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Survival and parasite spread in a spatial host-parasite model with host immunity

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Abstract

In this thesis, we introduce a stochastic model for the invasion of a parasite population in a spatially structured host population, which includes an individual-based adaptive immune response. We will call this the "Spatial Infection Model with Host Immunity" or SIMI for short.

In the SIMI, parasites move as independent simple random walks on a graph until they meet a vertex that is inhabited by a host. With a given probability, the host repels the infection, kills the parasite, and adapts its probability to repel the next infection. After a successful infection attempt, both the host and the attacking parasite die, and only the parasite leaves a random number of offspring.

We study the SIMI on the integer line $\mathbb{Z}$ and show that parasites have a positive survival probability if and only if the mean offspring are greater than the mean number of needed infection attempts. Furthermore, we study the speed at which the parasites invade the host population. If the probability of a host after repelling an infection, to also repel the next one does not grow fast enough, then parasites propagate across the host population at a linear speed. However, if that probability grows quickly enough, the propagation speed is polynomial with exponent < 1.

Finally we investigate the SIMI on higher-dimensional graphs with hosts that are either totally immune and never get infected or get infected in the first attempt. We show that the survival probability undergoes a phase transition in the frequency of totally immune hosts.

Zusammenfassung

In dieser Arbeit führen wir ein stochastisches Modell zur Beschreibung der Invasion einer Parasitenpopulation in eine räumlich strukturierte Wirtspopulation ein, wobei die Wirtspopulation über einen individuenbasierten adaptiven Verteidigungsmechanismus verfügt. Wir bezeichnen dieses Modell als „Spatial Infection Model with host Immunity", kurz SIMI.

Im SIMI bewegen sich Parasiten als unabhängige zufällige Irrfahrten auf einem Graphen, bis sie auf einen von einem Wirt besetzten Knoten treffen und diesen zu infizieren versuchen. Der Wirt wehrt mit einer gegebenen Wahrscheinlichkeit den Infektionsversuch ab, tötet den Parasiten und verändert seine Wahrscheinlichkeit, den nächsten Infektionsversuch abzuwehren. Ist ein Infektionsversuch erfolgreich, so töten sich der Wirt und der angreifende Parasit gegenseitig und nur der Parasit hinterlässt eine zufällige Anzahl an Nachkommen.

Wir betrachten das SIMI auf dem Graphen $\mathbb{Z}$ und zeigen, dass die Parasiten genau dann mit positiver Wahrscheinlichkeit für immer überleben können, wenn die mittlere Anzahl an Nachkommen größer als die mittlere Anzahl an nötigen Infektionsversuchen ist. Weiterhin analysieren wir die Geschwindigkeit, mit der Parasiten in die Wirtspopulation eindringen. Wächst die Wahrscheinlichkeit eines Wirts nicht schnell genug nach einem abgewehrten Infektionsversuch, auch den nächsten Versuch abzuwehren, so können die Parasiten sich mit linearer Geschwindigkeit in der Wirtspopulation ausbreiten. Fällt die Infektionswahrscheinlichkeit hingegen schnell genug, so ist die Ausbreitungsgeschwindigkeit nur polynomial schnell mit einem Exponenten < 1.

Abschließend betrachten wir das SIMI noch auf höherdimensionalen Graphen mit Wirten, die entweder vollständig immun sind und nie infiziert werden oder direkt beim ersten Versuch infiziert werden. Wir identifizieren in dieser Situation einen Phasenübergang in der Überlebenswahrscheinlichkeit der Parasiten in Abhängigkeit von der Häufigkeit vollständig immuner Wirte.

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Contents

List of Symbols

$\mathbb{E}[X]$	Expectation of the random variable X.
$\mathbb{V}[X]$	Variance of the random variable X.
$X \overset{\mathrm{d}}{=} Y$	X and Y are equal in distribution
$X_n \overset{\mathrm{d}}{\to} Y$	$(X_n)_{n\in\mathbb{N}}$ converges to Y in distribution.
C^D	Set of all functions with domain D and codomain C.
$\mathbb{N}_0 = \{0, 1, 2, \dots\}$	Set of all natural numbers including 0.
$\mathbb{Z} = \{\dots, -2, -1, 0, 1, 2, \dots\}$	Set of all integer numbers
$\mathbb{Z}_{\le x} = \{\dots, x-1, x\}$	Set of all integer numbers less or equal than x
$\mathbb{R} = (-\infty, \infty)$	Set of all real numbers.
$[n] = \{1, \dots, n\}$	Set of all natural numbers less or equal to n.
$\lfloor x \rfloor = \max\{k \in \mathbb{Z} : k \le x\}$	Largest integer part of x.
$\lceil x \rceil = \min\{k \in \mathbb{Z} : k \ge x\}$	Smallest integer bigger or equal than x.
$f = \mathcal{O}(g)$	g is an asymptotic upper bound for f.
$f = o(g)$	f is asymptotically negligible with respect to g.
$f = \Omega(g)$	g is an asymptotic lower bound for f.
$f = \Theta(g)$	g is an asymptotic lower and upper bound for f.
i.i.d.	independent and identically distributed.

Chapter 1

Introduction

1.1 Introduction

For a long time, researchers have been actively studying individual-based epidemiological models with a host and parasite dynamic (c.f. [8],[37],[9],[10],[34]). The purpose of this study is to explain how a population of parasites spreads among and infects a spatially structured population of hosts, where parasites require interaction with the hosts in order to reproduce and hosts have a resistance to parasite infection. There has been much research into the creation of mathematical models that capture a wide range of phenomena seen during the infection process while remaining sufficiently simplified to allow for rigorous treatment (c.f. [12],[42],[48]).
Building an interacting particle system that depicts the interaction between hosts and parasites at the micro-level is a common mathematical method for incorporating the spatial structure of the host population. In other words, it views each host and parasite as a distinct (discrete) entity, referred to as a particle of type H (resp. P), and it explains how each particle moves, interacts with other particles, reproduces, and dies. Liggett's books [30] and [31] are standard references for the construction and analysis of interacting particle systems.

The spread of a parasite population in a population of immobile hosts living on $\mathbb{Z}^d$, $d \geq 1$ can be described by a discrete time model that Telcs and Wormald introduced in [49]. They dubbed this model the egg model. To our best knowledge, Richard Durrett is credited with coining the term "frog model," which is the most common name for this model today ([39]). Renaming the terms "active" and "sleeping" frogs to reflect our perspective of parasites and hosts, the model works as follows. One host is placed on each site $x \in \mathbb{Z}^d \setminus \{\mathbf{0}\}$, and one parasite is placed at the site $\mathbf{0} \in \mathbb{Z}^d$. Until they are taken out of the system after getting infected, hosts stay in their starting position and don't move at all. All parasites move to a random, uniformly chosen neighboring site at each time step. Nothing more occurs if this site is occupied by other parasites or is empty. If a host lives on the site, however, the host gets infected, perishes, and is eliminated from the system forever. Additionally, the parasite that is infecting produces 2 new parasites at this vertex before dying. A later work by Popov, Alves, and Machado [2] expanded this model to include a random number of offspring, distributed as some $A \geq 1$ and independent of everything else for each infection. They demonstrated that the set of infected hosts satisfies a so-called shape theorem and grows linearly in time. Later, Ramirez and Sidoravicius in [40] modified the model and the shape theorem result to a continuous time setting, in which each parasite moves as a simple symmetric random walk in continuous time rather than moving all parasites at once. These results will be presented in a short survey in Section 2.1.

In these models, whenever a parasite attacks a host, the host immediately becomes infected and dies. This is obviously not a realistic assumption, as the host may have an immune system that can fend off a parasite infection and kill the attacking parasite without reproduction. In this thesis, we examine a similar host-parasite model as the frog model but with the addition that hosts have an immune response and might repel an infection attempt. Here is how we take this immune response into account. We consider a sequence $(p_m)_{m\in\mathbb{N}} \subset [0,1]$ and assume that every host can react to the occurrence of its previous parasite attacks. In the event that a parasite attacks the host at site $x \in \mathbb{Z}^d$ for the m-th time, the infection is prevented, independent of everything else, with a probability of $1 - p_m$. In this scenario, the parasite is eliminated and permanently removed from the system. With probability p_m, the infection attempt is successful, and a random number of parasites, independent of everything else and distributed as some A, which we may allow to be 0 with positive probability, are placed at site x. After a successful infection, the parasite kills the host, which is then permanently removed from the system. We call this model the Spatial Infection Model with host Immunity, or **SIMI** for short.

This mechanism brings the new issue of spatially dependent parasite deaths; hence, in this thesis, we will investigate, besides the speed of parasite spread, also the survival probability of the parasite population, i.e., the probability that at least one parasite remains alive at any given time. In [1], Alves, Machado, and Popov presented an alternative death mechanism for parasites, where at each step a parasite dies with probability p. We highlight the essential fact that, in their model, each parasite walks a geometrically distributed number of steps before being destroyed, so the routes taken by different parasites stay independent. This is no longer the case in our model, because knowing that a parasite has previously visited a specific vertex and successfully infected the host on that site affects the outcome of the next parasite that visits that site. In [1], they study parasites' survival and transience. For further information, see Section 2.1. In Chapter 5, we prove comparable results for our model in the particular case $p_m = p\delta_1(m)$, which means that either a host is infected the first time it is attacked with probability p or it is entirely immune and never gets infected.

The main focus of this thesis will be on examining the situation of the underlying graph $\mathbb{Z}$ and for which (moderate) assumptions on $(p_m)_{m\in\mathbb{N}}$ the behavior of linear growth, that is examined in the frog model, remains unaltered and under what assumptions on $(p_m)_{m\in\mathbb{N}}$ the system exhibits sublinear speed.
An important quantity is the number of parasites killed by a specific host, which is independent from everything else and distributed as

$$I := \inf\{m \geq 1 : B_m(p_m) = 1\},$$

where $\{B_m(p_m) : m \in \mathbb{N}\}$ are independent and $B_m(p_m)$ has a Bernoulli distribution with success probability p_m. Our first basic result demonstrates that a finite parasite population survives with positive probability if and only if $\mathbb{E}[I] < \mathbb{E}[A]$, which means that on average more offspring are generated at an infection than are needed for the infection to happen. In Chapter 3, we demonstrate that if

$$\mathbb{E}[I^{2+\varepsilon}] < \infty$$

for some $\varepsilon > 0$, the set of infected sites expands on a linear scale in time, conditioned on parasite survival. Also, for stronger moment assumptions on I, we derive a shape theorem.

In Chapter 4 we assume that I has a heavy tail, in the sense that for some $\alpha \in (1,2)$ and all $\alpha' > \alpha$ there is a $c > 0$ such that

$$\mathbb{P}(I \geq n) \geq cn^{-\alpha'}$$

for all $n \geq 1$. In this setting we show that the set of infected sites exhibits sublinear growth.

Chapter 2

Related work and main results

In this chapter, we lay out the thesis's main results, as well as provide a brief summary of related results from the literature.

Section 2.1 provides an overview of the frog model, which our SIMI generalizes. We will additionally emphasize how the strategies utilized may and will be applied to our model.
The results and proofs of the model evolving on the integer line $\mathbb{Z}$, which are included in Chapters 3 and 4, will be summarized in Section 2.2. The results in Chapter 3 have been obtained in collaboration with Cornelia Pokalyuk, and the results in Chapter 4 in collaboration with Matthias Birkner.
The scope of Chapter 5, which discusses the model with a particular choice of immunity distribution for different underlying graphs, will be finally outlined in Section 2.3.

2.1 A short survey on the frog model

The literature on the frog model that is relevant to the subject of this thesis will be briefly reviewed and discussed in this section. We will also demonstrate the extent to which we can utilize the approaches that have been provided in the literature for our model. We note that there is a vast literature regarding the frog model and its variants ([14],[36],[17],[20],[5],[18]), and, in this survey, we only discuss a selection of results that are in direct relation to our model.

To begin, we formally introduce the frog model described in the introduction. We consider the d-dimensional lattice $\mathbb{Z}^d$ with edge set $\{(x,y) \in \mathbb{Z}^d \times \mathbb{Z}^d : \|x-y\|_1 = 1\}$, where $\|(x_1, \dots, x_d)\|_1 := \sum_{i=1}^d |x_i|$.

Remark 2.1. *In this section on the frog model, we shall somewhat change (in comparison to the SIMI) the interpretation of how reproduction occurs following a successful infection for the sake of notation. As stated in the introduction, a random number of offspring are born following a host infection, and the infecting parasite dies. Since the amount of parasites in the frog model only grows, this would require the assumption that at least one offspring is produced in each infection. But because we intend to label every parasite in the subsequent construction, this interpretation would eliminate the label for the parasite that is causing the infection, needlessly complicating the notation. For this reason, in this section, we suppose that the infecting parasite survives the infection and we allow for the production of* 0 *offspring, which corresponded to* 1 *offspring in the previous interpretation. These two perspectives obviously result in the same process, which we now explain.*

Let the index set S be either $\mathbb{N}_0$ or $[0, \infty)$, and let A be a random variable that takes values in $\mathbb{N}_0$ with $\mathbb{P}(A \geq 1) > 0$. Since parasite death is not included in the conventional frog model, as was previously mentioned, the variable A represents the number of parasites that will be created during an infection, in addition to the infecting parasite. Let $\mathbf{A} = \{A_x : x \in \mathbb{Z}^d\}$ and $\{(Y_t^{x,i})_{t \in S} : i \in \mathbb{N}, x \in \mathbb{Z}^d\}$ be independent sets of random variables so that

- the number of offspring produced after the host at x is infected is described by the variable A_x, which is distributed as A for each $x \in \mathbb{Z}^d$. As a result, there will be $A_x + 1$ parasites at site x following the host's infection.
- according to $S = \mathbb{N}_0$ or $S = [0, \infty)$, the variables $(Y_t^{x,i})_{t \in S}$ are a simple symmetric random walk beginning in x in discrete (or continuous) time for every $x \in \mathbb{Z}^d, i \in \mathbb{N}$. The trajectory of the i-th parasite born on x will be defined as $(Y_t^{x,i})_{t \in S}$ for $x \in \mathbb{Z}^d$ and $i \leq A_x$. Again, we note that after a parasite is generated, its path is independent of everything else.

With $\inf \emptyset := \infty$, we set $t(x,y) = \inf\{t \in S | \exists 1 \leq i \leq A_x : Y_t^{x,i} = y\}$ for $x, y \in \mathbb{Z}^d$. If initially just the host at x gets infected, and every other host is still in the system, then, conditionally on $\{A_x \geq 1\}$,

$$T(x,y) := \inf_{\substack{k\in\mathbb{N}, x_0,x_1,\ldots,x_k\in\mathbb{Z}^d \\ x_0=x, x_k=y}} \{t(x_0,x_1)+t(x_1,x_2)+\ldots,t(x_{k-1},x_k)\}$$

is the time that the host at y gets infected. When just the host at x is initially infected and the offspring are determined by $\mathbf{A}$, we denote by

$$\mathcal{I}_t(x,\mathbf{A}) := \{y \in \mathbb{Z}^d : T(x,y) \le t\}$$

the set of sites that are not occupied by a host at time $t \in S$, i.e., the set of already infected sites.

We denote the frog model on $\mathbb{Z}^d$ with offspring given by $\mathbf{A} = \{A_x : x \in \mathbb{Z}^d\}$ and having the infecting parasite survive as $\mathrm{FM}(\mathbb{Z}^d, \mathbf{A})$. Keep in mind that collections $\mathbf{A}$ that are not i.i.d. are permitted by this definition. The definition of $\mathrm{FM}(G,\mathbf{A})$ for any graph $G = (V,E)$ is also evident.

2.1.1 Recurrence and transience

The recurrence and transience of parasites are the subjects of the first precise results on the frog model. A graph $G = (V,E)$ is referred to as vertex-transitive, as we recall, if for every $x, y \in V$ there exists a bijection $\phi : V \to V$ such that $\phi(x) = y$ and

$$\{\phi(u),\phi(v)\} \in E \iff \{u,v\} \in E.$$

This just means that the graph looks the same if viewed from different vertices.

Definition 2.2. *Let $G = (V,E)$ be a vertex-transitive graph, $\emptyset \in V$ be a distinguished vertex, and $\mathbf{A} = \{A_x : x \in V\}$ a collection of $\mathbb{N}_0$-valued random variables. If*

$$\mathbb{P}(\textit{if initially } \emptyset \textit{ is infected, then it is visited infinitely often by a parasite}) = 1.$$

then the frog model FM$(G,\mathbf{A})$ is referred to as recurrent. If not, it's referred to as transient.

Kosygina and Zerner demonstrated in [28, Theorem 1] that the probability above fulfills a zero-one law if $\mathbf{A}$ is an i.i.d. collection. For an explanation of their rather different notion of recurrence, see specifically Appendix A of their paper.

Going back to the frog model on $\mathbb{Z}^d$, we observe that even a single random walk is recurrent on $\mathbb{Z}^d$ for $d = 1, 2$. Because parasites remain in the system forever, the frog model's recurrence is trivially true. Higher dimensions, however, are more involved. In [49], Telcs and Wormald provided an answer to this question, demonstrating that if $d \geq 1$ and $A_x = 1$ almost surely for all $x \in \mathbb{Z}^d$, then the frog model is recurrent. We point out again that in the classic frog model, $A_x = 1$ means there are 2 parasites on the site x following the host's infection at site x. Popov later refined this result in [38] for a collection of offspring that is, in particular, not independent and identically distributed. For each $x \in \mathbb{Z}^d$, he assumed that

$$\mathbb{P}(A_x = 1) = 1 - \mathbb{P}(A_x = 0) = p(x)$$

for some function $p : \mathbb{Z}^d \to [0, 1]$ and that $\{A_x : x \in \mathbb{Z}^d\}$ is still independent. He determined the decay rate for p in this context, which separates the transient and recurrent phases.

Theorem 2.1 ([38] Theorem 1.1)**.** *Let* $d \geq 3$, $p : \mathbb{Z}^d \to [0, 1]$ *and* $\mathbf{A} = \{A_x : x \in \mathbb{Z}^d\}$ *be an independent collection with* $\mathbb{P}(A_x = 1) = 1 - \mathbb{P}(A_x = 0) = p(x)$ *for all* $x \in \mathbb{Z}^d \setminus \{\mathbf{0}\}$ *as well as* $A_{\mathbf{0}} = 1$ *almost surely. There exists* $\alpha_c(d) \in (0, \infty)$ *such that*

- *If* $\alpha < \alpha_c(d)$ *and* $p(x) \leq \frac{\alpha}{\|x\|^2}$ *for all* x *large enough, then* $FM(\mathbb{Z}^d, \mathbf{A})$ *is transient.*

- *If* $\alpha > \alpha_c(d)$ *and* $p(x) \geq \frac{\alpha}{\|x\|^2}$ *for all* x *large enough, then* $FM(\mathbb{Z}^d, \mathbf{A})$ *is recurrent.*

In particular, if $\mathbf{A}$ *is an i.i.d. collection, then the frog model* $FM(\mathbb{Z}^d, \mathbf{A})$ *is recurrent.*

We note that since the collection $\mathbf{A}$ considered in [38] is a priori not identically distributed, we cannot conclude that

$$\mathbb{P}(\mathbf{0} \text{ is visited infinitely many times}) = 0$$

in the transient case. In fact, in [38, Theorem 1.3] Popov constructs an example where this probability is strictly between 0 and 1.

2.1.2 Shape theorem on $\mathbb{Z}^d$

After being rescaled by time, the set $\mathcal{I}_n$ of infected hosts at time step n converges to a convex set. Alves, Machado, Popov, and Ravishankar initially proved this so-called shape theorem in [2] for the situation of $A = 1$ almost surely. Later, in [3], they extended it to any i.i.d. offspring collection $\mathbf{A}$. Recall that when we start with only the host at x infected, we denoted by $T(x, y)$ the time that the host at site y is infected, and

$$\mathcal{I}_n(x, \mathbf{A}) = \{y \in \mathbb{Z}^d : T(x, y) \leq n\}.$$

We set

$$\overline{\mathcal{I}}_n(x, \mathbf{A}) := \left\{ y + \left(-\frac{1}{2}, \frac{1}{2} \right]^d : y \in \mathcal{I}_n(x, \mathbf{A}) \right\} \subset \mathbb{R}^d.$$

The shape theorem now states the following quenched result.

Theorem 2.2 ([3] Theorem 1.1)**.** *For any $d \geq 1$ and any i.i.d. collection $\mathbf{A} = \{A_x : x \in \mathbb{Z}^d\}$, there is a non-empty convex symmetric set $\mathcal{A}_{d,\mathbf{A}} \subset \mathbb{R}^d$ such that conditionally on $A_0 \geq 1$, for almost all realizations $\eta \in \mathbb{N}_0^{\mathbb{Z}^d}$ of $\mathbf{A}$ and any $\varepsilon \in (0, 1)$ we have*

$$(1 - \varepsilon)\mathcal{A}_{d,\mathbf{A}} \subset \frac{\overline{\mathcal{I}}_n(\mathbf{0}, \eta)}{n} \subset (1 + \varepsilon)\mathcal{A}_{d,\mathbf{A}}$$

for all n large enough $\mathbb{P}_\eta$-almost surely. Here $\mathbb{P}_\eta = \mathbb{P}(\cdot|\mathbf{A} = \eta)$ is the conditional measure for a given offspring configuration η.

This theorem was later adapted by Ramirez and Sidoravicius in [40] to continuous time and $A = 1$ almost surely. In both cases the proof relies on Liggett's subadditive ergodic theorem [32] and that

$$T(x, y) \leq T(x, z) + T(z, y) \tag{2.1}$$

for any $x, y, z \in \mathbb{Z}^d$. The inclusion of parasite death eliminates this almost sure inequality in our model, the SIMI, as we will see in Chapter 3. This will occur because the parasite's path $Y^{x,i}$ is only utilized until it encounters a host and fails to create any offspring, be that due to the host's immunity or due to an infection with 0 offspring. But the hosts that remain in the system and, consequently, the routes taken by other parasites determine when this occurs; see specifically Example 5.5. Additionally, such an almost sure coupling will be prevented by the requirement to condition on the parasite population's survival in the SIMI. Because of this, even in the apparently simple situation of the underlying graph $\mathbb{Z}$, we will need to rely on an alternative construction that draws inspiration from the works [16],[15],[13] of Ramírez, Quastel, Comets, and Bérard and are discussed in the following section.

2.1.3 Renewal structure on $\mathbb{Z}$

A series of publications by Ramírez, Quastel, and Comets, as well as Ramírez and Bérard ([16],[15],[13]), established more detailed results using a renewal structure and the simple geometry of $\mathbb{Z}$. In their model initially one host on each x with $x > 0$ and $\eta(x)$ parasites on each x with $x \leq 0$ for some $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ are placed so that

$$\sum_{x \leq 0} \eta(x)\, \mathrm{e}^{\theta x} < \infty \tag{2.2}$$

for some $\theta > 0$. Due to the geometry of $\mathbb{Z}$, they can identify the state of the system by a tuple (r_t, η_t) with $\eta_0 = \eta$ and $r_0 = 0$. The quantity $r_t \in \mathbb{N}_0$, which they call the front of the process, represents the site that is infected at time t that is farthest from 0 in the positive direction, and $\eta_t \in \mathbb{N}_0^{\mathbb{Z}}$ represents the number of parasites at time t on each x with $x \leq r_t$. They examined a strong law of large numbers, a functional CLT, and large deviations for the process $(r_t)_{t\geq 0}$ as well as invariant distributions of η_t viewed from the front.

In Chapter 3 and Chapter 4, we will adopt initial configurations of type η on $\mathbb{Z}$, where only one half-line is filled with hosts and the other is filled with empty space or parasites. Their results rely on the construction of renewal times, which are as follows.

Theorem 2.3 ([15] Corollary 1)**.** *For $\theta > 0$ small enough and any $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ satisfying* (2.2)*, there is a sequence $(\kappa_n)_{n\in\mathbb{N}}$ of random times such that*

- *$\kappa_1, \kappa_2 - \kappa_1, \kappa_3 - \kappa_2, \ldots$ are independent, and*

  $$\{\kappa_{n+1} - \kappa_n : n \geq 1\}$$

  are identically distributed.

- $(r_{t\wedge\kappa_1})_{t\geq 0}, (r_{(\kappa_1+t)\wedge\kappa_2} - r_{\kappa_1})_{t\geq 0}, \dots$ *are independent and*

$$\{(r_{(\kappa_n+t)\wedge\kappa_{n+1}} - r_{\kappa_n})_{t\geq 0} : n \geq 1\}$$

  are identically distributed.

Furthermore $\mathbb{E}[|\kappa_{n+1} - \kappa_n|^2] < \infty$ *and* $\mathbb{E}[|r_{\kappa_{n+1}} - r_{\kappa_n}|^2] < \infty$.

Using this renewal structure, they showed the following results.

Theorem 2.4. *[[15] Theorem 1] For* $\theta > 0$ *small enough and any* $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *satisfying* (2.2)*, there exist* $v, \sigma^2 > 0$ *such that*

$$\lim_{t\to\infty} \frac{r_t}{t} = v$$

almost surely and

$$\sqrt{\varepsilon}\left(r_{\frac{t}{\varepsilon}} - \frac{vt}{\varepsilon}\right), \quad (t \geq 0)$$

converges in law as $\varepsilon \to 0$ *to a Brownian motion with variance* σ^2.

Theorem 2.5 ([15] Theorem 2)**.** *Let* $\theta > 0$ *be small enough and* $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *satisfying* (2.2)*. For* $t \geq 0$ *denote by* $\tau_{-r_t}\eta_t \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *the function*

$$\tau_{-r_t}\eta_t(x) := \eta_t(x + r_t), \quad (x \leq 0).$$

Then $(\tau_{-r_t}\eta_t)_{t\geq 0}$ *is a Feller process on the space of functions* $\mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *satisfying* (2.2)*. Also, there are exactly two invariant distributions* μ_∞ *and* $\delta_{\overline{0}}$*, where* $\delta_{\overline{0}}$ *is the point mass in the function* $\overline{0} : x \mapsto 0$*. For any* $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *satisfying* (2.2) *that is not the function* $\overline{0}$*,* $\tau_{-r_t}\eta_t$ *converges in distribution to* μ_∞ *as* $t \to \infty$*.*

Since any parasite at a site x with $x < r_{\kappa_n}$ at time κ_n moves diffusely, the renewal structure depends on establishing a lower growth bound for the front $(r_{\kappa_n+t})_{t\geq 0}$ that moves with linear speed using only newly (after time κ_n) generated parasites. In this way, only the newly generated parasites contribute to the front, because the old parasites cannot catch up to the linearly moving front. A comparable lower growth bound structure, which only takes into account parasites generated close to the front, is used in Chapter 3 and Chapter 4. We will establish a weakened version of the renewal structure, in which we can only demonstrate that the renewal times are almost surely finite, rather than that they have (certain) finite moments. Using this structure we show (only)

ergodicity of the process $(r_t)_{t\geq 0}$. Together with some conditional subadditivity property similar to (2.1), which, in particular, does not hold almost surely, this yields a strong law of large numbers (but no central limit theorem).
In a further work, Bérard and Ramírez obtain a large deviation principle based on a refinement of this renewal structure.

Theorem 2.6 ([13] Theorem 1)**.** *There exists a rate function* $I : [0,\infty) \to [0,\infty)$ *such that for every initial configuration* $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ *that satisfies* (2.2) *for all* $\theta > 0$, *we have*

$$\limsup_{t\to\infty} \frac{1}{t} \log \mathbb{P}\left(\frac{r_t}{t} \in C\right) \leq -\inf_{b\in C} I(b), \quad \textit{for all closed } C \subset [0,\infty)$$

and

$$\liminf_{t\to\infty} \frac{1}{t} \log \mathbb{P}\left(\frac{r_t}{t} \in G\right) \geq -\inf_{b\in G} I(b), \quad \textit{for all open } G \subset [0,\infty).$$

Also, with $v > 0$ *as in Theorem 2.4,* I *is identically zero on* $[0, v]$, *and it is positive, convex, and increasing on* (v,∞).

This result requires even finer control of the renewal structure than the functional CLT and thus is currently out of reach for our model.

2.1.4 Threshold frog model

In [26], Junge, McDonald, Pulla, and Reeves presented a variation of the frog model that also takes into account an immune response of hosts. Like our model, each host must be attacked a random number of times, i.i.d. over all hosts and according to some distribution, which they denote by τ. We note that, as described in the introduction, this viewpoint is equivalent to our viewpoint of having a sequence $(p_m)_{m\in\mathbb{N}} \subset [0,1]$ of success probabilities for the m-th infection attempt. In their model, however, in the event of an unsuccessful infection, the hosts do not eliminate the attacking parasite. Alternatively, the parasites can just sit on top of hosts, and once a parasite is generated, it is never taken out of the system. Therefore, by slightly modifying the proofs, the results on $\mathbb{Z}^d$ mentioned in Subsections 2.1.2 and 2.1.1 can be established. Consider the following construction to see this. Let $m := \inf\{k \geq 1 : \tau(k) > 0\}$, $\{A_x : x \in \mathbb{Z}^d\}$ be independent, and $\{I_x : x \in \mathbb{Z}^d\}$ be i.i.d. according to τ. We first put 1 host on each $x \in \mathbb{Z}^d \setminus \{\mathbf{0}\}$ with $I_x = m$ and $A_{\mathbf{0}}$ parasites on site $\mathbf{0}$. All other sites remain empty. The i-th parasite generated on site x travels according to a simple symmetric random walk $(Y_t^{x,i})_{t\in S}$. Whenever a parasite, say with label $(y,j)\in\mathbb{Z}^d\times\mathbb{N}$, jumps onto a site $x\in\mathbb{Z}^d$ with a (unmarked) host, it marks the host such that only the parasite with label (y,j) can interact with it. The host only becomes infected, and A_x many new parasites are created on site x, if the parasite with label (y,j) performs exactly $2(m-1)$ jumps back and forth between the site from whence it jumped onto x and the site x. If not, the host dies and is eliminated from the system without any new parasites getting generated. The threshold frog model, with immunities distributed as τ and offspring given by $\{A_x : x\in\mathbb{Z}^d\}$, clearly dominates this model. On the other hand, this model dominates a (possibly time-changed if $m>1$) frog model where the offspring are i.i.d., and the offspring at x are with probability $\frac{\tau(m)}{(2d)^{2(m-1)}}$ distributed as A_x and equal 0 with probability $1-\frac{\tau(m)}{(2d)^{2(m-1)}}$. This implies that the results found on $\mathbb{Z}^d$ also apply to the threshold frog model, as they were valid for any offspring distribution.

The threshold frog model is analyzed in [26] on the d-ary rooted tree $\widetilde{\mathbb{T}}^d$. The aforementioned construction is not applicable because results for arbitrary offspring distributions are not available in this setting (c.f. [22],[24]). The threshold frog model on $\widetilde{\mathbb{T}}^d$ with i.i.d. thresholds distributed as τ and i.i.d. offspring distributed as ξ is denoted by denoted by TFM$(\widetilde{\mathbb{T}}^d,\tau,\xi)$. They make the assumption that the offspring are Poisson distributed and i.i.d., with a parameter $\mu>0$ and obtain the following result on the recurrence of parasites.

Theorem 2.7 ([26] Theorem 1)**.** *Let τ be any distribution on $\mathbb{N}$ and let $\emptyset\in\widetilde{\mathbb{T}}^d$ be the root.*

$$\mu_c(\tau,\widetilde{\mathbb{T}}^d) := \inf\left\{\mu>0 : \begin{array}{c}\textit{in the TFM}(\widetilde{\mathbb{T}}^d,\tau,\mathrm{Poi}(\mu))\textit{ with }\emptyset\textit{ initially infected,}\\ \emptyset\textit{ is visited by infinitely often by parasites a.s.}\end{array}\right\}.$$

Then for all $d\geq 2$ we have

$$\mu_c(\tau,\widetilde{\mathbb{T}}^d)\in(0,\infty).$$

2.1.5 Frogs with geometric lifetime

Giving each parasite a geometric lifetime is one method to include parasite death that was introduced in [1] by Alves, Machado, and Popov. Every parasite in this discrete time model has a $1-p\in[0,1]$ chance of dying before taking a step.

Letting $\{D^{x,i} : x \in V, i \in \mathbb{N}\}$ be an i.i.d. collection of Geom$(1-p)$-distributed random variables, we thus substitute the stopped random walks

$$\{(Y_n^{x,i})_{0 \leq n < D^{x,i}} : x \in V, i \in \mathbb{N}\},$$

for the trajectories

$$\{(Y_t^{x,i})_{t \in \mathbb{N}_0} : x \in V, i \in \mathbb{N}\}.$$

On the graph $G = (V, E)$, with offspring given by $\mathbf{A} = \{A_x : x \in V\}$, and the probability p of surviving a step, we denote the frog model with geometric lifetime by $FM^*(G, \mathbf{A}, p)$.

This model was introduced by Alves, Machado, and Popov in [1] and later studied more extensively by Lebensztay, Machado, and Popov in [29] and by Rontes, Machado, and Sarkar in [19]. We present some of the results from [1], which in Chapter 5 will be (partially) adapted to our model.

To begin with, we note that using the construction from the introduction in this Section 2.1, that is, assigning each parasite its entire trajectory, it is not difficult to see that the system can be coupled in such a way that the event of survival parasites and the event of visiting $\mathbf{0}$ infinitely many times is monotone in p. As a result, we may provide the following definition.

Definition 2.3. *Let $G = (V, E)$ be a vertex-transitive graph and $\mathbf{A} = \{A_x : x \in V\}$ an i.i.d. collection of $\mathbb{N}_0$-valued random variables. We define*

$$p_c(G, \mathbf{A}) := \inf\{p \in (0, 1] : \mathbb{P}(\textit{the } FM^*(G, \mathbf{A}, p) \textit{ survives}) > 0\}$$

and $p_c'(G, \mathbf{A})$ as

$$\inf\left\{p \in (0,1] : \mathbb{P}\begin{pmatrix} \textit{if initially } \emptyset \textit{ is infected in the } FM^*(G, \mathbf{A}, p), \\ \textit{then it is visited infinitely often by a parasite} \end{pmatrix} > 0\right\}$$

The first result in [1] states that survival in this model on $\mathbb{Z}$ is almost surely impossible as long as the offspring numbers are not very high. In the SIMI considered in Chapter 5, this result will hold regardless of the offspring distribution.

Theorem 2.8 ([1] Theorem 1.1)**.** *If $\mathbb{E}[\max\{0, \log A\}] < \infty$, then $p_c(\mathbb{Z}, \mathbf{A}) = 1$.*

For higher dimensions they obtain a phase transition under some mild conditions.

Theorem 2.9 ([1] Theorem 1.3 and 1.4)**.** *Let $d \geq 2$ then*

- *if* $\mathbb{P}(A \geq 1) > 0$*, then* $p_c(\mathbb{Z}^d, \mathbf{A}) < 1$*.*

- *if* $\mathbb{E}[\max\{0, \log A\}^d] < \infty$*, then* $p_c(\mathbb{Z}^d, \mathbf{A}) > 0$*.*

These two results will also apply to our model in Chapter 5, where the positivity of the critical parameter even holds regardless of the offspring distribution. Also, they obtain the following asymptotic results for large dimensions, which we so far cannot show for our model but conjecture to be true as well.

Theorem 2.10 ([1] Theorem 1.8)**.** *It holds that*

$$\lim_{d\to\infty} p_c(\mathbb{Z}^d, \mathbf{A}) = \frac{1}{1+\mathbb{E}[A]},$$

where $\frac{1}{\infty} := 0$*.*

Regarding recurrence on $\mathbb{Z}^d$, they obtain the following result.

Theorem 2.11 ([1] Theorem 1.10 and 1.12)**.** *For any* $d \geq 1$ *we have the following:*

- *If* $\mathbb{E}[\max\{0, \log A\}^d] < \infty$*, then* $p_c'(\mathbb{Z}^d, \mathbf{A}) = 1$*.*

- *If* $\mathbb{P}(A \geq n) \geq (\log n)^{-\beta}$ *for some* $\beta < d$*, then* $p_c'(\mathbb{Z}^d, \mathbf{A}) = 0$*.*

In Chapter 5 we obtain a similar result, namely that recurrence cannot happen, i.e., $p_c' = 1$ on any graph, if $\mathbb{E}[A] < \infty$.
They also study this model on the d-regular tree $\mathbb{T}^d$ for $d \geq 3$ and obtain the following results.

Theorem 2.12 ([1] Theorem 1.2, 1.5 and 1.6)**.** *Let* $d \geq 3$*, then*

- *if there exists* $\delta > 0$ *such that* $\mathbb{E}[A^\delta] < \infty$*, then* $p_c(\mathbb{T}^d, \mathbf{A}) > 0$*.*

- *if* $\mathbb{E}[A^\delta] = \infty$ *for all* $\delta > 0$*, then* $p_c(\mathbb{T}^d, \mathbf{A}) = 0$*.*

Also,

- *if* $\mathbb{P}(A \geq 1) > 0$*, then* $p_c(\mathbb{T}^d, \mathbf{A}) < 1$*.*

The phase transition result will also apply to our model in Chapter 5, and on the tree $\mathbb{T}^d$ we are also able to show a similar result for the asymptotic of the critical parameter.

Theorem 2.13 ([1] Theorem 1.7)**.** *It holds that*

$$\lim_{d\to\infty} p_c(\mathbb{T}^d, \mathbf{A}) = \frac{1}{1+\mathbb{E}[A]},$$

where $\frac{1}{\infty} := 0$.

Finally, they show the following results for the recurrence on $\mathbb{T}^d$, which in our model are already encapsulated by the result of no recurrent phase on any graph described above.

Theorem 2.14 ([1] Theorem 1.9 and 1.11)**.** *For any* $d \geq 3$ *we have the following:*

- *If* $\mathbb{E}[A^\delta] < \infty$ *for all* $\delta \in (0,1)$*, then* $p_c'(\mathbb{T}^d, \mathbf{A}) = 1$.
- *If* $\mathbb{P}(A \geq n) \geq n^{-\beta}$ *for some* $\beta < \frac{\log(d-1)}{2\log d}$ *then* $p_c'(\mathbb{T}^d, \mathbf{A}) < 1$.

2.2 Infection on $\mathbb{Z}$

This section summarizes the results and proof strategies from Chapters 3 and 4. We consider the following scenario. The underlying graph is $\mathbb{Z}$, and initially only sites x with $x > 0$ are occupied by a host, and there is a possibly random $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$ such that each site x with $x \leq 0$ has $\eta(x)$ parasites. Because of the geometry of $\mathbb{Z}$, each host gets attacked separately. In particular, given the process is well-defined, for any $t \geq 0$ there is a site $r_t(\eta)$ such that there are no hosts on any site x with $x \leq r_t(\eta)$ and a configuration $\eta_t(\eta) \in \mathbb{N}_0^{\mathbb{Z}_{\leq r_t(\eta)}}$ such that there are $\eta_t(\eta)(x)$ parasites on each $x \leq r_t(\eta)$. This site $r_t(\eta)$ is referred to as the front of the process, while $\eta_t(\eta)$ represents the current parasite configuration. In Chapter 3, we analyze which conditions on η produce a well-defined process and prove that it is a strong Markov process. Furthermore, assuming $\mathbb{E}[A^2] < \infty$, we are able to show that it has the Feller property. To construct the process, we approximate the initial configuration η by a sequence $(\eta^l)_{l\in\mathbb{N}}$ with $\operatorname{supp} \eta^l \subset (-l, 0]$ such that $\eta^l \to \eta$ in an appropriate Polish space. Using a collection of independent random walks, we can construct the process starting with only finitely many parasites given by η^l. Then we show that for any $T \geq 0$ almost surely, uniformly over $t \in [0,T]$, the sequence $(r_t(\eta^l))_{l\in\mathbb{N}}$ is constant for large enough l and $((\eta_s(\eta^l))_{s\in[0,T]})_{l\in\mathbb{N}}$ converges in the uniform topology to some limit process. By construction, the resulting process will have càdlàg sample paths, because it is almost surely a uniform limit of a sequence of càdlàg paths. The strong Markov property will follow by showing that the corresponding semigroup preserves the bounded and uniformly continuous functions. The Feller property is obtained through calculating and bounding the quadratic variation of the martingale corresponding to the norm function on the state space. With that we can show that the norm of the process does not fall too fast with high probability, and hence for any compact set K there is a larger compact set K_0 such that starting outside of K_0 we enter K until time t only with small probability.

To explain the dynamics of the process, it is easier to think of the sequence $(p_m)_{m\in\mathbb{N}}$ of success probabilities for the m-th infection of a host. However, when analyzing the behavior, it is useful to count for each host how many infection attempts are needed before this host gets infected. We assume that the host at site x needs to be infected I_x-many times before it is infected and note that the collection $(I_x)_{x\geq 1}$ is i.i.d. and distributed as

$$I := \inf\{m \geq 1 : B_m(p_m) = 1\},$$

where $\{B_m(p_m) : m \geq 1\}$ is an independent collection and $B_m(p_m)$ is $\mathrm{Ber}(p_m)$ distributed for each $m \geq 1$. Also, we assume that after the host at site x with $x \geq 1$ is infected, there are A_x parasites born at site x, where $(A_x)_{x\geq 1}$ is i.i.d. distributed as some A.

Remark 2.4. *We point out that in contrast to the frog model in Section 2.1, we returned to the viewpoint of the infecting parasite to die even at a successful infection. Thus, after an infection at site x, there will be only A_x parasites sitting on vertex x, and we allow the case that $A_x = 0$ with positive probability.*

Because each host is attacked one after the other, we can directly calculate how many parasites need to die before the host at site x with $x > 0$ is infected. Namely, there are

$$\sum_{y=1}^{x} I_y$$

many parasites needed to infect the hosts at $1, 2, \ldots, x$. Since each infection of a site $y \in \{1, \ldots, x\}$ sets free A_y many new parasites, we obtain that the event of survival is given by

$$\bigcap_{x=1}^{\infty} \left\{ \sum_{y\leq 0} \eta(y) + \sum_{y=1}^{x-1} A_y \geq \sum_{y=1}^{x} I_y \right\}$$

and thus has positive probability if and only if

$$\max\left\{\mathbb{E}[A-I], \mathbb{P}\left(\sum_{y\leq 0}\eta(y)=\infty\right)\right\} > 0.$$

To analyze the speed of infection, we apply the following heuristic to explain the different behavior for finite and infinite second moments observed in Chapters 3 and 4. A typical random walk is at time t at a distance at most $\sqrt{t}$ from its origin. Hence, to infect a host at some site x, only the parasites at a distance of at most $\sqrt{t}$ participate in the infection with high probability. Since $\mathbb{E}[A] < \infty$, the law of large numbers implies that for large distances k, there are roughly $\Theta(k)$ parasites born inside $[x-k, x]$. Thus, in order to infect the host at x from site $x-1$, it takes roughly $\Theta(I_x^2)$ time units. See in particular Theorem 4.2 for a precise statement in this direction. In other words, the infection of site $n \gg 0$ takes roughly

$$\Theta\left(\sum_{x=1}^{n} I_x^2\right)$$

time units and thus grows linearly in n if I has finite second moments. If on the other hand I has a heavy tail, then the infection time of site n will grow superlinearly, which takes the speed of infection to a sublinear order.

2.2.1 Immunities with finite variance

In this section we consider the case that the variance of I is finite and will describe how we will, in Chapter 3, construct a lower bound for the front that is used to show linear growth. Assuming we are in the supercritical regime $\mathbb{E}[A] > \mathbb{E}[I]$, we will use tail bounds on the distribution of I to show that an auxiliary process, that is fed only from parasites born close to the front and lower bounds the actual process, already exhibits linear growth. Assuming for now that the initial configuration η is such that $(\eta(x))_{x\leq 0}$ is i.i.d. distributed as A, it works as follows. Consider some interval $[m, n)$ and note that until the time ρ_n at which the front leaves that interval, i.e., the first time that $r_{\rho_n} = n$, the parasites born at some site inside $[m, n)$ can only die at the hosts inside $(m, n]$. Hence, at time ρ_n, the amount $N_{m,n}$ of living parasites that were born at some site $x \in [m, n)$ is at least

$$\sum_{x=m}^{n-1} A_x - I_{x+1}. \tag{2.3}$$

Fixing some $\mathbb{E}[A] > \beta_A > \beta_I > \mathbb{E}[I]$, we obtain that for any $n \geq 1$ there is some random distance K_n, such

$$\sum_{x=n-K_n}^{n-1} A_x \geq \beta_A K_n \quad \text{and} \quad \sum_{x=n-K_n+1}^{n} Ix \leq \beta_I K_n,$$

and thus $N_{n-K_n,n} \geq (\beta_A - \beta_I)K_n$. Because living parasites cannot sit on top of hosts, this means that by the time that $\beta_I K_n$ of the parasites born inside $[n - K_n, n)$ reached the site n, the infection of site n must have already happened, which will give us the needed upper bound on the jump times of the front, and we will denote this auxiliary jump time by ν_n. Returning to arbitrary initial configurations, we find some random site $M \geq 1$, such that for any $n \geq 1$ we have $M + n - K_{M+n} \geq M$. Thus, (2.3) is a valid lower bound for $N_{M+n-K_{M+n},M+n}$, and ν_{M+n} is a valid upper bound for the jump time of the front onto site $M + n$.
Assuming that the tail of the immunity I falls fast enough, by supposing that $\mathbb{E}[I^{2+\varepsilon}] < \infty$ for some $\varepsilon > 0$, we will show that the distance K_n is small with sufficiently high probability such that the auxiliary jump times have finite expectation. By construction, two auxiliary jump times are independent conditionally on having disjoint intervals of influence $[n - K_n, n]$. Again using a small enough tail of I, we obtain that the sequence $(\nu_{M+n})_{n\in\mathbb{N}}$ is ϕ-mixing. This allows us to show that the auxiliary jump times satisfy an almost sure law of large numbers and thus the front of the process moves at least linearly fast. Coupling with a branching random walk shows that it, on the other hand, does not grow faster than linear. Precisely, we obtain the following.

Theorem 2.15. *[Theorem 3.2 in Chapter 3] Assume* $\mathbb{E}[I] < \mathbb{E}[A]$ *and that* $\mathbb{E}[I^{2+\varepsilon}] < \infty$ *for some* $\varepsilon > 0$*. Then for any initial configuration of parasites* $\eta \in \mathbb{N}_0^{\mathbb{Z}_{\leq 0}}$*, such that the process is well defined, we have conditioned on the survival of parasites*

$$0 < C_1 \leq \liminf_{t\to\infty} \frac{r_t}{t} \leq \limsup_{t\to\infty} \frac{r_t}{t} \leq C_2 < \infty$$

almost surely for some (deterministic) constants C_1, C_2*.*

Assuming smaller tails of I, we can also obtain estimates on the probability to move slower than linearly, which corresponds to a large deviation of the auxiliary jump times. This will allow us to construct a renewal time as in

Section 2.1 that we can show to be finite almost surely. In particular, this implies that the sequence of jump times of the front has a trivial tail sigma field and thus the limits considered in Theorem 2.15 are deterministic on the event of survival. Together with a subadditivity property of the front, we can show a law of large numbers for the front on an event with positive probability, which, by the non-randomness of the limits, then implies the law of large numbers on the whole event of survival. Precisely, we will show the following.

Theorem 2.16 (Theorem 3.3 in Chapter 3). *Suppose that for some $\alpha > \frac{3+\sqrt{11}}{2}$ and $\varepsilon_A > 0$ we have*

$$\mathbb{E}[A] > \mathbb{E}[I], \mathbb{E}[I^{2\alpha}] < \infty, \mathbb{E}[A^{\frac{4}{4\wedge\alpha-3}+\varepsilon_A}] < \infty \quad \textit{and} \quad \mathbb{P}(A \geq I+4) > 0$$

and initially there is only an amount of parasites distributed as A on vertex 0. Then there is a $\gamma > 0$ such that conditioned on the survival of parasites

$$\lim_{t\to\infty} \frac{r_t}{t} = \gamma$$

almost surely.

2.2.2 Immunities with a heavy tail

In this subsection we summarize the results and techniques used in Chapter 4. We assume that for some $\alpha \in (1,2)$ we have

$$\mathbb{P}(I \geq n) = l(n)n^{-\alpha} \tag{2.4}$$

for all $n \in \mathbb{N}$ and some slowly varying function l.

Under the assumption $\mathbb{E}[A] > \mathbb{E}[I]$, we can repeat the construction from the previous Section 2.2.1 and again obtain a site $M \geq 1$ and sequences $(K_{M+n})_{n\geq 1}$, $(\nu_{M+n})_{n\geq 1}$ as before. However, the auxiliary jump times will no longer have finite expectations but only have finite moments of any order $q < \frac{\alpha}{2}$. Hence, using this lower bound for the front, we will show that r_t grows faster than any function t^q for $q < \frac{\alpha}{2}$. On the other hand, for any $q > \frac{\alpha}{2}$, we will be able to show that it grows slower than t^q, in particular that it exhibits sublinear speed. The idea is the following. As described in the introduction of this section, to overcome an immunity of height $h \gg 1$, it takes $\Theta(h^2)$ time units. Now observing that an immunity of at least height h appears with probability $l(h)h^{-\alpha}$ and immunities are independent, this means that asymptotically, there always is an immunity of height $n^{\frac{1}{\alpha}-\varepsilon}$ before site n for any $\varepsilon > 0$. This barrier alone will slow down the time till infection of site n to the scale $n^{\frac{2}{\alpha}-\varepsilon}$. This will imply the following:

Theorem 2.17 (Theorem 4.1 and 4.5 in Chapter 4)**.** *Suppose that I satisfies* (2.4) *for some $\alpha \in (1,2)$. Then for any $q > \frac{\alpha}{2}$ we have*

$$\lim_{t\to\infty} \frac{r_t}{t^q} = 0.$$

Also, for any $q < \frac{\alpha}{2}$ we have conditioned on the survival of parasites

$$\lim_{t\to\infty} \frac{r_t}{t^q} = \infty.$$

In Chapter 4, we present a refinement of this theorem, where we bring the scale down to $t^{\frac{\alpha}{2}}\bar{l}(t)$ for some slowly varying function $\bar{l}$.
As part of the proof, we obtain a result that might be of independent interest. It is a refinement of the heuristic that it takes $\Theta(h^2)$ time units to infect a barrier of height $h \gg 1$.

Theorem 2.18 (Theorem 4.2, 4.3, and 4.4 in Chapter 4)**.** *Let $\mathbb{E}[A^2] < \infty$ and suppose that initially each site x with $x \leq 0$ is inhabited by an i.i.d. number of parasites distributed as A. For $\iota \in \mathbb{N}$ let X_ι be the infection time of site* 1*, conditioned on $I_1 = \iota$ and set*

$$c_\mu := \mathbb{E}[A]\sqrt{\frac{2}{\pi}}, \quad c_\sigma := \left(\frac{\mathbb{E}[A](2-\sqrt{2})}{\sqrt{\pi}} + \mathbb{V}[A]\frac{2\sqrt{2}-2}{\sqrt{\pi}}\right).$$

Then

$$K_\iota := \frac{X_\iota - \left(\frac{\iota}{c_\mu}\right)^2}{\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3}} \xrightarrow[\iota\to\infty]{\mathrm{d}} \mathcal{N}(0,1).$$

If in addition $\mathbb{E}[\exp(\lambda A)] < \infty$ for some $\lambda > 0$, then for any monotone function $f \in o\left(\sqrt{\iota}\right)$ there are constants $C_1, c_1 > 0$ such that for all $\iota \geq 1$ we have

$$\mathbb{P}(|K_\iota| \geq f(\iota)) \leq C_1 \exp\left(-c_1 f(\iota)\right).$$

Also, in this case there is a constant $c_3 > 0$ such that for any $\iota \geq 1$ and any $0 \leq w \leq c_3\iota^{\frac{1}{6}}$ we have

$$\frac{\mathbb{P}(K_\iota > w)}{1-\Phi(w)} = 1 + \mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right) \text{ and } \frac{\mathbb{P}(K_\iota \leq -w)}{\Phi(-w)} = 1 + \mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right),$$

where Φ is the cdf of the standard normal distribution.

In particular, the second part of this theorem implies that if I has a regularly varying tail with index $\alpha \in (1, 2)$, then $X_{I_1} = \rho_1$ has a regularly varying tail with index $\frac{\alpha}{2}$.

2.3 Infection on different graphs for a two-type host population

In this section we summarize the results from Chapter 5. We assume that there are only two types of hosts: susceptible hosts, which appear with probability p for some $p \in (0, 1]$, and completely immune hosts, which appear with probability $1 - p$. This corresponds to taking the sequence $(p_m)_{m \in \mathbb{N}}$ of success probabilities as $p_m = p\delta_1(m)$ for $m \geq 1$. This process is quite similar to the frog model with geometric lifetimes introduced in Section 2.1. In fact, some of the results and proofs can directly be translated to this model.

An important aspect is that, under the assumption that every infection produces at least one offspring, we can again take the viewpoint from Section 2.1 that the infecting parasite survives the infection. In that way, we can, for each site x, assign the set $\mathcal{R}_x$ of sites that will be visited by some parasite that was born after the host at x is infected. The collection of these sets is then conditionally independent, given which hosts are susceptible and which are completely immune. Also, in this way the infection process actually turns into a percolation problem, where a site y is reachable from x if $y \in \mathcal{R}_x$. Questions like the survival of frogs or the recurrence to the origin can then be expressed in terms of this percolation. For example, the survival of parasites is equivalent to the existence of a pairwise distinct sequence $\mathbf{0} = x_0, x_1, \ldots$ such that $x_{n+1} \in \mathcal{R}_{x_n}$ for all $n \in \mathbb{N}_0$. Recurrence to the origin would just mean that also $\mathbf{0} \in \mathcal{R}_{x_n}$ for infinitely many $n \in \mathbb{N}$.

Using this approach, we will analyze this model on general graphs and specifically show that the survival probability of parasites undergoes a phase transition on the integer lattice $\mathbb{Z}^d$ and the d-regular tree $\mathbb{T}_d$. Also under the mild assumption that $\mathbb{E}[A] < \infty$, we show that this model is never recurrent on any graph, because the completely immune hosts remain in the system forever.

Chapter 3

Infection on $\mathbb{Z}$: the finite Variance regime

3.1 Introduction

We are interested in the spread of a parasite in a spatially distributed host population. We model this scenario by placing susceptible (immobile) hosts on the vertices of a graph G. Later we will consider mainly $\mathbb{Z}$, that is, $G = (V, E)$ with vertex set $V = \mathbb{Z}$ and edge set $E = \{\{x, y\} : \|x - y\|_1 = 1\}$. Parasites infect the hosts and move on the lattice according to symmetric simple random walks in continuous time. As hosts often have an immune response against infections, we assume that whenever a parasite tries to infect a host, parasite reproduction might be prevented, and the parasite gets killed. In the case of a successful infection, the parasite kills the host and sets free a (possibly random) number of offspring. For simplicity we assume that hosts do not reproduce.

We can view this model as an extension of the frog model that has been introduced by Telcs and Wormland (1999, [49]). The classical frog model is an interacting particle system on some graph $G = (V, E)$, which evolves under the following dynamics. There are two types of particles, which are usually called *active frogs* and *sleeping frogs*, and each site $v \in V$ can host a finite number of frogs of the same type. Active frogs, independently of everything else, perform simple nearest neighbor random walks on G, and sleeping frogs do not move at all. Whenever an active frog jumps onto a vertex $v \in V$, all sleeping frogs on v immediately transform into active frogs and start performing their own simple nearest neighbor random walk, starting at v. The model can be formulated both in continuous and discrete time; however, we focus on the continuous case here. Interpreting active frogs as parasites and sleeping frogs as the offspring produced at an infection, in the classical frog model, an infection is always successful, and infecting parasites survive the infection. Therefore, in particular, the population of frogs can only grow larger.

In [2], Alves, Machado, and Popov showed a shape theorem for the set $S_d(n)$ of vertices visited by some active frog up to time n when $G = (\mathbb{Z}^d, \{\{x, y\} : \|x - y\|_1 = 1\})$ and at $n = 0$ there is one active frog in 0 and one sleeping frog on each other site $x \in \mathbb{Z}^d \setminus \{0\}$. Precisely, they showed that there is a convex (deterministic) set $\mathcal{A}_d$ such that for any $\varepsilon \in (0, 1)$

$$(1-\varepsilon)\mathcal{A}_d \subset \frac{S_d(n)}{n} \subset (1+\varepsilon)\mathcal{A}_d$$

for all n large enough almost surely. In [3] they improved this result to hold for random initial configurations, placing an i.i.d. number of sleeping frogs on each vertex. For the frog model in continuous time, Ramírez and Sidoravicius showed in [40] the shape theorem on $\mathbb{Z}^d$ with one sleeping frog on each site.

In the one-dimensional, time-continuous case, Quastel, Comets, and Ramírez improved upon this result in [15] and obtained a central limit theorem for the fluctuations of $S_1(t)$ around $\mathcal{A}_1 t$, and a large deviation principle was shown by Bérard and Ramírez in [13].

Next to the trivial survival of the frogs in the classical model, another main difference is that in the classical frog model, using a collection of independent simple symmetric random walks to assign each frog its trajectory after waking up yields an easy way to couple initial configurations in a monotone way. However, doing this in our model will not be a monotone coupling because when and where a specific parasite dies depends on the location of hosts that are still asleep; see Example 3.51. Hence, the trajectories of parasites will no longer be independent in this coupling. In particular, this means that the techniques relying on this monotone coupling, such as the sub-additivity arguments used in Ramirez and Sidoravicius ([40]) to show a shape theorem, cannot be applied to our model.

Importantly, techniques used by Quastel, Comets, and Ramírez in [16],[15] do not rely on this monotone coupling of the frog model but on the construction of a renewal structure. Inspired by these methods, we investigate our model by constructing a sequence of sites, from which the environment of future immunities and offspring numbers guarantees linear growth.

3.2 (Informal) model definition and main results

3.2.1 The spatial infection model with host immunity

Consider the graph $G = (\mathbb{Z}, \{\{x,y\} : \|x-y\|_1 = 1\})$ and consider two sites $\ell \leq r$ with $\ell \in \mathbb{Z} \cup \{-\infty\}$ and $r \in \mathbb{Z}$. Place one host at each vertex x with $x \notin [\ell, r]$. Equip each host with an immunity and denote the immunity corresponding to the host occupying the vertex x (if there is one) by I_x. We assume that $(I_x)_{x \notin [\ell,r]}$ is an i.i.d. sequence of $\mathbb{N}$-valued random variables, distributed as some I, and that I has a finite expectation, which we denote by μ_I. Furthermore, let $\eta \in \mathbb{N}_0^{\mathbb{Z}}$ with $\operatorname{supp} \eta \subset [\ell, r]$. Place on site $x \in [\ell, r]$ initially $\eta(x)$ parasites. Each parasite performs independently of all other parasites a time-continuous symmetric random walk with rate 2. Whenever a parasite jumps onto a vertex that is occupied by a host, the parasite attacks the host. If the initial immunity I_x of the host at site x is equal to i and the host is attacked for the ith time, the host and the parasite die, and A_x parasites are released at x, where $(A_x)_{x \in \mathbb{Z}}$ is an i.i.d. sequence of N_0-valued random variables, distributed as some A, independent of I, $(I_x)_{x \notin [\ell,r]}$ and A has a finite expectation, which we denote by μ_A. Otherwise, if the host has been attacked less than i times, only the parasite dies and the host survives. If a parasite jumps to an empty site, the parasite survives. In Section 3.5 we give a rigorous definition of the process on a state space that contains the position of the sites occupied by parasites or hosts as well as the remaining immunities of the hosts at sites next to sites free of hosts and show that it is a well-defined strong Markov process if the initial distribution of parasites is sufficiently well behaved. We call the corresponding process the spatial infection model with host immunity (SIMI, for short) with initial condition $\zeta = (\ell, r, \eta)$. If $\ell = -\infty$, only to the right of r hosts are placed. We call this case a one-sided host population and correspondingly the case $\ell \in \mathbb{Z}$ a two-sided host population.

Given the process is well defined, we can determine at each time point $t \geq 0$ the largest subinterval of $\mathbb{Z}$ which is not occupied by any host. We denote the boundaries of this interval by

$$r_t(\zeta) := \sup\left\{ x \geq r : \begin{array}{c} \text{In the SIMI with initial configuration } \zeta \\ \text{at time } t, \text{ there is no living host at site } x \end{array} \right\}$$

and call it the *right front* of the process and call (in the case $\ell \in \mathbb{Z}$)

$$\ell_t(\zeta) := \inf\left\{ x \leq \ell : \begin{array}{c} \text{In the SIMI with initial configuration } \zeta \\ \text{at time } t, \text{ there is no living host at site } x \end{array} \right\}$$

the *left front* of the process. Similarly, we denote by $\eta_t(\zeta) \in \mathbb{N}_0^{\mathbb{Z}}$ the amounts of parasites on each site at time t, by $\iota_t^\ell(\zeta)$ the remaining immunity of the host at site $\ell_t(\zeta) - 1$ at time t, and by $\iota_t^r(\zeta)$ the remaining immunity of the host at site $r_t(\zeta) + 1$ at time t. Then $(\ell_t, r_t, \eta_t, \iota_t^\ell, \iota_t^r)$ is enough information to describe the SIMI as a Markov process, and we obtain the following theorem.

Theorem 3.1. *There is a probability space $\mathbf{\Omega}' = (\Omega', \mathcal{F}', \mathbf{P}')$ such that for any (possibly random) initial placement of parasites and hosts given by $\zeta = (\ell, r, \eta)$ defined on some probability space $\mathbf{\Omega}'' = (\Omega'', \mathcal{F}'', \mathbf{P}'')$ and fulfilling the condition*

$$\mathbf{E}''\left[f_\theta(\zeta)\right] := \mathbf{E}''\left[\sum_{x\in\mathbb{Z}} \eta(x)\, \mathrm{e}^{\theta(x-r)}\right] < \infty$$

for some $\theta > 0$, the SIMI with initial configuration ζ can be constructed as a strong Markov process on the state space $(\mathbb{S}_\theta, d_\theta)$ with càdlàg paths on the product probability space $\mathbf{\Omega} = (\Omega, \mathcal{F}, \mathbf{P})$ of $\mathbf{\Omega}'$ and $\mathbf{\Omega}''$, where the state space $\mathbb{S}_\theta$ is given by

$$\left\{ \zeta = (\ell, r, \eta, \iota^\ell, \iota^r) \in (\mathbb{Z} \cup \{-\infty\}) \times \mathbb{Z} \times \mathbb{N}_0^{\mathbb{Z}} \times \mathbb{N} \times \mathbb{N} : \begin{array}{c} \ell \leq r, \operatorname{supp} \eta \subset [\ell, r] \\ f_\theta(\zeta) < \infty \end{array} \right\}$$

and

$$\begin{aligned} d_\theta(\zeta, \zeta') := {} & |r - r'| + |\ell - \ell'| + |\iota^\ell - (\iota^\ell)'| + |\iota^r - (\iota^r)'| \\ & + \sum_{x\in\mathbb{Z}} |\eta(x) - \eta'(x)|\, \mathrm{e}^{-\theta(x-(r\wedge r'))}. \end{aligned}$$

If in addition $\mathbb{E}[A^2] < \infty$, then this Markov process possesses the Feller property.

Remark 3.1. *In Section 3.5 we actually not only construct the process on $\mathbb{S}_\theta$ but also on a larger state space, which tracks additional information of the individual parasite trajectories. This will be helpful in the proof of our main results. In Section 3.5.2 we will construct the process carrying only the information above.*

Remark 3.2. *Via the distribution of I it is possible to model different responses of the hosts to a parasite. Taking any sequence $(p_m)_{m\in\mathbb{N}} \subset [0,1]$ and an independent sequence $(B_m)_{m\in\mathbb{N}}$ with $B_m \sim Ber(p_m)$, we can set*

$$I := \inf\{m \in \mathbb{N} : B_m = 1\}.$$

This means that the m-th infection attempt is successful with probability p_m. In the case that $p_m \equiv p$, this corresponds to no response of the host to previous infection attempts and a geometrically distributed I. However, taking $p_m \downarrow 0$ corresponds to hosts building up an immunity against infections each time that they successfully defend against an infection attempt. Taking on the other hand, $p_m \uparrow 1$ corresponds to parasites continuously damaging the host's defenses until they eventually succeed in infecting it. Controlling the speed at which p_m goes to 0 (resp. to 1) corresponds to how fast this immunity builds up (resp. how quickly the host gets damaged). For example, the choice $p_m = \frac{\alpha}{m+\alpha}$ with some $\alpha > 1$ yields the behavior $\mathbf{P}(I > m) \sim Cm^{-\alpha}$ for some constant $C = C(\alpha)$.

3.2.2 Main results on survival and speed of spread

Next we come to our main results concerning the probability of survival of the parasite population as well as the speed at which the parasite population spreads in the host population when we condition on survival.

For the rest of the chapter we fix some initial configuration ζ defined on $\mathbf{\Omega}''$ as in Theorem 3.1. We note that by construction the initial configuration ζ is independent of the immunities, the offspring numbers, as well as the trajectories of parasites that are used in the construction of the process, which are defined on $\mathbf{\Omega}'$. The SIMI with this random initial configuration is constructed by first sampling ζ and then constructing the process conditionally on the realization. The first results concern the probability of survival of the parasite population for infinite time, i.e., the following event:

$$\mathcal{S}(\zeta) := \bigcap_{t\geq 0} \left\{ \begin{array}{c} \text{In the SIMI with initial configuration } \zeta, \\ \text{there is at least one living parasite at time } t \end{array} \right\}.$$

One-sided host population

In this subsection we consider the case $\ell = -\infty$ and assume w.l.o.g. $r = 0$, that is, initially all sites to the left of and including the origin are either empty or occupied by parasites, and hosts are placed on all sites to the right of the origin. Since the initial condition is in this case always of the form $\zeta = (\ell, r, \eta) = (-\infty, 0, \eta)$, we shortly write η for the initial condition instead of ζ.

Since random walks are recurrent on $\mathbb{Z}$, as long as the parasite population is alive, at least one parasite will hit the front in a finite amount of time. Thus, the event of survival only depends on $(A_x)_{x>0}$ and $(I_x)_{x>0}$ and is given by

$$\mathcal{S}(\zeta) = \mathcal{S}(\eta) = \bigcap_{n=1}^{\infty} \left\{ \sum_{x \leq 0} \eta(x) + \sum_{k=1}^{n-1} A_k \geq \sum_{j=1}^{n} I_j \right\}.$$

This is just the event that a random walk with step distribution $A - I$ and starting at $\sum_{x \leq 0} \eta(x) - I_1$ stays non-negative. Hence, we can infer the classical result from [47, Lemma 6.1.3] to obtain the following

Lemma 3.3. *Assume $\mu_A := \mathbf{E}[A] > \mu_I := \mathbf{E}[I]$, and the initial configuration η satisfies*

$$\mathbf{P}\left(\sum_{x \leq 0} \eta(x) \geq I \right) =: \delta_0 > 0$$

then

$$\mathbf{P}(\mathcal{S}(\eta)) \geq \delta_0 \exp\left(-\sum_{n=1}^{\infty} \frac{1}{n} \mathbf{P}\left(\sum_{k=1}^{n} A_k < \sum_{j=2}^{n+1} I_j \right) \right) > 0.$$

If $\mu_A \leq \mu_I$, then

$$\mathcal{S}(\eta) = \left\{ \sum_{x \leq r} \eta(x) = \infty \right\}$$

Remark 3.4. *If η is such that*

$$\sum_{x \leq 0} \eta(x) \overset{d}{=} A,$$

then

$$\mathbf{P}(\mathcal{S}(\eta)) = \exp\left(-\sum_{n=1}^{\infty} \frac{1}{n} \mathbf{P}\left(\sum_{k=1}^{n} A_{k-1} < \sum_{j=1}^{n} I_j \right) \right).$$

Also, trivially, the inclusion

$$\left\{ \sum_{x \leq 0} \eta(x) = \infty \right\} \subset \mathcal{S}(\eta)$$

holds.

In the following, we sometimes drop the reference to the initial configuration and just write $\mathcal{S}$ instead of $\mathcal{S}(\eta)$ and assume we fixed some initial configuration η.

If the random variables $(I_k)_{k\in\mathbb{Z}}$ are geometrically distributed for some parameter p with $0 < p < 1$, the survival probability is given by the survival probability of a Galton-Watson process.

Lemma 3.5. *Suppose that $I \sim$Geom(p) for some $p \in \left(\frac{1}{\mu_A}, 1\right]$ and $\eta(x) = A_0\delta_{x,0}$, where A_0 is distributed as A conditioned to be > 0. Then*

$$\mathbf{P}(\Omega \setminus \mathcal{S}) = \sum_{m=1}^{\infty}\sum_{n=1}^{\infty}\mathbf{P}(A_0 = m|A_0 > 0)\frac{m}{n}\mathbf{P}\left(m + \sum_{k=1}^{n}\tilde{A}_k B_k = n\right) < 1$$

where $(B_k)_{k\geq 1}$ is an i.i.d. sequence of Bernoulli variables with parameter p, independent of $(\tilde{A}_k)_{k\geq 1}$, and $(\tilde{A}_k)_{k\geq 1}$ are independent and distributed as A_1. If, for some $a \in \mathbb{N}$, $A = a$ almost surely, we get the explicit formula

$$\mathbf{P}(\Omega \setminus \mathcal{S}) = \sum_{n=1}^{\infty}\frac{1}{n}\binom{an}{n-1}p^{n-1}(1-p)^{n(a-1)+1}$$

which is the unique solution $y \in (0, 1)$ to the equation

$$y = (py + 1 - p)^a. \tag{3.1}$$

Proof. Since the random variables $(I_k)_k$ are geometrically distributed, the number of parasites that are generated in n infection events (or attempts) is distributed as $\sum_{i=1}^{n} B_i\tilde{A}_i$. At the onset of the infection process, A_0 parasites are generated. Since at each infection event, the infecting parasite dies, the parasite population gets extinct at the infection event, at which for the first time the number of parasites equals the total number of happened infection events, i.e., at the τ-th infection event, with

$$\tau = \inf\{n|A_0 + \sum_{i=1}^{n} B_i\tilde{A}_i = n\}.$$

This number is the first generation at which the position $S_n = X_0 + \cdots + X_n$ of a random walk $(X_i)_{i\geq 0}$ with step sizes $X_i - X_{i-1} = B_i\tilde{A}_i - 1$ and started in $X_0 = A_0$ particles is 0. By the hitting time theorem [50],

$$\mathbf{P}(\tau = n|A_0 = m) = \frac{m}{n}\mathbf{P}(S_n = 0|S_0 = m).$$

Summing over all possible values for A_0 yields the first statement.
For the second statement, i.e., if $A = a$ almost surely, we calculate

$$\begin{aligned}
\mathbf{P}(\Omega \setminus \mathcal{S}) &= \sum_{m=1}^{\infty} \sum_{n=1}^{\infty} \mathbf{P}(A_0 = m | A_0 > 0) \frac{m}{n} \mathbf{P}\left(m + \sum_{k=1}^{n} \tilde{A}_k B_k = n\right) \\
&= \sum_{\ell=1}^{\infty} \frac{a}{a\ell} \mathbf{P}\left(\sum_{k=1}^{a\ell} B_k = \frac{a\ell - a}{a}\right) \\
&= \sum_{\ell=1}^{\infty} \frac{1}{\ell} \binom{a\ell}{\ell - 1} p^{\ell-1} (1-p)^{\ell(a-1)+1}.
\end{aligned}$$

Renaming ℓ into n yields the statement.
For the last statement, i.e., that the extinction probability solves equation (3.1), note that the extinction probability of the parasite population is equal to the extinction probability of a branching process with an offspring distribution with probability weights $p_0 = 1 - p$, $p_a = p$, and $p_i = 0$ for all $i \neq a$ started with a individuals. The generating function of this offspring distribution is $f(z) = (1-p+pz^a)$. Hence, a branching process with this offspring distribution started with a single individual dies with probability z, where $z \in (0, 1)$ solves

$$z = (1 - p + pz^a).$$

If the branching process is started with a individuals the extinction probability y solves

$$y = z^a = (1 - p + pz^a)^a = (1 - p + py)^a,$$

which yields the claim. □

Remark 3.6. *For geometrically distributed immunities, each infection attempt is successful with probability p, independent of how many attempts were already made at this host. Thus, the extinction probability is bounded by the expression above for any underlying infinite graph (V, E) on which the SIMI evolves and any initial host configuration. For recurrent graphs and infinitely large host populations, the extinction probability coincides.*

For immunity distributions that are not memoryless, each infection attempt's success depends on the number of previous infection attempts; thus the extinction probability cannot be bounded independent of the trajectories of parasites and hence depends on the underlying graph structure.

Definition 3.7. *For some fixed random initial configuration* η *such that* $\mathbf{P}(\mathcal{S}(\eta)) > 0$ *we denote by*

$$\mathbb{P}^\eta := \mathbf{P}(\cdot|\mathcal{S}(\eta))$$

the measure, conditioned on the survival of the parasites for infinite time. Similar to for $\mathcal{S}$*, we often drop the reference to the initial configuration and just write* $\mathbb{P}$ *instead of* $\mathbb{P}^\eta$*. Also, we denote by* $\mathbb{E}^\eta$ *(resp. just* $\mathbb{E}$*) the corresponding expectation operator.*

Given survival, we are interested in the speed of growth. Under mild conditions on the distribution of I, we obtain that (r_t) exhibits ballistic growth.

Theorem 3.2. *Assume that the distributions* A, I *fulfill the following conditions:*

$$\mathbf{E}[A] = \mu_A > \mu_I = \mathbf{E}[I] \tag{3.2}$$

and there is an

$$\alpha > 1 \quad \text{such that} \quad \mathbf{E}[I^{2\alpha}] < \infty. \tag{3.3}$$

Let η *be any initial configuration such that the SIMI is well-defined in the sense of Theorem 3.1 and satisfies* $\mathbf{P}(\mathcal{S}(\eta)) > 0$*. Then there are constants* C_1, C_2 *such that conditioned on the survival of the parasite population, i.e., under* $\mathbb{P}^\eta$*, almost surely the following holds:*

$$0 < C_1 \leq \liminf_{t\to\infty} \frac{r_t}{t} \leq \limsup_{t\to\infty} \frac{r_t}{t} \leq C_2 < \infty.$$

In Figure 3.2.2 below we depict a simulation of the process $(r_t)_{t\geq 0}$ for α close to the boundary of the parameter range in Theorem 3.2, namely $\alpha > 1.05$. We

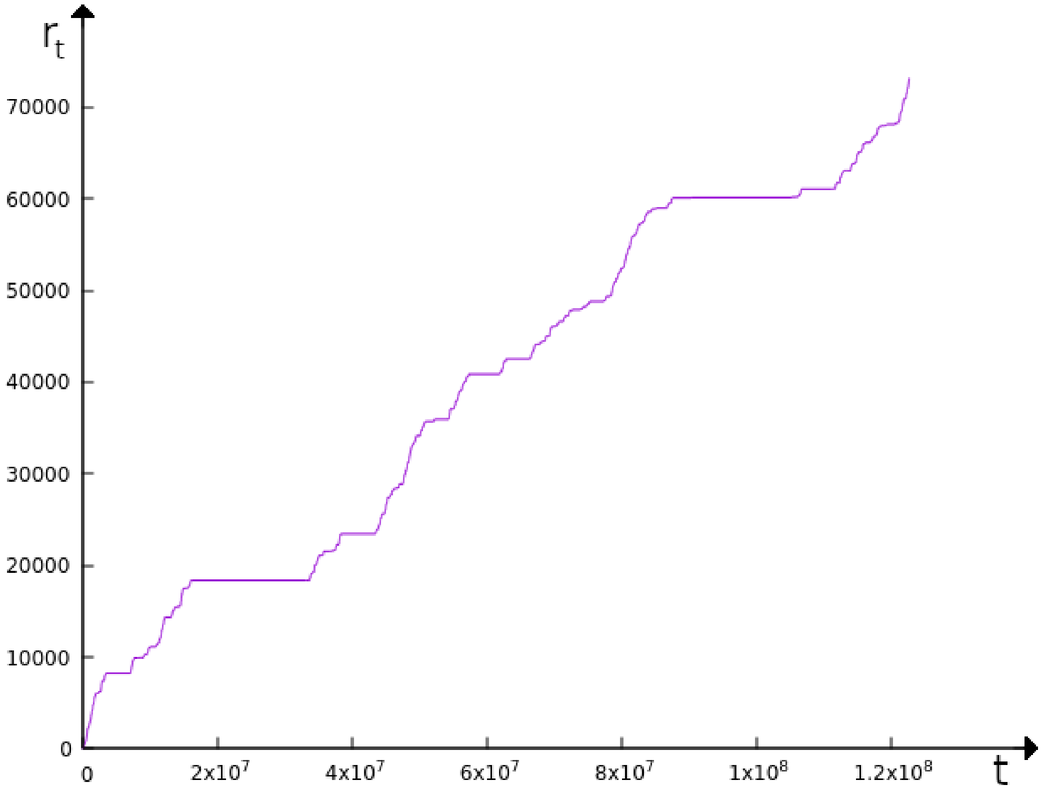


Figure 3.1: $(r_t)_{t\geq 0}$ for $\mathbf{P}(I \geq n) = \left(\frac{n-1}{3}+1\right)^{-2.1}$ and $A = 4$ a.s.

give a formal proof of Theorem 3.2 in Section 3.4. The main steps of the proof are as follows.

Sketch of the proof of Theorem 3.2

The upper bound follows by simply coupling with a branching random walk.

For the lower bound, a key observation is that only parasites quite close to the front push the front further. The reasons for this are that a) parasites can generate offspring only at the front, b) parasites move diffusively, and c) the tail of the immunity distribution falls so fast that sufficiently high barriers of immunities appear so rarely.

This structure motivates the construction of auxiliary jump times that upper bound the actual jump times from above but are based only on parasites born relatively close to the front. More precisely, to estimate the jump time from site $n-1$ to site n, we consider a small neighborhood left to n of random size K_n. The neighborhood is extended to the left until the number of parasites accumulating in the neighborhood is lower bounded by a number that grows linearly with the distance to the front; see Definition 3.8. Since by assumption the accumulated number of parasites grows on average faster than the accumulated number of immunities, one can show that the tail of the size K_n of the neighborhood falls quickly as long as the neighborhood does not cross the origin; see Lemma 3.15.

To control the movement of the front at sites whose corresponding neighborhoods would cross the origin, we proceed as follows. We show that there exists a site M from which on, the neighborhood of each site $M+n$ does not cross M for $n \geq k_0$ (with $k_0 \in \mathbb{N}$ depending on the tail of the immunity distribution as well as (inversely proportional) on the difference between the average number of parasite offspring numbers and average immunities, see (3.5)). This site M has a.s. a finite distance to the origin, and hence $M + k_0$ is reached a.s. in finite time; see Definition 3.11 and Lemma 3.14.

For sites $n \geq k_0$ we show by using results on collections of random walks hitting a one-sided barrier that the jump times from $M+n$ to $M+n+1$ have q-th moments for any $q \in [1, \frac{(4\wedge\alpha)+1}{2})$, see Lemma 3.17. Since neighborhoods of sites sufficiently far apart do not overlap with high probability, the corresponding auxiliary jump times only weakly depend on each other. More precisely, we show that the sequence of jump time $(\nu_{M+n})_{n\geq k_0}$ forms a ϕ-mixing sequence, see Lemma 3.19, which allows us to conclude a law of large numbers for $(\nu_{M+n})_{n\geq k_0}$ and show the claimed lower bound.

Under some stronger assumption, which we do not believe to be optimal, we can show the stronger result that the front satisfies an almost sure law of large numbers.

Theorem 3.3. *Suppose that for some $\alpha > \frac{3+\sqrt{11}}{2}$ and some $\varepsilon_A > 0$ we have*

- $\mathbf{E}[|I|^{2\alpha}] < \infty$, $\mathbb{E}[A^{\frac{4}{(4\wedge\alpha)-3}+\varepsilon_A}]$ *and* $\mathbf{P}(A - I \geq 4) > 0$.

Then, there is a (deterministic) $\gamma \in (0,\infty)$ such that, starting in the initial configuration given by $\eta = A\delta_0$ and conditioned on the survival of parasites, almost surely

$$\lim_{t\to\infty} \frac{r_t}{t} = \gamma.$$

As for Theorem 3.2, a proof of the theorem can be found in Section 3.4.
Sketch of the proof of Theorem 3.3
The approach is similar to the proof of Theorem 3.2. We also consider for each

site n a neighborhood of size K_n to the left of this site. However, to arrive not only at a lower bound but also on the convergence of r_t/t, it is not sufficient to construct a single site M. Instead, in Definition 3.12, we identify a sequence of sites $(M^i)_{i\geq 0}$ such that the upcoming births and immunities after each site M^i have the same properties as the site M, that is, the number of living parasites grows linearly in the distance of the front from each M^i, and in addition, even for small $n < k_0$, there are enough parasites born between M^i and $M^i + n - 1$ to ensure a fast infection of site $M^i + n$ with sufficiently high probability.

Then, in Lemma 3.37, we show a subadditivity property of the front in between reaching these good sites, conditionally on the event that the initial configuration of upcoming offspring and immunities is already good, i.e., $\{M^0 = 0\}$. In particular, we will use approximating jump times $\overline{\nu}_n^i = \nu_{M^i+n}$ defined similarly as ν_{n+M} (here defined to the right of M^i instead of M), which will be a ϕ-mixing sequence with $\sup_{n\geq 1} \mathbb{E}[|\overline{\nu}_n^i|^q] < \infty$ for all $q \in \left[1, \frac{(4\wedge\alpha)+1}{2}\right)$. With these approximating jump times, we show, in Lemma 3.21, that moving from one site M^i to the next M^{i+1} happens with finite expectation, which yields the claimed convergence, conditionally on $\{M^0 = 0\}$, after noting that $(M^{i+1} - M^i)_{i\geq 0}$ will be i.i.d. Finally, in Proposition 3.22, we construct a sequence of renewal sites from which on the front becomes independent of the past. This allows us to conclude that the limit of $\frac{r_t}{t}$ cannot be random, conditioned on survival, and thus, the limit of $\frac{r_t}{t}$ we obtained with positive probability must already hold almost surely.

Two-sided host population

In this subsection we investigate the survival probability in the two-sided model. We use the results on the one-sided model to obtain the following result on the positive probability of survival and linear spread.

Theorem 3.4. *Consider a two-sided host population with initial configuration $\zeta = (0, 0, A_0\delta_0)$. We make the same assumptions on A, I as in Theorem 3.2, but now further restricting*

$$\alpha > 3.$$

Then there is a positive probability for the parasites to survive for infinite time, *and there exists a* $v > 0$ *such that for any* $0 < \lambda < v$*, we have*

$$\mathbf{P}\left(\bigcap_{t\geq 0}\{\textit{all hosts inside } \{-\lfloor \lambda t\rfloor, \dots, \lfloor \lambda t\rfloor\} \textit{ are infected at time } t\}\right) > 0.$$

Sketch of the proof of Theorem 3.4 We construct an event of positive probability in which the right front is only driven by parasites born on a site x with $x \geq 1$, while the left front is driven only by parasites born on a site x with $x \leq -1$. We do this by showing that in the one-sided model started with a single parasite, there is a positive probability that the front always stays above $\lfloor \lambda t\rfloor$ and that for any time $t \geq 0$ there is no parasite on any site x with $x \leq -1-\lfloor \lambda t\rfloor$. Imposing this event on both the right and left fronts, after they reach 1 and -1, respectively, then yields that the two sides evolve as independent copies of the one-sided model, because parasites born on the right side never reach the linear line $-1 - \lfloor \lambda t\rfloor$, while the left front is always below this line, and vice versa for parasites born on the left side. This then yields the claim.

To show the result on the one-sided model, we first note that because in the one-sided model the new parasites get only added on the right front, the speed in the negative direction is bounded by the speed of random walk, which is on the scale $\sqrt{t}$ with high probability. Hence, with positive probability for all $t \geq 0$, there are no parasites to the left of $-1-\lfloor \lambda t\rfloor$ at time t. To see that with positive probability the front moves with linear speed, we use that $\alpha > 3$, which implies that for any $q \in \left(2, \frac{\alpha+1}{2}\right)$ we have $\mathbf{E}[|\nu_n|^q] < \infty$ for $n \geq 1$. This will allow us to obtain better estimates on the fluctuations of

$$\frac{1}{n}\sum_{k=1}^{n}\nu_k$$

around its mean v. We then show that the event

$$G_{k_0} := \left\{M = 0, \forall 1 \leq n < k_0 : \rho_n \leq \frac{n}{\lambda}\right\}$$

has positive probability, and that on the event G_{k_0}, by using tail estimates for sums of ϕ-mixing series, we also have

$$\rho_n \leq \rho_{k_0-1} + \sum_{k=k_0}^{n}\nu_k \leq \frac{n}{\lambda}$$

for all $n \geq k_0$ with positive probability.

3.3 Good sites and auxiliary jump times

We consider here mainly the case of a one-sided host population with initially $r = 0$. Also, w.l.o.g., we assume a random initial configuration $\zeta = (-\infty, 0, \eta)$ such that $\eta(0) \overset{d}{=} A$. If not, we can simply shift the process to 0 after the first jump, where, by definition of the process, $\eta_{\rho_1}(1) \overset{d}{=} A$, and use the strong Markov property.

In this section we construct the auxiliary jump times $\{\nu_n : n \in \mathbb{Z}\}$, see Definition 3.8, that will be used in the construction of a lower bound for the actual jump times of the front. We will also analyze the tails as well as the mutual dependencies of these jump times in Lemma 3.17 and Lemma 3.19. Furthermore, we will define the site M and the sequence of sites $(M^i)_{i \geq 0}$, see Definition 3.12, and analyze their properties. As explained in the sketches of the proofs for Theorem 3.2 and Theorem 3.3, we will use slightly different lower bounds for the jump times to show Theorem 3.2 than the one we are using to show Theorem 3.3. This difference appears only at the first k_0 sites after M and M^i, respectively. After that, ν_{M+n} and ν_{M^i+n} are defined analogously as upper bounds for the jump times for $n \geq k_0$.

The formal construction of the process will be given in Section 3.5. We shortly summarize some of the notation that will be introduced there, because we need it for the construction of the lower bound. We keep not only the current positions of parasites but also the places at which each parasite entered the system. Therefore we give each parasite a label $(x, i) \in \mathbb{Z} \times \mathbb{N}$, where x is its birthplace and i numerates all parasites that were born on that site. Also, as will become clear in the construction of the times $\{\nu_n : n \in \mathbb{Z}\}$, we need to follow the virtual paths of parasites after their death. The state space will hence be given by a 5-tuple $w = (r, \mathcal{L}, \mathcal{G}, F, \iota)$ with

$$r \in \mathbb{Z}, \mathcal{L} \subset \mathbb{Z} \times \mathbb{N}, \mathcal{G} \subset \mathbb{Z} \times \mathbb{N}, F : \mathcal{L} \cup \mathcal{G} \to \mathbb{Z}, \iota \in \mathbb{N}.$$

The entry r is the current position of the front, and ι is the current remaining immunity of the host at site $r + 1$. The set $\mathcal{L}$ consists of the labels of parasites that are currently alive, called living parasites, and $\mathcal{G}$ consists of the labels of parasites that already died (but were alive at some point in the past), called ghost parasites. The map F then assigns a current position to each parasite. There are, of course, some technical restrictions we need to make on these tuples to obtain a strong Markov process on this state space (see in particular

the assumptions in Theorem 3.1), which we defer to Section 3.5.
We now explain how we can think of our initial configuration $\zeta = (-\infty, 0, \eta)$ as an element of this state space that keeps track of more information. First, to obtain a Markov process, we need to keep track of the current remaining immunity and thus will extend our random initial configuration to $(-\infty, 0, \eta, I_1)$. Also we keep track of the position where a parasite entered the system instead of only following all actual parasite positions with η. We extend the configuration $(-\infty, 0, \eta, I_1)$ to an element of this new state space by assuming that every parasite is occupying the site on which it was born and there are no initial ghost parasites, i.e., to the configuration

$$(0, \{(x,i) \in \mathbb{Z} \times \mathbb{N} : x \leq 0, 1 \leq i \leq \eta(x)\}, \emptyset, (x,i) \mapsto x, I_1)\,.$$

With this identification we can assume to have a random initial configuration $w = (0, \mathcal{L}, \emptyset, F, I_1)$ defined on $\mathbf{\Omega}$. When the initial configuration is given by w, we denote by

$$w_t(w) = (r_t(w), \mathcal{L}_t(w), \mathcal{G}_t(w), F_t(w), \iota_t(w))$$

the configuration of the process at time t, by $\mathcal{S}(w)$ the event of survival of parasites for infinite time, i.e. $\mathcal{L}_t(w) \neq \emptyset$ for all $t \geq 0$, and by $\mathbb{P}^w$ the measure conditioned on this event. For the rest of this chapter we drop the reference to the initial configuration, by only writing $\mathbb{P}, \mathcal{S}, w_t$ instead of $\mathbb{P}^w, \mathcal{S}(w), w_t(w)$.
Also, we assume that there are independent collections

$$\mathbf{Y} = \{Y^{x,i} : x \in \mathbb{Z}, i \in \mathbb{N}\} = \{(Y^{x,i}_t)_{t \geq 0} : x \in \mathbb{Z}, i \in \mathbb{Z}\}$$

of i.i.d. continuous time simple symmetric random walks with rate 2 and starting at 0 as well as

$$\mathbf{I} = \{I_x : x \in \mathbb{Z}\}$$

of i.i.d. random variables distributed as I and

$$\mathbf{A} = \{A_x : x \in \mathbb{Z}\}$$

of i.i.d. random variables distributed as A. For some label $(x,i) \in \mathbb{Z} \times \mathbb{N}$, the path that the parasite with this label takes after it enters the system at some site $y \in \mathbb{Z}$ will be given by $y + Y^{x,i}$. We note that for $x > 0$ we will have $y = x$, but if the parasite was already alive in w, then it may be at a different site than its birthplace. Also for $x > 0$, the initial immunity of the host at x will be given by I_x, and the number of parasites that will be produced after the host at site x is infected will be given by A_x. Finally we denote by

$$\rho_n := \inf\{t \geq 0 : r_t \geq n\}$$

the time, when the front reaches site $n \geq 0$, i.e., when the host at site n gets infected.

With all the notation introduced, we now lay out the general approach. We identify a site M^0 such that from that site on, the upcoming births and deaths are in a good configuration, in the sense that the amount of living parasites grows linearly in the distance of the front to M^0 and the linear growth has some high enough slope. Why these properties are useful will become clear after we introduce the jump times $\{\nu_n : n \in \mathbb{Z}\}$ in Definition 3.8 that will be used to lower bound the front, which is also why we start this section by constructing these times before constructing $(M^i)_{i\geq 0}$. The constructed lower bound in particular will only use parasites born to the right of the site M^0, and hence not depend on the initial configuration anymore. After reaching the good site M^0, we simply repeat the procedure to find the next site $M^1 > M^0$, which has a good configuration of upcoming births and deaths. Iterating this yields a sequence $(M^i)_{i\geq 0}$ of good sites, such that even ignoring any parasites that were born before reaching M^i and only starting with A_{M^i} parasites at site M^i has a linear speed with high probability.

Then we establish a subadditivity property of the front that holds if we start with only A_0 parasites on 0 and no other parasites in the system and the first good site $M^0 = 0$. This allows us to prove the law of large numbers in the event that $M^0 = 0$, by controlling the tails of the hitting times of M^i. Then, showing that the limit of $\frac{r_t}{t}$ is not random, conditionally on survival, will show the strong law of large numbers in Theorem 3.3. For arbitrary initial configurations, this approach, however, does not work, and we will only show the weaker result of ballistic growth in Theorem 3.2.

In Definition 3.8 we will construct random times $\{\nu_n : n \in \mathbb{Z}\}$ on $\mathbf{\Omega}$ that will be used as the jump times for a lower bound of the front. Precisely, we will show that in the event that $\{M^i = k\}$, the time ν_{k+n} only depends on $\mathbf{A}, \mathbf{I}, \mathbf{Y}$ with an index inside $k + n - K_{k+n}$ for some random distance $K_{k+n} \leq n$ and is given by the first hitting time of a one-sided barrier by a collection of random walks.

In Lemma 3.15 we will show that this distance K_{k+n} does not become too large with high probability. In particular, this will show that on one hand the tails of ν_{M^i+k} fall fast enough in Lemma 3.17 and on the other that the sequence $(\nu_{M^i+n})_{n\geq 1}$ is weakly dependent, specifically that it is ϕ-mixing in Lemma 3.19. Also, in Proposition 3.10 we show that, still on the event $\{M^i = k\}$, we have $\nu_{k+n} \geq \rho_{k+n} - \rho_{k+n-1}$ for any $k \geq 0, n \geq 1$. The definition of M that is used in the proof of Theorem 3.2 will be slightly different and only yield that on the event $\{M = k\}$ we have $\nu_{k+n} \geq \rho_{k+n} - \rho_{k+n-1}$ for all $n \geq k_0$ with some explicit constant $k_0 \in \mathbb{N}$. The different treatment is due to the reason that we want every jump time above M^i to have a small tail, while for M we only need this eventually, i.e., for $n \geq k_0$.

We set $\overline{\nu}_n^i := \nu_{M^i+n}$, and using the tails of ν_n as well as their dependence, we want to obtain good bounds on

$$\sum_{j=1}^{n} \overline{\nu}_j^i \tag{3.4}$$

which is an upper bound for $\rho_{M^i+n} - \rho_{M^i}$. The tail estimates and the weak dependence, using standard results for ϕ-mixing sequences, allow us to control the moments of their partial sums (3.4) and in Lemma 3.20 show that the q-th moment only grows like $\mathcal{O}(n^{\frac{q}{2}})$, if $\alpha > 3$ and $q < \frac{(4\wedge\alpha)+1}{2}$, which will be useful in proving that moving from M^i to M^{i+1} happens with finite expectation.

3.3.1 Construction and basic properties of auxiliary jump times and good sites

Before constructing the good sites $(M^i)_{i\geq 0}$, we want to analyze a candidate for an upper bound of the jump times and under which conditions this actually is an upper bound and what tails these candidates have. These conditions then naturally lead to what properties the good sites $(M^i)_{i\geq 0}$ should satisfy in order to be able to define the jump times $(\overline{\nu}_n^i)_{n\geq 1}$ as an upper bound for the jump times $\rho_{M^i+n} - \rho_{M^i+n-1}$ that have the needed tail behavior of their partial sums (3.4).

The key idea in defining $\{\nu_n : n \in \mathbb{Z}\}$ is to obtain estimates on the number of living parasites when the front is at a certain position x, independent of the paths $\mathbf{Y}$, only relying on the random variables $\mathbf{A}, \mathbf{I}$. Then we estimate the time that these parasites would need to push the front further by establishing results on first hitting times of a one-sided barrier by a collection of simple symmetric random walks. Combining these two estimates, using the independence of $\mathbf{A}, \mathbf{I}, \mathbf{Y}$, we then obtain an upper bound, denoted by ν_n, for the times the process $(r_t)_{t\geq 0}$ takes to jump from $n-1$ to n, which was denoted by $\rho_n - \rho_{n-1}$. First we observe that for any $n \geq 1$ the number of parasites that die at site n is given by I_n, and the process $(r_t)_{t\geq 0}$ advances exactly when this many parasites have died. Hence, we have

$$\rho_{n+1} = \inf\{t \geq 0 : r_t \geq n+1\} = \inf\{t \geq \rho_n : |\mathcal{G}_t| - |\mathcal{G}_{\rho_n}| = I_{n+1}\}$$

and thus

$$|\mathcal{G}_{\rho_{n+m}}| - |\mathcal{G}_{\rho_n}| = \sum_{k=n+1}^{n+m} I_k.$$

for all $n \geq 0, m \geq 1$. In words, the amount of parasites that die during the time that the front needs to advance from site n to site $n+m$ is given by the sum of the immunities between $n+1$ and $n+m$. Because for $x > 0$, exactly A_x new parasites are added at x whenever the front jumps onto x, the number of living parasites at time ρ_{n+m} that have been generated at one of the sites $\{n, ..., n+m-1\}$ satisfies the inequality

$$|\mathcal{L}_{\rho_{n+m}} \cap (\{n, \ldots, n+m-1\} \times \mathbb{N})| \geq \sum_{k=n}^{n+m-1} A_k - \sum_{k=n+1}^{n+m} I_k.$$

This gives us a lower bound on the number of living parasites at time ρ_{n+m}, independent of the paths $\mathbf{Y}$, and leads to the following definition.

For the rest of this chapter we fix some

$$\beta_A \in (\mu_I, \mu_A), \qquad \beta_I \in (\mu_I, \beta_A).$$

Furthermore, we set

$$k_0 := \left\lceil \frac{\alpha+1}{\beta_A - \beta_I} \right\rceil. \tag{3.5}$$

Definition 3.8. *For any $k \geq 0$ we define*

$$m(A,k) := \inf\{j \geq k : \mathbf{P}(A = j) > 0\}, m(I,k) := \inf\{j \geq k : \mathbf{P}(I = j) > 0\},$$

and set $m_I := m(I,1), m_A := m(A, \beta_A \vee (4 + m(I,1)))$. For $1 \leq k < k_0$ we define

$$\underline{A}^{good}(k) := \left\{(a_1, \ldots, a_k) \in \mathbb{N}_0^k | \forall 1 \leq j \leq k : a_j \geq m_A\right\},$$

and

$$\underline{I}^{good}(k) := \left\{(i_1,\dots,i_k) \in \mathbb{N}^k | \forall 1 \le j \le k : i_j = m_I\right\}.$$

For $k \ge k_0$ *we define*

$$\underline{A}^{good}(k) := \left\{(a_1,\dots,a_k) \in \mathbb{N}_0^k : \sum_{j=1}^{k} a_j \ge \beta_A k\right\},$$

and

$$\underline{I}^{good}(k) := \left\{(i_1,\dots,i_k) \in \mathbb{N}^k : \sum_{j=1}^{k} i_j \le \beta_I k\right\}.$$

For $1 \le k < k_0$ *the set* $\underline{A}^{good}(k)$ *are the offspring constellations of length* k *such that on each vertex there are born at least* 4 *parasites more than the minimal immunity, and* $\underline{I}^{good}(k)$ *are the immunity constellations of length* k *such that each immunity has the minimal possible value. For* $k \ge k_0$ *the set* $\underline{A}^{good}(k)$ *are the offspring constellations of length* k *with on average at least* β_A *many parasites per site, while* $\underline{I}^{good}(k)$ *are the immunity constellations of length* k *with on average a strength of at most* β_I *per site. For* $n \in \mathbb{Z}$ *we now go backwards from site* n*, starting at* k_0 *steps, until we find two good configurations in both offspring and immunities. Precisely, we define*

$$K_n := \inf\left\{k \ge 1 : (A_{n-1},\dots,A_{n-k}) \in \underline{A}^{good}(k), (I_n,\dots,I_{n-k+1}) \in \underline{I}^{good}(k)\right\}$$

as the smallest distance greater than or equal to k_0 *where both the offsprings and immunities between* $n - K_n^m$ *and* n *are good, in the sense of the just defined sets. For* $k \in \mathbb{N}$ *and a good offspring constellation* $\mathbf{a} \in \underline{A}^{good}(k)$ *we define the corresponding labels of parasites below site* n *as*

$$\underline{\mathcal{V}}_n^{good}(k,\mathbf{a}) := \{(x,i) \in \mathbb{Z}\times\mathbb{N} : n-k \le x \le n-1, 1 \le i \le a_{n-x}\},$$

and define the random label set

$$\mathcal{W}_n := \underline{\mathcal{V}}_n^{good}(K_n,(A_{n-1},\dots,A_{n-K_n})).$$

For $(x,i) \in \mathbb{Z}\times\mathbb{N}$ *and* $k \in \mathbb{Z}$ *we define*

$$\tau_k^{x,i} := \inf\{t \ge 0 : Y_t^{x,i} = k\},$$

the first time the parasite with label (x,i) *has reached the site at distance* k *to the right of its birthplace, and*

$$\nu_n := \inf\left\{t \ge 0 : \sum_{(x,i)\in\mathcal{W}_n} \mathbb{1}_{\tau_{n-x}^{x,i} \le t} \ge \begin{cases} m_I K_n, & \text{if } 1 \le K_n < k_0 \\ \beta_I K_n, & \text{if } K_n \ge k_0 \end{cases}\right\}$$

as the first time at which at least a number equal to at least the accumulated sums of immunities between $n-K_n+1$ and n of parasites born between $n-K_n$ and $n-1$ reached site n.

Remark 3.9. *The role of the specific choice 4 will become clear in the proof of Lemma 3.17 and is just that 4 is the smallest integer that guarantees high enough moments.*
Because clearly $(\nu_n)_{n\in\mathbb{Z}}$ and $(K_n)_{n\in\mathbb{Z}}$ are stationary under the unconditioned law $\mathbf{P}$, we set $\nu := \nu_1, K := K_1$, to simplify notation when only stating properties depending on the distribution of a single variable.

The idea behind the definition of ν_n is the following. First, we ignore the deaths of parasites and use the collection $\mathbf{Y}$ to follow the (potentially virtual) paths of each parasite. We then want to distinguish which random walks correspond to living parasites and which correspond to ghost parasites at time $t=\rho_{n-1}$. The real process jumps to site n, when I_n many parasites, that were alive at time ρ_{n-1}, reached site n. Firstly, we note that placing these parasites back on the site where they were born and then following their trajectory only increases the first hitting time of site n. Hence, given $\mathcal{F}_{\rho_{n-1}}$, the time $\rho_n-\rho_{n-1}$ is smaller than the first time I_n many random walks, corresponding to parasites alive at time ρ_{n-1} and starting from their birthplace, reached site n. However, deciding which specific labels correspond to living parasites depends on the trajectories of all parasites before time ρ_{n-1} and thus is too complicated. Hence, for any $k\geq 1$, we only bound the amount of ghost parasites at time ρ_{n-1} that were born inside $[n-k,n-1]$. Once this amount of random walks and at least one additional random walk, all with labels in $[n-k,n-1]$, have reached site n, at least one of those (but we do not know which one) has to correspond to a parasite that was alive at time ρ_{n-1}. Thus, this gives an upper bound on the jump time from $n-1$ onto n. We will make this reasoning precise in the upcoming Proposition 3.10.
We note that if $n-K_n<0$, then the labels $\mathcal{W}_n$ are not necessarily corresponding to real parasites, depending on the initial configuration. But if $n-K_n\geq 0$, then $\mathcal{W}_n$ are exactly the labels of parasites that were born during the time $[\rho_{n-K_n},\rho_{n-1}]$. Because parasites can only die at sites to the right of their birthplace, an upper bound for the number of ghost parasites at time ρ_{n-1}, born inside $[n-K_n,n-1]$, is given by $I_{n-K_n+1}+\cdots+I_{n-1}$. The first and second

conditions in the definition of K_n exactly guarantee that the sum of immunities in $[n-K_n+1,n]$ is much smaller than the sum of parasites born in that interval. This will ensure that there are enough random walks corresponding to a parasite born in $[n-K_n, n-1]$, such that the time it takes for $I_{n-K_n+1}+\cdots+I_{n-1}$ many of those random walks to reach n has finite moments up to some high enough power, depending on the parameter α, which was chosen such that $\mathbf{E}[I^{2\alpha}] < \infty$. The different treatment for $k < k_0$ and $k \geq k_0$ comes from the fact that for $k \geq k_0$, the condition on the sums already guarantees a surplus of $(\beta_A - \beta_I)k_0 \geq \alpha + 1$ parasites, which will correspond to certain moments of ν_n conditionally on $K_n \geq k_0$; see the proof of Lemma 3.17. To also obtain moments estimates conditionally on $K_n < k_0$, we need to make the surplus of parasites for $k < k_0$ large enough and note that the definition of K_n makes this surplus at least $k(m_A - m_I) \geq 4k$.
We formalize the reasoning above in the following proposition, showing that ν_n is a lower bound for the jump time $\rho_n - \rho_{n-1}$ of the real front, if $K_n \leq n$.

Proposition 3.10. *For all* $n \geq k_0$ *we have that*

$$\mathbb{1}_{K_n \leq n}(\rho_n - \rho_{n-1}) \leq \nu_n$$

Proof. Clearly the right-hand side is non-negative, and hence it suffices to show the inequality on the event $K_n \leq n$. By definition of the process, placing all parasites alive at time ρ_n back to their birthplace, we obtain

$$\rho_n \leq \rho_{n-1} + \inf\left\{ t \geq 0 : \sum_{(x,i)\in\mathcal{L}_{\rho_{n-1}}} \mathbb{1}_{\tau^{x,i}_{n-x} \leq t} \geq I_n \right\}$$

and hence will show that, on $\{K_n \leq n\}$, the second term is smaller than ν_n. At time ν_n we have that

$$Z_n := \begin{cases} m_I K_n, & \text{if } 1 \leq K_n < k_0 \\ \lceil \beta_I K_n \rceil, & \text{if } K_n \geq k_0 \end{cases}$$

many random walks $(x + Y^{x,i}_t)_{t\geq 0}$ with birth label

$$(x,i) \in \mathcal{W}_n = \{(x,i) \in \mathbb{Z}\times\mathbb{N} : n - K_n \leq x < n, 1 \leq i \leq A_x\}$$

have reached site n, and since we are on $\{K_n \leq n\}$, these random walks correspond to parasites that were alive in the real process. Let us denote by $\mathcal{B} \subset \mathcal{W}_n$

the labels of the Z_n many parasites having reached site n at time ν_n. Since parasites can only die when jumping to the right of the front, and only I_x parasites die at each site x, we have that out of the parasites with labels inside $\mathcal{W}_n$, only $\sum_{j=1}^{K_n-1} I_{n-j}$ many can be ghosts at time ρ_{n-1}. In other words

$$\begin{aligned}|\mathcal{W}_n \cap \mathcal{L}_{\rho_{n-1}}| &\geq \sum_{j=1}^{K_n} A_{n-j} - \sum_{j=1}^{K_n-1} I_{n-j} = \sum_{j=1}^{K_n} A_{n-j} + I_n - \sum_{j=0}^{K_n-1} I_{n-j} \\ &= \sum_{j=1}^{K_n} A_{n-j} + I_n - \sum_{j=1}^{K_n} I_{n-j+1} \geq \sum_{j=1}^{K_n} A_{n-j} + I_n - Z_n.\end{aligned}$$

In particular, since $|\mathcal{B}| = Z_n$, this implies

$$\begin{aligned}|\mathcal{B} \cap \mathcal{L}_{\rho_{n-1}}| &= |\mathcal{W}_n \cap \mathcal{L}_{\rho_{n-1}}| - |(\mathcal{W}_n \setminus \mathcal{B}) \cap \mathcal{L}_{\rho_{n-1}}| \\ &\geq \sum_{j=1}^{K_n} A_{n-j} - Z_n + I_n - |\mathcal{W}_n \setminus \mathcal{B}| \\ &= \sum_{j=1}^{K_n} A_{n-j} - Z_n + I_n - \left(\sum_{j=1}^{K_n} A_{n-j} - Z_n\right) \geq I_n.\end{aligned}$$

Hence $|\mathcal{B} \cap \mathcal{L}_{\rho_{n-1}}| \geq I_n$ living parasites reached site n at time ν_n and thus

$$\nu_n \geq \inf \left\{ t \geq 0 : \sum_{(x,i) \in \mathcal{L}_{\rho_{n-1}}} \mathbb{1}_{\tau_{n-x}^{x,i} \leq t} \geq I_n \right\}.$$

This already concludes the proof. □

This proposition motivates the definition of the good sites $(M^i)_{i \geq 0}$ and M that will be used to prove Theorems 3.3 and 3.2. Namely, we want to define $(M^i)_{i \geq 0}$ and M in such a way that

$$\forall i \geq 0, n \geq 1 : K_{M^i+n} \leq n \quad \text{and} \quad \forall n \geq k_0 : K_{M+n} \leq n. \tag{3.6}$$

Because then, by Proposition 3.10, we have

$$\begin{gathered}\forall i \geq 0, n \geq 1 : \nu_{M^i+n} \geq \rho_{M^i+n} - \rho_{M^i+n-1} \quad \text{and} \\ \forall n \geq k_0 : \nu_{M+n} \geq \rho_{M+n} - \rho_{M+n-1}.\end{gathered} \tag{3.7}$$

Also, in this way, for any $i \geq 0$, the sequence $\{\nu_{M^i+n} : n \geq 1\}$, respectively $\{\nu_{M+n} : n \geq k_0\}$, conditionally on M^i, respectively conditionally on M, only depends on

$$\{A_x, I_{x+1}, Y^{x,j} : x \geq M^i, j \in \mathbb{N}\} \quad \text{resp.} \quad \{A_x, I_{x+1}, Y^{x,j} : x \geq M, j \in \mathbb{N}\},$$

and in particular will be independent of the initial configuration.
The treatment of the first k_0 sites after M^i will be slightly different from the treatment of the first k_0 sites after M, because in the former case we need even the jumps to these sites to have sufficient moments, while only relying on parasites that are born above M^i. In the definition of M, however, we can argue more simply and can define M as follows.

Definition 3.11. *Set* $L_0 = 0$ *and for* $k \geq 0$*, define*

$$L_{k+1} := \inf\{l \geq L_k + k_0 : K_l > l - L_k\}$$

and let

$$N := \inf\{k \geq 0 : L_{k+1} = \infty\}, \quad M := L_N.$$

Furthermore, we set

$$T := \inf\{t \geq 0 : r_t \geq M + k_0\}.$$

To define M^i we introduce some notation to treat the first k_0 sites differently than the other sites. We define

$$G : \bigcup_{n\in\mathbb{N}} \mathbb{N}_0^n \times \mathbb{N}^n \to \{0,1\},$$

such that for $n \in \mathbb{N}$ and $\mathbf{a} = (a_0, \dots, a_{n-1}) \in \mathbb{N}_0^n, \mathbf{i} = (i_1, \dots, i_n) \in \mathbb{N}^n$ we have $G(\mathbf{a}, \mathbf{i}) = 1$ if and only if

- for all $1 \leq j < (n+1) \wedge k_0$ it holds that

$$\begin{aligned} i_j &= \inf\{l \geq 1 : \mathbf{P}(I = l) > 0\}, \\ a_{j-1} &\geq \inf\{l \geq \beta_A \vee (i_j + 4) : \mathbf{P}(A = l) > 0\}. \end{aligned} \tag{3.8}$$

  Note that this is just the condition of a good configuration of length $j < k_0$ in Definition 3.8.

- for all $k_0 \leq j \leq n$ there is some $k_0 \leq i \leq j$ such that

$$(a_{j-i}, \dots, a_{j-1}) \in \underline{A}^{\text{good}}(i) \quad \text{and} \quad (i_{j-i+1}, \dots, i_j) \in \underline{I}^{\text{good}}(i).$$

Definition 3.12. *Let* $L_0^0 := 0$ *and recursively for* $k \geq 0$ *set*

$$L_{k+1}^0 := \inf\left\{l > L_k^0 : G((A_{L_k^0}, \dots, A_{l-1}), (I_{L_k^0+1}, \dots, I_l)) = 0\right\}$$

and define

$$N^0 := \inf\{k \geq 0 : L^0_{k+1} = \infty\}, \quad M^0 := L^0_{N^0}.$$

Then we set, recursively for $i \geq 0$, $L^{i+1}_0 := M^i + 1$ and for $k \geq 0$

$$L^{i+1}_{k+1} := \inf\left\{l > L^{i+1}_k : G((A_{L^{i+1}_k}, \dots, A_{l-1}), (I_{L^{i+1}_k+1}, \dots, I_l)) = 0\right\}$$

as well as

$$N^{i+1} := \inf\{k \geq 0 : L^{i+1}_{k+1} = \infty\}, \quad M^{i+1} := L^{i+1}_{N^{i+1}}.$$

For $j \geq 0, k \geq 1$ we define the event

$$\mathcal{G}_{j,j+k} := \bigcap_{m=1}^{k} \{G((A_j, \dots, A_{j+m-1}), (I_{j+1}, \dots, I_{j+m})) = 1\}$$

of good configurations between j and $j+k$ and set $\mathcal{G}_j := \mathcal{G}_{j,\infty}$. Also, we set

$$T^i := \inf\{t \geq 0 : r_t \geq M^i\}$$

and $\overline{\nu}^i_n := \nu_{M^i+n}$ for $n \geq 1$.

Remark 3.13. *We note that for all $j \geq 0$ we have*

$$\{M^i = j\} \subset \mathcal{G}_j \subset \bigcap_{n=1}^{\infty} \{K_{j+n} \leq n\}$$

and

$$\{M = j\} \subset \bigcap_{n=k_0}^{\infty} \{K_{j+n} \leq n\}.$$

To begin, we verify that the definitions above are actually well-defined and establish the following lemma.

Lemma 3.14. *We have $N < \infty$ almost surely. Also, if $\mathbf{P}(A - I \geq 4) > 0$ (c.f. (3.8)), then for any $i \geq 0$ we have $N^i < \infty$ almost surely. In particular, $(M^i)_{i \geq 0}$ and M are well-defined, and $T, T^0, T^1, \dots < \infty$ almost surely under $\mathbb{P}$.*

Proof. We recall $\mathcal{G}_j$ from Definition 3.12 and set $\mathcal{G} := \mathcal{G}_0$. We give the proof only for $(M^i)_{i \geq 0}$ and note that, using Remark 3.13, the results for M follow analogously.
For any $\mathbb{N}_0$-valued random variable X on $\mathbf{\Omega}$ and any $k \geq 0$, we recall

$$m(X, k) := \inf\{j \geq k : \mathbf{P}(X = j) > 0\}$$

and $m_I = m(I,1), m_A = m(A, \beta_A \vee (4 + m(I,1)))$ from Definition 3.8. Since m_I is the smallest value that I can take, the assumption $\mathbf{P}(A - I \geq 4) > 0$ together with $\beta_A < \mathbf{E}[A]$ implies that m_A is well defined. Then, by definition, for $1 \leq k < k_0$ we have

$$\{G((A_0, \dots, A_{k-1}), (I_1, \dots, I_k)) = 1\} = \bigcap_{j=1}^{k} \{A_{j-1} \geq m_A, I_j = m_I\}.$$

We observe that $\beta_I > \mathbf{E}[I] \geq m_I$ and by definition

$$m_A = m(A, \beta_A \vee (4 + m(I,1))) \geq \beta_A.$$

We obtain that the event

$$\bigcap_{j=1}^{k_0} \left\{ \begin{matrix} A_{j-1} \geq m_A, \\ I_j = m_I \end{matrix} \right\} \cap \bigcap_{m=1}^{\infty} \left\{ \sum_{k=1}^{m} A_{k_0+k-1} \geq \beta_A m, \sum_{k=1}^{m} I_{k_0+k} \leq \beta_I m \right\} \tag{3.9}$$

is contained in $\mathcal{G}$. The right event is that two independent random walks with step distribution $A - \beta_A$ and $\beta_I - I$ stay non-negative for all times, which has positive probability, since $\mathbf{E}[A] > \beta_A > \beta_I > \mathbf{E}[I]$. By assumption, the left event also has positive probability. The independence of the two events shows that $\mathbf{P}(\mathcal{G}) > 0$.

Analyzing N^0, we see that, by definition, we have that for $k, m \geq 0, n \geq k_0$ the event $\{L_k^0 = m, L_{k+1}^0 = m + n\}$ is given by

$$\{L_k^0 = m\} \cap \left(\bigcap_{j=1}^{k_0-1} \left\{ \begin{matrix} A_{m+j-1} \geq m_A, \\ I_{m+j} = m_I \end{matrix} \right\} \right) \cap \left(\bigcap_{j=k_0}^{n-1} \{K_{m+j} \leq j\} \right) \cap \{K_{m+n} > n\},$$

using the definition of K_m given in 3.8. For $1 \leq n < k_0$ the event $\{L_k^0 = m, L_{k+1}^0 = m + n\}$ is just given by

$$\{L_k^0 = m\} \cap \left(\bigcap_{j=1}^{n-1} \left\{ \begin{matrix} A_{m+j-1} \geq m_A, \\ I_{m+j} = m_I \end{matrix} \right\} \right) \cap (\{A_{m+n-1} < m_A\} \cup \{I_{m+n} \neq m_I\}).$$

In particular, going inductively through k, the event $\{L_k^0 = m\}$ only depends on $A_0, \dots, A_{m-1}$ and $I_1, \dots, I_m$, and the increments $L_1^0 - L_0^0, \dots, L_{k+1}^0 - L_k^0$ are independent under $\mathbf{P}$ conditionally on $L_k^0 < \infty$. Also, under $\mathbf{P}$ conditionally on $L_k^0 < \infty$, the increments $L_1^0 - L_0^0, \dots, L_k^0 - L_{k-1}^0$ have the same distribution. This yields that under $\mathbf{P}$, N^0 has a geometric distribution with success probability $\mathbf{P}(\mathcal{G}) > 0$ and is thus almost surely finite under $\mathbf{P}$ and hence also under $\mathbb{P}$.

An analogous argument, where in view of Remark 3.13 we only need to show the positive probability of the second event in (3.9), which holds with only the assumption $\mathbf{E}[I] < \mathbf{E}[A]$, shows that also N, under $\mathbf{P}$, has a geometric distribution with positive success probability and thus is almost surely finite.

We now investigate N^{i+1} for $i \geq 0$. Since by definition we have

$$\bigcap_{j=1}^{\infty}\{G((A_{M^i},\ldots,A_{M^i+j-1}),(I_{M^i+1},\ldots,I_{M^i+j}))=1\},$$

the offspring after M^i tend to be larger, and the immunities tend to be smaller. Hence, for any site $L_k^{i+1} > M^i$, it becomes more probable to never find a bad configuration above L_k^{i+1}, i.e., achieve the event $\{L_{k+1}^{i+1} = \infty\}$. We see that N^{i+1} is stochastically dominated by a geometric distribution with success probability $\mathbf{P}(\mathcal{G})$ and is thus also almost surely finite under $\mathbf{P}$ and thus also under $\mathbb{P}$.

We now show that also T^0 is almost surely finite under $\mathbb{P}$. We saw above that $M^0 < \infty$ almost surely, and on the event $\{M^0 = k\}$, the time T^0 is bounded by the following random time σ^k. For $j \geq 0$ let

$$S_j := \inf\left\{t \geq 0 \middle| \forall 0 \leq x \leq j \, \forall 0 \leq i \leq A_x : \max_{0\leq s\leq t} Y_s^{x,i} + x \geq j+1\right\}$$

be the time until all parasites that have been born on the first j sites reach site $j+1$ and

$$\sigma^k := \sum_{j=0}^{k-1} S_j$$

be the accumulation of these times.

Conditioned on parasites' survival, the time $\rho_{j+1} - \rho_j$ that the front needs to jump from j to $j+1$ is at most S_j. In particular, this implies that the time T^i to reach site M^i is bounded by

$$T^i \leq \sum_{k=0}^{\infty} \mathbb{1}_{M^i=k}\sigma^k$$

$\mathbb{P}$-almost surely. Analogously, the time T to reach site $M + k_0$ is bounded by

$$T \leq \sum_{k=0}^{\infty} \mathbb{1}_{M=k}\sigma^{k+k_0}$$

$\mathbb{P}$-almost surely.

Using [40, Theorem A.1], we can estimate the arrival times $\tau_k^{x,i}$ of random walks and derive for large enough t

$$\begin{aligned}
&\mathbf{P}(S_j > t)\\
&\quad \le \mathbf{P}\left(\max_{0\le x\le j} A_x > \log t\right) + \mathbf{P}\left(\max_{0\le x\le j} A_x \le \log t, \bigcup_{x=0}^{j}\bigcup_{i=1}^{\lfloor \log t\rfloor}\{\tau_{j+1-x}^{x,i} > t\}\right)\\
&\quad \le \frac{j\mathbf{E}[A]}{\log t} + \sum_{x=0}^{j}\sum_{i=1}^{\lfloor \log t\rfloor}\frac{2(j+1-x)}{\sqrt{2\pi t}}\cdot 2\\
&\quad \le \frac{j\mathbf{E}[A]}{\log t} + 2\log t\frac{(j+1)(j+2)}{\sqrt{2\pi t}} \to 0 \quad (t\to\infty),
\end{aligned}$$

and hence $S_j < \infty$ $\mathbf{P}$-almost surely and thus also $\sigma^k < \infty$ $\mathbf{P}$-almost surely. Consequently, also T_i and T are $\mathbb{P}$-almost surely finite. □

3.3.2 Auxiliary results

A key for analyzing the sequences $(M^i)_{i\ge 0}$ and $(\nu_n)_{n\in\mathbb{Z}}$ is an estimate of the tail of K. Using the moment assumptions on I and $A \ge 0$ a.s., we obtain the estimate for the probability of a bad configuration of length $k \ge k_0$

$$\mathbb{P}((A_{n-1},\dots,A_{n-k}) \notin \underline{A}^{\text{good}}(k) \text{ or } (I_n,\dots,I_{n-k+1}) \notin \underline{I}^{\text{good}}(k)) = \mathcal{O}(k^{-\alpha}).$$

Since K is the smallest distance at which a good configuration occurs, the event $\{K > n\}$ is contained in the event that all configurations with length $k = k_0, k_0+1,\dots,n$ are bad. Using classical results of Sparre-Andersen (c.f. [45]) on exactly these types of probabilities will allow us to improve the just-obtained estimate and give the following lemma.

Lemma 3.15. *For all $\varepsilon > 0$ there is a $C_K = C_K(\varepsilon) \ge 0$ such that for all $n \ge k_0$ we have*

$$\mathbf{P}(K > n) \le C_K n^{-(\alpha+1-\varepsilon)}.$$

The proof will be given in Section 3.3.3.

With the tail of K at hand, we can begin to analyze the sequence $(M^i)_{i\ge 0}$. As seen in the proof of Lemma 3.14, the number of trials N^0 stochastically dominates the amount of trials N^i for $i \ge 1$. Hence, the increments $M^{i+1} - M^i$ should be stochastically dominated by M^0. In addition, the event $\mathcal{G}_{M^{i+1}}$, that is, the condition of only good offspring numbers and immunities configurations after M^{i+1}, overrides the condition $\mathcal{G}_{M^i}$ of the previous good site. This means that the distribution of offspring numbers and immunities after M^i is the same for all $i \geq 0$, implying that $(M^{i+1} - M^i)_{i \geq 0}$ is i.i.d. under $\mathbb{P}$. Using the tail of K, we can also bound the tail of M^0 and thus the tail of $(M^{i+1} - M^i)_{i \geq 0}$. Precisely, we have the following lemma.

Lemma 3.16. *The sequence* $(M^{i+1} - M^i)_{i \geq 0}$ *is i.i.d. under* $\mathbb{P}$*, and for any* $\varepsilon > 0$ *there is a* $C \geq 0$ *such that for all* $l \in \mathbb{N}$ *we have*

$$\mathbb{P}(M^{i+1} - M^i \geq l) \leq \mathbb{P}(M^0 \geq l) \leq Cl^{-(\alpha - \varepsilon)}.$$

The proof will also be given in Section 3.3.3. Our estimate of the tail of $M^{i+1} - M^i$ is by a factor of order $\frac{1}{l}$ heavier than the tail of K because the event $\{\infty > L_1^0 > l\}$ is contained in the event that $\{K_j > j\}$ for some $j > l$. A union bound over these events yields the estimate.

Next, we consider the sequence $\{\nu_n : n \in \mathbb{Z}\}$. By construction, each jump time ν_n only depends on random variables with indices inside $[n - K_n, n]$. We will make use twofold of the just-obtained tail estimates for K. Firstly, we will establish tail estimates for ν by showing that if K is not too large, the surplus of parasites reaches the boundary sufficiently fast. Secondly, the tail estimates of K allow us to control the dependencies among the jump times $(\nu_n)_{n \in \mathbb{Z}}$, since conditionally on $K_{n+k} \leq k$, the variables ν_{n+k} and ν_n depend on different sets of independent random variables. We begin by stating the former result, which reads as follows.

Lemma 3.17. *For any* $q < \frac{(4 \wedge \alpha)+1}{2}$*, there is a* $C > 0$ *such that for all* $t > 0$ *we have*

$$\mathbf{P}(\nu > t) \leq Ct^{-q}.$$

In particular we have $\nu \in L^q(\Omega, \mathcal{F}, \mathbf{P})$ *for all* $q < \frac{(4 \wedge \alpha)+1}{2}$.

The proof will be given in Section 3.3.3. We note that the exponent in the tail of ν is half as large as in the tail of K, because a typical random walk is at a distance of $\sqrt{t}$ at time t. Hence, the event $\{\nu_n \leq t\}$ is only likely if $\{K_n \ll \sqrt{t}\}$. On the other hand, the different treatment of distance k_0 in the definition of K can be explained as follows. On the event $\{K_n = k\}$ with $\sqrt{t} \gg k \geq k_0$, at most $\lfloor \beta_I k \rfloor$ parasites out of a set of at least $\lceil \beta_A k \rceil$ independently moving parasites need to reach a one-sided boundary, which is at a distance at most

k from their starting point. At time t, a single parasite has not reached the boundary with probability $\mathcal{O}\left(\frac{k}{\sqrt{t}}\right)$, and thus, by independence, the probability that at least $(\beta_A - \beta_I)k$ parasites do not reach the boundary is of order $\mathcal{O}\left(\frac{k}{\sqrt{t}^{(\beta_A-\beta_I)k}}\right)$. Using $k \ll \sqrt{t}$, this expression will be maximized in $k = k_0$, and choosing $k_0 = \left\lceil \frac{\alpha+1}{\beta_A-\beta_I} \right\rceil$ yields the desired tail. For $\{K < k_0\}$ we can use the strong condition on the offspring and immunity configurations in the definition of K_n to obtain that there are at least Km_A parasites, and we wait for Km_I many to reach a one-sided boundary at a distance at most $k_0 - 1$. By definition, we have $Km_A - Km_I \geq 4$, which, analogously as above, gives that the probability of less than Km_I parasites having reached the boundary is bounded by $\mathcal{O}\left(\frac{1}{\sqrt{t}^{4+1}}\right)$.

Next, we deal with the sequences $(\overline{\nu}^i_n)_{n\geq 1}$ and $(\nu_{M+n})_{n\geq 1}$. By Lemma 3.16, each sequence $(\overline{\nu}^i_n)_{n\geq 1}$ has the same distribution, and thus it suffices to analyze the case $i = 0$, and we abbreviate $\overline{\nu}_n := \overline{\nu}^0_n$ for any $n \geq 1$. Also, we only perform the arguments for $(\overline{\nu}_n)_{n\geq 1}$ and note that similar results, with identical proofs, hold for $(\nu_{M+n})_{n\geq k_0}$.

By definition, the offspring and immunity configurations above M^0 are always good in the sense that $G((A_{M^0}, \dots, A_{M^0+n-1}), (I_{M^0+1}, \dots, I_{M^0+n})) = 1$. Clearly, this restriction affects the distribution of $\overline{\nu}_n$, and therefore the distribution of $\overline{\nu}_n$ differs from that of ν_n. However, this difference diminishes fast as n tends to infinity. A key observation is that the condition of having only good configurations above M^0 is, in fact, only a restriction on the first few sites after M^0. For large n, a bad configuration between M^0 and $M^0 + n$ would be a large deviation for $(A_{M^0}, \dots, A_{M^0+n-1})$ or $(I_{M^0+1}, \dots, I_{M^0+n})$, which is unlikely to happen. Because $\overline{\nu}_n$ only depends on variables with an index greater than $n - K_n$, this means that the distribution of $\overline{\nu}_n$ is only influenced by the restriction that all configurations above M^0 are good, by ruling out the anyway unlikely event of a large K_n. We thus obtain the following lemma.

Lemma 3.18. *The joint distributions of* $(\{\overline{\nu}_n, \overline{\nu}_{n+1}, \dots\})_{n\geq 1}$ *under* $\mathbb{P}$ *converge to the joint distribution of* $\{\nu_1, \nu_2, \dots\}$ *under* $\mathbf{P}$. *In particular, for any* $\varepsilon > 0$ *there is a* $C \geq 0$ *such that*

$$|\mathbb{P}((\overline{\nu}_n, \overline{\nu}_{n+1}, \dots) \in E) - \mathbf{P}((\nu_1, \nu_2, \dots) \in E)| \leq Cn^{-\alpha+\varepsilon}$$

for all $n \geq k_0, E \in \mathcal{B}([0, \infty)^{\mathbb{N}})$.

The proof will be given in Section 3.3.3, and we note that the same result holds for $(\nu_{M+n})_{n\geq k_0}$ with the same proof. The upper bound is derived from estimating the probability of a large $K_{n+j} > n+j$ for some $j \geq 0$ with a union bound.

Finally, we need to establish a weak dependence among the random variables $(\overline{\nu}_n)_{n\geq 1}$. As we will see, they form a ϕ-mixing sequence. This is not surprising because for $\overline{\nu}_{n+k}$ to be influenced by $\overline{\nu}_n$, we must have $K_{n+k} > k$, since otherwise the two variables use different parts of $\mathbf{A}, \mathbf{I}, \mathbf{Y}$. However, because the variables are defined above M^0, the immunities and offspring numbers used are not i.i.d. Similarly as in Lemma 3.18, we show that this restriction also diminishes for large k, which yields the following lemma.

Lemma 3.19. *For any $\varepsilon \in (0, \alpha)$ the sequence $(\overline{\nu}_n)_{n\geq 1}$ is ϕ-mixing under $\mathbb{P}$ with rate*

$$\sup_{\substack{E\in\mathcal{F}_{\leq m}, \mathbb{P}(E)>0,\\ B\in\mathcal{F}_{\geq m+n}}} |\mathbb{P}(B|E) - \mathbb{P}(B)| \leq \phi(n) := Cn^{-\alpha+\varepsilon},$$

where

$$\mathcal{F}_{\leq m} := \sigma(\overline{\nu}_j : 1 \leq j \leq m), \quad \mathcal{F}_{\geq m} := \sigma(\overline{\nu}_j : j \geq m).$$

The proof will be given in Section 3.3.3. There are two effects that make the events B and E depend on each other. The first is that every configuration of offspring numbers and immunities to the right of M^i is good. The second effect is that $B \in \mathcal{F}_{\geq m+n}$ depends on all random variables from $\mathbf{A}, \mathbf{I}, \mathbf{Y}$ with index less than $m+n$, in particular the same variables on which $E \in \mathcal{F}_{\leq m}$ depends. To deal with the first effect, for some large $k = \Theta(n)$ we split the event of having only good configurations to the right of M^i into the event $\mathcal{G}_{0,m+k}$ that there are only good configurations between M^i and site $M^i + m + k$ and the complement in $\mathcal{G}_{0,m+k}$ of the event $\mathcal{B}_{0,m+k}$ that for some $j > k$ there is a bad configuration between M^i and $M^i + m + j$. Using a union bound, the event $\mathcal{B}_{0,m+k}$ happens with probability $\mathcal{O}(k^{-\alpha+\varepsilon})$. To deal with the second effect, we split the event B into B intersected with the event that B is using variables with index less than $m+k$ and B intersected with the event that B uses only variables with index greater than $m+k$. Again using a union bound, the former event happens with probability $\mathcal{O}((n-k)^{-\alpha+\varepsilon})$. Now the remaining event B intersected with the event that B uses only variables with index greater than $m+k$ and the event $\mathcal{G}_{0,m+k} \cap E$ are independent, which will make the probability of their intersection

close to $\mathbb{P}(B)\mathbb{P}(E)$.
Given that the sequence $(\overline{\nu}_n)_{n\geq 1}$ is asymptotically stationary and has weak dependence, we can obtain a strong law of large numbers for it. To better control the fluctuations around the mean, we then use classical results on the tails of sums of ϕ-mixing sequences to obtain the following estimate.

Lemma 3.20. *If $\alpha > 3$, then for all $2 \leq q < \frac{(4\wedge\alpha)+1}{2}$, there exists a $C_q > 0$ such that for all $n \in \mathbb{N}$ we have*

$$\mathbb{E}\left[\max_{1\leq i\leq n}\left|\sum_{k=1}^{i}(\overline{\nu}_k - \mathbb{E}[\overline{\nu}_k])\right|^q\right] \leq C_q n^{\frac{q}{2}}.$$

The proof will be given in Section 3.3.3.
We will make use of this result twofold. The first application is to control the time the front needs to travel from one good site to the next and show it has a finite expectation. The other application will be to show that with positive probability the front moves at linear speed after a good site, which we will use to construct the almost surely finite renewal sites $(R^i)_{i\geq 0}$ in Proposition 3.22. Coming to the first application, we have the following.

Lemma 3.21. *Let T^1 be as in Definition 3.12. If $\alpha > \frac{3+\sqrt{11}}{2}$, then*

$$\mathbb{E}[T^1 | M^0 = 0] < \infty.$$

The proof will be given in Section 3.3.3 and relies on controlling large deviations of the sum of $(\overline{\nu}_k)_{k\geq 1}$ by using Lemma 3.20.
Furthermore, after a good site M^i is reached, we will show that with positive probability the front grows linearly fast at a certain small slope $\lambda > 0$ after a good site M^i is reached. At each good site M^i, the parasites that were generated to the left of M^i have a positive probability of never catching up to the linearly moving front. Iterating this procedure yields an almost surely finite renewal site $R^1 = M^{J^1}$, such that the front after reaching this site is only fed from parasites that are generated at a site x with $x \geq R^1$. Again, iterating the construction of R^1 will lead us to the following renewal structure that splits the jump times into independent epochs between these renewal sites.

Proposition 3.22. *Let $\alpha > 3$, $\mathbb{E}[I^{2\alpha}] < \infty, \mathbb{E}[A^{\frac{4}{4\wedge\alpha-3}+\varepsilon_A}] < \infty$ for some $\varepsilon_A > 0$ and assume the initial configuration of only A_0 parasites placed at vertex 0.*

There is a sequence $(R^i)_{i\geq 0}$ *of* $\mathbb{P}$*-almost surely finite renewal sites, such that* $R^0 = 0$ *almost surely and*

$$\{(R^{i+1} - R^i, \rho_{R^i+1} - \rho_{R^i}, \ldots, \rho_{R^{i+1}} - \rho_{R^{i+1}-1}) : i \geq 0\}$$

is an independent collection. The collection starting with $i \geq 1$ *is also identically distributed.*

The proof will be given in Section 3.3.3 and will make the construction described above rigorous.

In the proof of Theorem 3.3, we will make use of this renewal structure to obtain a zero-one law under $\mathbb{P}$ for the limit $\frac{r_t}{t}$, which will allow us to transfer a convergence with positive probability (on the event $\{M^0 = 0\}$) obtained through Liggett's Subadditive Ergodic Theorem [32] and Lemma 3.21 to a $\mathbb{P}$-almost sure convergence.

3.3.3 Proofs of auxiliary results

Proof of Lemma 3.15

We begin by establishing the following result on the asymptotic for coefficients of a power series. This will be useful because the probabilities we are interested in are given by such series; see Corollary 3.25 (cf. [45, Theorem 1]).

Lemma 3.23. *Let* $(w_n)_{n\in\mathbb{N}} \in \mathcal{O}(\mathrm{e}^{-\theta n}\, n^{-\gamma})$ *for some* $\theta \geq 0, \gamma > 1$*. Then, defining* $(c_n)_{n\in\mathbb{N}_0}$ *as the coefficients of the power series*

$$\sum_{n=0}^{\infty} c_n s^n := \exp\left(\sum_{n=1}^{\infty} w_n s^n\right) \qquad (|s| \leq 1),$$

we have $(c_n)_{n\in\mathbb{N}_0} \in \mathcal{O}(\mathrm{e}^{-\theta n}\, n^{-\gamma})$*.*

Proof. Let $C_w \geq 0$ be such that $|w_n| \leq C_w\, \mathrm{e}^{-\theta n}\, n^{-\gamma}$ for all $n \in \mathbb{N}$. We begin by investigating the coefficients of the power series defined by

$$\sum_{n=1}^{\infty} b_n(k) s^n := \left(\sum_{n=1}^{\infty} w_n s^n\right)^k \qquad (|s| \leq 1),$$

and show by induction over $k \in \mathbb{N}$ that, setting $C_1 := 2^{1+\gamma} \sum_{j=1}^{\infty} j^{-\gamma}$, we have

$$|b_n(k)| \leq C_w^k C_1^{k-1}\, \mathrm{e}^{-\theta n}\, n^{-\gamma}, \qquad \text{for all } n \in \mathbb{N}. \tag{3.10}$$

The induction root $k = 1$ holds by assumption, so we continue with the induction step. Let $k \geq 1$ and assume (3.10) holds; then for $|s| \leq 1$ we have

$$\begin{aligned}\sum_{n=1}^{\infty} b_n(k+1)s^n &= \left(\sum_{n=1}^{\infty} w_n s^n\right)^k \left(\sum_{n=1}^{\infty} w_n s^n\right) = \left(\sum_{n=1}^{\infty} b_n(k)s^n\right)\left(\sum_{n=1}^{\infty} w_n s^n\right) \\ &= \sum_{n=0}^{\infty}\sum_{j=0}^{n} w_{j+1}s^{j+1}b_{n-j+1}(k)s^{n-j+1} = \sum_{n=0}^{\infty} s^{n+2}\sum_{j=1}^{n+1} w_j b_{n-j+2}(k) \\ &= \sum_{n=2}^{\infty} s^n \sum_{j=1}^{n-1} w_j b_{n-j}(k).\end{aligned}$$

Now for $n \geq 2$ we obtain

$$\begin{aligned}\left|\sum_{j=1}^{n-1} w_j b_{n-j}(k)\right| &\leq C_w C_w^k C_1^{k-1} \sum_{j=1}^{n-1} \mathrm{e}^{-\theta j}\, j^{-\gamma}\, \mathrm{e}^{-\theta(n-j)}(n-j)^{-\gamma} \\ &\leq 2C_w^{k+1}C_1^{k-1}\,\mathrm{e}^{-\theta n} \sum_{j=1}^{\lfloor \frac{n}{2} \rfloor} (j(n-j))^{-\gamma} \\ &= 2C_w^{k+1}C_1^{k-1}\,\mathrm{e}^{-\theta n}\, n^{-\gamma} \sum_{j=1}^{\lfloor \frac{n}{2} \rfloor} \left(j\left(1-\frac{j}{n}\right)\right)^{-\gamma} \\ &\leq 2C_w^{k+1}C_1^{k-1}\,\mathrm{e}^{-\theta n}\, n^{-\gamma} \sum_{j=1}^{\lfloor \frac{n}{2} \rfloor} \left(j \cdot \frac{1}{2}\right)^{-\gamma} \\ &\leq 2C_w^{k+1}C_1^{k-1}\left(2^{\gamma}\sum_{j=1}^{\infty} j^{-\gamma}\right)\mathrm{e}^{-\theta n}\, n^{-\gamma} = C_w^{k+1}C_1^{k}\,\mathrm{e}^{-\theta n}\, n^{-\gamma}.\end{aligned} \tag{3.11}$$

This finishes the induction and shows (3.10) holds for all $k \in \mathbb{N}$. Noting that

$$\begin{aligned}\exp\left(\sum_{n=1}^{\infty} w_n s^n\right) &= 1 + \sum_{k=1}^{\infty}\frac{1}{k!}\left(\sum_{n=1}^{\infty} w_n s^n\right)^k = 1 + \sum_{k=1}^{\infty}\sum_{n=1}^{\infty}\frac{b_n(k)}{k!}s^n \\ &= 1 + \sum_{n=1}^{\infty} s^n \sum_{k=1}^{\infty}\frac{b_n(k)}{k!}\end{aligned}$$

we estimate

$$\left|\sum_{k=1}^{\infty}\frac{b_n(k)}{k!}\right| \leq \mathrm{e}^{-\theta n}\, n^{-\gamma}\sum_{k=1}^{\infty}\frac{1}{k!}C_w^k C_1^{k-1} = \frac{\mathrm{e}^{C_w C_1} - 1}{C_1}\,\mathrm{e}^{-\theta n}\, n^{-\gamma} = \mathcal{O}(\mathrm{e}^{-\theta n}\, n^{-\gamma}),$$

which finishes the proof. □

Definition 3.24. *We adopt the notation of [45] and, for $n \in \mathbb{N}$, denote by N_n^A the amount of partial sums*

$$\sum_{k=1}^{1}(\beta_A - A_k), \sum_{k=1}^{2}(\beta_A - A_k), \dots, \sum_{k=1}^{n}(\beta_A - A_k)$$

that are positive, and similarly we denote by N_n^I the amount of partial sums

$$\sum_{k=1}^{1}(I_k - \beta_I), \dots, \sum_{k=1}^{n}(I_k - \beta_I)$$

that are positive.

Corollary 3.25. *There is some $\theta > 0$ such that*

$$\mathbf{P}(N_n^I = n) = \mathcal{O}(n^{-(\alpha+1)}), \quad \mathbf{P}(N_n^A = n) = \mathcal{O}\left(\frac{\exp(-\theta n)}{n^{\frac{3}{2}}}\right)$$

Proof. As shown in [45, Theorem 1] we have

$$\sum_{n=0}^{\infty} \mathbf{P}(N_n^A = n)s^n = \exp\left(\sum_{n=1}^{\infty} \frac{\mathbf{P}\left(\sum_{j=1}^{n} A_j < \beta_A n\right)}{n} s^n\right),$$

Noting that $A \geq 0$ almost surely allows us to apply [4, Theorem 1] with

$$X_j = -A_j + \mu_A, \qquad a = \mu_A - \beta_A > 0$$

and conclude

$$\mathbf{P}\left(\sum_{j=1}^{n} A_j < \beta_A n\right) = \mathcal{O}\left(\frac{\exp(-\theta n)}{n^{\frac{1}{2}}}\right)$$

for some $\theta > 0$. If $\mathbf{P}(A < \beta_A) = \mathbf{P}(X_j > a) > 0$, the assumptions of [4, Theorem 1] are satisfied as explained before the theorem there, and if $\mathbf{P}(A < \beta_A) = 0$, then the left-hand side is just 0 and thus trivially the estimation holds. Now applying Lemma 3.23 yields the second claim. The first claim follows analogously from Lemma 3.23 and an application of Markov's as well as Rosenthal's inequality. Since, by assumption (3.3), $\mathbf{E}[I^{2\alpha}] < \infty$, we have

$$\begin{aligned}\mathbf{P}\left(\sum_{k=1}^{n} I_k > \beta_I n\right) = \mathbf{P}\left(\sum_{k=1}^{n} I_k - \mu_I > (\beta_I - \mu_I)n\right) &\leq \frac{\mathbf{E}\left[|\sum_{k=1}^{n} I_k - \mu_I|^{2\alpha}\right]}{(\beta_I - \mu_I)^{2\alpha} n^{2\alpha}} \\ &\leq \frac{C_{2\alpha}\mathbf{E}[|I_1 - \mu_I|^2]^\alpha n^\alpha}{(\beta_I - \mu_I)^{2\alpha} n^{2\alpha}} = \frac{C_{2\alpha}\mathbf{E}[|I_1 - \mu_I|^2]^\alpha}{(\beta_I - \mu_I)^{2\alpha}} n^{-\alpha}.\end{aligned}$$

□

Now we have all the ingredients to estimate the tail of K.

Proof of Lemma 3.15. First we observe that for $n \gg k_0$ large enough

$$\begin{aligned}\mathbf{P}(K > n) &\leq \mathbf{P}\left(\bigcap_{k=k_0}^{n}\left(\left\{\sum_{j=1}^{k} A_{1-j} < \beta_A k\right\} \cup \left\{\sum_{j=1}^{k} I_{2-j} > \beta_I k\right\}\right)\right) \\ &\leq \mathbf{P}(N_n^A + N_n^I \geq n - k_0 + 1) \\ &\leq \mathbf{P}(N_n^A \geq \lceil \lambda \log n \rceil) + \mathbf{P}(N_n^I > n - k_0 - \lceil \lambda \log n \rceil)\end{aligned}$$

for any $\lambda > 0$. Now using [45, Theorem 1, (3.3)] and then Corollary 3.25, we obtain for any $1 \leq k \leq n$

$$\mathbf{P}(N_n^A = k) \leq \mathbf{P}(N_k^A = k) = \mathcal{O}\left(\mathrm{e}^{-\theta k}\, k^{-\frac{3}{2}}\right)$$

and

$$\mathbf{P}(N_n^I = k) \leq \mathbf{P}(N_k^I = k) = \mathcal{O}\left(k^{-(\alpha+1)}\right).$$

Setting $\lambda = \frac{\alpha+1}{\theta}$, we have

$$\begin{aligned}\mathbf{P}(N_n^A \geq \lceil \lambda \log n \rceil) &= \sum_{k=\lceil \lambda \log n \rceil}^{n} \mathbf{P}(N_n^A = k) \leq \sum_{k=\lceil \lambda \log n \rceil}^{n} C_A\, \mathrm{e}^{-\theta k}\, k^{-\frac{3}{2}} \\ &\leq \sum_{k=\lceil \lambda \log n \rceil}^{n} C_A\, \mathrm{e}^{-\theta k} = C_A \frac{\mathrm{e}^{-\theta \lceil \lambda \log n \rceil} - \mathrm{e}^{-\theta(n+1)}}{1 - \mathrm{e}^{-\theta}} \\ &\leq \frac{C_A}{1 - \mathrm{e}^{-\theta}}\, \mathrm{e}^{-\theta \frac{\alpha+1}{\theta} \log n} = \mathcal{O}\left(n^{-(\alpha+1)}\right)\end{aligned}$$

and

$$\begin{aligned}\mathbf{P}(N_n^I > n - k_0 - \lceil \lambda \log n \rceil) &= \sum_{k=n-k_0-\lceil \lambda \log n \rceil + 1}^{n} \mathbf{P}(N_n^I = k) \\ &\leq \sum_{k=n-k_0-\lceil \lambda \log n \rceil + 1}^{n} C_I k^{-(\alpha+1)} \\ &\leq C_I (k_0 + \lceil \lambda \log n \rceil)(n - k_0 - \lceil \lambda \log n \rceil + 1)^{-(\alpha+1)} \\ &\leq 2 C_I \lambda n^{-(\alpha+1)} \frac{\log n}{(1 - \frac{2\lambda \log n}{n})^{\alpha+1}} \\ &= \mathcal{O}\left(n^{-(\alpha+1)} \log n\right),\end{aligned}$$

using that $2\lambda \log n > k_0 + \lceil \lambda \log n \rceil$ for n large enough. In particular, for any $\varepsilon > 0$ we have

$$\begin{aligned}\mathbf{P}(K > n) &\leq \mathbf{P}(N_n^A \geq \lceil \lambda \log n \rceil) + \mathbf{P}(N_n^I > n - k_0 - \lceil \lambda \log n \rceil) \\ &= \mathcal{O}\left(n^{-(\alpha+1)}\right) + \mathcal{O}\left(n^{-(\alpha+1)} \log n\right) = \mathcal{O}\left(n^{-(\alpha+1)+\varepsilon}\right)\end{aligned}$$

which finishes the proof. $\square$

Remark 3.26. *As seen in the proof, we actually obtain the better estimate*

$$\mathbf{P}(K > n) = \mathcal{O}\left(n^{-(\alpha+1)} \log n\right),$$

but in the proofs of Lemma 3.16 and Lemma 3.17 we will lose an n^{ε} factor anyway.

Proof of Lemma 3.16

Proof of Lemma 3.16. Clearly

$$\mathbb{P}(M^{i+1} - M^i \geq l) = \frac{1}{\mathbf{P}(\mathcal{S})} \sum_{j=0}^{\infty} \mathbf{P}(M^i = j, \mathcal{S}, M^{i+1} \geq j + l)$$

The event $\{M^i = j, \mathcal{S}, M^{i+1} \geq j + l\}$ is given by the intersection of an event $B^{<j}$ depending on $(A_0, \dots, A_{j-1})$ and $(I_1, \dots, I_j)$ defined through the event $\mathcal{S}$ and the event $\{M^i \geq j\}$, as well as the intersection of the event

$$\mathcal{G}_j = \bigcap_{m=1}^{\infty} \{G((A_j, \dots, A_{j+m-1}), (I_{j+1}, \dots, I_{j+m})) = 1\}$$

as also $\{M^i = j\}$ should be fulfilled and finally the intersection of some event $B_{>j}$ depending on $A_{j+1}, \dots$ and on $I_{j+2}, \dots$ defined through the event $\{M^{i+1} \geq j + l\}$. Precisely, $B_{>j}$ is the event that for some

$$k \geq 0 \text{ and } l_0 = 0 < l_1 < \dots < l_k$$

such that $l_k \geq l - 2 > l_{k-1}$ we have

$$\left\{ \begin{array}{c} \text{all configurations from } j + 1 + l_0 \text{ up to } j + 1 + l_1 - 1 \text{ are good} \\ \text{and the configuration from } j + 1 + l_0 \text{ to } j + 1 + l_1 \text{ is bad,} \\ \vdots \\ \text{all configurations from } j + 2 + l_{k-1} \text{ up to } j + 1 + l_k - 1 \text{ are good} \\ \text{and the configuration from } j + 2 + l_{k-1} \text{ to } j + 1 + l_k \text{ is bad.} \end{array} \right\}.$$

Using that $\mathbf{A}, \mathbf{I}$ are i.i.d. under $\mathbf{P}$, we obtain that

$$\begin{aligned}
\mathbb{P}(M^{i+1} - M^i \geq l) &= \frac{1}{\mathbf{P}(\mathcal{S})} \sum_{j=0}^{\infty} \mathbf{P}(B^{<j}) \mathbf{P}(\mathcal{G}_j, B_{>j}) \\
&= \mathbf{P}(\mathcal{G}_0, B_{>0}) \frac{1}{\mathbf{P}(\mathcal{S})} \sum_{j=0}^{\infty} \mathbf{P}(B^{<j}) \\
&= \mathbf{P}(\mathcal{G}_0, B_{>0}) \frac{1}{\mathbf{P}(\mathcal{S})} \sum_{j=0}^{\infty} \mathbf{P}(B^{<j}) \frac{\mathbf{P}(\mathcal{G}_j)}{\mathbf{P}(\mathcal{G}_j)} \\
&= \mathbf{P}(\mathcal{G}_0, B_{>0}) \frac{1}{\mathbf{P}(\mathcal{S})\mathbf{P}(\mathcal{G}_0)} \sum_{j=0}^{\infty} \mathbf{P}(B^{<j}, \mathcal{G}_j) \\
&= \mathbf{P}(\mathcal{G}_0, B_{>0}) \frac{1}{\mathbf{P}(\mathcal{S})\mathbf{P}(\mathcal{G}_0)} \sum_{j=0}^{\infty} \mathbf{P}(M^i = j, \mathcal{S}) \\
&= \frac{\mathbf{P}(\mathcal{G}_0, B_{>0})}{\mathbf{P}(\mathcal{G}_0)} = \mathbf{P}(B_{>0} | \mathcal{G}_0).
\end{aligned}$$

This yields that $(M^{i+1} - M^i)_{i \geq 0}$ are identically distributed. To see that $\mathbb{P}(M^{i+1} - M^i \geq l)$ is dominated by $\mathbb{P}(M^0 \geq l)$, note that the event $B_{>0}$ (which we just defined) is more likely to happen conditioned on survival, i.e., on the event

$$\bigcap_{m=1}^{\infty} \left\{ \sum_{k=1}^{m} A_{k-1} - I_k \geq 0 \right\},$$

rather than conditioned on $\mathcal{G}_0$, i.e.,

$$\mathbb{P}(M^0 \geq l) = \mathbf{P}(B_{>0} | \mathcal{S}) \geq \mathbf{P}(B_{>0} | \mathcal{G}_0) = \mathbb{P}(M^{i+1} - M^i \geq l).$$

The independence follows similarly after noting that

$$\mathcal{G}_j \cap \mathcal{G}_{j+k} = \mathcal{G}_{j+k} \cap \bigcap_{m=1}^{k} \{G((A_j, \ldots, A_{j+m-1}), (I_{j+1}, \ldots, I_{j+m})) = 1\}, \tag{3.12}$$

and the two events $\mathcal{G}_{j+k}$ and $\cap_{m=1}^{k} \{G((A_j, \ldots, A_{j+m-1}), (I_{j+1}, \ldots, I_{j+m})) = 1\}$) on the right-hand side are independent.

To obtain the tail estimate, we proceed as follows. We set $\delta_1 := \mathbf{P}(\mathcal{G}_0)$. Then for any $m \in \mathbb{N}$ and $l \geq 0$ we have

$$\begin{aligned}
\mathbb{P}(M^0 > l) &= \mathbb{P}(N^0 > m, M^0 > l) + \sum_{n=1}^{m} \mathbb{P}(N^0 = n, L_n^0 > l) \\
&\leq \mathbf{P}(N^0 > m) + \sum_{n=1}^{m} \mathbb{P}(l < L_n^0 < \infty).
\end{aligned}$$

As seen in the proof of Lemma 3.14, N^0 is geometrically distributed under $\mathbf{P}$, and hence the first part is equal to $(1-\delta_1)^m$. For $\lambda \in (0,1)$ and $n \in \{1,\dots,m\}$ we define the event

$$E_n^\lambda := \{L_1^0 - L_0^0 < l^\lambda, \dots, L_n^0 - L_{n-1}^0 < l^\lambda\}$$

such that on E_n^λ we have $L_n^0 < nl^\lambda$. For $l \geq m^{\frac{1}{1-\lambda}}$ we thus have

$$E_n^\lambda \cap \{l < L_n^0 < \infty\} = \emptyset.$$

Lemma 3.15 gives us that, fixing some $\varepsilon_K \in (0,\varepsilon)$, there is a $C_1 = C_1(\alpha,\varepsilon_K) \geq 0$ with

$$\begin{aligned}
\mathbb{P}(l < L_n^0 < \infty) = \mathbb{P}((E_n^\lambda)^C, l < L_n^0 < \infty) &\leq \sum_{k=1}^{n} \mathbb{P}(L_k^0 - L_{k-1}^0 \geq l^\lambda, l < L_n^0 < \infty) \\
&\leq \sum_{k=1}^{n} \mathbb{P}(l^\lambda \leq L_k^0 - L_{k-1}^0 < \infty) = n\mathbb{P}(l^\lambda \leq L_1^0 < \infty) \\
&\leq n\mathbb{P}\left(\bigcup_{j=\lfloor l^\lambda \rfloor} \{K_j > j\}\right) \leq C_1 n l^{-\lambda(\alpha-\varepsilon_K)}.
\end{aligned}$$

Now we choose $\lambda \in (\frac{\alpha-\varepsilon}{\alpha-\varepsilon_K}, 1), C_2 = \frac{\lambda(\alpha-\varepsilon_K)}{\log\frac{1}{1-\delta_1}}$ and $m = \lceil C_2 \log l \rceil$, then for l_0 large enough such that

$$l_0 > (1 + C_2 \log l_0)^{\frac{1}{1-\lambda}}$$

there is a $C_3 > 0$ such that for all $l \geq l_0$ we obtain

$$\mathbb{P}(M^0 > l) \leq l^{-\lambda(\alpha-\varepsilon_K)} + C_1 \frac{2 + 3C_2 \log l + (C_2 \log l)^2}{2} l^{-\lambda(\alpha-\varepsilon_K)} \leq C_3 l^{-\alpha+\varepsilon}.$$

Possibly increasing the constant C_3, this estimate also holds for any $0 \leq l < l_0$, which finishes the proof. □

Proof of Lemma 3.17

Now having a good control on the tail of K, we can use it to control the tail of ν. We split the event $\nu > t$ into the parts where $K \leq \lambda(t)$ and where $K > \lambda(t)$, for some suitable function $\lambda(t) \ll \sqrt{t}$; see (3.14) for a definition. We treat the first part by applying large deviation results on random walks and the second part by ignoring the random walk part and just estimating $K > \lambda(t)$ with Lemma 3.15.

Proof of Lemma 3.17. We recall the notations

$$m_I, m_A, \underline{A}^{\mathrm{good}}(k), \underline{I}^{\mathrm{good}}(k), \underline{\mathcal{V}}_n^{\mathrm{good}}(k,\mathbf{a}) \text{ and } \tau_k^{x,i}$$

from Definition 3.8 and define for

$$k \in \mathbb{N}, \mathbf{a} = (a_1, \dots, a_k) \in \underline{A}^{\mathrm{good}}(k)$$

the quantity

$$Z(k) := \begin{cases} m_I k, & \text{if } 1 \le k < k_0 \\ \beta_I k, & \text{if } k \ge k_0 \end{cases}$$

and random time

$$\mu_n(k,\mathbf{a}) := \inf \left\{ t \ge 0 : \sum_{(x,i) \in \underline{\mathcal{V}}_n^{\mathrm{good}}(k,\mathbf{a})} \mathbb{1}_{\tau_{n-x}^{x,i} \le t} \ge Z(k) \right\}.$$

Adopting the notation $\mu(k,\mathbf{a}) := \mu_1(k,\mathbf{a})$, we observe

$$\nu = \nu_1 = \sum_{k=1}^{\infty} \sum_{\mathbf{a} \in \underline{A}^{\mathrm{good}}(k)} \mu(k,\mathbf{a}) \mathbb{1}_{K=k} \prod_{j=1}^{k} \mathbb{1}_{A_{1-j}=a_j}.$$

Since $\mu(k,\mathbf{a})$ only depends on $\mathbf{Y}$, we obtain

$$\begin{aligned} &\mathbf{P}\left(K = k, \bigcap_{j=1}^{k} \{A_{1-j} = a_j\}, \nu \in B \right) \\ &\quad = \mathbf{P}\left(K = k, \bigcap_{j=1}^{k} \{A_{1-j} = a_j\} \right) \mathbf{P}(\mu(k,\mathbf{a}) \in B) \end{aligned} \tag{3.13}$$

for all $k \ge 1, \mathbf{a} \in \underline{A}^{\mathrm{good}}(k), B \in \mathcal{B}([0,\infty))$. In particular, setting

$$\lambda(t) := \lfloor t^{\frac{1}{2}-\varepsilon_1} \rfloor \tag{3.14}$$

for some $\varepsilon_1 > 0$ to be fixed later, we can bound $\mathbf{P}(\nu > t)$ by

$$\begin{aligned} &\mathbf{P}(\nu > t, K > \lambda(t)) + \sum_{k=1}^{\lambda(t)} \sum_{\mathbf{a} \in \underline{A}^{\mathrm{good}}(k)} \mathbf{P}\left(\nu > t, K = k, \bigcap_{j=1}^{k} \{A_{1-j} = a_j\} \right) \\ &\le C_K \lambda(t)^{-(\alpha+1-\varepsilon_K)} + \sum_{k=1}^{\lambda(t)} \sum_{\mathbf{a} \in \underline{A}^{\mathrm{good}}(k)} \mathbf{P}(\mu(k,\mathbf{a}) > t) \mathbf{P}\left(K = k, \bigcap_{j=1}^{k} \{A_{1-j} = a_j\} \right) \\ &\le C_K \lambda(t)^{-(\alpha+1-\varepsilon_K)} + \max_{\substack{1 \le k \le \lambda(t), \\ \mathbf{a} \in \underline{A}^{\mathrm{good}}(k)}} \mathbf{P}(\mu(k,\mathbf{a}) > t) \end{aligned} \tag{3.15}$$

for any $\varepsilon_K > 0$ and $C_K = C_K(\varepsilon_K)$ as in Lemma 3.15.
First we will show that for large enough t, the maximum over $k_0 \le k \le \lambda(t)$ is attained in k_0 and is in $\mathcal{O}\left(t^{-\frac{k_0(\beta_A-\beta_I)}{2}}\right)$. Then we will show that the maximum over $1 \le k < k_0$ is in $\mathcal{O}\left(t^{-\frac{5}{2}}\right)$, which for large t yields the desired tail behavior. Clearly for any $k \ge k_0, \mathbf{a} \in \underline{A}^{\mathrm{good}}(k)$ using a simple coupling argument, placing all walkers at the maximal distance shows

$$\begin{aligned} \mathbf{P}(\mu(k,\mathbf{a}) > t) &\le \mathbf{P}(\mu(k,(0,\dots,0,\lceil\beta_A k\rceil)) > t) \\ &= \mathbf{P}\left(\sum_{j=1}^{\lceil\beta_A k\rceil} \mathbb{1}_{\tau_k^{1-k,j} > t} \ge \lceil\beta_A k\rceil - \lceil\beta_I k\rceil + 1\right) \\ &= \mathbf{P}\left(\sum_{j=1}^{\lceil\beta_A k\rceil} \mathbb{1}_{\tau_k^{1-k,j} > t} \ge \frac{\lceil\beta_A k\rceil - \lceil\beta_I k\rceil + 1}{\lceil\beta_A k\rceil}\lceil\beta_A k\rceil\right) \end{aligned} \tag{3.16}$$

The last line of (3.16) is just the probability of a binomial distribution with success probability

$$\pi_k(t) := \mathbf{P}(\tau_k^{0,1} > t)$$

and $\lceil\beta_A k\rceil$ trials to be larger than $b_k\lceil\beta_A k\rceil$, with

$$b_k := \frac{\lceil\beta_A k\rceil - \lceil\beta_I k\rceil + 1}{\lceil\beta_A k\rceil}.$$

Thus we can apply [11, Eq. (5)], using as their parameters n, r, k the values $n = b_k\lceil\beta_A k\rceil, r = \frac{1}{b_k}, k = 0$ and noting that the error term R_0 is non-positive, to bound the last line of (3.16) by

$$\binom{\lceil\beta_A k\rceil}{b_k\lceil\beta_A k\rceil}\pi_k(t)^{b_k\lceil\beta_A k\rceil}(1-\pi_k(t))^{\lceil\beta_A k\rceil - b_k\lceil\beta_A k\rceil}\left(\frac{1-\pi_k(t)}{1-\frac{\pi_k(t)}{b_k}}\right). \tag{3.17}$$

Next, we estimate the success probability using [40, Theorem A.1] and obtain a constant $C_0 \ge 1$ such that for any $t \ge 0$ and $k \le t^{\frac{1}{2}-\varepsilon_1}$ we have

$$\pi_k(t) \le C_0\frac{k}{\sqrt{t}}. \tag{3.18}$$

Taking $t \ge t_0 := \left(\frac{2C_0\beta_A}{\beta_A-\beta_I}\right)^{\frac{1}{\varepsilon_1}}$ and any $k \le t^{\frac{1}{2}-\varepsilon_1}$ we arrive at

$$\pi_k(t) \le C_0 t^{-\varepsilon_1} \le \frac{\beta_A-\beta_I}{2\beta_A} < b_k. \tag{3.19}$$

To further bound (3.17), we estimate the binomial coefficient by the central coefficient and Stirling's formula, which gives

$$\binom{\lceil\beta_A k\rceil}{b_k\lceil\beta_A k\rceil} \le \binom{2\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}{\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil} \le \frac{\mathrm{e}^{\frac{1}{12\cdot 2\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}}\sqrt{2\pi\left(2\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil\right)}\left(\frac{2\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}{\mathrm{e}}\right)^{2\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}}{\left(\sqrt{2\pi\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}\left(\frac{\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}{\mathrm{e}}\right)^{\left\lceil\frac{\lceil\beta_A k\rceil}{2}\right\rceil}\right)^2}$$

$$\le 4^{\beta_A k}. \tag{3.20}$$

Next we estimate both $1-\pi_k(t)$ terms in (3.17) by 1 and note that by the choice of t_0, using (3.19), we can bound

$$\frac{1}{1-\frac{\pi_k(t)}{b_k}} \le \frac{1}{1-\frac{1}{2}} = 2. \tag{3.21}$$

Noting that $b_k\lceil\beta_A k\rceil = \lceil\beta_A k\rceil - \lceil\beta_I k\rceil + 1 \ge (\beta_A-\beta_I)k$, $t \ge t_0$, and combining the estimates (3.20),(3.21) and (3.18), we can bound the term in (3.17) by

$$2\cdot 4^{\beta_A k}\left(C_0\frac{k}{\sqrt{t}}\right)^{(\beta_A-\beta_I)k}. \tag{3.22}$$

We want to show that there is a $t_1 \ge t_0$ such that for all $t \ge t_1$ the maximum of (3.22) over $k_0 \le k \le t^{\frac{1}{2}-\varepsilon_1}$ is attained in k_0. To do so we treat k as a continuous variable and take the derivative with respect to k to show that it is negative. By a straightforward calculation we find that the derivative is given by

$$W(k,t,\beta_A,\beta_I)\cdot\left(C(\beta_A,\beta_I)+(\beta_A-\beta_I)\log\left(\frac{k}{\sqrt{t}}\right)\right)$$

for some positive expressions W and C. Explicitly,

$$W(k,t,\beta_A,\beta_I) = 2\cdot 4^{\beta_A k}\left(C_0\frac{k}{\sqrt{t}}\right)^{(\beta_A-\beta_I)k}$$

and

$$C(\beta_A,\beta_I) = \left(\log\left(C_0\right)+1\right)\left(\beta_A-\beta_I\right)+2\beta_A\log(2).$$

This means that the sign of the derivative is determined by the term in the brackets and calculating

$$\begin{aligned}
C(\beta_A,\beta_I)+(\beta_A-\beta_I)\log\left(\frac{k}{\sqrt{t}}\right) &\leq 0 \\
\iff (\beta_A-\beta_I)\log\left(\frac{k}{\sqrt{t}}\right) &\leq -C(\beta_A,\beta_I) \\
\iff k &\leq \sqrt{t}\exp\left(-\frac{C(\beta_A,\beta_I)}{(\beta_A-\beta_I)}\right)
\end{aligned}$$

yields that the derivative is negative if k is small. In particular, the expression in (3.22), for fixed t, is decreasing in k up to $\sqrt{t}\exp\left(-\frac{C(\beta_A,\beta_I)}{(\beta_A-\beta_I)}\right)$. Now taking

$$t_1 := \max\left\{t_0, \exp\left(\frac{C(\beta_A,\beta_I)}{\varepsilon_1(\beta_A-\beta_I)}\right)\right\}$$

we have $t^{\frac{1}{2}-\varepsilon_1} \leq \sqrt{t}\exp\left(-\frac{C(\beta_A-\beta_I)}{(\beta_A-\beta_I)}\right)$ for any $t \geq t_1$ and thus

$$\begin{aligned}
\max_{\substack{k_0\leq k\leq\lambda(t),\\ \mathbf{a}\in\underline{A}^{\text{good}}(k)}} \mathbf{P}(\mu(k,\mathbf{a})>t) &\leq 2\cdot 4^{\beta_A k_0}\left(C_0\frac{k_0}{\sqrt{t}}\right)^{(\beta_A-\beta_I)k_0} \\
&= C_1(k_0,\beta_A,\beta_I)t^{-\frac{(\beta_A-\beta_I)k_0}{2}}
\end{aligned}$$

with $C_1 = C_1(k_0,\beta_A,\beta_I) := 2\cdot 4^{\beta_A k_0}\left(C_0 k_0\right)^{(\beta_A-\beta_I)k_0}$. Next, we estimate that for $1 \leq k < k_0$ and $\mathbf{a} \in \underline{A}^{\text{good}}(k)$ we have at least $a_j \geq m_A \geq 4+m_I$ parasites on each site for $1 \leq j \leq k$ and thus, again by a coupling argument, obtain

$$\begin{aligned}
\mathbf{P}(\mu(k,\mathbf{a})>t) &\leq \mathbf{P}\left(\sum_{x=1}^{k}\sum_{i=1}^{m_A}\mathbb{1}_{\tau_x^{x,i}\leq t} < m_I k\right) \\
&\leq \mathbf{P}\left(\sum_{i=1}^{km_A}\mathbb{1}_{\tau_k^{0,i}\leq t} < km_I\right) \\
&= \sum_{j=0}^{km_I-1}\binom{km_A}{j}\mathbf{P}(\tau_k^{0,1}\leq t)^j\mathbf{P}(\tau_k^{0,1}>t)^{km_A-j} \\
&\leq C_2 t^{-\frac{k(m_A-m_I)+1}{2}} \leq C_2 t^{-\frac{5}{2}}
\end{aligned}$$

for some constant $C_2>0$ independent of k,t.
In particular, this implies that for large enough $t \geq t_1$ we have

$$\max_{\substack{1\leq k\leq\lambda(t),\\ \mathbf{a}\in\underline{A}^{\text{good}}(k)}} \mathbf{P}(\mu(k,\mathbf{a})>t) \leq \max\left\{C_1 t^{-\frac{(\beta_A-\beta_I)k_0}{2}}, C_2 t^{-\frac{5}{2}}\right\}$$

Choosing some $q < \frac{(4\wedge\alpha)+1}{2}$ and plugging this into estimate (3.15), fixing some $\varepsilon_1 \in \left(0, \frac{1}{2} - \frac{q}{\alpha+1}\right)$ and $\varepsilon_K := \alpha + 1 - \frac{q}{\frac{1}{2}-\varepsilon_1}$, we obtain a constant $C \geq 0$ such that for large enough $t \geq t_1$ we have

$$\begin{aligned}\mathbf{P}(\nu > t) &\leq C_K t^{-(\frac{1}{2}-\varepsilon_1)(\alpha+1-\varepsilon_K)} + \max_{\substack{1\leq k\leq\lambda(t),\\ \mathbf{a}\in\underline{A}^{\text{good}}(k)}} \mathbf{P}(\mu(k,\mathbf{a}) > t)\\ &\leq C_K t^{-q} + \max\left\{C_1 t^{-\frac{(\beta_A-\beta_I)k_0}{2}}, C_2 t^{-\frac{5}{2}}\right\} \leq C t^{-q}\end{aligned}$$

where we used that $\varepsilon_1, \varepsilon_K$ were exactly chosen in such a way that

$$\left(\frac{1}{2} - \varepsilon_1\right)(\alpha + 1 - \varepsilon_K) = q$$

and by definition

$$\min\left\{k_0\frac{\beta_A - \beta_I}{2}, \frac{5}{2}\right\} \geq \frac{(4\wedge\alpha)+1}{2} > q.$$

This shows the claimed tail behavior by possibly increasing the constant C for small $t \leq t_1$. Furthermore, by the layer-cake formula we obtain, fixing some $q' \in \left(q, \frac{(4\wedge\alpha)+1}{2}\right)$,

$$\begin{aligned}\mathbf{E}[|\nu|^q] &= \int_0^\infty q t^{q-1}\mathbf{P}(\nu > t)\,\mathrm{d}\,t\\ &\leq \int_0^{t_1} q t^{q-1}\,\mathrm{d}\,t + \int_{t_1}^\infty q t^{q-1} C t^{-q'}\,\mathrm{d}\,t \qquad (3.23)\\ &= t_1^q + \frac{qCt_1^{q-q'}}{q'-q} < \infty.\end{aligned}$$

□

Proof of Lemma 3.18

We start by showing that $(\overline{\nu}_n)_{n\geq1}$ is independent of M^0.

Lemma 3.27. *For* $E \in \mathcal{B}([0,\infty)^{\mathbb{N}})$ *we have*

$$\mathbb{P}\left((\overline{\nu}_1, \overline{\nu}_2, \dots) \in E\right) = \mathbf{P}\left((\nu_1, \nu_2, \dots) \in E \middle| M^0 = 0\right).$$

Proof. The claim follows analogously to the proof for Lemma 3.16. Using the notation used in that proof, we see that

$$\begin{aligned}&\mathbb{P}\left((\overline{\nu}_1, \overline{\nu}_2, \dots) \in E\right)\\ &\quad = \frac{1}{\mathbf{P}(\mathcal{S})}\sum_{j=0}^\infty \mathbf{P}(B^{<j}, \mathcal{G}_j, (\nu_{j+1}, \dots, \nu_{j+k_0-1}, \nu_{j+k_0}, \nu_{j+k_0+1}, \dots) \in E)\end{aligned}$$

and then we can perform the same steps as there, because

$$\mathcal{G}_j \cap \{(\nu_{j+1}, \dots, \nu_{j+k_0-1}, \nu_{j+k_0}, \nu_{j+k_0+1}, \dots) \in E\}$$

only depends on variables with index above j and $B^{<j}$ depends only on variables with index below j. $\square$

Corollary 3.28. *For any* $q \in \left[1, \frac{(\alpha \wedge 4)+1}{2}\right)$, *we have* $\mathbb{E}[|\overline{\nu}_n|^q] < \infty$.

Proof. For $n \geq 1$ the claim follows directly by Lemma 3.17 and Lemma 3.27, noting that

$$\mathbb{P}(\overline{\nu}_n > t) = \mathbf{P}(\nu_n > t | M^0 = 0) \leq \frac{\mathbf{P}(\nu_n > t)}{\mathbf{P}(M^0 = 0)}. \qquad \square$$

With this characterization of the joint distribution of $(\overline{\nu}_{k+n})_{n \geq 1}$ for any starting point $k \geq 0$, we can show that their joint distribution converges to the distribution of $(\nu_n)_{n \geq 1}$ for $k \to \infty$.

Proof of Lemma 3.18. For shorthand we write

$$\{\underline{\nu}_k \in E\} := \{(\nu_k, \nu_{k+1}, \dots) \in E\} \text{ and } \{\underline{\overline{\nu}}_k \in E\} := \{(\overline{\nu}_k, \overline{\nu}_{k+1}, \dots) \in E\}$$

for any $k \geq 1$. First we observe that by Lemma 3.27, for $n \geq k_0$ we have

$$|\mathbb{P}(\underline{\overline{\nu}}_n \in E) - \mathbf{P}(\underline{\nu}_1 \in E)| = \left| \frac{\mathbf{P}(\underline{\nu}_n \in E, M^0 = 0) - \mathbf{P}(M^0 = 0)\mathbf{P}(\underline{\nu}_1 \in E)}{\mathbf{P}(M^0 = 0)} \right|.$$

Hence it suffices to show

$$|\mathbf{P}(\underline{\nu}_n \in E, M^0 = 0) - \mathbf{P}(M^0 = 0)\mathbf{P}(\underline{\nu}_1 \in E)| \leq Cn^{-\alpha+\varepsilon}$$

for large n. We observe that for all $m \geq k_0$ we have

$$\{M^0 = 0\} = \mathcal{G}_{0,m} \setminus \left(\mathcal{G}_{0,m} \cap \bigcup_{j=m+1}^{\infty} \{K_j > j\} \right)$$

and hence

$$\mathbf{P}(M^0 = 0) = \mathbf{P}(\mathcal{G}_{0,m}) - \mathbf{P}\left(\mathcal{G}_{0,m}, \bigcup_{j=m+1}^{\infty} \{K_j > j\} \right). \tag{3.24}$$

In particular, we note that $\mathcal{G}_{0,m}$ only depends on $A_0, \dots, A_{m-1}, I_1, \dots I_m$. Next, we denote by

$$\widetilde{K}_n := \inf\{n - K_n, n + 1 - K_{n+1}, \dots\}$$

the smallest site, which is used to determine if $\underline{\nu}_n \in E$. In particular, because for any $m \geq 1$ the event $\{K_n \leq m\}$ only depends on $A_{n-m-1}, \dots, A_{n-1}$ and $I_{n-m}, \dots, I_n$, the event

$$\{\widetilde{K}_n \geq n-k, \underline{\nu}_n \in E\} \in \sigma(A_x, I_{x+1}, Y^{x,i} : x \geq n-k, i \in \mathbb{N}).$$

For $k_0 \leq k \leq n-k_0$, we estimate, repeatedly applying (3.24) and using the dependencies written above

$$\begin{aligned}
&|\mathbf{P}(\underline{\nu}_n \in E, M^0 = 0) - \mathbf{P}(M^0 = 0)\mathbf{P}(\underline{\nu}_1 \in E)| \\
&\quad \leq \mathbf{P}(\underline{\nu}_n \in E, \widetilde{K}_n < n-k, M^0 = 0) \\
&\qquad + |\mathbf{P}(\underline{\nu}_n \in E, \widetilde{K}_n \geq n-k, M^0 = 0) - \mathbf{P}(M^0 = 0)\mathbf{P}(\underline{\nu}_1 \in E)| \\
&\quad \leq \mathbf{P}(\widetilde{K}_n < n-k) + \mathbf{P}\left(\underline{\nu}_n \in E, \widetilde{K}_n \geq n-k, \mathcal{G}_{0,n-k}, \bigcup_{j=n-k+1}^{\infty} \{K_j > j\}\right) \\
&\qquad + \left|\mathbf{P}\left(\underline{\nu}_n \in E, \widetilde{K}_n \geq n-k, \mathcal{G}_{0,n-k}\right) - \mathbf{P}(M^0 = 0)\mathbf{P}(\underline{\nu}_1 \in E)\right| \\
&\quad \leq \mathbf{P}(\widetilde{K}_n < n-k) + \mathbf{P}\left(\bigcup_{j=n-k+1}^{\infty} \{K_j > j\}\right) \\
&\qquad + \left|\mathbf{P}\left(\underline{\nu}_n \in E, \widetilde{K}_n \geq n-k\right)\mathbf{P}\left(\mathcal{G}_{0,n-k}\right) - \mathbf{P}\left(\mathcal{G}_{0,n-k}\right)\mathbf{P}(\underline{\nu}_1 \in E)\right| \\
&\qquad + \mathbf{P}\left(\mathcal{G}_{0,n-k}, \bigcup_{j=n-k+1}^{\infty} \{K_j^{k_0} > j\}\right)\mathbf{P}(\underline{\nu}_1 \in E) \\
&\quad \leq \mathbf{P}(\widetilde{K}_n < n-k) + 2\mathbf{P}\left(\bigcup_{j=n-k+1}^{\infty} \{K_j > j\}\right) \\
&\qquad + \left|\mathbf{P}\left(\underline{\nu}_n \in E, \widetilde{K}_n \geq n-k\right) - \mathbf{P}(\underline{\nu}_n \in E)\right| \\
&\quad \leq 2\mathbf{P}(\widetilde{K}_n < n-k) + 2\mathbf{P}\left(\bigcup_{j=n-k+1}^{\infty} \{K_j > j\}\right) \\
&\quad \leq 2\sum_{j=0}^{\infty} \mathbf{P}(K_{n+j} > j+k) + 2\sum_{j=n-k+1}^{\infty} \mathbf{P}(K_{n+j} > j) \\
&\quad \leq 2\sum_{j=0}^{\infty} C(j+k)^{-(\alpha+1)+\varepsilon} + 2\sum_{j=n-k+1}^{\infty} Cj^{-(\alpha+1)+\varepsilon},
\end{aligned}$$

for any $\varepsilon > 0$ and some constant $C \geq 0$, using Lemma 3.15 in the last line. Now for $n > 2k_0$, plugging in $k = \lfloor \frac{n}{2} \rfloor$, we obtain a constant $C \geq 0$ such that

$$|\mathbb{P}(\overline{\underline{\nu}}_n \in E) - \mathbf{P}(\underline{\nu}_1 \in E)| \leq Cn^{-\alpha+\varepsilon},$$

which concludes the proof. □

With this convergence we can easily show that $(\overline{\nu}_n)_{n\geq k_0}$ has asymptotically the same moments as $(\nu_n)_{n\geq 1}$.

Corollary 3.29. *For all* $1 \leq q < \frac{(4\wedge\alpha)+1}{2}$ *we have*

$$\lim_{n\to\infty} \mathbb{E}[|\overline{\nu}_n|^q] = \mathbf{E}[|\nu|^q].$$

Proof. The layer cake formula yields

$$\begin{aligned}|\mathbb{E}[|\overline{\nu}_n|^q] - \mathbf{E}[|\nu|^q]| &= \left|\int_0^\infty qt^{q-1}\mathbb{P}(\overline{\nu}_n > t)\,\mathrm{d}\,t - \int_0^\infty qt^{q-1}\mathbf{P}(\nu > t)\,\mathrm{d}\,t\right| \\ &\leq \int_0^\infty qt^{q-1}|\mathbb{P}(\overline{\nu}_n > t) - \mathbf{P}(\nu > t)|\,\mathrm{d}\,t.\end{aligned}$$

Because

$$qt^{q-1}|\mathbb{P}(\overline{\nu}_n > t) - \mathbf{P}(\nu > t)| \leq qt^{q-1}\frac{2}{\mathbf{P}(M^0 = 0)}\mathbf{P}(\nu > t) \in L^1([0,\infty))$$

we can interchange the limit $n \to \infty$ with the integral and obtain from Lemma 3.18 that

$$\lim_{n\to\infty} |\mathbb{E}[|\overline{\nu}_n|^q] - \mathbf{E}[|\nu|^q]| = 0.$$ □

Proof of Lemma 3.19

We need to introduce some additional notation to make precise the reasoning from the sketch of the proof.

Definition 3.30. *For* $m \in \mathbb{N}$ *we define the index set*

$$\underline{C}^{good}(m) := \{(\mathbf{a},\mathbf{i}) \in \mathbb{N}_0^m \times \mathbb{N}^m \,|G(\mathbf{a},\mathbf{i}) = 1\}$$

of all possible good configurations $((A_0,\dots,A_{m-1}),(I_1,\dots,I_m))$ *given* $\{M^0 = 0\}$. *For* $m \in \mathbb{N}_0, n \in \mathbb{N}, (\mathbf{a},\mathbf{i}) \in \underline{C}^{good}(m)$ *we define the event that* $(A_0,\dots,A_{m-1})$ *equals* $\mathbf{a}$ *and* $(I_1,\dots,I_m)$ *equals* $\mathbf{i}$*, i.e.,*

$$\{\mathbf{A}_m = \mathbf{a}\} := \bigcap_{j=0}^{m-1}\{A_j = a_j\}, \{\mathbf{I}_m = \mathbf{i}\} := \bigcap_{k=1}^{m}\{I_k = i_k\}$$

Also, we define the event that, given $m \geq 1$ *and some* $(\mathbf{a},\mathbf{i}) \in \underline{C}^{good}(m)$*, also the upcoming random configuration after site* m *is good*

$$((a_1,\dots,a_m,A_m,\dots,A_{m+n-1}),(i_1,\dots,i_m,I_{m+1},\dots,I_{m+n})) \in \underline{C}^{good}(m+n).$$

That is, $\mathcal{G}_{m,n}(\mathbf{a},\mathbf{i})$ is the event

$$\bigcap_{x=m+1}^{m+n} \{G((a_0,\dots,a_{m-1},A_m,\dots,A_{m+n-1}),(i_1,\dots,i_m,I_{m+1},\dots,I_{m+n}))=1\}$$

with the obvious extension to $\mathcal{G}_{m,\infty}(\mathbf{a},\mathbf{i})$. We note that this is just an extension of the definition $\mathcal{G}_{0,n}$ from 3.12, where we fixed the first m entries. We observe that because the first m entries are fixed, the event $\mathcal{G}_{m,n}(\mathbf{a},\mathbf{i})$ only depends on $A_m,\dots,A_{m+n-1},I_{m+1},\dots,I_{m+n}$.
Also, we define the event $\mathcal{B}_{m,n}(\mathbf{a},\mathbf{i})$ that

$$((a_1,\dots,a_m,A_m,\dots,A_x),(i_1,\dots,i_m,I_{m+1},\dots,I_x)) \notin \underline{C}^{good}(m+x)$$

for some $x > m+n$. That is, $\mathcal{B}_{m,n}(\mathbf{a},\mathbf{i})$ is the event

$$\bigcup_{x=m+n+1}^{\infty} \left(\{G((a_0,\dots,a_{m-1},A_m,\dots,A_x),(i_1,\dots,i_m,I_{m+1},\dots,I_x))=0\}\right).$$

Again, $\mathcal{B}_{m,n}(\mathbf{a},\mathbf{i})$ only depends on $A_m,A_{m+1},\dots,I_{m+1},I_{m+2},\dots$.

Proof of Lemma 3.19. Using Lemma 3.27, we only need to show

$$\begin{aligned}&\left|\frac{\mathbf{P}\left(E,B|M^0=0\right)}{\mathbf{P}(E|M^0=0)} - \mathbf{P}(B|M^0=0)\right| \\ &= \left|\frac{\mathbf{P}(E,B,M^0=0)}{\mathbf{P}(E,M^0=0)} - \mathbf{P}(B|M^0=0)\right| \le Cn^{-\alpha+\varepsilon}\end{aligned} \tag{3.25}$$

for some $C > 0$, all $m \ge k_0, n \in \mathbb{N}$ and

$$E \in \sigma(\nu_1,\dots\nu_m), \mathbf{P}(E|M^0=0) > 0, B \in \sigma(\nu_k : k \ge m+n).$$

The idea is to split up the probability into different events, similarly as in the proof of Lemma 3.18, where one event is unlikely and on the other event we can use independence. Then, given $M^0 = 0$, we estimate how far above m the event E influences $\mathbf{A},\mathbf{I}$ and how far below $m+n$ the event B influences $\mathbf{A},\mathbf{I},\mathbf{Y}$. Making the distance n large, these areas of influence will be disjoint, and the two events will become independent, except on some unlikely event. We recall

$$\widetilde{K}_m = \inf\{m+j-K_{m+j} : j \ge 0\}$$

and that

$$\{\widetilde{K}_{m+n} \ge m+k, B\} \in \sigma(A_x, I_{x+1}, Y^{x,i} : x \ge m+k, i \in \mathbb{N}).$$

We also recall that, for any $l \geq k_0$, we have

$$\{M^0 = 0\} = \mathcal{G}_{0,l} \setminus (\mathcal{G}_{0,l} \cap \mathcal{B}_{0,l}) = \mathcal{G}_{0,l} \setminus \left(\mathcal{G}_{0,l} \cap \bigcup_{j=l+1}^{\infty} \{K_j > j\} \right).$$

With this in mind, we compute that for any $n > 2k_0$ and $k_0 < k \leq n - k_0$, the probability $\mathbf{P}(E, B, M^0 = 0)$ is equal to

$$\begin{aligned} &\mathbf{P}\left(E, B, \widetilde{K}_{m+n} \geq m+k, \mathcal{G}_{0,m+k}\right) \\ &- \mathbf{P}\left(E, B, \widetilde{K}_{m+n} \geq m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right) \\ &+ \mathbf{P}\left(E, B, \widetilde{K}_{m+n} < m+k, \mathcal{G}_{0,m+k}\right) \\ &- \mathbf{P}\left(E, B, \widetilde{K}_{m+n} < m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right). \end{aligned}$$

The first probability contains independent events and thus is equal to

$$\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right) \mathbf{P}\left(B, \widetilde{K}_{m+n} \geq m+k\right)$$

Now to estimate (3.25), we use the triangle inequality, putting together the first term with $-\mathbf{P}(B|M^0 = 0)$ and then each other term for itself. This gives that the term in (3.25) is bounded by

$$\begin{aligned} &\left| \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right) \mathbf{P}\left(B, \widetilde{K}_{m+n} \geq m+k\right)}{\mathbf{P}(E, M^0 = 0)} - \mathbf{P}(B|M^0 = 0) \right| \\ &+ \frac{\mathbf{P}\left(E, B, \widetilde{K}_{m+n} \geq m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} \\ &+ \frac{\mathbf{P}\left(E, B, \widetilde{K}_{m+n} < m+k, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} \\ &+ \frac{\mathbf{P}\left(E, B, \widetilde{K}_{m+n} < m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)}. \end{aligned}$$

To estimate these terms, we observe that for $(\mathbf{a}, \mathbf{i}) \in \underline{C}^{\text{good}}(m)$ and $l > k_0$, possibly $l = \infty$, we have

$$\begin{aligned} \mathbf{P}(\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E, \mathcal{G}_{0,m+l}) &= \mathbf{P}\left(\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E, \mathcal{G}_{m,m+l}(\mathbf{a}, \mathbf{i})\right) \\ &= \mathbf{P}\left(\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E\right) \mathbf{P}\left(\mathcal{G}_{m,m+l}(\mathbf{a}, \mathbf{i})\right). \end{aligned}$$

We note that

$$\mathcal{G}_{m,m+l}(\mathbf{a},\mathbf{i}) \supset \bigcap_{n=1}^{\infty} \left\{ \sum_{j=1}^{n} A_{m+j-1} \geq \beta_A n, \sum_{j=1}^{n} I_{m+j} \leq \beta_I n \right\} \tag{3.26}$$

for any $(\mathbf{a},\mathbf{i}) \in \underline{C}^{\mathrm{good}}(m)$. Because $\mu_I < \beta_I < \beta_A < \mu_A$, the right-hand side of (3.26) has positive probability, which we denote by δ.

We compute

$$\begin{aligned}
\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0=0)} &= \sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \frac{\mathbf{P}\left(\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E, \mathcal{G}_{0,m+k}\right)}{\sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \mathbf{P}\left((\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E, M^0 = 0\right)} \\
&= \sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \frac{\mathbf{P}\left((\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E\right)\mathbf{P}\left(\mathcal{G}_{m,k}(\mathbf{a},\mathbf{i})\right)}{\sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \mathbf{P}\left(\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E\right)\mathbf{P}\left(\mathcal{G}_{m,\infty}(\mathbf{a},\mathbf{i})\right)} \\
&\leq \sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \frac{\mathbf{P}\left((\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E\right)}{\sum_{(\mathbf{a},\mathbf{i})\in\underline{C}^{\mathrm{good}}(m)} \mathbf{P}\left((\mathbf{A}_m = \mathbf{a}, \mathbf{I}_m = \mathbf{i}, E\right)\delta} = \frac{1}{\delta}.
\end{aligned} \tag{3.27}$$

Hence, using the uniform bound (3.27), we can show for $k_0 < k' < k < n - k_0$ that

$$\begin{aligned}
&\left| \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0=0)} - 1 \right| = \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right) - \mathbf{P}(E, M^0=0)}{\mathbf{P}(E, M^0=0)} \\
&= \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0=0)} = \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, \bigcup_{j=m+k+1}^{\infty}\{K_j > j\}\right)}{\mathbf{P}(E, M^0=0)} \\
&\leq \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k'}, \bigcup_{j=m+k+1}^{\infty}\{K_j > j - m - k'\}\right)}{\mathbf{P}(E, M^0=0)} \\
&= \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k'}\right)\mathbf{P}\left(\bigcup_{j=m+k+1}^{\infty}\{K_j > j - m - k'\}\right)}{\mathbf{P}(E, M^0=0)} \\
&\leq \frac{1}{\delta}\sum_{j=1}^{\infty} \mathbf{P}(K_{j+m+k} > j + k - k') \leq C_1(k-k')^{-\alpha+\varepsilon},
\end{aligned} \tag{3.28}$$

for any $\varepsilon \in (0,\alpha)$ and some $C_1 = C_1(\varepsilon) \geq 0$, using Lemma 3.15. With this we can now begin to estimate each term of the triangle inequality used for (3.3.3). First, by an analogous argument as we used starting from the second line of (3.28),

$$\begin{aligned}
&\frac{\mathbf{P}\left(E, B, \widetilde{K}_{m+n} \geq m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0=0)} \\
&\leq \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0=0)} \leq C_1(k-k')^{-\alpha+\varepsilon}.
\end{aligned}$$

Similarly,

$$\begin{aligned}&\frac{\mathbf{P}\left(E, B, \widetilde{K}_{m+n} < m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)}\\ &\leq \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} \leq C_1(k-k')^{-\alpha+\varepsilon}.\end{aligned}$$

Next, using (3.27), we find

$$\begin{aligned}&\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, B, \widetilde{K}_{m+n} < m+k\right)}{\mathbf{P}(E, M^0 = 0)} \leq \frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}, \widetilde{K}_{m+n} < m+k\right)}{\mathbf{P}(E, M^0 = 0)}\\ =&\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)}\mathbf{P}\left(\widetilde{K}_{m+n} < m+k\right) \leq \frac{\mathbf{P}\left(\widetilde{K}_{m+n} < m+k\right)}{\delta} \leq C_2(n-k)^{-\alpha+\varepsilon}\end{aligned}$$

for some $C_2 = C_2(\varepsilon)$, using Lemma 3.15. Finally, to estimate the first term of (3.3.3) minus $\mathbf{P}(B|M^0 = 0)$, using the same split up as for (3.3.3) but now on $\mathbf{P}(B, M^0 = 0)$ (that is, with E replaced by Ω), we compute

$$\begin{aligned}&\left|\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)}\mathbf{P}\left(B, \widetilde{K}_{m+n} \geq m+k\right) - \mathbf{P}(B|M^0 = 0)\right|\\ \leq&\left|\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} - \frac{\mathbf{P}\left(\mathcal{G}_{0,m+k}\right)}{\mathbf{P}(M^0 = 0)}\right|\mathbf{P}\left(B, \widetilde{K}_{m+n} \geq m+k\right)\\ &+\frac{\mathbf{P}\left(B, \widetilde{K}_{m+n} \geq m+k, \mathcal{G}_{0,m+k}, \mathcal{B}_{0,m+k}\right)}{\mathbf{P}(M^0 = 0)}\\ &+\frac{\mathbf{P}\left(B, \widetilde{K}_{m+n} < m+k, M^0 = 0\right)}{\mathbf{P}(M^0 = 0)}\\ \leq&\left|\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} - \frac{\mathbf{P}\left(\mathcal{G}_{0,m+k}\right)}{\mathbf{P}(M^0 = 0)}\right| + C_1(k-k')^{-\alpha+\varepsilon} + C_2(n-k)^{-\alpha+\varepsilon}\\ \leq&\left|\frac{\mathbf{P}\left(E, \mathcal{G}_{0,m+k}\right)}{\mathbf{P}(E, M^0 = 0)} - 1\right| + \left|1 - \frac{\mathbf{P}\left(\mathcal{G}_{0,m+k}\right)}{\mathbf{P}(M^0 = 0)}\right| + C_1(k-k')^{-\alpha+\varepsilon} + C_2(n-k)^{-\alpha+\varepsilon}\\ \leq&3C_1(k-k')^{-\alpha+\varepsilon} + C_2(n-k)^{-\alpha+\varepsilon}.\end{aligned}$$

Now plugging in $k = \left\lceil \frac{2}{3}n \right\rceil, k' = \left\lceil \frac{1}{3}n \right\rceil$ and combining all estimates, we find a constant $C = C(\varepsilon) \geq 0$ such that

$$\left|\frac{\mathbf{P}(E, B, M^0 = 0)}{\mathbf{P}(E, M^0 = 0)} - \mathbf{P}(B|M^0 = 0)\right| \leq Cn^{-\alpha+\varepsilon}$$

for large enough $n \in \mathbb{N}$. Possibly increasing this constant C, the estimate holds already for all $n \in \mathbb{N}$, which finishes the proof. □

Proof of Lemma 3.20

First, we establish that the variance of the partial sum grows only linearly in n, given that the variance is finite.

Lemma 3.31. *If $\alpha > 3$, there is a $C > 0$ such that for all $n \geq 1$ we have*

$$\mathbb{E}\left[\left|\sum_{k=1}^{n}(\overline{\nu}_k - \mathbb{E}[\overline{\nu}_k])\right|^2\right] \leq Cn.$$

Proof. We set $Q_k := \overline{\nu}_k - \mathbb{E}[\overline{\nu}_k]$ and note that because $\alpha > 3$ we obtain from Lemma 3.17 that $(Q_k)_{k\in\mathbb{Z}} \subset L^2(\boldsymbol{\Omega})$. Now a classical result of Ibragimov [23, Lemma 1.1] states that ϕ-mixing implies weak correlations, in the sense that

$$\mathbb{E}[Q_m Q_{m+n}] \leq 2\sqrt{\phi(n)\mathbb{E}[Q_m^2]\mathbb{E}[Q_{m+n}^2]}.$$

Using Corollary 3.28 and Corollary 3.29, there is a constant $C_Q \geq 0$ such that $\mathbb{E}[Q_n^2] \leq C_Q$ for all $n \geq 1$. With this, we compute

$$\begin{aligned}
\mathbb{E}\left[\left(\sum_{k=1}^{n} Q_k\right)^2\right] &\leq \sum_{k=1}^{n}\sum_{j=1}^{n}|\mathbb{E}[Q_kQ_j]| = \sum_{k=1}^{n}\sum_{j=k}^{n}|\mathbb{E}[Q_kQ_j]| + \sum_{k=2}^{n}\sum_{j=1}^{k-1}|\mathbb{E}[Q_kQ_j]| \\
&= \sum_{k=1}^{n}\sum_{j=0}^{n-k}|\mathbb{E}[Q_kQ_{k+j}]| + \sum_{j=1}^{n}\sum_{k=1}^{n-j}|\mathbb{E}[Q_{j+k}Q_j]| \\
&= \sum_{k=1}^{n}\left(\mathbb{E}[Q_k^2] + 2\sum_{j=1}^{n-k}|\mathbb{E}[Q_kQ_{k+j}]|\right) \\
&\leq nC_Q + 2\sum_{k=1}^{n-1}\sum_{j=1}^{n-k} 2\sqrt{\phi(j)}C_Q \\
&\leq C_Q\left(n + 4C\sum_{k=1}^{n-1}\sum_{j=1}^{n-k} j^{-\frac{\alpha-\varepsilon}{2}}\right) \\
&\leq C_Q\left(n + 4C\sum_{k=1}^{n-1}\sum_{j=1}^{\infty} j^{-\frac{\alpha-\varepsilon}{2}}\right) \\
&\leq nC_Q\left(1 + 4C\sum_{j=1}^{\infty} j^{-\frac{\alpha-\varepsilon}{2}}\right),
\end{aligned}$$

where we used Lemma 3.19 for some $\varepsilon \in (0,1)$ and note the sum is finite, by the assumption $\alpha > 3$. □

Now it follows from classical results that the bounds on the second moments transfer to higher moments.

Proof of Lemma 3.20. Using the estimate in Lemma 3.31, we can conclude by a classical result for ϕ-mixing sequences from Ibragimov [23, Lemma 1.9] that

$$\mathbb{E}\left[\left|\sum_{k=1}^{n} \overline{\nu}_k - \mathbb{E}[\overline{\nu}_k]\right|^q\right] \leq C_! n^{\frac{q}{2}}$$

for some constant $C_1 > 0$. Thus, using another classical result of Serfling [44, Corollary B1], we already have

$$\mathbb{E}\left[\max_{1 \leq i \leq n}\left|\sum_{k=1}^{i} \overline{\nu}_k - \mathbb{E}[\overline{\nu}_k]\right|^q\right] \leq C n^{\frac{q}{2}}$$

for some constant $C_2 > 0$. ☐

Proof of Lemma 3.21

Proof of Lemma 3.21. We can make use of the variables $(\overline{\nu}_n)_{n\geq 1} = (\overline{\nu}^0_n)_{n\geq 1}$ to bound the time T^1 almost surely, namely

$$T^1 \leq \sum_{k=1}^{M^1 - M^0} \overline{\nu}_k.$$

Hence, we can estimate for any $\delta \in (0,1), \varepsilon \in (0, \alpha)$ and C_ε as in Lemma 3.16 that

$$\begin{aligned}\mathbb{P}(T^1 > t | M^0 = 0) &\leq \mathbb{P}(M^1 > t^\delta | M^0 = 0) + \mathbb{P}\left(\sum_{k=1}^{\lceil t^\delta \rceil} \overline{\nu}_k > t\right) \\ &\leq C_\varepsilon t^{-\delta(\alpha - \varepsilon)} + \mathbb{P}\left(\sum_{k=1}^{\lceil t^\delta \rceil} \overline{\nu}_k - \mathbb{E}[\nu_k] > t - \lceil t^\delta \rceil \sup_{k \geq 1} \mathbb{E}[\overline{\nu}_k]\right)\end{aligned}$$

For t large enough it holds that $t - \lceil t^\delta \rceil \sup_{k\geq 1} \mathbb{E}[\overline{\nu}_k] \geq \frac{t}{2}$. Hence, using the Markov inequality, we can estimate the probability in the last line by

$$\mathbb{E}\left[\left|\sum_{k=1}^{\lceil t^\delta \rceil} \overline{\nu}_k - \mathbb{E}[\overline{\nu}_k]\right|^q\right] \left|\frac{t}{2}\right|^{-q}$$

for any $q \in \left[1, \frac{(\alpha\wedge 4)+1}{2}\right)$. Using Lemma 3.20, we obtain a constant $C > 0$ such that for large enough t

$$\mathbb{E}\left[\left|\sum_{k=1}^{\lceil t^\delta \rceil} \overline{\nu}_k - \mathbb{E}[\overline{\nu}_k]\right|^q\right] \leq Ct^{\delta \frac{q}{2}}.$$

Now all that is left to check is that taking $\delta > \frac{1}{\alpha}$ close enough to $\frac{1}{\alpha}$ and a small $\varepsilon \in \left(0, \alpha - \frac{1}{\delta}\right)$, we can take $q < \frac{1+(\alpha\wedge 4)}{2}$ large enough, such that we also have $q\left(1 - \frac{\delta}{2}\right) > 1$. The condition for that to be possible is that

$$\frac{\alpha+1}{2} > \frac{2}{2-\frac{1}{\alpha}}$$

which is equivalent to

$$2\alpha^2 - 3\alpha - 1 > 0.$$

Solving for α yields that we must make the assumption

$$\alpha > \frac{3+\sqrt{11}}{2},$$

noting that this is also the reason why we chose the parameter $4 = \left\lceil \frac{3+\sqrt{11}}{2} \right\rceil$ in the definition of good configurations 3.8. ☐

Proof of Proposition 3.22

In this section we will show the existence of the renewal sites claimed in Proposition 3.22. The key idea is to observe that for each good site M^i there is a positive probability that the front grows linearly fast, and if it does not, then the probability that it falls below linear speed only at a large distance to M^i decreases sufficiently fast. Also, retrying for this linear growth at the next good site is independent from the last attempt. On the other hand, each parasite that is already generated before reaching the good site M^i only moves diffusely and thus has a positive probability of never catching up to a linearly moving front. Then for each parasite, we can repeat this trial until at some point none of the parasites generated below a certain good site will interact with the front after that good site is infected. This approach of a renewal-time point is inspired by the work of [15], in which, by showing finite moments of this renewal-time, even stronger results can be deduced.
We begin with establishing that the front can grow linearly fast after a good site with high probability.

Lemma 3.32. *Assume that* $\alpha > 3$ *and* $\lambda < \frac{1}{\sup_{j\geq 1}\mathbb{E}[\overline{\nu}_j^0]}$. *There is a* $\delta_1 > 0$ *such that*

$$\mathbb{P}\left(\bigcap_{k=1}^{\infty}\left\{\sum_{j=1}^{k}\overline{\nu}_j^0 \leq \frac{k}{\lambda}\right\}\right) \geq \delta_1.$$

Also, for $n \in \mathbb{N}$, *we have*

$$\mathbb{P}\left(\bigcap_{k=1}^{n}\left\{\sum_{j=1}^{k}\overline{\nu}_j^0 \leq \frac{k}{\lambda}\right\}, \bigcup_{m>n}\left\{\sum_{j=1}^{m}\overline{\nu}_j^0 > \frac{m}{\lambda}\right\}\right) \leq Cn^{-\frac{q}{2}}$$

for any $q < \frac{1+\alpha\wedge 4}{2}$ *and some* $C > 0$.

Proof. The first claim follows from Lemma 3.46 and will be shown in Section 3.4.3. The second claim can be seen as follows. For $\lambda < \frac{1}{\sup_{j\geq 1}\mathbb{E}[\overline{\nu}_j^0]}$ we have by Lemma 3.20 for any $q < \frac{1+\alpha\wedge 4}{2}$ that

$$\begin{aligned}
&\mathbb{P}\left(\bigcap_{k=1}^{n}\left\{\sum_{j=1}^{k}\overline{\nu}_j^0 \leq \frac{k}{\lambda}\right\}, \bigcup_{m>n}\left\{\sum_{j=1}^{m}\overline{\nu}_j^0 > \frac{m}{\lambda}\right\}\right) \leq \mathbb{P}\left(\sup_{m>n}\left\{\frac{1}{m}\sum_{j=1}^{m}\overline{\nu}_j^0 > \frac{1}{\lambda}\right\}\right)\\
&\leq \sum_{k=0}^{\infty}\mathbb{P}\left(\sup_{2^k n\leq m\leq 2^{k+1}n}\frac{1}{2^k n}\sum_{j=1}^{n}\overline{\nu}_j^0 > \frac{1}{\lambda}\right)\\
&\leq \sum_{k=0}^{\infty}\left(\left(\frac{1}{\lambda} - \sup_{j\geq 1}\mathbb{E}[\overline{\nu}_j^0]\right)2^k n\right)^{-q}\mathbb{E}\left[\left|\sum_{j=1}^{2^{k+1}n}\overline{\nu}_j^0 - \mathbb{E}[\overline{\nu}_j^0]\right|^q\right]\\
&\leq \sum_{k=0}^{\infty} C2^{-\frac{q}{2}k}n^{-\frac{q}{2}} \leq Cn^{-\frac{q}{2}}
\end{aligned}$$

for some $C > 0$ that may vary from line to line. □

We cite the following well-known fact about a simple symmetric random walk not moving ballistically with high probability.

Lemma 3.33. *Recall that* $(Y_t)_{t\geq 0}$ *is a simple symmetric random walk starting in* 0. *For any* $\lambda > 0$ *there is a* $\delta_2 > 0$ *such that*

$$\mathbb{P}\left(\bigcap_{t\geq 0}\{Y_t \leq 1 + \lfloor \lambda t\rfloor\}\right) \geq \delta_2.$$

Also, there are $C_1, c_2 > 0$ *such that for any* $n \in \mathbb{N}$ *we have*

$$\mathbb{P}\left(\bigcap_{k=1}^{n}\left\{\tau_k \geq \frac{k-1}{\lambda}\right\}, \bigcup_{m>n}\left\{\tau_m < \frac{m-1}{\lambda}\right\}\right) \leq C_1\exp(-c_2 n).$$

where

$$\tau_k = \inf\{t \geq 0 : Y_t \geq k\}.$$

Proof. This is a classically known result for random walks. A proof can be found in [16, Lemma 8]. $\square$

To construct the renewal sites, for any $j \geq 0$ we want to find a renewal site $j < R_{\text{good}}(j) < \infty$, such that the front after reaching $R_{\text{good}}(j)$ only depends on the parasites born at a site x with $x \geq R_{\text{good}}(j)$, and we can uniformly in j bound the tail of $R_{\text{good}}(j) - j$. Then we can iteratively define $R^{i+1} := R_{\text{good}}(R^i)$. To begin the construction, we first consider a single parasite (x, i), and we will show that there is an almost surely finite good site $M^{J_{\text{good}}(x,i)} > x$ such that after $T^{J_{\text{good}}(x,i)}$ the front moves linearly fast and the parasite (x, i) will be either dead or it will never reach the linearly moving front again. Then we will show that if we define

$$R_1(j) := M^{J^1_{\text{good}}(j)} := \sup_{0 \leq x \leq j, 1 \leq i \leq A_x} M^{J_{\text{good}}(x,i)}$$

for $j \geq 0$ we have

$$\lim_{n \to \infty} \sup_{j \geq 0} \mathbb{P}(R_1(j) - j > n) = 0.$$

In particular, none of the parasites born between 0 and j will catch up to the front after time $T^{J^1_{\text{good}}(j)}$.

Next, we observe that for some fixed $\delta > 0$, there is a probability of at least δ that also none of the parasites born between j and $R_1(j)$ catch up to the linear moving front after $T^{J^1_{\text{good}}(j)}$. If this happens, we have found the renewal site $R_{\text{good}}(j) = M^{J^1_{\text{good}}(j)}$. However, if some parasite born between j and $R_1(j)$ does catch up to the front after $T^{J^1_{\text{good}}(j)}$, arguing analogously as before, this does not happen too far away from $R_1(j)$. In particular, we can find another almost surely finite good site $R_2(j) = M^{J^2_{\text{good}}(j)}$ such that $\mathbb{P}(R_2(j) - j > n)$ goes to 0 uniformly over all $j \geq 0$ as $n \to \infty$ and none of the parasites generated between j and $R_1(j)$ catch up to the linearly moving front after $T^{J^2_{\text{good}}(j)}$. Again, there is a probability of at least δ that none of the parasites born between $R_1(j)$ and $R_2(j)$ catch up to the linearly moving front after time $T^{J^2_{\text{good}}(j)}$. If this event occurs, we have found the renewal site $R_{\text{good}}(j) = M^{J^2_{\text{good}}(j)}$. If the event does not occur, we repeat the procedure above for the parasites generated between $R_1(j)$ and $R_2(j)$, then for those between $R_2(j)$ and $R_3(j)$, and so on until at some $R_{\text{good}}(j) = M^{J_{\text{good}}(j)}$, none of the parasites generated before $T^{J_{\text{good}}(j)}$ will catch up to the linearly moving front. Furthermore, $\mathbb{P}(R_{\text{good}}(j) - j > n)$ tends to 0 uniformly over all $j \geq 0$ as $n \to \infty$. This will yield the renewal sites $(R^i)_{i \geq 0}$

by iteratively finding the next $R_{\text{good}}(R^i)$, from which on the front moves linearly and the parasites that were born below $R_{\text{good}}(R^i)$ never catch up to the front and thus don't influence the front anymore. The uniform tail bound will imply that $R^i < \infty$ for all $i \geq 0$.

Lemma 3.34. *Suppose the assumptions of Proposition 3.22. For any $j \geq 0$ there is an almost surely finite $R_{good}(j) > j$ such that after the front has reached $R_{good}(j)$, none of the parasites that were born at a site x with $x < R_{good}(j)$ reach the front anymore. Also, it holds that*

$$\lim_{n\to\infty} \sup_{j\geq 0} \mathbb{P}(R_{good}(j) - j > n) = 0.$$

Proof. We carry out the construction explained before this lemma.

For $x \geq 0$ and $i \in \mathbb{N}$, let

$$J_1(x,i) := J(x) := \inf\{k \geq 0 : M^k > x\}$$

be the index of the first good site after x. By Lemma 3.16, we have that

$$\mathbb{P}(M^{J(x)} - x > n) \leq C_1 n^{-q_1}$$

for any $q_1 < \alpha$ and a suitable $C_1 > 0$. At time $T^{J_1(x,i)}$, when the front is at $M^{J_1(x,i)}$, the parasite (x,i) can be either already dead, or it has to be at a site $y < M^{J_1(x,i)}$. We note here that since we condition on the survival of parasites, we have $T^{J_1(x,i)} < \infty$ almost surely under $\mathbb{P}$. If the parasite is already dead, we set

$$J_{\text{good}}(x,i) := J_1(x,i).$$

If the parasite (x,i) is still alive, then by Lemma 3.32 and Lemma 3.33, for some suitable λ small enough, there is a positive probability of at least $\delta_2\delta_1$ that the front after time $T^{J_1(x,i)}$ stays above the linear line $M^{J_1(x,i)} + \lfloor\lambda(t - T^{J_1(x,i)})\rfloor$, and the path of parasite (x,i) after reaching $M^{J_1(x,i)}$ stays below a linear line with slope $\frac{\lambda}{2}$. In particular, in this event the parasite (x,i) never influences the front again, and we set

$$J_{\text{good}}(x,i) := J_1(x,i).$$

If one of these events does not occur, then again by Lemma 3.32 and Lemma 3.33, the vertex $B_1(x,i)$ at which either the sum in Lemma 3.32 is too large or the hitting time in Lemma 3.33 is too small satisfies

$$\mathbb{P}(n < B_1(x,i) - M^{J_1(x,i)} < \infty | J_{\text{good}}(x,i) \neq J_1(x,i), M^{J_1(x,i)}) \leq C_2 n^{-\frac{q_2}{2}} \quad a.s.$$

for any $q_2 < \frac{1+\alpha\wedge 4}{2}$ and a suitable $C_2 > 0$. In this case, we repeat the process of finding the next good site after $B_1(x,i)$ and set

$$J_2(x,i) := J(B_1(x,i)) = \inf\{k \geq 0 : M^k > B_1(x,i)\},$$

which again satisfies

$$\mathbb{P}(M^{J_2(x,i)} - B_1(x,i) > n | J_{\text{good}}(x,i) \neq J_1(x,i), B_1(x,i)) \leq C_1 n^{-q_1} \quad a.s.$$

for $q_1 < \alpha$ and $C_1 > 0$ as before. If the parasite (x,i) is dead at time $T^{J_2(x,i)}$, we set

$$J_{\text{good}}(x,i) := J_2(x,i).$$

Otherwise, we first check if the accumulated sums of $(\overline{\nu}_k^{J_2(x,i)})_{k\geq 0}$ stay small in a sense of Lemma 3.32 and, consequently, the front stays above the linear line $M^{J_2(x,i)} + \lfloor \lambda(t - T^{J_2(x,i)}) \rfloor$, and if the path of the parasite (x,i) after reaching $M^{J_2(x,i)}$ stays below a linear line with slope $\frac{\lambda}{2}$ in the sense of Lemma 3.33. If this event occurs, the parasite (x,i) never reaches the front after $T^{J_2(x,i)}$, and we set

$$J_{\text{good}}(x,i) := J_2(x,i).$$

We note that $(\overline{\nu}_k^{J_2(x,i)})_{k\geq 1}$ depends only on variables with index above $M^{J_2(x,i)}$. Also, the time when the parasite (x,i) reaches $M^{J_2(x,i)}$ is a stopping time with respect to the filtration $\sigma(\mathbf{A}, \mathbf{I}, w_s : 0 \leq s \leq t)$, where we recall that $w_t \in \mathbb{L}_\theta$ is the state of the SIMI at time t; see Section 3.5. In particular, conditionally on $M^{J_2(x,i)}$, the path of the parasite (x,i) after reaching $M^{J_2(x,i)}$ is independent of the path of the parasite before reaching $M^{J_2(x,i)}$. This implies that the event $\{J_{\text{good}}(x,i) = J_2(x,i)\}$ occurs with probability at least $\delta_1\delta_2$, conditionally on $\{J_{\text{good}}(x,i) \neq J_1(x,i)\}$ and the values of $B_1(x,i), M^{J_2(x,i)}$.

Again, if the event does not occur, applying Lemma 3.32 and Lemma 3.33 and using the independence we just described, the site $B_2(x,i)$ at which either the accumulated sums of $(\overline{\nu}_k^{J_2(x,i)})_{k\geq 1}$ are above $\frac{k}{\lambda}$ or the path of the parasite (x,i) after reaching $M^{J_2(x,i)}$ is above a linear line with slope $\frac{\lambda}{2}$, satisfies

$$\mathbb{P}\left(n < B_2(x,i) - M^{J_2(x,i)} < \infty \,\middle|\, \begin{matrix} J_1(x,i) \neq J_{\text{good}}(x,i), \\ B_1(x,i), M^{J_2(x,i)} \end{matrix}\right) \leq C_2 n^{-\frac{q_2}{2}} \quad a.s.$$

with $q_2 < \frac{1+\alpha\wedge 4}{2}, C_2 > 0$ as above.
Iterating this procedure, we find that for $k \geq 1$, given the last attempt was not successful (i.e., we did not set $J_{\text{good}}(x,i) = J_k(x,i)$), then the next try is independent from the last try and successful with probability at least $\delta_1 \cdot \delta_2$, with δ_1, δ_2 as in Lemma 3.32 and Lemma 3.33. In particular, the number of needed attempts is stochastically dominated by a geometric distribution with success probability $\delta_1 \cdot \delta_2$. Also, as reasoned above, the $k+1$-th attempt costs a random number of vertices $B_{k+1}(x,i) - B_k(x,i)$, which is independent of the k-th attempt and satisfies

$$\begin{aligned}&\mathbb{P}\left(n < B_{k+1}(x,i) - B_k(x,i) < \infty \,|\, J_{\text{good}}(x,i) \neq J_k(x,i), B_k(x,i)\right)\\ &\quad \leq C_1 n^{-q_1} + C_2 n^{-\frac{q_2}{2}} \quad a.s.\end{aligned}$$

Arguing the same way as we did in the proof of Lemma 3.16, this yields that

$$\mathbb{P}(M^{J_{\text{good}}(x,i)} - x > n) \leq C_3 n^{-q_3}$$

for some $q_3 < \frac{1+\alpha\wedge 4}{4}$ and a $C_3 > 0$.
We now need to show the uniform limit

$$\lim_{n\to\infty} \sup_{j\geq 0} \mathbb{P}\left(\sup_{0\leq x\leq j, 1\leq i\leq A_x} M^{J_{\text{good}}(x,i)} > j+n\right) = 0.$$

By assumption $\alpha > 3$, and thus we can choose some $\varepsilon_A > 0$ and some $\vartheta \in \left(\frac{(4\wedge\alpha)-3}{4+\varepsilon_A((4\wedge\alpha)-3)}, \frac{(4\wedge\alpha)-3}{4}\right)$ and $q_3 \in \left(\vartheta+1, \frac{(4\wedge\alpha)+1}{4}\right)$. We now compute for any $0 \leq x \leq j$ that

$$\begin{aligned}&\mathbb{P}\left(\sup_{1\leq i\leq A_x} M^{J_{\text{good}}(x,i)} > j+n\right)\\ &\quad\leq \mathbb{P}\left(A > (j-x+n)^{\vartheta}\right) + \mathbb{P}\left(\bigcup_{i=1}^{(j-x+n)^{\vartheta}} \left\{M^{J_{\text{good}}} - x > j-x+n\right\}\right)\\ &\quad\leq \mathbb{P}(A > (j-x+n)^{\vartheta}) + (j-x+n)^{\vartheta} C_3 (j-x+n)^{-q_3}.\end{aligned}$$

By assumption on A, we can fix some $q_4 > 1$ such that $\mathbb{E}[A^{\frac{q_4}{\vartheta}}] < \infty$ and thus obtain

$$\sup_{j\geq 0} \sum_{0\leq x\leq j} \mathbb{P}(A > (j-x+n)^{\vartheta}) \leq \sum_{x\geq 0} \mathbb{P}(A > (x+n)^{\vartheta}) \leq C_4 n^{1-q_4}$$

for some constant C_4 independent of j and n. Using the definition of ϑ, we have $\vartheta - q_3 < -1$, and we see that for some constant C_5 independent of j and n, we have

$$\sup_{j\geq 0}\sum_{0\leq x\leq j}(j-x+n)^{\vartheta}(j-x+n)^{-q_3}\leq C_5 n^{1+\vartheta-q_3}.$$

In particular, we define

$$R_1(j):=\sup_{\substack{0\leq x\leq j\\ 1\leq i\leq A_x}} M^{J_{\text{good}}(x,i)}\quad\text{and}\quad J^1_{\text{good}}(j):=\sup_{\substack{0\leq x\leq j\\ 1\leq i\leq A_x}} J_{\text{good}}(x,i),$$

observing that $R_1(j)=M^{J^1_{\text{good}}(j)}$. By construction, the accumulated sums of $(\overline{\nu}_k^{J^1_{\text{good}}(j)})_{k\geq 1}$ grow at most linearly with slope $\frac{1}{\lambda}$ and, consequently, the front stays above $R_1(j)+\lfloor\lambda(t-T^{J^1_{\text{good}}(j)})\rfloor$ for $t\geq T^{J^1_{\text{good}}(j)}$ and none of the parasites born between 0 and j catch up to the linearly moving front after $T^{J^1_{\text{good}}(j)}$. Also, we have that

$$\sup_{j\geq 0}\mathbb{P}(R_1(j)-j>n)\leq C_4 n^{1-q_4}+C_5 n^{1+\vartheta-q_3}\overset{n\to\infty}{\to}0.$$

Next, we want to see that the parasites born between j and $R_1(j)$ have a positive probability to also stay below the linearly moving front after $T^{J^1_{\text{good}}(j)}$. We note that the paths of parasites generated between j and $R_1(j)$ are influenced by the event that there possibly are already good sites $M^{\ell}<R_1(j)$ from which the accumulated sums of $(\overline{\nu}_k^{\ell})_{k\geq 1}$ grow at most with slope $\frac{1}{\lambda}$. This event does occur if for some (x,i) with $0\leq x\leq j, 1\leq i\leq A_x$, we have $J_{\text{good}}(x,i)<J^1_{\text{good}}(j)$. However, knowing this event occurs only affects the paths of parasites until the time when these parasites reach $R_1(j)$. To see this, observe that, by definition, we have $\overline{\nu}^{\ell}_{M^{\ell+1}-M^{\ell}+k}=\overline{\nu}^{\ell+1}_k$ for any $\ell\geq 0, k\geq 1$. Hence, the event that the accumulated sums of $(\overline{\nu}_k^{J^1_{\text{good}}(j)})_{k\geq 1}$ grow at most linearly with slope $\frac{1}{\lambda}$ already implies that also for any $\ell<J^1_{\text{good}}(j)$ such that the accumulated sums of $(\overline{\nu}^{\ell}_k)_{1\leq k<R_1(j)-M^{\ell}}$ grow at most linearly with slope $\frac{1}{\lambda}$, already all the accumulated sums of $(\overline{\nu}^{\ell}_k)_{k\geq 1}$ grow at most linearly with slope $\frac{1}{\lambda}$. In particular, note that the event that the sums of $(\overline{\nu}^{\ell}_k)_{1\leq k<R_1(j)-M^{\ell}}$ grow at most linearly with slope $\frac{1}{\lambda}$ depends only on the paths of parasites until they reach $R_1(j)$, and the event that the accumulated sums of $(\overline{\nu}_k^{J^1_{\text{good}}(j)})_{k\geq 1}$ grow at most linearly with slope $\frac{1}{\lambda}$ depends only on parasites born at x with $x\geq R_1(j)$. In conclusion, this implies that after the time when a parasite generated between j and $R_1(j)$ reaches $R_1(j)$, its path is that of a (unconditioned) simple symmetric random walk and, consequently, has a probability of at least δ_2 to never catch up to a linearly moving line with slope $\frac{\lambda}{2}$.

We fix some large enough constant $L \in \mathbb{N}$, such that for some $\delta_3 \in (0,1)$ we have

$$C_4 L^{1-q_4} + C_5 L^{1+\vartheta-q_3} < 1 - \delta_3.$$

Then as computed above, we have $\sup_{j\geq 0} \mathbb{P}(R_1(j) - j > L) < 1 - \delta_3$. In the event $R_1(j) - j \leq L$ and

$$\sum_{k=0}^{R_1(j)-j-1} A_{j+k} \leq 2(\mathbb{E}[A]+4)L,$$

as argued above and using Lemma 3.33, with probability at least $\delta_2^{2(\mathbb{E}[A]+4)L}$, none of the parasites generated between j and $R_1(j)$ catch up to the linearly moving front after $T^{J^1_{\text{good}}(j)}$. We note that we can find some $\delta_4 > 0$ such that

$$\sup_{j\geq 0} \mathbb{P}\left(\sum_{k=0}^{R_1(j)-1} A_{j+k} > 2(\mathbb{E}[A]+4)L \,\middle|\, R_1(j) - j \leq L \right) < 1 - \delta_4.$$

Hence, with probability at least $\delta_2^{2(\mathbb{E}[A]+4)L}\delta_3\delta_4$, our search for the site $R_{\text{good}}(j)$ ends at $R_{\text{good}}(j) = R_1(j)$, and none of the parasites born between j and $R_1(j)$ catch up to the linearly moving front after $T^{J^1_{\text{good}}(j)}$.

If $R_1(j) - j > L$ or too many parasites were generated between j and $R_1(j)$, we can repeat the procedure to find $R_1(j)$, now starting at $R_1(j)$ instead of j. Thereby, we find a vertex $R_2(j) = M^{J^2_{\text{good}}(j)}$ such that none of the parasites born between j and $R_1(j)$ (hence also those generated between 0 and $R_1(j)$) catch up to the linearly moving front after $T^{J^2_{\text{good}}(j)}$ and we have

$$\lim_{n\to\infty} \sup_{j\geq 0} \mathbb{P}(R_2(j) - j > n) = 0.$$

Checking once more if $R_2(j) - R_1(j) \leq L$ and

$$\sum_{k=0}^{R_2(j)-R_1(j)-1} A_{R_1(j)+k} \leq 2(\mathbb{E}[A]+4)L,$$

we see that with probability at least $\delta_2^{2(\mathbb{E}[A]+4)L}\delta_3\delta_4$, also the parasites born between $R_1(j)$ and $R_2(j)$ do not contribute to the front after $T^{J^2_{\text{good}}(j)}$. Iterating this procedure, we find an almost surely finite site $R_{\text{good}}(j) = M^{J_{\text{good}}(j)} > j$ such that none of the parasites born between 0 and $R_{\text{good}}(j)$ contribute to the front after time $T^{J_{\text{good}}(j)}$, the sums of $(\overline{\nu}_k^{J_{\text{good}}(j)})_{k\geq 1}$ grow at most with slope $\frac{1}{\lambda}$, and

$$\lim_{n\to\infty} \sup_{j\geq 0} \mathbb{P}(R_{\text{good}}(j) > j + n) = 0. \qquad \square$$

With this renewal site $R_{\text{good}}(j)$ that has a uniform tail over j, we can now iteratively construct a sequence of renewal sites $(R^i)_{i\geq 0}$ simply by retrying for the next renewal site with $R_{\text{good}}(\cdot)$.

Proof of Proposition 3.22. We set $R^0 = 0$ and for $i \geq 0$ define

$$R^{i+1} := R_{\text{good}}(R^i) > R^i,$$

with $R_{\text{good}}(\cdot)$ as in Lemma 3.34. Using the uniform tail bound in Lemma 3.34, we obtain that for any $i \geq 0$, we have that $R^{i+1} < \infty$ almost surely, and by construction, none of the parasites generated below R^{i+1} contribute to the front after $\rho_{R^{i+1}}$. For each $i \geq 0$ and $\ell \geq 0, m > 0$, the event $\{R^{i+1} - R^i = m, R^i = \ell\}$ can be expressed as

$$G_{[0,\ell)} \cap G_{[\ell,\ell+m)} \cap G_{[\ell+m,\infty)}$$

for some events

$$G_{[\ell,\ell+m)} \in \sigma(A_x, I_{x+1}, Y^{x,i} : \ell \leq x < \ell+m, i \in \mathbb{N})$$
$$G_{[0,\ell)} \in \sigma(A_x, I_{x+1}, Y^{x,i} : 0 \leq x < \ell, i \in \mathbb{N})$$

and

$$G_{[\ell+m,\infty)} = \bigcap_{k=1}^{\infty} \left\{ K_{\ell+m+k} \leq k, \sum_{j=1}^{k} \nu_{\ell+m+j} \leq \frac{k}{\lambda} \right\} \in \sigma \begin{pmatrix} A_x, I_{x+1}, & x \geq \ell+m, \\ Y^{x,i} & i \in \mathbb{N} \end{pmatrix}.$$

Note in particular that these three events are independent. By construction of the renewal sites, we have that for any $B \in \mathcal{B}(\mathbb{R}^m)$ the event

$$\{R^{i+1} - R^i = m, R^i = \ell\} \cap \{(\rho_{k+1} - \rho_k : \ell \leq k < \ell+m) \in B\}$$

can be expressed as

$$G_{[0,\ell)} \cap \widetilde{G}_{[\ell,\ell+m)} \cap G_{[\ell+m,\infty)}$$

with $G_{[0,\ell)}, G_{[\ell+m,\infty)}$ as above and some event

$$G_{[\ell,\ell+m)} \supset \widetilde{G}_{[\ell,\ell+m)} \in \sigma(A_x, I_{x+1}, Y^{x,i} : \ell \leq x < \ell+m, i \in \mathbb{N}).$$

In particular, this implies the independence of

$$\{(R^{i+1} - R^i, \rho_{R^i+1} - \rho_{R^i}, \dots, \rho_{R^{i+1}} - \rho_{R^{i+1}-1}) : i \geq 0\},$$

and also that the subcollection with $i \geq 1$ is identically distributed. $\square$

3.4 Proofs of the main Theorems

3.4.1 Proof of Theorem 3.3

In this section, we will show that the process satisfies a strong law of large numbers, in the sense that

$$\lim_{t\to\infty} \frac{r_t}{t} = \gamma \quad \text{almost surely}$$

for some deterministic $\gamma > 0$. We recall the approach.

In Section 3.3 we identified a sequence $(M^i)_{i\geq 0} \subset \mathbb{Z}$, where the upcoming births and deaths are in a good configuration. In particular, the sequence only depends on $\mathbf{A}$ and $\mathbf{I}$, and the increments $(M^{i+1} - M^i)_{i\geq 0}$ are i.i.d.

The good state of upcoming births and deaths after each M^i allowed us to construct a lower bound for the front in Definition 3.12, only depending on parasites that are born to the right of M^i. In particular, in Lemma 3.21, using Lemma 3.20, we will be able to show that moving from M^i to M^{i+1} has finite expectation under our assumptions on α.

In Lemma 3.37 we will show a subadditivity property for the times of moving to each site $(M^i)_{i\geq 0}$ conditionally on the event that $\{M^0 = 0\}$, which yields a strong law of large numbers for the arrival times at the sites $(M^i)_{i\geq 0}$, conditionally on $\{M^0 = 0\}$. Since the increments of $(M^i)_{i\geq 0}$ are i.i.d., this yields also a strong law of large numbers for the infection times of any site n, conditionally on the event that $\{M^0 = 0\}$.

However, by Proposition 3.22, the limit of $\frac{\rho_n}{n}$ cannot be random, because the increments $(\rho_{n+1} - \rho_n)_{n\geq 0}$ have a $\mathbb{P}$-trivial tail sigma field. In particular, this will allow us to transfer the strong law of large numbers from the event $\{M^0 = 0\}$ to the entire event of survival.

The key in showing the subadditivity is to use a different coupling to construct the process, which is monotone in the initial configuration; see Proposition 3.58, in contrast to the construction that we used to define the auxiliary jump times; see also Example 3.51. In the construction, we will use a classical graphical representation using Poisson point processes to sample the jumps that happen on each site. We refer to Section 3.5.2 for the details. In this construction, the state of the process will consist of a triple (r, η, ι), where $r \in \mathbb{Z}$ is the position of the front, $\eta \in \mathbb{N}_0^{\mathbb{Z}}$ with $\operatorname{supp} \eta \subset (-\infty, r]$ is the number of living parasites on each site, and $\iota \in \mathbb{N}$ is the remaining immunity of the host at the site $r + 1$. In this notation we define the natural initial configurations

$$\zeta(r) := (r, A_r\delta_r, I_{r+1})$$

of starting with only A_r many parasites at the vertex r. For any initial configuration $\zeta = (r, \eta, \iota)$ as above and any time $t_0 \in \mathbb{R}$, we denote by

$$(r_t(\zeta; t_0), \eta_t(\zeta; t_0), \iota_t(\zeta; t_0)_{t \geq t_0}$$

the state of the SIMI at time t, when starting in the initial configuration ζ and using the Poisson point processes starting at time t_0. We will use that by Proposition 3.58, the coupling is such that for any initial time t_0, any $r \in \mathbb{Z}$, and configurations $\eta_1, \eta_2 \in \mathbb{N}_0^{\mathbb{Z}}$ with $\operatorname{supp} \eta_1, \operatorname{supp} \eta_2 \subset (-\infty, r]$, the following holds. If t_0 is a stopping time with respect to the information of the collections $\mathbf{A}, \mathbf{I}$ and the Poisson point processes up to time t, and η_1, η_2 are measurable with respect to the information of $\mathbf{A}, \mathbf{I}$ and the Poisson point processes up to time t_0, such that almost surely η_2 holds more parasites than η_1 in each interval around the front, then the front constructed from η_2 starting at time t_0 is always above the front constructed from η_1 starting at time t_0. In this coupling we define the following random variables, on which we want to apply Liggett's Subadditive Ergodic Theorem [32].

Definition 3.35. *In the coupling defined in Section 3.5.2, we define*

$$\widetilde{T}^i := \inf\{t \geq 0 : r_t(\zeta(0); 0) \geq M^i\}$$

and for $0 \leq m < n$ *we set*

$$X_{m,n} := \inf\{t \geq 0 : r_{\widetilde{T}^m + t}(\zeta(M^m); \widetilde{T}^m) \geq M^n\}.$$

Remark 3.36. *We note that* $X_{0,n}$ *always starts at the site* M^0. *Hence, only in the event* $\{M^0 = 0\}$ *do we have that* $X_{0,n} = \widetilde{T}^n$ *for* $n \geq 0$. *Also we note that by the definition of* $(M^i)_{i \geq 0}$, *the process started from* M^i *cannot die out, and thus* $X_{m,n} < \infty$ *almost surely for any* $0 \leq m < n$.

Lemma 3.37. *With* $(X_{m,n})_{0 \leq m < n}$ *as in Definition 3.35, we have that for some deterministic* $\rho > 0$

$$\lim_{n \to \infty} \frac{X_{0,n}}{n} = \rho$$

almost surely. In particular, we have

$$\lim_{n\to\infty} \frac{\widetilde{T}^n}{n} = \rho$$

almost surely on the event $\{M^0 = 0\}$.

Proof. We want to apply Liggett's Subadditive Ergodic Theorem. Since clearly $X_{m,n} \geq 0$ for all $0 \leq m < n$, we thus have to check the four conditions:

a) $\mathbb{E}[X_{0,n}] < \infty$ for all $n \in \mathbb{N}$

b) $X_{0,n} \leq X_{0,m} + X_{m,n}$ for all $0 \leq m < n$.

c) The joint distributions of $\{X_{m+1,m+k+1} : k \geq 1\}$ are the same as those of $\{X_{m,m+k} : k \geq 1\}$ for each $m \geq 0$.

d) For each $k \geq 1$, the process $\{X_{nk,(n+1)k} : n \geq 1\}$ is stationary and ergodic.

We now verify each condition.

a) This follows from Lemma 3.21 and property b), since clearly $T^1 \overset{\mathrm{d}}{=} \widetilde{T}^1$.

b) The configuration $\eta_{\widetilde{T}^m}(\zeta(M^0); \widetilde{T}^0)$ holds A_{M^m} parasites on site M^m and then all the remaining parasites that were generated between M^0 and M^m and are still alive. In particular, the configuration $\eta_{\widetilde{T}^m}(\zeta(M^0); \widetilde{T}^0)$ dominates the configuration $\zeta(M^m)$, which holds only A_{M^m} parasites on site M^m. By Proposition 3.58 and the strong Markov property of the process, this implies the subadditivity. We note here that for this to hold, we need to enlarge the state space of triples (r, η, ι) to also hold the information of all upcoming immunities and offspring, because the offspring and immunity configurations above M^m are always good and thus influence the future of the process. The state of the process will be given by a 4-tuple $(r, \eta, (\iota_n)_{n\geq1}, (a_n)_{n\geq1})$ where ι_n is the immunity of the host at $r + n$ and a_n are the offspring generated after the host at $r + n$ gets infected. Clearly the resulting process is still a strong Markov process with respect to the information of $\mathbf{A}, \mathbf{I}$ and the Poisson point processes up to time t, and clearly $\widetilde{T}^m$ is a stopping time with respect to this filtration.

c) This is clearly the case by translation invariance.

d) The stationarity follows again by translation invariance. To see the ergodicity, we note that $\widetilde{T}^m$ is a stopping time with respect to the information of $\mathbf{A}, \mathbf{I}$ and the Poisson point processes up to time t. Also, we note that by Lemma 3.16 we have

$$\{(M^{m+1} - M^m, A_{M^m}, \dots, A_{M^{m+1}-1}, I_{M^m+1}, \dots, I_{M^{m+1}}) : m \geq 0\}$$

is i.d.d. and, by definition, the process between M^m and M^nonly uses offspring $A_{M^m}, \dots, A_{M^n-1}$, immunities $I_{M^m+1}, \dots, I_{M^n}$, and the Poisson point processes between $\widetilde{T}^m$ and $\widetilde{T}^n$. Hence, the variables

$$(X_{nk,(n+1)k})_{n\geq 1}$$

use different parts of the collections $\mathbf{A}, \mathbf{I}$ and Poisson point processes. In particular, the sequence is not only ergodic but actually independent.

Having checked all the conditions, we can apply Liggett's Subadditive Ergodic Theorem and conclude the claimed almost sure convergence. Noting that, by definition, on the event $\{M^0 = 0\}$ we have $X_{0,n} = \widetilde{T}^n$ yields the second claim. □

We have established a law of large numbers for the hitting times of the good sites. To show the claimed law of large numbers for the front, we need the next proposition to transfer a law of large numbers of hitting times to a law of large numbers of the corresponding counting process.

Proposition 3.38. *Let $(X_n)_{n\geq 1}$ be a sequence of non-negative random variables such that there is a $\lambda > 0$ with*

$$\lim_{n\to\infty} \frac{1}{n} \sum_{j=1}^{n} X_j = \lambda$$

almost surely. Then

$$\lim_{t\to\infty} \frac{1}{t} \sup \left\{ n \geq 1 : \sum_{j=1}^{n} X_j \leq t \right\} = \frac{1}{\lambda}$$

almost surely.

Proof. We set

$$m_t := \sup \left\{ n \geq 1 : \sum_{j=1}^{n} X_j \leq t \right\}.$$

Let $\varepsilon > 0$ and let ω be such that

$$\lim_{n\to\infty} \frac{1}{n} \sum_{j=1}^{n} X_j(\omega) = \lambda.$$

We choose $n_0 = n_0(\omega) \in \mathbb{N}$ large enough such that

$$\left| \frac{1}{n} \sum_{k=1}^{n} X_k(\omega) - \lambda \right| < \varepsilon \quad \text{and} \quad \frac{n+1}{n} < 1 + \varepsilon$$

for all $n \geq n_0$. Set $t_0 = t_0(\omega) := \sum_{k=1}^{n_0} X_k(\omega)$. Clearly for all $t \geq t_0$ we have $m_t(\omega) \geq n_0$, thus we have

$$\frac{\sum_{k=1}^{m_t} X_k}{m_t}, \frac{\sum_{k=1}^{m_t+1} X_k}{m_t + 1} \in (\lambda - \varepsilon, \lambda + \varepsilon).$$

and by definition of m_t we have

$$\sum_{k=1}^{m_t} X_k \leq t < \sum_{k=1}^{m_t+1} X_k.$$

Dividing by m_t, we obtain

$$\lambda - \varepsilon < \frac{\sum_{k=1}^{m_t} X_k}{m_t} \leq \frac{t}{m_t} < \frac{m_t + 1}{m_t} \frac{\sum_{k=1}^{m_t+1} X_k}{m_t + 1} < (1 + \varepsilon)(\lambda + \varepsilon)$$

and hence $\lim_{t\to\infty} \frac{m_t}{t} = \frac{1}{\lambda} > 0$. $\square$

Proof of Theorem 3.3. By Lemma 3.37 we have that

$$\lim_{n\to\infty} \frac{T^n}{n} = \rho$$

for some $\rho \in (0, \infty)$ holds almost surely on the event $\{M^0 = 0\}$. Since the sequence of increments $(M^{k+1} - M^k)_{k\geq 0}$ is i.i.d. under $\mathbb{P}$, the strong law of large numbers implies that $\mathbb{P}$-almost surely

$$\lim_{n\to\infty} \frac{M^n}{n} = \mathbb{E}[M^1 - M^0].$$

For $n \in \mathbb{N}$ we set

$$Q_n := \sup\{m \geq 0 : M^m \leq n\},$$

then by Proposition 3.38 we have

$$\lim_{n\to\infty} \frac{Q_n}{n} = \frac{1}{\mathbb{E}[M^1 - M^0]}$$

$\mathbb{P}$-almost surely. Hence, on the event $\{M^0 = 0\}$ we almost surely have

$$\frac{\rho_n}{n} = \frac{T^{Q_n}}{Q_n}\frac{Q_n}{n} + \frac{\rho_n - T^{Q_n}}{n} \overset{n\to\infty}{\to} \frac{\rho}{\mathbb{E}[M^1 - M^0]}.$$

To see that the second summand

$$\frac{\rho_n - T^{Q_n}}{n}$$

tends to 0, simply note that by the definition of Q_n we have

$$0 \le \rho_n - T^{Q_n} < T^{Q_n+1} - T^{Q_n}.$$

Now we simply compute, using the estimates in the proof of Lemma 3.21, that for any $\varepsilon > 0$

$$\mathbb{P}(T^{Q_n+1} - T^{Q_n} > \varepsilon n) \le \mathbb{P}(T^1 > \varepsilon n | M^0 = 0) \le Cn^{-(1+\delta)}$$

for some suitable $C > 0$ and $\delta > 0$ small enough. In particular, the Borel-Cantelli Lemma implies

$$0 \le \lim_{n\to\infty} \frac{\rho_n - T^{Q_n}}{n} \le \lim_{n\to\infty} \frac{T^{Q_n+1} - T^{Q_n}}{n} = 0$$

$\mathbb{P}$-almost surely. With this we have shown that

$$\lim_{n\to\infty} \frac{\rho_n}{n} = \frac{\rho}{\mathbb{E}[M^1 - M^0]}$$

almost surely on the event $\{M^0 = 0\}$. By Proposition 3.22 and Kolmogorov's zero-one law (see e.g. [27, Theorem 2.37]), we obtain that the tail-sigma field

$$\bigcap_{i=0}^{\infty} \sigma(R^{k+1} - R^k, \rho_{R^k+1} - \rho_{R^k}, \ldots, \rho_{R^{k+1}} - \rho_{R^{k+1}-1} : k \ge i)$$

is $\mathbb{P}$-trivial. Noting that

$$\begin{aligned}&\bigcap_{i=0}^{\infty} \sigma(R^{k+1} - R^k, \rho_{R^k+1} - \rho_{R^k}, \ldots, \rho_{R^{k+1}} - \rho_{R^{k+1}-1} : k \ge i)\\ &\quad = \bigcap_{i=0}^{\infty} \sigma(R^{k+1} - R^k, \rho_{j+1} - \rho_j : k \ge i, j \ge R^i)\end{aligned}$$

and $\infty > R^i \ge i$ almost surely, yields that also

$$\mathcal{H}_{\text{tail},\rho} := \bigcap_{n=1}^{\infty} \sigma(\rho_{k+1} - \rho_k : k \ge n) \subset \bigcap_{i=0}^{\infty} \sigma\left(R^{k+1} - R^k, \rho_{j+1} - \rho_j : \begin{matrix} k \ge i, \\ j \ge R^i \end{matrix}\right)$$

is $\mathbb{P}$-trivial. Because $\rho_n < \infty$ almost surely under $\mathbb{P}$, the event

$$\left\{ \lim_{n\to\infty} \frac{\rho_n}{n} = \frac{\rho}{\mathbb{E}[M^1 - M^0]} \right\}$$

is contained in that tail-sigma field $\mathcal{H}_{\text{tail},\rho}$ and, as reasoned above, has positive probability. Thus, we must already have

$$\lim_{n\to\infty} \frac{\rho_n}{n} = \frac{\rho}{\mathbb{E}[M^1 - M^0]}$$

almost surely under $\mathbb{P}$.
Hence, again using Proposition 3.38, we obtain that

$$\lim_{t\to\infty} \frac{r_t}{t} = \frac{\mathbb{E}[M^1 - M^0]}{\rho}$$

$\mathbb{P}$-almost surely and have finished the proof of Theorem 3.3 by setting

$$\gamma := \frac{\mathbb{E}[M^1 - M^0]}{\rho}.$$

□

3.4.2 Proof of Theorem 3.2

In this section we prove the weaker result, which, however, works for a broader range of α and also any initial configuration w. Precisely, we want to show Theorem 3.2, i.e., that there are $C_1, C_2 > 0$ such that

$$C_1 \leq \liminf_{t\to\infty} \frac{r_t}{t} \leq \limsup_{t\to\infty} \frac{r_t}{t} \leq C_2$$

holds $\mathbb{P}$-almost surely. The upper bound follows by Equation (3.35). For the lower bound we use a quite similar construction as for M^0, however this time we don't give a special treatment to the first k_0 sites. We recall the definitions of $(L_k)_{k\geq 0}, N, M$ and T from Definition 3.11 and that $T < \infty$ holds $\mathbb{P}$-almost surely by Lemma 3.14. By definition, we have

$$K_{M+n} \leq n$$

for all $n \geq k_0$ and thus by Proposition 3.10 we have

$$\mathbb{1}_{t\geq T} \left(M + k_0 - 1 + \sup\left\{ n \geq 1 : \sum_{k=k_0}^{n} \nu_{M+k} \leq t - T \right\} \right) \leq r_t. \tag{3.29}$$

In light of Proposition 3.38, we hence need to show

$$\lim_{n\to\infty}\frac{1}{n}\left(T+\sum_{k=k_0}^{n}\nu_{M+k}\right)=\gamma \tag{3.30}$$

for some $\gamma > 0$. Because $T < \infty$ almost surely under $\mathbb{P}$, we only need to show that

$$\lim_{n\to\infty}\frac{1}{n}\sum_{k=k_0}^{n}\nu_{M+k}=\gamma$$

for some $\gamma > 0$. By Lemma 3.18, the variables $(\nu_{M+n})_{n\geq k_0}$ are asymptotically identically distributed, and by Lemma 3.19, they have weak dependence. We will use L^q-mixingales introduced by [35] to formally prove the claimed strong law of large numbers. We recall their definition next.

Definition 3.39. *Let* $\{X_i : i \geq 1\}$ *be a sequence of random variables on some probability space* $(\Xi, \mathcal{H}, P)$ *with* $E[|X_i|] < \infty$ *for all* $i \geq 1$ *and* $\{\mathcal{H}_i : i \in \mathbb{Z}\}$ *a nondecreasing sequence of sub* σ*-fields of* $\mathcal{H}$*. For* $q \geq 1$*, the collection* $\{X_i, \mathcal{H}_j : i \geq 1, j \in \mathbb{Z}\}$ *is called an* L^q*-mixingale if there exist nonnegative constants* $\{c_i : i \geq 1\}$ *and* $\{\psi(m) : m \geq 0\}$ *such that* $\lim_{m\to\infty}\psi(m) = 0$ *and for all* $i \geq 1, m \geq 0$ *we have*

- $\|E[X_i|\mathcal{H}_{i-m}]\|_q := \left(E\left[|E[X_i|\mathcal{H}_{i-m}]|^q\right]\right)^{\frac{1}{q}} \leq c_i\psi(m)$ *and*
- $\|X_i - E[X_i|\mathcal{H}_{i+m}]\|_q := \left(E\left[|X_i - E[X_i|\mathcal{H}_{i+m}]|^q\right]\right)^{\frac{1}{q}} \leq c_i\psi(m+1)$

We note that the first condition imposes the variables $\{X_i : i \geq 1\}$ to have zero mean, because

$$|E[X_i]| = |E[E[X_i|\mathcal{H}_{i-m}]]| \leq \|E[X_i|\mathcal{H}_{i-m}]\|_1 \leq \|E[X_i|\mathcal{H}_{i-m}]\|_q \leq c_i\psi(m) \to 0$$

as $m \to \infty$. We will thus verify the following lemma.

Lemma 3.40. *Set*

$$X_i := \nu_{M+k_0-1+i} - \mathbb{E}[\nu_{M+k_0-1+i}] \quad \textit{and} \quad \mathcal{H}_j := \begin{cases}\sigma(\nu_{M+k_0},\ldots,\nu_{M+k_0+j-1}), & j \geq 1\\ \{\emptyset,\Omega\}, & j \leq 0\end{cases}$$

for $i \geq 1, j \in \mathbb{Z}$*. Then for any* $1 < q < \frac{(4\wedge\alpha)+1}{2}$ *the collection* $\{X_i, \mathcal{H}_j : i \geq 1, j \in \mathbb{Z}\}$ *is an* L^q*-mixingale on the probability space* $(\Omega, \mathcal{F}, \mathbb{P})$*. In particular we have*

$$c_i = 2\|\nu_{M+k_0-1+i} - \mathbb{E}[\nu_{M+k_0-1+i}]\|_q \quad \textit{and} \quad \psi(m) = \phi(m)^{\frac{q-1}{q}}$$

with ϕ *as in Lemma 3.19.*

Proof. First we note that by Corollary 3.28 the expectations and conditional expectations exist and are finite. Next we note that the second condition of a L^q-mixingale is trivially fulfilled because X_i is $\mathcal{H}_i$ measurable; hence the left side is just 0. To verify the first condition we use the classical result for ϕ-mixing sequences of Serfling [43, Theorem 2.2] that shows

$$\mathbb{E}\left[|\mathbb{E}[X_i|\mathcal{H}_{i-m}|^q\right] \leq 2^q \phi(m)^{q-1} \mathbb{E}[|X_i|^q].$$

This already finishes the proof. □

To conclude the final convergence, we need the following lemma to deal with the error term that appears due to centering the not identically distributed variables $(\nu_{M+k_0-1+i})_{i\geq 1}$.

Lemma 3.41. *Let* $(a_n)_n \subset \mathbb{R}$ *be a sequence with* $\lim_{n\to\infty} a_n = 0$. *Then*

$$\lim_{n\to\infty} \frac{1}{n} \sum_{k=1}^{n} a_n = 0$$

Proof. Let $\varepsilon > 0$ and choose $N_1 \in \mathbb{N}$ such that $|a_n| < \min\left\{1, \frac{\varepsilon}{3}\right\}$ for all $n > N_1$. Then in particular for all $n > N_1$ we have

$$\frac{1}{n-N_1}\left|\sum_{k=N_1+1}^{n} a_k\right| < \min\left\{1, \frac{\varepsilon}{3}\right\}.$$

Setting

$$N_2 := \max\left\{N_1, \left\lceil \frac{3}{\varepsilon}\left|\sum_{k=1}^{N_1} a_k\right|\right\rceil, \left\lceil N_1 \frac{3}{\varepsilon}\right\rceil\right\}$$

we obtain for $n > N_2$

$$\begin{aligned}
\frac{1}{n}\left|\sum_{k=1}^{n} a_k\right| &= \frac{1}{n}\left|\sum_{k=1}^{N_1} a_k + \sum_{k=N_1+1}^{n} a_k\right| = \frac{1}{n}\left|\sum_{k=1}^{N_1} a_k + \frac{n-N_1}{n-N_1}\sum_{k=N_1+1}^{n} a_k\right| \\
&\leq \frac{1}{n}\left|\sum_{k=1}^{N_1} a_k\right| + \frac{1}{n}\frac{N_1}{n-N_1}\left|\sum_{k=N_1+1}^{n} a_k\right| + \frac{1}{n-N_1}\left|\sum_{k=N_1+1}^{n} a_k\right| \\
&< \left\lceil \frac{3}{\varepsilon}\left|\sum_{k=1}^{N_1} a_k\right|\right\rceil^{-1}\left|\sum_{k=1}^{N_1} a_k\right| + \left\lceil N_1\frac{3}{\varepsilon}\right\rceil^{-1} N_1 \cdot 1 + \frac{\varepsilon}{3} \leq \varepsilon,
\end{aligned}$$

which finishes the proof. □

With these tools at hand, we can now finally prove the needed law of large numbers.

Lemma 3.42. *It holds*

$$\lim_{n\to\infty} \frac{T + \sum_{k=k_0}^{n} \nu_{M+k}}{n} = \mathbf{E}[\nu]$$

$\mathbb{P}$*-almost surely.*

Proof. Using Lemma 3.14, we obtain that

$$\lim_{n\to\infty} \frac{T}{n} = 0$$

$\mathbb{P}$-almost surely.
Now, fixing some $q \in \left(1, \frac{(4\wedge\alpha)+1}{2}\right)$, we want to apply [25, Corollary 1] to conclude the convergence of

$$\lim_{n\to\infty} \frac{1}{n} \sum_{k=k_0}^{k_0+n} \nu_{M+k} - \mathbb{E}[\nu_{M+k}] = 0.$$

For this purpose, we have to check the following two conditions: we need to have $\sup_{i\geq 1} c_i < \infty$ and $\psi(m) = \mathcal{O}\left(\log(m)^{-(1+\delta)}\right)$ for some $\delta > 0$.
Using the constants given in Lemma 3.40 and applying Corollary 3.29, we see that

$$\begin{aligned} c_i &\leq 2\left(\|\nu_{M+k_0-1+i}\|_q + \|\mathbb{E}[\nu_{M+k_0-1+i}]\|_q\right) \\ &= 2\left(\mathbb{E}[|\nu_{M+k_0-1+i}|^q]^{\frac{1}{q}} + \mathbb{E}[\nu_{M+k_0-1+i}]\right) \\ &\to 2\left(\mathbf{E}[\nu^q]^{\frac{1}{q}} + \mathbf{E}[\nu]\right) \quad (i \to \infty). \end{aligned}$$

In particular, $\sup_{i\geq 1} c_i < \infty$, which is the first condition of [25, Corollary 1]. From Lemma 3.19 we obtain that

$$\psi(m) \leq C m^{(-\alpha+\varepsilon)\frac{q-1}{q}} = \mathcal{O}\left(\frac{1}{\log(m)^2}\right),$$

which is the second condition of [25, Corollary 1]. Hence we can apply the strong law of large numbers for L^q-mixingales to conclude

$$\lim_{n\to\infty} \frac{1}{n} \sum_{j=1}^{n} \nu_{M+k_0-1+j} - \mathbb{E}[\nu_{M+k_0-1+j}] = 0. \tag{3.31}$$

Thus putting everything together we obtain

$$\begin{aligned}
\lim_{n\to\infty}\left|\frac{1}{n}\left(T+\sum_{k=k_0}^{n}\nu_{M+k}\right)-\mathbf{E}[\nu]\right| &\leq \lim_{n\to\infty}\left|\frac{T}{n}\right|+\left|\frac{1}{n}\sum_{k=k_0}^{n}\nu_{M+k}-\mathbf{E}[\nu]\right| \\
&= \lim_{n\to\infty}\left|\frac{n-k_0+1}{n}\frac{1}{n-k_0+1}\sum_{k=k_0}^{n}\nu_{M+k}-\mathbb{E}[\nu_{M+k}]+\mathbb{E}[\nu_{M+k}]-\mathbf{E}[\nu]\right| \\
&\leq \lim_{n\to\infty}\left|\frac{1}{n-k_0+1}\sum_{k=k_0}^{n}\nu_{M+k}-\mathbb{E}[\nu_{M+k}]\right| \\
&\qquad+\left|\frac{1}{n-k_0+1}\sum_{k=k_0}^{n}\mathbb{E}[\nu_{M+k}]-\mathbf{E}[\nu]\right| \\
&= 0,
\end{aligned}$$

where in the last line we used (3.31) and Lemma 3.41, noting that by Corollary 3.29 we have $\lim_{n\to\infty}\mathbb{E}[\nu_{M+n}]=\mathbf{E}[\nu]$. □

Proof of Theorem 3.2. Using Lemma 3.42 and Proposition 3.38, we obtain the lower bound. For $\vartheta>0$ let f_ϑ be as in Theorem 3.1. For the upper bound we note that by (3.47), taking $\gamma>0$ large enough such that $c_{\gamma,\vartheta}>0$,

$$\begin{aligned}
\mathbf{P}(\mathcal{S}(\eta))\mathbb{P}(r_t>\gamma t)\leq \mathbf{P}(r_t>\gamma t) &= \int_\Omega \mathbf{P}(r_t(\eta(\omega))>\gamma t)\,\mathrm{d}\mathbf{P}(\omega) \\
&\leq \int_\Omega \mathrm{e}^{-c_{\gamma,\vartheta}t}f_\vartheta(\eta(\omega))\,\mathrm{d}\mathbf{P}(\omega)=\mathrm{e}^{-c_{\gamma,\vartheta}t}\,\mathbf{E}[f_\vartheta(\eta)].
\end{aligned}$$

By assumption the initial configuration satisfies $\mathbf{E}[f_\vartheta(\eta)]<\infty$, since otherwise the whole process is not even well defined. This concludes the proof, because this bound is clearly integrable in t. □

3.4.3 Proof of Theorem 3.4

We finally consider the SIMI on $\mathbb{Z}$, where initially all vertices $x\neq 0$ are inhabited by a host and there are a random number of active parasites, distributed according to A at the origin. Since we start with only finitely many active parasites, we do not need to worry about the state space topology, as a coupling with a branching random walk again shows that the number of infected sites, hence the number of active parasites, grows at most linearly in time. However, since deaths can now occur at both boundaries, which carry their individual immunities, the event of survival can, a priori, no longer be expressed independent of the paths given by $\mathbf{Y}$. In the special case that I has a geometric distribution with parameter $p \in (0,1]$, this, however, is still possible, because the infection probability does not depend on the number of previous attempts, i.e., $\mathbf{P}(I = k+1 | I > k) = p$ for all $k \geq 0$. In the general case, however, $\mathbf{P}(I = k+1|I > k)$ does depend on k, which will make a successful infection dependent on the number of parasites that died at each boundary. Using Lemma 3.46, we can, however, get rid of this dependence by considering the event that parasites born on some $x > 0$ never reach the left host boundary and parasites born on $x < 0$ never reach the right host boundary. We recall the following classical result on the speed of continuous-time simple symmetric random walks on $\mathbb{Z}$:

Lemma 3.43. *[16, Lemma 8] Let $\{X_t : t \geq 0\}$ be a continuous time simple symmetric random walk on $\mathbb{Z}$ with jump rate 2, starting from $x \leq -1$ on some probability space $(\Omega', \mathcal{F}', P)$. For any $c > 0$, let*

$$\tau_c := \inf\{t \geq 0 : X_t \geq \lfloor ct \rfloor\},$$

then

$$P(\tau_c = \infty) \geq \begin{cases} 1 - \mathrm{e}^{(1+x)\theta_c}, & x \leq -2 \\ \exp\left(-\frac{2}{c}\right)\left(1 - \mathrm{e}^{-\theta_c}\right), & x = -1 \end{cases}$$

where $\theta_c > 0$ is the positive solution of $c\theta - 2(\cosh\theta - 1) = 0$.

Definition 3.44. *For $j \geq 1$ we set*

$$K_{n,j} := \inf\left\{k \geq j : \sum_{\ell=1}^{k} A_{n-\ell} \geq \beta_A k, \sum_{\ell=1}^{k} I_{n+1-\ell} \leq \beta_I k\right\}.$$

Analogously we define

$$\mathcal{W}_{n,j} := \{(x,i) \in \mathbb{Z} \times \mathbb{N} : n - K_{n,j} \leq x \leq n-1, 1 \leq i \leq A_x\}$$

and

$$\nu_{n,j} := \inf\left\{t \geq 0 : \sum_{(x,i)\in\mathcal{W}_{n,j}} \mathbb{1}_{\tau^{x,i}_{n-x} \leq t} \geq \beta_I K_{n,j}\right\}.$$

Finally we define for any $l \in \mathbb{Z}, n \geq 1$ the time

$$\nu_n(l) := \min\{\nu_{l+n,1}, \ldots, \nu_{l+n,n\wedge k_0}\}.$$

Remark 3.45. *Analogously to Lemma 3.10, we obtain that*

$$\mathbb{1}_{K_{n,j}\leq n}(\rho_n - \rho_{n-1}) \leq \nu_{n,j}$$

for all $n \geq 1, 1 \leq j \leq n$. *Clearly* $K_{n,j} \leq K_{n,j+1}$ *and hence for any* $l \in \mathbb{Z}, n \geq 1$ *also*

$$\mathbb{1}_{K_{l+n,n\wedge k_0}\leq n}(\rho_{l+n} - \rho_{l+n-1}) \leq \nu_n(l).$$

Furthermore, the sequence $(\nu_n(l))_{n\geq k_0}$ *is* ϕ*-mixing and has finite* q*-th moments for any* $q < \frac{\alpha+1}{2}$ *which follows analogously as Lemma 3.17 and Lemma 3.19.*

Lemma 3.46. *Assume* $\alpha > 3$. *Then for any* $\gamma < \frac{1}{\mathbf{E}[\nu_{1,k_0}]}$ *we have*

$$\mathbf{P}\left(\bigcap_{k=1}^{\infty}\{K_{k,k\wedge k_0} \leq k\}, \bigcap_{n=1}^{\infty}\left\{\sum_{k=1}^{n}\nu_k(0) \leq \frac{n}{\gamma}\right\}\right) > 0.$$

Proof. We recall

$$m(X,k) = \inf\{j \geq k : \mathbf{P}(X = j) > 0\}$$

for any random variable X on $\mathbf{\Omega}$. We let $\mu := \mathbb{E}[\nu_{1,k_0}]$ and $\gamma < \frac{1}{\mu}$. For $n \in \mathbb{N}, \varepsilon \in (0, \frac{1}{\gamma})$ we define $G_{n,\varepsilon}$ to be the event that

$$I_1 = \cdots = I_n = m(I,1), A_0 = \cdots = A_{n-1} = m(A,\beta_A),$$

and all random walks $\{Y^{x,i} : 0 \leq x < n, 1 \leq i \leq m(A,\beta_A)\}$ take $n + k_0$ steps to the right before time ε. By definition of the event, we have

$$G_{n,\varepsilon} \subset \bigcap_{k=1}^{n}\{K_{k,k_0} = k \wedge k_0, \nu_k(0) < \varepsilon\}$$

and clearly $\mathbf{P}(G_{n,\varepsilon}) > 0$ for all $n \in \mathbb{N}, \varepsilon \in (0, \frac{1}{\gamma})$. Next let $H_{n,\varepsilon}$ be the event

$$\bigcap_{k=1}^{\infty}\left\{K_{n+k,k\wedge k_0} \leq k, \sum_{j=1}^{k}\nu_{n+j,j\wedge k_0} < \frac{n+k}{\gamma} - n\varepsilon\right\},$$

which is independent of $G_{n,\varepsilon}$. By the definitions of $G_{n,\varepsilon}$ and $H_{n,\varepsilon}$ we have

$$\bigcap_{k=1}^{\infty}\{K_{k,k\wedge k_0} \leq k\} \cap \bigcap_{n=1}^{\infty}\left\{\sum_{k=1}^{n}\nu_k(0) \leq \frac{n}{\gamma}\right\} \supset G_{n,\varepsilon} \cap H_{n,\varepsilon},$$

hence, using the independence of $G_{n,\varepsilon}$ and $H_{n,\varepsilon}$, we only need to show that $\mathbf{P}(H_{n,\varepsilon}) > 0$ for some $n \in \mathbb{N}, \varepsilon \in (0, \frac{1}{\gamma})$. Observe that

$$\begin{aligned}\mathbf{P}(H_{n,\varepsilon}^C) \leq \mathbf{P}&\left(\bigcup_{k=1}^{\infty}\{K_{n+k,k\wedge k_0} > k\}\right)\\ &+ \mathbf{P}\left(\bigcup_{k=1}^{k_0}\left\{\sum_{j=1}^{k}\nu_{n+j,j} \geq \delta\left(\frac{n+k}{\gamma} - n\varepsilon\right)\right\}\right)\\ &+ \mathbf{P}\left(\bigcup_{k=k_0+1}^{\infty}\left\{\sum_{j=k_0+1}^{k}\nu_{n+j,k_0} \geq (1-\delta)\left(n\left(\frac{1}{\gamma} - \varepsilon\right) + \frac{k-k_0}{\gamma}\right)\right\}\right)\end{aligned} \tag{3.32}$$

for any $\delta \in (0,1)$ such that $\frac{1-\delta}{\gamma} > \mu$.

The first term does not depend on n, because the random variables $(K_{n,j})_{n\in\mathbb{Z}}$ are identically distributed, and the complement of the event considered in the first term is contained in the event

$$\bigcap_{k=1}^{\infty}\left\{\sum_{j=1}^{k} I_{n+j} \leq \beta_I k, \sum_{j=1}^{k} A_{n+j-1} \geq \beta_A k\right\},$$

which has positive probability. In particular, the first term of (3.32) is smaller than 1.

For the second term of (3.32) we observe that

$$\begin{aligned}\mathbf{P}&\left(\bigcup_{k=1}^{k_0}\left\{\sum_{j=1}^{k}\nu_{n+j,j} \geq \delta\left(\frac{n+k}{\gamma} - n\varepsilon\right)\right\}\right)\\ &= \mathbf{P}\left(\bigcup_{k=1}^{k_0}\left\{\sum_{j=1}^{k}\nu_{j,j} \geq \delta\left(\frac{n+k}{\gamma} - n\varepsilon\right)\right\}\right),\end{aligned}$$

which tends to 0 for $n \to \infty$, because $\nu_{1,1}, \ldots, \nu_{k_0,k_0} < \infty$ almost surely by the same proof as Lemma 3.17. To estimate the last term, we note that by an analogous statement as claimed in Lemma 3.20, for any $2 < q < \frac{\alpha+1}{2}$ we have

$$\begin{aligned}\mathbf{P}&\left(\sum_{j=k_0+1}^{k}\nu_{n+j,k_0} \geq (1-\delta)\left(n\left(\frac{1}{\gamma} - \varepsilon\right) + \frac{k-k_0}{\gamma}\right)\right)\\ &= \mathbf{P}\left(\sum_{j=1}^{k-k_0}\nu_{j,k_0} - \mu \geq (1-\delta)\left(n\left(\frac{1}{\gamma} - \varepsilon\right) + \frac{k-k_0}{\gamma}\right) - (k-k_0)\mu]\right)\\ &\leq C(k-k_0)^{\frac{q}{2}}\left((k-k_0)\left(\frac{1-\delta}{\gamma} - \mu\right) + n(1-\delta)\left(\frac{1}{\gamma} - \varepsilon\right)\right)^{-q}.\end{aligned}$$

Now for $\vartheta \in \left(\frac{q+2}{2q}, 1\right)$ Young's inequality yields

$$\begin{aligned}
&(k-k_0)\left(\frac{1-\delta}{\gamma}-\mu\right)+n(1-\delta)\left(\frac{1}{\gamma}-\varepsilon\right)\\
=&\vartheta\frac{k-k_0}{\vartheta}\left(\frac{1-\delta}{\gamma}-\mu\right)+(1-\vartheta)\frac{n(1-\delta)}{1-\vartheta}\left(\frac{1}{\gamma}-\varepsilon\right)\\
\geq&\left[\frac{k-k_0}{\vartheta}\left(\frac{1-\delta}{\gamma}-\mu]\right)\right]^{\vartheta}\left[\frac{n(1-\delta)}{1-\vartheta}\left(\frac{1}{\gamma}-\varepsilon\right)\right]^{1-\vartheta}
\end{aligned}$$

and thus we can estimate the third term in (3.32) using the union bound with

$$\sum_{k=k_0+1}^{\infty} C(k-k_0)^{\frac{q}{2}-\vartheta q}\left[\frac{1}{\vartheta}\left(\frac{1-\delta}{\gamma}-\mu]\right)\right]^{-q\vartheta}\left[\frac{n(1-\delta)}{1-\vartheta}\left(\frac{1}{\gamma}-\varepsilon\right)\right]^{q(\vartheta-1)}.$$

By definition, $\frac{q}{2}-\vartheta q < -1$, hence the sum is finite, and clearly $n^{q(\vartheta-1)}$ goes to zero as n tends to ∞. Hence for large enough n the sum in (3.32) is less than 1, which yields that $\mathbf{P}(H_{n,\varepsilon}) > 0$ and finishes the proof. □

Proof of Theorem 3.4. We will construct a subset $\mathcal{V} \subset \mathcal{S}$ of the event of survival, which has positive probability. On $\mathcal{V}$ we will have $A_0 = 2, I_1 = I_{-1} = 1$, as well as linearly moving left and right fronts only using parasites born on the right or left side, respectively, while parasites from the other side do not catch up to the front. For simplicity we assumed that $\mathbf{P}(A = 2) > 0, \mathbf{P}(I = 1) > 0$. In the following it will be clear how to adapt the proof to other cases.
Analogously to $(K_{n,j})_{j\geq 1,n\in\mathbb{Z}}, (\nu_{n,j})_{j\geq 1,n\in\mathbb{Z}}$, one constructs $(\hat{K}_{n,j})_{j\geq 1,n\in\mathbb{Z}}$, $(\hat{\nu}_{n,j})_{j\geq 1,n\in\mathbb{Z}}$ on $\boldsymbol{\Omega}$ by reflecting $\mathbf{I}, \mathbf{A}, \mathbf{Y}$ around the origin, i.e.,

$$\hat{K}_{n,j} = \inf\left\{k \geq j : \sum_{i=n+1}^{n+k} A_i \geq \beta_A k, \sum_{i=n}^{n+k-1} I_i \leq \beta_I k\right\},$$

$\hat{\nu}_{n,j}$ is the first time more than $\beta_I \hat{K}_{n,j}$ parasites born between $n+1$ and $n+\hat{K}_{n,j}$ reached site n. Finally setting $\hat{\nu}_n(l) := \min\{\hat{\nu}_{l-n,1}, \dots, \hat{\nu}_{l-n,n\wedge k_0}\}$ for $n \geq 1$ and $l \in \mathbb{Z}$, we observe by Lemma 3.46 that for $\gamma < \frac{1}{\mathbf{E}[\nu_{1,k_0}]}$

$$\begin{aligned}
&\mathbf{P}\left(\bigcap_{k=1}^{\infty}\{K_{k,k\wedge k_0} \leq k\}, \bigcap_{n=1}^{\infty}\left\{\sum_{k=1}^{n}\nu_k(0) \leq \frac{n}{\gamma}\right\}\right)\\
&\quad= \mathbf{P}\left(\bigcap_{k=1}^{\infty}\{\hat{K}_{k,k\wedge k_0} \leq k\}, \bigcap_{n=1}^{\infty}\left\{\sum_{k=1}^{n}\hat{\nu}_k(0) \leq \frac{n}{\gamma}\right\}\right)
\end{aligned}$$

is positive. We define the events

$$B_{\text{right}}(\gamma) := \bigcap_{x>0} \bigcap_{i=1}^{A_x} \bigcap_{t\geq 0} \left\{ x + Y_t^{x,i} > -\lfloor \gamma t \rfloor \right\},$$

$$B_{\text{left}}(\gamma) := \bigcap_{x<0} \bigcap_{i=1}^{A_x} \bigcap_{t\geq 0} \left\{ x + Y_t^{x,i} < \lfloor \gamma t \rfloor) \right\}.$$

Applying Lemma 3.43 and due to the independence of $\mathbf{Y}$ and $\mathbf{A}$, we obtain that $B_{\text{right}}(\gamma)$ is independent of $B_{\text{left}}(\gamma)$ and

$$\begin{aligned} \mathbf{P}(B_{\text{left}}(\gamma)) &= \mathbf{P}(B_{\text{right}}(\gamma)) \\ &\geq \mathbf{E}\left[\left(\exp\left(-\frac{2}{\gamma}\right) \left(1 - \mathrm{e}^{-\theta_\gamma}\right) \right)^{A_1} \right] \prod_{x=2}^{\infty} \mathbf{E}\left[\left(\left(1 - \mathrm{e}^{(1-x)\theta_\gamma}\right) \right)^{A_x} \right]. \end{aligned}$$

Taylor expanding

$$\mathbf{E}[(1-z)^A] = 1 - \mathbf{E}[A]z + h(z)z$$

for $z \in (0,1)$ and some $|h(z)| = o(1)$ as $z \to 0$, and that for some $C > 1$ we have

$$\log(1-z) \geq -Cz \quad \text{for all} \quad 0 \leq z \leq \max_{x\geq 2} \mathrm{e}^{-(1-x)\theta_\gamma} \left(\mathbf{E}[A] - h\left(\mathrm{e}^{(1-x)\theta_\gamma}\right) \right)$$

yields

$$\begin{aligned} &\prod_{x=2}^{\infty} \mathbf{E}\left[\left(1 - \mathrm{e}^{(1-x)\theta_\gamma}\right)^{A_x} \right] \\ &\quad = \exp\left(\sum_{x=2}^{\infty} \log\left(1 - \mathbf{E}[A]\, \mathrm{e}^{(1-x)\theta_\gamma} + h\left(\mathrm{e}^{(1-x)\theta_\gamma}\right) \mathrm{e}^{(1-x)\theta_\gamma}\right) \right) \\ &\quad \geq \exp\left(-\sum_{x=2}^{\infty} C\, \mathrm{e}^{(1-x)\theta_\gamma} \left(\mathbf{E}[A] - h\left(\mathrm{e}^{(1-x)\theta_\gamma}\right) \right) \right) > 0. \end{aligned}$$

In conclusion, this yields $\mathbf{P}(B_{\text{left}}(\gamma)) = \mathbf{P}(B_{\text{left}}(\gamma)) > 0$ Next we define

$$C_{\text{right}}(\gamma) := \bigcap_{k=1}^{\infty} \{K_{1+k,k\wedge k_0} \leq k\} \cap \bigcap_{n=1}^{\infty} \left\{ \sum_{k=1}^{n} \nu_k(1) \leq \frac{n}{\gamma} \right\}$$

$$C_{\text{left}}(\gamma) := \bigcap_{k=1}^{\infty} \{\hat{K}_{-1-k,k\wedge k_0} \leq k\} \cap \bigcap_{n=1}^{\infty} \left\{ \sum_{k=1}^{n} \hat{\nu}_k(-1) \leq \frac{n}{\gamma} \right\}.$$

To show that $\mathbf{P}((B_{\text{right}}(\gamma), C_{\text{right}}(\gamma)) > 0$ we will have to show an analog result as in Lemma 3.46 but under the measure $\mathbf{P}(\cdot | B_{\text{right}}(\gamma))$.

First we note that $\{Y^{x,i} : x > 0, i \in \mathbb{N}\}$ is still an independent collection, just not an identically distributed one, under the measure $\mathbf{P}(\cdot|B_{\text{right}}(\gamma))$. Because clearly the event $B_{\text{right}}(\gamma)$ gives the random walks a drift to the right, for any $x > 0, i \in \mathbb{N}$ and $n \in \mathbb{N}, t \geq 0$ we have

$$\mathbf{P}\left(\sup_{0\leq s\leq t} Y_s^{x,i} < n \,\middle|\, B_{\text{right}}(\gamma)\right) \leq \mathbf{P}\left(\sup_{0\leq s\leq t} Y_s^{x,i} < n\right).$$

Reasoning just as in Lemma 3.17, we obtain $\nu_1(1), \dots, \nu_{k_0-1}(1) < \infty$ almost surely under $\mathbf{P}(\cdot|B_{\text{right}}(\gamma))$ and $\nu_{k_0}(1), \nu_{k_0+1}(1), \dots \in L^q(\Omega, \mathcal{F}, \mathbf{P}(\cdot|B_{\text{right}}(\gamma)))$ for any $2 \leq q < \frac{\alpha+1}{2}$. Moreover, the arguments in Lemma 3.19 only depend on $\mathbf{A}$ and $\mathbf{I}$, thus $\nu_1(1), \nu_2(1), \dots$ is also ϕ-mixing under the measure $\mathbf{P}(\cdot|B_{\text{right}}(\gamma))$. Hence, one obtains analogously to the proof of Lemma 3.46 that

$$\mathbf{P}(C_{\text{right}}(\gamma)|B_{\text{right}}(\gamma)) > 0.$$

In particular, this means that for any $0 < \gamma_1 < \gamma_2 < \frac{1}{\mathbf{E}[\nu_{1,k_0}]}$ and $\varepsilon > 0$ the event $\mathcal{V}$, given by the intersection of

$\{A_0 = 2\}$ and $\{I_1 = I_{-1} = 1\}$,

Parasite $(0,1)$ jumps for the first time at time $\tau_1^{0,1} \in (1, 1+\varepsilon)$ and jumps onto site 1,

Parasite $(0,2)$ jumps for the first time at time $\tau_{-2}^{0,2} \in (1, 1+\varepsilon)$ and jumps onto site -1,

$$B_{\text{right}}(\gamma_1) \cap C_{\text{right}}(\gamma_2) \cap B_{\text{left}}(\gamma_1) \cap C_{\text{left}}(\gamma_2)$$

has positive probability. Choosing now

$$\gamma_2 \in \left(0, \frac{1}{\mathbf{E}[\nu_{1,k_0}]}\right), \quad \gamma_1 \in (0, \gamma_2), \quad \text{and} \quad \varepsilon \in \left(0, \frac{1}{\gamma_1} - \frac{1}{\gamma_2}\right)$$

we have that on the event $\mathcal{V}$ the right and left host boundaries $(r_t)_{t\geq 0}, (l_t)_{t\geq 0}$ satisfy

$$r_t \geq \begin{cases} 0, & t < \tau_1^{0,1} \\ 1 + \lfloor \gamma_2(t - \tau_1^{0,1}) \rfloor, & t \geq \tau_1^{0,1} \end{cases} \quad \text{and} \quad l_t \leq \begin{cases} 0, & t < \tau_{-1}^{0,2} \\ -1 - \lfloor \gamma_2(t - \tau_{-1}^{0,2}) \rfloor, & t \geq \tau_{-1}^{0,2}. \end{cases}$$

Recalling the sets $\mathcal{L}_t$ containing the labels of living parasites at time t, $\mathcal{G}_t$ containing the labels of parasites that died until time t, and $F_t(x,i) \in \mathbb{Z}$ as the position of the parasite with label (x, i) at time t, on the event $\mathcal{V}$ it also holds that

$$\{F_t(x,i) : (x,i) \in \mathcal{L}_t \cup \mathcal{G}_t, x > 0\} \begin{cases} = \emptyset, & t < \tau_1^{0,1} \\ \subset \mathbb{Z}_{>-\lfloor \gamma_1 (t - \tau_1^{0,1}) \rfloor}, & t \geq \tau_1^{0,1} \end{cases}$$

and

$$\{F_t(x,i) : (x,i) \in \mathcal{L}_t \cup \mathcal{G}_t, x < 0\} \begin{cases} = \emptyset, & t < \tau_{-1}^{0,2} \\ \subset \mathbb{Z}_{<\lfloor \gamma_1 (t - \tau_{-1}^{0,2}) \rfloor}, & t \geq \tau_{-1}^{0,2} \end{cases}.$$

The choice of parameters gives us now that

$$\begin{aligned} \forall t \geq \tau_1^{0,1} : \min_{\substack{(x,i) \in \mathcal{L}_t \cup \mathcal{G}_t, \\ x > 0}} F_t(x,i) > l_t \\ \forall t \geq \tau_{-1}^{0,2} : \max_{\substack{(x,i) \in \mathcal{L}_t \cup \mathcal{G}_t, \\ x < 0}} F_t(x,i) < r_t. \end{aligned}$$

In words, any parasite born on some $x > 0$ moves slower than with linear speed γ_1 to the left and thus never catches up to the left front of hosts, which moves at least at linear speed γ_2, and vice versa for parasites born on $x < 0$. Hence, on the given event, the actual process with both directions filled with hosts moves just as two copies of the process with just one side filled, conditioned on the event $B_{\text{right}}(\gamma_1) \cap C_{\text{right}}(\gamma_2)$. As by definition of the event $C_{\text{right}}(\gamma_2)$ these processes survive, we obtain the survival of the process with initially all sites $x \neq 0$ inhabited by a host. □

3.5 Construction of the spatial infection model with host immunity

In this section we formally construct the SIMI on $\mathbb{Z}$ with initial configurations as above as a strong Markov process on some probability space. We construct the process in two different ways. The first is to assign each parasite a label and sample its entire path after it enters the system by picking from a collection of i.i.d. simple symmetric random walks $(Y^{x,i})_{x \in \mathbb{Z}, i \in \mathbb{N}}$. Of course the sampled path will become a virtual path once the parasite has died; nonetheless, it is still sampled entirely, as this is needed to construct the auxiliary jump times. We will call the so-constructed process the *tagged* system.

The second construction is to assign each site x in $\mathbb{Z}$ with a collection of Poisson point processes $\{P_{x,n}^{\rightarrow}, P_{x,n}^{\leftarrow} : n \in \mathbb{N}\}$, which will be used to determine the jump times and directions of parasites leaving the site x, where only the Poisson point processes with index $n \leq \eta_{t-}(x)$ are allowed to be used. In this construction we won't be tracking each parasite individually, but only the amounts of parasites on each site. We call the so-constructed process the *untagged* system. The natural coupling for different initial configurations in this system will allow us to show that the front is almost surely monotone in the initial configuration, whereas for the tagged system, as Example 3.51 shows, this is not the case. Using this monotone coupling, we can then follow the lines of [15] to show the Feller property of the constructed Markov process.

3.5.1 Tagged system

We first construct the process in a coupled way for any finite starting configuration and then define the process for arbitrary starting configurations as the almost sure limit of the processes started in certain approximating, finite initial configurations. We will carry out this construction in detail. A similar construction is used in [15, 16], but they rely on an almost sure monotonicity argument that, as we will see in Example 3.51, does not hold in our case. However, we follow the same approach of first defining the process for initial configurations with finitely many parasites and then extending it to infinitely many parasites by performing a limit in the state space.

In Definition 3.47 we give the state space in which the limit will be defined, and in Proposition 3.49 we show that this space is Polish. In Proposition 3.52 we then show the claimed convergence, and in Theorem 3.5 we show the strong Markov property of the process.

We consider a probability space $\mathbf{\Omega}' = (\Omega', \mathcal{F}', \mathbf{P}')$ on which the following independent random variables are defined.

There is a simple symmetric random walk starting in 0 and jumping at rate 2 called $Y = (Y_t)_{t\geq 0}$ and an independent collection

$$\mathbf{Y} := \{Y^{x,i} : x \in \mathbb{Z}, i \in \mathbb{N}\}$$

of simple symmetric random walks starting in 0 and jumping at rate 2.

There is an $\mathbb{N}_0$-valued random variable $A \in L^1(\mathbf{\Omega}')$ and a collection

$$\mathbf{A} := \{A_k : k \in \mathbb{Z}\}$$

of i.i.d. $\mathbb{N}_0$-valued variables, distributed as A.
There is an $\mathbb{N}$-valued random variable $I \in L^1(\boldsymbol{\Omega}')$ and a collection

$$\mathbf{I} := \{I_k : k \in \mathbb{Z}\}$$

of i.i.d. $\mathbb{N}$-valued variables, distributed as I.
We give the construction of the process for a one-sided host population. The simpler case of a two-sided host population is treated in Remark 3.50. To begin the construction, we first specify the state space of the process. Because of the geometry of $\mathbb{Z}$ and since parasites jump only to nearest neighbors, the set of sites occupied by hosts and the set of sites free of hosts is separated by a single site $r \in \mathbb{Z}$, which we call the (right) front in the following. In the definition of the approximating jump times $\{\nu_n : n \in \mathbb{Z}\}$, we used the virtual paths of ghost parasites after their birth. For this reason, we include those in the state space and make the following definition.

Definition 3.47. *A parasite configuration is a 5-tuple $w = (r, \mathcal{L}, \mathcal{G}, F, \iota)$ with*

$$r \in \mathbb{Z}, \mathcal{L}, \mathcal{G} \subset \mathbb{Z} \times \mathbb{N}, F : \mathcal{L} \cup \mathcal{G} \to \mathbb{Z}, \iota \in \mathbb{N}$$

such that

- *parasites are either dead or alive: $\mathcal{L} \cap \mathcal{G} = \emptyset$,*
- *hosts to the right of r are not yet infected:*

$$\sup\{x \in \mathbb{Z} | \exists i \in \mathbb{N} : (x,i) \in \mathcal{L} \cup \mathcal{G}\} \leq r,$$

- *living parasites cannot sit on top of hosts:* $\sup\{F(x,i) : (x,i) \in \mathcal{L}\} \leq r$,
- *and the technical conditions that for some $\theta > 0$*

$$\sum_{(x,i) \in \mathcal{L}} \exp(\theta F(x,i)) < \infty \qquad \text{and} \qquad |\mathcal{G}| < \infty. \tag{3.33}$$

For $\theta > 0$ we denote by $\mathbb{L}_\theta$ the space of all parasite configurations that satisfy (3.33) *and define*

$$\begin{aligned} \xi(w, w', x, i) &:= \left| \mathbb{1}_{(x,i) \in \mathcal{L}}\, \mathrm{e}^{\theta(F(x,i) - r)} - \mathbb{1}_{(x,i) \in \mathcal{L}'}\, \mathrm{e}^{\theta(F'(x,i) - r')} \right|, \\ \xi'(w, w', x, i) &:= |\mathbb{1}_{(x,i) \in \mathcal{G}} F(x,i) - \mathbb{1}_{(x,i) \in \mathcal{G}'} F'(x,i)| \end{aligned}$$

for $w = (r, \mathcal{L}, \mathcal{G}, F, \iota), w' \in \mathbb{L}_\theta, (x,i) \in \mathbb{Z} \times \mathbb{N}$, *in order to define the metric* d_θ *on* $\mathbb{L}_\theta$ *by*

$$d_\theta(w,w') := |r - r'| + |\iota - \iota'| + \sum_{(x,i)\in\mathbb{Z}\times\mathbb{N}} \xi(w,w',x,i) + \xi'(w,w',x,i).$$

Remark 3.48. *For a configuration* $w = (r, \mathcal{L}, \mathcal{G}, F, \iota)$*, the site* r *will be the rightmost site without host cells. The set* $\mathcal{L}$*, called living parasites, will be the birth labels of parasites that are still alive, and* $\mathcal{G}$*, called ghost parasites, will be the birth labels of parasites that were alive at some time but already died.* F *assigns each parasite its current position, and* ι *is the immunity of site* $r+1$*, or equivalently the number of attempts needed before the next successful infection.*

As we will see later, the metric d_θ is sufficient to define the process for initial configurations with infinitely many parasites, by approximation with finitely many parasites. But first we need to make sure that the state space above has at least some good properties.

Proposition 3.49. *Let* $\theta > 0$*, then* $(\mathbb{L}_\theta, d_\theta)$ *defined above is a complete and separable metric space. Also,* $(\mathbb{L}_\theta, d_\theta)$ *is not locally compact.*

Proof. It is clear that d_θ defines a metric. Moreover, because $\mathbb{L}_\theta$ contains the function space

$$\left\{ \eta : \mathbb{N}_0 \to \mathbb{N}_0 : \sum_{n=0}^{\infty} \eta(n)\, \mathrm{e}^{-\theta n} < \infty \right\}$$

it cannot be locally compact, simply by considering the sequence of configurations placing $\lfloor \varepsilon\, \mathrm{e}^{\theta n} \rfloor$ living parasites on site $r - n$ and leaving all other sites empty, which is a sequence with no convergent subsequence in a ε-Ball.
Now we show that $(\mathbb{L}_\theta, d_\theta)$ is separable. The set

$$\mathbb{A} := \{(r, \mathcal{L}, \mathcal{G}, F, \iota) \in \mathbb{L}_\theta : |\mathcal{L}| < \infty\}$$

is countable, which can be seen by observing that as sets

$$\begin{aligned}\mathbb{A} &= \bigcup_{k=0}^{\infty} \bigcup_{m=0}^{\infty} \{(r, \mathcal{L}, \mathcal{G}, F, \iota) \in \mathbb{L}_\theta : |\mathcal{L}| = k\ , |\mathcal{G}| = m\} \\ &\overset{\sim}{\subset} \bigcup_{k=0}^{\infty} \bigcup_{m=0}^{\infty} \mathbb{Z} \times \binom{\mathbb{Z}\times\mathbb{N}}{k} \times \binom{\mathbb{Z}\times\mathbb{N}}{m} \times \mathbb{Z}^{m+k} \times \mathbb{N}.\end{aligned}$$

For $l \geq 1$ we define a map $w^l : \mathbb{L}_\theta \to \mathbb{A}$ as follows. For $w = (r, \mathcal{L}, \mathcal{G}, F, \iota)$ set

$$\mathcal{L}^l(w) := \{(x,i) \in \mathcal{L} : F(x,i) > r - l\} \text{ and } w^l(w) := \Big(r, \mathcal{L}^l(w), \mathcal{G}, F_{|_{\mathcal{L}^l(w)\cup\mathcal{G}}}, \iota\Big),$$

that is, we consider only living parasites that are placed at a distance less than l to the front. Using (3.33), and that by definition $F(x,i) - r + l > 0$ for all $(x,i) \in \mathcal{L}^l(w)$, we obtain

$$|\mathcal{L}^l(w)| < \mathrm{e}^{\theta l} \sum_{(x,i)\in\mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) < \infty.$$

Thus $w^l(w) \in \mathbb{A}$ for all $l \in \mathbb{N}, w \in \mathbb{L}_\theta$. Since

$$\mathcal{L}^1(w) \subset \mathcal{L}^2(w) \subset \dots \quad \text{and} \quad \mathcal{L} = \bigcup_{l=1}^{\infty} \mathcal{L}^l(w),$$

Condition (3.33) yields

$$d_\theta(w, w^l(w)) = \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) \to 0 \quad (l \to \infty).$$

This shows that $\mathbb{A}$ is dense, and thus $\mathbb{L}_\theta$ is separable.
Next, we show that $\mathbb{L}_\theta$ is also complete. Suppose that

$$(w_n)_{n\in\mathbb{N}} = ((r_n, \mathcal{L}_n, \mathcal{G}_n, F_n, \iota_n))_{n\in\mathbb{N}}$$

is a Cauchy sequence in $\mathbb{L}_\theta$. Choosing $\varepsilon = 1$ we find an $N_0 \in \mathbb{N}$ such that $d_\theta(w_n, w_m) < 1$ for all $n, m \geq N_0$. Since $d_\theta(w_n, w_m)$ is at least

$$|r_n - r_m| + |\iota_n - \iota_m| + \sum_{(x,i)\in\mathcal{G}_n\cup\mathcal{G}_m} |\mathbb{1}_{(x,i)\in\mathcal{G}_n} F_n(x,i) - \mathbb{1}_{(x,i)\in\mathcal{G}_m} F_m(x,i)|,$$

which is integer valued, this implies that there is an $r \in \mathbb{Z}, \mathcal{G} \subset \mathbb{Z} \times \mathbb{N}, \iota \in \mathbb{N}$ and $\widetilde{F} : \mathcal{G} \to \mathbb{Z}$ such that

$$r_n = r, \quad \mathcal{G}_n = \mathcal{G}, \quad (F_n)_{|\mathcal{G}} = \widetilde{F}, \quad \iota_n = \iota$$

for all $n \geq N_0$. This yields that for $m, n \geq N_0$ we have

$$d(w_n, w_m) = \sum_{(x,i)\in\mathbb{Z}\times\mathbb{N}} \mathrm{e}^{-\theta r} \left| \mathbb{1}_{(x,i)\in\mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i)\in\mathcal{L}_m} \mathrm{e}^{\theta F_m(x,i)} \right|.$$

For $l \in \mathbb{N}$, setting

$$\varepsilon(l) := \mathrm{e}^{-\theta(l-1)} - \mathrm{e}^{-\theta l},$$

we define

$$N_l := \inf\{N \geq N_{l-1} | \forall m, n \geq N : d(w_n, w_m) < \varepsilon(l)\}.$$

By definition of $\varepsilon(l)$, this means that $w^l(w_n) = w^l(w_m)$ for all $l \in \mathbb{N}$ and $m, n \geq N_l$. We define

$$\mathcal{L} := \bigcup_{l=1}^{\infty} \mathcal{L}^l(w_{N_l}),$$

as well as $F : \mathcal{L} \cup \mathcal{G} \to \mathbb{Z}$ by

$$F(x,i) := \mathbb{1}_{(x,i)\in\mathcal{L}} F_{N_l}(x,i) + \mathbb{1}_{(x,i)\in\mathcal{G}} \widetilde{F}(x,i),$$

where $l \in \mathbb{N}$ is such that $(x,i) \in \mathcal{L}^l(w_{N_l})$ and set $w := (r, \mathcal{L}, \mathcal{G}, F, \iota)$, noting that for $l \in \mathbb{N}$ we have $w^l(w) = w^l(w_{N_l})$. Now let $\varepsilon > 0$ and $L \in \mathbb{N}$ such that

$$\varepsilon(L) \leq \varepsilon.$$

For fixed $l > L$ and all $n, m \geq N_L$ we have $w^L(w_n) = w^L(w_m) = w^L(w)$ and obtain

$$\begin{aligned}
&\sum_{(x,i)\in\mathcal{L}^l(w_n)\cup\mathcal{L}^l(w_m)} \mathrm{e}^{-\theta r} \left|\mathbb{1}_{(x,i)\in\mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i)\in\mathcal{L}_m} \mathrm{e}^{\theta F_m(x,i)}\right| \\
=& \sum_{(x,i)\in(\mathcal{L}^l(w_n)\cup\mathcal{L}^l(w_m))\setminus\mathcal{L}^L(w)} \mathrm{e}^{-\theta r} \left|\mathbb{1}_{(x,i)\in\mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i)\in\mathcal{L}_m} \mathrm{e}^{\theta F_m(x,i)}\right| \\
\leq& \sum_{(x,i)\in(\mathcal{L}_n\cup\mathcal{L}_m)\setminus\mathcal{L}^L(w)} \frac{\mathrm{e}^{-\theta r}}{1-\mathrm{e}^{-\theta}} \left|\mathbb{1}_{(x,i)\in\mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i)\in\mathcal{L}_m} \mathrm{e}^{\theta F_m(x,i)}\right| \\
=& \frac{d_\theta(w_n, w_m)}{1-\mathrm{e}^{-\theta}} < \frac{\varepsilon}{1-\mathrm{e}^{-\theta}},
\end{aligned}$$

where the inequality in the third line can be shown as follows. For each $(x,i) \in (\mathcal{L}_n \cup \mathcal{L}_m) \setminus \mathcal{L}^L(w)$ we distinguish between four cases

$$\begin{aligned}
\text{I: } &(x,i) \notin \mathcal{L}^l(w_n) \text{ and } (x,i) \notin \mathcal{L}^l(w_m) \\
\text{II: } &(x,i) \in \mathcal{L}^l(w_n) \text{ and } (x,i) \notin \mathcal{L}^l(w_m) \\
\text{III: } &(x,i) \notin \mathcal{L}^l(w_n) \text{ and } (x,i) \in \mathcal{L}^l(w_m) \\
\text{IV: } &(x,i) \in \mathcal{L}^l(w_n) \text{ and } (x,i) \in \mathcal{L}^l(w_m).
\end{aligned}$$

In the first case we just added a positive term so the inequality holds, and in the last case we just divided the already existing term by $1 - \mathrm{e}^{-\theta} < 1$, which only makes it larger. In the second case we have to show that

$$\mathrm{e}^{\theta(F_n(x,i)-r)} \leq \frac{\exp(\theta(F_n(x,i)-r)) - \exp(\theta(F_m(x,i)-r))}{1-\mathrm{e}^{-\theta}}.$$

Because $(x,i) \notin \mathcal{L}^l(w_m)$, it holds that $F_m(x,i) - r \leq -l$ and $(x,i) \in \mathcal{L}^l(w_n) \setminus \mathcal{L}^L(w_n)$ implies $-l < F_n(x,i) - r \leq -L$. Hence, it remains to show that

$$\mathrm{e}^{-\theta y} \leq \frac{\mathrm{e}^{-\theta y} - \mathrm{e}^{-\theta z}}{1 - \mathrm{e}^{-\theta}}$$

for all $y \in \{L, \ldots, l-1\}, z \geq l$. For fixed y, the right-hand side is clearly increasing in z, and thus it suffices to show the inequality for $z = l$. But for $z = l$ we have that

$$\frac{\mathrm{e}^{-\theta y}}{\mathrm{e}^{-\theta y} - \mathrm{e}^{-\theta l}} = \frac{1}{1 - \mathrm{e}^{-\theta(l-y)}},$$

which attains its maximum at $y = l - 1$ and thus yields the claimed inequality. The third case is analogous to the second one.
Hence, letting $m \to \infty$, we obtain

$$\sum_{(x,i) \in \mathcal{L}^l(w_n) \cup \mathcal{L}^l(w)} \mathrm{e}^{-\theta r} \left| \mathbb{1}_{(x,i) \in \mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i) \in \mathcal{L}} \mathrm{e}^{\theta F(x,i)} \right| \leq \frac{\varepsilon}{1 - \mathrm{e}^{-\theta}}$$

for any $n \geq N_L$. Thus

$$\begin{aligned}
&\sum_{(x,i) \in \mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) \\
&\quad \leq \sum_{(x,i) \in \mathcal{L}^l(w_n) \cup \mathcal{L}^l(w)} \mathrm{e}^{-\theta r} \left| \mathbb{1}_{(x,i) \in \mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i) \in \mathcal{L}} \mathrm{e}^{\theta F(x,i)} \right| \\
&\qquad + \sum_{(x,i) \in \mathcal{L}^l(w_n)} \exp(\theta(F_n(x,i) - r)) \\
&\quad \leq \frac{\varepsilon}{1 - \mathrm{e}^{-\theta}} + \sum_{(x,i) \in \mathcal{L}_n} \exp(\theta(F_n(x,i) - r)) < \infty.
\end{aligned}$$

Letting $l \to \infty$ yields $w \in \mathbb{L}_\theta$ and

$$d(w_n, w) = \sum_{(x,i) \in \mathcal{L}_n \cup \mathcal{L}} \mathrm{e}^{-\theta r} \left| \mathbb{1}_{(x,i) \in \mathcal{L}_n} \mathrm{e}^{\theta F_n(x,i)} - \mathbb{1}_{(x,i) \in \mathcal{L}} \mathrm{e}^{\theta F(x,i)} \right| \leq \frac{\varepsilon}{1 - \mathrm{e}^{-\theta}}$$

for any $n \geq N_L$, thus

$$\lim_{n \to \infty} w_n = w$$

in $\mathbb{L}_\theta$. This shows that $(\mathbb{L}_\theta, d_\theta)$ is complete and thus finishes the proof. □

We begin by constructing the process for a finite starting configuration. That is, for any $w \in \mathbb{A}$ we now use the collections $\mathbf{Y}, \mathbf{A}, \mathbf{I}$ to define a strong Markov process

$$(X_t(w))_{t \geq 0} = ((r_t, \mathcal{L}_t, \mathcal{G}_t, F_t, \iota_t)(w))_{t \geq 0}$$

with càdlàg sample paths in $\mathbb{A}$ on the probability space $\mathbf{\Omega}'$.

Let $w \in \mathbb{A}$ and set $\sigma_0 := 0, \rho_0 = 0, r_0 := r, \iota_0 := \iota, \mathcal{L}_0 := \mathcal{L}, \mathcal{G}_0 = \mathcal{G}$ and

$$F_t(x,i) := F(x,i) + Y_t^{x,i} \text{ for all } (x,i) \in \mathcal{L}_0 \cup \mathcal{G}_0, t \geq \sigma_0.$$

Assume that for $n \geq 0$ we have already defined

$$\sigma_0, \dots, \sigma_n, \quad (r_t, \mathcal{L}_t, \mathcal{G}_t, F_t, \iota_t) \in \mathbb{A} \text{ for all } 0 \leq t \leq \sigma_n \text{ and } \rho_0, \dots, \rho_{r_{\sigma_n}-r} \leq \sigma_n.$$

If $\mathcal{L}_{\sigma_n} = \emptyset$, we set $r_t = r_{\sigma_n}, \mathcal{L}_t = \emptyset, \mathcal{G}_t = \mathcal{G}_{\sigma_n}, \iota_t = \iota_{\sigma_n}$ for all $t > \sigma_n$ and $\sigma_m = \infty$ for all $m > n$.

Otherwise, if $\mathcal{L}_{\sigma_n} \neq \emptyset$, let

$$\sigma_{n+1} := \inf\{t > \sigma_n \mid \exists (x,i) \in \mathcal{L}_{\sigma_n} : F_t(x,i) = r_{\sigma_n} + 1\}.$$

By construction we have $0 < |\mathcal{L}_{\sigma_n}| \leq |\mathcal{L}| + \sum_{i=1}^n A_{r+i} < \infty$, thus $\sigma_n < \sigma_{n+1} < \infty$ almost surely, and there is almost surely a unique $(x_n, i_n) \in \mathcal{L}_{\sigma_n}$ such that $F_{\sigma_{n+1}}(x_n, i_n) = r_{\sigma_n} + 1$. Moreover, $\sigma_{n+1} - \sigma_n$ is stochastically dominated by an exponentially distributed random variable with random parameter $|\mathcal{L}| + \sum_{i=1}^n A_{r+i}$, corresponding to the case that any previous infection was successful, all living parasites are located on r_{σ_n}, and the first jump goes to the right. In particular, because $\mathbf{E}[A] < \infty$ and thus

$$\sum_{n=0}^{\infty} \frac{1}{|\mathcal{L}| + \sum_{i=1}^n A_{r+i}} = \infty$$

almost surely, this implies that $\lim_{n\to\infty} \sigma_n = \infty$ almost surely.

For $t \in (\sigma_n, \sigma_{n+1})$ we set $r_t = r_{\sigma_n}, \iota_t = \iota_{\sigma_n}, \mathcal{L}_t = \mathcal{L}_{\sigma_n}, \mathcal{G}_t = \mathcal{G}_{\sigma_n}$ and then finally set $\mathcal{G}_{\sigma_{n+1}} = \mathcal{G}_{\sigma_n} \cup \{(x_n, i_n)\}$.

- If $\iota_{\sigma_n} = 1$: Set $r_{\sigma_{n+1}} = r_{\sigma_n} + 1, \iota_{\sigma_{n+1}} = I_{r_{\sigma_n}+1}, \rho_{r_{\sigma_{n+1}}-r} = \sigma_{n+1}$. Also, if $A_{r_{\sigma_{n+1}}} > 0$ set

  $$\mathcal{L}_{\sigma_{n+1}} = \mathcal{L}_{\sigma_n} \setminus \{(x_n, i_n)\} \cup \{(r_{\sigma_{n+1}}, 1), \dots, (r_{\sigma_{n+1}}, A_{r_{\sigma_{n+1}}})\}$$

  with $F_t(r_{\sigma_{n+1}}, i) = r_{\sigma_{n+1}} + Y_{t-\sigma_{n+1}}^{r_{\sigma_{n+1}}, i}$ for $1 \leq i \leq A_{r_{\sigma_{n+1}}}, t \geq \sigma_{n+1}$, and if $A_{r_{\sigma_{n+1}}} = 0$ set

  $$\mathcal{L}_{\sigma_{n+1}} = \mathcal{L}_{\sigma_n} \setminus \{(x_n, i_n)\}.$$

- If $\iota_{\sigma_n} > 1$: Set $r_{\sigma_{n+1}} = r_{\sigma_n}, \iota_{\sigma_{n+1}} = \iota_{\sigma_n} - 1$ and

  $$\mathcal{L}_{\sigma_{n+1}} = \mathcal{L}_{\sigma_n} \setminus \{(x_n, i_n)\}.$$

Remark 3.50. *If the host population is two-sided, then any initial configuration considered contains only finitely many parasites. Hence the above construction can easily be adapted to construct the process in this case.*

Before we continue and define $((X_t(w))_{t\geq 0}$ for any $w \in \mathbb{L}_\theta$ by using the approximation $\lim_{l\to\infty} w^l(w) = w$ in $\mathbb{L}_\theta$, we will show some useful inequalities. For $w = (r, \mathcal{L}, \mathcal{G}, F, \iota) \in \mathbb{L}_\theta$ and $(x, i) \in \mathcal{L} \cup \mathcal{G}, m \in \mathbb{N}_0$ we set $[m] = \{1, \dots, m\}$ and define the maps

$$\begin{aligned} F^{(x,i),\pm}(w) &: \mathcal{L} \cup \mathcal{G} \to \mathbb{Z} \\ (y,j) &\mapsto \begin{cases} F(x,i) \pm 1, & (y,j) = (x,i) \\ F(y,j), & \text{else} \end{cases} \\ F^{(x,i),m}(w) &: \mathcal{L} \cup \{r+1\} \times [m] \cup \mathcal{G} \to \mathbb{Z} \\ (y,j) &\mapsto \begin{cases} r+1, & y = r+1 \text{ or } (y,j) = (x,i) \\ F(y,j), & \text{else} \end{cases} \end{aligned}$$

and note that for $m = 0$ we have $F^{(x,i),0} = F^{(x,i),+}$. With these maps, for $m \in \mathbb{N}_0, k \in \mathbb{N}$ and $(x, i) \in \mathcal{L} \cup \mathcal{G}$ we define the configurations

$$\begin{aligned} w^{(x,i),\pm} &:= (r, \mathcal{L}, \mathcal{G}, F^{(x,i),\pm}(w), \iota), \\ w^{(x,i),m,k} &:= (r+1, \mathcal{L} \setminus \{(x,i)\} \cup \{r+1\} \times [m], \mathcal{G} \cup \{(x,i)\}, F^{(x,i),m}(w), k) \\ w^{(x,i),\,\mathrm{f}} &:= (r, \mathcal{L} \setminus \{(x,i)\}, \mathcal{G} \cup \{(x,i)\}, F^{(x,i),+}(w), \iota - 1). \end{aligned}$$

For $\vartheta \geq \theta$ we define the functions

$$\begin{aligned} f_\vartheta &: \mathbb{L}_\theta \to \mathbb{R} \\ w &\mapsto \sum_{(x,i)\in\mathcal{L}\cup\mathcal{G}} \exp(\vartheta F(x,i)). \end{aligned}$$

and note that

$$\begin{aligned} |f_\vartheta(w^{(x,i),\pm}) - f_\vartheta(w)| &= \mathrm{e}^{\vartheta F(x,i)} \left| \mathrm{e}^{\pm\vartheta} - 1 \right| \\ |f_\vartheta(w^{(x,i),m,k}) - f_\vartheta(w)| &= \mathrm{e}^{\vartheta r} \left(\mathrm{e}^{\vartheta}(m+1) - 1 \right) \\ |f_\vartheta(w^{(x,i),\mathrm{f}}) - f_\vartheta(w)| &= \mathrm{e}^{\vartheta r} \left(\mathrm{e}^{\vartheta} - 1 \right). \end{aligned}$$

A simple calculation shows that for any $w \in \mathbb{A}$ we have

$$\begin{aligned} Lf_\vartheta(w) &:= \lim_{t \to 0+} \frac{\mathbf{E}[f_\vartheta(X_t(w)) - f_\vartheta(w)]}{t} \\ &= \sum_{(x,i) \in \mathcal{L} \setminus \mathcal{L}^1(w) \cup \mathcal{G}} f_\vartheta(w^{(x,i),+}) + f_\vartheta(w^{(x,i),-}) - 2f_\vartheta(w) \\ &\quad + \sum_{(x,i) \in \mathcal{L}^1(w)} f_\vartheta(w^{(x,i),-}) + \mathbb{1}_{\iota=1} \sum_{m=0}^{\infty} \sum_{k=1}^{\infty} b_m e_k f_\vartheta(w^{(x,i),m,k}) \\ &\qquad + \mathbb{1}_{\iota>1} f_\vartheta(w^{(x,i),\,\mathrm{f}}) - 2f_\vartheta(w), \end{aligned}$$

where $e_k = \mathbf{P}(I = k)$ and $b_m = \mathbf{P}(A = m)$. This immediately follows from the construction of $X_t(w)$ using a finite subset of $\mathbf{Y}, \mathbf{I}, \mathbf{A}$. To shorten notation we set

$$\mathbb{1}_{\iota=1} \sum_{m=0}^{\infty} \sum_{k=1}^{\infty} b_m e_k =: \sum_{m,k} \delta_m^k,$$

and compute

$$\begin{aligned} Lf_\vartheta(w) = &\sum_{(x,i) \in \mathcal{L} \setminus \mathcal{L}^1(w) \cup \mathcal{G}} \sum_{(y,j) \in \mathcal{L} \cup \mathcal{G}} \mathrm{e}^{\vartheta F^{(x,i),+}(y,j)} + \mathrm{e}^{\vartheta F^{(x,i),-}(y,j)} - 2\,\mathrm{e}^{\vartheta F(y,j)} \\ &+ \sum_{(x,i) \in \mathcal{L}^1(w)} \Bigg(\sum_{(y,j) \in \mathcal{L} \cup \mathcal{G}} \mathrm{e}^{\vartheta F^{(x,i),-}(y,j)} - 2\,\mathrm{e}^{\vartheta F(y,j)} \\ &\qquad + \sum_{m,k} \delta_m^k \sum_{(y,j) \in \mathcal{L} \cup \{r+1\} \times [m] \cup \mathcal{G}} \mathrm{e}^{\vartheta F^{(x,i),m,k}(y,j)} \\ &\qquad + \mathbb{1}_{\iota>1} \sum_{(y,j) \in \mathcal{L} \cup \mathcal{G}} \mathrm{e}^{\vartheta F^{(x,i),+}(y,j)} \Bigg) \\ = &\sum_{(x,i) \in \mathcal{L} \setminus \mathcal{L}^1(w) \cup \mathcal{G}} \mathrm{e}^{\vartheta(F(x,i)+1)} + \mathrm{e}^{\vartheta(F(x,i)-1)} - 2\,\mathrm{e}^{\vartheta F(x,i)} \\ &+ \sum_{(x,i) \in \mathcal{L}^1(w)} \mathrm{e}^{\vartheta(r-1)} - 2\,\mathrm{e}^{\vartheta r} \\ &+ \sum_{m,k} \delta_m^k \Bigg(\mathrm{e}^{\vartheta(r+1)} + \sum_{(y,j) \in \{r+1\} \times [m]} \mathrm{e}^{\vartheta(r+1)} \Bigg) \\ &+ \mathbb{1}_{\iota>1}\,\mathrm{e}^{\vartheta(r+1)} \\ = &\sum_{(x,i) \in \mathcal{L} \setminus \mathcal{L}^1(w)} \mathrm{e}^{\vartheta F(x,i)} (\mathrm{e}^{\vartheta} + \mathrm{e}^{-\vartheta} - 2) \\ &+ \sum_{(x,i) \in \mathcal{L}^1(w)} \mathrm{e}^{\vartheta r} \left(\mathrm{e}^{-\vartheta} - 2 + \left(1 + \mathbb{1}_{\iota=1} \sum_{m=0}^{\infty} m b_m \right) \mathrm{e}^{\vartheta} \right) \end{aligned}$$

This shows that $Lf_\vartheta(w) \in [\lambda_{1,\vartheta} f_\vartheta(w), \lambda_{2,\vartheta} f_\vartheta(w)]$ for

$$0 < \mathrm{e}^{\vartheta} + \mathrm{e}^{-\vartheta} - 2 =: \lambda_{1,\vartheta} < \mathrm{e}^{-\vartheta} - 2 + (1 + \mathbf{E}[A])\, \mathrm{e}^{\vartheta} =: \lambda_{2,\vartheta}.$$

Thus

$$\mathbf{E}[f_\vartheta(X_t(w))] \leq \mathrm{e}^{\lambda_{2,\vartheta} t}\, f_\vartheta(w) \tag{3.34}$$

and $(f_\vartheta(X_t(w)))_{t\geq 0}$ is a nonnegative submartingale. Doob's inequality yields

$$\mathbf{P}\left(\sup_{0\leq s\leq t} f_\vartheta(X_s(w)) \geq M\right) \leq \frac{\mathbf{E}[f_\vartheta(X_t(w))]}{M}.$$

Since by definition

$$r_t(w) = \begin{cases} \sup_{0\leq s\leq t} \sup_{(x,i)\in\mathcal{L}_s(w)} F_s(w)(x,i), & \text{if } \sup_{0\leq s\leq t} \max_{(x,i)\in\mathcal{L}} F_s(x,i) \geq r \\ r, & \text{else} \end{cases}$$

we obtain for $t \geq 0$ that

$$\begin{aligned} \mathbf{P}(r_t(w) - r > \gamma t) &= \mathbf{P}\left(r_t(w) - r > \gamma t,\ \sup_{0\leq s\leq t} \max_{(x,i)\in\mathcal{L}} F_s(x,i) \geq r\right) \\ &= \mathbf{P}\left(\sup_{0\leq s\leq t} \sup_{(x,i)\in\mathcal{L}_s(w)} F_s(w)(x,i) - r > \gamma t,\ \sup_{0\leq s\leq t} \max_{(x,i)\in\mathcal{L}} F_s(x,i) \geq r\right) \\ &\leq \mathbf{P}\left(\sup_{0\leq s\leq t} f_\vartheta(X_s(w)) > \mathrm{e}^{\vartheta(r+\gamma t)}\right) \leq \mathrm{e}^{-c_{\gamma,\vartheta} t}\, f_\vartheta(w)\, \mathrm{e}^{-\vartheta r}, \end{aligned} \tag{3.35}$$

with $c_{\gamma,\vartheta} := \gamma\vartheta - \lambda_{2,\vartheta} > 0$ for large γ.

Similarly as in [16], we constructed the model in a way that allows us to couple arbitrary initial configurations $w \in \mathbb{A}$. However, in our coupling the front $(r_t(w))_{t\geq 0}$ is not monotone in the initial condition. To see this, we give the following concrete example.

Example 3.51. Let

$$\mathcal{L}_1 = \{(1,1),(1,2)\}, \mathcal{L}_2 = \mathcal{L}_1 \cup \{(0,1),(0,2)\}$$

and

$$w_i = (1, \mathcal{L}_i, \emptyset, (x,i) \mapsto x, 1) \quad (i \in \{1,2\}).$$

We will show that for all $t_0 > 0$

$$\mathbf{P}(r_{t_0}(w_1) \geq 4, r_{t_0}(w_2) \leq 3) > 0.$$

For a label $(x, i) \in \mathbb{Z} \times \{1, 2\}$ let $(t^n_{x,i})_{n\in\mathbb{N}}$ be the i.i.d. Exp(2)-distributed jump times of $Y^{x,i}$. We assume that all jumps occurring are jumps to the right, $I_2 = I_3 = I_4 = 1$, i.e., every infection attempt is successful, and $A_2 = A_3 = A_4 = 2$, which clearly has positive probability. We begin by investigating the system started from configuration 2, where initially $(0, 1), (0, 2), (1, 1), (1, 2)$ are active. Assume

$$t^1_{0,2} > t_0, \tag{3.36}$$

and hence particle $(0, 2)$ does not move at all before time t_0, which happens with positive probability. Next, assume that

$$t^1_{0,1} + t^2_{0,1} < \min\{t^1_{1,1}, t^1_{1,2}\} \tag{3.37}$$

hence particle $(0, 1)$ is the first which reaches site 2 and dies, after waking up particles on site 2 at time $t^1_{0,1} + t^2_{0,1}$. Next, we assume

$$t^1_{0,1} + t^2_{0,1} + t^1_{2,1} < \min\{t^1_{1,1} + t^2_{1,1}, t^1_{1,2} + t^2_{1,2}, t^1_{0,1} + t^2_{0,1} + t^1_{2,2}\}, \tag{3.38}$$

so that particle $(2, 1)$ wakes up the particles on site 3 and dies at time $t^1_{0,1} + t^2_{0,1} + t^1_{2,1}$. At last, we assume

$$t^1_{1,1} + t^2_{1,1} + t^3_{1,1} < \min\left\{\begin{matrix} t^1_{1,2} + t^2_{1,2} + t^3_{1,2}, t^1_{0,1} + t^2_{0,1} + t^1_{2,2}, \\ t^1_{0,1} + t^2_{0,1} + t^1_{2,1} + t^1_{3,1}, t^1_{0,1} + t^2_{0,1} + t^1_{2,1} + t^1_{3,2} \end{matrix}\right\} \tag{3.39}$$

and hence particle $(1, 1)$ wakes up the particles on site 4 at time $T_2 = t^1_{1,1} + t^2_{1,1} + t^3_{1,1}$.

Next, we study the system started in configuration 1, where initially only $\{(1, 1), (1, 2)\}$ are active. We assume

$$t^1_{1,1} < t^1_{1,2} \tag{3.40}$$

and hence particle $(1, 1)$ dies when waking up the particles on site 2. Next we assume

$$t^1_{1,2} + t^2_{1,2} < \min\{t^1_{1,1} + t^1_{2,1}, t^1_{1,1} + t^1_{2,2}\} \tag{3.41}$$

which means particle $(1, 2)$ dies when waking up the particles on site 3. Next we assume that

$$t^1_{1,1} + t^1_{2,1} + t^2_{2,1} < \min\{t^1_{1,1} + t^1_{2,2}, t^1_{1,2} + t^2_{1,2} + t^1_{3,1}, t^1_{1,2} + t^2_{1,2} + t^1_{3,2}\} \tag{3.42}$$

and hence particle $(2,1)$ wakes up the particles on site 4 at time $T_1 = t^1_{1,1} + t^1_{2,1} + t^2_{2,1}$. Now if

$$t^1_{1,1} + t^1_{2,1} + t^2_{2,1} < t_0 < t^1_{1,1} + t^2_{1,1} + t^3_{1,1} \tag{3.43}$$

we have $T_1 < t_0 < T_2$ or, in other words,

$$r_{t_0}(w_2) \leq 3 < 4 \leq r_{t_0}(w_1). \tag{3.44}$$

Clearly, the event that (3.36), (3.37), (3.38), (3.39), (3.40), (3.41), (3.42), and (3.43) has positive probability, which concludes the proof.
The following table depicts an example configuration for times $(t^n_{x,i})_{1\leq n\leq 3}$ that satisfies the assumptions above for $t_0 = 9$ (times that don't appear in any condition are left blank and can attain any value, as they do not matter for the outcome).

	$(0,1)$	$(0,2)$	$(1,1)$	$(1,2)$	$(2,1)$	$(2,2)$	$(3,1)$	$(3,2)$
$t^1_{x,i}$	1	11	4	5	3	9	6	6
$t^2_{x,i}$	1		1.5	1	1			
$t^3_{x,i}$			4	4				

In this example we have $T_1 = 8$, but $T_2 = 9.5$.

This example also shows that we cannot simply use that for $t \geq 0$ the map $l \mapsto r_t(w^l(w))$ is monotone to define $r_t(w)$ as its limit like it was done in [16]. In contrast, we use that almost surely $l \mapsto r_t(w^l(w))$ is constant for large enough l, because the additional random walks have not yet reached site r.

Proposition 3.52. *Let $r \in \mathbb{Z}$ be fixed and $w = (r, \mathcal{L}, \mathcal{G}, F, I_{r+1})$ be a random initial configuration taking values in $\mathbb{L}_\theta$, defined on $\mathbf{\Omega}$, that is independent of*

$$\{A_x, I_{x+1} : x > r, i \in \mathbb{N}\} \cup \mathbf{Y}$$

and such that

$$\mathbf{E}\left[\sum_{(x,i)\in\mathcal{L}} \exp(\theta(F(x,i) - r))\right] < \infty.$$

Then there is a set $B^w \in \mathcal{F}$, depending only on w, such that $\mathbf{P}(B^w) = 1$ and for all $\omega \in B^w$ and all $T \geq 0$

$$\{(X_t(w^l(w))(\omega))_{t\in[0,T]} : l \in \mathbb{N}\}$$

is a Cauchy sequence in the uniform topology on $D([0,T], \mathbb{L}_\theta)$.

Proof. Let $w = (r, \mathcal{L}, \mathcal{G}, F, I_{r+1})$ be as above and let $l \in \mathbb{N}$. By the independence assumption, we can construct the processes

$$(X_t(w^l(w)))_{t\geq 0}$$

by first sampling a realization of w and then using the collections $\mathbf{Y}, \mathbf{I}, \mathbf{A}$ to obtain the process with that initial configuration. We will show that for all $T \geq 0$ these processes almost surely converge uniformly over $t \in [0, T]$ in $\mathbb{L}_\theta$. Hence, we fix an $\varepsilon > 0$ and $T \geq 0$. We set

$$B^w := \bigcap_{S=1}^{\infty} \bigcap_{n=1}^{\infty} \bigcup_{l=1}^{\infty} \left\{ \sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) \leq \frac{1}{n} \right\}$$

and note that by continuity from above and below of $\mathbf{P}$ we have

$$\mathbf{P}(B^w) = \lim_{S\to\infty} \lim_{n\to\infty} \lim_{l\to\infty} \mathbf{P}\left(\sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) \leq \frac{1}{n} \right)$$

We now investigate the probability

$$\mathbf{P}\left(\sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right).$$

Since for a simple symmetric random walk $(Y_t)_{t\geq 0}$ jumping at rate 2, the process

$$(\exp(\theta Y_t - 2t(\cosh\vartheta - 1)))_{t\geq 0}$$

is a càdlàg martingale, for any $k \geq 1$, also

$$(M_t^{l,k})_{t\geq 0} := \left(\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r) - 2t(\cosh\vartheta - 1)) \right)_{t\geq 0}$$

is a càdlàg martingale w.r.t.

$$(\mathcal{H}_t)_{t\geq 0} := \left(\sigma\left(w, \mathbb{1}_{(x,i)\in\mathcal{L}} Y_s^{x,i} : (x,i) \in \mathbb{Z}\times\mathbb{N}, 0 \leq s \leq t\right)\right)_{t\geq 0}.$$

Thus, Doob's inequality yields

$$\mathbf{P}\left(\sup_{0\leq t\leq S} M_t^{l,k} > \lambda \right) \leq \frac{1}{\lambda}\mathbf{E}[M_0^{l,k}] = \frac{1}{\lambda}\mathbf{E}\left[\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) \right] \tag{3.45}$$

for any $\lambda > 0$. For fixed $t \geq 0$ the sequence

$$\left(\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) \right)_{k\geq 1}$$

is increasing almost surely, since only more positive terms get added for each k. Thus

$$\begin{aligned}
&\mathbf{P}\left(\sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right) \\
&= \mathbf{P}\left(\bigcup_{k=1}^{\infty} \left\{ \sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right\} \right) \\
&= \lim_{k\to\infty} \mathbf{P}\left(\left\{ \sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right\} \right).
\end{aligned}$$

Together with (3.45), using $\lambda = \frac{\exp(-2S(\cosh\theta - 1))}{n}$, we obtain

$$\begin{aligned}
&\mathbf{P}\left(\sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right) \\
&\leq n\exp(2(\cosh\vartheta - 1)S) \lim_{k\to\infty} \mathbf{E}\left[\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) \right] \\
&\overset{\text{mon. conv.}}{=} n\exp(2(\cosh\vartheta - 1)S)\mathbf{E}\left[\sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) - r)) \right].
\end{aligned} \tag{3.46}$$

By the assumption

$$\mathbf{E}\left[\sum_{(x,i)\in\mathcal{L}} \exp(\theta(F(x,i) - r)) \right] < \infty$$

we can apply dominated convergence to take the limit $l \to \infty$ inside the expectation, which yields

$$\lim_{l\to\infty} \mathbf{P}\left(\sup_{0\leq t\leq S} \sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)} \exp(\theta(F(x,i) + Y_t^{x,i} - r)) > \frac{1}{n} \right) = 0,$$

because the sum

$$\sum_{(x,i)\in\mathcal{L}} \exp(\theta(F(x,i)-r))$$

has finite expectation, thus in particular it is almost surely finite and hence its tailsums converge to 0 almost surely. In conclusion, this yields the claim that $\mathbf{P}(B^w)=1$. Choosing $n=2$ yields that

$$B^w \subset \bigcap_{S=1}^{\infty}\bigcup_{l=1}^{\infty}\left\{\sup_{\substack{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w),\\ 0\le t\le S}} F(x,i)+Y_t^{x,i}<r\right\}.$$

In particular, this means that for all $\omega\in B^w$ there is an $N(\omega,T)$ such that for all $l\ge N(\omega,T)$, none of the living parasites with initial position below $r-l$ have even reached r by time T and were just moving as simple random walks without any interaction. Hence for $k>0$ the configurations $X_t(w^l(w))$ and $X_t(w^{l+k}(w))$ only differ by the parasites with birthlabel in $\mathcal{L}^{l+k}(w)\cap(\mathcal{L}\setminus\mathcal{L}^l(w))$. Thus for all $\omega\in B, t\in[0,T]$ and $l\ge N(\omega,T), k\ge 0$

$$\begin{aligned}
&d_\theta(X_t(w^l(w)),X_t(w^{l+k}(w))\\
&\quad=\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\cap(\mathcal{L}\setminus\mathcal{L}^l(w))}\exp(\theta(F(x,i)+Y_t^{x,i}-r_t(w^l(w)))\\
&\quad\le\sum_{(x,i)\in\mathcal{L}^{l+k}(w)\cap(\mathcal{L}\setminus\mathcal{L}^l(w))}\exp(\theta(F(x,i)+Y_t^{x,i}-r))\\
&\quad\le\sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)}\exp(\theta(F(x,i)+Y_t^{x,i}-r)).
\end{aligned}$$

By definition of B^w, for all $\omega\in B^w$ we can choose $S=\lfloor T+1\rfloor, n=\lceil\frac{1}{\varepsilon}\rceil$, there is an $N'(\omega,T,\varepsilon)\ge N(\omega,T)$ such that for all $l\ge N'(\omega,T,\varepsilon)$

$$\sup_{0\le t\le S}\sum_{(x,i)\in\mathcal{L}\setminus\mathcal{L}^l(w)}\exp(\theta(F(x,i)+Y_t^{x,i}-r))\le\frac{1}{n},$$

hence, for all $k\ge 0, t\in[0,T]$

$$d_\theta(X_t(w^l(w)),X_t(w^{l+k}(w)))\le\varepsilon.$$

which is the claim. □

Remark 3.53. *This shows that for all $\omega\in B^w$ the sequence*

$$\{(X_t(w^l(w(\omega)))(\omega))_{t\ge0}: l\in\mathbb{N}\}$$

converges to a limit in $D([0,\infty),\mathbb{L}_\theta)$, which we denote by $(X_t(w)(\omega))_{t\ge0}$.

By taking the limits $\lim_{l\to\infty} X_t(w^l(w)) = X_t(w)$ in (3.34) and (3.35), we obtain

$$\mathbf{P}(r_t(w) - r > \gamma t | w) \le \mathrm{e}^{-c_{\gamma,\vartheta} t} f_\vartheta(w)\, \mathrm{e}^{-\vartheta r} \tag{3.47}$$

and

$$\mathbf{E}[f_\vartheta(X_t(w))|w] \le \mathrm{e}^{\lambda_{2,\vartheta} t} f_\vartheta(w).$$

For any $t \ge 0$ we define linear operators on the space of bounded measurable functions $\mathrm{B}(\mathbb{L}_\theta)$ by

$$\begin{aligned} S_t : \mathrm{B}(\mathbb{L}_\theta) &\to \mathrm{B}(\mathbb{L}_\theta) \\ f &\mapsto \mathbf{E}[f(X_t(\cdot))] \end{aligned}$$

and observe that

$$\|S_t\| = \sup_{\|f\|\le 1} \sup_{w\in\mathbb{L}_\theta} |\mathbf{E}[f(X_t(w))]| \le \sup_{\|f\|\le 1} \mathbf{E}[\|f\|] = 1.$$

However, considering the sequence $w_n = (0, \{0\} \times \{1,\dots,n\}, \emptyset, x \mapsto x, 1)$ and $f : w \mapsto \mathbb{1}_{r>0}$, it is easy to see that the map $t \mapsto S_t f$ is not continuous for general $f \in B(\mathbb{L}_\theta)$. To show the Markov and then the strong Markov property of $(X_t(w))_{t\ge 0}$, we will show that $(S_t)_{t\ge 0}$ forms a semi-group on the class $\mathrm{BUC}(\mathbb{L}_\theta)$ of bounded and uniformly continuous functions, i.e.

$$\begin{aligned} \forall t \ge 0 \forall f \in \mathrm{BUC}(\mathbb{L}_\theta) &: S_t f \in \mathrm{BUC}(\mathbb{L}_\theta) \\ \forall s,t \ge 0 \forall f \in \mathrm{BUC}(\mathbb{L}_\theta) &: S_{s+t} f = S_s(S_t f). \end{aligned}$$

It is classically known, e.g., [7, Theorem 2.1], that $\mathrm{BUC}(\mathbb{L}_\theta)$ are convergence determining, and hence the semi-group property shows the Markov property. The strong Markov property follows because $\mathrm{BUC}(\mathbb{L}_\theta)$ is a class of continuous functions, and the sample paths are càdlàg by construction. We begin with introducing some notation to obtain a result of the dependence of $(X_t(w))_{t\ge 0}$ from its initial configuration.

Definition 3.54. *Let $w, w' \in \mathbb{L}_\theta$ with $r = r', \iota = \iota'$ and $F_{|\mathcal{G}} = F'_{|\mathcal{G}'}$. Then we call*

$$\overline{\mathcal{L}}(w,w') := \left\{ (x,i) \in \mathcal{L} \cup \mathcal{L}' : \begin{array}{c} (x,i) \notin \mathcal{L} \text{ or } (x,i) \notin \mathcal{L}' \text{ or} \\ (x,i) \in \mathcal{L} \cap \mathcal{L}' \text{ and } F(x,i) \ne F'(x,i) \end{array} \right\}$$

the distinguishing parasites for w and w'.

Lemma 3.55. *For all $\varepsilon > 0$ and $T \geq 0$ there is a $\delta \in (0,1)$ such that for all $w, w' \in \mathbb{L}_\theta$ with*

$$d_\theta(w, w') < \delta$$

there is a $(\sigma(Y_s^{x,i} : 0 \leq s \leq t, (x,i) \in \overline{\mathcal{L}}(w,w')))_{t \geq 0}$ stopping time τ, such that

- $\mathbf{P}(\tau \leq T) < \varepsilon$,
- $\sup_{0 \leq t \leq T} \mathbb{1}_{\tau > T} d_\theta(X_t(w), X_t(w')) < \varepsilon$.

Proof. If $d_\theta(w, w') < \delta$, then $\delta < 1$ implies $r = r', \mathcal{G} = \mathcal{G}', F_{|\mathcal{G}} = F'_{|\mathcal{G}}, \iota = \iota'$, which we assume for the rest of the proof. We define $\widetilde{F}(w, w') : \mathcal{L} \cup \mathcal{L}' \cup \mathcal{G} \to \mathbb{Z}$ by

$$(x,i) \mapsto \begin{cases} F(x,i), & (x,i) \in \mathcal{G} \\ F(x,i), & (x,i) \in \mathcal{L} \cup \mathcal{L}' \setminus \mathcal{L}' \\ F'(x,i), & (x,i) \in \mathcal{L} \cup \mathcal{L}' \setminus \mathcal{L} \\ F(x,i) \vee F'(x,i), & (x,i) \in \mathcal{L} \cap \mathcal{L}' \end{cases}.$$

For $n \in \mathbb{N}$ we define

$$A_T^n := \left\{ \sup_{0 \leq t \leq T} \sum_{(x,i) \in \overline{\mathcal{L}}(w,w')} \exp(\theta(\widetilde{F}(w,w')(x,i) + Y_t^{x,i} - r)) \leq \frac{1}{n} \right\}.$$

For $\omega \in A_T^n$, none of the frogs that distinguish w and w' reached $r+1$ by time T in either $X_t(w)$ or $X_t(w')$; therefore, these configurations only differ by the current positions of frogs in $\overline{\mathcal{L}}(w,w')$. Hence, $r_t(w)(\omega) = r_t(w')(\omega)$ and

$$\begin{aligned} d_\theta(X_t(w), X_t(w')) = & \sum_{(x,i) \in (\mathcal{L} \cup \mathcal{L}') \setminus \mathcal{L}'} \mathrm{e}^{\theta(F(x,i) + Y_t^{x,i} - r_t(w))} \\ & + \sum_{(x,i) \in (\mathcal{L} \cup \mathcal{L}') \setminus \mathcal{L}} \mathrm{e}^{\theta(F'(x,i) + Y_t^{x,i} - r_t(w))} \\ & + \sum_{(x,i) \in \mathcal{L} \cap \mathcal{L}' \cap \overline{\mathcal{L}}(w,w')} \mathrm{e}^{\theta(Y_t^{x,i} - r_t(w))} \left| \mathrm{e}^{\theta F(x,i)} - \mathrm{e}^{\theta F'(x,i)} \right| \\ \leq & \sum_{(x,i) \in \overline{\mathcal{L}}(w,w')} \exp(\theta(\widetilde{F}(w,w')(x,i) + Y_t^{x,i} - r)). \end{aligned}$$

This implies

$$\sup_{0 \leq t \leq T} d_\theta(X_t(w), X_t(w')) \mathbb{1}_{A_T^n} \leq \frac{1}{n}.$$

Now we define

$$\tau^n := \inf\left\{t \geq 0 : \sum_{(x,i)\in\overline{\mathcal{L}}(w,w')} \exp(\theta(\widetilde{F}(w,w')(x,i) + Y_t^{x,i} - r)) > \frac{1}{n}\right\}$$

which clearly is an $(\sigma(Y_s^{x,i} : 0 \leq s \leq t, (x,i) \in \overline{\mathcal{L}}(w,w')))_{t\geq 0}$-stopping time and note that

$$\{\tau^n > T\} = A_T^n.$$

Analogously to the estimation (3.46) in the proof of Proposition 3.52, we have

$$\begin{aligned}\mathbf{P}\left(\Omega \setminus A_T^n\right) &\leq n\exp(2T(\cosh\theta - 1)) \sum_{(x,i)\in\overline{\mathcal{L}}(w,w')} \exp(\theta(\widetilde{F}(w,w')(x,i) - r)) \\ &\leq n\exp(2T(\cosh\theta - 1))\frac{d_\theta(w,w')}{1-\mathrm{e}^{-\theta}},\end{aligned}$$

where the last inequality follows from

$$|\,\mathrm{e}^{\theta F(x,i)} - \mathrm{e}^{\theta F'(x,i)}\,| \geq (1-\mathrm{e}^{-\theta})\,\mathrm{e}^{\theta(F(x,i)\vee F'(x,i))}\,.$$

Hence choosing $n := \left\lfloor 1 + \frac{1}{\varepsilon}\right\rfloor$ and

$$\delta = \frac{1-\mathrm{e}^{-\theta}}{n^2\exp(2T(\cosh\theta - 1))}$$

yields the claim. □

With this refinement we can show that S_t maps $\mathrm{BUC}(\mathbb{L}_\theta)$ onto itself.

Lemma 3.56. *Let* $f \in \mathrm{BUC}(\mathbb{L}_\theta)$ *and* $T \geq 0$. *Then for any* $\varepsilon > 0$ *there is a* $\delta > 0$ *such that for all* $w, w' \in \mathbb{L}_\theta$

$$d_\theta(w,w') < \delta \quad \Rightarrow \quad \sup_{0\leq t\leq T} |\mathbf{E}[f(X_t(w)) - f(X_t(w'))]| < \varepsilon.$$

In particular, $S_t f \in \mathrm{BUC}(\mathbb{L}_\theta)$ *for any* $t \geq 0$.

Proof. Fix $f \in \mathrm{BUC}(\mathbb{L}_\theta)$ and let $\varepsilon > 0$. Because f is uniformly continuous, there is a $\varepsilon_0 \in \left(0, \frac{\varepsilon}{4\|f\|_\infty}\right)$ such that $d_\theta(w,w') < \varepsilon_0$ implies $|f(w) - f(w')| < \frac{\varepsilon}{2}$. Now by Lemma 3.55 we find a $\delta \in (0,1)$ such that for all $w, w' \in \mathbb{L}_\theta$ with $d_\theta(w,w') < \delta$ there is a random time τ with

$$\mathbf{P}(\tau \leq T) < \varepsilon_0$$

and

$$\sup_{0\le t\le T} \mathbb{1}_{\tau>T} d_\theta(X_t(w), X_t(w')) < \varepsilon_0.$$

Then for any $w, w' \in \mathbb{L}_\theta$ with $d_\theta(w, w') < \delta$ and all $t \in [0, T]$ we have

$$\begin{aligned}|\mathbf{E}[f(X_t(w)) - f(X_t(w'))]| &\le \mathbf{E}[\mathbb{1}_{\tau>T}|f(X_t(w)) - f(X_t(w'))|] + \mathbf{E}[\mathbb{1}_{\tau\le T}2\|f\|_\infty] \\ &< \frac{\varepsilon}{2} + 2\|f\|_\infty\varepsilon_0 < \varepsilon.\end{aligned}$$

Since $w \mapsto \mathbf{E}[f(X_t(w))]$ is clearly bounded by $\|f\|_\infty$, this finishes the proof. □

Lemma 3.57. *For $f \in \mathrm{BUC}(\mathbb{L}_\theta), w \in \mathbb{L}_\theta$ and $s, t \ge 0$ we have*

$$(S_{s+t}f)(w) = (S_s(S_t f))(w).$$

Proof. First we note, that for $w \in \mathbb{A}$ we already know that $(X_t(w))_{t\ge0}$ is a Markov process in $\mathbb{A}$, hence

$$S_{s+t}f(w) = (S_s(S_t f))(w)$$

for any $w \in \mathbb{A}, f \in \mathrm{BUC}(\mathbb{L}_\theta)$.
Let $\varepsilon > 0$ and choose $\delta_1 \in \left(0, \frac{\varepsilon}{2\|f\|}\right)$ as in Lemma 3.56 with $T = s + t$. Then choose $\delta_2 \in (0, \delta_1)$ as in Lemma 3.55 with $T = s + t, \varepsilon = \delta_1$. Finally choose $l \in \mathbb{N}$ such that $d_\theta(w, w^l(w)) < \delta_2$ and compute

$$\begin{aligned}|S_{s+t}f(w) - S_sS_tf(w)| &\le |S_{s+t}f(w) - S_{s+t}f(w^l(w))| \\ &\quad + |S_{s+t}f(w^l(w)) - S_sS_tf(w^l(w))| \\ &\quad + |S_sS_tf(w^l(w)) - S_sS_tf(w)| \\ &\le \varepsilon + 0 + |S_sS_tf(w^l(w)) - S_sS_tf(w)|.\end{aligned}$$

Now to estimate the final term we choose τ as in Lemma 3.55 corresponding to $w, w^l(w)$ and compute

$$\begin{aligned}|S_sS_tf(w^l(w)) - S_sS_tf(w)| &= \left|\mathbf{E}\left[S_tf(X_s(w^l(w))) - S_tf(X_s(w))\right]\right| \\ &\le \mathbf{E}\left[\mathbb{1}_{\tau>t+s}\left|S_tf(X_s(w^l(w))) - S_tf(X_s(w))\right|\right] \\ &\quad + \mathbf{E}\left[\mathbb{1}_{\tau\le t+s}\left|S_tf(X_s(w^l(w))) - S_tf(X_s(w))\right|\right] \\ &\le \varepsilon + 2\|f\|\delta_1 < 2\varepsilon.\end{aligned}$$

Because these estimations hold for any $\varepsilon > 0$, this concludes the proof. □

This shows that for any $w \in \mathbb{L}_\theta$ the process $(X_t(w))_{t\geq 0}$ is a Markov process. To show the strong Markov property we simply use that its semi-group preserves the separating class $\mathrm{BUC}(\mathbb{L}_\theta)$ of functions that, in particular, are continuous.

Theorem 3.5. *For $w \in \mathbb{L}_\theta$ the process $(X_t(w))_{t\geq 0}$ is strong Markov with respect to its natural filtration and almost surely has càdlàg sample paths.*

Proof. By construction, $(X_t(w))_{t\geq 0}$ has càdlàg sample paths for all $w \in \mathbb{A}$, and by uniform convergence,

$$\lim_{l\to\infty} \sup_{0\leq t\leq T} d_\theta(X_t(w), X_t(w^l(w))) = 0,$$

so also $(X_t(w))_{t\geq 0}$ has càdlàg sample paths.
Let σ be an almost surely finite $(\mathcal{F}_t(w))_{t\geq 0}$ stopping time; then there is a sequence $(\sigma_n)_{n\in\mathbb{N}}$ of $(\mathcal{F}_t(w))_{t\geq 0}$ stopping times with a countable range, such that $\sigma_n \downarrow \sigma$ for $n \to \infty$. Because each σ_n has a countable range, we obtain that $(X_t(w))_{t\geq 0}$ is strong Markov at σ_n. Using $\sigma_n \geq \sigma$ we obtain $\mathcal{F}_\sigma(w) \subset \mathcal{F}_{\sigma_n}(w)$ and hence for each $f \in \mathrm{BUC}(\mathbb{L}_\theta)$ the right continuity of $t \mapsto X_t(w)$ and the continuity of $w \mapsto \mathbf{E}[f(X_t(w))]$ yield

$$\begin{aligned}
\mathbf{E}[f(X_{\sigma+t}(w))|\mathcal{F}_\sigma(w)](\omega) &= \lim_{n\to\infty} \mathbf{E}[f(X_{\sigma_n+t}(w))|\mathcal{F}_\sigma(w)](\omega) \\
&= \lim_{n\to\infty} \mathbf{E}[\mathbf{E}[f(X_{\sigma_n+t}(w))|\mathcal{F}_{\sigma_n}(w)]|\mathcal{F}_\sigma(w)](\omega) \\
&= \lim_{n\to\infty} \mathbf{E}\left[\int_\Omega f(X_t(X_{\sigma_n}(w))(\omega'))\,\mathrm{d}\mathbf{P}(\omega')\middle| \mathcal{F}_\sigma(w)\right](\omega) \\
&= \mathbf{E}\left[\int_\Omega f(X_t(X_\sigma(w))(\omega'))\,\mathrm{d}\mathbf{P}(\omega')\middle| \mathcal{F}_\sigma(w)\right](\omega) \\
&= \int_\Omega f(X_t(X_\sigma(w)(\omega))(\omega'))\,\mathrm{d}\mathbf{P}(\omega').
\end{aligned}$$

This concludes the proof, because $\mathrm{BUC}(\mathbb{L}_\theta)$ is separating. ☐

3.5.2 Untagged system

In this subsection we construct the untagged system as described at the beginning of this section. In the construction we only consider finite initial configurations. The extension to infinite initial configurations follows by similar ideas as in the previous section. In Proposition 3.58 we show that this coupling is monotone in the initial configuration.

In this construction we no longer keep track of the birthplaces of parasites and just store the current configuration of all parasites. Thus the state space of configurations will be given by

$$\mathbb{S}_\theta := \left\{ (r, \eta, \overline{\eta}, \iota) \in \mathbb{Z} \times \mathbb{N}_0^{\mathbb{Z}} \times \mathbb{N}_0^{\mathbb{Z}} \times \mathbb{N} : \begin{array}{c} \operatorname{supp} \eta \subset (-\infty, r], \sum_{x \in \mathbb{Z}} \overline{\eta}(x) < \infty, \\ \sum_{x \le r} \eta(x)\, \mathrm{e}^{\theta(x-r)} < \infty \end{array} \right\}.$$

The front is given by r; for $x \in \mathbb{Z}$, the number of living parasites on site x is given by $\eta(x)$, and the number of ghost parasites on x is given by $\overline{\eta}(x)$, and finally the immunity of the host at $r+1$ is given by ι. To construct the process we will use a collection of Poisson point processes to sample the jumps for each site. To this end, let $\{P_{x,n}^{\leftarrow}, P_{x,n}^{\rightarrow} : x \in \mathbb{Z}, n \in \mathbb{N}\}$ and $\{G_{x,n}^{\leftarrow}, G_{x,n}^{\rightarrow} : x \in \mathbb{Z}, n \in \mathbb{N}\}$ be independent collections of independent Poisson point processes on $\mathbb{R}$ with intensity 1 and set

$$P(x,n) := \sum_{k=1}^{n} P_{x,k}^{\leftarrow} + P_{x,k}^{\rightarrow}, \quad G(x,n) := \sum_{k=1}^{n} G_{x,k}^{\leftarrow} + G_{x,k}^{\rightarrow}$$

which are independent Poisson point processes on $\mathbb{R}$ with intensity $2n$. By convention we set $P(x,0) := G(x,0) := \emptyset$. We assume that these processes are defined on the same probability space as $\mathbf{A}, \mathbf{I}$.

For $l, r \in \mathbb{Z}$, a configuration $\eta \in \mathbb{N}_0^{\mathbb{Z}}, \overline{\eta} \in \mathbb{N}_0^{\mathbb{Z}}$ with $\operatorname{supp} \eta, \operatorname{supp} \overline{\eta} \subset [l, r]$, $\iota \in \mathbb{N}$, and a time $t_0 \in \mathbb{R}$, we define the process $(\zeta_t(r, \eta, \overline{\eta}, \iota; t_0))_{t \ge t_0}$ given by the tuple

$$(r_t(r, \eta, \overline{\eta}, \iota; t_0), \eta_t(r, \eta, \overline{\eta}, \iota; t_0), \overline{\eta}_t(r, \eta, \overline{\eta}, \iota; t_0) \iota_t(r, \eta, \overline{\eta}, \iota; t_0))_{t \ge t_0}$$

as follows. The collection $\{P_{x,n}^{\leftarrow} : x \in \mathbb{Z}, n \in \mathbb{N}\}$ gives the time points at which a living parasite jumps from x to $x-1$, where a jump time $t \in P_{x,n}$ is only allowed to be used if $\eta_{t-}(x) \ge n$. Analogously, the times that a living parasite jumps from x to $x+1$ are given by $\{P_{x,n}^{\rightarrow} : x \in \mathbb{Z}, n \in \mathbb{N}\}$. The collection $\{G_{x,n}^{\leftarrow}, G_{x,n}^{\rightarrow} : x \in \mathbb{Z}, n \in \mathbb{N}\}$ determines the jumps of ghost parasites in the same way. Whenever for some time t a jump of a living parasite onto the site $r_{t-}+1$ happens, we use ι_{t-} to determine the outcome of the infection attempt. If $\iota_{t-} = 1$, then

$$r_t = r_{t-} + 1, \eta_t := \eta_{t-} - \delta_{r_{t-}} + A_{r_t} \delta_{r_t}, \overline{\eta}_t := \overline{\eta}_t + \delta_{r_t} \text{ and } \iota_t := I_{r_t+1}.$$

Otherwise, simply

$$r_t = r_{t-}, \iota_t = \iota_{t-} - 1, \overline{\eta}_t := \overline{\eta}_t + \delta_{r_t+1} \text{ and } \eta_t = \eta_{t-} - \delta_{r_t}.$$

It is clear that the so-constructed process $(r_t(r,\eta,\overline{\eta},\iota;0))_{t\geq 0}$ has the same distribution as the process $(r_t(w))_{t\geq 0}$ constructed from the tagged system in the previous Section 3.5 with w given by

$$(r,\{(x,i)\in\mathbb{Z}\times\mathbb{N}:1\leq i\leq\eta(x)\},\{(x,i)\in\mathbb{Z}\times\mathbb{N}:1\leq i\leq\overline{\eta}(x)\},(x,i)\mapsto x,\iota).$$

Also, it is clear that the resulting process is a strong Markov process with respect to its natural filtration and also with respect to the filtration

$$\sigma(\mathbf{A},\mathbf{I},\zeta,\{[0,t]\cap P(x,n),[0,t]\cap G(x,n):x\in\mathbb{Z},n\in\mathbb{N}\}).$$

In this coupling we have the following monotonicity property.

Proposition 3.58. *Let $t_0\in\mathbb{R}, l,r\in\mathbb{Z}$ and $\eta^1,\eta^2\in\mathbb{N}_0^{\mathbb{Z}}$ with*

$$\operatorname{supp}\eta_1,\operatorname{supp}\eta_2\subset(l,r]$$

such that

$$\sum_{k\geq x}\eta^1(k)\leq\sum_{k\geq x}\eta^2(k)$$

for all $x\in\mathbb{Z}$. In particular, we allow t_0,r,η^1,η^2 to be random and the conditions above to hold almost surely. Let $(r_t^1,\eta_t^1,\iota_t^1)_{t\geq t_0}$ be the process with initial configuration (r,η^1,I_{r+1}) at time t_0 and let $(r_t^2,\eta_t^2,\iota_t^2)_{t\geq t_0}$ be the process with initial configuration (r,η^2,I_{r+1}) at time t_0. Then almost surely for all $t\geq t_0$ we have

$$r_t^1\leq r_t^2.$$

Proof. For $n\geq 0$ we set

$$\rho_n^1:=\inf\{t\geq t_0:r_t^1\geq r+n\},\quad \rho_n^2:=\inf\{t\geq t_0:r_t^2\geq r+n\}.$$

First we note that the event of parasite extinction in the i-th process for $i\in\{1,2\}$ is given by

$$\mathcal{D}^i=\bigcup_{n\geq 1}\left\{\sum_{k=1}^{n}I_{r+k}>\sum_{x\leq r}\eta^i(x)+\sum_{k=1}^{n-1}A_{r+k}\right\}.$$

Let $n_{\mathrm{d}}^i\geq 1$ be the random number such that the extinction in the i-th process occurs when the front is at $r+n_{\mathrm{d}}^i-1$ and τ_{d}^i be the time at which it occurs. In particular, by assumption, we have $n_{\mathrm{d}}^1\leq n_{\mathrm{d}}^2$. We will now show that for

$0 \leq n < n_{\mathrm{d}}^1$ we have $\rho_n^1 \geq \rho_n^2$. Since by definition, we have $\rho_{n_{\mathrm{d}}^1}^1 = \infty$, this shows the claim. For $t \in [t_0, \rho_1^1 \wedge \rho_1^2)$ the amount of parasites that died so far in the i-th process is given by $I_{r+1} - \iota_t^i$. Since both processes use the same Poisson point process, accounting for the lost mass due to parasite death, this implies that

$$I_{r+1} - \iota_t^1 + \sum_{k \geq x} \eta_t^1(k) \leq I_{r+1} - \iota_t^2 + \sum_{k \geq x} \eta_t^2(k)$$

for all $x \in \mathbb{Z}$ and $t \in [t_0, \rho_1^1 \wedge \rho_2^1)$. In particular, since ρ_1^i is given by

$$\inf \left\{ s \geq t_0 : \left| \left\{ t \in [t_0, s] \cap \sum_{k=1}^{\infty} P_{r,k}^{\rightarrow} : t \in P(r, \eta_{t-}^i(r)) \right\} \right| = I_{r+1} \right\},$$

we obtain that $\rho_1^2 \leq \rho_1^1$, because the only way for $\eta_t^2(r)$ to be less than $\eta_t^1(r)$ is if the difference has already tried to infect the host at $r+1$. Arguing analogously as above, we then must have

$$-\iota_t + \sum_{k=r+1}^{r_t^1+1} I_k + \sum_{k \geq x} \eta_t^1(k) \leq -\iota_t + \sum_{k=r+1}^{r_t^2+1} I_k + \sum_{k \geq x} \eta_t^2(k)$$

for all $x \in \mathbb{Z}$ and $t \in [\rho_1^2, \rho_2^2 \wedge \rho_2^1)$, which again implies $\rho_2^2 \leq \rho_2^1$. Repeating this yields $\rho_n^2 \leq \rho_n^1$ for all $0 \leq n < n_{\mathrm{d}}^1$ and thereby finishes the proof. □

With this monotonicity result, we can show the Feller property claimed in Theorem 3.1 by following the same argumentation as done for the classical frog model in [15, section 6].

Proof of Theorem 3.1. This proposition implies that the constructed process is monotone in the initial configuration; in particular, for any $\zeta = (r, \eta, \overline{\eta}, \iota) \in \mathbb{S}_\theta$ and $l \in \mathbb{N}$, we can define

$$\zeta^l = (r, \mathbb{1}_{x > r-l} \eta(\cdot), \overline{\eta}, \iota)$$

which contains only finitely many parasites. By the lemma above, we then have that for any fixed $t \geq 0$ the sequence

$$(r_t(\zeta^l; 0))_{l \geq 1}$$

is almost surely monotone and in particular has a limit

$$r_t(\zeta; 0) := \lim_{l \to \infty} r_t(\zeta^l; 0) \in \mathbb{Z} \cup \{+\infty\}.$$

Following the same arguments as in [15, section 6], this yields that we obtain a well-defined strong Markov process

$$(r_t(\zeta), \eta_t(\zeta), \overline{\eta}_t(\zeta), \iota_t(\zeta); 0)_{t\geq 0}$$

for any configuration $\zeta \in \mathbb{S}_\theta$. Also, setting $a_m := \mathbb{P}(A = m)$ and $i_k := \mathbb{P}(I = k)$ the process has the generator

$$\begin{aligned} Lf(\zeta) = &\sum_{\substack{x,y\leq r\\ |x-y|=1}} \eta(x)(f(r, \eta - \delta_x + \delta_y, \overline{\eta}, \iota) - f(r, \eta, \overline{\eta}, \iota)) \\ &+ \sum_{\substack{x,y\in\mathbb{Z}\\ |x-y|=1}} \overline{\eta}(x)(f(r, \eta, \overline{\eta} - \delta_x + \delta_y, \iota) - f(r, \eta, \overline{\eta}, \iota)) \\ &+ \eta(r)\begin{pmatrix} \mathbb{1}_{\iota=1}\sum_{m=0}^\infty a_m \sum_{k=1}^\infty i_k f(r+1, \eta - \delta_r + m\delta_{r+1}, \overline{\eta} + \delta_{r+1}, k) \\ +\mathbb{1}_{\iota>1} f(r, \eta - \delta_r, \overline{\eta} + \delta_{r+1}, \iota) \\ -f(r, \eta, \overline{\eta}, \iota) \end{pmatrix} \end{aligned}$$

acting over functions $f \in \mathrm{BUC}(\mathbb{S}_\theta)$ such that the sums above converge. In particular, for $\vartheta \geq \theta > 0$ and

$$f_\vartheta(\zeta) := \sum_{x\in\mathbb{Z}} (\eta + \overline{\eta})(x)\,\mathrm{e}^{\vartheta x},$$

and $\zeta \in \mathbb{S}_\theta$ with only finitely many living parasites we can compute

$$Lf_\vartheta(\zeta) \in [(\mathrm{e}^\vartheta + \mathrm{e}^{-\vartheta} - 2)f_\vartheta(\zeta), (\mathrm{e}^{-\vartheta} + \mathbb{E}[A]\,\mathrm{e}^\vartheta - 2)f_\vartheta(\zeta)]$$

and

$$(L(f_\vartheta^2) - 2f_\vartheta Lf_\vartheta)(\zeta) \leq \mathbb{E}[A^2]\lambda_{3,\vartheta} f_{2\vartheta}(\zeta) \tag{3.48}$$

for some constant $\lambda_{3,\vartheta} \in (0, \infty)$. We note that the introduction of ghost parasites is necessary to obtain the lower bound for $Lf_\vartheta(\zeta)$. These claims follow by just multiplying out f_ϑ^2, plugging it in the generator L, and then carefully going through the cases for different x_1, x_2, y_1, y_2 to see the cancellations, and we omit this lengthy calculation at this point. For $\zeta \in \mathbb{S}_\theta$ let $\mathbb{P}_\zeta$ be the completion with respect to the canonical filtration on the space of càdlàg functions $D([0, \infty), \mathbb{S}_\theta)$ of the measure

$$\mathbb{P}((\zeta_t(\zeta; 0))_{t\geq 0} \in \cdot).$$

Then using the estimations above and following the same argumentation as in [15, section 6], we can see that $(\mathbb{P}_\zeta)_{\zeta\in\mathbb{S}_\theta}$ forms a Feller process on $\mathbb{S}_\theta$, by first identifying the compact sets of $\mathbb{S}_\theta$ as in [15, Lemma 22] and then using (3.48) to obtain an analog of [15, Lemma 23] and conclude the result as in [15, Proposition 5]. Finally we observe that forgetting about the ghost parasites, that is projecting the process onto its other three components, is continuous and retains the Markov property and the Feller property. $\square$

Chapter 4

Infection on $\mathbb{Z}$: the heavy-tailed immunity regime

4.1 Introduction

In this chapter, we further study the host and parasite model on the integer line $\mathbb{Z}$, which was introduced in Chapter 3. The construction details can be found in Chapter 3. We will now briefly describe the model and outline the scope of this chapter. In this model, hosts are motionless, with one host sitting on each positive vertex x, with $x > 0$. Parasites move as independent, simple, symmetric random walks on $\mathbb{Z}$, without interaction with other parasites, and attempt to infect any host they encounter. We assume that hosts have an immune response that permits them to prevent infection and kill the attacking parasite. The hosts adapt to the parasites and become more difficult to infect as more parasites have been successfully repelled. In Chapter 3, we focused on the case when hosts adapt only slowly to parasites, while this chapter investigates quickly adapting hosts. To be explicit, we assume that for some sequence $(p_m)_{m\in\mathbb{N}} \subset [0,1]$, the chance that a host is infected when attacked for the m-th time is equal to p_m, independent of anything else. The number of attacks on each host before infection is distributed as follows:

$$I := \inf\{m \geq 1 : S_m = 1\},$$

where $(S_m)_{m\geq 1}$ is an independent sequence of Bernoulli variables, with $S_m \sim \mathrm{Ber}(p_m)$. In Chapter 3, we assumed that this distribution has finite moments of order $\mathbb{E}[I^{2+\varepsilon}] < \infty$ for some $\varepsilon > 0$. In this chapter, we will investigate the situation where I has a regularly varying tail of index $\alpha \in (1,2)$. Specifically, I will not have a finite second moment. Using Stirling's formula for the Γ-function, we can explain why this assumption can be thought of as hosts that adapt faster to an attacker. If we let

$$p_m = p_m(\alpha) = \frac{\alpha}{\alpha + m} \qquad (m \geq 1)$$

then

$$\mathbb{P}(I > n) = \prod_{m=1}^{n} (1 - p_m) = \prod_{m=1}^{n} \frac{m}{\alpha + m} = \frac{\Gamma(\alpha+1)\Gamma(n+1)}{\Gamma(\alpha+n+1)} \sim Cn^{-\alpha}. \tag{4.1}$$

Clearly the map $\alpha \mapsto p_m(\alpha)$ is increasing for each m, and thus, for larger α, the probabilities of successful infection fall more slowly, or equivalently, the immunity builds up more slowly for higher α.

The aim of this chapter is to establish that assuming a behavior like (4.1) yields a front that does not move on a different scale than $t^{\frac{\alpha}{2}}$ in a sense made precise in the upcoming Theorems 4.1 and 4.5.

4.2 Main results

In this section we will present the main results of this chapter and briefly sketch the proofs.

4.2.1 Upper growth bound for the front

The first main result establishes that assuming the hosts adapt quickly to the parasites yields a sublinear speed of infection.

Theorem 4.1. *Suppose there is an $\alpha \in (1,2)$ such that I has a regularly varying tail of index α, i.e.*

$$\mathbb{P}(I > n) = n^{-\alpha} l(n) \tag{4.2}$$

for all $n \in \mathbb{N}$ and some slowly varying function l and suppose that $\mathbb{E}[A^{\vartheta}] < \infty$ for some $\vartheta > 2\alpha$. Then there is some slowly varying function b_2 such that if initially each vertex $x \in \mathbb{Z}$ with $x \leq 0$ is inhabited by an i.i.d. amount of parasites distributed as A, then we have

$$\lim_{t\to\infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} = 0$$

almost surely.

4.2.2 CLT for the infection time of large immunities

As part of the proof of Theorem 4.1, but also of independent interest, we obtain the following central limit theorem for the infection time of a host with large immunity $\iota \to \infty$.

Theorem 4.2. *Suppose that* $\mathbb{E}[A^2] < \infty$ *and set*

$$c_\mu := \mathbb{E}[A]\sqrt{\frac{2}{\pi}}, \quad c_\sigma := \left(\frac{\mathbb{E}[A](2-\sqrt{2})}{\sqrt{\pi}} + \mathbb{V}[A]\frac{2\sqrt{2}-2}{\sqrt{\pi}}\right).$$

If initially each vertex $x \in \mathbb{Z}$ *with* $x \leq 0$ *is inhabited by an i.i.d. amount of parasites distributed as* A *and the host at the site* 1 *has immunity equal to some deterministic* $\iota \in \mathbb{N}$*, we denote by* $X_\iota = \rho_1$ *the infection time of that host. We then have the following:*

$$K_\iota := \frac{X_\iota - \left(\frac{\iota}{c_\mu}\right)^2}{\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3}} \underset{\iota\to\infty}{\overset{\mathrm{d}}{\to}} \mathcal{N}(0,1).$$

Assuming regularity of the offspring, we can even establish the following two moderate deviation bounds.

Theorem 4.3. *Suppose that* $\mathbb{E}[\exp(\lambda A)] < \infty$ *for some* $\lambda > 0$ *and let* K_ι *be as in Theorem 4.2. Then for any monotone function* $f \in o\left(\sqrt{\iota}\right)$ *there are constants* $C_1, c_1 > 0$ *such that for all* $\iota \geq 1$ *we have*

$$\mathbb{P}(|K_\iota| \geq f(\iota)) \leq C_1 \exp\left(-c_1 f(\iota)\right).$$

If we have $\mathbb{E}[\exp(\lambda A)] < \infty$ *for all* $\lambda \in \mathbb{R}$*, then there are constants* $C_2, c_2 > 0$ *such that*

$$\mathbb{P}(|K_\iota| \geq f(\iota)) \leq C_2 \exp\left(-c_2 f(\iota)^2\right).$$

Theorem 4.4. *Suppose that* $\mathbb{E}[\exp(\lambda A)] < \infty$ *for some* $\lambda > 0$ *and let* K_ι *be as in Theorem 4.2. Then there are constants* $c_3 > 0$ *such that for any* $\iota \geq 1$ *and any* $0 \leq w \leq c_3\iota^{\frac{1}{6}}$ *we have*

$$\frac{\mathbb{P}(K_\iota > w)}{1-\Phi(w)} = 1 + \mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right) \text{ and } \frac{\mathbb{P}(K_\iota \leq -w)}{\Phi(-w)} = 1 + \mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right).$$

4.2.3 Lower growth bound for the front

Using a similar approach as in Chapter 3, we can also establish a lower bound for the infection speed.

Theorem 4.5. *Suppose that for some* $\alpha' \in (1,2]$ *we have*

$$\mathbb{E}[I^{\alpha'}] < \infty.$$

Then for any $q < \frac{\alpha'}{2}$ *we have*

$$\lim_{t\to\infty} \frac{r_t}{t^q} = \infty.$$

4.2.4 Proof sketches of the main results

Sketch of the proofs of Theorems 4.2, 4.3, 4.4. The proofs rely on the key idea that a random walk at time t has not reached a distance greater than $\sqrt{t}$ with high probability. Hence, the infection of a host up to time t can only rely on parasites that were born at a distance at most $\Theta(\sqrt{t})$ to the host. Since the offspring generated at an infection are i.i.d., the law of large numbers implies that there are only $\mathbb{E}[A]\Theta(\sqrt{t})$ many parasites that were born at a distance less than $\Theta(\sqrt{t})$. In particular, this means that if the host has an immunity of height h, then it takes on the scale $t = \Theta(h^2)$ time steps until $\mathbb{E}[A]\Theta(\sqrt{t}) \approx h$, and thus, the infection of that host will also require $\Theta(h^2)$ time units. Making this heuristic precise, we will obtain Theorem 4.2 by calculating the asymptotic expectation and variance of the number of parasites that already arrived at a host. Showing a Lindeberg condition will yield the central limit theorem, and estimating the moment-generating function of this object will yield the moderate deviation results. □

Sketch of the proof of Theorem 4.1. Using the tail assumption on I, we see that sufficiently large immunities appear frequently enough. By Theorem 4.2 and weaker concentration bounds as in Theorem 4.3, the infection of a host with an immunity $h \geq n^{\frac{1}{2}+\delta}$ will take $n^{1+2\delta}$ time units with high probability. Thus the infection of this host alone will slow down the spread of parasites below linear speed. □

Sketch of the proof of Theorem 4.5. We apply the same construction as in Chapter 3 to obtain a good site M, such that starting from M, the amount of parasites generated between M and $M+n$ grows at least linearly in n with a sufficiently large slope, and the amount of parasites needed to infect the hosts between M and $M+n$ grows at most linearly with a sufficiently small slope. Using this surplus of parasites generated to the right of M, we construct a sequence $(\nu_{M+n})_{n\geq k_0}$ of approximate jump times that upper bound the time between the infection of the host at $M+n-1$ and the infection of the host at $M+n$. For details of this construction we refer to Chapter 3. Using our moment assumption on I will show that the sequence $(\nu_{M+n})_{n\geq k_0}$ has finite moments of any order $q<\frac{\alpha'}{2}$ and is sufficiently fast ϕ-mixing. These two facts will imply that for any $q<q'<\frac{\alpha}{2}$, the sequence $(|\nu_{M+n}|^{q'})_{n\geq k_0}$ satisfies a strong law of large numbers, and using that $x\mapsto x^{q'}$ is concave will show that $\rho_{M+n}-\rho_{M+k_0}\leq\sum_{k=k_0}^{n}\nu_{M+k}$ grows slower than $n^{\frac{1}{q}}$. $\square$

4.3 Proofs of Results

4.3.1 Construction of the process

For a detailed construction of the process, we refer to Chapter 3 and here only quickly recall the notation.

Definition 4.1. *We assume an independent collection*

$$\mathbf{Y}=\{Y^{x,i}:x\in\mathbb{Z},i\in\mathbb{N}\}=\{(Y_t^{x,i})_{t\geq 0}:x\in\mathbb{Z},i\in\mathbb{N}\}$$

of i.i.d. simple symmetric random walks in continuous time starting at 0*,*

$$\mathbf{A}=\{A_x:x\in\mathbb{Z}\}$$

of i.i.d. $\mathbb{N}_0$*-valued variables distributed as* A *and*

$$\mathbf{I}=\{I_x:x\in\mathbb{Z}\}$$

of i.i.d. $\mathbb{N}$*-valued variables distributed as* I*.*
Also, we define the hitting times.

$$\tau_k^{x,i}:=\inf\left\{t\geq 0:Y_t^{x,i}=k\right\}$$

for $(x,i)\in\mathbb{Z}\times\mathbb{N}$ *and* $k\in\mathbb{Z}$*.*

For $x \in \mathbb{Z}$, A_x will be the parasites that are generated after the host at x is infected, and I_x will be the number of parasites that need to attack the host at x before it gets infected. For $x \in \mathbb{Z}$ and $i \in \mathbb{N}$, the i-th parasite that is generated on site x will follow the path $x + Y^{x,i}$.

More precisely, the process evolves as follows. Initially every vertex x with $x \leq 0$ holds A_x many parasites. We give each parasite a label $(x, i) \in \mathbb{Z} \times \mathbb{N}$, where x is its initial position and i enumerates the A_x many parasites with the initial position x. Then a parasite with label (x, i) moves according to the random walk $(x + Y_t^{x,i})_{t \geq 0}$ until it meets a host. At this time the parasite is killed and the label (x, i) is no longer used in the process. We denote by ρ_1 the first time that out of the collection

$$\mathcal{L}_0 = \{(x, i) : x \leq 0, 1 \leq i \leq A_x\},$$

there are I_1 many labels

$$\mathcal{G}_{\rho_1} = \{(x_1^1, i_1^1), \ldots, (x_{I_1}^1, i_{I_1}^1)\}$$

such that $(x + Y_t^{x,i})_{t \geq 0}$ already reached the vertex 1 at time ρ_1. Then we add parasites with labels $(1, 1), \ldots, (1, A_1)$, which will move according to $(1 + Y_{t-\rho_1}^{1,i})_{t \geq 0}$ to our collection

$$\mathcal{L}_{\rho_1} = \mathcal{L}_0 \setminus \mathcal{G}_{\rho_1} \cup \{(1, 1), \ldots, (1, A_1)\}.$$

Iterating this procedure, we obtain a sequence $(\rho_n)_{n \geq 1}$ of random times such that at ρ_n there are I_n many labels out of the collection of parasites at time ρ_{n-1} that reached the vertex n, and these labels then get removed from the collection of living parasites. We call

$$r_t := \sup\{n \geq 0 : \rho_n \leq t\}$$

the front of the process and ρ_n the infection time of the host at site n. We represent the state of this process as a tuple

$$(r_t, \mathcal{L}_t, \mathcal{G}_t, F_t, \iota_t), \tag{4.3}$$

where r_t is the position of the front, $\mathcal{L}_t$ are the labels of living parasites at time t, $\mathcal{G}_t$ are the labels of parasites that were removed up to time t, $F_t : \mathcal{L}_t \cup \mathcal{G}_t \to \mathbb{Z}$ assigns each parasite its position at time t, and $\iota_t \in \mathbb{N}$ is the remaining immunity of the host at site $r_t + 1$. In Chapter 3 we show that this process, with the initial configuration above, is well defined as a strong Markov process on a suitable state space.

4.3.2 Proof of Theorems 4.2, 4.3 and 4.4

In this section we will prove the central limit theorem 2.18. To begin with, we formally introduce the object of interest using the notation developed in Section 4.3.1.

Definition 4.2. *For $t \geq 0, n \in \mathbb{Z}$ we define the count of arrived random walks.*

$$B_{t,n} := \sum_{x=1}^{\infty} \sum_{i=1}^{A_{n-x}} \mathbb{1}_{\tau_x^{n-x,i} \leq t}$$

and for $\iota \geq 0$ the following random times

$$X_{\iota,n} := \inf \{t \geq 0 : B_{t,n} \geq \iota\}.$$

For notational convenience we also define

$$B_t := \sum_{x=1}^{\infty} \sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t}, \quad X_\iota = \inf\{t \geq 0 : B_t \geq \iota\},$$

noting that $(B_t)_{t \geq 0}, \{(B_{t,n})_{t \geq 0} : n \in \mathbb{Z}\}$ are identically distributed and thus also $(X_\iota)_{\iota \geq 0}, \{(X_{\iota,n})_{\iota \geq 0} : n \in \mathbb{Z}\}$ are identically distributed.

Remark 4.3. *When initially all parasites below n are alive and at their birthplace and $I_n = \iota$, i.e., the initial configuration in the sense of Section 4.3.1*

$$(n-1, \{(x,i) \in \mathbb{Z} \times \mathbb{N} : x < n, 1 \leq i \leq A_x\}, \emptyset, (x,i) \mapsto x, \iota)$$

then $B_{t,n}$ is the amount of initial parasites that reached site n at time t, and $X_{\iota,n}$ is the infection time of site n.

Lemma 4.4. *We recall the initial condition described in Section 4.3.1*

$$w_{\mathit{full}} = (0, \{(x,i) \in \mathbb{Z} \times \mathbb{N} : x \leq 0, 1 \leq i \leq A_x\}, \emptyset, (x,i) \mapsto x, I_1),$$

where every parasite below 0 is awake and at its birthplace. Then almost surely, we have

$$\rho_n = \inf\{t \geq 0 : r_t(w_{\mathit{full}}) \geq n\} \geq X_{I_n,n}.$$

for any $n \geq 1$.

Proof. At time ρ_n there are I_n many random walks, corresponding to living parasites at time ρ_{n-1}, that reached site n. Because we use the same random walks to compute $X_{I_n,n}$, all of those random walks started from the same location in $X_{I_n,n}$ but at time 0, whereas for ρ_n they possibly started at a later time. Precisely, the random walk with label (x, i) started at time $\rho_x \geq 0$ for $x < n, 1 \leq i \leq A_x$. This already shows the almost sure inequality. $\square$

Since B_t is the sum of the independent random variables

$$\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t},$$

it should be expected that centering and norming B_t yields an object that is approximately normally distributed for large t. Hence the first step is to establish an asymptotic expression for the expectation and variance of B_t for large t.

Lemma 4.5. *If $\mathbb{E}[A] < \infty$ then as t approaches infinity, we have*

$$\mathbb{E}[B_t] = \mathbb{E}[A] \left(\sqrt{\frac{2t}{\pi}} + \mathcal{O}(1) \right)$$

and if $\mathbb{E}[A^2] < \infty$ we also have

$$\mathbb{V}[B_t] = \left(\frac{\mathbb{E}[A](2 - \sqrt{2})}{\sqrt{\pi}} + \mathbb{V}[A] \frac{2\sqrt{2} - 2}{\sqrt{\pi}} \right) \left(\sqrt{t} + \mathcal{O}(1) \right)$$

Proof. For $x \in \mathbb{N}, t \geq 0$ let

$$p(x, t) := \mathbb{P} \left(\sup_{0 \leq s \leq t} Y_t \geq x \right)$$

and observe that by the reflection principle we have

$$p(x, t) = 2\mathbb{P}(Y_t \geq x) - \mathbb{P}(Y_t = x).$$

Then, because for each $x \geq 1$ the variable A_x is independent of the i.i.d. collection $\{\tau_x^{x,i} : i \geq 1\}$, we obtain by Wald's first identity (e.g. [27, Theorem 5.5]) and the reflection principle that

$$\begin{aligned} \mathbb{E}[B_t] = \mathbb{E} \left[\sum_{x=1}^{\infty} \sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t} \right] &= \sum_{x=1}^{\infty} \mathbb{E} \left[\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t} \right] = \sum_{x=1}^{\infty} \mathbb{E}[A] p(x, t) \\ &= \mathbb{E}[A] \sum_{x=1}^{\infty} 2\mathbb{P}(Y_t \geq x) - \mathbb{P}(Y_t = x) \\ &= \mathbb{E}[A] \left(2\mathbb{E}[Y_t \mathbb{1}_{Y_t \geq 0}] + \mathbb{P}(Y_t \geq 1) \right). \end{aligned}$$

Since $x \mapsto x\mathbb{1}_{x\geq 0}$ is Lipschitz continuous with Lipschitz constant 1, we obtain by the Berry-Esseen bound for the 1-Wasserstein distance, see e.g. [41], that

$$\mathbb{E}[Y_t\mathbb{1}_{Y_t\geq 0}] = \sqrt{t}\mathbb{E}[Z\mathbb{1}_{Z\geq 0}] + \mathcal{O}(1),$$

with $Z \sim \mathcal{N}(0,1)$. Calculating

$$\mathbb{E}[Z\mathbb{1}_{Z\geq 0}] = \int_0^\infty \frac{z}{\sqrt{2\pi}}\,\mathrm{e}^{-\frac{z^2}{2}}\,\mathrm{d}\,z = \frac{1}{\sqrt{2\pi}}$$

yields the first claim, since clearly $\mathbb{P}(Y_t \geq 1) \leq 1$.
For the second claim we observe that the collection

$$\left(\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i}\leq t}\right)_{x\geq 1}$$

is independent and thus

$$\mathbb{V}[B_t] = \sum_{x=1}^{\infty} \mathbb{V}\left[\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i}\leq t}\right].$$

Because for each $x \geq 1$ the variable A_x is independent of the i.i.d. collection $\{\tau_x^{x,i} : i \geq 1\}$ we obtain by the Blackwell-Girshick equality (e.g. [27, Theorem 5.10] that

$$\begin{aligned}\mathbb{V}\left[\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i}\leq t}\right] &= \mathbb{V}[A]\mathbb{E}[\mathbb{1}_{\tau_x^{x,1}\leq t}]^2 + \mathbb{E}[A]\mathbb{V}[\mathbb{1}_{\tau_x^{x,1}\leq t}]\\ &= \mathbb{V}[A]p(x,t)^2 + \mathbb{E}[A]p(x,t)(1-p(x,t))\\ &= p(x,t)\mathbb{E}[A] + p(x,t)^2(\mathbb{V}[A]-\mathbb{E}[A]).\end{aligned}$$

Thus, we end up with

$$\begin{aligned}\mathbb{V}[B_t] =& \sum_{x=1}^{\infty} p(x,t)\mathbb{E}[A] + p(x,t)^2(\mathbb{V}[A]-\mathbb{E}[A])\\ =& \mathbb{E}[B_t] + (\mathbb{V}[A]-\mathbb{E}[A])\sum_{x=1}^{\infty} p(x,t)^2.\end{aligned}$$

Squaring out $p(x,t)^2 = 4\mathbb{P}(Y_t \geq x)^2 - 4\mathbb{P}(Y_t \geq x)\mathbb{P}(Y_t = x) + \mathbb{P}(Y_t = x)^2$, we compute

$$\sum_{x=1}^{\infty} |4\mathbb{P}(Y_t \geq x)\mathbb{P}(Y_t = x) + \mathbb{P}(Y_t = x)^2| \leq \sum_{x=1}^{\infty} 5\mathbb{P}(Y_t = x) \leq \frac{5}{2}.$$

Next, we note that $\mathbb{P}(Y_t \geq x)^2$ is the probability that two independent random walks are both greater than or equal to x. Thus,

$$\begin{aligned}\sum_{x=1}^{\infty} \mathbb{P}(Y_t \geq x)^2 &= \sum_{x=1}^{\infty} \mathbb{P}(\min\{Y_t^{0,1}, Y_t^{0,2}\} \geq x) \\ &= \mathbb{E}[\min\{Y_t^{0,1}, Y_t^{0,2}\} \mathbb{1}_{\min\{Y_t^{0,1}, Y_t^{0,2}\} \geq 0}].\end{aligned}$$

Similar to before, we thus obtain by the Berry-Esseen bound [41] that we have

$$\mathbb{E}[\min\{Y_t^{0,1}, Y_t^{0,2}\} \mathbb{1}_{\min\{Y_t^{0,1}, Y_t^{0,2}\} \geq 0}] = \sqrt{t}\mathbb{E}[\min\{Z_1, Z_2\} \mathbb{1}_{\min\{Z_1, Z_2\} \geq 0}] + \mathcal{O}(1)$$

with $Z_1, Z_2 \sim \mathcal{N}(0,1)$ i.i.d.. A simple computation now shows

$$\begin{aligned}\mathbb{E}[\min\{Z_1, Z_2\} \mathbb{1}_{\min\{Z_1, Z_2\} \geq 0}] &= 2 \int_0^\infty \int_0^x y \frac{\mathrm{e}^{-\frac{y^2}{2}}}{\sqrt{2\pi}} \,\mathrm{d}\, y \frac{\mathrm{e}^{-\frac{x^2}{2}}}{\sqrt{2\pi}} \,\mathrm{d}\, x \\ &= \frac{1}{\pi} \int_0^\infty \left(1 - \mathrm{e}^{-\frac{x^2}{2}}\right) \mathrm{e}^{-\frac{x^2}{2}} \,\mathrm{d}\, x \\ &= \frac{1}{\pi} \int_0^\infty \mathrm{e}^{-\frac{x^2}{2}} \,\mathrm{d}\, x - \frac{1}{\pi} \int_0^\infty \mathrm{e}^{-x^2} \,\mathrm{d}\, x \\ &= \frac{1}{\sqrt{2\pi}} - \frac{1}{2\sqrt{\pi}} = \frac{\sqrt{2}-1}{2\sqrt{\pi}}.\end{aligned}$$

Putting everything together, this yields

$$\begin{aligned}\mathbb{V}[B_{t,0}] &= \sqrt{t} \left(4 \frac{\sqrt{2}-1}{2\sqrt{\pi}} (\mathbb{V}[A] - \mathbb{E}[A]) + \sqrt{\frac{2}{\pi}} \mathbb{E}[A] \right) + \mathcal{O}(1) \\ &= \sqrt{t} \left(\frac{2-\sqrt{2}}{\sqrt{\pi}} \mathbb{E}[A] + 2 \frac{\sqrt{2}-1}{\sqrt{\pi}} \mathbb{V}[A] \right) + \mathcal{O}(1).\end{aligned}$$ □

Using this asymptotic and that B_t is the sum of independent variables

$$\sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t}$$

we can establish a central limit theorem for $(B_t)_{t \geq 0}$, which then extends to a central limit theorem for $(X_\iota)_{\iota \geq 0}$ by using the duality

$$\{X_\iota \leq t\} = \{B_t \geq \iota\}$$

for any $t \geq 0, \iota \geq 0$.

Proof of Theorem 4.2. By definition, for $|w| \leq \sqrt{\frac{c_\mu \iota}{4c_\sigma}}$ we have

$$\{K_\iota \leq w\} = \left\{ X_\iota \leq \left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3} \right\} = \left\{ B_{\left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3}} \geq \iota \right\} \tag{4.4}$$

To show the claim, we will first establish a central limit theorem for $(B_t)_{t\geq 0}$ and then carry it over to $(X_\iota)_{\iota \geq 1}$ by using (4.4). For $t > 0$ we denote $\sigma_t^2 := \mathbb{V}[B_t]$ and for $x = 1, \dots, \lceil t \rceil$ we set

$$Z_{t,x} := \frac{1}{\sigma_t} \sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t} - \mathbb{E}[A] p(x,t)$$

and

$$Z_{t,\lceil t \rceil + 1} := \frac{1}{\sigma_t} \sum_{x=\lceil t \rceil + 1}^{\infty} \sum_{i=1}^{A_x} \mathbb{1}_{\tau_x^{x,i} \leq t} - \mathbb{E}[A] p(x,t).$$

We note that for each $t > 0$, the collection $(Z_{t,x})_{x=1,\dots,\lceil t \rceil + 1}$ is centered, independent, and sums to $\frac{B_t}{\sigma_t}$, thus

$$\mathbb{V}\left[\sum_{x=1}^{\lceil t \rceil + 1} Z_{t,x}\right] = 1.$$

Hence, to establish a central limit theorem, it suffices to check the Lindeberg condition (e.g. [27, Theorem 15.44]):

$$\lim_{t\to\infty} \sum_{x=1}^{\lceil t \rceil + 1} \mathbb{E}[Z_{t,x}^2 \mathbb{1}_{|Z_{t,x}| > \varepsilon}] = 0$$

for any $\varepsilon > 0$. First, we note that as seen in the proof of Lemma 4.5, we have

$$\sigma_t^2 \mathbb{E}[Z_{t,\lceil t \rceil + 1}^2] = \sum_{x=\lceil t \rceil + 1}^{\infty} \mathbb{E}[A] p(x,t) + (\mathbb{V}[A] - \mathbb{E}[A]) p(x,t)^2.$$

For any $\vartheta \in (0,1]$ we have

$$\begin{aligned} \mathbb{P}(Y_t \geq x) \leq \mathrm{e}^{-\vartheta x} \mathbb{E}[\mathrm{e}^{\vartheta Y_t}] &= \mathrm{e}^{-\vartheta x} \sum_{k=0}^{\infty} \mathrm{e}^{-t} \frac{(t)^k}{k!} \left(\frac{\mathrm{e}^{\vartheta} + \mathrm{e}^{-\vartheta}}{2}\right)^k \\ &= \exp(-\vartheta x + t(\cosh\vartheta - 1)) \leq \exp(-\vartheta x + \vartheta^2 t) \end{aligned}$$

Plugging in $\vartheta = \frac{1}{\sqrt{t}}$ for $t \geq 1$ yields $\mathbb{P}(Y_t \geq x) \leq \exp\left(-\frac{x}{\sqrt{t}} + 1\right)$. Using the reflection principle, we hence obtain

$$p(x,t) = \mathbb{P}\left(\sup_{0\leq s\leq t} Y_s \geq x\right) \leq 2\mathbb{P}(Y_t \geq x) \leq 2\,\mathrm{e}^{1-\frac{x}{\sqrt{t}}}.$$

This yields

$$\begin{aligned}\sigma_t^2\mathbb{E}[Z_{t,\lceil t\rceil+1}^2] &\leq 2\,\mathrm{e}\,\mathbb{E}[A]\frac{\exp\left(-\frac{\lceil t\rceil+1}{\sqrt{t}}\right)}{1-\exp\left(-\frac{1}{\sqrt{t}}\right)} + 4\,\mathrm{e}^2(\mathbb{V}[A]-\mathbb{E}[A])\frac{\exp\left(-2\frac{\lceil t\rceil+1}{\sqrt{t}}\right)}{1-\exp\left(-\frac{2}{\sqrt{t}}\right)}\\ &\leq C_1\sqrt{t}\exp\left(-\sqrt{t}\right)\overset{t\to\infty}{\to} 0\end{aligned}$$

for some constant $C_1 = C_1(\mathbb{E}[A],\mathbb{V}[A])$. On the other hand, using that for large $t \geq 0$ we have

$$Z_{t,x}^2 \leq (A_x + \mathbb{E}[A])^2$$

we have by dominated convergence

$$\lim_{t\to\infty}\mathbb{E}[Z_{t,x}^2\mathbb{1}_{|Z_{t,x}|>\varepsilon}] = 0.$$

for any $x \geq 1$. This already shows the Lindeberg condition and thus proves that

$$\sup_{w\in\mathbb{R}}\left|\mathbb{P}\left(\frac{B_t-\mathbb{E}[B_t]}{\sigma_t}\leq w\right)-\Phi(w)\right|\overset{t\to\infty}{\to} 0, \tag{4.5}$$

where Φ is the cdf of the standard normal distribution $\mathcal{N}(0,1)$.
To obtain the CLT for $(X_\iota)_{\iota\geq 1}$ we proceed as follows. Taylor-expanding the square root, we have for $|w| \leq \sqrt{\frac{c_\mu\iota}{4c_\sigma}}$ that

$$\begin{aligned}c_\mu\sqrt{\left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3}} &= \iota\sqrt{1+w\sqrt{\frac{4c_\sigma}{c_\mu\iota}}}\\ &= \iota + \sqrt{\frac{c_\sigma}{c_\mu}}w\sqrt{\iota} - \frac{c_\sigma w^2}{2c_\mu}\left(1+r_1(\iota,w)\right)\end{aligned}$$

with $|r_1(\iota,w)| = \mathcal{O}\left(\frac{|w|}{\sqrt{\iota}}\right)$. Similar we obtain for $|w| \leq \sqrt{\frac{c_\mu\iota}{4c_\sigma}}$

$$\begin{aligned}\sqrt{c_\sigma}\left(\left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{\frac{4c_\sigma}{c_\mu^5}\iota^3}\right)^{\frac{1}{4}} &= \sqrt{\frac{\iota c_\sigma}{c_\mu}}\left(1+w\sqrt{\frac{4c_\sigma}{c_\mu\iota}}\right)^{\frac{1}{4}}\\ &= \sqrt{\frac{\iota c_\sigma}{c_\mu}}\left(1+\frac{w}{2}\sqrt{\frac{c_\sigma}{c_\mu\iota}}\left(1+r_2(\iota,w)\right)\right)\end{aligned}$$

with $|r_2(\iota,w)| = \mathcal{O}\left(\frac{|w|}{\sqrt{\iota}}\right)$. We set $t(\iota,w) := \left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{\frac{4c_\sigma}{c_\mu}\iota^3}$ and

$$\overline{B}_{\iota,w} := \frac{B_{t(\iota,w)} - c_\mu\sqrt{t(\iota,w)}}{\sqrt{c_\sigma}t(\iota,w)^{\frac{1}{4}}}$$

and by the expansions above, obtain that for $|w| \leq \sqrt{\frac{c_\mu \iota}{4c_\sigma}}$, the event in (4.4) is equal to the event that

$$\begin{aligned}\overline{B}_{\iota,w} &\geq -\frac{w}{1+\frac{w}{2}\sqrt{\frac{c_\sigma}{c_\mu \iota}}\,(1+r_2(\iota,w))} - \frac{c_\sigma w^2(1+r_1(\iota,w))}{2\sqrt{\iota c_\sigma c_\mu}\left(1+\frac{w}{2}\sqrt{\frac{c_\sigma}{c_\mu \iota}}\,(1+r_2(\iota,w))\right)}\\ &= -w(1+r_3(\iota,w)),\end{aligned}$$

for some $|r_3(\iota,w)| = \mathcal{O}\left(\frac{|w|}{\sqrt{\iota}}\right)$. Using that by Lemma 4.5 we have

$$\mathbb{E}[B_{t(\iota,w)}] = c_\mu\sqrt{t(\iota,w)} + \overline{r}_1(\iota,w), \quad \mathbb{V}[B_{t(\iota,w)}] = c_\sigma\sqrt{t(\iota,w)} + \overline{r}_2(\iota,w)$$

with $\sup_{\iota\geq 1, |w|\leq\sqrt{\frac{c_\mu\iota}{4c_\sigma}}} \max\{\overline{r}_1(\iota,w), \overline{r}_2(\iota,w)\} < \infty$. We finally obtain that the event $\{K_\iota \leq w\}$ in (4.4) is equal to

$$\frac{B_{t(\iota,w)} - \mathbb{E}[B_{t(\iota,w)}]}{\sqrt{\mathbb{V}[B_{t(\iota,w)}]}} \geq -w(1+r_3(\iota,w))\sqrt{1+\frac{\overline{r}_2(\iota,w)}{\mathbb{V}[B_{t(\iota,w)}]}} - \frac{\overline{r}_1(\iota,w)}{\sqrt{\mathbb{V}[B_{t(\iota,w)}]}}. \quad (4.6)$$

Using (4.5) and that the normal distribution is symmetric and has a continuous cdf, we thus obtain that for any $w \in \mathbb{R}$ we have

$$\lim_{\iota\to\infty} \mathbb{P}(K_\iota \leq w) = \Phi(w). \qquad \square$$

Assuming higher regularity of A, we can also bound the higher absolute central moments by Rosenthal's inequality.

Lemma 4.6. *For $q > 2$ there exists a $C_q > 0$ such that*

$$\mathbb{E}\left[|B_{t,n} - \mathbb{E}[B_{t,n}]|^q\right] \leq C_q \mathbb{E}[A^q] t^{\frac{q}{4}}.$$

Proof. By Rosenthal's inequality, there are constants $C_1(q), C_2(q)$ such that we have

$$\begin{aligned}\mathbb{E}\left[|B_{t,n} - \mathbb{E}[B_{t,n}]|^q\right] &\leq C_1(q)\sum_{x=1}^{\infty}\mathbb{E}\left[\left|\sum_{i=1}^{A_x}\mathbb{1}_{\tau_x^{x,i}\leq t} - \mathbb{E}[A]p(x,t)\right|^q\right]\\ &\quad + C_2(q)\left(\sum_{x=1}^{\infty}\mathbb{E}\left[\left|\sum_{i=1}^{A_x}\mathbb{1}_{\tau_x^{x,i}\leq t} - \mathbb{E}[A]p(x,t)\right|^2\right]\right)^{\frac{q}{2}}\end{aligned} \quad (4.7)$$

Using Lemma 4.5, we can bound the second sum by $C_3(q)\mathbb{E}[A^2]t^{\frac{q}{4}}$.
To bound the first sum, we note that there is some constant $C_4(q)$ such that

$$(x+y)^q \leq C_4(q)(x^q + y^q)$$

for all $x, y \geq 0$. Hence, we can bound the first sum in (4.7) by

$$C_1(q)C_4(q)\sum_{x=1}^{\infty}\mathbb{E}\left[\left|\sum_{i=1}^{A_x}\mathbb{1}_{\tau_x^{x,i}\leq t}\right|^q\right] + C_1(q)C_4(q)\sum_{x=1}^{\infty}\mathbb{E}[A]^q p(x,t)^q. \tag{4.8}$$

Because $q > 2$, we have $p(x,t)^q \leq p(x,t)$, and thus the second sum in (4.8) can, using Lemma 4.5, again be bounded by $C_5(q)\mathbb{E}[A]^{q+1}\sqrt{t}$. To bound the remaining sum, setting $a_n = \mathbb{P}(A = n)$, we calculate

$$\begin{aligned}
\mathbb{E}\left[\left|\sum_{i=1}^{A_x}\mathbb{1}_{\tau_x^{x,i}\leq t}\right|^q\right] &= \sum_{n=1}^{\infty} a_n \mathbb{E}\left[\left|\sum_{i=1}^{n}\mathbb{1}_{\tau_x^{x,i}\leq t}\right|^q\right] \\
&= \sum_{n=1}^{\infty} a_n \sum_{k=0}^{n} k^q \binom{n}{k} p(x,t)^k (1-p(x,t))^{n-k} \\
&\leq \sum_{n=1}^{\infty} a_n n^{q-1} \sum_{k=0}^{n} k \binom{n}{k} p(x,t)^k (1-p(x,t))^{n-k} \\
&= \sum_{n=1}^{\infty} a_n n^q p(x,t) = \mathbb{E}[A^q]p(x,t).
\end{aligned}$$

And hence, using Lemma 4.5, we can bound the first sum in (4.8) by $\mathbb{E}[A^q]C_6(q)\sqrt{t}$.

Combining all of these estimates, and noting that $\mathbb{E}[A] \leq \mathbb{E}[A^2] \leq \mathbb{E}[A^q]$, we can find a constant $C_q > 0$ such that

$$\mathbb{E}\left[|B_{t,n} - \mathbb{E}[B_{t,n}]|^q\right] \leq C_q \mathbb{E}[A^q] t^{\frac{q}{4}},$$

which concludes the proof. □

Assuming even more regularity on A, namely finite exponential moments of some positive order, we can bound the moment generating function of the centered and normed amount B_t.

Lemma 4.7. *Suppose that $\mathbb{E}[\exp(\vartheta A)] < \infty$ for some $\vartheta > 0$. Then there is a constant C_1 such that for all $t > 0$ and $\lambda \in \left[-\sqrt{\mathbb{V}[B_t]}, \sqrt{\mathbb{V}[B_t]}\right]$ such that $\mathbb{E}\left[\exp\left(\frac{\lambda}{\sqrt{\mathbb{V}[B_t]}}A\right)\right] < \infty$ we have*

$$\mathbb{E}\left[\exp\left(\lambda\frac{B_t - \mathbb{E}[B_t]}{\sqrt{\mathbb{V}[B_t]}}\right)\right] \leq \exp\left(\frac{\lambda^2}{2} + C_1\frac{|\lambda|^3}{t^{\frac{1}{4}}}\right).$$

Proof. We set $\sigma^2 := \mathbb{V}[B_t], \mu := \mathbb{E}[B_t], a_n := \mathbb{P}(A = n)$ and

$$Z_t := \frac{B_t - \mu}{\sigma}$$

and let $t > 0$ and $\lambda \in [-\sigma, \sigma]$ such that $\mathbb{E}\left[\exp\left(\frac{\lambda}{\sigma} A\right)\right] < \infty$. Using the independence for different x and that $(1 + p(\exp(\cdot) - 1))^n$ is the moment generating function of a binomial distribution $\mathrm{Bin}(n, p)$, we can compute

$$\begin{aligned}
\mathbb{E}[\exp(\lambda Z_t)] &= \mathbb{E}\left[\exp\left(\frac{\lambda}{\sigma}\sum_{x=1}^{\infty}\sum_{i=1}^{A_x}\mathbb{1}_{\tau_x^{x,i}\leq t} - \mathbb{E}[A]p(x,t)\right)\right] \\
&= \prod_{x=1}^{\infty}\mathbb{E}\left[\sum_{n=0}^{\infty}\mathbb{1}_{A_x = n}\exp\left(\frac{\lambda}{\sigma}\left(\sum_{i=1}^{n}\mathbb{1}_{\tau_x^{x,i}\leq t} - \mathbb{E}[A]p(x,t)\right)\right)\right] \\
&= \prod_{x=1}^{\infty}\sum_{n=0}^{\infty} a_n \mathbb{E}\left[\exp\left(\frac{\lambda}{\sigma}\sum_{i=1}^{n}\mathbb{1}_{\tau_x^{x,i}\leq t}\right)\right]\exp\left(-\frac{\lambda}{\sigma}\mathbb{E}[A]p(x,t)\right) \\
&= \prod_{x=1}^{\infty}\sum_{n=0}^{\infty} a_n \left(1 + p(x,t)\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)\right)^n \exp\left(-\frac{\lambda}{\sigma}\mathbb{E}[A]p(x,t)\right) \\
&= \prod_{x=1}^{\infty}\mathbb{E}\left[\left(1 + p(x,t)\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)\right)^A\right]\exp\left(-\frac{\lambda}{\sigma}\mathbb{E}[A]p(x,t)\right).
\end{aligned}$$

Note that because $p(x,t) < 1$ and by the assumption $\mathbb{E}\left[\exp\left(\frac{\lambda}{\sigma}A\right)\right] < \infty$, the expression is well defined.
Setting now

$$h(z) := \exp\left(-\frac{\lambda}{\sigma} z\mathbb{E}[A]\right)\mathbb{E}\left[\left(1 + z\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)\right)^A\right], \quad (z \in [0,1))$$

we want to find the Taylor expansion of h up to the second order. For this we write $G(z) := \mathbb{E}[z^A], s_z := 1 + z\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)$ and compute

$$h'(z) = \exp\left(-\frac{\lambda}{\sigma} z\mathbb{E}[A]\right)\left(-\frac{\lambda}{\sigma}\mathbb{E}[A]G(s_z) + \left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)G'(s_z)\right),$$

$$\begin{aligned}
h''(z) = \exp\left(-\frac{\lambda}{\sigma} z\mathbb{E}[A]\right)\Bigg(&\frac{\lambda^2}{\sigma^2}\mathbb{E}[A]^2 G(s_z) - 2\frac{\lambda}{\sigma}\mathbb{E}[A]\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)G'(s_z) \\
&+ \left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)^2 G''(s_z)\Bigg)
\end{aligned}$$

$$\begin{aligned}
h'''(z) = \exp\left(-\frac{\lambda}{\sigma} z\mathbb{E}[A]\right)\Bigg(&-\frac{\lambda^3}{\sigma^3}\mathbb{E}[A]^3 G(s_z) + 3\frac{\lambda^2}{\sigma^2}\mathbb{E}[A]^2\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)G'(s_z) \\
&- 3\frac{\lambda}{\sigma}\mathbb{E}[A]\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)^2 G''(s_z) + \left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)^3 G'''(s_z)\Bigg).
\end{aligned}$$

Because

$$G^{(n)}(1) = \mathbb{E}[A(A-1)\cdots(A-n+1)]$$

for any $n \geq 1$ we thus have

$$\begin{aligned} h(z) = R_2(z) + 1 + z\mathbb{E}[A]\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1 - \frac{\lambda}{\sigma}\right) \\ + \frac{z^2}{2}\left(\mathbb{E}[A]^2\left(\frac{\lambda^2}{\sigma^2} - 2\frac{\lambda}{\sigma}\left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)\right) + \left(\mathrm{e}^{\frac{\lambda}{\sigma}} - 1\right)^2\mathbb{E}[A^2 - A]\right), \end{aligned}$$

with $|R_2(z)| \leq \frac{|\lambda|^3}{\sigma^3}(1 + \mathcal{O}(\frac{|\lambda|}{\sigma}))z^3$. Using the power series expansion of the exponential function, we further obtain

$$h(z) = R_2(z) + z\mathbb{E}[A]\frac{\lambda^2}{2\sigma^2}\left(1 + \mathcal{O}\left(\frac{|\lambda|}{\sigma}\right)\right) + \frac{z^2}{2}\frac{\lambda^2}{\sigma^2}\left(\mathbb{V}[A] - \mathbb{E}[A] + \mathcal{O}\left(\frac{|\lambda|}{\sigma}\right)\right).$$

Using the series expansion of the logarithm, we thus find $\log(h(z))$ is equal to

$$\frac{\lambda^2}{2\sigma^2}\left(z\mathbb{E}[A]\left(1 + \mathcal{O}\left(\frac{|\lambda|}{\sigma}\right)\right) + z^2\left(\mathbb{V}[A] - \mathbb{E}[A] + \mathcal{O}\left(\frac{|\lambda|}{\sigma}\right)\right)\right) + R_3(z)$$

with $|R_3(z)| \leq |R_2(z)| + \frac{\lambda^4}{\sigma^4}\left(1 + \mathcal{O}\left(\frac{|\lambda|}{\sigma}\right)\right)z^2$. Using this estimate, and that as shown in Lemma 4.5, we have

$$\sigma^2 = \sum_{x=1}^{\infty}\mathbb{E}[A]p(x,t) + (\mathbb{V}[A] - \mathbb{E}[A])p(x,t)^2 = \Theta(\sqrt{t}),$$

we find

$$\begin{aligned} \mathbb{E}[\exp(\lambda Z_t)] &= \prod_{x=1}^{\infty} h(p(x,t)) = \exp\left(\sum_{x=1}^{\infty}\log(h(p(x,t)))\right) \\ &= \exp\left(\frac{\lambda^2}{2} + \mathcal{O}\left(\sqrt{t}\frac{|\lambda|^3}{\sigma^3}\right)\right) = \exp\left(\frac{\lambda^2}{2} + \mathcal{O}\left(\frac{|\lambda|^3}{t^{\frac{1}{4}}}\right)\right). \end{aligned}$$

We note here that by choice $|\lambda| \leq \sigma$ and hence the higher powers of $\frac{|\lambda|}{\sigma}$ are absorbed in the $\mathcal{O}\left(\frac{|\lambda|^3}{\sigma^3}\right)$-term. Fixing some suitable constant C_1 to bound the $\mathcal{O}\left(\frac{|\lambda|^3}{t^{\frac{1}{4}}}\right)$ finishes the proof. □

Proof of Theorem 4.3. We adopt the definition $t(\iota, w) = \left(\frac{\iota}{c_\mu}\right)^2 + w\sqrt{4\frac{c_\sigma}{c_\mu}\iota^3}$ from the proof of Theorem 4.2. By assumption, for large enough $\iota \geq 1$ we have $w = f(\iota) = o(\sqrt{\iota}) \leq \sqrt{\frac{c_\mu \iota}{4c_\sigma}}$ and hence the event $\{|K_\iota| \geq f(\iota)\}$ is equal to the event that

$$\{B_{t(\iota,f(\iota))} < \iota\} \cup \{B_{t(\iota,-f(\iota))} \geq \iota\}.$$

Again, by the assumption $w = f(\iota) = o(\sqrt{\iota}) \leq \sqrt{\frac{c_\mu \iota}{4c_\sigma}}$, we can apply the Taylor expansions in the proof of Theorem 4.2. Thus, we see that the events above are equal to

$$\{B_{t(\iota,f(\iota))} < \iota\} = \left\{ \frac{B_{t(\iota,f(\iota))} - \mathbb{E}[B_{t(\iota,f(\iota))}]}{\sqrt{\mathbb{V}[B_{t(\iota,f(\iota))}]}} < -f(\iota)(1 + r_1(\iota)) \right\}$$
$$\{B_{t(\iota,-f(\iota))} \geq \iota\} = \left\{ \frac{B_{t(\iota,-f(\iota))} - \mathbb{E}[B_{t(\iota,-f(\iota))}]}{\sqrt{\mathbb{V}[B_{t(\iota,-f(\iota))}]}} \geq f(\iota)(1 + r_2(\iota)) \right\}$$

for some $r_1(\iota) = o(1), r_2(\iota) = o(1)$. The exponential Markov inequality, combined with Lemma 4.7, yields that there is a C_1 such that for any $\lambda > 0$ and $\iota \geq 1$ large enough we have

$$\mathbb{P}(B_{t(\iota,f(\iota))} < \iota) \leq \frac{\exp\left(\frac{\lambda^2}{2} + C_1 \frac{\lambda^3}{\sqrt{\iota}}\right)}{\exp\left(\lambda f(\iota)(1 + r_1(\iota))\right)}$$

and

$$\mathbb{P}(B_{t(\iota,-f(\iota))} \geq \iota) \leq \frac{\exp\left(\frac{\lambda^2}{2} + C_1 \frac{\lambda^3}{\sqrt{\iota}}\right)}{\exp\left(\lambda f(\iota)(1 + r_2(\iota))\right)}.$$

In particular, choosing $\lambda = 1$ and $\iota \geq 1$ large enough, we obtain

$$\mathbb{P}(|K_\iota| \geq f(\iota)) \leq 2 \exp\left(1 - \frac{f(\iota)}{2}\right).$$

Possibly increasing the constant $C_1 \geq 2\,\mathrm{e}$ for small ι yields the claim. If we assume $\mathbb{E}[\exp(\lambda A)] < \infty$ for all $\lambda \in \mathbb{R}$ we can minimize the estimation above by choosing for $i = 1, 2$

$$\lambda_i := \frac{\sqrt{12C_1 f(\iota)\sqrt{\iota}(1 + r_i(\iota)) + \iota} - \sqrt{\iota}}{6C_1} = f(\iota)(1 + r_i(\iota) + \widetilde{r}_i(\iota))$$

for some $\widetilde{r}_i(\iota) = o(1)$. Plugging this in yields the better estimation

$$\mathbb{P}(|K_\iota| \geq f(\iota)) \leq C_2 \exp\left(-c_2 f(\iota)^2\right)$$

for some $C_2, c_2 > 0$ and all $\iota \geq 1$. $\square$

Proof of Theorem 4.4. Let $Z_t = \frac{B_t - \mathbb{E}[B_t]}{\sqrt{\mathbb{V}[B_t]}}, C_1$ be as in Lemma 4.7, and $\Delta = \frac{t^{\frac{1}{4}}}{2C_1} < \mathbb{V}[B_t]$ for t large enough. Then, using Lemma 4.7 and [46, Remark 1″], choosing their parameters $H = 1$ and $\overline{\delta}$ as in their equation (6), we have for $1 \leq w \leq \frac{10t^{\frac{1}{4}}}{311C_1}$ that

$$\frac{1-\mathbb{P}(Z_t \leq w)}{1-\Phi(w)} = \exp\left(\frac{w^3}{\Delta}\lambda\left(\frac{w}{\Delta}\right)\right)\left(1+f_1\left(\frac{20}{311},1\right)\frac{w}{\Delta}\right) \quad \text{and}$$
$$\frac{\mathbb{P}(Z_t \leq -w)}{\Phi(-w)} = \exp\left(-\frac{w^3}{\Delta}\lambda\left(-\frac{w}{\Delta}\right)\right)\left(1+f_2\left(\frac{20}{311},1\right)\frac{w}{\Delta}\right),$$

where $\lambda(t)$ is the power series of Cramèr, which depends on the cumulants of Z_t, and f_1, f_2 are defined in [46]. In particular, for ι large enough and some constants $c_3 > 0$ and $0 \leq w \leq c_3\iota^{\frac{1}{6}}$, we obtain using (4.6), and noting that $|w| = \mathcal{O}\left(\iota^{\frac{1}{6}}\right)$ makes all the error terms small, that

$$\frac{\mathbb{P}(K_\iota > w)}{1-\Phi(w)} = 1+\mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right) \quad \text{and} \quad \frac{\mathbb{P}(K_\iota \leq -w)}{\Phi(-w)} = 1+\mathcal{O}\left(\frac{1+w^3}{\sqrt{\iota}}\right). \qquad \square$$

4.3.3 Proof of Theorem 4.1

In this section we will prove the upper bound on the speed of infection claimed in Theorem 4.5. The approach will be to use the results established for $(X_\iota)_{\iota\geq 1}$ and, in particular, Lemma 4.6 and Lemma 4.4 to show in Lemma 4.8 that the infection time of a host with immunity ι with high probability takes at least $\Omega(\iota^2)$ time units. Finally, fixing some suitable slowly varying function b, we use the tail assumption on I to show that for large enough n, there is a host with immunity $\Omega\left(n^{\frac{1}{\alpha}}b(n)\right)$ that needs to be infected before the front reaches n. Using this reasoning, we show in Lemma 4.9 that the infection times are on a superlinear scale. Finally, we will use the relation

$$r_t = \sup\{n \geq 0 : \rho_n \leq t\}$$

to establish that if $(\rho_n)_{n\geq 0}$ grows superlinearly, then $(r_t)_{t\geq 0}$ has to grow sublinearly with the inverse exponent as ρ_n.

The first lemma makes the heuristic described in the introduction precise and shows that deviations of $X_{\iota,n}$ below the order ι^2 become exceedingly rare for large immunities ι.

Lemma 4.8. *For any $\beta > \mathbb{E}[A]\sqrt{\frac{2}{\pi}}$ and $q > 2$, there is a $C_1 > 0$ such that for any $\iota \geq 1$ we have*

$$\mathbb{P}\left(X_{\iota,n} \leq \left(\frac{\iota}{\beta}\right)^2\right) \leq C_1\mathbb{E}[A^q]\iota^{-\frac{q}{2}}.$$

Proof. Fix $\beta > \mathbb{E}[A]\sqrt{\frac{2}{\pi}}$ and note that by Lemma 4.5 for large enough ι we have

$$\mathbb{E}\left[B_{\left(\frac{\iota}{\beta}\right)^2,n}\right] = \mathbb{E}[A]\sqrt{\frac{2}{\pi}}\frac{\iota}{\beta} + \mathcal{O}(1) < \iota.$$

Hence, using Lemma 4.6 and the Markov inequality, for ι large enough we obtain

$$\begin{aligned}
\mathbb{P}\left(X_{\iota,n} \leq \left(\frac{\iota}{\beta}\right)^2\right) &= \mathbb{P}\left(B_{\left(\frac{\iota}{\beta}\right)^2,n} \geq \iota\right)\\
&\leq \mathbb{P}\left(\left|B_{\left(\frac{\iota}{\beta}\right)^2,n} - \mathbb{E}\left[B_{\left(\frac{\iota}{\beta}\right)^2,n}\right]\right|^q \geq \left(\iota - \mathbb{E}\left[B_{\left(\frac{\iota}{\beta}\right)^2,n}\right]\right)^q\right)\\
&\leq \frac{C_q\mathbb{E}[A^q]\left(\frac{\iota}{\beta}\right)^{\frac{q}{2}}}{\left(\iota - \mathbb{E}\left[B_{\left(\frac{\iota}{\beta}\right)^2,n}\right]\right)^q} = \frac{C_q\mathbb{E}[A^q]\left(\frac{\iota}{\beta}\right)^{\frac{q}{2}}}{\left(\iota - \mathbb{E}[A]\sqrt{\frac{2}{\pi}}\frac{\iota}{\beta} + \mathcal{O}(1)\right)^q}\\
&= \frac{C_q\mathbb{E}[A^q]}{\beta^{\frac{q}{2}}\left(1 - \frac{\mathbb{E}[A]}{\beta}\sqrt{\frac{2}{\pi}} + \mathcal{O}\left(\frac{1}{\iota}\right)\right)}\iota^{-\frac{q}{2}} =: C_1\mathbb{E}[A^q]\iota^{-\frac{q}{2}}.
\end{aligned}$$

Possibly increasing the constant C_1 this estimate then also holds for any $\iota \geq 1$, which finishes the proof. □

With the help of the lower bound $X_{I_n,n} \leq \rho_n$ and the trivial bound $\rho_{n+1} \geq \rho_n$ for any $n \in \mathbb{N}$, we can now show that almost surely the infection times grow superlinearly for large n, because

$$\left(\sup_{1\leq k\leq n} X_{I_k,k}\right)_{n\geq 1}$$

already grows superlinear.

Lemma 4.9. *There is a smooth, slowly varying function* $b_1 : [1,\infty) \to (0,\infty)$ *and an almost surely finite* $N \in \mathbb{N}$ *such that for all* $n \geq N$ *we have*

$$\rho_n \geq n^{\frac{2}{\alpha}} b_1(n)$$

Proof. Recall the assumption that

$$\mathbb{P}(I \geq n) = n^{-\alpha} l(n)$$

for some slowly varying function l. Fix some smooth, slowly varying function

$$b : [1,\infty) \to (0,\infty)$$

such that

$$\left(\exp\left(-\frac{l\left(n^{\frac{1}{\alpha}}b(n)\right)}{b(n)^{\alpha}}\right)\right)_{n\in\mathbb{N}} \in l^1(\mathbb{N})$$

and define a sequence of barrier sites

$$B_n := \inf\left\{k \geq 1 : I_k > n^{\frac{1}{\alpha}}b(n)\right\}. \tag{4.9}$$

B_n is geometrically distributed with success probability $\mathbb{P}\left(I > n^{\frac{1}{\alpha}}b(n)\right)$. Using the assumption on I, the limit

$$\left(1-\frac{1}{x}\right)^x \uparrow \frac{1}{\mathrm{e}} \quad (x \to \infty),$$

and that $x \mapsto x^{\frac{1}{\alpha}}b(x)$ is eventually increasing, we obtain that for large enough n we have

$$\begin{aligned}\mathbb{P}(B_n > n) &\leq \left(1 - n^{-1}b(n)^{-\alpha}l\left(n^{\frac{1}{\alpha}}b(n)\right)\right)^n \\ &\leq \exp\left(-\frac{l\left(n^{\frac{1}{\alpha}}b(n)\right)}{b(n)^{\alpha}}\right)\end{aligned}$$

In particular, using the Borel-Cantelli lemma, this implies that there is an almost surely finite $N_0 \in \mathbb{N}$ such that for all $n \geq N_0$ we have

$$B_n \leq n. \tag{4.10}$$

We fix some $q \in (2\alpha, \vartheta)$ such that $\mathbb{E}[A^q] < \infty$ and some $\beta > \mathbb{E}[A]\sqrt{\frac{2}{\pi}}$. Because B_n depends only on $\mathbf{I}$ and $(X_{k,n})_{k\geq 1, n\in\mathbb{Z}}$ depends only on $\mathbf{Y}, \mathbf{A}$, using Lemma 4.8, we obtain that

$$\mathbb{P}\left(X_{\left\lceil n^{\frac{1}{\alpha}}b(n)\right\rceil, B_n} \leq \left(\frac{\left\lceil n^{\frac{1}{\alpha}}b(n)\right\rceil}{\beta}\right)^2\right) \leq C_1\mathbb{E}[A^q]n^{-\frac{q}{2\alpha}}b(n)^{-\frac{q}{2}}$$

for all $n \geq 1$. By definition, $\frac{q}{2\alpha} > 1$, and thus the Borel-Cantelli lemma and the eventual monotonicity of $x \mapsto x^{\frac{1}{\alpha}}b(x)$ imply that there is an almost surely finite $N_1 \in \mathbb{N}$ such that for all $n \geq N_1$ we have

$$X_{\left\lceil n^{\frac{1}{\alpha}}b(n)\right\rceil, B_n} > \left(\frac{n^{\frac{1}{\alpha}}b(n)}{\beta}\right)^2. \tag{4.11}$$

In conclusion, we obtain that for any $n \geq N_0 \vee N_1$ we have

$$\rho_n \overset{(4.10)}{\geq} \rho_{B_n} \overset{\text{Lemma 4.4}}{\geq} X_{I_{B_n}, B_n} \overset{(4.9)}{\geq} X_{\left\lceil n^{\frac{1}{\alpha}} b(n) \right\rceil, B_n} \overset{(4.11)}{>} \left(\frac{n^{\frac{1}{\alpha}} b(n)}{\beta} \right)^2 .$$

Setting $N := N_0 \vee N_1$ and $b_1 := \frac{b^2}{\beta^2}$ already shows the claim. □

Proof of Theorem 4.1. Let b_1 be as in Lemma 4.9, the event $\mathcal{N} \in \mathcal{F}$ with $\mathbb{P}(\mathcal{N}) = 0$ such that for any $\omega \in \Omega \setminus \mathcal{N}$ there is an $N = N(\omega)$ with

$$\rho_n \geq n^{\frac{2}{\alpha}} b_1(n)$$

for all $n \geq N$.

Clearly $r_t \geq 0$, and hence it suffices to show

$$\limsup_{t \to \infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} = 0$$

almost surely for some slowly varying function $b_2(t)$. On the event

$$\left\{ \limsup_{t \to \infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} > 0 \right\},$$

there exists an increasing sequence of random times $(T_k)_{k \geq 1}$ with $\lim_{k \to \infty} T_k = \infty$ and

$$r_{T_k} > \frac{\limsup_{t \to \infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)}}{2} T_k^{\frac{\alpha}{2}} b_2(T_k)$$

for all $k \geq 1$. By definition, setting $V := \frac{\limsup_{t \to \infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)}}{2}$ means that

$$\rho_{\left\lceil V T_k^{\frac{\alpha}{2}} b_2(T_k) \right\rceil} \leq T_k$$

for all $k \geq 1$. We choose a smooth, slowly varying function $b_2 : [1, \infty) \to (0, \infty)$ such that

$$\lim_{t \to \infty} b_2(t)^{\frac{2}{\alpha}} b_1 \left(t^{\frac{\alpha}{2}} b_2(t) \right) = 0$$

and observe that for $k(\omega)$ large enough we thus have

$$T_k(\omega) < \left\lceil V(\omega) T_k(\omega)^{\frac{\alpha}{2}} b_2(T_k(\omega)) \right\rceil^{\frac{2}{\alpha}} b_1 \left(\left\lceil V(\omega) T_k(\omega)^{\frac{\alpha}{2}} b_2(T_k(\omega)) \right\rceil \right).$$

Now, if there is some

$$\omega \in \left\{ \limsup_{t \to \infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} > 0 \right\} \cap (\Omega \setminus \mathcal{N}),$$

then for $k(\omega)$ large enough such that

$$\left\lceil VT_k(\omega)^{\frac{\alpha}{2}} b_2(T_k(\omega))\right\rceil \geq N(\omega),$$

we would have the contradiction

$$T_k < \left\lceil VT_k^{\frac{\alpha}{2}} b_2(T_k)\right\rceil^{\frac{2}{\alpha}} b_1\left(\left\lceil VT_k^{\frac{\alpha}{2}} b_2(T_k)\right\rceil\right) \leq \rho_{\left\lceil VT_k^{\frac{\alpha}{2}} b_2(T_k)\right\rceil} \leq T_k.$$

Hence,

$$\left\{\limsup_{t\to\infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} > 0\right\} \subset \mathcal{N}$$

and thus

$$\mathbb{P}\left(\limsup_{t\to\infty} \frac{r_t}{t^{\frac{\alpha}{2}} b_2(t)} > 0\right) = 0,$$

which concludes the proof. □

4.3.4 Proof of Theorem 4.5

For the details of the construction, we refer to Chapter 3 and now only shortly summarize the results. We assume that the initial configuration is given by some random tuple

$$(0, \mathcal{L}, \emptyset, F, I_1)$$

as in (4.3) such that

$$|\mathcal{L}| \geq I_1$$

with positive probability. As shown in Lemma 3.3, there is a positive probability for the parasites to survive, and, by abuse of notation, in this section we denote by $\mathbb{P}$ the probability measure conditioned on this event of survival and by $\mathbb{E}$ the corresponding expectation, as all results will only be stated under this conditioned measure. In this setting we obtain the following results following the constructions and proofs of Chapter 3.

Lemma 4.10. *Suppose that $\alpha' \in (1,2]$ is such that $\mathbb{E}[I^{\alpha'}] < \infty$. There is an almost surely finite M and an explicit constant $k_0 \in \mathbb{N}$ such that $\rho_{M+k_0} < \infty$ almost surely conditioned on the survival of parasites. Furthermore, there is a sequence $(\nu_{M+n})_{n\geq k_0}$ such that for all $n \geq k_0$ we have*

$$\rho_{M+n} - \rho_{M+n-1} \leq \nu_{M+n}$$

and for all $q < \frac{\alpha'}{2}$ *we have* $\mathbb{E}[|\nu_{M+n}|^q] < \infty$ *for all* $n \geq k_0$ *and*

$$\lim_{n\to\infty} \mathbb{E}[|\nu_{M+n}|^q] = \gamma_q$$

for some constants $(\gamma_q)_{q<\frac{\alpha'}{2}}$. *Also, the sequence* $(\nu_{M+n})_{n\geq k_0}$ *is* ϕ*-mixing with*

$$\sup_{\substack{E\in\sigma(\nu_{M+j}:1\leq j\leq n),\mathbb{P}(E)>0,\\ B\in\sigma(\nu_{M+j}:j\geq n+k)}} |\mathbb{P}(B|E) - \mathbb{P}(B)| \leq Ck^{-\alpha'+1+\varepsilon}.$$

Proof. The construction and proofs are given in Chapter 3. To avoid confusion, we note here that the results in Chapter 3 were under the assumption $\mathbb{E}[I^{2\alpha}] < \infty$ for some $\alpha > 1$, whereas in this section we assumed $\mathbb{E}[I^{\alpha'}] < \infty$ for some $\alpha' \in (1,2]$. In particular, take note of the factor 2 in the exponent of the assumption in Chapter 3.
We can follow the same proofs as given in Chapter 3, and the main difference is that under our assumption $\mathbb{E}[I^{\alpha'}] < \infty$ for $\alpha \in (1,2]$ we obtain, by the one big jump principle, the estimate

$$\mathbb{P}\left(\sum_{k=1}^{n} I_k > \beta_I n\right) = \mathcal{O}\left(n^{1-\alpha'}\right).$$

Plugging in this estimate in the crucial Lemma 3.15 yields the corresponding result with an $\mathcal{O}\left(n^{-\alpha'+\varepsilon}\right)$ bound. The results above then follow from this estimate as in Chapter 3 and correspond to the results given in Proposition 3.10, Lemma 3.17, Lemma 3.19, and Corollary 3.29. □

Proof of Theorem 4.5. Fix some $q < \frac{\alpha'}{2}$ and a $q' \in \left(q, \frac{\alpha'}{2}\right)$. Arguing analogously as in Lemma 3.42 will establish an almost sure law of large numbers for $(|\nu_{M+k}|^{q'})_{k\geq k_0}$ and, in particular, show that

$$\lim_{n\to\infty} \frac{1}{n}\left(|\rho_{M+k_0-1}|^{q'} + \sum_{k=k_0}^{n} |\nu_{M+k}|^{q'}\right) = \gamma_{q'}$$

with $\gamma_{q'}$ as in Lemma 4.10. Hence, using that $x \mapsto x^{q'}$ is concave since $q' < 1$, we obtain

$$0 \leq \frac{1}{n^{\frac{1}{q}}}\left(\rho_{M+k_0-1} + \sum_{k=k_0}^{n} \nu_{M+k}\right) \leq \frac{1}{n^{\frac{1}{q}-\frac{1}{q'}}}\left(\frac{|\rho_{M+k_0-1}|^{q'} + \sum_{k=k_0}^{n} |\nu_{M+k}|^{q'}}{n}\right)^{\frac{1}{q'}}.$$

As argued above, the second term converges to $\gamma_{q'}^{\frac{1}{q'}}$ and the first term converges to 0, since $q < q'$. Hence we obtain

$$\lim_{n\to\infty} \frac{1}{n^{\frac{1}{q}}} \left(\rho_{M+k_0-1} + \sum_{k=k_0}^{n} \nu_{M+k} \right) = 0. \tag{4.12}$$

An analog of Proposition 3.38 will finish the proof.

Proposition 4.11. *Let* $(X_n)_{n\geq 1}$ *be a sequence of non-negative random variables such that for* $q \in (0,1)$ *we have*

$$\lim_{n\to\infty} \frac{1}{n^{\frac{1}{q}}} \sum_{j=1}^{n} X_j = 0$$

almost surely. Then

$$\lim_{t\to\infty} \frac{1}{t^q} \sup \left\{ n \geq 1 : \sum_{j=1}^{n} X_j \leq t \right\} = \infty$$

almost surely

Proof. We set

$$m_t := \sup \left\{ n \geq 1 : \sum_{j=1}^{n} X_j \leq t \right\}.$$

Let $C > 0$ and let ω be such that

$$\lim_{n\to\infty} \frac{1}{n^{\frac{1}{q}}} \sum_{j=1}^{n} X_j(\omega) = 0.$$

We choose $n_0 = n_0(\omega) \in \mathbb{N}$ large enough such that

$$0 \leq \frac{1}{n^{\frac{1}{q}}} \sum_{k=1}^{n} X_k(\omega) < \frac{1}{(2C)^{\frac{1}{q}}} \quad \text{and} \quad \frac{n+1}{n} \leq 2$$

for all $n \geq n_0$. Set $t_0 = t_0(\omega) := \sum_{k=1}^{n_0} X_k(\omega)$. Clearly for all $t \geq t_0$ we have $m_t(\omega) \geq n_0$, thus we have

$$0 \leq \frac{\sum_{k=1}^{m_t+1} X_k}{(m_t+1)^{\frac{1}{q}}} < \frac{1}{(2C)^{\frac{1}{q}}} \tag{4.13}$$

and by definition of m_t we have

$$\sum_{k=1}^{m_t} X_k \leq t < \sum_{k=1}^{m_t+1} X_k. \tag{4.14}$$

Taking the reciprocal, taking the q-th power, and multiplying by $\frac{m_t+1}{2}$, this yields

$$C \overset{(4.13)}{<} \frac{m_t+1}{2\left(\sum_{k=1}^{m_t+1} X_k\right)^q} \overset{(4.14)}{<} \frac{m_t+1}{2t^q} \leq \frac{m_t}{t^q}$$

for all $t \geq t_0$. As C was arbitrary, this finishes the proof. $\square$

Applying proposition 4.11 with $X_1 = \rho_{M+k_0-1}, X_j = \nu_{M+k_0+j-2}$ for $j \geq 2$, using (4.12) finishes the proof of Theorem 4.5, since

$$r_t = \sup\{n \geq 0 : \rho_n \leq t\} \geq \sup\left\{n \geq 1 : \sum_{k=1}^{n} X_k \leq t\right\},$$

where we define $\sup \emptyset := 0$. $\square$

Chapter 5

Infection in higher dimensions for a two-type host population

5.1 Introduction

In this chapter, we investigate the spread of parasites in a spatially distributed host population on more general graphs $G = (V, E)$. The main focus will be on the integer lattice $\mathbb{Z}^d$ for $d \geq 2$ and the d-regular tree $\mathbb{T}_d$ for $d \geq 3$. By abuse of notation, we denote by $\mathbf{0}$ a distinguished vertex in any graph G, which only for $\mathbb{Z}^d$ will actually be the origin, and assume that initially the host at $\mathbf{0}$ is infected and a random number of parasites, distributed as some random variable A, is placed at $\mathbf{0}$. Parasites move on G according to symmetric simple random walks in discrete time and attempt to infect a host and reproduce when they jump onto a host. As hosts often have an immune response against infections, we assume that a host with probability $1 - p \in [0, 1)$ is completely immune (immune for short) to infection; that is, whenever a parasite tries to infect such a host, parasite reproduction is prevented and the parasite is killed. If the host is not immune, it is called susceptible. In this case, the attacking parasite kills the host, the attacking parasite reproduces (and dies afterwards), and sets free a random number of offspring, distributed as A and independent of everything else. For simplicity we assume that hosts do not reproduce.

Remark 5.1. *We point out the important difference that in the setting of this chapter, the immunity of a host does not get reduced, and (completely) immune hosts remain in the system forever, whereas in Chapters 3 and 4, conditioned* *on the survival of parasites, every host will die eventually.*

We note here that the infecting parasite also dies at a successful infection, and we allow for 0 offspring to be produced at an infection. Hence, at which steps the parasite population decreases depends on the two parameters p and $\mathbb{P}(A = 0)$. In this chapter we investigate the survival probability of the parasite population and show that there is a phase transition for a positive survival probability in the parameter p on both $\mathbb{Z}^d$ and $\mathbb{T}_d$. Also we investigate recurrence to the origin and show that this does not happen on any graph if the offspring distribution has a finite mean. We will call our model the Spatial Infection Model with host Immunity, or SIMI for shorthand. In Chapter 3 and Chapter 4, we carry out a more thorough analysis of a similar model on $\mathbb{Z}$, where hosts can lose their immunity after getting attacked a random number of times.

Our model generalizes the frog model that was introduced by Telcs and Wormland (1999, [49]). The frog model is a classical interacting particle system on some graph $G = (V, E)$, which involves two types of particles, which are usually called *active frogs* and *sleeping frogs*. Each site $v \in V$ can host a finite number of frogs of the same type; sleeping frogs do not move, and active frogs perform simple nearest neighbor random walks on G. All sleeping frogs on a vertex $v \in V$ immediately transform into active frogs after an active frog jumps onto the vertex v. In our model, the active frogs correspond to parasites, and the sleeping frogs on a vertex $v \in V$ correspond to the offspring that are produced after the host at v gets infected. In this sense, in the case that $p = 1$ and that there is almost surely at least one offspring produced after a successful infection, our model coincides with the classical frog model, where the number of sleeping frogs on each vertex is i.i.d. distributed as $A - 1$.

It was shown by Alves, Machado, and Popov in [2, 3] that the frog model on $\mathbb{Z}^d$ satisfies a shape theorem for the set $S_d(n)$ of vertices visited by some active frog up to time n. They showed that, if an i.i.d. amount of sleeping frogs is placed on each vertex, there is a convex deterministic set $\mathcal{A}_d$, possibly depending on the distribution of sleeping frogs per vertex, such that for any $\varepsilon \in (0, 1)$

$$(1-\varepsilon)\mathcal{A}_d \subset \frac{S_d(n)}{n} \subset (1+\varepsilon)\mathcal{A}_d$$

for all n large enough almost surely.

We will use this result to show our main result, Theorem 5.3. The proof relies on coupling with a supercritical site percolation and using that, due to the shape theorem, if all hosts in a large region are susceptible, then with high probability an infection starting in that region will reach any vertex in a suitable subregion after a linear amount of steps. Making the region big enough and then p close to 1 will allow us to conclude that the coupled site percolation is supercritical and show the positive survival probability.

Next to the trivial survival of the frogs in the classical model, another main difference from a mathematical standpoint is the following. In the classical frog model, using a collection of independent simple symmetric random walks to assign each frog its trajectory after waking up yields an intuitive way to couple initial configurations in a monotone way. However, doing this in our model will not be a monotone coupling if we allow for 0 offspring to be produced after a successful infection. This happens because when and where a specific parasite dies depends on the location of hosts that are still alive and will produce 0 offspring. But this, of course, depends on whether another parasite has already reached that vertex. A concrete example of this phenomenon can be found in Example 5.5. Also, we note that due to immune hosts remaining in the system forever, the trajectories of parasites are no longer independent, as they possibly die at the same immune host.

In [1], Alves, Machado, and Popov introduced and studied a different way of introducing a death mechanic to the frog model. In their model, each frog, independent of everything else, has a lifetime that is geometrically distributed with parameter $\widetilde{p} \in [0, 1)$. That is, each time a frog takes a step, it dies with probability $\widetilde{p}$. We note that in this setting, the trajectories of frogs after awakening are still independent. Also, because the death mechanic only depends on $\widetilde{p}$, in contrast to our model where it also depends on $\mathbb{P}(A = 0)$, it is directly clear that the survival probability of frogs is monotone in the parameter $\widetilde{p}$.

A similar model, that does not include the death of frogs but sleepy frogs that need to be visited a random number of times before waking up, was introduced by Junge, McDonald, Pulla, and Reeves in [26]. However, because visiting frogs do not die upon meeting a sleepy frog and just keep on moving without waking up the frog, the trajectories of frogs remain independent, and the shape theorem on $\mathbb{Z}^d$ remains unchanged; see Section 2.1. They study the process on d-ary trees using quite different methods from ours.

5.2 Main results

In this section we present the main results of this chapter. We will establish a phase transition for the probability of survival of the parasite population in the parameter p. Also, we investigate recurrence to the origin and show that under some mild assumptions on the offspring distribution, recurrence cannot occur on any graph. First, we present results on the survival of the parasite population, and then we lay out the results on the recurrence to the origin. Also, we further distinguish the results on the integer lattice $\mathbb{Z}^d$ and the d-regular tree $\mathbb{T}_d$.

5.2.1 Survival of the parasite population

In this section we will, for any graph G and offspring distributed as A, investigate the value of the critical parameter $p_c(G, A)$, which is defined as

$$\inf\left\{ p \in (0,1] : \mathbb{P}\left(\begin{array}{c} \text{The parasite population in the SIMI on } G \\ \text{with offspring distribution } A \text{ and} \\ \text{susceptible hosts appearing with probability } p \\ \text{survives forever.} \end{array} \right) > 0 \right\}.$$

In Definition 5.7 we will give a formal definition of $p_c(G, A)$ after constructing the process and show in Lemma 5.6 that $p_c(G, A)$ is a critical parameter, in the sense that for $p > p_c(G, A)$ the parasite population on G survives with positive probability and for $p < p_c(G, A)$ it dies out almost surely. First, we note that on a finite graph $G = (V, E)$ the critical parameter $p_c(G, A)$ is trivially 0 for any offspring distribution, because with probability $(\mathbb{P}(A \geq 1)p)^{|V|} > 0$ there is no completely immune host at all, and every infection produces at least one offspring. Hence, in the following we always assume that G is an infinite graph. Our first result states that on any (infinite) graph this critical parameter is positive for any A that has finite expectation.

Theorem 5.1. *For any infinite graph G we have*

$$p_c(G, A) \geq \min\left\{1, \frac{1}{\mathbb{E}[A]}\right\},$$

where $\frac{1}{\infty} := 0$.

A proof will be given in Section 5.4 and relies on coupling with a subcritical Galton-Watson process.

Also, on vertex-transitive graphs we can couple the SIMI with a site percolation to show that the critical parameter must be positive.

Theorem 5.2. *For any vertex-transitive graph G and any offspring distribution A we have*

$$p_c(G, A) \geq \widetilde{p}_c(G),$$

where $\widetilde{p}_c(G)$ is the critical parameter for a site percolation on G. In particular $p_c(\mathbb{Z}, A) = 1$.

Proof. We recall that in a site percolation on G with parameter $p \in [0, 1]$, every vertex is open with probability p, and for $p < \widetilde{p}_c(G)$, almost surely there is no path of infinite length using only open vertices. In particular, this means that for $p < \widetilde{p}_c(G)$, almost surely there is some finite $\mathbf{0} \in \mathcal{J} \subset V$, such that initially every vertex $x \in \mathcal{J} \setminus \{\mathbf{0}\}$ is inhabited by a susceptible host and every vertex $x \in V \setminus \mathcal{J}$, for which there is a $y \in \mathcal{J}$ with graph distance $d(x, y) = 1$, is inhabited by a completely immune host. Since every neighbor of $\mathcal{J}$ is completely immune, a parasite dies when it attempts to leave the finite set $\mathcal{J}$. Thus, the parasite population dies out in finite time. □

5.2.2 Survival on $\mathbb{Z}^d$

Our main theorems will establish that $p_c(\mathbb{Z}^d, A) < 1$ for all $d \geq 2$ under certain conditions on A. The proof relies on coupling with a supercritical site percolation.

Our main theorem states the following.

Theorem 5.3. *For any $d \geq 2$ and A such that $A \geq 1$ almost surely and $\mathbb{E}[A] > 1$, we have*

$$p_c(\mathbb{Z}^d, A) < 1.$$

As a corollary we immediately obtain the following result for general A.

Theorem 5.4. *Let $d \geq 2$ and A such that $\mathbb{E}[A] > 1$. Let $\widetilde{A}$ be a random variable that is distributed as A conditioned to be at least 1, and suppose*

$$\mathbb{P}(A = 0) < 1 - p_c(\mathbb{Z}^d, \widetilde{A}).$$

Then also

$$p_c(\mathbb{Z}^d, A) < 1.$$

5.2.3 Survival on $\mathbb{T}_d$

Similar to $\mathbb{Z}^d$, we obtain a phase transition whenever at least one offspring is generated in an infection.

Theorem 5.5. *Let $A \geq 1$ almost surely and $\mathbb{E}[A] > 1$ and $d \geq 3$. Then*

$$p_c(\mathbb{T}_d, A) < 1.$$

Using the same argument as on $\mathbb{Z}^d$, we will obtain the following.

Theorem 5.6. *Let $d \geq 3$ and A such that $\mathbb{E}[A] > 1$. Let $\widetilde{A}$ be a random variable that is distributed as A conditioned to be at least 1, and suppose*

$$\mathbb{P}(A = 0) < 1 - p_c(\mathbb{T}_d, \widetilde{A}).$$

Then also

$$p_c(\mathbb{T}_d, A) < 1.$$

For a large degree d, parasites will jump onto a new site still inhabited by a host most of the time, and hence, the survival will approximately be like that of a Galton-Watson process. Precisely we obtain the following asymptotic.

Theorem 5.7. *Suppose that $1 < \mathbb{E}[A] < \infty$, then*

$$\lim_{d \to \infty} p_c(\mathbb{T}_d, A) = \frac{1}{\mathbb{E}[A]}.$$

5.2.4 Recurrence to the origin

In this section we will investigate for any vertex-transitive graph $G = (V, E)$ the recurrence to the origin, that is, the probability

$$\vartheta(G, p, A) := \mathbb{P}\left(\begin{array}{c}\text{In the SIMI on } G \text{ with initially only the origin } \mathbf{0} \text{ infected,}\\ \text{offspring distributed as } A \text{ and}\\ \text{susceptible hosts appearing with probability } p,\\ \text{the origin } \mathbf{0} \text{ is visited by a parasite infinitely often}\end{array}\right).$$

Our main result reads that on any vertex-transitive graph, this probability is 0 for any $p < 1$ and offspring distribution with finite expectation.

Theorem 5.8. *Let G be a vertex-transitive graph, $p \in [0, 1)$, and A be such that $\mathbb{E}[A] < \infty$. Then*

$$\vartheta(G, p, A) = 0.$$

Remark 5.2. *For the case $p = 1$, the recurrence of this model on general graphs is still open. It is known to be recurrent on any $\mathbb{Z}^d$ for $d \geq 1$ and any offspring distribution (c.f. [38]). Also, depending on the offspring distribution, the frog model can be recurrent or transient on $\mathbb{T}_d$ for any $d \geq 3$ (c.f. [21]). For almost surely 2 offspring, it is recurrent on $\mathbb{T}_3$ and transient on $\mathbb{T}_6$, but the behavior on $\mathbb{T}_4$ and $\mathbb{T}_5$ is not solved (c.f. [22]).*

5.3 Construction of the Process

In this section we construct the SIMI on G. Although it is intuitively clear that the survival probability should be monotone in the parameter p, Example 5.5 shows that we cannot conclude that simply by relying on the monotonicity of the classical frog model construction. For that reason, we consider two ways of constructing the model, which were also used in Chapter 3 for similar reasons. The first approach is the classical way to assign each parasite that enters the system a label $(x, i) \in V \times \mathbb{N}$ and sample its entire path $(Y_n^{x,i})_{n \geq 0}$. We note that the path $(Y_n^{x,i})_{n \geq 0}$ will get sampled for all $n \geq 0$ but only be used until the time that the parasite dies. The second approach will assign each vertex $x \in V$ sequences $(D_n^x)_{n \in \mathbb{N}}$ of jump directions that a parasite will perform to leave that vertex after jumping onto it. The two constructions satisfy two different important almost sure path properties that will be shown in Lemma 5.4 and 5.6.
To perform the construction, we assume to have a probability space $\mathbf{\Omega}$ on which the following independent collections are defined. We assume there is an i.i.d. collection

$$\mathbf{U} := \{U_x : x \in V\}$$

which are uniformly distributed on $(0, 1)$. For $p \in (0, 1]$ we then define

$$\mathbf{I}^p := \{I_x^p : x \in V\} := \{1 + \infty \cdot \mathbb{1}_{U_x > p} : x \in V\}$$

and we assume there is $A \in L^1(\mathbf{\Omega}; \mathbb{N}_0)$ and an i.i.d. collection

$$\mathbf{A} := \{A_x : x \in V\}$$

distributed as A and independent of $\mathbf{U}$. For the first construction, we assume an independent collection

$$\mathbf{Y} := \{Y^{x,i} : x \in V, i \in \mathbb{N}\} := \{(Y_n^{x,i})_{n \geq 0} : x \in V, i \in \mathbb{N}\}$$

of simple symmetric random walks on G such that $Y^{x,i}$ starts in x and is independent of $\mathbf{A}, \mathbf{U}$ for all $x \in V, i \in \mathbb{N}$.
To perform the second construction, we assume an independent collection

$$\mathbf{D} := \{D_n^x : x \in V, n \in \mathbb{N}\}$$

such that D_n^x is uniformly distributed over $\mathcal{N}_x \subset V$, the neighborhood of x in G, and independent of $\mathbf{U}, \mathbf{A}, \mathbf{Y}$ for all $x \in V, n \in \mathbb{N}$.
For $q \in [1, \infty]$ we define the q-norm on $\mathbb{Z}^d$

$$\|x\|_q := \begin{cases} \left(\sum_{j=1}^d |x_j|^q\right)^{\frac{1}{q}}, & q < \infty \\ \max\{|x_1|, \dots, |x_d|\}, & q = \infty \end{cases}$$

and define for $r \geq 0$ the closed q-ball

$$B_q^d(x, r) := \{y \in \mathbb{R}^d : \|x - y\|_q \leq r\}.$$

For $x, y \in \mathbb{Z}^d$ we define the distance $d_q(x, y) = \|x - y\|_q$ and note that $d := d_1$ is simply the graph distance in $\mathbb{Z}^d$, i.e., the number of edges in the shortest path from x to y.
For any finite set $\mathcal{J} \subset \mathbb{Z}^d$ we define its boundary

$$\partial \mathcal{J} := \{y \in \mathbb{Z}^d \setminus \mathcal{J} | \, \exists x \in \mathcal{J} : \|x - y\|_1 = 1\}$$

and set $\overline{\mathcal{J}} := \mathcal{J} \cup \partial \mathcal{J}$.
On $\mathbb{T}_d$ we note that for any $x, y \in \mathbb{T}_d$ there is a unique path from x to y and define the graph distance $d(x, y)$ to be the number of edges contained in that path. For $x, y \in \mathbb{T}_d$ we say that $x \geq y$ if y is contained in the unique path from $\mathbf{0}$ to x. For a finite set $\mathcal{J} \subset \mathbb{T}_d$ we again define its boundary

$$\partial \mathcal{J} := \{y \in \mathbb{T}_d \setminus \mathcal{J} | \exists x \in \mathcal{J} : d(x, y) = 1\}$$

and again $\overline{\mathcal{J}} := \mathcal{J} \cup \partial \mathcal{J}$.
The state space of the process will be given by tupels

$$\mathbb{S} := \left\{ (\mathcal{I}, \eta) \,\middle|\, \begin{matrix} \mathcal{I} \subset V \text{ finite}, \eta : \overline{\mathcal{I}} \to \mathbb{N}_0 \cup \{-1, -\infty\} \text{ with} \\ \eta(\mathcal{I}) \subset \mathbb{N}_0, \eta(\partial \mathcal{I}) \subset \{-1, -\infty\} \end{matrix} \right\}.$$

The set $\mathcal{I}$ are the currently infected sites without hosts, and η gives the amount of parasites on each infected site $x \in \mathcal{I}$ and the immunity of each site $x \in \partial \mathcal{I}$

that is reachable in one jump from an infected site. For any $p \in (0,1]$ and initial configuration $(\mathcal{I}, \eta) \in \mathbb{S}$, we will construct the SIMI $(\mathcal{I}_t^p, \eta_t^p)_{t\geq 0}$ as a strong Markov process defined on $\boldsymbol{\Omega}$ and taking values in $\mathbb{S}$, equipped with the discrete topology, as well as prove basic properties of the so-coupled processes for different initial configurations in the upcoming subsections 5.3.1 and 5.3.2. We specify the following natural type of random initial configurations.

Definition 5.3. *Let $p \in (0,1]$ and $\mathcal{I} \subset V$ be finite. The random initial configuration $(\mathcal{I}, \eta^{reg,p})$ is defined as*

$$\eta^{reg,p}(w) = \begin{cases} A_w, & w \in \mathcal{I} \\ -I_w^p, & w \in \partial\mathcal{I} \end{cases}.$$

The upcoming constructions, however, will be performed for any initial configuration $(\mathcal{I}, \eta) \in \mathbb{S}$.

5.3.1 Parasite-wise path construction

In this subsection we construct the SIMI by assigning each parasite a label and sampling its entire path at once. We call this the parasite-wise construction.

Suppose there is some initial configuration $(\mathcal{I}, \eta) \in \mathbb{S}$ and a $p \in (0,1]$. To distinguish the two constructions, we will denote the process constructed in this section by $(\widetilde{\mathcal{I}_t^p}(\mathcal{I}, \eta), \widetilde{\eta_t^p}(\mathcal{I}, \eta))_{n\geq 0}$. Also, we will not indicate the underlying graph $G = (V, E)$ on which the process evolves in our notation and always assume that the underlying graph is clear from the context.

The dynamics can be described as follows. We assign each parasite a label $(x, i) \in V \times \mathbb{N}$, where x is the location of the parasite and i enumerates the parasites on the same site x. A parasite with label (x, i) moves along the trajectory $(Y_n^{x,i})_{n\geq 0}$ until it visits a vertex $y \in V$ that is not yet infected. If $I_y^p = \infty$, the parasite is killed and the label (x, i) is removed from the system, and we no longer use $(Y_n^{x,i})_{n\geq 0}$. If $I_y^p = 1$ and $A_y = 0$, then the parasite is also killed and the label (x, i) is removed from the system, but the site y is added to the set of infected sites. If $I_y^p = 1$ and $A_y \geq 1$, then the site y is added to the set of infected sites, the label (x, i) remains in the system, and the labels $(y, 1), \ldots, (y, A_y - 1)$ are added to the system as parasites that follow the trajectory $(Y_n^{y,j})_{n\geq 0}$ for $j = 1, \ldots, A_y - 1$.

We assume that there is some deterministic mechanism to determine the order in which the labels are processed in each time step. For a more formal way of constructing the process, we refer to Chapter 3.

In the following we make the assumption that $A \geq 1$ almost surely. Hence, the second case in the construction does not appear, and labels of parasites only get removed if the parasite visits an immune host.
Then, by construction, the i-th parasite that is generated at some site $x \in V$, follows the path $(Y_n^{x,i})_{n\geq 0}$ until it visits a vertex $y \in V \setminus \mathcal{I}$ with $I_y^p = \infty$. Hence, it is useful to define for any $(x,i) \in V \times \mathbb{N}$ the lifetime and set of vertices visited by the parasite with label (x,i):

$$\begin{aligned} \tau_{x,i}^p(\mathcal{I}) &:= \inf\{n \geq 0 : Y_n^{x,i} \notin \mathcal{I} \text{ and } I^p_{Y_n^{x,i}} = \infty\} \\ \mathcal{V}_{x,i}^p(\mathcal{I}) &:= \{Y_n^{x,i} : 0 \leq n < \tau_{x,i}^p(\mathcal{I})\}. \end{aligned} \tag{5.1}$$

From the construction it is clear that the set

$$\mathcal{I}_\infty^p(\mathcal{I}, \eta^{\text{reg},p}) := \bigcup_{n\geq 0} \widetilde{\mathcal{I}_n^p}(\mathcal{I}, \eta^{\text{reg},p})$$

of vertices that eventually get infected when the initial configuration is given by $(\mathcal{I}, \eta^{\text{reg},p})$ can be described as follows. A vertex $x \in V$ is in $\mathcal{I}_\infty^p(\mathcal{I}, \eta^{\text{reg},p})$, if and only if $x \in \mathcal{I}$ or $x \in V \setminus \mathcal{I}$ and for some $n \geq 1$ there exist

$$x_0 \in \mathcal{I}, i_0 \in \{1, \ldots, A_{x_0}\} \text{ and } x_1, \ldots, x_n \in V \setminus \mathcal{I},\ i_1, \ldots, i_{n-1} \in \mathbb{N} \tag{5.2}$$

with $1 \leq i_m \leq A_{x_m} - 1$ for all $m \in \{1, \ldots n-1\}$, $x_n = x$ and $x_{k+1} \in \mathcal{V}^p_{x_k,i_k}(\mathcal{I})$ for all $k \in \{0, \ldots, n-1\}$. The following lemma is evident.

Lemma 5.4. *Let $0 < p < p' \leq 1$ and $\mathcal{I} \subset \mathcal{I}' \subset V$ be finite, and suppose that $A \geq 1$ almost surely. Then we have*

$$\mathcal{I}_\infty^p(\mathcal{I}, \eta^{reg,p}) \subset \mathcal{I}_\infty^{p'}(\mathcal{I}', \eta^{reg,p'})$$

almost surely. Also, the event that the parasite population with initial configuration $(\mathcal{I}, \eta^{reg,p})$ survives for infinite time is given by the event that

$$\{|\mathcal{I}_\infty^p(\mathcal{I}, \eta^{reg,p})| = \infty\}.$$

Proof. Because $I_x^p \geq I_x^{p'}$ for all $x \in V$, we obtain

$$\tau_{x,i}^p(\mathcal{I}) \leq \tau_{x,i}^{p'}(\mathcal{I}')$$

and thus

$$\mathcal{V}^{p}_{x,i}(\mathcal{I}) \subset \mathcal{V}^{p'}_{x,i}(\mathcal{I}')$$

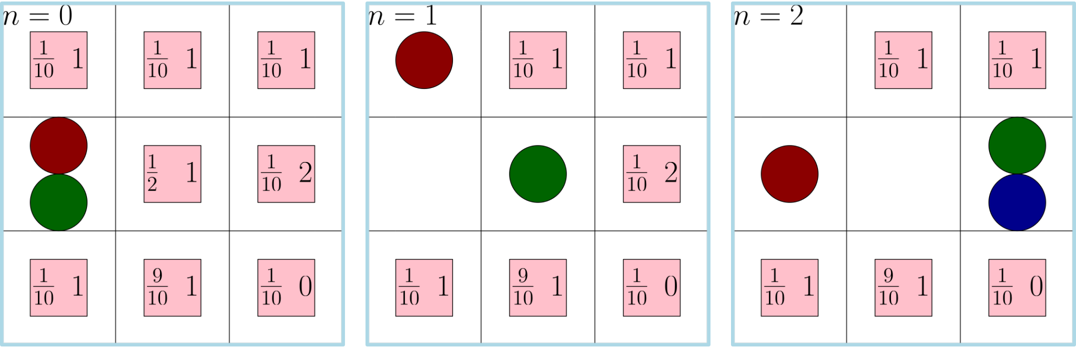
for all $(x, i) \in V \times \mathbb{N}$. This already shows the claim, because if $x \in \mathcal{I}^{p}_{\infty}(\mathcal{I}, \eta^{\mathrm{reg},p}) \setminus \mathcal{I}'$ and

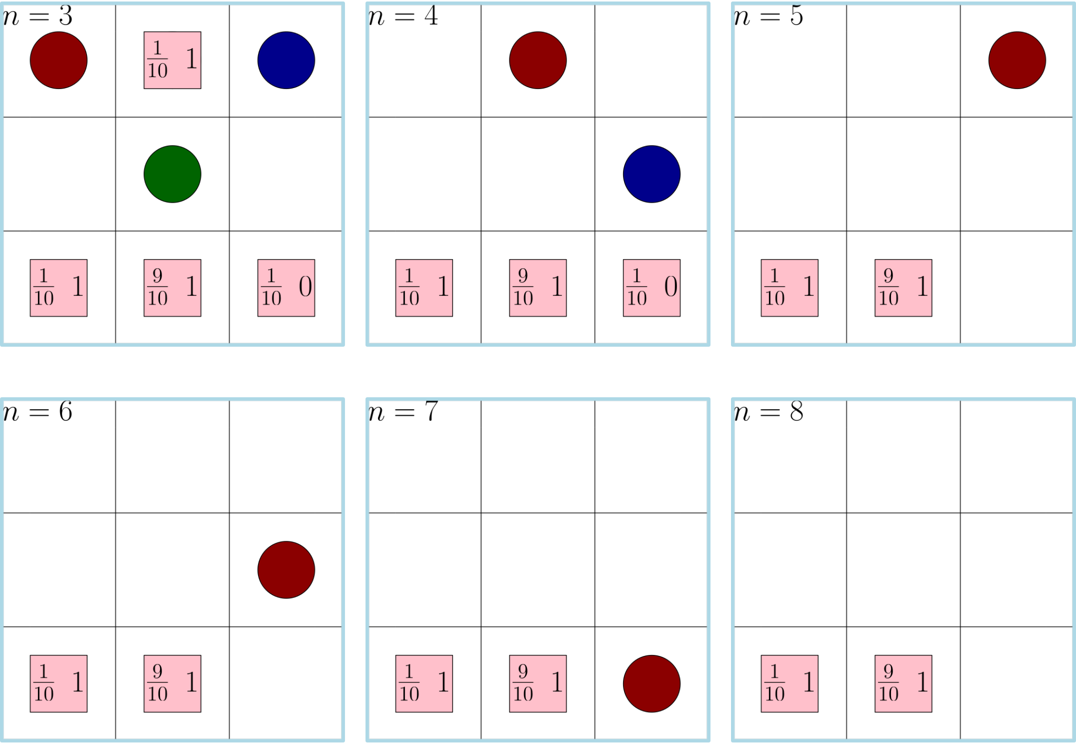
$$x_0 \in \mathcal{I}, i_0 \in \{1, \dots, A_{x_0}\} \text{ and } x_1, \dots, x_n \in V \setminus \mathcal{I},\ i_1, \dots, i_{n-1} \in \mathbb{N}$$

is a sequence as in (5.2), then, starting at the largest $k \in \{0, \dots, n-1\}$ such that $x_k \in \mathcal{I}'$, it is also a sequence that shows $x \in \mathcal{I}^{p'}_{\infty}(\mathcal{I}', \eta^{\mathrm{reg},p'})$.
The second claim is trivially true, because $\tau^{p}_{x,i}(\mathcal{I}), |\mathcal{V}^{p}_{x,i}(\mathcal{I})| < \infty$ almost surely for all labels $(x, i) \in V \times \mathbb{N}$, which shows the $\subset$ inclusion, and it takes at least $d(x, y)$ time steps for the infection to spread from x to y, which shows the $\supset$ inclusion. ☐

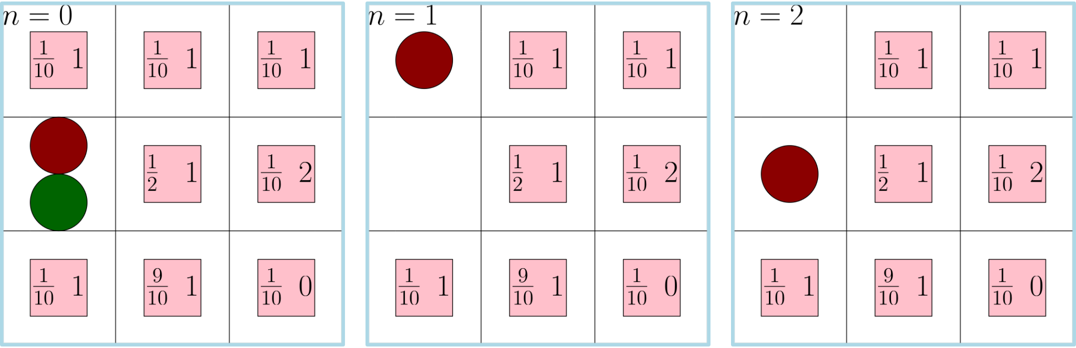
To finish this subsection, we give a concrete example that shows that in this coupling, we can have the process with p survive but the process with p' die out if we allow for $A = 0$ with positive probability.

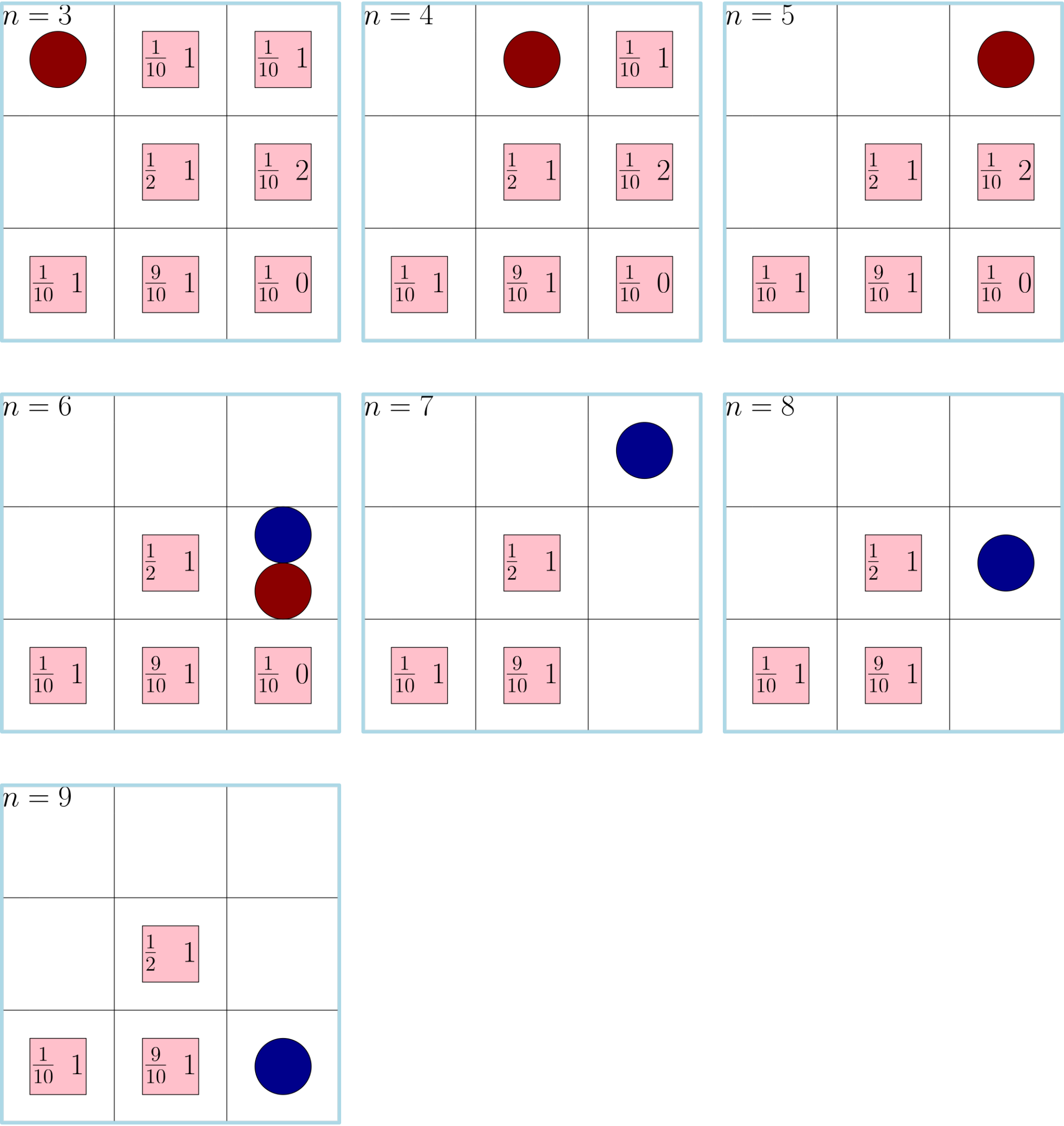
Example 5.5. We give a realization of $\mathbf{Y}, \mathbf{U}, \mathbf{A}$ on $\mathbb{Z}^2$ where the process with a higher probability of susceptible hosts dies out and the process with lower probability survives.
In the following, each square represents a living host, and each circle represents a parasite, with their coloring corresponding to their label. The left number in each host is the value of U_x, determining if the host is immune, and the right number is the value of A_x. We follow the infections for the cases $p = \frac{1}{4}$ and $p' = \frac{3}{4}$. If a parasite disappears, then it jumped onto a neighboring immune host. We begin the case of $p' = \frac{3}{4}$:





In this case the infection died out after 8 steps. Now we investigate how the infection behaves with the same parasite movement but $p = \frac{1}{4}$, which means the host in the center is now immune and prevents the green parasite from waking up the blue parasite early.





In this case the blue parasite does not die when jumping onto the bottom right site, because the host on that vertex was already killed by the green parasite. This blue parasite can now start a new infection and allow for a survival of parasites. This example motivates the upcoming construction to show that we can construct a monotone coupling in the parameter p and thus justify the term of a critical p in Definition 5.7.

5.3.2 Vertex-wise path construction

In this subsection we construct the SIMI by assigning each vertex a sequence of directions in which arriving parasites will leave the vertex. We call this the vertex-wise construction.

The goal is to establish an analog for Lemma 5.4 in the case that $A = 0$ with positive probability, which for the previous parasitewise construction is not true in the case of $A = 0$ with positive probability as seen in Example 5.5.

Suppose there is some initial configuration $(\mathcal{I}, \eta) \in \mathbb{S}$ and a $p \in (0, 1]$. For readability, we drop the reference to the initial configuration and in the following just write $\mathcal{I}_n^p, \eta_n^p$ instead of $\mathcal{I}_n^p(\mathcal{I}, \eta), \eta_n^p(\mathcal{I}, \eta)$. Also, we again leave out the reference to the graph on which the process is defined, as the construction steps are analogous for any graph. To perform the proof of Lemma 5.6, we need to introduce some notation and carry out the construction in a very detailed manner. Informally speaking, at each time step $n \geq 0$, we draw an i.i.d. collection of jump directions, using $\{D_n^x : x \in V, n \in \mathbb{N}\}$ that each parasite will perform and then calculate what the new state is after these jumps, according to the dynamics of the model. For the coupling in Lemma 5.6, we then need to keep track of which random variables are used exactly to sample the jump directions.

At time $n = 0$ we set $\mathcal{I}_0^p = \mathcal{I}$ and $\eta_0^p = \eta$. Also we define,

$$\mathcal{T}_0^p := \{(x, i) \in \mathcal{I} \times \mathbb{N} : 1 \leq i \leq \eta(x)\}$$

and the map $N_0^p = \eta_{|\mathcal{I}}$.

For $n \geq 0$ we now define the state of the process at time $n + 1$. First, we label the elements

$$\mathcal{T}_n^p = \left\{(x_{n,1}^p, i_{n,1}^p), \ldots, (x_{n,k_n}^p, i_{n,k_n}^p)\right\}$$

according to some deterministic labeling rule with $k_n := \#\mathcal{T}_n^p$. We will perform these jumps in this order and construct the sequence of states

$$(\mathcal{I}_{n,j}^p, \eta_{n,j}^p, \mathcal{T}_{n,j}^p, N_{n,j}^p)_{j=1,\ldots,k_n}$$

that the process is in after the j-th jump at time n given by $(x_{n,j}^p, i_{n,j}^p)$. Then we will set

$$(\mathcal{I}_{n+1}^p, \eta_{n+1}^p, \mathcal{T}_{n+1}^p, N_{n+1}^p) := (\mathcal{I}_{n,k_n}^p, \eta_{n,k_n}^p, \mathcal{T}_{n,k_n}^p, N_{n,k_n}^p)$$

as the state of the process after all the jumps at time n have been performed. We begin by defining $\mathcal{I}_{n,0}^p := \mathcal{I}_n^p, \eta_{n,0}^p := \eta_n^p, \mathcal{T}_{n,0}^p := \mathcal{T}_n^p, N_{n,0}^p := N_n^p$. Then for each $j = 1, \dots, k_n$, we do the following steps. We use $D_{i^p_{n,j}}^{x^p_{n,j}}$ to determine the destination of the current jump and thus set $y^p_{n,j} := D_{i^p_{n,j}}^{x^p_{n,j}}$. We distinguish between the following cases:

- $y^p_{n,j} \in \mathcal{I}^p_{n,j-1}$: The site is already infected. Here we set

$$\begin{aligned}
\mathcal{I}^p_{n,j} &:= \mathcal{I}^p_{n,j-1}, \\
\mathrm{dom}(\eta^p_{n,j}) &:= \mathrm{dom}(\eta^p_{n,j-1}), \\
\eta^p_{n,j}(w) &:= \begin{cases} \eta^p_{n,j-1}(x^p_{n,j}) - 1, & w = x^p_{n,j} \\ \eta^p_{n,j-1}(y^p_{n,j}) + 1, & w = y^p_{n,j} \\ \eta(w), & \text{else} \end{cases} \\
\mathrm{dom}(N^p_{n,j}) &:= \mathrm{dom}(N^p_{n,j-1}), \\
N^p_{n,j}(w) &:= \begin{cases} N^p_{n,j-1}(y^p_{n,j}) + 1 =: m^p_{n,j}, & w = y^p_{n,j} \\ N^p_{n,j-1}(w), & \text{else} \end{cases} \\
\mathcal{T}^p_{n,j} &:= \big(\mathcal{T}^p_{n,j-1} \cup \{(y^p_{n,j}, m^p_{n,j})\}\big) \setminus \{(x^p_{n,j}, i^p_{n,j})\}.
\end{aligned}$$

- $y^p_{n,j} \notin \mathcal{I}^p_{n,j-1}$ and $\eta^p_{n,j-1}(y^p_{n,j}) = -1$: The site is inhabited by a susceptible host. Here we set

$$\begin{aligned}
\mathcal{I}^p_{n,j} &:= \mathcal{I}^p_{n,j-1} \cup \{y^p_{n,j}\}, \\
\mathrm{dom}(\eta_{n,j}) &:= \overline{\mathcal{I}^p_{n,j}}, \\
\eta^p_{n,j}(w) &:= \begin{cases} \eta^p_{n,j-1}(x^p_{n,j}) - 1, & w = x^p_{n,j} \\ A_{y^p_{n,j}}, & w = y^p_{n,j} \\ -I^p_w, & w \in \partial\{y^p_{n,j}\} \cap \left(\mathbb{Z}^d \setminus \overline{\mathcal{I}^p_{n,j-1}}\right) \\ \eta^p_{n,j-1}(w), & \text{else} \end{cases} \\
\mathrm{dom}(N^p_{n,j}) &:= \mathcal{I}^p_{n,j}, \\
N^p_{n,j}(w) &:= \begin{cases} A_{y^p_{n,j}}, & w = y^p_{n,j} \\ N^p_{n,j-1}(w), & \text{else} \end{cases} \\
\mathcal{T}^p_{n,j} &:= \left(\mathcal{T}^p_{n,j-1} \cup \{(y^p_{n,j}, i) : 1 \le i \le A_{y^p_{n,j}}\}\right) \setminus \{(x^p_{n,j}, i^p_{n,j})\}.
\end{aligned}$$

  We note that for this construction we do not need to distinguish between the cases $A_{y^p_{n,j}} = 0$ or $A_{y^p_{n,j}} \ge 1$.

- $y^p_{n,j} \notin \mathcal{I}^p_{n,j-1}$ and $\eta^p_{n,j-1}(y^p_{n,j}) = -\infty$: The site is inhabited by an immune host. Here we set

$$\begin{aligned} \mathcal{I}^p_{n,j} &:= \mathcal{I}^p_{n,j-1}, \\ \operatorname{dom}(\eta^p_{n,j}) := \operatorname{dom}(\eta^p_{n,j-1}),\ \eta^p_{n,j}(w) &:= \begin{cases} \eta^p_{n,j-1}(x^p_{n,j}) - 1, & w = x^p_{n,j} \\ \eta(w), & \text{else} \end{cases} \\ N^p_{n,j} &:= N^p_{n,j-1} \\ \mathcal{T}^p_{n,j} &:= \mathcal{T}^p_{n,j-1} \setminus \{(x^p_{n,j}, i^p_{n,j})\}. \end{aligned}$$

Finally we set $\mathcal{I}^p_{n+1} := \mathcal{I}^p_{n,k_n}, \eta^p_{n+1} := \eta^p_{n,k_n}, \mathcal{T}^p_{n+1} := \mathcal{T}^p_{n,k_n}, N^p_{n+1} := N^p_{n,k_n}$, which finishes the construction.

It is clear that the processes $(\mathcal{I}^p_n(\mathcal{I}, \eta), \eta^p_n(\mathcal{I}, \eta))_{n\geq 0}$ and $(\widetilde{\mathcal{I}^p_n}(\mathcal{I}, \eta), \widetilde{\eta^p_n}(\mathcal{I}, \eta))_{n\geq 0}$ have the same distribution, and we now want to show an equivalent of Lemma 5.4 that also holds if $A = 0$ with positive probability.

Lemma 5.6. *Let $0 < p < p' \leq 1$, $\emptyset \neq \mathcal{I} \subset \mathcal{I}' \subset \mathbb{Z}^d$ and suppose A takes values in $\mathbb{N}_0$. Then we have*

$$\mathcal{I}^p_n(\mathcal{I}, \eta^{reg,p}) \subset \mathcal{I}^{p'}_n(\mathcal{I}', \eta^{reg,p'})$$

for all $n \geq 0$ almost surely. In particular we have

$$\bigcup_{n\geq 0} \{\#\eta^{p'}_n(\mathcal{I}', \eta^{reg,p'}) = 0\} \subset \bigcup_{n\geq 0} \{\#\eta_n(\mathcal{I}, \eta^{reg,p}) = 0\},$$

where for any $\eta : \mathbb{Z}^d \to \mathbb{N}_0 \cup \{-1, -\infty\}$ we denote by $\#\eta$ the value

$$\sum_{x\in\mathbb{Z}^d} \mathbb{1}_{\eta(x)>0}\eta(x).$$

Proof. For readability we drop the reference to the initial configuration and, e.g., simply write $\mathcal{I}^p_n$ instead of $\mathcal{I}^p_n(\mathcal{I}, \eta^{\text{reg},p})$ and $\mathcal{I}^{p'}_n$ instead of $\mathcal{I}^{p'}_n(\mathcal{I}', \eta^{\text{reg},p'})$. We do the same for any other variable in the construction of the process, i.e., for any variable used in the construction of $((\mathcal{I}^{p'}_n, \eta^{p'}_n)(\mathcal{I}', \eta^{\text{reg},p'}))_{n\geq 0}$ we only keep the sup-index p' to distinguish between the two processes.

For $n \geq 1$ we define the sets

$$\mathcal{S}^p_n := \bigcup_{m=0}^{n-1} \mathcal{T}^p_m, \quad \mathcal{S}^{p'}_n := \bigcup_{m=0}^{n-1} \mathcal{T}^{p'}_m.$$

The elements of $\mathcal{S}^p_n$ correspond to the jumps that happened before time n in the unprimed process, and analogously $\mathcal{S}^{p'}_n$ are the jumps in the primed process.

We now show by induction that the following conditions hold for all $n \geq 0$:

a) $\mathcal{I}_n^p \subset \mathcal{I}_n^{p'}$.

b) $N_n^p(x) \leq N_n^{p'}(x)$ for all $x \in \mathcal{I}_n^p$.

c) $\mathcal{T}_n^p \subset \mathcal{T}_n^{p'} \cup \mathcal{S}_n^{p'}$.

By assumption the induction hypothesis holds for $n = 0$, since $I_x^p \geq I_x^{p'}$ for all $x \in V$.

To perform the induction step, assume that the induction hypothesis holds for all $0 \leq m \leq n$. In the construction of the state at time $n+1$, we have to go through each

$$(x_{n,1}^p, i_{n,1}^p), \ldots, (x_{n,k_n}^p, i_{n,k_n}^p) \in \mathcal{T}_n^p$$

and show that the induction hypothesis still holds after performing each of these jumps. Again, we distinguish between the outcome of each of these jumps, recalling $y_{n,j}^p = D_{i_{n,j}^p}^{x_{n,j}^p}$ is the site the jump lands on.

- $y_{n,j}^p \notin \mathcal{I}_{n,j-1}^p$ and $\eta_{n,j-1}^p(y_{n,j}^p) = -1$: By c), this jump also occurred in the primed process, and by the coupling, the host was also already infected or susceptible. In any case, this means that the jumps $\{(y_{n,j}^p, i) : 1 \leq i \leq A_{y_{n,j}}\}$ that get added in the unprimed process also got added in the primed process, and thus a), b), and c) still hold.

- $y_{n,j}^p \in \mathcal{I}_{n,j-1}^p$: By c), this jump also occurred in the primed process. If even $y_{n,j}^p \in \mathcal{I}_n^p$, then by a) the site was also already infected in the primed process. By b), the newly added jump $(y_{n,j}^p, N_{n,j}^p(y_{n,j}^p))$ was also added to the primed process, and hence a), b), and c) also hold at time $n+1$. If $y_{n,j}^p \in \mathcal{I}_{n,j-1}^p$ but not $y_{n,j}^p \in \mathcal{I}_n^p$, then for some $1 \leq \ell < j$ we had $y_{n,\ell}^p \notin \mathcal{I}_{n,\ell-1}^p$ and $\eta_{n,\ell-1}^p(y_{n,\ell}^p) = -1$. In this case, by c), this jump $(x_{n,\ell}^p, i_{n,\ell}^p)$ also occurred in the primed process, and by the argument above for the first case, a), b), and c) still hold for $n+1$.

- $y_{n,j}^p \notin \mathcal{I}_{n,j-1}^p$ and $\eta_{n,j-1}^p(y_{n,j}^p) = -\infty$: In this case we have $\mathcal{I}_{n,j}^p = \mathcal{I}_{n,j-1}^p$ and $N_{n,j}^p = N_{n,j-1}^p$ and only $\mathcal{T}_{n,j}^p$ gets smaller. Hence the conditions a), b) and c) trivially hold.

This finishes the induction and shows the first claim. The second claim follows by noting that we still have

$$\bigcup_{n \geq 0} \{\#\eta_n^p = 0\} = \left\{ \left| \bigcup_{n \geq 0} \mathcal{I}_n^p \right| < \infty \right\}.$$

□

This result may seem like the construction in Section 5.3.1 was not necessary. However, in the case of $A \geq 1$, the fact that the infection can be calculated by following the sets

$$\{\mathcal{V}^p_{x,i}(\mathcal{I}) : (x,i) \in V \times \mathbb{N}\}$$

is an important feature that the vertex-wise construction in this section does not provide. The key consequence of this is that in the parasite-wise construction, the infection that started from some vertex x almost surely is contained in the infection starting from some vertex $y \neq x$ after it infected x. In the vertex-wise construction of this section, this almost sure relation is no longer true, because if the process was already running when x was infected, we use different parts of $\mathbf{D}$ to determine the jumps than we use if we freshly start the infection at x. In particular, for the proof of Theorem 5.3, we make use of this feature of the parasite-wise construction to couple the process with a supercritical site percolation.

5.4 Proofs of the results

In this section we prove the theorems stated in Section 5.2. First we formally define the object of interest, the critical parameter $p_c(G, A)$, as follows.

Definition 5.7. *Let $d \geq 2$ and $G = (V, E)$ be a graph, then the value*

$$p_c(G, A) := \inf \left\{ p \in (0,1] : \mathbb{P}\left(\bigcap_{n \geq 0} \{\#\eta^p_t(\{\mathbf{0}\} \subset V, \eta^{reg,p}) > 0\} \right) > 0 \right\}$$

is called the critical parameter for the SIMI on G.

Remark 5.8. *Note that by Lemma 5.6, the survival probability is monotone in $p \in (0,1]$; thus $p_c(G, A)$ is actually the critical parameter.*

Proof of Theorem 5.1. Let $p < \min\left\{1, \frac{1}{\mathbb{E}[A]}\right\}$. On any infinitely large graph, the amount of sites visited by a simple symmetric random walk is infinite. Since completely immune hosts remain in the system forever, and thus each newly visited site is a completely immune host with probability $1-p > 0$, each parasite will eventually hit a susceptible host and produce 0 offspring or hit a completely immune host. Say the parasite with label (x,i) hits some host at a vertex

$y \in V$. Then, if it is the first time that this host is attacked by a parasite, with probability p the host is susceptible and the parasite generates offspring distributed as A, and with probability $1-p$ the host is completely immune and no offspring are generated. If the host at vertex v was already visited by a different parasite than (x, i), then the host has to be a completely immune host, or else it would have been killed by that other parasite. Hence, in this case no offspring are generated. This means that the limit

$$\lim_{n\to\infty} \#\eta_n^p$$

is stochastically dominated by the limit

$$\lim_{n\to\infty} \xi_n$$

where $(\xi_n)_{n\geq 0}$ is a Galton-Watson process with offspring distributed as A with probability p and 0 else. Since this Galton-Watson process has mean offspring $p\mathbb{E}[A] < 1$, the claim follows. $\square$

5.4.1 Proofs of survival results

5.4.2 Proofs for $\mathbb{Z}^d$

Proof of Theorem 5.3. For p close enough to 1, we will couple the SIMI with a supercritical site percolation on $\mathbb{Z}^d$ such that if there is percolation, then the parasite population in the SIMI survives. The idea is to find large areas with only susceptible hosts that will be completely infected if one of the hosts in the center of that area gets infected. Finding an infinite chain of these areas will yield the result.

We note that for $p = 1$, and because $A \geq 1$ almost surely, the construction in Section 5.3.1 is exactly the construction of the classical frog model with random offspring distribution given by $A - 1$. For this model, the set of infected sites satisfies a shape theorem (see [2]). For $x \in \mathbb{Z}^d$ we abbreviate

$$\xi_n^x := \widetilde{\mathcal{I}_n^1}(\{x\}, \eta^{\text{reg},1} - \delta_x)$$

for the set of infected sites in the SIMI at time n with initially only site x infected and $p = 1$. We note here that we initially place only $A_x - 1$ parasites on site x because only those will be added in the system if site x is infected in an already running process. Also we note that due to the assumption $\mathbb{E}[A] > 1$ we have $\mathbb{P}(A \geq 2) > 0$.

Next, we set

$$\overline{\xi}_n^x := \left\{ y + \left(-\frac{1}{2}, \frac{1}{2}\right]^d : y \in \xi_n^x \right\}.$$

Then let $\emptyset \neq \mathcal{A}_d \subset B_1^d(\mathbf{0}, 1)$ be the asymptotic shape of the frog model with offspring distributed as $A - 1$. This means that there is an event $B \in \mathcal{F}$ with $\mathbb{P}(B | A_{\mathbf{0}} \geq 2) = 1$ such that for any $\omega \in B$ and any $\varepsilon \in (0, 1)$ there is an $n_0 = n_0(\omega, \varepsilon)$ such that

$$(1 - \varepsilon)\mathcal{A}_d \subset \frac{\overline{\xi}_n^{\mathbf{0}}(\omega)}{n} \subset (1 + \varepsilon)\mathcal{A}_d$$

for all $n \geq n_0$.

We fix some $\varepsilon \in (0, 1)$, then choose $r > 0$ such that

$$B_\infty^d(\mathbf{0}, r) \subset \mathcal{A}_d,$$

which is possible since $\mathcal{A}_d$ is symmetric, convex, and contains more than 1 point (see [2, Theorem 1.1]), and set

$$R(N) := \left\lceil \frac{N}{r(1 - \varepsilon)} \right\rceil.$$

By taking $N \in \mathbb{N}$ large enough, we can make

$$\theta(N) := \mathbb{P}\left((1 - \varepsilon) B_\infty^d(\mathbf{0}, r) \subset \frac{\overline{\xi}_{R(N)}^{\mathbf{0}}}{R(N)} \middle| A_0 \geq 2 \right)$$

as close to 1 as we want. By the definition of $R(N)$, the event

$$(1 - \varepsilon) B_\infty^d(\mathbf{0}, r) \subset \frac{\overline{\xi}_{R(N)}^{\mathbf{0}}}{R(N)}$$

implies that $B_\infty^d(\mathbf{0}, N) \subset \overline{\xi}_{R(N)}^{\mathbf{0}}$. This means that with a probability $\theta(N)$ as close to 1 as we want, the entire ball $B_\infty^d(\mathbf{0}, N)$ is infected after $R(N)$ steps.

For the coupling of the SIMI with $p \neq 1$ with a supercritical site percolation, we will make p close enough to 1 (depending on N) such that with sufficiently high probability, for each $x \in \mathbb{Z}^d$ there is a large area $V_N(x)$ around $B_\infty^d(x, N)$ with only susceptible hosts. Thus, if x is infected, then after $R(N)$ steps, the entire ball $B_\infty^d(x, N)$ will be infected with probability at least $\theta(N)$, because the SIMI inside $V_N(x)$ is just the frog model. In particular, the existence of an infinite chain of such balls $(B^d_\infty(x_n, N))_{n\geq 1}$ with $x_{n+1} \in B^d_\infty(x_n, N)$ implies the survival of the parasite population. For convenience we assume that N is odd and for

$$x \in N\mathbb{Z}^d = \{(x_1, \dots, x_d) \in \mathbb{Z}^d : N|x_1, \dots, N|x_d\}$$

define

$$V_N(x) = x + \left[\frac{1-N}{2} - R(N), \frac{N-1}{2} + R(N)\right]^d = B^d_\infty\left(x, \frac{N-1}{2} + R(N)\right).$$

We now declare a site percolation on $N\mathbb{Z}^d$ as follows. We say x is open if

$$G_I(x) := \bigcap_{y \in V_N(x)\cap\mathbb{Z}^d} \{I^p_y = 1\}$$

and

$$G_F(x) := \bigcap_{L\in F(x)} \bigcup_{j\in L\cap\mathbb{Z}^d} \{A_j \geq 2, B^d_\infty(j, N) \subset \overline{\xi}^j_{R(N)}\},$$

where $F(x)$ are $2d$ many $(d-1)$-dimensional faces of the cube

$$x + \left[\frac{1-N}{2}, \frac{N-1}{2}\right]^d.$$

The event $G_I(x) \cap G_F(x)$ means that for each face $L \in F(x)$ there is a vertex $j \in L$ such that if j gets infected, then in the frog model and, due to the event $G_I(x)$, also in the SIMI a sufficiently large ball around j will be completely infected after $R(N)$ time steps. Clearly $G_I(x)$ and $G_F(x)$ are independent for each $x \in N\mathbb{Z}^d$. Also, by the independence of $\mathbf{I}^p$, we have $\mathbb{P}(G_I(x)) = p^{(N+2R(N))^d}$, and to calculate the probability of $G_F(x)$ we first note that for each face $L \in F(x)$

$$\mathbb{P}\left(\bigcup_{j\in L\cap\mathbb{Z}^d} \{A_j \geq 2, B^d_\infty(j, N) \subset \overline{\xi}^j_{R(N)}\}\right) \geq (1 - \mathbb{P}(A = 1)^{N^{d-1}})\theta(N).$$

Hence, using that the $2d$ events in the intersection are trivially $2d$-dependent, using [33, Theorem B26]

$$\mathbb{P}(G_F(x)) \geq \left(1 - \left(1 - \theta(N)\left(1 - \mathbb{P}(A = 1)^{N^{d-1}}\right)\right)^{\frac{1}{2d}}\right)^{4d}.$$

Taking N large enough and p close to 1, we can make

$$\mathbb{P}(G_I(x), G_F(x)) \geq \rho$$

for any $\rho \in (0,1)$. Next we observe that for any $L \in F(x)$, the frog model started from any $j \in L$ cannot leave the set $V_N(x)$ until time $R(N)$, because parasites can only move to their neighbors in each time step. Hence, if

$$\|x - x'\|_\infty \geq N + 2R(N),$$

then $G_I(x) \cap G_F(x)$ is independent of $G_I(x') \cap G_F(x')$. In other words, the collection

$$\{\mathbb{1}_{G_I(x),G_F(x)} : x \in N\mathbb{Z}^d\}$$

is K-dependent with

$$K = \left(6 + \frac{4}{r(1-\varepsilon)}\right)^d.$$

In particular, choosing $\rho \in (0,1)$ such that

$$\left(1 - (1-\rho)^{\frac{1}{K}}\right)^2 > p'_c(d),$$

where $p'_c(d)$ is the critical parameter of Bernoulli site percolation on $\mathbb{Z}^d$, we obtain using [33, Theorem B26] again that with positive probability there is percolation.

Now, using Lemma 5.4, in the event that $\mathbf{0}$ is in the infinite cluster of this percolation and that the initial parasites in $\mathbf{0}$ reach all sites of $B^d_\infty\left(\mathbf{0}, \frac{N+1}{2}\right)$ before leaving $V_N(\mathbf{0})$, the SIMI will survive for infinite time. As argued above, this happens with positive probability, and thus we can conclude that

$$p_c(\mathbb{Z}^d, A) < 1. \qquad \square$$

Proof of Theorem 5.4. We define the immunities $\widetilde{I}^p_x := 1 + \infty\mathbb{1}_{U_x > p} + \infty\mathbb{1}_{A_x = 0}$. Using these immunities, only vertices with $A_x \geq 1$ can be infected, and the resulting process will be given by the SIMI with $\widetilde{p} = \max\{0, p - \mathbb{P}(A = 0)\}$ and offspring distributed as $\widetilde{A}$. Also, this process clearly is dominated by the original process with offspring distributed as A and immunity probability $1 - p$. Hence the claim follows by Theorem 5.3. $\square$

5.4.3 Proofs for $\mathbb{T}_d$

Proof of Theorem 5.5. For $x \neq \mathbf{0} \in \mathbb{T}_d$ we denote by $\mathbb{T}^+_d(x) = \{y \in \mathbb{T}_d : y \geq x\}$. Fix some vertex $x_{0,\mathbf{0}}$ adjacent to the root $\mathbf{0}$ and set $\mathbb{T}^+_d := \mathbb{T}_d \setminus \mathbb{T}^+_d(x_{0,\mathbf{0}})$. For $(x,i) \in \mathbb{T}_d \times \mathbb{N}$ we denote by

$$\mathcal{W}^{x,i}_n := \{Y^{x,i}_m : 0 \leq m \leq n\}$$

the set of vertices ever visited by the parasite (x,i) up to time n in the case $p=1$, and simply write $\mathcal{W}_n := \mathcal{W}_n^{\mathbf{0},1}$. Also, for any finite connected set $\mathcal{J} \subset \mathbb{T}_d$ with $\mathbf{0} \in \mathcal{J}$ we denote by

$$\partial_e(\mathcal{J}) := \mathcal{J} \setminus \{x \in \mathcal{J} | \exists y \in \mathcal{J} : y > x\}$$

the external boundary of $\mathcal{J}$, that is, the set of vertices from which $\mathcal{J}$ can be left in one jump. We make the following observations: Since a random walk on $\mathbb{T}_d$ is transient, we have

- with positive probability the walk never leaves $\mathbb{T}_d^+$, i.e.,

$$\theta := \mathbb{P}\left(\bigcap_{n\geq 0}\{\mathcal{W}_n \subset \mathbb{T}_d^+\}\right) > 0$$

- $|\partial_e(\mathcal{W}_n)|$ is nondecreasing and $|\partial_e(\mathcal{W}_n)| \to \infty$ almost surely as $n \to \infty$.

To show a positive survival probability, we construct a supercritical Galton-Watson process $(\xi_n)_{n\geq 0}$ that is dominated by the SIMI. Initially we set $\zeta_0 = \{\mathbf{0}\}$ and $\xi_0 := |\zeta_0|$. If for all $1 \leq i \leq A_{\mathbf{0}}$ we have

$$\mathcal{W}_n^{\mathbf{0},i} \notin \mathbb{T}_d^+$$

for some $n \geq 0$, then we set $\zeta_1 := \emptyset, \xi_1 := 0$. Else, we let

$$j_{1,\mathbf{0}} := \inf\{1 \leq i \leq A_{\mathbf{0}} | \forall n \geq 0 : \mathcal{W}_n^{\mathbf{0},i} \in \mathbb{T}_d^+\}$$

and set

$$\zeta_1 := \partial_e\left(\mathcal{V}^p_{\mathbf{0},j_{1,\mathbf{0}}}(\{\mathbf{0}\})\right) \setminus \left\{Y^{\mathbf{0},j_{1,\mathbf{0}}}_{\tau^p_{\mathbf{0},j_{1,\mathbf{0}}}-1}\right\} \subset \mathbb{T}_d^+$$

the external boundary of the set of sites visited by the parasite $(\mathbf{0}, j_{1,\mathbf{0}})$, excluding the site from which it jumped onto a completely immune host. Again we set $\xi_1 := |\zeta_1|$. We note that by construction we have $\mathbb{T}_d(x) \cap \mathbb{T}_d(y) = \emptyset$ for $x, y \in \zeta_1$ with $x \neq y$.

For $n \geq 1$, if $\zeta_n = \emptyset$, we set $\zeta_{n+1} = \emptyset$ and $\xi_{n+1} = 0$. Else, for each $x \in \zeta_n$, we determine the offspring of x as follows. If $A_x = 1$, then x has no offspring. If $A_x \geq 2$ and for all $1 \leq i \leq A_x - 1$ we have

$$\mathcal{W}_n^{x,i} \notin \mathbb{T}_d(x)$$

for some $n \geq 1$ then x has no offspring. Else, we set

$$j_{n+1,x} := \inf\{1 \leq i \leq A_x - 1 | \forall n \geq 1 : \mathcal{W}_n^{x,i} \in \mathbb{T}_d(x)\}$$

and define the offspring of x as

$$\partial_e \left(\mathcal{V}^p_{x,j_{n+1,x}}(\{x\}) \right) \setminus \left\{ Y^{x,j_{n+1,x}}_{\tau^p_{x,j_{n+1,x}}-1} \right\} \subset \mathbb{T}_d^+(x).$$

Finally we define ζ_{n+1} as the union of all offspring of elements in ζ_n and $\xi_{n+1} := |\zeta_{n+1}|$.

Because the exploration for offspring only considers a so-far unexplored subtree, we obtain that $(\xi_n)_{n\geq 0}$ is a Galton-Watson process. Also, it is clear that by taking p close to 1 we can make this process supercritical, because the amount of visited sites $|\mathcal{V}^p_{x,j_{n+1,x}}(\{x\})|$ has a geometric distribution with parameter $1-p$ and thus goes to ∞ as p approaches 1. $\square$

Proof of Theorem 5.7. The proof is analogous to [1]. To highlight why this approach also works in our model, we give the proof here again.

Since by Theorem 5.1 we have $p_c(\mathbb{T}_d, A) \geq \frac{1}{\mathbb{E}[A]}$, it suffices to show that for any $p > \frac{1}{\mathbb{E}[A]}$ the SIMI survives on $\mathbb{T}_d$ for large enough d. For $s \in \mathbb{N}$, let $A^{(s)} := A\mathbb{1}_{A\leq s}$ and note that by monotone convergence $\mathbb{E}[A^{(s)}] \to \mathbb{E}[A]$. Thus, for s large enough, $p > \frac{1}{\mathbb{E}[A^{(s)}]}$ and it suffices to show that the SIMI on $\mathbb{T}_d$ with offspring distributed as $A^{(s)}$ survives with positive probability. We construct an auxiliary process $(\widetilde{\xi}_n)_{n\geq 0}$ that is dominated by the living parasites at time n and also dominates a supercritical Galton-Watson process. Initially all parasites on $\mathbf{0}$ belong to $\widetilde{\xi}_0$. For $n \geq 0$ the collection $\widetilde{\xi}_{n+1}$ will consist of parasites at distance $n+1$ to the root and will be constructed as follows. We assume some deterministic rule for the order in which the parasites are treated. Then if a parasite in $\widetilde{\xi}_n$ jumps, the following happens:

- If the parasite jumps towards the root, it is removed without offspring.
- If the parasite jumps onto some vertex at distance $n+1$ from the root and a different parasite has already jumped to that vertex, then it is removed without offspring.
- If the parasite jumps onto some vertex at distance $n+1$ from the root, it is the first parasite to jump onto that vertex, and the host on that vertex is completely immune, then it is removed without offspring.

- If the parasite jumps onto some vertex at distance $n+1$ from the root, is the first parasite to jump onto that vertex, and the host on that vertex is susceptible, then any new parasites generated (according to $A^{(s)}$) on that vertex are added to $\widetilde{\xi}_{n+1}$ as its offspring.

We note that by definition, each vertex can only be inhabited by at most s parasites in $\widetilde{\xi}_n$. Also, because offspring can only get generated whenever a parasite jumps onto a never before visited vertex, the probability for that host to be susceptible is p, independent of everything else in $\widetilde{\xi}_n$. Hence, $(\widetilde{\xi}_n)_{n\geq 0}$ dominates a Galton-Watson process with mean offspring

$$\frac{d-s}{d}\mathbb{E}[A^{(s)}]p.$$

This corresponds to the worst case that $d-(s-1)$ directions are already used up by the other parasites on the vertex and 1 direction is towards the root, resulting in at least $d-s$ free directions. Taking d large enough, this can be made greater than 1 and thus the Galton-Watson process, and hence the SIMI, survives with positive probability. $\square$

5.4.4 Proof on recurrence

Proof of Theorem 5.8. We will show that, with probability 1, there are only finitely many vertices $\mathcal{H} \subset V$, such that the parasites that will be produced if $v \in \mathcal{H}$ is infected reach $\mathbf{0}$. Clearly, using Lemma 5.6, we obtain that replacing the offspring distribution A by $\widetilde{A}$ that is distributed as A conditioned to be at least 1, will increase the recurrence probability; hence $\vartheta(G,p,A) \leq \vartheta(G,p,\widetilde{A})$. For the SIMI with offspring distributed as $\widetilde{A}$, we can then make use of the variables defined in (5.1) to study the behavior of the model. We fix some $p \in [0,1)$ and for $x \in V \setminus \{\mathbf{0}\}$ set

$$\mathcal{R}_x := \bigcup_{i=1}^{\widetilde{A}_x - 1} \mathcal{V}^p_{x,i}(\{x\}),$$

the vertices that will be reached by some parasite that was activated at x. Also, we define

$$\mathcal{R}_{\mathbf{0}} := \bigcup_{i=1}^{\widetilde{A}_{\mathbf{0}}} \mathcal{V}^p_{\mathbf{0},i}(\{\mathbf{0}\})$$

the set of vertices visited by the initially activated parasites. Because G is vertex transitive and in $\mathbf{0}$ we activate parasites distributed as $\widetilde{A}$ instead of just $\widetilde{A}-1$, it follows immediately that $\mathbb{P}(\mathbf{0} \in \mathcal{R}_x) \leq \mathbb{P}(x \in \mathcal{R}_{\mathbf{0}})$. We calculate

$$\begin{aligned}\sum_{x \neq \mathbf{0}} \mathbb{P}(\mathbf{0} \in \mathcal{R}_x) \leq \sum_{x \neq \mathbf{0}} \mathbb{P}(x \in \mathcal{R}_{\mathbf{0}}) = \mathbb{E}\left[|\mathcal{R}_{\mathbf{0}} \setminus \{\mathbf{0}\}|\right] &= \mathbb{E}\left[\left|\bigcup_{i=1}^{\widetilde{A}_{\mathbf{0}}} \mathcal{V}^p_{\mathbf{0},i} \setminus \{\mathbf{0}\}\right|\right] \\ \leq \mathbb{E}\left[\sum_{i=1}^{\widetilde{A}_{\mathbf{0}}} \left|\mathcal{V}^p_{\mathbf{0},i} \setminus \{\mathbf{0}\}\right|\right] &= \mathbb{E}[\widetilde{A}]\mathbb{E}\left[\left|\mathcal{V}^p_{\mathbf{0},1}\right|\right] < \infty.\end{aligned}$$

By the Borel-Cantelli Lemma there are almost surely only finitely many $x \neq \mathbf{0}$ such that $\mathbf{0} \in \mathcal{R}_x$. Hence, $\mathbf{0}$ is almost surely only finitely often visited by parasites. □

Chapter 6

Conclusion and open problems

In this chapter we briefly recapitulate the major results of this thesis and point out some possible further open questions in the model.
The aim of this thesis was the study of a stochastic infection model that we introduced, called the Spatial Infection Model with host Immunity, or SIMI for short. The main focus of this work lied on the SIMI evolving on the integer line $\mathbb{Z}$ and investigating the scale at which parasites invade a given host population. Also, we briefly discussed the situation of a specific type of immune response on higher dimensional graphs.

We managed to show that on the integer line $\mathbb{Z}$, the parasite population can only survive with positive probability, if the average number of offspring produced in an infection is larger than the mean number of parasites that are needed to infect a host. If the parasite population survives, it will invade arbitrarily deep into the host population and eventually infect every host. In particular, we assumed in our model that the offspring distribution has a finite expectation. In the continuous time setting, there has been study into the question of explosion for offspring with no finite expectation (c.f. [5]), i.e., they studied the probability of creating infinitely many offspring in finite time. This leads to the following question.

Open problem 1 If we allow offspring distributions, for which the frog model explodes as in [5] or grows superlinearly as in [6]. Does the introduction of immunities with similarly large tails prevent explosion respectively slow down the speed of infection in the SIMI to a linear scale?

On the lattice $\mathbb{Z}^d$ with $d \geq 2$ we only showed a positive survival probability for parasites under a specific assumption on the distribution of immunities, that is much more restrictive than just an assumption on the expected value.

Open problem 2 How does the process evolve for arbitrary immunity distributions on higher dimensional $\mathbb{Z}^d$ with $d \geq 2$? Which assumptions on this distribution yield a positive probability for survival of parasites? Given that the parasites survive, will every (not completely immune) host get infected eventually?

On the integer line $\mathbb{Z}$, we showed that the speed at which parasites invade the host population depends on the speed at which the hosts adapt to the parasites. Specifically, we showed that if the hosts do not adapt fast enough, the parasites will invade at least a distance proportional to the time deep into the host population. Assuming that the hosts adapt even slower, we were able to show that the invaded distance divided by the time converges to a deterministic quantity. A key ingredient was the construction of a renewal time point κ as in [16],[15],[13], though we took the stand point of a renewal site $R^1 = r_\kappa$ because we were not really interested in properties of κ besides that it is finite, which is equivalent to R^1 being finite. At this time κ, only parasites that were generated after κ will contribute to the front. We only showed that for a specific initial configuration, this time is almost surely finite, which established an ergodicity of the front process $(r_t)_{t\geq 0}$. In [15] bounds on the second moment of this time are obtained and assuming the very restricting $I < A$ almost surely, one can essentially copy the proof of [15], with offspring given by $A - I$, to obtain a similar structure in the SIMI. The difficulty that appears in the general setting lies in the construction of the renewal times. This is done by repeatedly trying to achieve the renewal event that the front moves linearly fast and none of the parasites below the front catch up to that linear speed. For a fixed $\delta_0 > 0$, we can only assure the probability for a renewal event to be at least δ_0, if we are at a good site in the sense of Chapter 3 and the parasites that were generated below the front are also not too close to the front. So, if we want to bound the number of trials by a geometric distribution with parameter δ_0, then we must only allow an attempt for a renewal event if we are in such a good situation. However, in case the renewal event is not achieved, we cannot obtain good bounds on the next time that we are in such a good configuration. This is because in a failed attempt for a renewal event, the front is moving too slow and thus it might take untypically long to reach the next good site. During this untypical long time, the parasites below the front have had enough time to also be in an untypical configuration that piles up too many parasites close to the front.

Open problem 3 Can we, for a broader range of I (assuming only finite moments up to some order), establish moment bounds for the renewal times κ and r_κ, that will lead to a functional CLT and an invariant distribution of the parasite population viewed from the front as in [15], or even large deviation results as in [13]?

Another point of interest was the study of quickly adapting hosts in the sense of Chapter 4. In this setting, assuming that I is regularly varying with index α, we were able to show that the invasion distance is not polynomially above or below the scale $t^{\frac{\alpha}{2}}$. In future work with Matthias Birkner, we want to investigate the following refinement of this fact.

Open problem 4 Is there a stable limit theorem for the front? That is, does $\frac{r_t}{t^{\frac{\alpha}{2}}}$ converge in distribution to some limit law?

To see why such a conjecture is reasonable we apply the following heuristic. The CLT in Theorem 2.18 suggests that for high enough regularity of the offspring distribution, the infection of hosts with high immunity $h \gg 1$ is very tightly on the scale h^2. Using the regularly varying tail of the immunity I, we have that for large distances $M \gg 1$ and small $\varepsilon > 0$, the number of immunities in $[1, M]$ with height at least $\varepsilon M^{\frac{1}{\alpha}}$ is roughly $\mathrm{Poi}(\varepsilon^{-\alpha})$-distributed. Suppose that $\widetilde{I}_1, \dots, \widetilde{I}_{N_\varepsilon}$ are those high immunities in $[1, M]$, where $N_\varepsilon \sim \mathrm{Poi}(\varepsilon^{-\alpha})$. Then $\widetilde{I}_k \overset{\mathrm{d}}{\approx} \varepsilon M^{\frac{1}{\alpha}} I$ and these high immunities appear at a distance on the scale $\Omega(\varepsilon^\alpha M)$. To overcome these immunities we need parasites born at a distance on the scale $\Omega(\varepsilon M^{\frac{1}{\alpha}})$. Hence it should be reasonable to assume that the infection of these large immunities is roughly described by the quantity given in Theorem 2.18. That is, the infection of the host with immunity I_k happens really on a time scale $\left(\frac{\widetilde{I}_k}{c_\mu}\right)^2$, each infection is approximately independent and the infection time of all hosts $1, \ldots, N_\varepsilon$ would be roughly on the scale

$$(1+o(1)) \sum_{j=1}^{N_\varepsilon} \left(\frac{\widetilde{I}_j}{c_\mu} \right)^2 \overset{\mathrm{d}}{=} (1+o(1)) M^{\frac{2}{\alpha}} \sum_{j=1}^{N_\varepsilon} \left(\frac{\varepsilon I_j}{c_\mu} \right)^2 .$$

The independence of infections would suggest that for $\lambda \geq 0$ we have

$$\begin{aligned} \mathbb{E}\left[\exp\left(-\lambda \sum_{j=1}^{N_\varepsilon} \left(\frac{\varepsilon I_j}{c_\mu} \right)^2 \right) \right] &\approx \exp\left(\varepsilon^{-\alpha} \left(\mathbb{E}\left[\mathrm{e}^{-\lambda \left(\frac{\varepsilon I}{c_\mu} \right)^2} \right] - 1 \right) \right) \\ &\approx \exp\left(\varepsilon^{-\alpha} \left(\mathrm{e}^{-\widetilde{c} \varepsilon^\alpha \lambda^{\frac{\alpha}{2}}} - 1 \right) \right) \overset{\varepsilon \to 0}{\to} \exp\left(-\widetilde{c} \lambda^{\frac{\alpha}{2}} \right) . \end{aligned}$$

Taking $M \to \infty$ and $\varepsilon \to 0$ would yield that

$$\frac{\text{time to infect all large immunities in } [1, M]}{M^{\frac{2}{\alpha}}}$$

is approximately $\frac{\alpha}{2}$-stable distributed. Using the lower bound established in Theorem 4.5 we can show that in between these large immunities the front moves with speed at least $c \left(\varepsilon M^{\frac{1}{\alpha}} \right)^{\alpha - 2}$ for some $c > 0$. Hence, the time spend between the large immunities is roughly given by

$$\frac{M}{c \left(\varepsilon M^{\frac{1}{\alpha}} \right)^{\alpha - 2}} = c^{-1} \varepsilon^{2-\alpha} M^{\frac{2}{\alpha}} .$$

In particular, it should disappear in the limit $\varepsilon \to 0$ and yield that

$$\frac{\text{time to infect } M}{M^{\frac{2}{\alpha}}} \approx \frac{\text{time to infect all large immunities in } [1, M]}{M^{\frac{2}{\alpha}}} \approx T,$$

where T is a stable subordinator with index $\frac{\alpha}{2}$. This would then imply that $\frac{r_t}{t^{\frac{\alpha}{2}}}$ is approximately Mittag-Leffner-distributed.

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