

Multiscale analysis of particle systems

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March 6, 2020

Abstract

Lecture notes regarding the multi-scale analysis of reaction diffusion particle systems. These notes are still in a very rudimentary form and being frequently updated; in particular, some proofs have a few details omitted and a few rough approximations, and the bibliographical references are yet very scarce. Comments and suggestions are very much appreciated. These lecture notes are based on mini-courses given in TU Darmstadt and Università Roma Tre in 2019. I am thankful to the organizers and the participants for creating a very stimulating and participative atmosphere.

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1 Introduction

In preparation.

Convention regarding constants and terminology

We use $c, c', c'', C, C'' \dots$ for arbitrary constants, whose values may change from line to line. When we want to emphasize that the constant depends only on the dimension, we write c_d but the value of c_d may also change from line to line. When we want to fix a constant and use it with the same meaning throughout a section, we will use numbered indices such as c_1, c_2, \dots .

We let $\text{Poisson}(\lambda)$ denote a Poisson random variable of parameter λ that is independent of everything else. We use a similar notation for other distributions such as Bernoulli. We also let $\text{PPP}(\lambda)$ stand for a Poisson point process of intensity λ .

2 Particle System

We consider a system of particles on \mathbb{Z}^d starting from a Poisson point process of intensity μ ; that is, at time 0 the number of particle at each vertex of \mathbb{Z}^d is given by an independent Poisson random variable of intensity μ . Then, from time 0, particles move as independent simple random walks on \mathbb{Z}^d . Let η_t denote the configuration of particles at time t , where η_t is the counting measure so that, for all $\Lambda \subset \mathbb{Z}^d$,

$$\eta_t(\Lambda) := \sum_{x \in \Lambda} \eta_t(x) = \text{“\# particles in } \Lambda \text{ at time } t\text{”}.$$

Thus, we have that

$$\{\eta_0(x)\}_{x \in \mathbb{Z}^d} \text{ are i.i.d. Poisson random variables of parameter } \mu. \tag{2.1}$$

2.1 Invariant measure

The next theorem shows that the Poisson point process is an invariant measure for the particle system. In other words, the particle system we consider here is in equilibrium.

Theorem 2.1. *For any given $t \geq 0$, η_t is a Poisson point process of intensity μ on \mathbb{Z}^d .*

Proof. Fix $t > 0$ and $x, y \in \mathbb{Z}^d$. Let $N_t(x \rightarrow y)$ be the number of particles that start from x at time 0 and are located at y at time t . Using the thinning property of Poisson random variables we obtain that, for any given $x \in \mathbb{Z}^d$,

$$\{N_t(x \rightarrow y)\}_{y \in \mathbb{Z}^d} \text{ are independent Poisson random variables, each of intensity } \mu p_t(x, y), \quad (2.2)$$

where $p_t(x, y)$ is the probability that a random walk starting from x is located at y at time t . Using (2.1) we obtain that the $N_t(x \rightarrow y)$ are also independent across different values of x . Hence,

$$\eta_t(y) = \sum_{x \in \mathbb{Z}^d} N_t(x \rightarrow y),$$

which is a sum of independent Poisson random variables. From the superposition property of Poisson random variables, we have that $\eta_t(y)$ is a Poisson random variable of intensity

$$\sum_{x \in \mathbb{Z}^d} \mu p_t(x, y) = \sum_{x \in \mathbb{Z}^d} \mu p_t(y, x) = \mu.$$

Using (2.2) we obtain that the $\eta_t(y)$ are independent across different values of y , completing the proof. \square

2.2 Meeting times

The central problem we will look at is the spread of an infection among the particles. In order to analyze this problem, we will need to control the probability that particles meet¹ within a certain time interval. This is the context of the next theorem.

Theorem 2.2. *Assume that two particles are located at distance ℓ from one another at time 0. There exists a constant c_d such that the probability that the particles meet before time ℓ^2 is at least c_d for $d = 1$, at least $\frac{c_d}{\log \ell}$ for $d = 2$ and at least $\frac{c_d}{\ell^{d-2}}$ for $d \geq 3$.*

Proof. Let X_t and Y_t be the location at time t of each of the particles; hence, $\|X_0 - Y_0\|_1 = \ell$. Let M_s be the amount of time that the particles spend co-located at the same vertex during the time interval $[0, s]$; more formally,

$$M_s = \int_0^s \mathbf{1}(X_t = Y_t) dt.$$

We want to derive a lower bound to

$$\mathbb{P}(M_s > 0) = \frac{\mathbb{E}(M_s)}{\mathbb{E}(M_s | M_s > 0)}. \quad (2.3)$$

Denoting by $p_t(x, y)$ the probability that a random walk goes from x to y in time t , we have that

$$\mathbb{E}(M_s) = \int_0^s \mathbb{P}(X_t = Y_t) dt = \int_0^s \sum_{x \in \mathbb{Z}^d} p_t(X_0, x) p_t(Y_0, x) dt.$$

Since $p_t(Y_0, x) = p_t(x, Y_0)$ we obtain that

$$\mathbb{E}(M_s) = \int_0^s \sum_{x \in \mathbb{Z}^d} p_t(X_0, x) p_t(x, Y_0) dt = \int_0^s p_{2t}(X_0, Y_0) dt = \frac{1}{2} \int_0^{2s} p_{t'}(X_0, Y_0) dt',$$

¹That is, that the particles are at the same vertex at the same time

where the last step follows from a change of variable $t' = 2t$. Recalling that s is of order $\ell^2 = \|X_0 - Y_0\|_1^2$, for us it will be enough to use the lower bound

$$\mathbb{E}(M_s) \geq \frac{1}{2} \int_s^{2s} p_{t'}(X_0, Y_0) dt' \geq \begin{cases} c\sqrt{s}, & d = 1, \\ c, & d = 2, \\ \frac{c}{s^{d-2}}, & d \geq 3, \end{cases}$$

for some constant c . The final bounds follow from the local CLT (see, Lemma B.1). On the other hand $\mathbb{E}(M_s | M_s > 0)$ is at most the expected time that a random walk that starts from the origin spends at the origin during $[0, s]$, which is the Green's function up to time s and is known to behave as

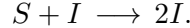
$$\begin{cases} c\sqrt{s}, & d = 1, \\ c \log(s), & d = 2, \\ c, & d \geq 3, \end{cases}$$

for some other constant c . Plugging these two bounds into (2.3) establishes the theorem. \square

3 Frog Model

Most of these notes will be devoted to analyze the spread of infection, which we define in Section 4. Before going into this model, we discuss a simpler process, called the *frog model*.

In the frog model, there are two types of particles, S (meaning *susceptible*) and I (meaning *infected*). S particles do not move (or, equivalently, we say that they jump at rate $D_S = 0$) and are initially distributed as a Poisson point process of intensity μ in \mathbb{Z}^d . The I particles, in turn, start from a single particle initially placed at the origin. This I particle move at rate $D_I = 1$. Whenever an I particle jumps onto a site occupied by S particles, the S particles all turn to type I (and, hence, start moving independently of one another as simple random walks at rate $D_I = 1$). This is usually represented by the reaction formula



We refer to this model as the *frog model with SI dynamics*. We let $\eta_t^S(x), \eta_t^I(x)$ be the number of S and I particles, respectively, that are located at site x at time t . As before, we take η_t^S, η_t^I to be the counting measure so that, for all $\Lambda \subset \mathbb{Z}^d$, we have

$$\eta_t^S(\Lambda) = \sum_{x \in \Lambda} \eta_t^S(x) \quad \text{and} \quad \eta_t^I(\Lambda) = \sum_{x \in \Lambda} \eta_t^I(x).$$

The frog model is also called *stochastic combustion model*. In this context, I particles are regarded as *heat particles* which diffuse and spread the heat to *inert particles* (modelled by the S particles). Once heated, the inert particles become heat particles and start to diffuse as well.

The frog model was introduced in 1999 by Telcs and Wormald [38], who defined it as a branching process where particles never die and branch only on their first visit to a vertex. In [38], it was showed that the frog model is recurrent in all dimensions, which is intended to mean that $\eta_t(0) \geq 1$ for infinitely many values of t .

Theorem 3.1 (Recurrence in the frog model [38]). *For all $d \geq 1$, each particle will eventually become infected almost surely.*

For a more thorough discussion regarding the recurrence problem, refer to the survey by Popov [30], and the recent work of Hoffman, Johnson and Junge [20] who proved a phase transition between recurrence and transience for the frog model on trees.

3.1 Positive speed and shape theorem

We consider the problem of spread of infection in the frog model. Since infected particles move as simple random walks, the originally infected particles (that is, the particles that were located at the origin at time 0) are likely to be at time t within distance of order \sqrt{t} from the origin. But since the infection can spread between particles, it is natural to believe that the infection could spread faster than \sqrt{t} . In particular, we would like to see whether the infection spreads with *positive speed*.

Definition 3.2 (Positive speed of propagation). We say that the frog model has *positive speed of propagation* (or just *positive speed*) if, for all large enough t , there is an infected particle whose distance to the origin has order t . More precisely, there exists a constant $c = c(d, \mu) > 0$ such that

$$\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{ct}) \geq 1 \text{ for all large enough } t, \text{ almost surely,}$$

where we recall that \mathcal{B}_r stands for a ball of radius r centered at the origin.

A positive answer to the above question was given by Alves, Machado, Popov and Ravishankar [3], building on earlier results by Alves, Machado and Popov [1] and Ramírez and Sidoravicius [31]. In fact, [3] proves a stronger result, which we will discuss below. But before that, we state the theorem on the positive speed of propagation since the proof of this theorem is the central content of this section.

Theorem 3.3. *For $d \geq 2$ and any $\mu > 0$, the frog model with SI dynamics has positive speed.*

As we mentioned above, [3] proved a stronger result, which goes under the name of *shape theorem*. Let A_t be the set of sites of \mathbb{Z}^d which were infected at least once during $[0, t]$; that is,

$$A_t = \left\{ x \in \mathbb{Z}^d : \exists s \in [0, t] \text{ for which } \eta_s^I(x) \geq 1 \right\}.$$

Then we transform A_t into a subset of \mathbb{R}^d by adding cubes of side length 1 centered at the sites of A_t to obtain $\tilde{A}_t = \bigcup_{x \in A_t} (x + [-1/2, 1/2]^d)$. We consider \tilde{A}_t , instead of A_t , since $\frac{\tilde{A}_t}{t} := \bigcup_{x \in \tilde{A}_t} \frac{x}{t}$ is a simply connected subset of \mathbb{R}^d , whereas $\frac{A_t}{t}$ is just a collection of points. We are now ready to state the shape theorem result of Alves, Machado, Popov and Ravishankar. We will not prove this result, as it goes out of the scope of our discussion here.

Theorem 3.4 ([1, 31, 3]). *In the frog model, for any $d \geq 1$ and any $\mu > 0$, there exists a compact subset \mathcal{S} of \mathbb{R}^d such that for any $\varepsilon > 0$ we have*

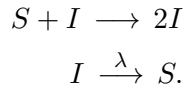
$$(1 - \varepsilon)\mathcal{S} \subset \frac{\tilde{A}_t}{t} \subset (1 + \varepsilon)\mathcal{S} \text{ for all } t \text{ large enough, almost surely.}$$

The set \mathcal{S} is called the *limit shape*. The above theorem can be interpreted as a type of law of large numbers for a sequence of random subsets $\tilde{A}_1, \tilde{A}_2, \dots$ of \mathbb{R}^d . As we pointed out above, Theorem 3.4 is an extension of an earlier result of Alves, Machado and Popov [1] and Ramírez and Sidoravicius [31] who independently established the shape theorem for the frog model when, in the initial configuration, each site $x \in \mathbb{Z}^d \setminus \{0\}$ has exactly one susceptible particle. The main difference between [1] and [31] is that in [1] the particles perform *discrete time* random walks, whereas in [31] the particles perform *continuous time* random walks. We remark that [31] also showed that \mathcal{S} is not an Euclidean ball and that the distribution of the particles at time t converges weakly to a Poisson point process.

In dimension one, more can be said about the frog model. Using a regeneration time argument, Comets, Quastel and Ramírez [11] proved that the fluctuations around the limit shape are Gaussian. Refer to the survey [21] for a more thorough discussion.

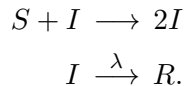
3.2 SIS and SIR dynamics

There are two other variants of the frog model (and of spread of infection in general) that we will discuss: the SIS and the SIR dynamics. They include an additional parameter $\lambda > 0$. In the SIS, we allow I particles to “heal” at rate λ , turning back to type S. The reaction formulas become



Note that, as defined above, if an I particle is at the same site of other I particles and decides to turn to type S, it instantaneously gets reinfected by the other I particles, and becomes of type I again. In other words, I particles can effectively turn into type S only when they are alone at a site.

In the SIR dynamics, there is a third type of particle, denoted R (meaning *removed* or *dead*). Each I particle dies at rate λ , turning to type R. This is an irreversible transition, since R particles never change types. So, the reaction formulas become



It is also possible to combine these two dynamics, for example, by letting I particles turn to type S at some rate and to type R at some other rate. But we will not look at this variant here.

3.3 Phase transition in the SIR dynamics

We now turn our attention to the SIR dynamics for the frog model. A central question here is whether the infection survives.

Definition 3.5 (Survival of the infection). We say that the infection *survives* if we have that $\mathbb{P}(\eta_t^I(\mathbb{Z}^d) \geq 1 \text{ for all } t \geq 0) > 0$. If the infection does not survive, then we say that the infection *dies out*.

Note that, with positive probability, all particles that are initially at the origin die out before any particle jumps into or out of the origin. So, for all $\mu > 0$ and $\lambda > 0$, the infection dies out with positive probability. That is the reason why, in the definition of survival above, we only require the infection to survive with positive probability.

Alves, Machado and Popov [2] showed that the infection survives for small enough λ in dimensions $d \geq 2$. (In fact, [2] considers the frog model in discrete time, but the proof carries through to continuous time.)

Theorem 3.6 ([2, Theorem 1.3–1.5]). *In the frog model with SIR dynamics, for $d \geq 2$ and all $\mu > 0$, there exists λ_c such that if $\lambda < \lambda_c$ then the infection survives, otherwise the infection dies out.*

They also showed that, in dimension $d = 1$, the infection dies out for any $\mu > 0$ and $\lambda > 0$.

Theorem 3.7 ([2, Theorem 1.1]). *In the frog model with SIR dynamics, for $d = 1$, all $\mu > 0$ and all $\lambda > 0$, the infection dies out almost surely.*

The above proofs can be adapted to show that in dimension $d \geq 2$ and for all $\mu > 0$, the infection survives in the SIS dynamics for all small enough λ . An open question is what happens in the SIS dynamics at very large density, since particles get immediately reinfected when they heal at sites where there are other infected particles.

Question 3.8. *In the frog model with SIS dynamics, is there a value $\mu_c < \infty$ such that, for all $\mu > \mu_c$, it happens that the infection survives for all $\lambda < \infty$?*

In Section 3.4, we will present the proof of positive speed for the frog model in $d \geq 2$, which will be a single-scale argument using a widely used techniques: comparison with percolation.

3.4 Proof of positive speed: a single-scale argument via percolation

In this section we will prove that the frog model has positive speed of propagation in the SI dynamics, which is the result we stated in Theorem 3.3. The proof we will present here is inspired by the argument used in [2], which actually establishes the phase transition in the SIR dynamics (Theorem 3.6 above). We will discuss how the proof we present here can be adapted to the SIR dynamics in Remark 3.9.

Before turning to the proof, we introduce a representation of the frog model as a percolation process, which intuitively explains why positive speed happens. Later we will see that this representation does not hold in the “standard” model of spread of infection (that is, with $D_S = D_I = 1$), which gives rise to fundamental challenges in the analysis.

3.4.1 Frog model as a percolation process

Fix a large enough value τ . For each particle of η_0 , sample a random walk path of time-length τ . That is, define a collection

$$\begin{aligned} (X_{x,i}(t))_{t \in [0, \tau]} \text{ for each } x \in \mathbb{Z}^d \text{ and } i \in \{1, 2, \dots, \eta_0(x)\}, \text{ where } X_{x,i}(0) = x \text{ and} \\ X_{x,i}(t) \text{ is the location at time } t \text{ of the } i\text{th particle that started from } x. \end{aligned} \quad (3.1)$$

With the above construction, if a particle (call it p) that starts from the origin is such that its path intersects a site x with $\eta_0^S(x) \geq 1$, which we will refer to as

$$0 \rightsquigarrow x,$$

then the particles that start from x will turn to type I within time τ . Note that it is not necessarily true that it will be p that infects the particles from x , since it could happen that, on its way to x , p infected other particles that move to x faster than p . But, undoubtedly, we obtain that the particles that start from x will get infected during the time $[0, \tau]$. So, in some sense, the frog model is an *abelian process*, which is to mean that time plays a less important role. In other words, once we have fixed the collection of paths $\{(X_{x,i}(t))_{t \in [0, \tau]} : x \in \mathbb{Z}^d, i \in \{1, 2, \dots, \eta_0(x)\}\}$, if there exists a sequence of sites x_1, x_2, \dots, x_k such that

$$0 \rightsquigarrow x_1 \rightsquigarrow x_2 \rightsquigarrow \dots \rightsquigarrow x_k,$$

then regardless of the exact times at which particles will jump (thus, regardless of the order at which particles jump), we obtain that, for each $i \in \{1, 2, \dots, k\}$, the particles in x_i turn into type I during the interval $[0, i\tau]$.

In order to show that positive speed occurs, it is enough to show that the percolation process obtained from the union of the paths $X_{x,i}$ percolate in an oriented way. That is, it suffices to show that there exists an infinite sequence of sites x_1, x_2, \dots such that

$$\|x_i\|_1 > \|x_{i-1}\|_1 \text{ for each } i \geq 2, \quad \text{and} \quad 0 \rightsquigarrow x_1 \rightsquigarrow x_2 \rightsquigarrow x_3 \rightsquigarrow \dots. \quad (3.2)$$

We refer to a path as above as an *infection path*. When such a path occurs, we obtain that $\|x_i\|_1 \geq i$ by the first part of (3.2), which then implies that the infection reaches out to a site of distance at least i from the origin by time $i\tau$. It is possible to show that, for any $\mu > 0$, such an infection path occurs if we set τ large enough and we relax the definition of the paths to allow the particles that start from the origin to move for an arbitrarily large amount of time. We will first do the proof μ large (Section 3.4.2) and then will give a more robust argument for all μ (Section 3.4.3).

3.4.2 Positive speed for μ large: oriented percolation

For didactic purpose, we will carry out the proof of Theorem 3.3 in two steps: first for large enough μ , which allows a direct comparison with oriented percolation, and then for all $\mu > 0$ via a single-scale renormalization argument.

Proof of Theorem 3.3 for large μ . We fix a value τ . Recall that $X_{x,i}(t)$ for $t \in [0, \tau]$ is the path that the i -th particle born at x perform for time t after turning to type I; see (3.1). We say that a site x is *good* (or *open*) if it contains at least one S particle at time 0 which jumps to all neighbors of x within time τ after it turned to type I. In other words, x is good if

$$\text{there exists } i \in \{1, 2, \dots, \eta_0^S(x)\} \text{ such that } X_{x,i} \supset x + \mathcal{B}_1;$$

that is, $X_{x,i}$ contains all neighbors of x .

Now, for any fixed x and i , the probability that $X_{x,i} \supset x + \mathcal{B}_1$ is bounded below by some constant $c_1 = c_1(d, \tau) > 0$. Since particles born at x move independently of one another, using the thinning property of Poisson random variables we obtain that the number of particles that are born at x and do what we specify above is a Poisson random variable of parameter μc_1 . Hence, the probability that a site is good is the probability that this Poisson random variable is at least 1, which is $1 - e^{-\mu c_1}$.

Thus, with μ large enough, we can make $1 - e^{-\mu c_1}$ strictly larger than $p_c^{\text{site}, \uparrow}(\mathbb{Z}^d)$, the critical probability for oriented site percolation on \mathbb{Z}^d . Since the event that a site is good is independent across different sites, we obtain from oriented percolation that, with positive probability, the origin is in an infinite oriented path of good sites, where by an oriented path we mean a sequence of neighboring sites x_0, x_1, x_2, \dots such that $\|x_{i+1}\|_1 = \|x_i\|_1 + 1$ for all $i \geq 0$. When the origin belongs to one such path, letting $0 = x_0, x_1, x_2, \dots$ denote this path, the fact that the origin is good implies that a particle from the origin visits all neighbors of the origin. In particular, $0 \rightsquigarrow x_1$, since x_1 is a neighbor of the origin. Hence, the infection reaches distance i from the origin in time at most τi , establishing positive speed.

If the origin is not part of an oriented path of good sites, an event that happens with positive probability, we only need to let a particle from the origin move for as long as necessary (maybe

for longer than time τ) until it reaches a site that is part of an infinite oriented path of good sites. When this happens, from that time onwards, the infection will propagate with positive speed. Since the time it takes for the particle from the origin to reach one such path is almost surely finite, the proof is completed. (This last part will be carried out in more details at the end of the full proof below). \square

3.4.3 Full proof of positive speed: single-scale renormalization

Here we present the proof of Theorem 3.3 via a single-scale renormalization. This is by now a classical argument, which has been used to establish several results, especially in percolation. We introduced the frog model exactly to present this type of argument, as it will serve as the basis of our more elaborate constructions of a multi-scale renormalization in Section 7.

We would like to mimic the proof presented in Section 3.4.2 for large μ . The problem is that if μ is small, then a site is likely to be empty of particles, and cannot directly send the infection to its neighbors. To go around this problem, we will consider large enough boxes, whose side lengths grow with μ .

Imagine a tessellation of \mathbb{Z}^d in very large boxes, and fix one such box. The box is so large that it is very likely that it has several particles from η_0^S . When this is the case and an infected particle gets inside this box, the infected particle has a good chance of visiting several of the sites hosting particles from η_0^S in the box. So such particles will get infected and will start moving. If several of them get infected, then it becomes likely that at least one of them will quickly move to a nearby box, allowing the infection to spread there as well. The goal is to show that this causes a cascading effect, similar to what happened in Section 3.4.2 when the infection reached a site belonging to an infinite oriented path of good sites. The difference is that here our aim is to show that there will be an infinite path of good *boxes*, where a good box is a box that satisfies the property mentioned above (namely, that if the infection enters the box, then it can quickly spread to nearby boxes).

Now we make the above argument rigorous. With the sole exception of the particles that start from the origin, for any other particle that gets infected, we only observe its path during a time interval of length τ after the infection, using the paths $X_{x,i}$ defined in (3.1). Now, tessellate \mathbb{Z}^d into disjoint cubes of side length L . So cube $Q(i)$ is defined as

$$Q(i) := iL + \left[-\frac{L}{2}, \frac{L}{2}\right]^d.$$

Also we define the *center* of $Q(i)$ as the inner cube of side-length $L/3$ in $Q(i)$; that is, the center of $Q(i)$ is the cube

$$Q^{\text{center}}(i) := iL + \left[-\frac{L}{6}, \frac{L}{6}\right]^d.$$

Later we will take L large with respect to μ , but for the moment just set τ as a function of L by

$$\tau := L^2.$$

For each cube we say that the cube is *good* if all the following events happen:

1. The first $L/3$ vertices of $Q(i)$ visited by infected particles contain in total at least $\mu L/6$ particles from η_0^S , call the set of such particles from η_0^S as \mathcal{P} ,
2. For each cube $Q(j)$ neighboring $Q(i)$ (that is, with $\|j - i\|_1 = 1$) at least one particle from \mathcal{P} visits $Q^{\text{center}}(j)$ within time L^2 of its infection.

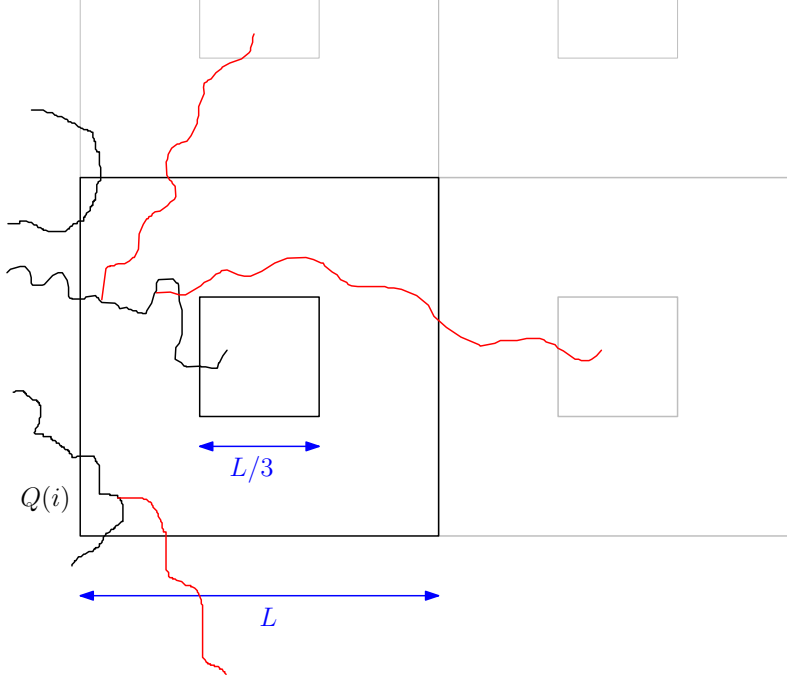


Figure 1: Definition of good cubes. The black paths represent infected particles entering the center of the cube; as they traverse the annulus of the cube they infect several particles, which then move to neighboring centers.

Note that this event gives exactly the argument we intuitively described in the beginning of the proof, where good boxes play the role of good sites. In particular, one can find an oriented path of good cubes, and if a particle from the origin visits the center of a cube in this path within time s , we have that, for any positive integer k , after time $s + k\tau = s + L^2k$ there is an infected particle from a site of distance at least $-\sqrt{s \log(s)} + (k-1)L$; the term $-\sqrt{s \log(s)}$ comes from the fact that particles that start from the origin will not move a distance larger than $\sqrt{s \log(s)}$ by time s , with probability going to 1 as $s \rightarrow \infty$. We get the term $(k-1)L$, instead of kL , because we do not know where the infection is located in the center of the first and last boxes so there could be a variation of at most $\frac{2L}{3} \leq L$. This implies that the infection will spread with speed at least

$$\liminf_{k \rightarrow \infty} \frac{-\sqrt{s \log(s)} + (k-1)L}{s + L^2k} = \frac{1}{L} > 0.$$

We wrote the above event in a more informal way, for the sake of clarity. We now turn to the proof of the theorem, where we start by presenting a construction of the frog model that will allow us to define the event that a cube is good in a more suitable way.

Full proof of Theorem 3.3. In order to show that there exists an infinite oriented path of good cubes, we would like to compare the good cubes with an independent percolation process. For this, we need that the events that $\{Q(i) \text{ is good}\}$ are independent across different i , and that the probability of each of these events is large enough.

We start with a simple observation. Note that, in the second part of the event that $\{Q(i) \text{ is good}\}$, we need to compute the probability that a particle moves from $Q(i)$ to $Q^{\text{center}}(j)$ in time L^2 , where

$\|i - j\|_1 = 1$. But, for any $x \in Q(i)$, a consequence of the local CLT (see, for example, Lemma B.1) is that

$$\sum_{y \in Q^{\text{center}}(j)} p_{L^2}(x, y) \leq \frac{c}{(L^2)^{d/2}} |Q^{\text{center}}(j)| = \frac{c(L/3)^d}{(L^2)^{d/2}} = c_1(d),$$

where we recall that $p_{L^2}(x, y)$ is the probability that a random walk starting from x is at site y at time L^2 .

Now we are ready to present the construction of the frog model. In this construction, we do not sample at time 0 the values of the random variables η_0^S . Instead, to each cube $Q(i)$, associate a pile \mathcal{L}_i of L^d independent Poisson random variables of parameter μ . Associate as well another pile, \mathcal{L}'_i , this time having infinitely many elements, where each element is an independent Bernoulli random variable of parameter c_1 . Then, when an infected particle visits for the first time a site from $Q(i)$, call this site x , then we take the first Poisson random variable from \mathcal{L}_i and set $\eta_0^S(x)$ be this number. We also remove this number from \mathcal{L}_i . In other words, we add to x as many susceptible particles as is given by the first number in \mathcal{L}_i , and remove this number from \mathcal{L}_i . Note that since there is an infected particle at x at that time, all such susceptible particles become infected. Next, we consider an ordering of the neighboring boxes of $Q(i)$, and call it the current neighbor as the first neighboring box of $Q(i)$ in the ordering. Then, for each susceptible particle that we added to x , in turn, we take one Bernoulli random variable from \mathcal{L}'_i . If one such Bernoulli random variable is equal to 1, then we couple the random walk trajectory that the particle will do during time L^2 so that it ends at the center of the current neighbor. In this case, we also switch the current neighbor to the next neighboring box in the ordering. On the other hand, if the Bernoulli random variable is equal to zero, then we will not care about what the particle will actually do, but what one needs to do is to couple the trajectory of the particle for the next L^2 steps given the information that the Bernoulli random variable is zero.

Note that, if it happens that an infected particle enters $Q^{\text{center}}(i)$, then at least $L/3$ numbers will be used from \mathcal{L}_i . If these numbers provide at least $\mu L/6$ susceptible particles, then the first $\mu L/6$ numbers from \mathcal{L}'_i will be used. And if these numbers sum to at least $2d$, we can couple the particles added in $Q(i)$ so that for each neighboring box of $Q(i)$ at least one particle will be at the center of that neighboring box after time L^2 . So, for concreteness, we say that the cube is *good* if all the following events happen:

- (E_1) The first $L/3$ numbers in \mathcal{L}_i sum to at least $\mu L/6$, and
- (E_2) The first $\mu L/6$ numbers in \mathcal{L}'_i sum to at least $2d$.

Since the above is measurable with respect to the numbers in the lists \mathcal{L}_i and \mathcal{L}'_i , and the \mathcal{L}_i and \mathcal{L}'_i are independent across different i , we have that

the events that $\{Q(i) \text{ is good}\}$ are independent across different i .

Now we compute the probability that a box is good. Note that

$$\mathbb{P}(Q(i) \text{ is bad}) = \mathbb{P}(E_1^c) + \mathbb{P}(E_2^c) = \mathbb{P}(\text{Poisson}(\mu L/3) \leq \mu L/6) + \mathbb{P}(\text{Binomial}(\mu L/6, c_1)).$$

Then a standard Chernoff bound gives that there exists a constant $c = c(d)$ such that

$$\mathbb{P}(Q(i) \text{ is bad}) \leq \exp(-c\mu L).$$

The proof is completed by noting that $\mathbb{P}(Q(i) \text{ is good})$ goes to 1 with L , so we can set L large enough so that $\mathbb{P}(Q(i) \text{ is good}) > p_c^{\text{site}, \uparrow}(\mathbb{Z}^d)$, the critical probability for oriented site percolation on \mathbb{Z}^d . So we obtain that good *boxes* percolate in an oriented way; so there exists an infinite path of boxes that is oriented in \mathbb{Z}^d . Hence, if such an infinite oriented path of good boxes contains the box centered at the origin, then we obtain that the infection spreads with positive speed as explained above.

On the other hand, if the box centered at the origin is not in an infinite path, then we proceed as follows. Consider the times s_1, s_2, \dots such that s_i is the first time that the originally infected particle from the origin reaches the boundary of a box of ℓ_∞ distance i from the origin; this distance is in term of the ℓ_∞ distance between the indices of the boxes, that is, the ℓ_∞ distance between the boxes $Q(i)$ and $Q(j)$ is $\|i - j\|_\infty$. At each s_i , the particle that is at the boundary of the given box has a positive probability of jumping all the way to the center of that box. If this happen and the box is good, then the good event is triggered because at least $L/3$ sites from the box are visited by an infected particle. Because good boxes form a supercritical oriented percolation process, there is a positive probability that this box is connected to infinity via an oriented path of good boxes. If this does not happen, then we can wait until the next time s_k , where k is the smallest value so that all boxes that were observed in the previous step are within ℓ_∞ distance $k - 1$ from the origin. And then we iterate. Since each iteration finds a percolating good box (i.e., a good box with an infinite oriented path of good boxes) with positive probability, eventually such an oriented path will be hit by the infection. \square

Remark 3.9 (SIS and SIR dynamics). We note that the above proof also establishes that SIS and SIR dynamics survive with positive probability for the frog model. For this, we only need a small change in the definition of good box. We use the thinning property of Poisson point processes to define the particle system η' which only contains the particles that move for at least time $\tau = L^2$ before healing or dying from the infection. Then, after fixing L so that $\mathbb{P}(Q(i) \text{ is good}) > p_c^{\text{site}, \uparrow}(\mathbb{Z}^d)$, we can choose λ small enough, so that $\mathbb{P}(Q(i) \text{ is good}) > p_c^{\text{site}, \uparrow}(\mathbb{Z}^d)$ even if we replace η with η' .

3.5 Proof of an upper bound on the speed

We give a linear upper bound on the speed of propagation, to show that the frog model cannot spread faster than ballistic.

Theorem 3.10 (Upper bound on the speed). *In the frog model in the SI dynamics, there exists a constant $C = C(d, \mu) > 0$ such that, for any t ,*

$$\mathbb{P}\left(\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{Ct}) \geq 1\right) \rightarrow 0 \quad \text{as } t \rightarrow \infty.$$

Before turning to the proof of the above theorem, recall that the I particles of the frog model form a branching random walk where branching occurs only at the first visit of each site. Therefore the I particles are stochastically dominated by a branching random walk which branches at each step. Since at each branching time the number of offsprings is a Poisson random variable of parameter μ , which is finite, then this branching random walk is at most ballistic. Below we will do a more direct approach to illustrate how the first moment method can be used in this case.

First, we give one definition that we will use later on as well.

Definition 3.11 (Genealogical path). A *genealogical path* p_0, p_1, \dots is a sequence of particles where particle p_i infected particle p_{i+1} ; for the definition of a genealogical path we assume that p_i is the particle that *first* infected p_{i+1} , so p_{i+1} was an S particle when p_i transmitted the infection to it. If the infection reaches distance Ct from the origin by time t , then there is a genealogical path that gets to distance Ct within time t .

Proof of Theorem 3.10. We will apply the first moment method to calculate the expected number of genealogical paths (see Definition 3.11). Instead of defining the path as a sequence of particles, we can define the path by its number k of hops (where a *hop* is meant to correspond to a transmission of the infection from one particle to the next, so that $k + 1$ is the number of particles involved in this genealogical path) and three sequences: the number of jumps $m_1, m_2, \dots, m_k \geq 1$ of each particle, the displacements $x_1, x_2, \dots, x_k \in \mathbb{Z}^d$ of each particle, and numbers $j_0, j_1, \dots, j_{k-1} \geq 1$. We impose that

$$\|x_i\|_1 \leq m_i \text{ for all } i \geq 1. \quad (3.3)$$

The path starts at x_0 , which will be taken to be the origin. We need to choose a particle to start the genealogical path. Since the site x_0 may contain several particles at time 0, we select the j_0 th particle (in some predetermined order) from x_0 to be the particle p_0 of the path. So j_0 is a number that indicates which particle we follow from the S particles present at a given site (such S particles will at that moment turn to I particles). We follow particle p_0 until it makes m_1 jumps. If at that time p_0 is not at site x_1 , then the path is not valid. Otherwise, we select the j_1 th S particle from x_1 (which became an I particle when p_0 jumped to x_1), and let this be p_1 . If the number of S particles at x_1 is smaller than j_1 , the path is not valid. We then repeat this procedure to obtain p_2, p_3, \dots ; note that p_i will be found at site $x_1 + x_2 + \dots + x_i$. This procedure ends when p_{k-1} jumps onto $x_1 + x_2 + \dots + x_k$, where the path ends.

Let G_t be the number of genealogical paths, as described above, that reach to distance Ct at time t . With x_0 being the origin, we have

$$\mathbb{E}(G_t) \leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i \geq Ct}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 \leq m_i}} \sum_{j_0, \dots, j_{k-1} \geq 1} \mathbb{P} \left(\left\{ \sum_{i=1}^k \mathcal{J}_i(m_i) \leq t \right\} \cap_{i \in J_+} \left\{ \mathcal{N}_i \geq j_i \right\} \right),$$

where $\mathcal{J}_i(m_i)$ is the time that particle p_{i-1} takes to perform m_i jumps, and \mathcal{N}_i is the number of S particles found by p_{i-1} when it jumps onto $x_1 + x_2 + \dots + x_i$. Note that $\sum_{i=1}^k \mathcal{J}_i(m_i)$ is a sum of $\sum_{i=1}^k m_i$ independent exponential random variables of rate 1, so the probability that it is smaller than t is equal to the probability that a Poisson random variable of parameter t is at least $\sum_{i=1}^k m_i$. Since \mathcal{N}_i is a Poisson random variable of mean μ , we get that

$$\begin{aligned} \mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i = M}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 \leq m_i}} \mathbb{P}(\text{Poisson}(t) \geq M) \sum_{j_0, \dots, j_{k-1} \geq 1} \prod_{i=0}^{k-1} \mathbb{P}(\text{Poisson}(\mu) \geq j_i) \\ &= \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i = M}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 \leq m_i}} \mathbb{P}(\text{Poisson}(t) \geq M) \mu^k \\ &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i = M}} \mathbb{P}(\text{Poisson}(t) \geq M) \mu^k \prod_{i=1}^k (c_d m_i)^d, \end{aligned}$$

where the equality follows from the fact that $\sum_{j=1}^{\infty} \mathbb{P}(\text{Poisson}(\mu) \geq j) = \mathbb{E}(\text{Poisson}(\mu)) = \mu$, and the last step follows from the fact that the number of sites of \mathbb{Z}^d with ℓ_1 norm at most m_i is upper bounded by $c_d m_i^d$ for some constant c_d . Now using standard bounds for the tail of Poisson random variables (cf. Lemma A.1), we get

$$\mathbb{E}(G_t) \leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i = M}} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \mu^k \prod_{i=1}^k (c_d m_i)^d.$$

Using Lagrange multipliers the product at the end is maximized when $c_d m_i = cM/k$ for all i , thus

$$\begin{aligned} \mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 1 \\ \sum_{i=1}^k m_i = M}} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \mu^k \left(\frac{cM}{k}\right)^{dk} \\ &\leq \sum_{k=1}^{\infty} \sum_{M=Ct \vee k}^{\infty} \binom{M-1}{k-1} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \mu^k \left(\frac{cM}{k}\right)^{dk} \\ &= \sum_{M=Ct}^{\infty} \sum_{k=1}^M \binom{M-1}{k-1} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \mu^k \left(\frac{cM}{k}\right)^{dk} \\ &\leq \sum_{M=Ct}^{\infty} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \sum_{k=1}^M \binom{M-1}{k-1} \left(\frac{c\mu M}{k}\right)^{dk}. \end{aligned}$$

Analyzing the derivative of $\left(\frac{c\mu M}{k}\right)^k$ as a function of k , we obtain that this term is maximized when $k = \frac{c\mu M}{e}$. Thus,

$$\begin{aligned} \mathbb{E}(G_t) &\leq \sum_{M=Ct}^{\infty} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \exp\left(\frac{cd\mu M}{e}\right) \sum_{k=1}^M \binom{M-1}{k-1} \\ &\leq \sum_{M=Ct}^{\infty} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) \exp\left(\frac{cd\mu M}{e}\right) 2^{M-1}. \end{aligned}$$

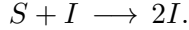
The above is at most e^{-ct} since $\log\left(\frac{M}{t}\right)$ is lower bounded by an arbitrarily large constant as C from Ct in the range of M can be set large enough with respect to μ and d . \square

4 Spread of infection

We now turn our attention to the main model here. In few words, this model corresponds to the frog model (in the SI dynamics) with $D_S = D_I = 1$. In this section, we will define the model and the quantities we are interested in, and present the results that are known. We will only start analyzing this model in Section 5.

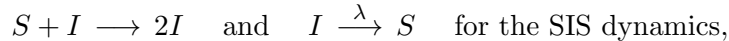
We now define the model explicitly. There are two types of particles, S (standing for *susceptible*) and I (standing for *infected*). We let η_0^S be a Poisson point process of intensity μ in \mathbb{Z}^d , and let $\eta_0^I(\mathbb{Z}^d) = \eta_0^I(0) = 1$. We set $D_S = D_I = 1$, so all particles perform independent simple random

walks on \mathbb{Z}^d from time 0, and an S particle turns to type I whenever it shares a site with an I particle. So the reaction formula is given by

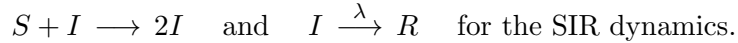


We henceforth unambiguously refer to the above process as *spread of infection*. (The frog model is also a model for the spread of an infection, but to avoid confusion we will always explicitly mention the name frog model when talking about that process, and will use the term spread of infection to refer only to the model with $D_S = D_I = 1$.)

Above we defined spread of infection with SI dynamics. As in the frog model (see Section 3.2), we can define spread of infection with SIS or SIR dynamics. Recall that these variants have an additional parameter λ and are defined by the reaction formulas



and



4.1 Challenges not presented in the frog model

The first question we might ask ourselves is whether the techniques employed in the analysis of the frog model can be made to work for the spread of infection. We will try to give a few intuitive explanations about why the spread of infection brings additional challenges to the analysis.

For simplicity assume that initially there is only one particle at the origin (the one from η_0^I), and call this particle p . Assume that p has moved for a time t , during which it traversed a space-time path γ without encountering any S particle. Assume also that p jumps at time t to a site x where it has not been before. In the frog model, we have that the number of S particles found at x at time t is a Poisson random variable of intensity μ . The only information one needs to infer this is that x is not visited by γ .

On the other hand, in the spread of infection, the number of particles at x is also a Poisson random variable, but the intensity is different. The intensity is given by μ times the probability that a random walk starting from x at time t , and moving backwards in time from time t to 0, does so without colliding with the space-time path γ . So this intensity heavily depends on the shape of γ . In other words, as we observe the particle system, we gain information about the environment of S particles beyond the sites that were observed.

4.2 Main results with SI dynamics

As in the frog model, the main question we will address is whether there is *positive speed* for the infection.

Definition 4.1 (Positive speed). We say that infection spreads with *positive speed* if for all large enough t there is an infected particle of distance larger than ct from the origin, for some constant c . In other words, there exists a constant $c = c(d, \mu) > 0$ such that

$$\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{ct}) \geq 1 \text{ for all large enough } t, \text{ almost surely,}$$

where we recall that \mathcal{B}_r stands for a ball of radius r centered at the origin.

The study of the spread of infection was already being discussed and promoted in the 70s by Spitzer. However, the first rigorous treatment of this question appeared only in the early 2000s with Kesten and Sidoravicius, who published a series of articles related to this question. In the first of their paper [22], they analyzed the branching random walk with catalysts model (which we will discuss in Section 9.1.3). They developed an intricate multi-scale analysis, which serves as the basis of the multi-scale analysis developed in their later works, and became a very influential technique in the analysis of several particle systems. In particular, Kesten and Sidoravicius adapted this multi-scale analysis to show in [23] that the infection spreads with positive speed.

Theorem 4.2 (Positive speed [23]). *There exists $c = c(d, \mu) > 0$ such that, almost surely, $\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{ct}) \geq 1$ for all large enough t .*

We will give the proof of the above theorem later in Section 7. The proof we will present here will be different (and slightly simpler) than the one in [23]; it will follow a multi-scale renormalization scheme. We present this alternative proof since the technique of multi-scale renormalization has already found application to the analysis of several other processes, including random interacements [37], activated random walks [34], random walks in changing environments [19], multi-particle diffusion limited aggregation [33], and even percolation [10].

In Section 8 we will discuss a more powerful multi-scale analysis which is closer in spirit to the one of Kesten and Sidoravicius, and which has been further developed by Stauffer [36] and Gracar and Stauffer [17, 16]. These two extensions, in particular [17], put the multi-scale analysis into a percolation framework, through the construction of a geometrical structure called a *Lipschitz surface*.

Kesten and Sidoravicius also showed a shape theorem for the set of vertices visited by infected particles [25]. This is one of the few instances where a shape theorem was proved for a model which is not subadditive². We will not provide a proof of the shape theorem, as it goes beyond the scope of our discussion here. But, for the sake of completeness, we will state this result. For this, let A_t be the set of sites of \mathbb{Z}^d which were infected at least once during $[0, t]$; that is,

$$A_t = \left\{ x \in \mathbb{Z}^d : \exists s \in [0, t] \text{ for which } \eta_s^I(x) \geq 1 \right\}.$$

Then extend A_t to \mathbb{R}^d by adding cubes of side length 1 centered at the sites of A_t to obtain

$$\tilde{A}_t = \bigcup_{x \in A_t} \left(x + [-1/2, 1/2]^d \right).$$

Theorem 4.3 ([25]). *In the SI dynamics, for any $d \geq 1$ and any $\mu > 0$, there exists a compact subset \mathcal{S} of \mathbb{R}^d such that for any $\varepsilon > 0$ we have*

$$(1 - \varepsilon)\mathcal{S} \subset \frac{\tilde{A}_t}{t} \subset (1 + \varepsilon)\mathcal{S} \text{ for all } t \text{ large enough, almost surely.}$$

In dimension one, Bérard and Ramírez [7] proved a central limit theorem for the so-called *front* of the infection (that is, the rightmost infected particle). It is shown in [7] via a regeneration argument that the fluctuations of the front of the infection (around the value given by the shape theorem) are Gaussian. See also [21] for a survey on spread of infection and the frog model.

²This is another illustration of a difference between the spread of infection and the frog model discussed in Section 3. While the frog model is subadditive, the spread of infection is not.

4.3 SIS dynamics

Using a similar multi-scale analysis as in [23], Kesten and Sidoravicius showed in [24] that in the SIS dynamics the infection survives if λ (the rate of healing) is small enough.

Definition 4.4 (Survival of the infection). We say that the infection *survives* if

$$\mathbb{P}\left(\eta_t^I(\mathbb{Z}^d) \geq 1 \text{ for all } t \geq 0\right) > 0.$$

If the infection does not survive, then we say that the infection *dies out*.

Theorem 4.5 (Survival of the infection in SIS [24]). *In the SIS dynamics, for $d \geq 1$, for all $\mu > 0$, there exists λ_c such that if $\lambda < \lambda_c$ then the infection survives with positive probability.*

They showed the converse case if the SIS dynamics is changed slightly. They assume that a particle does not get immediately reinfected when it goes from I to S in a site with other I particles. Instead, they assume that a particle can only get infected if it jumps onto an infected particle or if an infected particle jumps onto it (so only jumps of particles can trigger an infection). Under this assumption, [24] also established that if $\lambda > \lambda_c$, then the infection dies out almost surely.

In the model we consider, with instantaneous reinfections, it is an open problem to say whether there are large enough densities for which the infection survives regardless of λ .

Question 4.6. *In the SIS dynamics, is there a value $\mu_c < \infty$ such that for all $\mu > \mu_c$ the infection survives for all $\lambda < \infty$?*

4.4 SIR dynamics

It is an open problem to establish a phase transition in the SIR dynamics. This is particularly challenging since the particle system obtained after removing R particles is not anymore stationary. It is not difficult to convince oneself that such a phase transition cannot occur in dimension 1; for this case, the infection dies out almost surely for any $\mu > 0$ and any $\lambda > 0$. The main reason is that it takes time t for the infection to reach to distances of order t from the origin (due to the positive speed of propagation, which is true even without particles dying), but it takes an amount of time of order only $\log t$ for a set of t particles to die (this holds because the probability that a given particle survive for time at least s after being infected is $e^{-\lambda s}$). So, if the number of infected particles is very large, it should tend to decrease in a short amount of time. As a consequence, as the infection spreads, the set of infected particles will be comprised of two small sets of order 1 (one forming the left front and the other forming the right front). Eventually these two small sets will die before transmitting the infection any further.

Question 4.7. *In the SIR dynamics, for any $d \geq 2$ and any $\mu > 0$, is there a value $\lambda_c > 0$ such that for all $\lambda < \lambda_c$ the infection survives, whereas for all $\lambda > \lambda_c$ the infection dies out?*

4.5 Random conductance model

In [17, 16], Gracar and Stauffer showed that a certain percolation structure that they call *Lipschitz surface* occurs, and using this they showed that the infection spreads with positive speed in the random conductance model. In this model, we equip \mathbb{Z}^d with i.i.d. conductances. We will consider

the conductances to be *uniformly elliptic*, which means that there are constants $0 < c < c' < \infty$ so that all conductances are in the interval $[c, c']$. Then, particles move as simple random walks, but when a particle decides to jump, it chooses a neighbor with probability proportional to the conductance of the edge between them.

Theorem 4.8 (Positive speed for random conductances [17, 16]). *Let $d \geq 2$, and consider the random conductance model with uniformly elliptic conductances. For any $\mu > 0$, there exists $c = c(d, \mu) > 0$ such that, almost surely, $\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{ct}) \geq 1$ for all large enough t .*

Gracar and Stauffer also showed that in the SIS dynamics the infection survives when λ is small.

Theorem 4.9 (Survival of the infection in SIS in the random conductance [17, 16]). *Let $d \geq 2$, and consider the random conductance model with uniformly elliptic conductances. In the SIS dynamics, for all $\mu > 0$, there exists λ_c such that if $\lambda < \lambda_c$ then the infection survives with positive probability.*

4.6 Different initial configurations

In [21] it is left as an open problem to establish positive speed when the initial configuration of S particles is not i.i.d. Poisson. This question has not been addressed explicitly. However, it is implied by the proof of Gracar and Stauffer [17, 16], which we stated above in Theorem 4.8. We will discuss this in Section 8, when we present the technique of Lipschitz surface from [17]. Given an initial configuration of S particles $\omega \in \mathbb{N}^{\mathbb{Z}^d}$, we let \mathbb{P}_ω be the measure induced by the SI dynamics starting from ω and one additional I particle at the origin.

Theorem 4.10 (Positive speed with general starting configurations). *Let $d \geq 2$. For any $\mu > 0$, let ν_μ be the measure of a Poisson point process on \mathbb{Z}^d and $c = c(\mu, d)$ be a constant. Then, for any $t > 0$, there exists $\Omega_t \subset \mathbb{N}^{\mathbb{Z}^d}$ with $\nu_\mu(\Omega_t) \rightarrow 1$ as $t \rightarrow \infty$ such that starting from a configuration $\omega \in \Omega_t$ we obtain that $\mathbb{P}_\omega(\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{ct}) \geq 1) \rightarrow 1$ as $t \rightarrow \infty$.*

4.7 $D_S \neq D_I$ with $D_S, D_I > 0$

One of the main open problems left by Kesten and Sidoravicius [23] (see also [21]) is to establish positive speed when $D_S \neq D_I$ but both rates are positive. In fact, papers in the physics literature conjecture that the speed depend only on D_I .

Question 4.11. *In the SI dynamics, is there positive speed when $D_S \neq D_I$ with $D_S, D_I > 0$? Moreover, does the speed depend only on D_I ?*

4.8 Zero range process

In [5], Baldasso and Teixeira analyzed the case where the particle system move according to a zero range process in dimension $d = 1$. In this case, under mild conditions, which guarantee the existence of a non-trivial invariant measure for the particle system, they were able to show that the infection spreads with positive speed. Their proof involve a multi-scale renormalization argument. This model falls out of the scope of these notes, so we refer the reader to [5] for more information.

5 First proofs for the spread of infection

In this section we give some initial proofs for the problem of spread of infection with $D_S = D_I = 1$ in the SI dynamics. In Section 5.1 we show that the infection cannot spread faster than ballistic, which refines the first moment method described for the corresponding proof for the frog model in Section 3.5. Next, in Section 5.2, we show that by time t the infection reaches a distance of order at least $\frac{t}{(\log t)^c}$ from the origin. This result will build upon the single-scale argument used to prove positive speed for the frog model, given in Section 3.4.3, and will serve as a basis for the multi-scale renormalization we will develop to show the actual positive speed in Section 7.

5.1 Upper bound on the speed

We give a linear upper bound on the speed of propagation, to show that the infection cannot travel faster than ballistic. A similar argument is given in [23].

Theorem 5.1 (Upper bound on the speed). *There exists a constant $C = C(d, \mu) > 0$ such that, for any t ,*

$$\mathbb{P}\left(\eta_t^I(\mathbb{Z}^d \setminus \mathcal{B}_{Ct}) \geq 1\right) \rightarrow 0 \quad \text{as } t \rightarrow \infty.$$

Remark 5.2. It is possible to prove the above theorem with a comparison to a branching random walk. This is because each time an I particle jumps to a given site z which is not occupied by I particles, then

$$\begin{aligned} &\text{the number of S particles at } z \text{ at time } t \text{ is a Poisson random variable of mean} \\ &\mu \text{ times the probability that a particle at } z \text{ at time } t \text{ was not infected before.} \end{aligned} \quad (5.1)$$

So this number is stochastically dominated by a Poisson random variable of mean μ . With this, we obtain that the set of infected particles is stochastically dominated by a branching random walk with finite expected offspring. The maximum displacement of such branching random walks is ballistic, which gives a linear upper bound on the speed of propagation. Below we will do a more direct approach, using a careful first moment method.

We start by recalling the definition of a genealogical path.

Definition 5.3 (Genealogical path). A *genealogical path* p_0, p_1, \dots is a sequence of particles where particle p_i infected particle p_{i+1} ; for the definition of a genealogical path we assume that p_i is the particle that *first* infected p_{i+1} , so p_{i+1} was an S particle when p_i transmitted the infection to it. If the infection reaches distance Ct from the origin by time t , then there is a genealogical path that gets to distance Ct within time t .

Proof of Theorem 5.1. The proof here uses a (non-immediate, but tedious) first moment method. It resembles the corresponding proof for the frog model (Theorem 3.10), but there are additional details. To make the proof here self-contained, we will repeat some definitions. Nonetheless, it may be helpful to look at the proof of Theorem 3.10 since the proof strategy is the same and the argument there is simpler. Our strategy will be to apply a first moment method to calculate the expected number of genealogical paths (cf. Definition 5.3).

Instead of defining the path as a sequence of particles, we can define the path by its number k of hops (as before, a *hop* corresponds to a transmission of the infection from one particle to the next

one in the path) and three sequences: the number of jumps $m_1, m_2, \dots, m_k \geq 0$ of each particle, the displacement $x_1, x_2, \dots, x_k \in \mathbb{Z}^d$ of each particle, and numbers $j_0, j_1, \dots, j_{k-1} \in \mathbb{Z} \setminus \{0\}$. We impose that

$$\|x_i\|_1 \leq m_i \text{ for all } i \geq 1. \quad (5.2)$$

Note that, unlike in the proof of the frog model, we allow the m_i to be zero and the j_i to be negative; we will explain this below.

The path starts at x_0 , which will be taken to be the origin, but x_0 may contain several particles at time 0, so we select the j_0 th particle (in some predetermined order) from x_0 to be the particle p_0 of the path. We will always have $j_0 \geq 1$, and the j_i will represent the number of the particle we will start to follow, with negative and positive values meaning different sets of particles as we explain now. We follow particle p_0 until it makes m_1 jumps. If at that time p_0 is not at site x_1 , then the path is not valid. Otherwise, we consider the value of j_1 . If $j_1 > 0$, we look at all the particles in x_1 that were S particles immediately before p_0 jumped to x_1 . If the number of such particles is smaller than j_1 , the path is not valid. Otherwise, we select the j_1 th such S particle (which became an I particle when p_0 jumped to x_1), and let this be p_1 . If, on the other hand, $j_1 < 0$, then we count how many S particles jump onto x_1 before p_0 jumps out of x_1 . If that number is smaller than $-j_1$, the path is not valid. Otherwise, we select the $(-j_1)$ th such particle and let it be p_1 . We repeat this procedure to obtain p_2, p_3, \dots ; note that p_i will be found at site $x_1 + x_2 + \dots + x_i$. This procedure ends when p_{k-1} jumps onto $x_1 + x_2 + \dots + x_k$, where the path ends. Since in the frog model S particles do not move, the case of an S particle jumping on a site with an I particle does not occur. We add the possibility of having j_i negative to take such cases into consideration. Because of this one may also have $m_i = 0$.

In fact, if $m_i = 0$, it means that p_{i-1} will not jump; hence, x_i is the origin. In this case, p_i will be a particle that jumps onto p_{i-1} before p_{i-1} jumps out of $x_1 + x_2 + \dots + x_{i-1}$. In other words,

$$\text{for any } i \geq 1, \text{ if } m_i = 0, \text{ we have } j_i < 0. \quad (5.3)$$

Moreover, when $j_i < 0$, we know that when particle p_{i-1} is at site $y := x_1 + x_2 + \dots + x_i$, it has to wait S particles to jump onto y . In order to model this, we will give a Poisson clock to p_{i-1} of rate $1 + \mu$, with 1 being the rate at which p_{i-1} jumps out of y and μ being an upper bound on the rate at which S particles jump onto y ; see (5.1).

We will refer to this Poisson clock as the *clock* of p_{i-1} . Each time this Poisson clock rings, a decision has to be made: with probability at least $\frac{1}{1+\mu}$ we make p_{i-1} jump out of y , and with probability at most $\frac{\mu}{1+\mu}$ we make an S particle jumps onto y . We refer to this as the *jump decision* of p_{i-1} . We recall the following useful property of Poisson processes:

$$\text{jump decisions and the time between rings of the clock are independent random variables.} \quad (5.4)$$

Let G_t be the number of genealogical paths, as described above, that reach to distance Ct at time t . Given j_1, j_2, \dots, j_k , let J_- denote the set of i such that $j_i < 0$, and J_+ denote the set of i such

that $j_i > 0$. Then, with x_0 being the origin, we have

$$\begin{aligned}
\mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i \geq Ct}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 = m_i}} \sum_{j_0, \dots, j_{k-1} \in \mathbb{Z} \setminus \{0\}} \\
&\quad \mathbb{P} \left(\left\{ \sum_{i=1}^k \mathcal{J}_i(m_i) + \sum_{i \in J_-} \mathcal{W}_i(-j_i) \leq t \right\} \cap_{i \in J_+} \left\{ \mathcal{N}_i \geq j_i \right\} \cap_{i \in J_-} \left\{ \mathcal{D}_i > -j_i \right\} \right) \\
&\leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i \geq Ct}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 = m_i}} \sum_{j_0, \dots, j_{k-1} \in \mathbb{Z} \setminus \{0\}} \\
&\quad \mathbb{P} \left(\left\{ \sum_{i=1}^k \mathcal{J}_i(m_i) \leq t \right\} \cap_{i \in J_+} \left\{ \mathcal{N}_i \geq j_i \right\} \cap_{i \in J_-} \left\{ \mathcal{D}_i > -j_i \right\} \right),
\end{aligned}$$

where $\mathcal{J}_i(m_i)$ is the time that particle p_{i-1} takes to perform m_i jumps, $\mathcal{W}_i(-j_i)$ (valid only for $j_i < 0$) is the time for the clock of p_{i-1} to ring $-j_i$ times, \mathcal{N}_i is the number of S particles found by p_{i-1} when it jumps onto $x_1 + x_2 + \dots + x_i$, and \mathcal{D}_i is the number of jump decisions taken by p_{i-1} before p_{i-1} decides to jump out of $x_1 + x_2 + \dots + x_i$. Using 5.4, all these variables are independent, which gives

$$\begin{aligned}
\mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i \geq Ct}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 = m_i}} \sum_{j_0, \dots, j_{k-1} \in \mathbb{Z} \setminus \{0\}} \mathbb{P} \left(\sum_{i=1}^k \mathcal{J}_i(m_i) \leq t \right) \\
&\quad \prod_{i \in J_+} \mathbb{P}(\mathcal{N}_i \geq j_i) \prod_{i \in J_-} \mathbb{P}(\mathcal{D}_i > -j_i) \quad (5.5)
\end{aligned}$$

Using (5.1) we have that \mathcal{N}_i is stochastically dominated by a Poisson random variable of parameter μ , thus

$$\prod_{i \in J_+} \mathbb{P}(\mathcal{N}_i \geq j_i) \leq \prod_{i \in J_+} \mathbb{P}(\text{Poisson}(\mu) \geq j_i). \quad (5.6)$$

Moreover, \mathcal{D}_i is a geometric random variable of success probability $\frac{1}{1+\mu}$, which yields

$$\prod_{i \in J_-} \mathbb{P}(\mathcal{D}_i > -j_i) = \prod_{i \in J_+} \left(\frac{\mu}{1+\mu} \right)^{-j_i} = \left(\frac{\mu}{1+\mu} \right)^{\sum_{i \in J_+} |j_i|}. \quad (5.7)$$

Note that

$$\sum_{j \in \mathbb{Z} \setminus \{0\}} \mathbb{P}(\text{Poisson}(\mu) \geq j) \left(\frac{\mu}{1+\mu} \right)^{|j| \mathbf{1}(j < 0)} = \sum_{j=1}^{\infty} \left(\mathbb{P}(\text{Poisson}(\mu) \geq j) + \left(\frac{\mu}{1+\mu} \right)^j \right) = 2\mu.$$

Using this, and plugging (5.6) and (5.7) into (5.5), we sum over all values of j_i to obtain

$$\begin{aligned}
\mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i \geq Ct}} \sum_{\substack{x_1, \dots, x_k \\ \|x_i\|_1 = m_i}} \mathbb{P} \left(\sum_{i=1}^k \mathcal{J}_i(m_i) \leq t \right) (2\mu)^k \\
&\leq \sum_{k=1}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i \geq Ct}} \mathbb{P} \left(\sum_{i=1}^k \mathcal{J}_i(m_i) \leq t \right) (2\mu)^k \prod_{i=1}^k (1 + c_d m_i)^d,
\end{aligned}$$

where the last step follows since, for any m_i , there are at most $(1 + c_d m_i)^d$ sites x_i with $\|x_i\|_1 \leq m_i$. Now note that $\sum_{i=1}^k \mathcal{J}_i(m_i)$ is a sum of $\sum_{i=1}^k m_i$ exponential random variables of rate 1, so the probability that this sum is at most t is equal to the probability that a Poisson random variable of parameter t is larger than $\sum_{i=1}^k m_i$. Denoting $\sum_{i=1}^k m_i$ by M , we obtain

$$\begin{aligned} \mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i = M}} \mathbb{P}\left(\sum_{i=1}^k \mathcal{J}_i(m_i) \leq t\right) (2\mu)^k \prod_{i=1}^k (1 + c_d m_i)^d \\ &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i = M}} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) (2\mu)^k \prod_{i=1}^k (1 + c_d m_i)^d, \end{aligned}$$

where in the last step we used standard bounds for the tail of Poisson random variables (cf. Lemma A.1). Using Lagrange multipliers the product at the end is maximized when $1 + c_d m_i = cM/k$ for all i , thus

$$\begin{aligned} \mathbb{E}(G_t) &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \sum_{\substack{m_1, \dots, m_k \geq 0 \\ \sum_{i=1}^k m_i = M}} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) (2\mu)^k \left(\frac{cM}{k}\right)^{dk} \\ &= \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \binom{M+k-1}{k-1} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) (2\mu)^k \left(\frac{cM}{k}\right)^{dk} \\ &\leq \sum_{k=1}^{\infty} \sum_{M=Ct}^{\infty} \exp\left(-cM \log\left(\frac{M}{t}\right)\right) 2^M (4\mu)^k \left(\frac{cM}{k}\right)^{dk}, \end{aligned} \tag{5.8}$$

where in the last inequality we used the simple bound $\binom{M+k-1}{k-1} \leq 2^{M+k}$. Now note that

$$\sum_{k=1}^{\infty} (4\mu)^k \left(\frac{cM}{k}\right)^{dk} \leq \sum_{k=1}^{\infty} \left(\frac{4c\mu M}{k}\right)^{dk}.$$

Since the term in the sum is maximized when $k = \frac{4c\mu M}{e} < 2c\mu M$, we obtain

$$\begin{aligned} \sum_{k=1}^{\infty} \left(\frac{4c\mu M}{k}\right)^{dk} &\leq 4c\mu M \exp\left(\frac{4cd\mu M}{e}\right) + \sum_{k=4c\mu M}^{\infty} \left(\frac{4c\mu M}{k}\right)^{dk} \\ &\leq \exp(c'\mu M) + 2^{-4dc\mu M} \\ &\leq \exp(2c'\mu M). \end{aligned}$$

Plugging the above bound into (5.8), we get

$$\mathbb{E}(G_t) \leq \sum_{M=Ct}^{\infty} \exp\left(-cM \log\left(\frac{M}{t}\right) + c\mu M\right),$$

which is at most $e^{-c't}$ if the constant C in the range of M is large enough with respect to μ and d . \square

5.2 Almost tight lower bound on speed of propagation

Before establishing the positive speed result (which we will do in Section 7), we first show in this section that the infection cannot spread much slower than linear in time.

Theorem 5.4 (Almost linear lower bound on the speed). *Let $c = \frac{d+2}{d}$, then for any $t > 0$ we have*

$$\mathbb{P} \left(\eta_t^I \left(\mathbb{Z}^d \setminus \mathcal{B}_{\frac{t}{(\log t)^c}} \right) \geq 1 \right) \rightarrow 1 \quad \text{as } t \rightarrow \infty.$$

To prove the above theorem, we will try to employ a similar strategy as the one we used to obtain the positive speed for the frog model in Theorem 3.3. The first challenge we encounter is that when the infection gets inside a box, the number of S particles present in that box depends on the time the infection entered the box. This is a crucial difference with the frog model, in which it was enough to look at the S particles that started in that box (which does not change over time since S particles do not move). To go around this (and other problems) we will need a more subtle definition of boxes. We will develop the framework now before going into the details of the proof.

5.2.1 Space-time tessellation

We will need to define boxes in space and time; that is, boxes will be subsets of $\mathbb{Z}^d \times \mathbb{R}$. Tessellate space-time into boxes of spatial length L and time length $S := \delta L^2$, where δ will be a small enough constant that we will fix first, and then let L be large enough. So, for each $i \in \mathbb{Z}^d$ and $\tau \in \mathbb{Z}$, we obtain a box

$$Q(i, \tau) := \left(iL + \left[-\frac{L}{2}, \frac{L}{2}\right]^d \right) \times (\tau S + [0, S]). \quad (5.9)$$

We define the *base* of box $Q(i, \tau)$ as the center of the box in space at the first time of the box:

$$Q^{\text{base}}(i, \tau) := \left(iL + \left[-\frac{L}{6}, \frac{L}{6}\right]^d \right) \times \{\tau S\} \subset Q(i, \tau).$$

We will sometimes abuse notation and use $Q^{\text{base}}(i, \tau)$ to denote the subset of \mathbb{Z}^d induced by the space-time region above.

We now define the event that a box is good. Inspired by the definition of a good box in the proof for the frog model in Section 3.4.3, we would like to define $Q(i, \tau)$ to be good in a way that if there is an I particle (call it p_0) at $Q^{\text{base}}(i, \tau)$, then p_0 spreads the infection to several other particles in $Q(i, \tau)$, and then for each neighboring box of $Q(i, \tau)$ at least one of such newly infected particles move to that box. So the amount of time S that $Q(i, \tau)$ spans is split into two intervals: the first one $[\tau S, \tau S + S']$ during which p_0 infects several other particles, and then $[\tau S + S', (\tau + 1)S]$ during which the newly infected particles move to neighboring boxes. The problem is that during the first interval, the probability that a particle meets p_0 is not independent from the probability that another particle meets p_0 . For example, if p_0 moves atypically quickly and exits the box, it could happen that p_0 does not meet any of the particles. In order to control this probability, we will consider a more restrictive event, where the particles that could meet p_0 are forced to be well spreadout in the box.

First, consider the following box contained in $Q(i, \tau)$:

$$Q^{\text{half}}(i, \tau) := \left(iL + \left[-\frac{L}{4}, \frac{L}{4}\right]^d \right) \times (\tau S + [0, S']). \quad (5.10)$$

Note that $Q^{\text{half}}(i, \tau)$ is a space-time region, where the spatial region is given by a cube with half the size of the spatial region of $Q(i, \tau)$, which motivates the choice of notation. Note also that

$$Q^{\text{base}}(i, \tau) \subset Q^{\text{half}}(i, \tau) \subset Q(i, \tau).$$

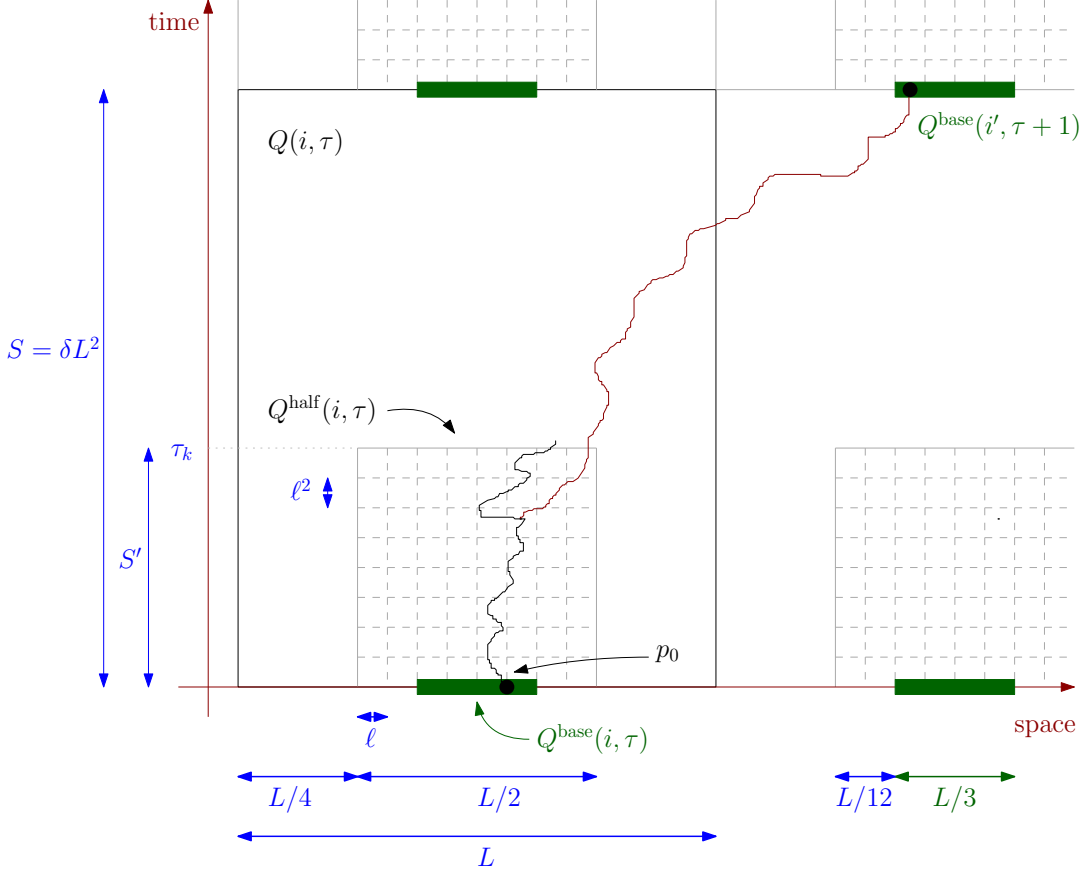


Figure 2: Definition of the space-time region $Q(i, \tau)$ and its division in $Q^{\text{base}}(i, \tau)$ (the green line segment) and $Q^{\text{half}}(i, \tau)$ (the tessellated region). The infected particle p_0 departs from $Q^{\text{base}}(i, \tau)$ and while moving within $Q^{\text{half}}(i, \tau)$ encounters several other particles (to whom p_0 transmits the infection). At least one such particle then moves to $Q^{\text{base}}(i', \tau + 1)$ where $Q(i', \tau + 1)$ is a neighbor of $Q(i, \tau)$ (that is, $\|i - i'\|_1 = 1$).

Now we tessellate $(iL + [-\frac{L}{4}, \frac{L}{4}]^d)$, the spatial region of $Q^{\text{half}}(i, \tau)$, into disjoint sub-boxes of side length ℓ ; refer to Figure 2. We set $k = \frac{S'}{\ell^2}$, we assume that k is an integer and then, for each $j \in \{0, 1, 2, \dots, k\}$, we set the times $\tau_j = \tau S + j\ell^2$. Thus $\tau_k = \tau S + S'$.

Definition 5.5 (Good boxes). Fix a box $Q(i, \tau)$. Assume that there is an infected particle (which we distinguish from the others) in $Q^{\text{base}}(i, \tau)$, and call it p_0 . For each $j \in \{1, 2, \dots, k\}$, let p_j be one particle (chosen according to some arbitrary order) that is at the same site as p_0 at time τ_j and is different from p_0, p_1, \dots, p_{j-1} ; if p_0 is alone at a site at time τ_j or only shares a site with particles from $\{p_1, p_2, \dots, p_{j-1}\}$, we set $p_j = \emptyset$. Given a constant $c_1 = c_1(\mu, d) > 0$, we say that $Q(i, \tau)$ is good if the following events all hold:

(E_1) For each $j \in \{1, 2, \dots, k\}$, the distinguished particle p_0 is inside $Q^{\text{half}}(i, \tau)$ at time τ_j .

- (E₂) For each sub-box and each $j \in \{0, 1, 2, \dots, k-1\}$, there are at least $\frac{\mu \ell^d}{2}$ particles at the sub-box at time τ_j ; call this set of particles \mathcal{P}_j but select exactly $\mu \ell^d / 2$ particles from each sub-box to put into \mathcal{P}_j .
- (E₃) For each $j \in \{0, 1, 2, \dots, k-1\}$, the particles of \mathcal{P}_j are inside $Q(i, \tau)$ at time $\tau S + S'$.
- (E₄) For each $j \in \{1, 2, \dots, k\}$, if $M_j = \mathbf{1}(p_j \neq \emptyset)$, then $\sum_{j=1}^k M_j \geq c_1 k$.
- (E₅) For each neighboring box $Q(i', \tau + 1)$ of i (thus $\|i' - i\|_1 = 1$), one of the particles from $\{p_1, p_2, \dots, p_k\}$ go to $Q^{\text{base}}(i', \tau + 1)$.

Despite being already a much more involved definition of a good box than the one we had for the frog model, this definition is still not strong enough. The issue is that we need to define the event above so that it does not depend on the particles outside of $Q(i, \tau)$; in particular, this is not at all clear as we are looking at a distinguished *infected* particle p_0 , whose existence depends on the whole spread of infection up to time τS . We will stick with the above definition for the moment not to overload the proof with technical constructions. Afterwards, in Section 5.2.4, we explain a construction that can be used to take care of this issue.

Remark 5.6. In fact, it would suffice to define a box $Q(i, \tau)$ to be good if just the events E_4 and E_5 hold, while the events E_1, E_2 and E_3 could appear only inside the proof that establishes that $E_4 \cap E_5$ holds with high probability. But we chose to define the event that $Q(i, \tau)$ is good in a more explicit manner so as to highlight the intermediate steps used to establish $E_4 \cap E_5$.

5.2.2 Probability of good boxes

Later we will take L to be large enough, but now we set S' and ℓ as functions of L by the following relations:

$$S' = L, \quad \ell = \left(\frac{L}{\delta}\right)^{\frac{1}{d+2}}. \quad (5.11)$$

We choose the relation above because $S' = L$ will be a good choice for us later on, when we will use this event in the multi-scale analysis, whereas the choice for ℓ is made to optimize the bound in the lemma below.

Lemma 5.7. *Fix a box $Q(i, \tau)$ and let ℓ and S' be as in (5.11). Then for any small enough δ there exists a constant $c = c(\mu, d, \delta)$ so that*

$$\mathbb{P}(Q(i, \tau) \text{ is bad}) \leq \exp\left(-cL^{\frac{d}{d+2}}\right),$$

for all large enough L .

Proof. First, we write

$$\mathbb{P}(Q(i, \tau) \text{ is bad}) \leq \mathbb{P}(E_1^c) + \mathbb{P}(E_2^c) + \mathbb{P}(E_3^c \cap E_2) + \mathbb{P}(E_4^c \cap E_1 \cap E_2) + \mathbb{P}(E_5^c \cap E_3 \cap E_4). \quad (5.12)$$

For E_1 , we use the union bound on $i \in \{1, 2, \dots, k\}$ and then the bounds on the displacement of random walks (cf. Lemma B.1) to obtain

$$\begin{aligned} \mathbb{P}(E_1^c) &\leq \sum_{j=1}^k \mathbb{P}\left(p_0 \text{ is outside } Q^{\text{half}}(i, \tau) \text{ at time } \tau_j\right) \\ &\leq \sum_{j=1}^k \exp\left(-\frac{c'(L/12)^2}{S'}\right) \leq \frac{S'}{\ell^2} \exp\left(-\frac{c'(L/12)^2}{S'}\right). \end{aligned} \quad (5.13)$$

We will only apply the relation in (5.11) at the very end. The only thing that we need to keep in mind here from (5.11) is that the terms outside the exponential (which are polynomial in L) can be easily absorbed in the constant c' . For E_2 , we use that the particle system is in stationarity, which means that the number of particles at a given sub-box is a Poisson random variable of intensity μ . Hence, taking the union bound on all sub-boxes (in space and time), and using a Chernoff bound for Poisson random variables (cf. Lemma A.2) we have

$$\mathbb{P}(E_2^c) \leq \left(\frac{(L/2)^d}{\ell^d}\right) \left(\frac{S'}{\ell^2}\right) \mathbb{P}\left(\text{Poisson}(\mu\ell^d) \leq \frac{\mu\ell^d}{2}\right) \leq \left(\frac{(L/2)^d}{\ell^d}\right) \left(\frac{S'}{\ell^2}\right) \exp(-c\mu\ell^d). \quad (5.14)$$

For E_3 , we again use the union bound on all sub-boxes (in space and time) and the union bound on all $\frac{\mu\ell^d}{2}$ particles inside each sub-box, a fact that is given by E_2 . Then, each such particle has to traverse a distance of at least $L/4$, which is the distance between the spatial region of $Q^{\text{half}}(i, \tau)$ and the boundary of the spatial region of $Q(i, \tau)$ (refer to Figure 2). Thus, using the bounds on the displacement of random walks (cf. Lemma B.1), we have

$$\begin{aligned} &\mathbb{P}(E_3^c \cap E_2) \\ &\leq \left(\frac{(L/2)^d}{\ell^d}\right) \left(\frac{S'}{\ell^2}\right) \left(\frac{\mu\ell^d}{2}\right) \mathbb{P}(\text{a random walk moves more than } L/4 \text{ in time at most } S') \\ &\leq \left(\frac{(L/2)^d}{\ell^d}\right) \left(\frac{S'}{\ell^2}\right) \left(\frac{\mu\ell^d}{2}\right) \exp\left(-\frac{c'(L/4)^2}{S'}\right). \end{aligned} \quad (5.15)$$

The event E_4 is a little bit more delicate. First let x_1, x_2, \dots, x_k be the location of p_0 at times $\tau_1, \tau_2, \dots, \tau_k$. Since we are under E_1 , we have that $x_j \in Q^{\text{half}}(i, \tau)$ for all j . From now on, we just fix x_1, x_2, \dots, x_k . Note that $M_j = \mathbf{1}(p_j \neq \emptyset)$. Now since $x_j \in Q^{\text{half}}(i, \tau)$, there exists a sub-box that contains x_j . Denote by R_j the spatial region of this sub-box (thus, $x_j \in R$). Since there are at least $\frac{\mu\ell^d}{2}$ particles inside R_j at time τ_{j-1} , the probability that one given such particle is at x_j at time τ_j is at least

$$\frac{c}{(\ell^2)^{d/2}}$$

since the distance between two sites inside the same sub-box is at most $\sqrt{d}\ell$ and $\tau_j - \tau_{j-1} = \ell^2$; here we apply the local CLT stated in Lemma B.1. Now we use the fact that there are at least $\frac{\mu\ell^d}{2}$ particles in R_j at time τ_{j-1} and, in fact, there are at least $\frac{\mu\ell^d}{2} - j$ particles if we disregard p_1, p_2, \dots, p_{j-1} . But using the value of S' and the fact that δ can be set small enough with respect to μ , we have

$$\frac{\mu\ell^d}{2} - j \geq \frac{\mu\ell^d}{2} - \frac{S'}{\ell^2} = \frac{\mu\ell^d}{2} - \frac{\delta\ell^{d+2}}{\ell^2} \geq \frac{\mu\ell^d}{3}.$$

Thus the probability that at least one of the particles is at x_j at time τ_j is at least

$$1 - \left(1 - \frac{c}{(\ell^2)^{d/2}}\right)^{\frac{\mu\ell^d}{2} - j} \geq 1 - \left(1 - \frac{c}{(\ell^2)^{d/2}}\right)^{\frac{\mu\ell^d}{3}}. \quad (5.16)$$

The important property is that there exists a constant $c_2 \in (0, 1)$ depending only on μ and d (and not on ℓ) so that

$$1 - \left(1 - \frac{c}{(\ell^2)^{d/2}}\right)^{\frac{\mu \ell^d}{3}} \geq c_2. \quad (5.17)$$

So, we would like to claim that for each j there is a probability at least c_2 that M_j is 1. Then, by setting c_1 smaller than c_2 and using concentration for the sum of the M_j we would like to claim that E_4 holds with very large probability. The problem is that the M_j are not independent of one another and, in fact, the events E_1 and E_2 depend on the configuration of particles during the whole of $[\tau_0, \tau_k]$. We go around this by refining the events E_1 and E_2 , and changing the definition of M_j . For each $j \in \{1, 2, \dots, k\}$, we define the events

$$E_{1,j} = \left\{x_j \in Q^{\text{half}}(i, \tau)\right\},$$

and

$$E_{2,j} = \left\{\text{at time } \tau_{j-1} \text{ each sub-box has at least } \frac{\mu \ell^d}{2} \text{ particles}\right\}.$$

Note that $E_1 = \bigcap_{j=1}^k E_{1,j}$ and $E_2 = \bigcap_{j=1}^k E_{2,j}$. We now change the definition of M_j by defining the event

$$\bar{M}_j = \mathbf{1}(\{p_j \neq \emptyset\} \cup E_{1,j}^c \cup E_{2,j}^c),$$

and we have that

$$\mathbb{P}(E_4^c \cap E_1 \cap E_2) \leq \mathbb{P}\left(\sum_{j=1}^k \bar{M}_j < c_1 k\right).$$

Now let \mathcal{F}_j be the σ -algebra produced by $\bar{M}_{j'}$ for $j' \in \{1, 2, \dots, j-1\}$. Since \mathcal{F}_j includes only events that happen up to time τ_{j-1} for the particles that are not p_0 , for any $F \in \mathcal{F}_j$ we obtain that

$$\begin{aligned} \mathbb{P}(\bar{M}_j = 1 \mid F) &= \mathbb{P}(\bar{M}_j = 1 \mid F \cap E_{1,j} \cap E_{2,j}) \mathbb{P}(E_{1,j} \cap E_{2,j} \mid F) \\ &\quad + \mathbb{P}(\bar{M}_j = 1 \mid F \cap \{E_{1,j}^c \cup E_{2,j}^c\}) \mathbb{P}(\{E_{1,j}^c \cup E_{2,j}^c\} \mid F) \\ &= \mathbb{P}(\bar{M}_j = 1 \mid F \cap E_{1,j} \cap E_{2,j}) \mathbb{P}(E_{1,j} \cap E_{2,j} \mid F) + \mathbb{P}(\{E_{1,j}^c \cup E_{2,j}^c\} \mid F) \\ &\geq \mathbb{P}(\bar{M}_j = 1 \mid F \cap E_{1,j} \cap E_{2,j}) \geq c_2, \end{aligned}$$

where the second-last inequality follows since the line above is a linear combination between $\mathbb{P}(\bar{M}_j = 1 \mid F \cap E_{1,j} \cap E_{2,j})$ and 1, and the last inequality follows from (5.16) and (5.17). So the sum $\sum_{j=1}^k \bar{M}_j$ stochastically dominates the sum of i.i.d. Bernoulli random variables of parameter c_2 . Therefore, using a Chernoff bound for Binomial random variables (see Lemma A.3), we have

$$\mathbb{P}(E_4^c \cap E_1 \cap E_2) \leq \mathbb{P}(\text{Binomial}(k, c_2) < c_1 k) \leq \exp(-ck). \quad (5.18)$$

Finally, for E_5 , we just need to notice that under E_3 and E_4 , we find $c_1 k$ infected particles at time τ_k inside $Q^{\text{half}}(i, \tau)$. So their distance to $Q^{\text{base}}(j', \tau)$ (in ℓ_1 norm) is at most $d(L + L/12)$. Since $S - S'$ is of order S , we can use the local CLT (cf. Lemma B.1) to obtain that each infected particle will be inside $Q^{\text{half}}(i, \tau)$ with probability at least

$$\frac{c(L/3)^d}{(S - S')^{d/2}} \geq c'.$$

Hence,

$$\mathbb{P}(E_5^c \cap E_3 \cap E_4) \leq \exp(-ck). \quad (5.19)$$

Now plugging (5.13), (5.14), (5.15), (5.18) and (5.19) into (5.12), and using the values of ℓ and S' completes the proof. \square

5.2.3 Finishing the proof of Theorem 5.4

Proof of Theorem 5.4. Mimicking the proof for the frog model, we would like to find an infinite (in space and time) path of good boxes. Even though Lemma 5.7 gives that, by setting L large enough, we can make the probability of a given box being good arbitrarily close to 1, the event that a box is good is not independent from other boxes. This prevents us from comparing directly with oriented percolation, as we did in the frog model. To illustrate this dependence, note that the event E_2 requires several particles to be present in the base of a box. If a very large region in space (say, for example, of side-length $100L$) is empty of particles at time 0, it is likely that, during a time interval of length S , the bulk of this region (that is, away from the boundary) will remain empty of particles. This implies that correlations do not decay exponentially fast, which in fact establishes that the set of good boxes cannot be shown to stochastically dominate a (Bernoulli, independent) percolation process. It is exactly to circumvent this problem that multi-scale arguments have been developed. We will explain some of them in Sections 7 and 8.

Here we will resort to a simpler solution, we will allow L to be large enough not only with respect to μ and d but also with respect to t , in order to show that all boxes we need to look at up to time t will be good (via a simple application of the union bound). First, note that if all boxes are good in the space-time region $[-t^2, t^2] \times [0, t]$, then at time t the infection reaches distance $\frac{t}{S}L - L/6$, where the negative term is to account for the distance between the infection and the boundary of the base in the last box. Now it remains to set $L = c(\log t)^{\frac{d+2}{d}}$, where c is a large enough constant depending on μ and d . Then, applying Lemma 5.7 and taking the union bound over all boxes, the probability that all boxes in $[-t^2, t^2] \times [0, t]$ are good is at least

$$1 - \left(\frac{2t^2}{L}\right)^d \left(\frac{t}{S}\right) \exp(-c \log t) \rightarrow 1, \quad \text{as } t \rightarrow \infty. \quad (5.20)$$

□

Remark 5.8. In the proof above, if it had turned out that L were independent of t , then we would have established positive speed since the speed obtained is

$$\frac{\frac{t}{S}L - L/6}{t} \rightarrow \frac{1}{\delta L}, \quad \text{as } t \rightarrow \infty \text{ with } L \text{ fixed.}$$

However, L is not independent of t . If we were to set L to be independent of t , then the probability that a box is good would not be close enough to 1 to apply the union bound in (5.20). This implies that if we set L to be independent of t , then the infection will enter bad boxes. In fact, if we set L independent of t , we will observe clusters of bad boxes of arbitrarily large size as time goes to infinity. The multi-scale arguments we explain in Sections 7 and 8 will give a way to control the location of bad boxes, to show that the good boxes are much more numerous and drastically overwhelm the negative effect that bad boxes may produce.

5.2.4 Defining good boxes formally

We give a more pedantic definition of the event that a box is good, given in Definition 5.5. For each box $Q(i, \tau)$, and each site $x \in Q(i, \tau)$, associate to x a random walk path $\gamma_x: [\tau S, (\tau + 1)S] \rightarrow \mathbb{Z}^d$ of time length S . If there is an infected particle in $Q^{\text{base}}(i, \tau)$, we choose one of them (according to some pre-defined order of the sites in $Q^{\text{base}}(i, \tau)$), and let this particle move from τS to $(\tau + 1)S$ using the path γ_x , where x is the location of that particle in $Q^{\text{base}}(i, \tau)$. Then we replace the event E_1 from Definition 5.5 by the event

(E'_1) For each $x \in Q^{\text{base}}(i, \tau)$, $\gamma_x \subset Q^{\text{half}}(i, \tau)$.

By taking the union bound on $x \in Q^{\text{base}}(i, \tau)$ it follows that one can obtain a bound of the same order as the one obtained for E_1 in (5.13). Similarly, the event E_4 can be replaced by

(E'_4) For each $x \in Q^{\text{base}}(i, \tau)$ and each $j \in \{1, 2, \dots, k\}$, if M_j is the indicator for the event that there is a particle from $\mathcal{P}_{j-1} \setminus \{p_1^x, p_2^x, \dots, p_{j-1}^x\}$ at $\gamma_x(\tau_j)$, where p_j^x being the particle found at time $\tau_{j'}$ at site $\gamma_x(\tau_{j'})$, then $\sum_{j=1}^k M_j \geq c_1 k$.

By taking the union bound on $x \in Q^{\text{base}}(i, \tau)$ it follows that one can obtain a bound of the same order as the one obtained for E_4 in (5.18).

With these two changes, the event that a box is good does not depend on how the infection evolved before time τS .

6 Local mixing

In this section we will show a very important technique to control dependences on this model. In particular, we will show that if inside a box there is a large enough density of particle, with some density β , then after some time the configuration of particles inside the box (away from the boundary) is “sandwiched” between two Poisson process of densities $(1 - \varepsilon)\beta$ and $(1 + \varepsilon)\beta$. Intuitively, this gives a way to claim that the particles get close to stationary locally (deep within the box).

This kind of argument was introduced by Sinclair and Stauffer in [35]. It also appeared in [29, 36], and was adapted to the random conductance model in [16]. The version we present here is due to Popov and Teixeira, who generalized the argument in [35] to apply to random interlacements, and did that developing a very nice framework.

Theorem 6.1 (Local mixing). *Let Q be a cube of side length L , tessellated into sub-cubes of side length ℓ . Assume that at time 0 each sub-cube contains at least $\beta_- \ell^d$ and at most $\beta_+ \ell^d$ particles from η_0 , and that $\eta_0(\mathbb{Z}^d \setminus Q) = 0$. Let particles move for time T as independent random walks. There are constants $c_1, c_2, c_3 > 0$ such that, for any $\varepsilon > 0$, if $T \geq \frac{c_1 \ell^2}{\varepsilon^2}$ any we take $Q' \subset Q$ with $d(Q', \partial Q) \geq c_2 \sqrt{T \log \varepsilon^{-1}}$, letting Ψ_+ and Ψ_- be Poisson point processes on Q' independent of η_0 of intensity $(1 + \varepsilon)\beta_+$ and $(1 - \varepsilon)\beta_-$, respectively, there exists a coupling $\tilde{\mathbb{P}}$ between Ψ_+, Ψ_- and η_T so that*

$$\tilde{\mathbb{P}}(\forall S \subseteq Q' \Psi_-(S) \leq \eta_T(S) \leq \Psi_+(S)) \geq 1 - \exp\left(-c_3 \varepsilon^2 \beta_- T^{d/2}\right).$$

We note that in the local mixing theorem (Theorem 6.1), the location of the particles of η_0 can be arbitrarily correlated. As long as each sub-box satisfies the density condition, it is possible to recover Poisson point processes after letting particles move for a time interval of order ℓ^2 , which is the time necessary for particles to be able to move to neighboring sub-cubes.

Before moving to the proof of Theorem 6.1, we describe two ideas.

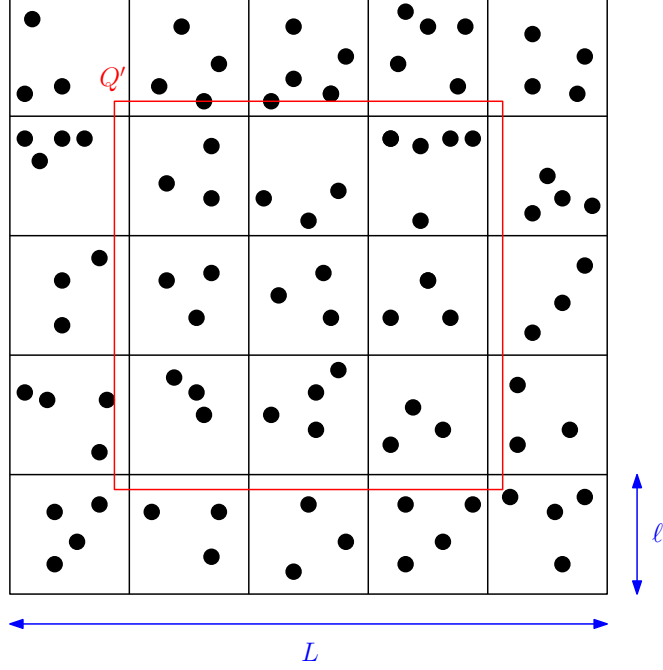


Figure 3: Illustration of the local mixing theorem with $\beta_- \ell^d = 3$ and $\beta_+ \ell^d = 5$.

6.1 Coupling of Poisson point processes

Fix values $\lambda_+ > \lambda_- > 0$. We describe a standard procedure to couple two Poisson point processes Ψ_+ and Ψ_- of intensity λ_+ and λ_- , respectively, so that

$$\Psi_+ \supseteq \Psi_- . \tag{6.1}$$

Let Ω be the space on which the two processes are defined. We just sample a Poisson point process of intensity one in $\Omega \times \mathbb{R}_+$; so points have the form $(\psi_i, h_i)_i$ and h_i is denoted the *height* of point ψ_i . Then all points of height at most λ_- belong to Ψ_- and all points of height at most λ_+ belong to Ψ_+ . Since $\lambda_+ > \lambda_-$ we establish (6.1). See Figure 4.

6.2 Simulating a random variable via a Poisson point process

Let X be a random variable on Ω with density function $g: \Omega \rightarrow \mathbb{R}_+$. Here we show how to sample X using a Poisson point process Ψ of intensity 1 on $\Omega \times \mathbb{R}_+$.

First sample Ψ and let $(\psi_i, h_i)_i$ be the points of Ψ . Define

$$\xi := \inf \{ \varphi > 0 : \exists i \text{ for which } \varphi g(\psi_i) \geq h_i \} .$$

We extend the above definition for any $S \subseteq \Omega$, by writing

$$\xi^S := \inf \{ \varphi > 0 : \exists i \text{ for which } \varphi g(\psi_i) \geq h_i \text{ and } \psi_i \in S \} . \tag{6.2}$$

Note that $\xi = \xi^\Omega$.

Then the lemma below establishes the construction of X as ψ_i .

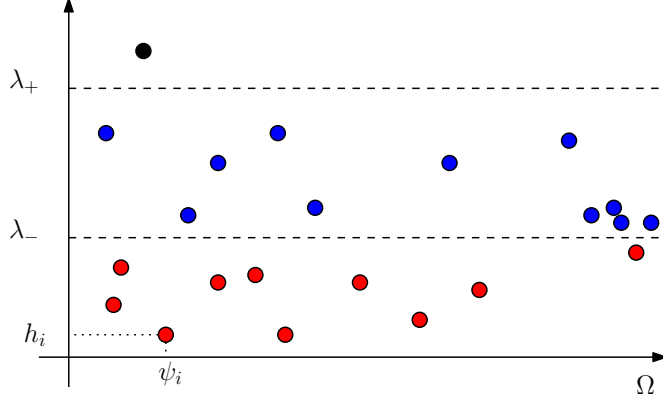


Figure 4: Illustration of the coupling of two Poisson point processes. Ψ_+ comprises the blue and red points, whereas Ψ_- comprises only the red points.

Lemma 6.2. *Given Ψ, X, g and ξ as above, we obtain the following properties. Then there exists a unique i such that $\xi g(\psi_i) = h_i$, and the distribution of ψ_i is g .*

Proof. The uniqueness of i follows from standard properties of Poisson processes. Let $\text{Exp}(\nu)$ denote an exponential random variable of rate ν . Then, for any $S \subset \Omega$, we obtain

$$\mathbb{P}(X \in S) = \mathbb{P}(\xi^{S^c} > \xi^S) = \mathbb{P}\left(\text{Exp}\left(\int_{S^c} g\right) > \text{Exp}\left(\int_S g\right)\right) = \frac{\int_S g}{\int_S g + \int_{S^c} g} = \int_S g.$$

□

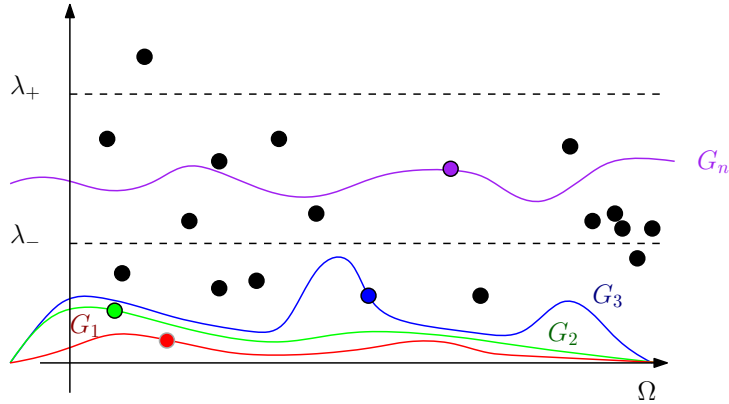


Figure 5: Illustration of how variables X_1, X_2, \dots can be sampled using a Poisson point process. The red, green, blue and purple lines represent the graphs of the functions G_1, G_2, G_3 and G_n , respectively. The colored points indicates the points of the Poisson point process that is intersected by each colored line.

If we have a sequence of random variables X_1, X_2, \dots to be sampled in order, and if g_i is the density of X_i conditioned on the values of X_1, X_2, \dots, X_{i-1} , then the above procedure can be used replacing (6.2) by

$$\xi_i^S := \inf\{\varphi > 0: \exists i \text{ for which } h_i \in (G_{i-1}(\psi_i), G_{i-1}(\psi_i) + \varphi g_i(\psi_i))\},$$

where $G_i: \Omega \rightarrow \mathbb{R}_+$ is defined as

$$G_0 \equiv 0 \quad \text{and} \quad G_i := \sum_{j=1}^i \psi_j g_j = G_{i-1} + \psi_i g_i. \quad (6.3)$$

Then if after sampling X_1, X_2, \dots, X_n we have that for all $\psi \in \Omega$ it holds that $G_n(\psi) \in (\lambda_-, \lambda_+)$, then X_1, \dots, X_n stochastically dominates a Poisson point process of intensity λ_- and are stochastically dominated by a Poisson point process of intensity λ_+ , which are coupled as described in Section 6.1; see Figure 5.

6.3 Proof of local mixing

Proof of Theorem 6.1. Now we put the ideas of the previous two sections together to proof Theorem 6.1. We let $\Omega = Q'$. Assume that each sub-cube has exactly $\beta \ell^d$ particles (so $\beta = \beta_- = \beta_+$). Here we will establish the lower bound $\eta_T \supseteq \Psi_-$; the proof for the upper bound is identical. We move the $n := \beta \ell^d$ particles in Q one by one, and let X_i be the location of the i th particle at time T . Let g_i be the density function of X_i . Since particles move independently, g_i is the same regardless of the values of X_1, X_2, \dots, X_{i-1} . In order to establish the theorem we will derive a lower bound for the following probability:

$$\mathbb{P}(\forall z \in Q' \ G_n(z) \geq (1 - \varepsilon)\beta) \geq 1 - \sum_{z \in Q'} \mathbb{P}(G_n(z) < (1 - \varepsilon)\beta),$$

where G_n is defined in (6.3). Now for a given $z \in Q'$ and any $\theta > 0$, we use Chernoff bound to write

$$\begin{aligned} \mathbb{P}(G_n(z) < (1 - \varepsilon)\beta) &= \mathbb{P}\left(\exp(-\theta G_n(z)) > \exp(-\theta(1 - \varepsilon)\beta)\right) \\ &\leq \exp(\theta(1 - \varepsilon)\beta) \mathbb{E}(\exp(-\theta G_n(z))) \\ &= \exp(\theta(1 - \varepsilon)\beta) \prod_{i=1}^n \mathbb{E}(\exp(-\theta \xi_i g_i(z))) \\ &= \exp(\theta(1 - \varepsilon)\beta) \prod_{i=1}^n \left(\frac{1}{1 + \theta g_i(z)}\right), \end{aligned}$$

where in the second last step we used the definition of G_n and the fact that the ξ_i are independent, and in the last step that ξ_i are exponential random variables of rate 1. We can now use the fact that $\log(1 + x) \geq x - x^2$ for all $x \in (0, 1/2)$ to write the fraction in a different way. For simplicity, we will just use that $\log(1 + x) \geq x(1 - \varepsilon/2)$ for x small enough. Thus,

$$\text{we will require that } \theta g_i(z) \leq \frac{\varepsilon}{100} \text{ for all } i, z, \quad (6.4)$$

allowing us to write

$$\mathbb{P}(G_n(z) < (1 - \varepsilon)\beta) \leq \exp\left(\theta(1 - \varepsilon)\beta - (1 - \varepsilon/2)\theta \sum_{i=1}^n g_i(z)\right). \quad (6.5)$$

We now turn to deriving a lower bound for $\sum_{i=1}^n g_i(z)$. Let B denote a sub-cube, and let x_i be the location of the i th particle at time 0. For each B , let I_B denote the values of i for which $x_i \in B$; hence, $|I_B| = \beta \ell^d$ for all B . Note that

$$\sum_{i=1}^n g_i(z) = \sum_B \sum_{i \in I_B} p_T(x_i, z) = \sum_B \sum_{i \in I_B} p_T(z, x_i).$$

Using Lemma B.2, and writing $\bar{p}_B = \frac{1}{\ell^d} \sum_{x \in B} p_T(z, x)$ the average value of $p_T(x, z)$ across $x \in B$, we obtain

$$\sum_{i=1}^n g_i(z) \geq \sum_B \sum_{i \in I_B} \bar{p}_B \exp\left(-\frac{d\ell^2}{2T}\right) = \sum_B \beta \ell^d \bar{p}_B = \beta \exp\left(-\frac{d\ell^2}{2T}\right) \sum_{x \in Q} p_T(z, x).$$

Since $z \in Q'$, we obtain

$$\sum_{i=1}^n g_i(z) \geq \beta \exp\left(-\frac{d\ell^2}{2T}\right) \left(1 - e^{-\frac{cc_2 T \log \varepsilon^{-1}}{T}}\right) \geq \beta(1 - \varepsilon^2).$$

Plugging this bound into (6.5), we finally obtain

$$\begin{aligned} \mathbb{P}(G_n(z) < (1 - \varepsilon)\beta) &\leq \exp(\theta(1 - \varepsilon)\beta - (1 - \varepsilon/2)\theta\beta(1 - \varepsilon^2)) \\ &\leq \exp\left(-\frac{\varepsilon\beta\theta}{3}\right). \end{aligned}$$

We can still set θ and it is enough to set θ as large as possible, with the constraint given by (6.4). Since $g_i(z) \geq \frac{c}{T^{d/2}}$, we can set θ of the order of $\varepsilon T^{d/2}$, which completes the proof. \square

7 Multi-scale renormalization

Here we establish the positive speed of propagation for the infection, Theorem 4.2, via a multi-scale renormalization argument. This type of multi-scale argument has been widely used to analyze several models, most notably the model of random interlacements, where it already appeared when Sznitman introduced the model in [37].

We will make one simplification in this section. We will assume that

$$\begin{aligned} &\text{there is a constant } C > 0 \text{ such that, } \textit{almost surely}, \text{ for any time } t \in \mathbb{R} \text{ and any } s \geq 0 \\ &\text{each particle moves distance at most } Cs \text{ during the time interval } [t, t + s]. \end{aligned} \quad (7.1)$$

At the end, in Section 7.6 we discuss how to get rid of this assumption.

Now we start by introducing a tessellation very similar to the one in the proof of the almost positive speed in Theorem 5.4. We recommend the reader to first look at the proof of Theorem 5.4 before continuing, as several aspects of that proof will be used here.

7.1 Defining scale 1

We fix a small constant δ and a large number L . The value of δ is fixed first, and then we take L large enough later.

Partition space-time into boxes of spatial length $L/3$ and time length $S_1 := \delta L^2$. Then we construct boxes of spatial length L and time length S_1 so that the box $Q_1(i, \tau)$ is given by

$$Q_1(i, \tau) := \left(i\frac{L}{3} + \left[-\frac{L}{2}, \frac{L}{2}\right]^d\right) \times (\tau S_1 + [0, S_1]).$$

Note that this is different from the definition of the space-time boxes in Section 5.2, which is given in (5.9), because here boxes overlap. In particular, the boxes in Section 5.2 were disjoint

(disregarding boxes that overlap only at their boundaries), whereas here each box overlaps with other 3^d boxes. This will be essential because here we will necessarily run into bad boxes. Thus, as we are following an infected particle and it enters a bad box, we will have little control on how the infection spreads inside this box. So we cannot guarantee that an infected particle will be present in a neighboring box. What we will do in such situations is to keep following the same infected particle as it traverses the bad box. When the time of that box ends, the infected particle will be somewhere in Z^d , but the way our tessellation is defined guarantees that the particle will be at the “base” of *some* box, where we define the *base* of $Q_1(i, \tau)$ as

$$Q_1^{\text{base}}(i, \tau) := \left(i \frac{L}{3} + \left[-\frac{\varepsilon L}{6}, \frac{\varepsilon L}{6} \right]^d \right) \times \{\tau S_1\};$$

hence, for any given τ , the base of the boxes $Q(\cdot, \tau)$ tessellate Z^d . For any set Λ in space-time, we define its spatial projection as

$$\mathcal{S}(\Lambda) = \left\{ x \in \mathbb{Z}^d : \exists s \in \mathbb{R} \text{ for which } (x, s) \in \Lambda \right\}.$$

Now we define the event that $Q_1(i, \tau)$ is good.

Definition 7.1. Assume that there is an infected particle in $Q_1^{\text{base}}(i, \tau)$, which we denote by p_0 . Let $S' = L$. We say that $Q(i, \tau)$ is good if the following holds:

1. Considering only the particles located in $Q(i, \tau)$ at time τS_1 , during the time interval $[\tau S_1, \tau S_1 + S']$, p_0 transmits the infection to at least $c_1 L^{\frac{d}{d+2}}$ such particles, for some fixed constant $c_1 = c_1(d, \mu)$.
2. For each box $Q(i', \tau + 1)$ with $\|i' - i\|_\infty = 3$ (so $\mathcal{S}(Q(i, \tau))$ and $\mathcal{S}(Q(i', \tau + 1))$ intersect in a set of dimension at most $d - 1$), one of the infected particles above go to $Q^{\text{base}}(i', \tau + 1)$.

The events above are essentially events E_4 and E_5 in Definition 5.5, where ℓ has been replaced by its value $\left(\frac{L}{\delta}\right)^{\frac{1}{d+2}}$ and δ is a small constant. For an illustration, see figure 2 in the proof of Theorem 5.4, and for a more thorough description on how this event can be defined so that it is measurable locally see Section 5.2.4. Note that the event $\{Q(i, \tau) \text{ is good}\}$ is an *increasing event*, in the sense that if $\{Q(i, \tau) \text{ is good}\}$ for a certain configuration, then $\{Q(i, \tau) \text{ is good}\}$ also holds if we add one particle to the previous configuration.

The lemma below gives the probability that a box is bad.

Lemma 7.2. *Fix a box $Q(i, \tau)$. Then, for small enough c_1 in Definition 7.1, there is a constant $c = c(d, \mu, c_1) > 0$ so that, for any L large enough,*

$$\mathbb{P}(Q_1(i, \tau) \text{ is bad}) \leq \exp(-cL^{\frac{d}{d+2}}).$$

Proof. The proof is essentially identical to the proof of Lemma 5.7. The main difference is that here we restrict to the particles located in $Q(i, \tau)$ at time τS_1 . We proceed as follows. We tessellate $\mathcal{S}(Q(i, \tau))$ into cubes of side length $L^{1/3}$ and require that each such cube has at least $\frac{9\mu L^{d/3}}{10}$ particles at time τS_1 . Now, using the local mixing result (Theorem 6.1) from time τS_1 to any given time $s \in [\tau S_1 + S'/2, \tau S_1 + S']$ (where we recall that $S' = L$), the particles that are “deep inside” $\mathcal{S}(Q(i, \tau))$ at time s (that is, away from the boundary of $\mathcal{S}(Q(i, \tau))$, for example, inside a region

analogous to Q^{half} from (5.10)) stochastically dominate a Poisson point process of intensity at least $\frac{8\mu}{9}$ with probability at least

$$1 - \exp\left(-cL^{d/2}\right).$$

Since $L^{d/2}$ is much larger than $L^{\frac{d}{d+2}}$ for all $d \geq 1$, applying the local mixing is not going to change the final probability that a box is good. Then, we apply local mixing and the union bound for all values of s of the type τ_j (see the proof of Lemma 5.7) inside the interval $[\tau S_1 + S'/2, \tau S_1 + S']$, where we skipped the interval $[\tau S_1, \tau S_1 + S'/2]$ to leave enough time for local mixing to take place. \square

7.2 Defining higher scales

Now we develop a multi-scale renormalization framework. We introduce boxes at higher scales by setting $L_1 = L$ and, for $k \geq 2$, defining

$$L_k := C_L k^{10d} L_{k-1}, \quad (7.2)$$

with C_L being a fixed and large constant, which may depend on L , and the exponent $10d$ being just a large number that we have not tried to optimize. (For concreteness it will be enough for our purpose to take $C_L = L^2$.) The variable k will be an index for the scale (so, the larger k , the larger the scale is). Note that the scale grows faster than exponential, since

$$L_k = C_L k^{10d} L_{k-1} = C_L^2 (k(k-1))^{10d} L_{k-2} = C_L^{k-1} (k!)^{10d} L_1.$$

We will see that setting the scales to grow exponentially fast (such as $L_k = CL_{k-1}$ for some constant C) will not be enough here. For $k \geq 2$, we also set

$$S_k := \delta L L_k, \quad (7.3)$$

and define the space time box $Q_k(i, \tau)$ as

$$Q_k(i, \tau) := \left(i \frac{L_k}{3} + \left[-\frac{L_k}{2}, \frac{L_k}{2} \right]^d \right) \times (\tau S_k + [0, S_k]).$$

with its *enlargement*

$$Q_k^{\text{enlarge}}(i, \tau) := \left(i \frac{L_k}{3} + \left[-\frac{5L_k}{8}, \frac{5L_k}{8} \right]^d \right) \times \{\tau S_k\}. \quad (7.4)$$

Note that $\mathcal{S}(Q_k^{\text{enlarge}}(i, \tau))$ is a cube of side length $\frac{5L_k}{4}$ and

$$\text{the distance between } \mathcal{S}(Q_k(i, \tau)) \text{ and } \partial \mathcal{S}(Q_k^{\text{enlarge}}(i, \tau)) \text{ is } \frac{L_k}{8}. \quad (7.5)$$

7.3 Good boxes at higher scales

Before defining what a good box at higher scale is, we discuss the general strategy which gives a kind of recipe for defining good boxes at higher scale at most applications of this multi-scale renormalization argument. Then we will need to tweak the definition of good boxes (which usually depend on the exact application one has in mind) so that we end with the definition we will need.

7.3.1 Recipe for defining good boxes at higher scales

The general strategy is to impose a condition of the following type: fix a positive integer a and define

$$Q_k(i, \tau) \text{ is } \textit{bad} \text{ if it contains at least } a \text{ } \textit{disjoint} \text{ bad boxes of scale } k-1. \quad (7.6)$$

Sometimes the word *disjoint* is replaced by *well separated*, as this is used with a lemma establishing that disjoint (or well separated) boxes are roughly independent; this will be evident when we bound the probability that a box is good in Section 7.4. Henceforth we fix $a = 2$, as this will be enough for our purposes. However, a usually depends on the application: one just carries out the whole calculation using the variable a , and then discovers what the requirement is needed from a .

The intuition behind (7.6) is the following. Let $\tilde{\rho}_k$ be the probability that a box of scale k is bad. (We use the notation $\tilde{\rho}_k$ instead of ρ_k , because ρ_k will be defined slightly different later on to represent the probability that a box of scale k is bad.) Then, if disjoint boxes were *independent* of one another, we get that

$$\tilde{\rho}_k \leq \left(\left(\frac{L_k}{L_{k-1}/3} \right)^d \frac{S_k}{S_{k-1}} \right)^2 \tilde{\rho}_{k-1}^2,$$

where the combinatorial term $\left(\left(\frac{L_k}{L_{k-1}/3} \right)^d \frac{S_k}{S_{k-1}} \right)^2$ just counts the number of ways to choose two boxes of scale $k-1$ inside a box of scale k , and $\tilde{\rho}_{k-1}^2$ is the probability that two disjoint boxes of scale $k-1$ are bad, assuming independence. (The two powers of 2 in the equation above would become a if we did not have $a = 2$.) Continuing the recursion we get

$$\tilde{\rho}_k = \tilde{\rho}_1^{2^{k-1}} \prod_{i=1}^{k-1} \left(\left(\frac{L_{k+1-i}}{L_{k-i}/3} \right)^d \frac{S_{k+1-i}}{S_{k-i}} \right)^{2^i}.$$

Then the hope is that the term in the product is much smaller than the first term. One can usually prove this by induction. First, assume that $\tilde{\rho}_k \leq \tilde{\rho}_1^{C_k 2^{k-1}}$, where C_k is to be set later, and note that for $k = 1$ this is true by setting $C_1 = 1$. Assume that this is true for all values up to $k-1$. Then, for $\tilde{\rho}_k$ one does

$$\begin{aligned} \tilde{\rho}_k &\leq \left(\left(\frac{L_k}{L_{k-1}/3} \right)^d \frac{S_k}{S_{k-1}} \right)^2 \tilde{\rho}_{k-1}^2 \\ &\leq \left(\left(\frac{L_k}{L_{k-1}/3} \right)^d \frac{S_k}{S_{k-1}} \right)^2 \tilde{\rho}_1^{2C_{k-1}2^{k-2}} \\ &= \left(\left(\left(\frac{L_k}{L_{k-1}/3} \right)^d \frac{S_k}{S_{k-1}} \right)^2 \tilde{\rho}_1^{(C_{k-1}-C_k)2^{k-1}} \right) \tilde{\rho}_1^{C_k 2^{k-1}}. \end{aligned} \quad (7.7)$$

At this point, one tries to take C_k decreasing with k so that $C_{k-1} - C_k$ is positive but not too close to zero to have $(C_{k-1} - C_k) 2^{k-1}$ to be a large power in the $\tilde{\rho}_1$ term, making the term inside the parenthesis smaller than 1 (so that the combinatorial term gets killed). At the same time, C_k cannot decrease too quickly with k , because we also need that $\liminf_{k \rightarrow \infty} C_k > 0$. But this can be easily achieved; for example, we can choose $C_k = C_{k-1} - \frac{1}{k^2}$. Then, if all the above works out, for $C_* = \liminf_{k \rightarrow \infty} C_k$, we establish

$$\tilde{\rho}_k \leq \tilde{\rho}_1^{C_* 2^{k-1}}.$$

Our problem (and the problem to be faced in essentially all applications of a multi-scale analysis), of course, is that the disjoint boxes are not independent at all. Therefore, we will obtain a recursion of the type

$$\tilde{\rho}_k \leq (\text{“combinatorial term”})^2 (\tilde{\rho}_{k-1}^2 + \text{“error term”}),$$

where the “error term” will express how well we can control the dependences between two disjoint boxes. We will try to make the error term smaller than $\tilde{\rho}_{k-1}^2$, which would yield

$$\tilde{\rho}_k \leq (\text{“combinatorial term”})^2 2\tilde{\rho}_{k-1}^2,$$

so the two can be incorporated into the combinatorial term and all the reasoning above would go through.

7.3.2 Actual definition of good boxes

In order to control the error term, we will need to enrich the definition of bad boxes given in (7.6). Recall the definition of the enlargement of a box in (7.4).

Definition 7.3. The box $Q_k(i, \tau)$ is *good* if, considering only the particles that are inside $Q_k^{\text{enlarge}}(i, \tau)$ to decide whether boxes of scale $k-1$ in $Q_k(i, \tau)$ are good or bad, $Q_k(i, \tau)$ does not contain 2 *disjoint* bad boxes of scale $k-1$.

Note that since the spatial center of a box of scale k is $i\frac{L_k}{3}$, cubes of side length $\frac{L_k}{3}$ centered at $i\frac{L_k}{3}$ tessellate \mathbb{Z}^d . As a consequence, two disjoint boxes of scale $k-1$ must have distance at least $L_{k-1}/3$. We will use this distance and the fact that particles must come from the enlargement of each box to control the dependences. Note that, given two disjoint boxes of scale k , we have from (7.5) that

$$\text{the distance between their enlargements is at least } \frac{L_k}{3} - 2\frac{L_k}{8} = \frac{L_k}{12}. \quad (7.8)$$

7.3.3 Definition of ρ_k

We will make ρ_k stand for the probability that a given box of scale k is bad. However, as we hinted in Section 7.3.1, we will define ρ_k in a slight different way. We will need to consider different intensities of particles at each scale. Let $\varepsilon_1 = \varepsilon > 0$ small enough and, for $k \geq 2$, define

$$\varepsilon_k := \varepsilon_{k-1} - \frac{\varepsilon}{k^2} \geq \frac{\varepsilon}{4}. \quad (7.9)$$

We emphasize that we pick ε small, then we pick δ small enough in the definition of scale 1 and then at the end we take L large enough.

Let \mathbb{P}_k be the probability measure induced by the process where η_0^S is obtained from a Poisson point process of intensity $(1 - \varepsilon_k)\mu$. Since the event that $Q_1(i, \tau)$ is good is an increasing event, we have that

$$\mathbb{P}(Q(i, \tau) \text{ is good}) \geq \mathbb{P}_1(Q(i, \tau) \text{ is good}),$$

and for any $k \geq 1$ we have

$$\mathbb{P}_{k+1}(Q_k(i, \tau) \text{ is good}) \geq \mathbb{P}_k(Q_k(i, \tau) \text{ is good}). \quad (7.10)$$

For any $k \geq 1$, we define

$$\rho_k := \mathbb{P}_k(Q_k(i, \tau) \text{ is bad}).$$

By translation-invariance, the above probability does not depend on (i, τ) .

7.4 Probability that a higher scale box is good

Note that the bound in Lemma 7.2 gives that

$$\rho_1 \leq \exp\left(-cL^{\frac{d}{d+2}}\right), \quad (7.11)$$

since ε is small enough and the new definition of bad boxes is compatible to the one we had in Lemma 7.2: the enlargement $Q_1^{\text{enlarge}}(i, \tau)$ contains $Q_1(i, \tau)$ at time τS_1 .

Note that to show that a box $Q_k(i, \tau)$ of scale k is bad, we need to control how particles move from $Q_k^{\text{enlarge}}(i, \tau)$ to the enlargement of the boxes of scale $k-1$ inside $Q_k(i, \tau)$.

Lemma 7.4. *Let $\Lambda \subset \mathcal{S}\left(Q_k^{\text{enlarge}}(i, \tau)\right)$ be such that the distance between Λ and $\partial Q_k^{\text{enlarge}}(i, \tau)$ is at least $\frac{L_k}{16}$. Let s be a time such that $\tau S_k + S_{k-1} \leq s \leq \tau S_k + S_k$. Take $\zeta \geq \frac{\varepsilon}{10k^2}$. Then, let \mathcal{E} be the event that, from the set of particles that are in $Q_k^{\text{enlarge}}(i, \tau)$, the ones that are in Λ at time s contains a Poisson point process of intensity $(1-\zeta)(1-\varepsilon_k)\mu$, which is independent of the particles in $Q_k^{\text{enlarge}}(i, \tau)$. Then, there is a constant $c = c(d)$ such that*

$$\mathbb{P}_k(\mathcal{E}) \geq 1 - \exp\left(-c\zeta^2\mu S_{k-1}^{d/2}\right).$$

Proof. This is just an application of local mixing, Theorem 6.1. To do this, we only need to tessellate $\mathcal{S}\left(Q_k^{\text{enlarge}}(i, \tau)\right)$ into cubes of side length $\sqrt{\frac{S_{k-1}\zeta^2}{c_1}}$, where c_1 is the constant from Theorem 6.1, and then note that the distance between Λ and $Q_k^{\text{enlarge}}(i, \tau)$ is at least

$$\frac{L_k}{16} = \frac{\delta L S_k}{16} \geq c_2 \sqrt{S_k \log \zeta^{-1}} \geq c_2 \sqrt{s \log \zeta^{-1}}.$$

□

Now we try to implement the reasoning discussed in Section 7.3 in the following lemma.

Lemma 7.5. *The ρ_k satisfy the following recursion for $k \geq 2$ and some constant c :*

$$\rho_k \leq \underbrace{\left(\frac{3L_k}{L_{k-1}}\right)^{2(d+1)}}_{\text{combinatorial term}} \underbrace{\left(\rho_{k-1}^2 + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right)\right)}_{\text{error term}}.$$

Proof. Let $Q_k(i, \tau)$ be a box of scale k . We start by observing that ρ_k is at most

$$\left(\left(\frac{L_k}{L_{k-1}/3}\right)^d \frac{S_k}{S_{k-1}}\right)^2 \left(\sup_{\substack{Q_{k-1}(j,s), Q_{k-1}(j',s') \subset Q_k(i,\tau) \\ Q_{k-1}(j,s) \cap Q_{k-1}(j',s') = \emptyset}} \mathbb{P}_k(Q_{k-1}(j,s), Q_{k-1}(j',s') \text{ are bad})\right), \quad (7.12)$$

where the first term accounts for the total number of ways one can choose two boxes of scale $k-1$ inside $Q_k(i, \tau)$, and the second term is the probability that two boxes of scale $k-1$ are bad. For simplicity, let $Q = Q_{k-1}(j, s)$ and $Q' = Q_{k-1}(j', s')$, and assume without loss of generality that $s' \geq s$. We split the proof into three cases, which are illustrated in Figure 6.

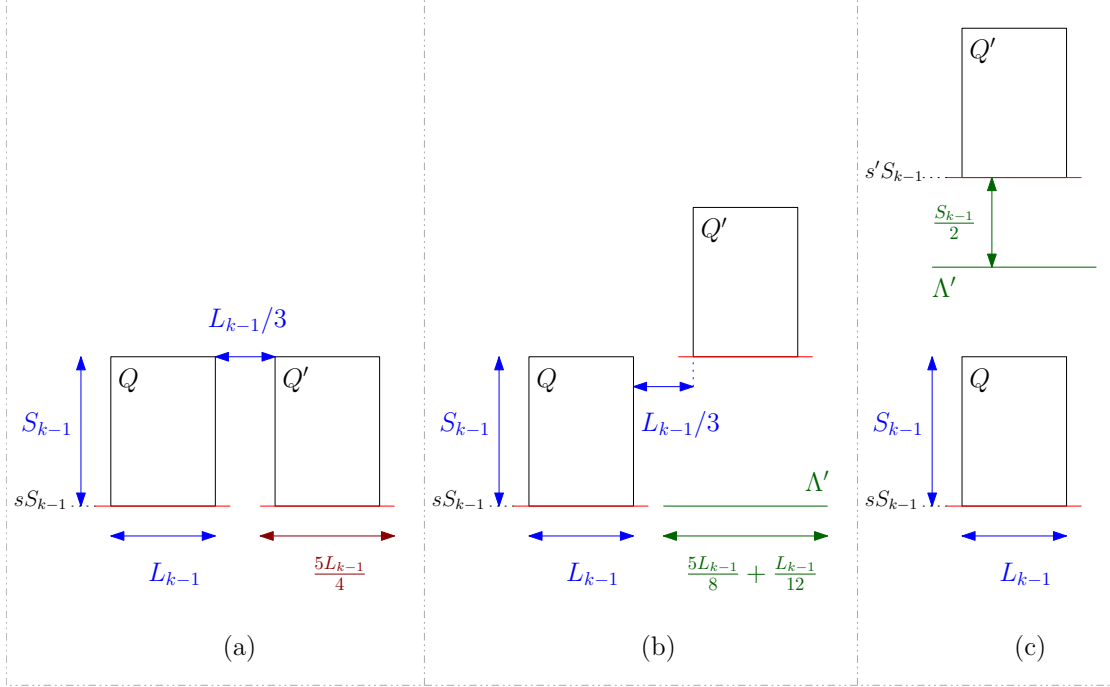


Figure 6: The three possible cases for two disjoint bad boxes of scale $k - 1$ inside a box of scale k . The red lines under each box represent their enlargements, defined in (7.4). The green lines illustrate the sets Λ' in the proof of Lemma 7.5.

Case (a): $s = s'$. In this case the enlargement of Q and Q' are disjoint. Let Λ be the union of the spatial enlargements of Q and that of Q' . Also set ζ such that $(1 - \zeta)(1 - \varepsilon_k) = (1 - \varepsilon_{k-1})$. Note that

$$\zeta = 1 - \left(\frac{1 - \varepsilon_{k-1}}{1 - \varepsilon_k} \right) \geq 1 - (1 - \varepsilon_{k-1} + \varepsilon_k) \geq \varepsilon_{k-1} - \varepsilon_k = \frac{\varepsilon}{k^2}.$$

Therefore, Lemma 7.4 gives that the particles from $Q_k^{\text{enlarge}}(i, \tau)$ contain a Poisson point process of intensity $(1 - \zeta)(1 - \varepsilon_k)\mu = (1 - \varepsilon_{k-1})\mu$ at the enlargements of Q and Q' , an event denoted by \mathcal{E} . But these enlargements are disjoint, therefore if $sS_{k-1} \geq \tau S_k + S_{k-1}$ we have

$$\begin{aligned} \mathbb{P}_k(Q \text{ and } Q' \text{ are bad}) &\leq \mathbb{P}_{k-1}(Q \text{ is bad}) \mathbb{P}_{k-1}(Q' \text{ is bad}) + \mathbb{P}_k(\mathcal{E}^c) \\ &= \rho_{k-1}^2 + \exp\left(-\frac{c\mathcal{E}}{k^2} S_{k-1}^{d/2}\right). \end{aligned} \quad (7.13)$$

If $sS_{k-1} = \tau S_k$, then we do not need to use the event \mathcal{E} since Q and Q' already start at the enlargement of $Q_k(i, \tau)$.

Case (b): $s' = s + 1$, then we will again use the fact that they are disjoint and apply the local mixing technique. But here it is slightly more involved since we need to apply the local mixing twice. Let $\Lambda' \subset \mathbb{Z}^d$ be the cube $j' \frac{L_{k-1}}{3} + \left[-\frac{5L_{k-1}}{8} - \frac{L_{k-1}}{12}, \frac{5L_{k-1}}{8} + \frac{L_{k-1}}{12}\right]$; see Figure 6(b). Note that Λ' contains the spatial enlargement of Q' . Then, let Λ be defined as the union of the spatial region of the enlargement of Q with Λ' . Note that such a Λ satisfies the condition of Lemma 7.4, so we obtain the event \mathcal{E} that the particles from $Q_k^{\text{enlarge}}(i, \tau)$ contain a Poisson point process of intensity $(1 - \zeta)(1 - \varepsilon_k)\mu$ inside Λ at time s where now we set ζ so that $(1 - \zeta)^2(1 - \varepsilon_k) = 1 - \varepsilon_{k-1}$.

Note that

$$\zeta = 1 - \sqrt{\frac{1 - \varepsilon_{k-1}}{1 - \varepsilon_k}} \geq \frac{\varepsilon_{k-1} - \varepsilon_k}{2} = \frac{\varepsilon}{2k^2}. \quad (7.14)$$

(As in case (a), the above step is only required if $sS_{k-1} \geq \tau S_k + S_{k-1}$, otherwise \mathcal{E} is already satisfied.) Now note that Λ' does not intersect the spatial region of the enlargement of Q since the distance between the spatial regions of the enlargements of Q and Q' is at least $\frac{L_{k-1}}{12}$, cf. (7.8). So we will apply the local mixing again, this time from Λ' to the enlargement of Q' . To do this, consider the particles that are in Λ' at time sS_{k-1} and let $\bar{\mathcal{E}}$ be the event that after these particles moved upto time $s'S_{k-1}$, inside the enlargement of Q' they contain a Poisson point process of intensity $(1 - \zeta)^2(1 - \varepsilon_k)\mu = (1 - \varepsilon_{k-1})\mu$. Note that the distance between Λ' and the spatial enlargement of Q' is $\frac{L_{k-1}}{12}$, and that particles will move during a time interval of length S_{k-1} from sS_{k-1} to $s'S_{k-1}$. Since $\frac{L_{k-1}}{12}$ is larger than $c_2\sqrt{S_{k-1}}\log\zeta^{-1}$, for all $k \geq 2$, where c_2 is the constant from Theorem 6.1 and the inequality holds when $k = 2$ because δ is small enough, we can apply Theorem 6.1 to obtain that

$$\begin{aligned} \mathbb{P}_k(Q \text{ and } Q' \text{ are bad}) &\leq \mathbb{P}_{k-1}(Q \text{ is bad})\mathbb{P}_{k-1}(Q' \text{ is bad}) + \mathbb{P}_k(\mathcal{E}^c) + \mathbb{P}_k(\bar{\mathcal{E}}^c) \\ &= \rho_{k-1}^2 + \exp\left(-\frac{c\varepsilon}{k^2}S_{k-1}^{d/2}\right). \end{aligned} \quad (7.15)$$

Case (c): $s' > s + 1$. This is the most delicate one. We will again apply the local coupling (Theorem 6.1) twice, using the fact that there is time difference of length at least S_{k-1} between Q and Q' . Let Λ be the spatial enlargement of Q , and let

$$\Lambda' \text{ be the cube } j'\frac{L_{k-1}}{3} + \left[-\frac{5L_{k-1}}{8} - \frac{L_{k-1}}{12}, \frac{5L_{k-1}}{8} + \frac{L_{k-1}}{12}\right]^d.$$

We will first apply the local mixing from $Q_k^{\text{enlarge}}(i, \tau)$ to Λ (as we did in the previous two cases as well), and then apply the local mixing from Λ' at time

$$r := \left(s' - \frac{1}{2}\right)S_{k-1}$$

to the enlargement of Q' ; see Figure 6(c). Set

$$\zeta \text{ such that } (1 - \zeta)^3(1 - \varepsilon_k) = 1 - \varepsilon_{k-1},$$

thus $\zeta \geq \frac{\varepsilon}{3k^2}$ using the same reasoning as in (7.14). Tessellate Λ' into sub-cubes of side-length $\ell := \sqrt{\frac{S_{k-1}\zeta^2}{2c_1}}$; which we will just refer to as the sub-cubes. Then, considering the set \mathcal{P} of the particles that are inside $Q_k^{\text{enlarge}}(i, \tau)$, define the events

$$\mathcal{E} = \{\text{the particles from } \mathcal{P} \text{ that are in } \Lambda \text{ at time } sS_{k-1} \text{ contain a PPP } ((1 - \zeta)(1 - \varepsilon_k)\mu)\},$$

and

$$\mathcal{D} = \left\{ \text{each sub-cube contains at least } (1 - \zeta)^2(1 - \varepsilon_k)\mu\ell^d \text{ particles from } \mathcal{P} \text{ at time } r \right\}.$$

Note that

$$\mathbb{P}_k(\mathcal{E}^c) + \mathbb{P}_k(\mathcal{D}^c) \leq \exp\left(-c\zeta^2S_{k-1}^{d/2}\right) + \exp\left(-c\zeta^{d+2}S_{k-1}^{d/2}\right),$$

where the first term follows from local mixing and the second term follows from local mixing and the Chernoff bound for Poisson random variables: note that ℓ^d is of the order of $S_{k-1}^{d/2}\zeta^d$ and we are asking a Poisson random variable to be larger than $(1 - \zeta)$ times its expected value. Thus,

$$\mathbb{P}_k(\mathcal{E}^c) + \mathbb{P}_k(\mathcal{D}^c) \leq \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right). \quad (7.16)$$

Finally, let \mathcal{P}' be the particles of \mathcal{P} that are found in the sub-cubes at time r . Define the event

$$\mathcal{E}' = \left\{ \text{the particles from } \mathcal{P}' \text{ that are in the enlargement of } Q' \text{ contain a PPP } ((1 - \zeta)^3(1 - \varepsilon_k)\mu) \right\}.$$

Now we proceed by doing

$$\begin{aligned} & \mathbb{P}_k(Q \text{ and } Q' \text{ are bad}) \\ & \leq \mathbb{P}_k(\{Q \text{ and } Q' \text{ are bad}\} \cap \mathcal{E} \cap \mathcal{D}) + \mathbb{P}_k(\mathcal{E}^c) + \mathbb{P}(\mathcal{D}^c) \\ & \leq \mathbb{P}_k(\{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) \mathbb{P}_k(Q' \text{ is bad} \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) + \mathbb{P}_k(\mathcal{E}^c) + \mathbb{P}(\mathcal{D}^c) \\ & \leq \mathbb{P}_{k-1}(Q \text{ is bad}) \mathbb{P}_k(Q' \text{ is bad} \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right), \end{aligned}$$

where for the last term in the last step we used (7.16). Now we use the event \mathcal{E}' to bound $\mathbb{P}_k(Q' \text{ is bad} \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D})$ by

$$\mathbb{P}_k(\{Q' \text{ is bad}\} \cap \mathcal{E}' \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) + \mathbb{P}_k(\mathcal{E}'^c \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}).$$

Since the time at which the event \mathcal{D} takes place (that is, at which the event is measurable) is between the times corresponding to \mathcal{E}' and $\{Q \text{ is bad}\} \cap \mathcal{E}$, we can use the the Markov property and local mixing to infer that

$$\mathbb{P}_k(\mathcal{E}'^c \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) \leq \exp\left(-c\zeta^2 S_{k-1}^{d/2}\right)$$

and

$$\mathbb{P}_k(\{Q' \text{ is bad}\} \cap \mathcal{E}' \mid \{Q \text{ is bad}\} \cap \mathcal{E} \cap \mathcal{D}) \leq \mathbb{P}_{k-1}(Q' \text{ is bad}).$$

Putting everything together we obtain

$$\begin{aligned} \mathbb{P}_k(Q \text{ and } Q' \text{ are bad}) & \leq \mathbb{P}_{k-1}(Q \text{ is bad}) \mathbb{P}_{k-1}(Q \text{ is bad}) + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right) \\ & \leq \rho_{k-1}^2 + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right). \end{aligned} \quad (7.17)$$

Putting all three cases together (that is, using (7.13), (7.15) or (7.17), depending on the case) into (7.12) completes the proof by noting that in the combinatorial term we have $\frac{S_k}{S_{k-1}} = \frac{L_k}{L_{k-1}}$. \square

7.5 Completing the proof of positive speed

First, we simplify the bound in Lemma 7.5.

Lemma 7.6. Fix any $\gamma \in (0, 1)$. Then, if C_L , the constant in the definition of L_k in (7.2), grows not faster than polynomially in L , and if L is large enough with respect to $\mu, d, \delta, \varepsilon$ and γ , we obtain that

$$\rho_k \leq \rho_1^{(1-\gamma)2^{k-1}}.$$

Proof. If we ignore the combinatorial and the error terms in Lemma 7.5, we obtain that

$$\rho_{k-1}^2 \geq \rho_1^{2^{k-1}}, \quad k \geq 2.$$

We want to show that this is larger than the error term in Lemma 7.5. For this, using the definition of S_k in (7.3) and the one of L_k in (7.2), we have that

$$\exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right) \leq \exp\left(-\frac{c'\varepsilon^{d+2}L^{d/2}L_{k-1}^{d/2}}{k^{2d+4}}\right) \leq \exp\left(-\frac{c'\varepsilon^{d+2}C_L^{(k-2)d/2}(k-1)!5d^2L^d}{k^{2d+4}}\right).$$

Comparing this with (7.11), we note that for all L large enough we get that the error term is smaller than ρ_{k-1}^2 for all $k \geq 2$: in fact, for small k , we use that L is large enough because the error term is exponential in L^d while ρ_{k-1}^2 is exponential in $L^{\frac{d}{d+2}}$, but when k is large we use that ρ_{k-1}^2 is exponential in 2^k while the error term is exponential in L_{k-1} but L_{k-1} grows faster than exponentially. Thus,

$$\rho_k \leq \left(\frac{3L_k}{L_{k-1}}\right)^{2(d+1)} 2\rho_{k-1}^2.$$

Now we implement the strategy described in Section 7.3.1. We assume that $\rho_k \leq \rho_1^{C_k 2^{k-1}}$, which is true for $k = 1$ if we set $C_1 = 1$. Then, to prove by induction, we assume that the above holds up to $k - 1$. Then, following the steps described in (7.7) and in the paragraph afterwards, it suffices to set C_k so as to have

$$2\left(\frac{3L_k}{L_{k-1}}\right)^{2(d+1)} \rho_1^{(C_{k-1}-C_k)2^{k-1}} \leq 1.$$

But setting $C_k = C_{k-1} - \frac{\gamma}{10k^2}$, we have that the above is true for all $k \geq 2$ because

$$\frac{3L_k}{L_{k-1}} = 3C_L k^{10d},$$

so it grows only polynomially in k and, for small k , C_L grows at most polynomially in L while ρ_1 decreases as a stretched exponential in L . Since

$$\liminf_{k \rightarrow \infty} C_k = \liminf_{k \rightarrow \infty} 1 - \sum_{j=2}^k \frac{1}{10j^2} \geq 1 - \gamma,$$

the proof is completed. □

We are now ready to conclude the proof of positive speed of propagation.

Proof of Theorem 4.2. Let k be defined so that $S_k = t$ (assume that one can choose k so that the equality is satisfied). We need to show that the box of scale k centered at the origin being good implies that the infection has positive speed of propagation. Consider a good box $Q_k(i, \tau)$ of scale k and assume that there is an infected particle at some vertex $x \in Q_k^{\text{base}}(i, \tau)$ at time τS_k . Let

$\zeta_k = \sum_{i=1}^k \frac{\zeta}{i^2}$, for a fixed small $\zeta > 0$ so that $\zeta_k \leq \frac{1}{2}$ for all $k \geq 1$. Then, we will show that, at time $(\tau + 1)S_k$, we have an infected particle at some position y such that

$$\|y - x\|_2 \geq \frac{L_k}{3}(1 - \zeta_k). \quad (7.18)$$

This is true for $k = 1$, and we assume that this is true up to $k - 1$. Since $Q_k(i, \tau)$ is good, there is at most one bad box of scale $k - 1$ inside it (including possibly overlapping boxes). There are two cases: either the infection manages to exit $Q_k(i, \tau)$ during $[\tau S_k, (\tau + 1)S_k]$ or it does not. In the first case, the infection has to be within distance $2CS_{k-1}$ from the spatial boundary of $Q_k(i, \tau)$ at time $(\tau + 1)S_k$. This is because the only way the infection can move back inside the box is the presence of a bad box at the boundary. But then, the assumption (7.1) on the speed of particles gives that particles cannot move deep inside $Q_k(i, \tau)$. In this case we have

$$\|y - x\|_2 \geq \frac{L_k}{3} - 2CS_{k-1} = \frac{L_k}{3} - 2C\delta LL_{k-1} = \frac{L_k}{3} \left(1 - \frac{6\delta CL}{C_L k^{10d}} \right),$$

which gives (7.18).

Now we assume that the infection does not manage to exit $Q_k(i, \tau)$. Then, at each time interval of length S_{k-1} , as the infection goes through a good box of scale $k - 1$, the infection traverses distance at least $(1 - \zeta_{k-1})L_{k-1}/3$ by the induction hypothesis. Since there are no 2 disjoint bad boxes of scale $k - 1$ in $Q_k(i, \tau)$, we have that the number of bad boxes is at most c_d . So we have that

$$\begin{aligned} \|y - x\|_2 &\geq \left(\frac{S_k}{S_{k-1}} - c_d \right) \frac{L_{k-1}}{3} (1 - \zeta_{k-1}) - c_d CS_{k-1} \\ &= \left(\frac{L_k}{L_{k-1}} - c_d \right) \frac{L_{k-1}}{3} (1 - \zeta_{k-1}) - c_d CS_{k-1}, \end{aligned}$$

where CS_{k-1} represents the backtrack that the infection can suffer through the bad boxes. Thus, using that $\zeta_k \leq 1/2$ for all k , we have

$$\|y - x\|_2 \geq \frac{L_k}{3}(1 - \zeta_{k-1}) \left(1 - \frac{c_d}{C_L k^{10d}} - \frac{3c_d CS_{k-1}}{L_k} \right) \geq \frac{L_k}{3}(1 - \zeta_k).$$

□

7.6 Getting rid of assumption (7.1)

In order to remove the assumption that random walks are not faster than ballistic, we add this assumption to the definition that a box is good. For each box $Q_k(i, \tau)$ and each site $x \in \mathcal{S}(Q_k^{\text{base}}(i, \tau))$, we let $J_k(x, \tau)$ be a vector of $\frac{S_k}{S_{k-1}}$ independent random variables, the j th one giving the number of jumps an infected particles that is at x at time τS_k gives during the time interval $\tau S_k + [(i - 1)S_{k-1}, iS_{k-1}]$. Recall that at each time we choose just one infected particle to follow, and when a particle is at $x \in Q_k^{\text{base}}(i, \tau)$, we let the number of jumps of this particle along the time interval of $Q_k(i, \tau)$ to be given by $J_k(x, \tau)$.

Now we are ready to define good boxes. Fix a constant $C_{\text{rw}} > 0$ and take the following definition.

Definition 7.7. The box $Q_k(i, \tau)$ is *good* if the following two things happen:

- (E₁) For each $x \in \mathcal{S}(Q_k^{\text{base}}(i, \tau))$ and each $j \in \{1, 2, \dots, \frac{S_k}{S_{k-1}}\}$, the j th element of $J_k(x, \tau)$ is at most $C_{\text{rw}}S_{k-1}$.
- (E₂) Considering only the particles that are inside $Q_k^{\text{enlarge}}(i, \tau)$ to decide whether boxes of scale $k-1$ in $Q_k(i, \tau)$ are good or bad, $Q_k(i, \tau)$ does not contain 2 *disjoint* bad boxes of scale $k-1$.

Now we choose C_{rw} to be some large (but universal) constant, and take the union bound on x and j to obtain

$$\mathbb{P}(E_1^c) \leq \left(\frac{L_k}{3}\right)^d \left(\frac{S_k}{S_{k-1}}\right) \exp(-cC_{\text{rw}}S_{k-1}) \leq \exp(-c'C_{\text{rw}}S_{k-1}),$$

for some constant $c' > 0$. Now, updating the definition of ρ_k to be compatible with Definition 7.7, we obtain the following recursion (cf. Lemma 7.5):

$$\begin{aligned} \rho_k &\leq \left(\frac{3L_k}{L_{k-1}}\right)^{2(d+1)} \left(\rho_{k-1}^2 + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right)\right) + \mathbb{P}_k(E_1^c) \\ &\leq \left(\frac{3L_k}{L_{k-1}}\right)^{2(d+1)} \left(\rho_{k-1}^2 + \exp\left(-\frac{c\varepsilon^{d+2}S_{k-1}^{d/2}}{k^{2d+4}}\right)\right) + \exp(-c'C_{\text{rw}}S_{k-1}). \end{aligned}$$

Using the same reasoning as in Lemma 7.6, we have that, for $k \geq 2$,

$$\rho_{k-1}^2 \geq \exp(-c'C_{\text{rw}}S_{k-1}).$$

In fact, for large k the term S_{k-1} in the right-hand side grows faster than exponentially, and for small k the term S_{k-1} grows like L^2 . So it is a much faster growth than that of ρ_{k-1} (see Lemma 7.6). Thus, we obtain

$$\rho_k \leq \rho_1^{(1-\gamma)2^{k-1}},$$

and everything discussed in the previous sections go through.

8 Multi-scale analysis and Lipschitz percolation

(Yet to be written.)

9 Beyond spread of infection

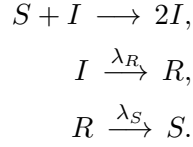
In this section we will illustrate several processes (beyond spread of infection) that belong to the class of reaction-diffusion particle systems. We split the discussion in this section into two parts, depending on whether the particle system moves according to independent random walks (as discussed so far) or to an exclusion process.

9.1 Reaction-diffusion particle systems

9.1.1 Spread of infection: SIRS dynamics

This is a combination of SIS and SIR dynamics. There are three types of particles, S, I and R, and there are two parameters λ_R and λ_S , besides μ . The initial configuration is as in the SI, SIS

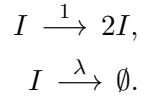
and SIR dynamics (η_0^S is a Poisson point process of intensity μ , $\eta_0^I(\mathbb{Z}^d) = \eta_0^I(0) = 1$ has only one particle at the origin, and $\eta_0^R(\mathbb{Z}^d) = 0$). The reaction formulas are



This model represents the case that when a particle heals it may be immune from the infection for some time, but later become susceptible again.

9.1.2 Branching random walk

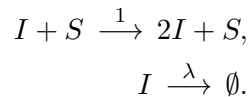
We will have only one type of particle (call it I). A branching random walk with binary branching at rate 1 and death rate λ can be represented by taking the initial configuration $\eta_0^I(\mathbb{Z}^d) = \eta_0^I(0) = 1$ and the reaction formulas



In fact, the frog model (with SIR dynamics) is a model of branching random walk, where the I -particles branch only in their first visit to a site. There is a vast literature on Branching random walk, but treating this model is beyond the scope of this notes.

9.1.3 Branching random walks with catalysts

There are two types of particles, S and I , as in the spread of infection model. S particles are regarded as catalysts and remain in their state forever. Meanwhile, I particles branch only when they share a site with an S particle, and the rate of branching is the number of S particles in that site. Moreover, I particles die at rate λ , independent of the other particles. The system is characterized by the following formulas

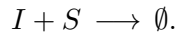


Note that the above formulas conserve the number of S particles. In fact, the S particles only serve as catalysts that trigger the branching of I particles. For the sake of clarity, we remark that the first reaction formula states that for each I particle and for each S particle in the same site as the I particle, there is a rate 1 Poisson clock that triggers the reaction given by the formula.

This model played an important role in the development of multi-scale analysis techniques for particle systems due to the seminal work of Kesten and Sidoravicius [22], which was later extended to analyse the spread of infection with SI and SIS dynamics, and also extended by Stauffer [36] and Gracar and Stauffer [17] to develop more general and robust multi-scale techniques.

9.1.4 Annihilating random walks

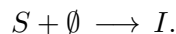
There are two types of particles, S and I, both jumping at rate one ($D_I = D_S = 1$). One particle of each type annihilate each other instantaneously when they are at the same site. We can represent this by the following formula:



For more information about annihilating random walks we refer to [8] and references therein.

9.1.5 Internal diffusion limited aggregation (IDLA)

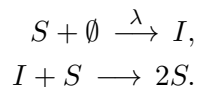
There are two types of particles, S and I (standing for *inactive*). Only S particles move ($D_I = 0, D_S = 1$). When an S particle is alone at a site, it instantaneously turns into I, while I particles never change state. We obtain the formula



There is a vast literature on IDLA, and treating this model is beyond the scope of this notes. For more information we refer the reader to the original paper of Diaconis and Fulton [13] and the recent work [6] and references therein.

9.1.6 Activated random walks (ARW)

There are two types of particles, S and I (standing for *inactive*). Only S particles move ($D_I = 0, D_S = 1$). When an S particle is alone at a site, at rate λ it turns into I. Moreover, when an S particle jumps at a site occupied by an I particle, then the I particle turns into S. We obtain the following formulas



Note that IDLA can be viewed as the limit of activated random walks when $\lambda \rightarrow \infty$. There has been several recent results about ARW, we refer the reader to the survey [32].

9.1.7 General setting

A reaction-diffusion particle system is then composed of four ingredients:

- A set Σ of types for the particles, such as $\Sigma = \{S, I, R\}$,
- Initial configurations for the particles, η_0^σ for each $\sigma \in \Sigma$,
- The jump rates of each type, $D_\sigma \geq 0$ for each $\sigma \in \Sigma$,
- A set of reaction formulas, which can be either instantaneous reactions such as $S + I \longrightarrow 2I$ or reactions that happen at a certain rate such as $I \xrightarrow{\lambda} R$.

9.2 Reaction-diffusion by the exclusion process

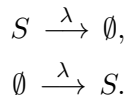
Up to now we have only considered the case that particles move as independent random walks. In this section we will discuss one possible variation, which gives rise to a myriad of new processes.

Let D_σ denote the rate at which particles of type σ try to jump. Each particle of type σ then have a Poisson clock of rate $2dD_\sigma$ and, when the clock rings, the particle chooses a neighbor uniformly at random and *if the neighbor is empty* (that is, it is not occupied by a particle of any type), the particle jumps to the neighbor. On the other hand, if the neighbor is occupied, the particle does not jump and, moreover, if the neighbor is occupied by a particle of type σ' and there is a reaction formula with left-hand side represented by the *directed* sum $\sigma + \sigma'$, the reaction is performed. The order of the terms in the left-hand side of the reaction formula is important, as it specifies which type of particle was attempting to jump.

As a consequence, we will have at most one particle per site at all times; thus $\sum_{\sigma \in \Sigma} \eta_t^\sigma(x) \in \{0, 1\}$ for all $t \geq 0$ and all $x \in \mathbb{Z}^d$. Reactions may also happen at empty sites, which will be represented as \emptyset .

9.2.1 Birth-death particle system

This is a model studied by De Masi, Ferrari and Lebowitz [12]; see also [15]. There is one type of particle, S, and $D_S = 1$. Then, at rate λ , there is creation or deletion of particles according to the following reaction formulas



Note that there is no reaction when particles jump.

9.2.2 Multi-particle diffusion limited aggregation (MDLA)

There are two types of particles, S and I (standing for *inactive*). The jump rates are $D_S = 1$ and $D_I = 0$, so only S particles may jump and trigger a reaction. We take the initial configuration to be $\eta_0^I(\mathbb{Z}^d) = \eta_0^I(0) = 1$ and η_0^S being a product of Bernoulli measures of parameter $\mu \in (0, 1)$ on $\mathbb{Z}^d \setminus \{0\}$. Then when an S particle attempts to jump onto a site occupied by an I particle, the S particle turns into I. The reaction formulas is the following



Above we write $I + I$ instead of $2I$, as a way to emphasize that sites cannot host more than one particle. As with the left-hand side, the order of the terms in the right-hand side matter. For example, the reaction formula $S + I \longrightarrow I + S$ would mean that the S particle turns into I and the I particle turns into S.

For existing works in this model see [33], where Sidoravicius and Stauffer used a multi-scale analysis to analyze MDLA in dimensions $d \geq 2$.

9.3 Beyond particle systems

Using the exclusion process as a form of diffusion, as explained in Section 9.2, allows us to model several stochastic processes as a reaction diffusion particle system. Examples include growth processes and classical interacting particles systems from Liggett's book [28].

The way this is achieved is by introducing a *virtual* type of particle, which we will call type V. Particles of type V will occupy *all* the sites that are not occupied by the other types (in other words, V particles occupy all *vacant* sites). Because all sites have at least one particle, no particle move, and several processes can be modeled in this way, including contact process, voter model, majority dynamics and first passage percolation. Below we illustrate this with three growth processes based on first passage percolation. Nonetheless, we will not spend much time in this type of processes, since their nature is very different from an actual reaction diffusion particle system; they are not based on a mobile, *diffusive* system of particles.

We decided to mention this alternative here as the techniques discussed in this note have also been employed in the analysis of such processes.

9.3.1 First passage percolation

This is a model of spread of infection with SI dynamics. There are two types of particles, I (for *infected*) and V (for *vacant*), and the initial configuration is $\eta_0^I(\mathbb{Z}^d) = \eta_0^I(0) = 1$, and $\eta^V(x) = 1$ for all $x \in \mathbb{Z}^d \setminus \{0\}$. Note that there are no empty sites, so particles do not jump. But the jump rate $D_I = 1$ is used to trigger the reaction formula

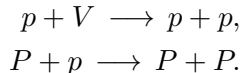


Since no other reaction formula has been specified, I particles do not trigger any reaction. The above characterizes first passage percolation with *exponential* passage times (of rate D_I).

First passage percolation is by now a classical process, and we refer the reader to the book [4] for further information.

9.3.2 Prey-predator first passage percolation

There are three types of particles P (predator), p (prey), and V (vacant). Initially we have $\eta_0^P(\mathbb{Z}^d) = \eta_0^P(0) = 1$ and $\eta_0^p(\mathbb{Z}^d) = \eta_0^p(x) = 1$ for some neighbor x of the origin. For all $y \in \mathbb{Z}^d \setminus \{0, x\}$, we have $\eta_0^V(y) = 1$. The process evolves as prey conquer sites with V particles, and predators conquer sites with preys. The reaction formulas are as follows

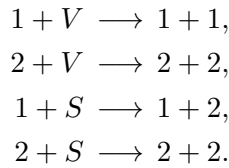


An interesting question is whether the prey can survive for some value of $D_p < D_P$. For further information on this model, see [26] and references therein.

9.3.3 First passage percolation in hostile environment

This model was introduced by Sidoravicius and Stauffer [33] as a means to analyzing the aforementioned MDLA process (see also [9]), but it is an interesting model in its own right. There are four types of particles: 1 (standing for *type 1*), 2 (standing for *type 2*), S (standing for *type 2 seed*), V (standing for *vacant*).

We start with $\eta_0^1(\mathbb{Z}^d) = \eta_0^1(0) = 1$, and let η_0^S be a product of Bernoulli measures on $\mathbb{Z}^d \setminus \{0\}$ of parameter μ . Then for each $x \in \mathbb{Z}^d \setminus \{0\}$ for which $\eta_0^S(x) = 0$ we set $\eta_0^V(x) = 1$. Then S particles turn into type 2 when type 1 or 2 try to jump at the site of the S particle. Also, V particles turn into type 1 or 2 whenever a type 1 or 2 particle, respectively, tries to jump onto the site of the V particle. For the jump rates, we have $D_S = 0$ (so type 2 seeds do not trigger any reaction, they just wait), $D_1 = 1$ and $D_2 = \lambda$ so different types can spread at different rates when $\lambda \neq 1$, and D_V is irrelevant. The reaction formulas are as follows



10 Multi-scale analysis in percolation

10.1 Particle percolation

We start defining a percolation process based on η_t , which we henceforth call *particle percolation*.

Definition 10.1 (*t*-open sites). Given η_t , we say that a vertex

$$x \in \mathbb{Z}^d \text{ is } t\text{-open iff } \eta_t(x) \geq 1.$$

Definition 10.2 (Critical densities). We define two critical values. First, let μ_c be the critical value for percolation of occupied sites, defined as the value which satisfies

$$1 - e^{-\mu_c} = p_c^{\text{site}},$$

where $p_c^{\text{site}} = p_c^{\text{site}}(\mathbb{Z}^d)$ is the critical probability for site percolation on \mathbb{Z}^d . Similarly, let μ_c^V be the critical value for percolation of vacant sites, defined as the value which satisfies

$$e^{-\mu_c^V} = p_c^{\text{site}}.$$

The above definition and stationarity of η_t (Theorem 2.1) imply that, for all $\mu > \mu_c$ and any given $t \geq 0$ we have

$$\mathbb{P}\left(0 \xrightarrow{t} \infty\right) > 0,$$

where $\{0 \xrightarrow{t} \infty\}$ denotes the event that the origin is in an infinite cluster of *t*-open sites. Since there are uncountably many values for *t*, it is a priori unclear whether for $\mu > \mu_c$ there could be times for which percolation occurs. The theorem below settles this question; it has essentially the same proof as in the corresponding result for dynamical percolation [18]. Let \mathcal{C}_t^∞ be the event that there exists an infinite cluster of *t*-open sites.

Theorem 10.3 (No exceptional times away from criticality). *In particle percolation, for any $\mu > \mu_c$, we have $\mathbb{P}(\mathcal{C}_t^\infty \text{ for all } t) = 1$. Conversely, for any $\mu < \mu_c$, we have $\mathbb{P}(\{\mathcal{C}_t^\infty\}^c \text{ for all } t) = 1$.*

Proof. Take ε small enough and consider a site x open during $[i\varepsilon, (i+1)\varepsilon]$ if there exists a particle at x at time $i\varepsilon$ that does not move during that time interval. Then, the probability that x is open at the i th slot according to the above definition is

$$1 - \exp(-\mu e^{-\varepsilon}),$$

since $e^{-\varepsilon}$ is the probability that a particle does not move during an interval of length ε . Since $\mu > \mu_c$, taking ε small enough makes the above probability larger than p_c^{site} . So there is an infinite cluster with probability 1 during $[i\varepsilon, (i+1)\varepsilon]$. Since the number of slots is countable, we obtain that there is an infinite cluster for all times.

For the second part, we use a similar strategy. We consider a site open during $[i\varepsilon, (i+1)\varepsilon]$ if there exists a particle at x at some time during that interval. For any site y , a particle starting from y can only be at x after time ε if it makes at least $\|x - y\|_1$ jumps during a time interval of length ε . The probability that a random walk makes j jumps during a time interval of length $\varepsilon \leq \frac{1}{2e}$ is given by (cf. Lemma A.1)

$$\mathbb{P}(\text{Poisson}(\varepsilon) \geq j) \leq 2 \exp\left(-\varepsilon - j \left(\log\left(\frac{j}{\varepsilon}\right) - 1\right)\right) \leq \exp\left(-cj \log\left(\frac{j}{\varepsilon}\right)\right),$$

where the last inequality holds for all small enough ε and $j \geq 1$, and some constant c . Since there are at most $(2d)^j$ particles at ℓ_1 -distance j from x , we obtain that the probability that x is open at slot i is

$$1 - e^{-\mu} + e^{-\mu} \left(1 - \exp\left(-\mu \sum_{j=1}^{\infty} (2d)^j \exp\left(-cj \log\left(\frac{j}{\varepsilon}\right)\right)\right)\right).$$

For small enough ε , the above probability is at most

$$1 - e^{-\mu} + e^{-\mu} \left(1 - \exp\left(-\mu \exp\left(-c \log\left(\frac{1}{\varepsilon}\right)\right)\right)\right) \leq 1 - e^{-\mu} + e^{-\mu} \mu \varepsilon^c < p_c^{\text{site}},$$

where the last inequality holds because by choosing ε small enough we can make the left-hand side arbitrarily close to $1 - e^{-\mu} < p_c^{\text{site}}$. \square

10.1.1 Percolation time

The percolation time was introduced by Sinclair and Stauffer [35], in the context of a particle system moving in continuous time and continuous space. But the definition of the percolation time makes sense in any percolation process that updates over time.

Definition 10.4 (Percolation time). The percolation time T_{perc} is the first time that the origin belongs to the infinite cluster of open sites; that is,

$$T_{\text{perc}} := \inf\{t \geq 0: 0 \xrightarrow{t} \infty\}.$$

We first study the percolation time in so-called *dynamical percolation*. In dynamical percolation, at time 0 each site is open or closed with probability p and $1 - p$, respectively. Moreover, each site has a Poisson clock of rate 1, and when the clock of a site x rings, then x refreshes its state: it becomes open or closed with probability p and $1 - p$, respectively, independent of anything else.

Dynamical percolation was introduced in 1997 by Häggström, Peres and Steif [18], and independently by Itai Benjamini.

Theorem 10.5 (Percolation time in dynamical percolation). *In dynamical percolation, for all $d \geq 2$ and all $p > p_c$, there exists a constant $c = c(d, p) > 0$ such that*

$$\mathbb{P}(T_{\text{perc}} > t) \leq \exp(-ct).$$

Proof. Let s be large enough so that

$$p' := (1 - e^{-s})p > p_c^{\text{site}}.$$

Divide the interval $[0, t]$ into subintervals of length s . For the i th interval, say that a site is open at interval i if its state was refreshed during $((i - 1)s, is]$ and the site is open at time is . Note that the open sites in this definition are independent across different i . Therefore,

$$\begin{aligned} \mathbb{P}(T_{\text{perc}} > t) &\leq \prod_{i=1}^{t/s} \mathbb{P}(0 \text{ is not in the infinite cluster of open sites at interval } i) \\ &\leq (1 - \theta(p'))^{t/s}, \end{aligned}$$

where $\theta(p')$ is the probability that the origin is in the infinite cluster of Bernoulli percolation of parameter p' . \square

10.1.2 Percolation time in particle percolation

The percolation time for particle percolation was initially studied by Sinclair and Stauffer [35] in the model of particles moving as independent Brownian motions in \mathbb{R}^d , and also analyzed by Peres, Sinclair, Sousi and Stauffer [29]. The results of those papers are expected to hold also for the discrete-space setting of these notes. The expected behavior of the percolation time is the following.

Question 10.6. *In particle percolation, does it hold that $\mathbb{P}(T_{\text{perc}} > t)$ is at most $\exp\left(-\frac{ct}{\log t}\right)$ in $d = 2$ and $\exp(-ct)$ in $d \geq 3$?*

It is known that $\mathbb{P}(T_{\text{perc}} > t)$ cannot decay faster than stated above [29, 35, 14], in particular the above bounds are lower bounds on the probability that the origin is s -closed for all $s \in [0, t]$. Establishing the upper bound, in turn, remains a challenging open problem. The best upper bounds on the above questions were obtained by Peres, Sinclair, Sousi and Stauffer [29] in 2013 for the model in continuous space.

Theorem 10.7 ([29, Theorem 1.6]). *For all $d \geq 2$ and all $\mu > \mu_c$, there exists $c = c(d, \mu)$ such that*

$$\mathbb{P}(T_{\text{perc}} > t) \leq \exp\left(-\frac{ct}{t^{3+6/d}}\right).$$

10.1.3 Detection (percolation of vacant sets)

We say that a space-time site (x, s) , $x \in \mathbb{Z}^d$ and $s \in \mathbb{R}$, is vacant if $\eta_s(x) = 0$.

Definition 10.8. Define the event $\left\{0 \xrightarrow{v\uparrow} \infty\right\}$ as the event that there is an infinite path from the space-time origin $(0, 0)$ that is oriented in time and only visits vacant space-time sites.

Note that in the definition above path does not need to go to infinity in time and, in fact, when $\mu < \mu_c^v$, with positive probability this event holds for a path that remains at time 0; recall the value of μ_c^v from Definition 10.2.

The existence of the above path corresponds to the problem of detecting the presence of a mobile target, whose goal is to avoid being detected by the particle system η_t . It has been established by Stauffer [36] (in the model in continuous space) that if μ is large enough then the target cannot avoid detection. The proof of this theorem involves a multi-scale analysis in the spirit of Section 8, and in fact includes the case that the space-time path of the target is allowed to move backwards in time. It also establishes almost tight bounds for dimensions $d \geq 3$.

Definition 10.9. Define the event $\left\{(0, 0) \xrightarrow{v} \infty\right\}$ as the event that there is an infinite path from the space-time origin $(0, 0)$ that only visits vacant space-time sites.

Let $\mathcal{B}_t^1 = [-t, t]$ be the one-dimensional ball of radius t , $\partial\mathcal{B}_t^1$ be its external boundary, and $\mathbb{Z}^d \times \partial\mathcal{B}_t^1$ be the corresponding space-time region. Then $\left\{(0, 0) \xrightarrow{v} \mathbb{Z}^d \times \partial\mathcal{B}_t^1\right\}$ is the event that the target avoids detection up to time t or $-t$ via a space-time path that can move backwards in time.

Theorem 10.10 ([36, Theorem 1.6]). *There exists a value $\mu_0 = \mu_0(d)$ and constants c, C depending on c, C such that, for all $\mu > \mu_0$, we have*

$$\mathbb{P}\left(\left\{(0, 0) \xrightarrow{v} \mathbb{Z}^d \times \partial\mathcal{B}_t^1\right\}\right) \leq \begin{cases} \exp\left(-\frac{ct}{(\log t)^{c'}}\right), & \text{in } d = 2 \\ \exp(-ct), & \text{in } d \geq 3. \end{cases}$$

A central question is whether the critical probability for the event that the target can avoid detection forever is different than μ_c^v . If this is the case, then there are values of μ for which the target can avoid detection only through space-time paths that leave time 0.

Question 10.11. *Does there exist $\mu'_c > \mu_c^v$ such that for $\mu \in (\mu_c^v, \mu'_c)$ we have*

$$\mathbb{P}\left(0 \xrightarrow{v\uparrow} \infty\right) > 0?$$

We conclude this section with a quick remark regarding the detection of a static target, which is equivalent to estimating the first time that the origin is occupied by at least one particle. Sharp results can be obtained regarding this time. For example, it is known [29, 35, 14] that, for any $t \geq 0$, the probability that the origin is s -closed for all $s \in [0, t]$ behaves as $\exp(-c\sqrt{t})$ in $d = 1$, $\exp(-c\frac{t}{\log t})$ in $d = 2$, and $\exp(-ct)$ in $d \geq 3$, and the constant $c = c(d, \mu)$ can be computed explicitly.

A Standard large deviation results

Lemma A.1 (Upper tail of Poisson). *For any $\lambda > 0$ and any $x \geq 2e\lambda$, we have*

$$\mathbb{P}(\text{Poisson}(\lambda) \geq x) \leq 2 \exp\left(-\lambda - x \left(\log\left(\frac{x}{\lambda}\right) - 1\right)\right).$$

Proof. Let X be a Poisson random variable of parameter λ . Then

$$\mathbb{P}(X \geq x) = \sum_{z=x}^{\infty} e^{-\lambda} \frac{\lambda^z}{z!} \leq \sum_{z=x}^{\infty} e^{-\lambda} \left(\frac{\lambda e}{z}\right)^z.$$

Since $x \geq 2e\lambda$, the last term is at most 2^{-z} , which yields $\mathbb{P}(X \geq x) \leq 2e^{-\lambda} \left(\frac{\lambda e}{x}\right)^x$. \square

Lemma A.2 (Lower tail of Poisson). *For any $\lambda > 0$ and any $\varepsilon > 0$, we have*

$$\mathbb{P}(\text{Poisson}(\lambda) < (1 - \varepsilon)\lambda) \leq (1 - \varepsilon)\lambda \exp\left(-\frac{\varepsilon^2 \lambda}{2}\right).$$

Proof. Let X be a Poisson random variable of parameter λ . Then

$$\mathbb{P}(X < (1 - \varepsilon)\lambda) = \sum_{z=0}^{(1-\varepsilon)\lambda-1} e^{-\lambda} \frac{\lambda^z}{z!} \leq (1 - \varepsilon)\lambda e^{-\lambda} \left(\frac{\lambda e}{(1 - \varepsilon)\lambda}\right)^{(1-\varepsilon)\lambda},$$

where in the inequality we use the fact that the largest term of the sum is when $z = (1 - \varepsilon)\lambda$, and the fact that $z! \geq (z/e)^z$. Now we use the fact that $(1 - \log(1 - \varepsilon))(1 - \varepsilon) \leq 1 - \frac{\varepsilon^2}{2}$ for all $\varepsilon \in (0, 1)$, which yields

$$\mathbb{P}(X < (1 - \varepsilon)\lambda) \leq (1 - \varepsilon)\lambda e^{-\lambda + (1 - \varepsilon^2/2)\lambda} = (1 - \varepsilon)\lambda \exp\left(-\frac{\varepsilon^2 \lambda}{2}\right).$$

\square

Lemma A.3 (Chernoff bound for Binomial).

B Estimates for simple random walks

In this section, we let $(Z_t)_{t \geq 0}$ be a continuous-time random walk on \mathbb{Z}^d starting from the origin, and recall that $p_t(x, y)$ is the probability that a random walk starting from x is at site y at time t .

Lemma B.1 (Probability bounds). *For any $\alpha > 0$ there exist constants $C, c > 0$ depending on α such that for any $t > 0$ and any $x \in \mathbb{Z}^d$ for which $\|x\|_1 \leq \alpha\sqrt{t}$, we have*

$$\frac{c}{t^{d/2}} \leq p_t(0, x) \leq \frac{C}{t^{d/2}}.$$

Moreover, there exists c' such that for any $t \geq 0$ and any $\ell \geq 1$, we have

$$\mathbb{P}\left(\bigcup_{s \in [0, t]} \{\|Z_s\|_1 \geq \ell\}\right) \leq \exp\left(-\frac{c'\ell^2}{t}\right).$$

Proof. The first part follows from the local central limit theorem in [27, Theorem 2.1.1]. The second part follows by considering each dimension an then using the bound for one-dimensional random walk (which uses the reflection principle). \square

Lemma B.2 (Collision of random walks). *For $t \geq 0$ and $x, y \in \mathbb{Z}^d$, let $p_t(x, y)$ be the probability that a particle that is at x at time 0 is located at y at time t . Then, if $\|x - y\|_1 \leq \sqrt{t}$, then*

$$p_t(0, x) \leq p_t(0, y) \exp\left(\frac{\|x - t\|_2^2}{2t}\right).$$

Proof. Essentially a consequence of the local CLT. \square

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