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Maria Deijfen
Olle Häggström

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Postal address:

Mathematical Statistics
Dept. of Mathematics
Stockholm University
SE-106 91 Stockholm
Sweden

Internet:

http://www.math.su.se/matstat

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The initial configuration is irrelevant for the possibility of mutual unbounded growth in the two-type Richardson model

Maria Deijfen *
Olle Häggström †

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Abstract

The two-type Richardson model describes the growth of two competing infections on $\mathbb{Z}^d$. At time 0 two disjoint finite sets $\xi_1, \xi_2 \subset \mathbb{Z}^d$ are infected with type 1 and type 2 infection respectively. An uninfected site then becomes type 1 (2) infected at a rate proportional to the number of type 1 (2) infected nearest neighbors and once infected it remains so forever. The main result in this paper is, loosely speaking, that the choice of the initial sets ξ_1 and ξ_2 is irrelevant in deciding whether the event of mutual unbounded growth for the two infection types has positive probability or not.

Keywords: Richardson's model, first-passage percolation, initial configuration, competing growth

AMS 2000 Subject Classification: Primary 60K35
Secondary 82B43.

*Stockholm University. E-mail: mia@matematik.su.se
†Chalmers University of Technology. E-mail: olleh@math.chalmers.se

1 Introduction

This paper is concerned with certain models for random growth and competition on the cubic lattice $\mathbb{Z}^d$ in dimension $d \geq 2$. The Richardson model, introduced in Richardson (1973), is one of the simplest models for growth on $\mathbb{Z}^d$. Each site is in either of two states, denoted by 0 and 1, and the set of sites in state 1 increases to cover all of $\mathbb{Z}^d$. The dynamics is that a site in state 0 is transferred to state 1 at a rate proportional to the number of nearest neighbors in state 1 and a site in state 1 remains there forever. This is equivalent to first-passage percolation with i.i.d. exponential passage times.

In Häggström and Pemantle (1998) a generalized version of the Richardson model is introduced. There are now three possible states, denoted by 0, 1 and 2 respectively, for each site. A site in state 0 is transferred to state 1 (2) with rate λ_1 (λ_2) times the number of nearest neighbors in state 1 (2) and the states 1 and 2 are absorbing. Here $\lambda_1, \lambda_2 > 0$ are the parameters of the model. For disjoint sets $\xi_1, \xi_2 \subset \mathbb{Z}^d$, let $P^{\lambda_1,\lambda_2}_{\xi_1,\xi_2}$ denote the probability law of the generalized process started at time 0 with the sites in ξ_1 being in state 1, the sites in ξ_2 in state 2 and the rest of $\mathbb{Z}^d$ in state 0. The states 1 and 2 may be thought of as representing two different types of infection and the model then describes the growth of two infections competing for space on $\mathbb{Z}^d$. There are two possible scenarios: Either one of the infection types at some point completely surrounds the other, preventing the surrounded type from growing any further, or both infection types keep growing indefinitely. Write A for the latter event, that is,

$$A = \{\text{both infection types reach sites arbitrarily far away from the origin}\}.$$

If the initial sets ξ_1 and ξ_2 are finite, clearly A^c has positive probability. To decide whether A has positive probability or not is more intricate. First, assume that $\xi_1 = \{\mathbf{0}\}$ and $\xi_2 = \{\mathbf{1}\}$, where $\mathbf{n} = (n, 0, \ldots, 0)$. Intuitively, A should in this case occur with positive probability if and only if $\lambda_1 = \lambda_2$. This intuition is partly confirmed in Häggström and Pemantle (1998,2000). The main result in the first paper is that if $\lambda_1 = \lambda_2$ and $d = 2$, then $P^{\lambda_1,\lambda_2}_{\mathbf{0},\mathbf{1}}(A) > 0$. In the second paper it is proved that if $d \geq 2$ and λ_1 is held fixed, then $P^{\lambda_1,\lambda_2}_{\mathbf{0},\mathbf{1}}(A) = 0$ for all but at most countably many values of λ_2. The aim in the present paper is to show that the choice of initial sets is basically irrelevant for these results. Of course, if one set completely surrounds the other, then mutual unbounded growth is ruled out. To formulate our main result, we therefore employ the following definition:

Definition 1.1 Let ξ_1 and ξ_2 be two disjoint finite subsets of $\mathbb{Z}^d$. We say

that one of the sets (ξ_i) *strangles* the other (ξ_j) if there exists no infinite self-avoiding path in $\mathbb{Z}^d$ that starts at a vertex in ξ_j and that does not intersect ξ_i. The pair (ξ_1, ξ_2) is said to be *fertile* if neither of the sets strangles the other.

The main result is as follows:

Theorem 1.1 *Let (ξ_1, ξ_2) and (ξ_1', ξ_2') be two fertile pairs of disjoint finite subsets of $\mathbb{Z}^d$. For all choices of (λ_1, λ_2), we have*

$$P^{\lambda_1,\lambda_2}_{\xi_1,\xi_2}(A) > 0 \Leftrightarrow P^{\lambda_1,\lambda_2}_{\xi_1',\xi_2'}(A) > 0.$$

This implies that mutual unbounded growth has positive probability when starting from $(\{\mathbf{0}\}, \{\mathbf{1}\})$ if and only if it occurs with positive probability for every other fertile initial configuration as well. Hence the results in Häggström and Pemantle (1998,2000) extend to arbitrary initial sets, as desired.

Häggström and Pemantle (1998) proved a special case of Theorem 1.1, namely the case when $d = 2$, $\lambda_1 = \lambda_2$ and (ξ_1, ξ_2) and (ξ_1', ξ_2') consist of single sites. The proof readily extends to the case where λ_1 and λ_2 are arbitrary and ξ_1 and ξ_2 are both connected sets. However, the proof fails to extend to more general initial configurations, and, since it uses planarity, it is unclear whether it extends to the case $d \geq 3$. These difficulties are overcome in the present paper.

We mention also that a related model for competing growth in continuous space was studied by Deijfen *et al* (2003), and the results obtained there include a kind of continuum analogue of our main result.

2 Preliminaries

In this section we give a concrete construction of the two-type Richardson model that suits our purposes. We also introduce some notation and formulate a lemma that will be important in the proof of Theorem 1.1.

To begin with, note that, by time-scaling and symmetry, we may restrict our attention to two-type processes with rates $(1, \lambda)$ for some $\lambda \leq 1$. To build up such a process, define the distance between two sites $x = (x_1, \ldots, x_d)$ and $y = (y_1, \ldots, y_d)$ on $\mathbb{Z}^d$ by $\delta(x, y) = \sum_{i=1}^d |x_i - y_i|$ and call two sites nearest neighbors if they are located at distance 1 from each other. Independently for each ordered pair (x, y) of nearest neighbor sites on $\mathbb{Z}^d$, associate a unit rate Poisson process $P^{(x,y)}$ and, for $\lambda \in [0, 1]$, write $\lambda P^{(x,y)}$ for the thinning of

$P^{(x,y)}$ obtained by removing each Poisson occurrence with probability $1-\lambda$. Intuitively, at the times of the occurrences in the process $P^{(x,y)}$, we imagine that a channel between x and y is opened so that type 1 infection can be transferred from x to y, that is, if x is type 1 infected at such a time, then y will become type 1 infected as well. The type 2 infection is controlled analogously by the process $\lambda P^{(x,y)}$.

To formally define the growth process, let Γ_n^i denote the set of type i infected sites after n infections and let T_n denote the time point for the nth infection. Also, for a set $\eta \subset \mathbb{Z}^d$, define $\partial\eta$ to be the set of sites in η that has at least one nearest neighbor in η^c, that is,

$$\partial\eta = \{x \in \eta;\ \exists y \in \mathbb{Z}^d \backslash \eta \text{ with } \delta(x,y) = 1\}.$$

The sequences $\{\Gamma_n^1\}$, $\{\Gamma_n^2\}$ and $\{T_n\}$ are obtained inductively as follows:

1. Let $\Gamma_0^1 = \xi_1$, $\Gamma_0^2 = \xi_2$ and $T_0 = 0$.
2. Given Γ_n^1, Γ_n^2 and T_n, define $T_{n+1} = \min\{\acute{T}_{n+1}^1, \acute{T}_{n+1}^2\}$, where

   $$\acute{T}_{n+1}^1 = \inf\{T > T_n;\ T \in P^{(x,y)} \text{ for some pair } (x,y) \text{ such that } x \in \partial\Gamma_n^i \text{ and } y \notin \Gamma_n^1 \cup \Gamma_n^2\}$$

   and $\acute{T}_{n+1}^2$ is defined analogously but with $P^{(x,y)}$ replaced by $\lambda P^{(x,y)}$.
3. If $T_{n+1} = \acute{T}_{n+1}^1$, then $\Gamma_{n+1}^2 = \Gamma_n^2$ and $\Gamma_{n+1}^1 = \Gamma_n^1 \cup \{y\}$, where y is the site such that $\acute{T}_{n+1} \in P^{(x,y)}$. If $T_{n+1} = \acute{T}_{n+1}^2$, then Γ_n^2 is updated in the same way while Γ_n^1 is left unchanged.

The set of type i infected sites at time $t \in [T_n, T_{n+1})$ is given by $\Gamma_i(t) = \Gamma_n^i$ and the total set of infected sites at time t is $\Gamma(t) = \Gamma_1(t) \cup \Gamma_2(t)$. When the initial sets need to be clear from the notation they will be included as superscript, for instance $\Gamma^{\xi_1,\xi_2}(t)$ denotes the set of infected sites at time t in a process started from the sets (ξ_1, ξ_2). By standard properties of the Poisson process, the time until an infected site infects an uninfected nearest neighbor is exponentially distributed and hence $\{\Gamma(t)\}$ is a Markov process.

We remark that in the original construction of the two-type Richardson model given in Häggström and Pemantle (1998,2000), the type 1 and the type 2 infections are generated by independent Poisson processes. More precisely, to each nearest neighbor pair (x,y) two independent Poisson processes $P_1^{(x,y)}$ and $P_2^{(x,y)}$ with rates 1 and λ respectively are attached. The process $P_1^{(x,y)}$ then controls the type 1 infection and $P_2^{(x,y)}$ controls the type 2 infection. However, in the present article we will always assume that the type 1 and

the type 2 infections are generated by the same Poisson process as described above. Obviously this gives a growth process with the same distribution as the original one.

One way of describing the evolution of the infection is to study the *infection graph*, denoted by Ψ. It consists of two disjoint graphs, Ψ_1 and Ψ_2, describing the type 1 and the type 2 infection respectively. These are generated as follows: For $i = 1, 2$, let $\Psi_i(t)$ be the graph with vertex set $\Gamma_i(t)$ and edge set obtained by putting an edge between two nearest neighbor sites $x, y \in \Gamma_i(t)$ if and only if, at some time $t' \leq t$, x was infected by y or vice versa. Define $\Psi_i = \lim_{t\to\infty} \Psi_i(t)$, where the limit exists since both the vertex set and the edge set of $\Psi_i(t)$ is increasing in t, and let $\Psi = \Psi_1 \cup \Psi_2$. In the one-type Richardson model started from a single infected site, Ψ is a tree and its features have been studied in Newman (1995) and Häggström and Pemantle (1998). In general, Ψ is a forest, that is, each connected component is a tree.

Clearly mutual unbounded growth for the two infection types in the two-type model occurs if and only if both Ψ_1 and Ψ_2 contain an infinite path. The following lemma relates the existence of such paths to the boundary configuration of the initial set. To formulate it, extend the notation for the infection graphs to incorporate the initial sets, so that $\Psi_i^{\zeta_1,\zeta_2}$ denotes the type i infection graph for a process started from (ζ_1, ζ_2).

Lemma 2.1 *Consider two growth processes with the same infection rates $(1, \lambda)$, $\lambda \leq 1$, and generated by the same Poisson processes, but started from two different finite initial configurations (ζ_1, ζ_2) and (ζ_1', ζ_2'). Assume that $\zeta_1 \cup \zeta_2 = \zeta_1' \cup \zeta_2' = \zeta$ and $\zeta_2 \cap \partial\zeta \subset \zeta_2' \cap \partial\zeta$.*

(a) *If $\Psi_2^{\zeta_1,\zeta_2}$ contains an infinite path, then so does $\Psi_2^{\zeta_1',\zeta_2'}$.*

(b) *If there is an infinite path in $\Psi_1^{\zeta_1,\zeta_2}$ starting at some site $x \in \partial\zeta \cap \zeta_1 \cap \zeta_1'$, then the same path is present in $\Psi_1^{\zeta_1',\zeta_2'}$ as well.*

Proof: Write ζ° for the interior of ζ, that is, $\zeta^\circ = \zeta \backslash \partial\zeta$. We will show that

$$\Gamma_1^{\zeta_1,\zeta_2}(t)\backslash\zeta^\circ \supset \Gamma_1^{\zeta_1',\zeta_2'}(t)\backslash\zeta^\circ \tag{1}$$

and

$$\Gamma_2^{\zeta_1,\zeta_2}(t)\backslash\zeta^\circ \subset \Gamma_2^{\zeta_1',\zeta_2'}(t)\backslash\zeta^\circ \tag{2}$$

for all t. To this end, order the time points for the infections in the two growth processes in one single sequence $\{\tilde{T}_n\}_{n\geq 0}$ where $\tilde{T}_0 := 0$. Note that, since the growth processes are generated by the same Poisson processes, infections can

take place simultaneously in both processes. Hence an infection time $\tilde{T}_n$ can represent an infection that occurs in both processes. Assume that (1) and (2) hold for $t = \tilde{T}_n$. The only way for (1) to fail at $t = \tilde{T}_{n+1}$ is then that a site that is uninfected at time $\tilde{T}_n$ in the process started from (ζ_1, ζ_2) becomes type 1 infected in the process started from (ζ_1', ζ_2'). However, it is easily seen that if this should be the case, then the same infection must take place in the process started from (ζ_1, ζ_2) as well. Hence both sets $\Gamma_1^{\zeta_1,\zeta_2}(\tilde{T}_n)\backslash\zeta^\circ$ and $\Gamma_1^{\zeta_1',\zeta_2'}(\tilde{T}_n)\backslash\zeta^\circ$ are extended by the same site and thus (1) is preserved at time $\tilde{T}_{n+1}$. Analogously it can be seen that (2) is preserved at $\tilde{T}_{n+1}$. Furthermore, by assumption, the type 2 infected part of $\partial(\zeta_1 \cup \zeta_2)$ is a subset of the type 2 infected part of $\partial(\zeta_1' \cup \zeta_2')$, implying that (1) and (2) hold for $t = \tilde{T}_0$. It follows by induction over n that the inclusions (1) and (2) hold for all $t \in \{\tilde{T}_n\}$ and clearly they must then hold for all $t \geq 0$. Part (a) follows immediately from (2).

To establish (b), we first show that

$$\Gamma^{\zeta_1,\zeta_2}(t) \supset \Gamma^{\zeta_1',\zeta_2'}(t) \text{ for all } t \geq 0. \tag{3}$$

To this end, assume that the site $y \notin \zeta$ is infected at time $t > 0$ in the process started from (ζ_1', ζ_2'). If y is type 1 infected it follows from (1) that y is (type 1) infected at time t in the process started from (ζ_1, ζ_2) as well. So suppose y is type 2 infected. Then there is an infection chain with passage time at most t that leads from some site in ζ_2' to y. Clearly, unless some site in the chain becomes type 1 infected before it is reached by the type 2 infection, the same chain is present also in the process started from (ζ_1, ζ_2). However, the fact that a site in the chain is type 1 infected can only decrease the time it takes for the infection to reach y. Hence y is infected at the latest at time t in the process started from (ζ_1, ζ_2) and (3) follows.

Now let $\{v_n\}$ and $\{e_n\}$ denote the vertex and edge set respectively of the infinite path starting at $x = v_0$ in $\Psi_1^{\zeta_1,\zeta_2}$. We will call a site v_n *successful* in the process started from (ζ_1', ζ_2') if it is type 1 infected and infects the site v_{n+1} via the edge e_n at the latest at the time when v_{n+1} is infected in the process started from (ζ_1, ζ_2). Using (3), it follows easily by induction over n that all vertices in $\{v_n\}$ are successful in the process started from (ζ_1', ζ_2'). Hence $\{v_n\} \cup \{e_k\} \subset \Psi_1^{\zeta_1',\zeta_2'}$, as desired. □

3 Proof of Theorem 1.1

We are now in a position to prove Theorem 1.1. The proof is based on a coupling of the processes $P_{\xi_1,\xi_2}^{\lambda_1,\lambda_2}$ and $P_{\xi_1',\xi_2'}^{\lambda_1,\lambda_2}$ that has certain similarities with

the coupling used in the proof of Proposition 1.1 in Deijfen *et al* (2003). The geometrical aspects of our proof are, however, quite different.

Proof of Theorem 1.1: Pick finite sets $\xi_1, \xi_2, \xi_1', \xi_2' \subset \mathbb{Z}^d$ such that the pairs (ξ_1, ξ_2) and (ξ_1', ξ_2') are fertile. We will show that if $P^{\lambda_1,\lambda_2}_{\xi_1,\xi_2}(A) > 0$, then $P^{\lambda_1,\lambda_2}_{\xi_1',\xi_2'}(A) > 0$ as well. Interchanging the roles of (ξ_1, ξ_2) and (ξ_1', ξ_2') in the below arguments gives the reverse implication. As pointed out before, by time-scaling and symmetry, it suffices to consider the case when $\lambda_1 = 1$ and $\lambda_2 \leq 1$, that is, when the type 1 infection has rate 1 and is more powerful than the type 2 infection.

To begin with, we need some notation. For a finite set $\eta \subset \mathbb{Z}^d$, let $\bar{m}(\eta)$ and $\underline{m}(\eta)$ be the points in $\mathbb{Z}^d$ with coordinates

$$\bar{m}_i(\eta) = \max\{x_i;\ x_i \text{ is the } i\text{th coordinate of a point in } \eta\}$$

and

$$\underline{m}_i(\eta) = \min\{x_i;\ x_i \text{ is the } i\text{th coordinate of a point in } \eta\}$$

respectively and define

$$B_\eta = \{x \in \mathbb{Z}^d;\ \underline{m}_i(\eta) \leq x_i \leq \bar{m}_i(\eta) \text{ for all } i = 1, \ldots, d\},$$

that is, B_η is the smallest box that contains the set η. Write B_η^{+k} for the box B_η enlarged by k sites in each direction, that is,

$$B_\eta^{+k} = \{x \in \mathbb{Z}^d;\ \underline{m}_i(\eta) - k \leq x_i \leq \bar{m}_i(\eta) + k \text{ for all } i = 1, \ldots, d\}.$$

Finally, let $\xi = \xi_1 \cup \xi_2 \cup \xi_1' \cup \xi_2'$.

Now, first consider a process started from (ξ_1, ξ_2) and let τ be the time when the box B_ξ^{+2} is fully infected in this process, that is,

$$\tau = \inf\{t;\ B_\xi^{+2} \subset \Gamma^{\xi_1,\xi_2}(t)\}.$$

Then consider a process started from (ξ_1', ξ_2') coupled with the one started from (ξ_1, ξ_2) in such a way that it evolves independently up to time τ and then uses the same Poisson processes as the process started from (ξ_1, ξ_2) to generate the infections after time τ. The notation for this coupled process is equipped with a hat-symbol, for instance $\hat{\Gamma}^{\xi_1',\xi_2'}(t)$ denotes the set of infected sites at time t. We will describe a scenario for the time interval $[0, \tau]$ in the coupled process that – combined with Lemma 2.1 – guarantees that both infection types grow unboundedly in this process given that they do so in the process started from (ξ_1, ξ_2). To this end, assume that mutual unbounded growth occurs in the process started from (ξ_1, ξ_2), that is, assume that both

infection graphs $\Psi_1^{\xi_1,\xi_2}$ and $\Psi_2^{\xi_1,\xi_2}$ contain an infinite path. Let x_1 be the last site on $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ that is touched by an infinite path in $\Psi_1^{\xi_1,\xi_2}$ and let $\tilde{x}_1$ be the last site on ∂B_ξ^{+2} that is touched by the path through x_1. (Here "last" refers to time, that is, sites are ordered with respect to the time when they are infected.) For simplicity we assume that $\Gamma^{\xi_1,\xi_2}(\tau)$ has no holes so that there are no uninfected sites completely surrounded by $\Gamma^{\xi_1,\xi_2}(\tau)$. The desired scenario for the coupled process is as follows:

1. By definition of the box $B_{\xi_1'\cup\xi_2'}$, at time 0 there are at least two infected sites on $\partial B_{\xi_1'\cup\xi_2'}$. If none of these is type 1 infected, assume that some site on $\partial B_{\xi_1'\cup\xi_2'}$ becomes type 1 infected before any type 2 infection takes place. This is possible because of the assumption that ξ_1' is not strangled by ξ_2'.

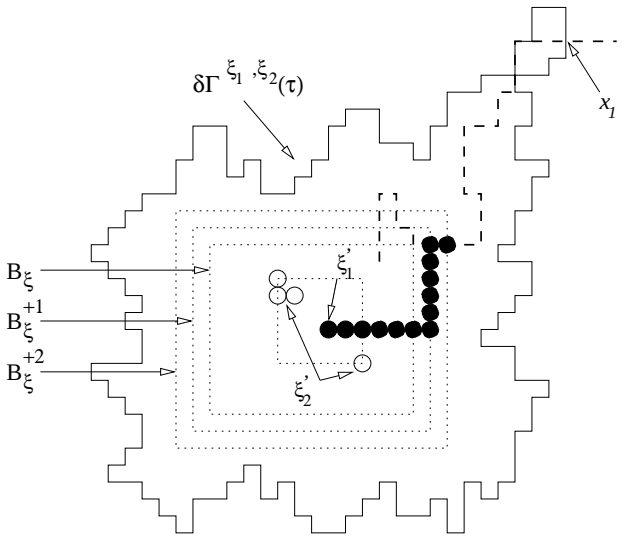
2. Pick a type 1 infected point x on $\partial B_{\xi_1'\cup\xi_2'}$ and assume that the type 1 infection reaches ∂B_ξ^{+1} via the shortest possible path from x without any type 2 infections occurring. Also without any type 2 infections occurring, suppose that the type 1 infection wanders the shortest way along ∂B_ξ^{+1} to the nearest neighbor of the site $\tilde{x}_1 \in \partial B_\xi^{+2}$ and then moves out to B_ξ^{+2} by infecting $\tilde{x}_1$. If $\tilde{x}_1$ happens to be a corner point of B_ξ^{+2} it does not have a nearest neighbor on B_ξ^{+1}. To deal with this case, let $\tilde{\tilde{x}}_1$ be the last (in time) non-corner point on B_ξ^{+2} that is touched by the infinite path through x_1. Suppose then that the type 1 infection wanders along ∂B_ξ^{+1} to the nearest neighbor of $\tilde{\tilde{x}}_1$, moves out to B_ξ^{+2} by infecting $\tilde{\tilde{x}}_1$ and then follows the infinite type 1 path to $\tilde{x}_1$.

   The configuration at this stage of the construction consists of the initial sets (ξ_1', ξ_2') and a type 1 path linking the set ξ_1' to the point $\tilde{x}_1$ on ∂B_ξ^{+2}, see Figure 1(a).

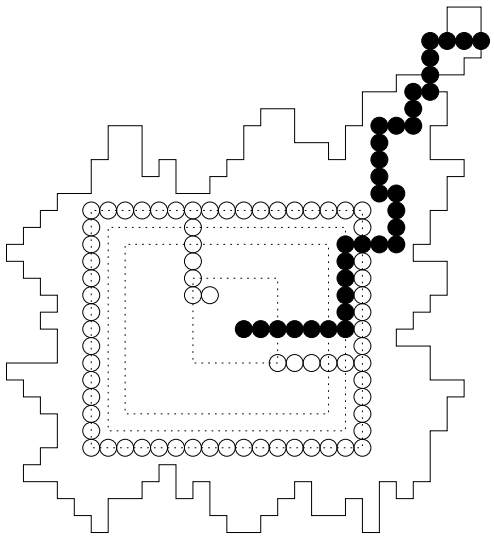
3. Now assume that the type 1 infection lies still while the type 2 infection wanders out from ξ_2' to ∂B_ξ^{+2} and invades all sites on ∂B_ξ^{+2} except $\tilde{x}_1$ (and possibly also $\tilde{\tilde{x}}_1$ and one or more corner points on the type 1 path between $\tilde{x}_1$ and $\tilde{\tilde{x}}_1$), which is already type 1 infected. Since ξ_2' is not strangled by ξ_1', a path from ξ_2' to ∂B_ξ^{+2} does indeed exist.

4. Suppose that the type 1 infection wanders from $\tilde{x}_1$ to the site x_1 on $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ along the infinite path through x_1 in $\Psi_1^{\xi_1,\xi_2}$ while no type 2 infections occur.

   To summarize, at this stage all sites on ∂B_ξ^{+2} except $\tilde{x}_1$ (and possibly also $\tilde{\tilde{x}}_1$ and one or more corner points on the type 1 path between $\tilde{x}_1$



(a) Configuration after Step 2. The dashed line indicates the infinite type 1 path through x_1 in the process started from (ξ_1, ξ_2).



(b) Configuration after Step 4.

Figure 1: Development of the infection in the process started from (ξ_1', ξ_2'). Black circles represent type 1 infected sites and white circles represent type 2 infected sites.

and $\tilde{\tilde{x}}_1$) are type 2 infected. We also have a type 1 path, passing ∂B_ξ^{+2} at $\tilde{x}_1$, that reaches from ξ_1' to x_1, see Figure 1(b).

5. Assume that $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ is infected as follows: If there are sites on $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ that can not be reached from ∂B_ξ^{+2} using paths in $\Gamma^{\xi_1,\xi_2}(\tau)$ without using sites on the type 1 path through x_1 – this is the case if x_1 is located on a cape as displayed in Figure 1 – suppose that the type 2 infection lies still until the type 1 infection has invaded these sites, one at a time, starting from x_1. Then assume that the rest of $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ is type 2 infected while no type 1 infections occur. Note that the sites on $\partial\Gamma^{\xi_1,\xi_2}(\tau)$ that can not be reached without using sites on the type 1 path through x_1 must constitute a connected subset of $\partial\Gamma^{\xi_1,\xi_2}(\tau)$. Also, some thought reveals that these sites must be type 1 infected in the process started from (ξ_1, ξ_2).

6. Suppose that the interior of $\Gamma^{\xi_1,\xi_2}(\tau)$ is filled with infection without any sites outside $\Gamma^{\xi_1,\xi_2}(\tau)$ being infected.

7. Let T denote the time when the above scenario is completed. Assume that $T \leq \tau$ and suppose that no infections at all take place in the time interval $(T, \tau]$.

The above scenario clearly has positive probability because it depends only on finitely many infections. Furthermore, given this scenario, the following hold at time τ:

- $\hat{\Gamma}^{\xi_1',\xi_2'}(\tau) = \Gamma^{\xi_1,\xi_2}(\tau) := \Gamma$;
- $\left(\Gamma_2^{\xi_1,\xi_2}(\tau) \cap \partial\Gamma\right) \subset \left(\hat{\Gamma}_2^{\xi_1',\xi_2'}(\tau) \cap \partial\Gamma\right)$;
- $x_1 \in \Gamma_2^{\xi_1,\xi_2}(\tau) \cap \hat{\Gamma}^{\xi_1',\xi_2'}(\tau) \cap \partial\Gamma$.

After time τ the coupled process is based on the same Poisson processes that were used to generate the process started from (ξ_1, ξ_2). It follows from Lemma 2.1 with $(\zeta_1, \zeta_2) = \left(\Gamma_1^{\xi_1,\xi_2}(\tau), \Gamma_2^{\xi_1,\xi_2}(\tau)\right)$ and $(\zeta_1', \zeta_2') = \left(\Gamma_1^{\xi_1',\xi_2'}(\tau), \Gamma_2^{\xi_1',\xi_2'}(\tau)\right)$ that there is at least one infinite path in both $\hat{\Psi}_1^{\xi_1',\xi_2'}$ and $\hat{\Psi}_2^{\xi_1',\xi_2'}$. Hence we have mutual unbounded growth in the coupled process.

Now let A_{ξ_1,ξ_2} denote the event that both infection types grow unboundedly in the process started from (ξ_1, ξ_2) and let $\hat{A}_{\xi_1',\xi_2'}$ denote the same event in the coupled process. Trivially

$$P(\hat{A}_{\xi_1',\xi_2'}) \geq P(\hat{A}_{\xi_1',\xi_2'} | A_{\xi_1,\xi_2}) P(A_{\xi_1,\xi_2}). \tag{4}$$

The above reasoning shows that if both infection types grow unboundedly in the process started from (ξ_1, ξ_2), then the scenario described in 1-7 guarantees that they do so in the coupled process as well. Hence the first factor on the right-hand side in (4) is positive. The last factor on the right-hand side is positive by assumption. Thus $P(\hat{A}_{\xi_1',\xi_2'}) > 0$ and, since $P(\hat{A}_{\xi_1',\xi_2'}) = P^{1,\lambda_2}_{\xi_1',\xi_2'}(A)$, we are done. □

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