If both sites are distinct and occupied then site x becomes occupied.

While the contact process has been intensively studied during the past 35 years, much less attention has been paid to the sexual reproduction process. Noble [14] and Neuhauser [13] investigated a particular case of the process (1) in which individuals are located on the rescaled lattice $\epsilon\mathbb{Z}$, and offspring are produced by pairs of adjacent (distance ϵ apart) occupied sites. In [14], the offspring is sent to either site adjacent to the parent pair with equal probability, and adjacent sites exchange their contents at rate ϵ^{-2} which is referred to as fast stirring. In [13], an offspring produced by a pair of occupied sites $(y, y + \epsilon)$ is sent to a site chosen at random according to a certain transition probability, the offspring has access to an ever-growing number of sites as $\epsilon \downarrow 0$ which is referred to as long range dispersal. In both [14] and [13], it is proved that if the birth rate λ exceeds some critical value then the process survives (i.e., has a stationary distribution with a positive density of occupied sites) provided $\epsilon > 0$ is sufficiently small, the focus is on the exact estimate of this critical value when $\epsilon \downarrow 0$. Durrett and Gray [5] and later Chen [1, 2] also studied the problem of survival of a stochastic spatial model with sexual reproduction, called symmetric sexual reproduction process, in dimensions $d \geq 2$. In their model, site x becomes occupied at rate λ whenever a pair of sites adjacent to x and Euclidean distance $\sqrt{2}$ apart are occupied. In contrast, the main purpose of this article is not on survival so we will assume from now on that the birth rate λ is fixed so that the model described by the transition rates in (1) survives in the sense that there exists a stationary distribution with a positive density of occupied sites.

The stochastic model $\{\xi_t : t \geq 0\}$ we introduce in this article is a multitype version of the sexual reproduction process (1) describing the evolution of a population of diploid individuals. The state space maps the d -dimensional integer lattice into the set $\{0, aa, ab, bb\}$. One shall think of sites in state 0 as being empty, and sites in state aa , ab , and bb as being occupied by a diploid individual with genotype aa , ab , and bb , respectively. While the demographic evolution is described by the transition rates (1), at each birth, the genotype of the offspring is determined according to the Mendel's laws: the genotype of an offspring produced by the parent pair (y_1, y_2) will be the combination of one of the two alleles of the individual at y_1 and one of the two alleles of the individual at y_2 . The alleles are chosen at random, independently and uniformly. We call this process the sexual reproduction process with genotypes, abbreviated by SRG from now on. Recall that the transition probability $p(x, y)$ is translation invariant and symmetric, which implies the existence of some probability density function $q(x)$ such that $p(x, y) = q(y - x)$. For technical reasons, we assume in addition that $q(x)$ has variance $\sigma^2 < \infty$.

The main objective of this article is to prove that the behavior of the SRG is similar to that of the voter model [3, 9] and the multitype contact process [12] in the sense that the process clusters in one and two dimensions whereas alleles a and b may coexist (there exists a stationary distribution with a positive density of each genotype) in higher dimensions. Although the results are similar, the birth mechanism of the sexual reproduction process is too sophisticated so that the long-term behavior of the SRG can be understood by using the techniques of [3, 9, 12]. In particular, our proof relies of a variety of new techniques introduced for this purpose.

The non-spatial model. Before we study the behavior of the spatially explicit model, we look at its mean-field approximation [6], that is, we pretend that all sites are independent and that the system is spatially homogeneous. This then results in a system of differential equations for

the densities of homozygous and heterozygous. Let u_{aa} (respectively, u_{bb}) denote the density of homozygous of type a (respectively, b), and u_{ab} the density of heterozygous. The first step is to investigate the demographic density $u = u_{aa} + u_{ab} + u_{bb}$. It follows from the dynamics that

$$\frac{du}{dt} = -u + \lambda(1-u)u^2. \quad (2)$$

When $\lambda \leq 4$, any solution of (2) converges to 0, whereas when $\lambda > 4$, there are two additional equilibriums which are both positive, namely

$$\rho_u = \frac{\lambda - \sqrt{\lambda^2 - 4\lambda}}{2\lambda} \quad \text{and} \quad \rho_s = \frac{\lambda + \sqrt{\lambda^2 - 4\lambda}}{2\lambda}.$$

If the initial density is strictly smaller (respectively, strictly larger) than ρ_u then the density converges to 0 (respectively, ρ_s), i.e., 0 and ρ_s are stable while ρ_u is unstable. Returning to the model including genotypes, the mean-field ordinary differential equations can be written

$$\frac{du_{aa}}{dt} = -u_{aa} + \lambda(1-u) \left(u_{aa} + \frac{u_{ab}}{2}\right)^2 \quad (3)$$

$$\frac{du_{ab}}{dt} = -u_{ab} + 2\lambda(1-u) \left(u_{aa} + \frac{u_{ab}}{2}\right) \left(u_{bb} + \frac{u_{ab}}{2}\right) \quad (4)$$

$$\frac{du_{bb}}{dt} = -u_{bb} + \lambda(1-u) \left(u_{bb} + \frac{u_{ab}}{2}\right)^2. \quad (5)$$

To find the equilibrium states, we let

$$\sigma_a = \frac{2u_{aa} + u_{ab}}{2(u_{aa} + u_{ab} + u_{bb})} \quad \text{and} \quad \sigma_b = \frac{2u_{bb} + u_{ab}}{2(u_{aa} + u_{ab} + u_{bb})}$$

denote the frequencies of genes of type a and b . Then, equations (2) and (3) imply that

$$\frac{du_{aa}}{dt} = -u_{aa} + \lambda(1-u)\sigma_a^2 u^2 = -u_{aa} + \sigma_a^2 \left(\frac{du}{dt} + u\right)$$

so that $u_{aa} = \sigma_a^2 u$ at the equilibrium. By symmetry, $u_{bb} = \sigma_b^2 u$ and so $u_{ab} = 2\sigma_a\sigma_b u$ at the equilibrium. To compute the fractions of genes of type a and b at the equilibrium, we observe that combining equations (3), (4) and (5), we obtain

$$\frac{d}{dt} \left(\frac{2u_{aa} + u_{ab}}{2u} \right) = \frac{d}{dt} \left(\frac{2u_{bb} + u_{ab}}{2u} \right) = 0,$$

that is, the fractions of genes are preserved by the dynamics. In conclusion, the demographic evolution is described by equation (2) while the genes mix up in the population in such a way that, at the equilibrium,

$$u_{aa} = \sigma_a^2(0)u \quad u_{ab} = 2\sigma_a(0)\sigma_b(0)u \quad u_{bb} = \sigma_b^2(0)u$$

where $\sigma_a(0)$ and $\sigma_b(0)$ denote the fractions of genes of type a and b at time 0. This is referred to as the Hardy-Weinberg equilibrium in population genetics.

Note that the behavior of the mean-field approximations of the voter model and the multitype contact process are similar. For the voter model, the densities of types are preserved, while for the multitype contact process, only the frequencies of types are preserved. For the SRG, the preserved quantities are the frequencies of genes of type a and of type b . In conclusion, provided the birth rate is large enough to ensure survival, the mean-field approximations of all three models predict coexistence, i.e., existence of a stable equilibrium with a positive density of each type.

The spatially explicit model. It has been proved for the voter model and the multitype contact process that the inclusion of a spatial structure in the form of local interactions translates into a spatial segregation in one and two dimensions, while both types of particles may coexist in higher dimensions. The result for the voter model is due to Clifford and Sudbury [3] and Holley and Liggett [9], and the result for the multitype contact process to Neuhauser [12]. For both models, the key of the proof is duality. The dual process starting at $\{x, y\}$ allows to trace the history of the individuals at sites x and y back to time 0 by keeping track of their ancestors, so to determine the state of these sites at the current time from the configuration at earlier time. In the voter model, the dual process is a system of coalescing random walks. The ancestral lines of the individuals at sites x and y eventually coalesce with probability 1 in dimensions $d \leq 2$, whereas there is a positive probability that they never coalesce in dimensions $d \geq 3$. The result for the voter model follows from the fact that coalescence of the ancestral lines is equivalent to the existence of a common ancestor that determines the (common) type of x and y . In the terminology of population genetics, x and y are said to be identical by descent. The dual process of the multitype contact process is more complicated. However, the ancestral lines can be divided into independent and identically distributed pieces so that the same argument as for the voter model applies.

Our analysis of the SRG also relies on duality. The techniques employed, however, are quite different, and our proof requires the introduction of a number of new concepts. To formulate our main result, we let $g(i, x, t) \in \{0, a, b\}$ denote the type of the i th gene ($i = 1, 2$) of the individual, if it exists, located at site x at time t . By convention, 0 denotes the absence of individual.

Theorem 1 *Assume that initially the random variables $\{g(i, x, 0) : x \in \mathbb{Z}^d, i = 1, 2\}$ are independent and $= a$ and $= b$ with probability θ and $1 - \theta$, respectively. Then, the process ξ_t converges in distribution to the measure π as $t \rightarrow \infty$ with*

$$\begin{aligned} \pi &= \theta \pi_{aa} + (1 - \theta) \pi_{bb} && \text{in } d \leq 2 \\ &= \nu_\theta && \text{in } d \geq 3, \end{aligned}$$

where π_{aa} and π_{bb} denote the limits starting from all sites occupied by individuals of genotype aa and genotype bb , respectively, and where ν_θ is a translation invariant measure under which the densities of genes of type a and b are both positive whenever $0 < \theta < 1$.

Recall that the birth rate λ has been fixed so that the upper invariant measure of the sexual reproduction process (1) has a positive density of occupied sites. To prove Theorem 1, we will need to make the following technical assumption

Conjecture 2 *The dual process $\{\hat{\eta}_s(x, t) : s \geq 0\}$ of the sexual reproduction process (1) starting at space-time point (x, t) lives forever or dies out exponentially fast, i.e.,*

$$P(T < \inf \{s \geq 0 : \hat{\eta}_s(x, t) = \emptyset\} < \infty) \leq C_1 \exp(-\gamma_1 T)$$

for suitable $C_1 < \infty$ and $\gamma_1 > 0$.

We refer the reader to Section 3 for a rigorous definition of $\{\hat{\eta}_s(x, t) : s \geq 0\}$, the dual process of the sexual reproduction process. The estimate in Conjecture 2 is well-known for the contact process (and the dual process of the contact process since the contact process is self-dual). The proof relies on the analogous estimate for oriented percolation together with the fact that, viewed on suitable length and time scales, the contact process dominates oriented percolation (see for

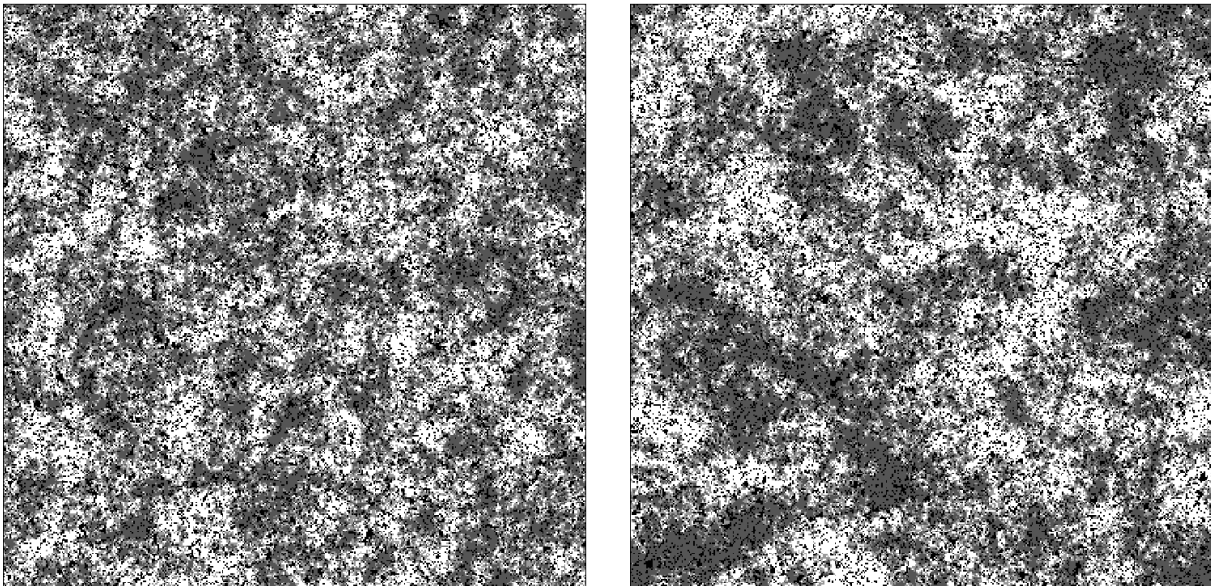


FIGURE 1. Snapshots of the process with birth rate $\lambda = 7.8$ at times 100 and 1000, respectively. In both realizations, the process evolves on the 400×400 square with periodic boundary conditions and starts from the “all heterozygous” configuration. The color code is black = 0, dark grey = aa , pale grey = ab , and white = bb .

instance Lemma 7, Section 11.b, in [4]). Unfortunately, we do not know how to prove Conjecture 2 for the sexual reproduction process. Lemma 3.1 below, however, strongly suggests that the dual process of the process (1) grows like a contact process from which a proof of Conjecture 2 (using again a comparison with oriented percolation) would follow.

2. Sketch of the proof

The key to prove Theorem 1 is duality. The strategy is similar to that of the proof of the analogous result for the voter model [3, 9] and the multitype contact process [12]. The idea is to keep track of the ancestors of the i th gene of the individual at site x and of the j th gene of the individual at site y by going backwards in time. The aim is to prove that the resulting ancestral lines coalesce for almost all realizations of the process if and only if $d \leq 2$. This implies that both genes are asymptotically identical by descent (and so identical) in low dimensions $d \leq 2$ while they may be different in higher dimensions $d \geq 3$. In view of the birth mechanism (sexual reproduction), the dual process of the SRG appears to be more complicated than the dual processes of the voter model and the multitype contact process. In particular, our proof mainly relies on the introduction of a number of new concepts that we now define intuitively to facilitate the understanding of the global strategy. These key concepts are written in *italics* below.

Topology of the dual process. The first consequence of sexual reproduction is that the dual process starting at (x, t) consists of a finite collection of finite subsets of \mathbb{Z}^d rather than a finite collection of sites as for the multitype contact process or a single site as for the voter model. That is, the dual process starting at (x, t) is given by

$$\hat{\eta}_s(x, t) = \{B_1, B_2, \dots, B_n\}, \quad 0 \leq s \leq t,$$

where each $B_k \subset \mathbb{Z}^d$ is a finite set containing the ancestors (the two parents, or one parent and two grand parents, or the four grand parents, ...) of the individual at site x at time $t \geq 0$. To investigate the topology of the dual process, we will consider a collection μ of independent coin flips which assign the value 1 (Heads) or 2 (Tails) to each birth occurrence, and will construct a new process called μ -process in the following way: at each birth attempt, we pick one of both parents at random as indicated by the corresponding coin flip, and pretend that the birth occurs if the chosen site is occupied and the target site empty. The genotypes of the parent and its offspring are unimportant in this construction. This makes the μ -process a contact process. We call μ -ancestral tree the dual process of the μ -process starting at space-time point (x, t) . We will prove that the dual process of the SRG lives forever if and only if for any collection of coin flips μ , the μ -ancestral tree lives forever. Moreover, conditioned on survival, each set B belonging to the dual process has a nonempty intersection with each of the μ -ancestral trees.

The ancestral path. The second step is to keep track of the ancestor of the i th gene of the individual at (x, t) through a process $g_s(i, x, t)$ referred to as *ancestral path*. As for the multitype contact process, the elements of the dual process can be arranged according to the order they determine the type of (x, t) . This order relationship will be referred to as *ancestor hierarchy*, and the minimal element for this order denoted by $B_s(x, t)$ and called *first ancestor set*. This set contains all the actual ancestors of (x, t) . To identify which of these ancestors is the actual carrier of the i th gene of (x, t) , we will introduce an additional set-valued process $H_s(i, x, t)$ containing all the *potential carriers* at time $t - s$ of the gene under consideration. Since, at each birth, the gene we are tracking down originates from exactly one of both parents, there exists a collection μ of coin flips such that the set $\{H_s(i, x, t) : s \geq 0\}$ is equal to the μ -ancestral tree starting at (x, t) . In particular, results of the previous subsection imply that, conditioned on survival of the dual process,

$$B_s(x, t) \cap H_s(i, x, t) \neq \emptyset \quad \text{at any time } s \geq 0. \quad (6)$$

By construction, the ancestral path follows the first ancestor in the intersection (6) going backwards in time. The mathematical definition of first ancestor in this context will be given later.

Renewal points. After constructing the ancestral path, the next step is to break its evolution at some points called *renewal points* in order to define an embedded random walk. To define renewal points in the case of the SRG, we introduce the concept of a *family*. Let $B \subset \mathbb{Z}^d$ be a finite set and let $t \geq 0$. Then, the family of (B, t) , denoted by $\mathcal{F}_s(B, t)$, can be seen as a generalization of the dual process starting from a finite set rather than a single site. Families have some nice properties, including the following Markov type property:

$$\mathcal{F}_{s+u}(B, t) = \bigcup_{D \in \mathcal{F}_s(B, t)} \mathcal{F}_u(D, t - s) \quad \forall s, u \geq 0, \quad \forall B \subset \mathbb{Z}^d \text{ finite.}$$

Relying on the previous equation, we will prove that the family of (B, t) lives forever if and only if the dual process starting at (z, t) lives forever for any $z \in B$, and that when it does not, it dies out exponentially fast. Renewal points will be defined as the space-time locations of the ancestral path occurring when the family of the first ancestor set lives forever. To prove that the sequence of renewal points $\{(S_j, T_j) : j \geq 1\}$ performs a random walk, we will first show that, if the individual present at the j th renewal point transmits its k_j th gene on its way up to (x, t) , then

$$g_{s+T_j}(i, x, t) = g_s(k_j, S_j, t - T_j).$$

This implies that the original ancestral path can be defined by gluing together the ancestral paths starting at consecutive renewal points, which is the key to prove that the sequence of renewal points performs a random walk. In other respects, using that families live forever or die out exponential fast, we will obtain that the spatio-temporal displacements between consecutive renewal points have exponential bounds. Techniques developed in [12], Sections 3-5, then imply that the random walk defined by the sequence of renewal points is recurrent in $d \leq 2$ and transient in $d \geq 3$.

Identity by descent. The proof of Theorem 1 is now straightforward. The idea is that recurrence of the sequence of renewal points in $d \leq 2$ translates by duality into a spatial segregation through the fact that occupied sites are asymptotically identical by descent. In contrast, transience in $d \geq 3$ implies that distinct ancestral paths may evolve indefinitely without overlapping, which allows different individuals to have different genotypes. See [12] for more details.

3. Duality and contact type substructure

This section is devoted to the construction of the dual process. The aim is also to exhibit somewhat interesting connections between the dual process of the sexual reproduction process and the dual process of the contact process (see Proposition 3.3 below).

Construction of the SRG. The first step is to construct the process (1), from collections of independent Poisson processes, which is referred to as Harris' graphical representation [7]. The construction of the SRG only requires an additional collection of independent coin flips. These coin flips indicate which gene an offspring inherits from its parents. For any $y, z_1, z_2 \in \mathbb{Z}^d$, we consider the two collections of independent Poisson processes

$$\begin{array}{lll} \text{arrival times:} & T_n(y, z_1, z_2) & U_n(y) \\ \text{rate:} & \lambda q(z_1 - y) q(z_2 - y) & 1 \end{array}$$

We draw an arrow from z_1 to y and an arrow from z_2 to y at time $T_n(y, z_1, z_2)$ to indicate that a birth may occur: if sites z_1 and z_2 are both occupied then site y becomes occupied if it is not already. We also put a death mark "x" at site y at time $U_n(y)$ to indicate that if site y is occupied then it becomes empty. To construct the SRG starting from $\xi_0 : \mathbb{Z}^d \rightarrow \{0, aa, ab, bb\}$, we first order (artificially) at random the genes of each individual, and assume by convention that, if a birth occurs at site y at time $T_n(y, z_1, z_2)$, then the i th gene, $i = 1, 2$, of the individual at site y originates from the individual at site z_i . To determine which genes an offspring inherits from its parents, we introduce a collection of independent random variables $\nu(\cdot)$ with

$$P(\nu(n, y, z_1, z_2) = (i, j)) = 1/4 \quad \forall n \geq 1, \quad \forall y, z_1, z_2 \in \mathbb{Z}^d, \quad \forall i, j = 1, 2. \quad (7)$$

Then, condition on the event that $\nu(n, y, z_1, z_2) = (i, j)$, if it exists the offspring sent to site y at the arrival time $T_n(y, z_1, z_2)$ inherits the i th gene of site z_1 and the j th gene of site z_2 .

Definition of the dual process. The dual process $\{\hat{\eta}_s(x, t) : 0 \leq s \leq t\}$ starting at space-time point (x, t) allows us to keep track of the ancestors of the individual at site x at time t by going backwards in time. In the case of the sexual reproduction process, the dual process is a collection of finite subsets of \mathbb{Z}^d which starts from the singleton $\hat{\eta}_0(x, t) = \{x\}$, and evolves as follows:

- 1a. If a birth event occurs from sites z_1 and z_2 to site y at time $t - s$ then $\hat{\eta}_s(x, t)$ is obtained from $\hat{\eta}_{s-}(x, t)$ as follows: for each set $B \in \hat{\eta}_{s-}(x, t)$ which contains y , we add a set B' which is obtained from B by removing y and adding z_1 and z_2 .

- 1b. If a death event occurs at site y at time $t - s$ then $\hat{\eta}_s(x, t)$ is obtained from $\hat{\eta}_{s-}(x, t)$ by removing any set B containing y .

Later on, the event described in 1a above will be written $B \rightarrow B'$ at time $t - s$. A nice property of the dual process is that it allows us to deduce the state of site x at time t from the configuration at earlier times. More precisely, it follows from the previous construction that

$$x \in \eta_t \quad \text{if and only if} \quad B \subset \eta_{t-s} \quad \text{for some} \quad B \in \hat{\eta}_s(x, t) \quad (8)$$

where η_t is identified with the set of occupied sites: $\eta_t \equiv \{z \in \mathbb{Z}^d : \eta_t(z) = 1\}$. The dual process is naturally defined only for $0 \leq s \leq t$ but it is convenient to assume that the Poisson processes in the construction are defined for negative times and $\hat{\eta}_s(x, t)$ for all $s \geq 0$.

μ -ancestral trees. To understand the topology of the dual process, we will compare its structure with the well-known tree structure of the contact process. The first step is to define a new process from the graphical representation introduced above supplemented with a collection of independent coin flips. We introduce a collection of independent random variables $\mu(\cdot)$ with

$$P(\mu(n, y, z_1, z_2) = 1) = P(\mu(n, y, z_1, z_2) = 2) = 1/2 \quad \forall n \geq 1, \quad \forall y, z_1, z_2 \in \mathbb{Z}^d. \quad (9)$$

We define a new process ζ_t^μ that maps \mathbb{Z}^d into $\{0, 1\}$ as follows.

1. If the label $\mu(n, y, z_1, z_2) = i$ and the parent site z_i is occupied at time $T_n(y, z_1, z_2)$ then, regardless of the state of the other parent site, y becomes occupied if it is not already.
2. An individual at site y at time $U_n(y)$, if it exists, is killed.

In other words, at each birth occurrence, we pick one of both parent sites at random and pretend that the birth occurs whenever the chosen site is occupied and the target site is empty. It follows that the evolution of ζ_t^μ at site $y \in \mathbb{Z}^d$ is described by the transition rates

$$c_{0 \rightarrow 1}(y, \zeta^\mu) = \lambda \sum_z q(z - y) \zeta^\mu(z) \quad \text{and} \quad c_{1 \rightarrow 0}(y, \zeta^\mu) = 1. \quad (10)$$

The transition rates in (10) indicate that ζ_t^μ is the contact process with birth parameter λ and dispersal kernel q . Given a graphical representation and a collection $\mu(\cdot)$, we call ζ_t^μ the μ -process associated to the sexual reproduction process introduced in (1) constructed from the same graphical representation. We let $\hat{\zeta}_s(\mu, x, t)$ denote the dual process of the μ -process starting at (x, t) and call μ -ancestral tree the space-time set $\{\hat{\zeta}_s(\mu, x, t) : s \geq 0\}$. Let

$$\Theta_s(x, t) = \{\hat{\zeta}_s(\mu, x, t) \text{ for some } \mu(\cdot)\} = \bigcup_{\mu(\cdot)} \hat{\zeta}_s(\mu, x, t).$$

Then, $\Theta_s(x, t)$ is a finite collection of finite subsets of \mathbb{Z}^d that starts at $\Theta_0(x, t) = \{\{x\}\}$ and evolves according to the following rules:

- 2a. If a birth event occurs from sites z_1 and z_2 to site y at time $t - s$ then $\Theta_s(x, t)$ is obtained from $\Theta_{s-}(x, t)$ in the following way: we remove each set $A \in \Theta_{s-}(x, t)$ which contains y and add two sets A' and A'' which are obtained from A by adding z_1 and z_2 , respectively.
- 2b. If a death event occurs at site y at time $t - s$ then $\Theta_s(x, t)$ is obtained from $\Theta_{s-}(x, t)$ by removing y from any set $A \in \Theta_{s-}(x, t)$.

To conclude this section, we prove that the dual process of the sexual reproduction process lives forever if and only if for any collection $\mu(\cdot)$ of independent coin flips the corresponding μ -ancestral tree lives forever. The necessary condition only is useful to prove Theorem 1. However, we consider that the equivalence is sufficiently interesting in itself to give its complete proof.

Lemma 3.1 *Assume that $\hat{\eta}_s(x, t) \neq \emptyset$. Let $A \in \Theta_s(x, t)$ and $B \in \hat{\eta}_s(x, t)$. Then $A \cap B \neq \emptyset$.*

PROOF. Since at any time $s \geq 0$ the dual process is finite with probability 1, we can order the birth events and the death events occurring in the dual process and prove the result by induction on the number of occurrences of Poisson processes contained in the dual process. The property to be proved is satisfied at time $s = 0$ since $\hat{\eta}_0(x, t) = \Theta_0(x, t) = \{\{x\}\}$. Assume that the property is satisfied by time s (until time s^-), with $t - s$ denoting the arrival time of a Poisson process occurring in the dual process, and let $A \in \Theta_s(x, t)$ and $B \in \hat{\eta}_s(x, t)$.

1. Assume first that $t - s = T_n(y, z_1, z_2)$ for some $y, z_1, z_2 \in \mathbb{Z}^d$. Then, rule 1a above implies that there exists $B' \in \hat{\eta}_{s^-}(x, t)$ such that

$$B = B' \quad \text{or} \quad B = B' \cup \{z_1, z_2\} - \{y\}.$$

- (a) Assume that $B = B'$. In this case, we apply rule 2a to find a set $A' \in \Theta_{s^-}(x, t)$ such that $A' \subset A$. By assumption, we have $A' \cap B' \neq \emptyset$ so that $A \cap B \neq \emptyset$.
- (b) Assume that $B = B' \cup \{z_1, z_2\} - \{y\}$. If $y \notin A$ then $A \in \Theta_{s^-}(x, t)$ so that

$$A \cap B = (A - \{y\}) \cap B = A \cap (B - \{y\}) \supset A \cap B' \neq \emptyset.$$

If $y \in A$ then either z_1 or z_2 belongs to A so that $A \cap B \neq \emptyset$.

2. Assume that $t - s = U_n(y)$ for some $y \in \mathbb{Z}^d$. By rule 2b, there is a set $A' \in \Theta_{s^-}(x, t)$ such that $A = A' - \{y\}$. Moreover, rule 1b implies that $y \notin B$ and $B \in \hat{\eta}_{s^-}(x, t)$. Putting things together, we deduce that

$$A \cap B = (A' - \{y\}) \cap B = A' \cap (B - \{y\}) = A' \cap B.$$

By assumption, we have $A' \cap B \neq \emptyset$ (since $B \in \hat{\eta}_{s^-}(x, t)$). In particular, $A \cap B \neq \emptyset$.

This completes the proof. \square

Lemma 3.2 *Assume that $\eta_0 \equiv 1$ and $A \neq \emptyset$ for any $A \in \Theta_t(x, t)$. Then at any time $s \leq t$*

$$A \cap \eta_{t-s} \neq \emptyset \quad \text{for any} \quad A \in \Theta_s(x, t).$$

PROOF. As previously, we prove the result by induction on the number of occurrences of Poisson processes. Since $\eta_0 \equiv 1$ the property to be proved holds for $s = t$. Assume that the property holds until time $t - s$, the arrival time of a Poisson process. Let $A \in \Theta_s(x, t)$.

1. Assume that $t - s = T_n(y, z_1, z_2)$ for some $y, z_1, z_2 \in \mathbb{Z}^d$.
 - (a) Assume that $y \notin A$. Then rule 2b above implies that $A \in \Theta_s(x, t)$ so that

$$A \cap \eta_{t-s^-} \supset A \cap \eta_{t-s} \neq \emptyset.$$

(b) Assume that $y \in A$ and $z_1 \notin \eta_{t-s}$. Then $A' = A \cup \{z_1\} \in \Theta_s(x, t)$ so that

$$A \cap \eta_{t-s^-} \supset A \cap \eta_{t-s} = (A \cup \{z_1\}) \cap \eta_{t-s} = A' \cap \eta_{t-s} \neq \emptyset.$$

(c) By symmetry, the same holds when $y \in A$ and $z_2 \notin \eta_{t-s}$.

(d) Assume that $y \in A$ and $z_1, z_2 \in \eta_{t-s}$. Then the individuals at z_1 and z_2 give birth to an individual which is sent to site y so that $y \in \eta_{t-s^-}$. In particular,

$$A \cap \eta_{t-s^-} \supset \{y\} \neq \emptyset.$$

2. Assume that $t - s = U_n(y)$ for some $y \in \mathbb{Z}^d$. Then we have $\eta_{t-s^-} = \eta_{t-s} - \{y\}$. Moreover, rule 2b implies that the set $A' = A - \{y\}$ belongs to $\Theta_s(x, t)$. It follows that

$$A \cap \eta_{t-s^-} = A \cap (\eta_{t-s} - \{y\}) = (A - \{y\}) \cap \eta_{t-s} = A' \cap \eta_{t-s} \neq \emptyset.$$

This completes the proof. \square

Proposition 3.3 *We have $\hat{\eta}_s(x, t) \neq \emptyset$ for any $0 \leq s \leq t$ if and only if*

$$(A \neq \emptyset \text{ for any } A \in \Theta_s(x, t)) \text{ for any } 0 \leq s \leq t.$$

PROOF. Assume that $\hat{\eta}_s(x, t) \neq \emptyset$. Let $B \in \hat{\eta}_s(x, t)$. Then, Lemma 3.1 implies that

$$A \supset A \cap B \neq \emptyset \quad \text{for any } A \in \Theta_s(x, t).$$

Reciprocally, assume that for any set $A \in \Theta_t(x, t)$, $A \neq \emptyset$. Since $\Theta_0(x, t) = \{\{x\}\}$, an application of Lemma 3.2 with $s = 0$ gives $\eta_t(x) = 1$ provided the process starts from the all occupied configuration. The duality relationship (8) then implies that $\hat{\eta}_s(x, t) \neq \emptyset$ for any $0 \leq s \leq t$. \square

4. Keeping track of the genes

The duality relationship (8) indicates whether a site is occupied or not at a given time depending on the configuration of the system at earlier times. Since we are interested in the genotypes as well, we also need to determine the spatial location at earlier times of the ancestors of the genes of the individual under consideration. More precisely, given $x \in \mathbb{Z}^d$ and $t \geq 0$, we will define two processes denoted by $g_s(i, x, t)$, $i = 1, 2$, indicating the spatial location at time $t - s$ of the ancestor of the i th gene of the individual at (x, t) . These processes are embedded in the dual process.

The first ancestor set. As for the multitype contact process [12], the elements of the dual process starting at (x, t) are arranged according to the order they determine the genotype of the individual located at site x at time t . This order relationship will be referred to as the ancestor hierarchy. In contrast with the multitype contact process, the ancestor hierarchy for the SRG is only a partial order but it has a unique minimal element. Another difference between the multitype contact process and the SRG is that, in the former, each particle has exactly one parent, whereas in the latter, each particle has exactly two parents. It follows that, for the multitype contact process, the first ancestor reduces to a single site. The particle at this site, if it exists, is of the same type

as the particle at site x at time t . In the case of the SRG, the minimal element of the dual process is a set which is linearly growing with respect to s . This set is denoted by $B_s(x, t)$ later, and called first ancestor set at time $t - s$.

To define the first ancestor set, the first step is to extend the concept of dual process to the concept of family. For any finite set $B \subset \mathbb{Z}^d$ and any time t , we let $\mathcal{F}_s(B, t)$ denote the backwards process defined in the following way. A set D belongs to $\mathcal{F}_s(B, t)$ if and only if there is a sequence of times $s_0 = 0 < s_1 < \dots < s_{n+1} = s$ and sets $D_1 = B, \dots, D_n, D_{n+1} = D$ such that

1. For $i = 1, 2, \dots, n$, $D_i \rightarrow D_{i+1}$ at time $t - s_i$ and
2. For $i = 0, 1, \dots, n$, there is no death mark in D_{i+1} between times $t - s_{i+1}$ and $t - s_i$.

Recall that the notation $D_i \rightarrow D_{i+1}$ has been defined in 1a above (see page 7).

Definition 4.1 *The backwards process $\mathcal{F}_s(B, t)$ is called the family of (B, t) .*

The reader will observe that, when $B = \{x\}$, the family of (B, t) is equal to the dual process starting at (x, t) . In particular, a family can be seen as an extension of the dual process starting from a finite set rather than a single site.

We now give a formal algorithm to determine the first ancestor set of the dual process, and refer the reader to the left hand picture of Figure 2 for a concrete example where the first ancestor set is drawn in thick lines. For simplicity, we have drawn the picture assuming that each parent pair is a pair of nearest neighbors. Let $B_0 = \{x\}$ and a dual time $s \geq 0$. To determine $B_s(x, t)$ we first define by induction a sequence of finite subsets B_i as follows:

$$B_i \rightarrow B_{i+1} \text{ at time } t - u_i \text{ for some } u_i \leq s \quad \text{and} \quad \mathcal{F}_{s-u_i}(B_{i+1}, t - u_i) \neq \emptyset \quad (11)$$

with u_i maximal. The sequence halts at $i = n$ when there is no set B_{i+1} such that (11) holds. We then define the first ancestor set at dual time s by setting

$$B_s(x, t) = B_{i^*} \quad \text{where } i^* = \min \{0 \leq i \leq n : B_i \in \hat{\eta}_s(x, t)\}.$$

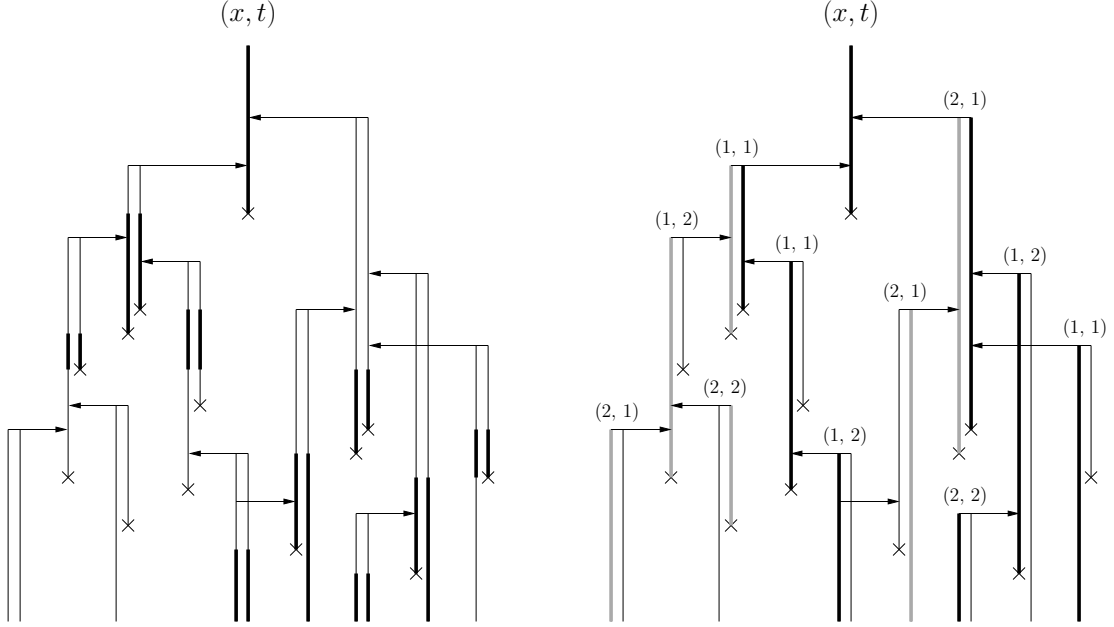
Note that $B_n \in \hat{\eta}_s(x, t)$ so that i^* is well defined. Moreover, by construction, provided all the sites in the first ancestor set $B_s(x, t)$ are occupied at time $t - s$, the genotype of the individual at site x at time t is determined by the genotypes of the individuals in $B_s(x, t)$ at time $t - s$.

The set of the potential carriers. The first ancestor set is linearly growing in time, containing two parents, or one parent and two grand parents, or four grand parents, etc. To determine which one of these individuals carries the i th gene ($i = 1, 2$) of the individual under consideration, we introduce an additional set-valued process, denoted by $H_s(i, x, t)$ and defined from the Harris' graphical representation and the collection of coin flips introduced in (7). The process evolves according to the following rules, starting at $H_0(i, x, t) = \{x\}$.

- 3a. If a birth occurs at site $y \in H_{s-}(i, x, t)$ at time $t - s = T_n(y, z_1, z_2)$ then

$$H_s(i, x, t) = H_{s-}(i, x, t) \cup \{z_1\} \quad \text{or} \quad H_s(i, x, t) = H_{s-}(i, x, t) \cup \{z_2\}$$

depending on whether y gave its first or second gene when it has been added to the dual process, respectively. If the birth occurs at site $y = x$ before a \times is encountered at site x then the set $H_s(i, x, t)$, $i = 1, 2$, is obtained from $H_{s-}(i, x, t)$ by adding site z_i .

FIGURE 2. $B_s(x, t)$ and $H_s(i, x, t)$, $i = 1, 2$.

3b. If a death occurs at $y \in H_{s-}(i, x, t)$ at time $t - s$ then $H_s(i, x, t) = H_{s-}(i, x, t) - \{y\}$.

See Figure 2, picture on right, for an example. The processes $H_s(i, x, t)$, $i = 1, 2$, are drawn in grey and black thick lines, respectively, and constructed from the graphical representation and the collection of independent coin flips $\nu(\cdot)$. For simplicity, we have drawn the picture assuming that for each parent pair (z_1, z_2) , we have $z_2 = z_1 + 1$. Note that rules 3a and 3b imply that there exists another collection of coin flips $\mu(\cdot)$ whose law is given by (9) such that the space-time set

$$H(i, x, t) = \{H_s(i, x, t) : s \geq 0\}$$

is equal to the μ -ancestral tree starting at (x, t) . In particular, as for the multitype contact process, the elements of $H_s(i, x, t)$ are arranged according to the order they determine $\zeta_t^\mu(x)$, where the interacting particle system ζ_t^μ is the contact process introduced in (10). This ancestor hierarchy induces a total order that we denote by \prec later.

In the case of the multitype contact process, the ancestor hierarchy has first been described by Neuhauser [12] and defined recently in a more rigorous way by Lanchier [11]. The basic idea is to introduce a function ϕ_s that maps the dual process into a set S_∞ of sequences:

$$\phi_s : H_s(i, x, t) \longrightarrow S_\infty = \{\{1, 2, \dots\} \cup \{\infty\}\}^{\mathbb{N}}.$$

The set S_∞ is additionally equipped with the usual lexicographic order \ll where

$$(u_1, u_2, \dots) \ll (v_1, v_2, \dots) \quad \text{if and only if} \quad \begin{cases} u_i = v_i & \text{for } i = 1, 2, \dots, n-1 \\ u_n < v_n \end{cases}$$

for some positive integer n . The function ϕ_s is strictly monotone in the sense that

$$\text{for all } x_1, x_2 \in H_s(i, x, t), \quad \phi_s(x_1) \ll \phi_s(x_2) \quad \text{if and only if} \quad x_2 \prec x_1. \quad (12)$$

The ancestor hierarchy on the dual process $H_s(i, x, t)$ is thus naturally induced by the lexicographic order on S_∞ through the function ϕ_s . The function ϕ_s corresponds to a labelling of the μ -ancestral tree and is defined inductively by going backwards in time. The original branch starting at site x at dual time 0 is labelled (∞, ∞, \dots) . Now, assume that a birth event from x_1 to x_2 occurs at dual time s_0 to include site x_1 to the dual process, and let

$$\phi_{s_0}(x_2) = (u_1, u_2, \dots, u_n, \infty, \dots) \text{ with } u_i < \infty \text{ for } i = 1, 2, \dots, n$$

denote the label on the parent branch (the one at site x_2 at dual time s_0). Then, we set

$$\phi_{s_0}(x_1) = (u_1, u_2, \dots, u_n, m, \infty, \dots)$$

if the new branch at site x_1 is the m th one (going backwards in time) originated from the branch at site x_2 . Also, $\phi_s(x_1) = \phi_{s_0}(x_1)$ until a death mark \times is encountered at site x_1 when the site is removed from the dual process. This construction implies that the first ancestor as defined in (12) through the mapping ϕ_s is the actual ancestor of the individual at site x at time t for the contact process ζ_t^μ . In particular, provided it is located in the first ancestor set $B_t(x, t)$ at time 0, this ancestor carries the i th gene of the individual at site x at time t for the SRG.

The position of the i th gene. We now define a process $g_s(i, x, t)$ which indicates the actual position at time $t - s$ of the ancestor of the i th gene of (x, t) . By construction of the SRG from the graphical representation and the collection of independent coin flips $\nu(\cdot)$ defined in (7), we have

$$g_s(i, x, t) \in B_s(x, t) \cap H_s(i, x, t) \text{ at any time } s \geq 0$$

provided the intersection $B_s(x, t) \cap H_s(i, x, t)$ is nonempty. To determine the location of the actual ancestor at time $t - s$, we write

$$H_s(i, x, t) = \{g_s(i, 1), g_s(i, 2), \dots, g_s(i, n_s)\}$$

with the convention that $g_s(i, k) \prec g_s(i, \ell)$ if and only if $k < \ell$, and set

$$g_s(i, x, t) = g_s(i, k_0) \quad \text{where } k_0 = \min \{1 \leq k \leq n_s : g_s(i, k) \in B_s(x, t)\}. \quad (13)$$

By construction, the i th gene of the individual at (x, t) is of the same type as the j th gene of the individual at site $g_s(i, x, t)$ at time $t - s$ where j is determined by the collection of independent coin flips $\nu(\cdot)$. See Figure 3, picture on left, for an illustration where $g_s(i, x, t)$, $i = 1, 2$, are drawn in grey thick lines and black thick lines for $i = 1$ and $i = 2$, respectively. In the general case, the existence of the ancestral path $g_s(i, x, t)$ is insured by the following

Lemma 4.2 *Assume that $\eta_t(x) \neq 0$. Then $B_s(x, t) \cap H_s(i, x, t) \neq \emptyset$ for all $0 \leq s \leq t$.*

PROOF. First of all, the assumption $\eta_t(x) \neq 0$ implies that

$$\hat{\eta}_s(x, t) \neq \emptyset \quad \text{at any time } s \leq t \quad (14)$$

so that the first ancestor set $B_s(x, t) \in \hat{\eta}_s(x, t)$ is well defined. Moreover, as previously mentioned, the space-time set $H(i, x, t)$ is equal to the μ -ancestral tree starting at (x, t) for some collection of coin flips $\mu(\cdot)$. In particular,

$$H_s(i, x, t) \in \Theta_s(x, t) \quad \text{at any time } s \leq t. \quad (15)$$

Lemma 3.1 together with (14) and (15) then implies that

$$B_s(x, t) \cap H_s(i, x, t) \neq \emptyset \quad \text{at any time } s \leq t.$$

This completes the proof. \square

5. Coalescing ancestral paths. Proof of Theorem 1

The proof of Theorem 1 essentially relies on an idea of Kuczek [10] that consists in breaking the evolution of the backwards process $g_s(i, x, t)$ into independent and identically distributed pieces at certain points called renewal points. Since the dual process grows linearly in time, between two consecutive renewal points $g_s(i, x, t)$ is contained in a triangle-shaped set. In addition, we prove exponential bounds on the width and height of the triangles which makes the sequence of renewal points a recurrent random walk in $d \leq 2$, and a transient random walk in $d \geq 3$.

Properties of the families. To define renewal points, we first prove some of the properties of the concept of family introduced in Definition 4.1 above.

Definition 5.1 *Let a finite set $B \subset \mathbb{Z}^d$, and a time $t \geq 0$. We say that (B, t) lives forever if its family lives forever, i.e.,*

$$\mathcal{F}_s(B, t) \neq \emptyset \quad \text{at any time } s \geq 0.$$

We provide comparisons between the families of (B, t) and (z, t) when $z \in B$, and some estimates on the extinction time of a family. More precisely, we prove that a family lives forever or dies out exponentially fast. These results are stated in Lemmas 5.2-5.4 below.

Lemma 5.2 *Assume that (x, t) lives forever. Then at any time $s \geq 0$ there exists $B \in \mathcal{F}_s(x, t)$ such that $(B, t - s)$ lives forever.*

PROOF. Let $u \geq 0$ and $B \in \mathcal{F}_s(x, t)$. Then the definition of family implies that

$$\mathcal{F}_{s+u}(x, t) = \bigcup_{B \in \mathcal{F}_s(x, t)} \mathcal{F}_u(B, t - s).$$

In particular, if (x, t) lives forever then there exists $B \in \mathcal{F}_s(x, t)$ such that $\mathcal{F}_u(B, t - s) \neq \emptyset$ at any time $u \geq 0$, i.e., $(B, t - s)$ lives forever. This completes the proof. \square

Lemma 5.3 *For any finite set $B \subset \mathbb{Z}^d$,*

$$\tau(B, t) := \inf \{s \geq 0 : \mathcal{F}_s(B, t) = \emptyset\} = \inf \{\tau(z, t) : z \in B\}.$$

In particular, (B, t) lives forever if and only if (z, t) lives forever for any site $z \in B$.

PROOF. Let $z_0 \in B$ such that $s_0 := \tau(z_0, t) = \inf \{\tau(z, t) : z \in B\}$. Then for any site $z \in B$ there exists a finite set $B_z \in \mathcal{F}_{s_0}^-(z, t)$. By construction,

$$D := \bigcup_{z \in B} B_z \in \mathcal{F}_{s_0}^-(B, t)$$

so that $\mathcal{F}_{s_0^-}(B, t) \neq \emptyset$. This implies that $\tau(B, t) \geq \inf \{\tau(z, t) : z \in B\}$.

To prove the converse, let $D \in \mathcal{F}_{s_0^-}(B, t)$. Then, by definition of the family of (B, t) ,

$$D = \bigcup_{z \in B} B_z \quad \text{for some } B_z \in \mathcal{F}_{s_0^-}(z, t), \quad z \in B. \quad (16)$$

Since $s_0 = \tau(z_0, t)$ there is a death mark \times at some site $y \in B_{z_0}$ at time $t - s_0$. The expression (16) implies that $y \in D$ at time $t - s_0$ so $D \notin \mathcal{F}_{s_0}(B, t)$. This holds for any set D so that we can conclude that $\mathcal{F}_{s_0}(B, t) = \emptyset$ and then $\tau(B, t) \leq \inf \{\tau(z, t) : z \in B\}$. \square

Lemma 5.4 *Assume that (B, t) lives forever and that $B \rightarrow D$ at time t . Provided Conjecture 2 holds, there exist $C_1 < \infty$ and $\gamma_1 > 0$ such that*

$$P(s < \tau(D, t) < \infty) \leq 2C_1 \exp(-\gamma_1 s).$$

PROOF. Since $B \rightarrow D$ at time t , there exist $y \in B$ and $z_1, z_2 \in \mathbb{Z}^d$ such that

$$t = T_n(y, z_1, z_2) \text{ for some } n \geq 1 \quad \text{and} \quad D = B \cup \{z_1, z_2\} - \{y\}.$$

Since (B, t) lives forever, Lemma 5.3 implies that (z, t) lives forever for any $z \in B$. In particular, a new application of the previous lemma leads to

$$\begin{aligned} P(s < \tau(D, t) < \infty) &\leq P(s < \tau(z, t) < \infty \text{ for some } z \in D) \\ &\leq P(s < \tau(z_i, t) < \infty \text{ for some } i \in \{1, 2\}) \leq 2 \times P(s < \tau(z_1, t) < \infty) \end{aligned}$$

so that we just need to prove that

$$P(s < \tau(z_1, t) < \infty) \leq C_1 \exp(-\gamma_1 s),$$

which is exactly the statement of Conjecture 2. \square

Renewal points. The definition of renewal points for the SRG is formulated by using together the first ancestor set and the concept of a family. We first define inductively a sequence of stopping times σ_k , $k \geq 0$, as follows. Let $\sigma_0 = 0$ and denote by σ_1 the first time we encounter a death mark \times at site x by going backwards in time, starting from (x, t) . As long as $\sigma_k < \infty$, we let

$$\sigma_{k+1} = \inf \{s > \sigma_k : \mathcal{F}_{s-\sigma_k}(B_{\sigma_k}(x, t), t - \sigma_k) = \emptyset\}$$

be the first time $(B_{\sigma_k}(x, t), t - \sigma_k)$ dies out. See the left-hand side of Figure 3 for a picture of the sequence of stopping times. If $(B_{\sigma_k}(x, t), t - \sigma_k)$ lives forever then $\sigma_{k+1} = \infty$ and we let $T_1 = \sigma_k$ be the first renewal time, and

$$S_1 = g_{T_1}(i, x, t)$$

be the location of the i th gene at time $t - T_1$. The j th renewal point (S_j, T_j) is defined by using the same algorithm but replacing the first ancestor set $B_s(x, t)$ with the first ancestor set of the dual process starting at the previous renewal point, namely $B_s(S_{j-1}, t - T_{j-1})$. Let

$$S_n = x + \sum_{j=1}^n X_j \quad \text{and} \quad T_n = \sum_{j=1}^n \tau_j$$

so that X_j and τ_j respectively denote the spatial displacement and the temporal displacement between consecutive renewal points.

Proposition 5.5 *Assume that (x, t) lives forever. Then (X_j, τ_j) , $j \geq 1$, form an independent and identically distributed family of random vectors on $\mathbb{Z}^d \times \mathbb{R}^+$. Moreover,*

$$P(\|X_j\| > s) \leq C_2 \exp(-\gamma_2 s) \quad \text{and} \quad P(\tau_j > s) \leq C_2 \exp(-\gamma_2 s)$$

for suitable $C_2 < \infty$ and $\gamma_2 > 0$.

The key to prove that the vectors (X_j, τ_j) , $j \geq 1$, are independent and identically distributed is introduced in the following gluing lemma. Here is the basic idea. We assume that the individual present at the j th renewal point gives its k_j th gene on its way up to (x, t) , and set

$$\Delta_j = \{g_s(k_j, S_j, t - T_j) : 0 \leq s < \tau_{j+1}\}.$$

By using the properties of the Harris' graphical representation, it is not difficult to prove that the sets $\Delta_j - (S_j, t - T_j)$, $j \geq 0$, are independent and identically distributed (see Lemma 5.7 below for the details). Lemma 5.6 states that the ancestral path $g_s(i, x, t)$ can be constructed by gluing together the sets Δ_j , $j \geq 0$. This implies that $\{g_s(i, x, t) : s \geq 0\}$ itself can be divided into independent and identically distributed pieces. We now make this argument precise.

Lemma 5.6 (gluing lemma) *For any $j \geq 0$, let $B_{j,s} = B_s(S_j, t - T_j)$ and assume that the individual at site S_j at time $t - T_j$ gives its k_j th gene on its way up to (x, t) . Then*

$$g_{s+T_j}(i, x, t) = g_s(k_j, S_j, t - T_j) \quad \text{and} \quad B_{j,s} \subset B_{s+T_j}(x, t) \quad \text{for any } s \geq 0.$$

PROOF. We prove the result by induction. First of all, when $j = 0$, the property to be proved holds by definition since $S_0 = x$ and $T_0 = 0$. Assume that

$$g_{s+T_{j-1}}(i, x, t) = g_s(k_j, S_{j-1}, t - T_{j-1}) \quad \text{and} \quad B_{j-1,s} \subset B_{s+T_{j-1}}(x, t) \quad \text{for some } j \geq 1.$$

By setting $s = \tau_j$ in the previous equation, we get

$$S_j = g_{T_j}(i, x, t) = g_{\tau_j}(k_j, S_{j-1}, t - T_{j-1}) \in B_{j-1, \tau_j} \subset B_{T_j}(x, t).$$

Moreover, the definition of renewal time implies that $(B_{j-1, \tau_j}, t - T_j)$ lives forever. In particular, it follows from Lemma 5.3 that $(S_j, t - T_j)$ lives forever. In other respects, the construction of the dual process together with the inclusion $B_{j-1, \tau_j} \subset B_{T_j}(x, t)$ implies that

$$B_{j,s} \subset B_{s+T_j}(x, t) \quad \text{for any } s \geq 0.$$

Let $H_{j,s} = H_s(k_j, S_j, t - T_j)$. Since $S_j \in H_{T_j}(i, x, t)$, and the processes $H_s(i, x, t)$ and $H_{j,s}$ are constructed from the same collection of coin flips, we get

$$H_{j,s} \subset H_{s+T_j}(i, x, t) \quad \text{for any } s \geq 0.$$

In particular,

$$B_{j,s} \cap H_{j,s} \subset B_{s+T_j}(x, t) \cap H_{s+T_j}(i, x, t) \quad \text{for any } s \geq 0. \quad (17)$$

We now observe that (13) implies that

$$\phi_{T_j}(z) \ll \phi_{T_j}(S_j) \quad \text{for any } z \in B_{T_j}(x, t) \cap H_{T_j}(i, x, t), \quad z \neq S_j.$$

Let $\phi_{T_j}(S_j) = (u_1, u_2, \dots, u_n, \infty, \dots)$ with $u_i < \infty$. Then, the definition of ϕ_s tells us that

$$\phi_{s+T_j}(z) = (u_1, u_2, \dots, u_n, v_{n+1}, \dots) \quad \text{if and only if } z \in H_{j,s}.$$

This, together with (17), implies that the set $B_{j,s} \cap H_{j,s}$ contains the minimal elements of the set $B_{s+T_j}(x, t) \cap H_{s+T_j}(i, x, t)$ for the order \prec . Finally, since $(S_j, t - T_j)$ lives forever, Lemma 3.1, assures us that the intersection $B_{j,s} \cap H_{j,s}$ is nonempty for any $s \geq 0$ so that

$$g_s(k_j, S_j, t - T_j) = g_{s+T_j}(i, x, t) \quad \text{for any } s \geq 0.$$

This completes the proof. \square

Lemma 5.7 *Assume that (x, t) lives forever. Then, the vectors (X_j, τ_j) , $j \geq 1$, are independent and identically distributed.*

PROOF. For any $j \geq 0$, let

$$\Delta_j = \{g_s(k_j, S_j, t - T_j) : 0 \leq s < \tau_{j+1}\}.$$

First of all, since the backwards process $g_s(k_j, S_j, t - T_j)$ is constructed from the dual process starting at $(S_j, t - T_j)$, the random set Δ_j depends on parts of the graphical representation that are between time $t - T_{j+1}$ and time $t - T_j$. This implies that, for any $j_1 < \dots < j_n$, the random sets $\Delta_{j_1}, \dots, \Delta_{j_n}$ are determined by disjoint parts of the graph, and so are independent:

$$P(\Delta_{j_k} \in B_{j_k} \mid S_{j_k}, 1 \leq k \leq n) = \prod_{k=1}^n P(\Delta_{j_k} \in B_{j_k} \mid S_{j_k}) \quad (18)$$

for any measurable sets B_{j_1}, \dots, B_{j_n} . In other respects, the graphical representation is translation invariant in space (since the evolution rules of the process are) and time (due to the loss of memory of the exponential distribution). It follows that

$$P(\Delta_{j_1} - (S_{j_1}, t - T_{j_1}) \in B) = P(\Delta_{j_2} - (S_{j_2}, t - T_{j_2}) \in B) \quad (19)$$

for any measurable set B . Now, by Lemma 5.6,

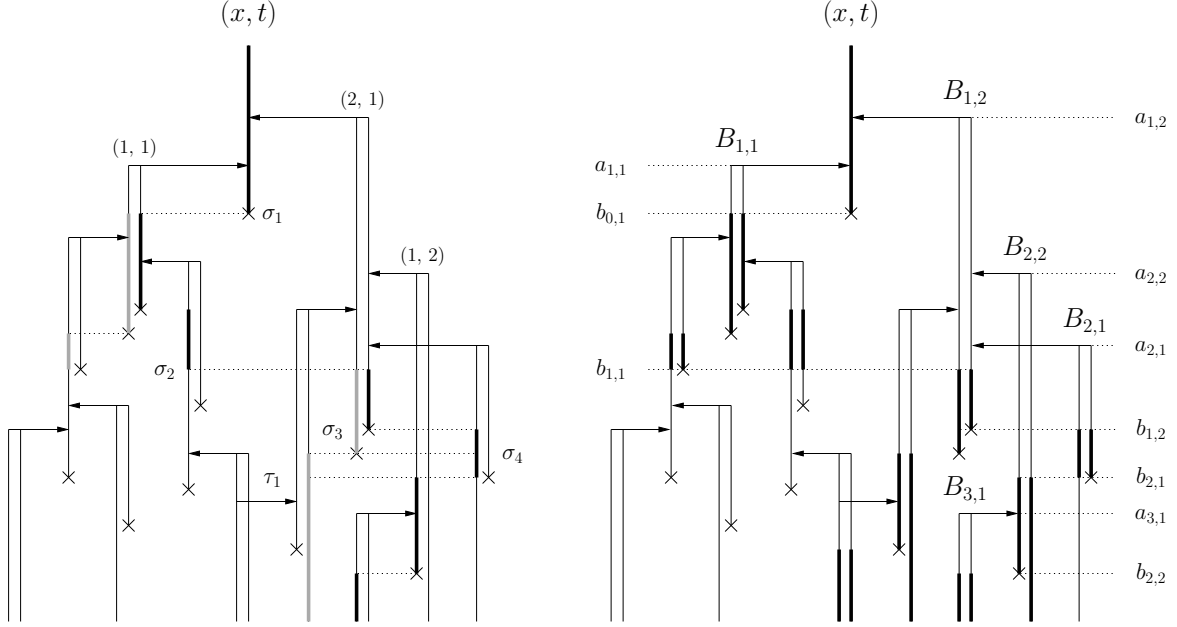
$$\Delta_j = \{g_s(i, x, t) : T_j \leq s < T_{j+1}\}.$$

This, together with equations (18) and (19), implies that the vectors (X_j, τ_j) , $j \geq 1$, are independent and identically distributed. This completes the proof. \square

The last step is to prove that the width $\|X_j\|$ and height τ_j of the triangles can be bounded by a random variable that has exponentially decaying tails. Since the tree structure of the dual process grows at most linearly in time, the existence of $C_2 < \infty$ and $\gamma_2 > 0$ such that

$$P(\|X_j\| > s) \leq C_2 \exp(-\gamma_2 s)$$

follows from the analogous result for τ_j . To prove the latter, the key idea is to show that, whenever the process $g_s(i, x, t)$ jumps within a new family, this family lives forever or dies out quickly, and that a geometric number of trials suffices to find the first renewal time.

FIGURE 3. $g_s(i, x, t)$, $i = 1, 2$, and illustration of Lemma 5.8.

Lemma 5.8 *There exist $C_2 < \infty$ and $\gamma_2 > 0$ such that $P(\tau_1 > s) \leq C_2 \exp(-\gamma_2 s)$.*

PROOF. The result follows from Lemma 5.4 and the construction shown in Figure 3, picture on right, that we now describe in details. We set $B_{0,1} = \{x\}$, $a_{0,1} = 0$, and

$$b_{0,1} = \inf \{s \geq 0 : U_n(x) = t - s \text{ for some } n \geq 1\}.$$

Let $B_{1,j} \subset \mathbb{Z}^d$ and $a_{1,j} > 0$, $j = 1, 2, \dots, n$, such that

$$B_{0,1} \rightarrow B_{1,j} \text{ at time } t - a_{1,j}$$

with $0 < a_{1,n} < \dots < a_{1,1} < b_{0,1}$, and

$$N_1 = \inf \{j \geq 1 : (B_{1,j}, t - a_{1,j}) \text{ lives forever}\}.$$

In our picture, $N_1 = 2$ since $(B_{1,1}, t - a_{1,1})$ does not live forever. Since (x, t) lives forever, it follows from Lemma 5.2 that the random variable N_1 is well defined ($N_1 \leq n$). Moreover, there is a positive probability depending only on the birth parameter λ that the set $B_{1,j}$ lives forever. This implies that the random variable N_1 is geometrically distributed. For any integer $j \leq N_1 - 1$, we denote by $b_{1,j}$ the first time the family of $(B_{1,j}, t - a_{1,j})$ dies out, i.e.,

$$b_{1,j} = \inf \{s > a_{1,j} : \mathcal{F}_{s-a_{1,j}}(B_{1,j}, t - a_{1,j}) = \emptyset\}.$$

The definition of N_1 implies that $b_{1,j} < \infty$ for any $j \leq N_1 - 1$. To define b_{1,N_1} , we first observe that the set B_{1,N_1} is obtained from $B_{0,1}$ by removing site x and adding two other sites z_1 and z_2 . Only one of these two sites, say z_1 , may contain the gene we are interested in. Then, we let

$$b_{1,N_1} = \inf \{s \geq a_{1,N_1} : U_n(z_1) = t - s \text{ for some } n \geq 1\}.$$

To find the first renewal time, we let

$$\rho_1 = \sup \{b_{1,j} : j \leq N_1 - 1\}.$$

In our picture, $\rho_1 = b_{1,1}$. First of all, since $b_{0,1} \geq a_{1,j}$ for all $1 \leq j \leq N_1 - 1$,

$$\rho_1 \leq b_{0,1} + \sup \{b_{1,j} - a_{1,j} : j = 1, 2, \dots, N_1 - 1\} \leq b_{0,1} + \sum_{j=1}^{N_1-1} (b_{1,j} - a_{1,j}). \quad (20)$$

In other respects, $(B_{1,j}, t - a_{1,j})$ does not live forever when $1 \leq j \leq N_1 - 1$, and $B_{1,j}$ is generated from $B_{0,1}$ that lives forever so Lemma 5.4 implies that

$$P(b_{1,j} - a_{1,j} > s) = P(\tau(B_{1,j}, t - a_{1,j}) > s) \leq 2C_1 \exp(-\gamma_1 s) \quad (21)$$

for all $1 \leq j \leq N_1 - 1$. Since N_1 is geometrically distributed, (20) and (21) imply that

$$P(\rho_1 > s) \leq C_3 \exp(-\gamma_3 s) \quad (22)$$

for suitable $C_3 < \infty$ and $\gamma_3 > 0$. We now observe that if $b_{1,N_1} > \rho_1$ then the gene we are keeping track jumps to site z_1 at dual time ρ_1 . If (z_1, ρ_1) lives forever then $\rho_1 = \tau_1$ is the first renewal time, and the lemma follows from the previous estimate (22). Otherwise, we define a time ρ_2 by using the same algorithm as above starting from $(z_1, t - a_{1,N_1})$ instead of (x, t) , and so on. After a geometric number of trials K we obtain $\rho_K = \tau_1$. In our picture, $\tau_1 = \rho_2 = b_{2,1}$. This, together with the inequality in (22), implies the result. This completes the proof of the lemma which, together with Lemma 5.7, implies Proposition 5.5. \square

Theorem 1 follows from Proposition 5.5 by using the same techniques as in [12], Sections 3-5. (See Section 2 for an intuitive idea of the proof.)

References

- [1] H. N. Chen. On the stability of a population growth model with sexual reproduction on \mathbb{Z}^2 . *Ann. Probab.*, 20(1):232–285, 1992.
- [2] H. N. Chen. On the stability of a population growth model with sexual reproduction on \mathbb{Z}^d , $d \geq 2$. *Ann. Probab.*, 22(3):1195–1226, 1994.
- [3] P. Clifford and A. Sudbury. A model for spatial conflict. *Biometrika*, 60:581–588, 1973.
- [4] R. Durrett. *Lecture notes on particle systems and percolation*. The Wadsworth & Brooks/Cole Statistics/Probability Series. Wadsworth & Brooks/Cole Advanced Books & Software, Pacific Grove, CA, 1988.
- [5] R. Durrett and L. Gray. Some peculiar properties of a particle system with sexual reproduction. In *Stochastic spatial processes*, volume 1212 of *Lecture Notes in Math*. Springer, New York, 1986.
- [6] R. Durrett and S. A. Levin. The importance of being discrete (and spatial). *Theoret. Pop. Biol.*, 46:363–394, 1994.
- [7] T. E. Harris. Nearest neighbor markov interaction processes on multidimensional lattices. *Adv. Math.*, 9:66–89, 1972.
- [8] T. E. Harris. Contact interactions on a lattice. *Ann. Probability*, 2:969–988, 1974.

- [9] R. A. Holley and T. M. Liggett. Ergodic theorems for weakly interacting infinite systems and the voter model. *Ann. Probability*, 3(4):643–663, 1975.
- [10] T. Kuczek. The central limit theorem for the right edge of supercritical percolation. *Ann. Probab.*, 17:1322–1332, 1989.
- [11] N. Lanchier. Two-scale multitype contact process. *Preprint*.
- [12] C. Neuhauser. Ergodic theorems for the multitype contact process. *Probab. Theory Related Fields*, 91(3-4):467–506, 1992.
- [13] C. Neuhauser. A long range sexual reproduction process. *Stochastic Process. Appl.*, 53(2):193–220, 1994.
- [14] C. Noble. Equilibrium behavior of the sexual reproduction process with rapid diffusion. *Ann. Probab.*, 20(2):724–745, 1992.

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