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Aline Marguet, Charline Smadi

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PARASITE INFECTION IN A CELL POPULATION: ROLE OF THE PARTITIONING KERNEL

ALINE MARGUET AND CHARLINE SMADI

Abstract. We consider a cell population subject to a parasite infection. Cells divide at a constant rate and, at division, share the parasites they contain between their two daughter cells. The sharing may be asymmetrical, and its law may depend on the quantity of parasites in the mother. Cells die at a rate which may depend on the quantity of parasites they carry, and are also killed when this quantity explodes. We study the survival of the cell population as well as the mean quantity of parasites in the cells, and focus on the role of the parasites partitioning kernel at division.

Key words and phrases: Continuous-time branching Markov processes, Structured population, Long time behaviour, Birth and Death Processes

MSC 2000 subject classifications: 60J80, 60J85, 60H10.

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Introduction

We are interested in the modelling of a parasite infection in a cell population, and, in particular, in the role of the stochasticity of repartition of the parasites at cell division. From the pioneering work of Kimmel [13], several models and associated analysis have been

proposed, both in discrete [4, 5, 1, 2] and continuous time [8, 7]. The asymmetric repartition of parasites is taken into account in all of those work: in [4, 20], each parasite chooses to go to one daughter cell with probability p (and to the other with probability $1-p$), and in [5], a random environment is considered (the probability generating functions of the number of parasites at birth in the two daughter-cells of each cell in the population are i.i.d random variables). In branching-within-branching models, independently for each parasite and with the same distribution, the descendants are shared between the daughter cells. A different approach has been proposed in [8], removing the independence property of the sharing of parasites descending from different lineages. Following the dynamics of the ($\mathbb{R}$-valued) quantity of parasites inside the cells (rather than a discrete count), this model assumes that a cell with x parasites, splits into two daughter cells with a quantity of parasites Θx and $(1-\Theta)x$ respectively, with Θ a random variable on $[0,1]$. Here, we extend this approach and explore the role of the random variable Θ in the proliferation of the infection. We assume that cells divide at a constant rate. Their death rate may depend on the quantity of parasites they contain and they may additionally be killed when this quantity explodes. The dynamics of the quantity of parasites in a cell is given by a Stochastic Differential Equation (SDE) with drift, diffusion and positive jumps. At division the parasites of a cell are shared between its two daughters according to a partitioning kernel which may depend on the quantity of parasites. Similarly as in [13, 4, 5, 8, 7, 1, 2, 20] we are interested in the long time behaviour of the parasite infection. More precisely, we will study the number of cells alive, as well as the number of parasites in the cells at large time. This work complements [19], where we considered division rates which could depend on the quantity of parasites contained in the cells but fixed partitioning kernels at division. Assuming here that the division rate is constant allows us to consider partitioning kernels depending on the quantity of parasites in the cell at division, and to focus on the effect of the partitioning kernel on the long time behaviour of the infection. In particular, we compare partitioning strategies and show that a symmetrical division (half of the parasites in each daughter cell) is the worst choice for the cell population in terms of survival. We give quantitative conditions on the level of infection for the cell population to survive, for both uniform and equal sharing partitioning kernels. We also explore numerically the difference between deterministic and random partitioning, highlighting the fact that randomness and asymmetry seem to be the keys to survival. In particular, we prove that any symmetric partitioning kernel is better for survival than its deterministic counterpart with the same expected minimum value. Finally, we prove that whatever the growth of the parasites, there exist partitioning kernels enabling the cell population to survive the infection.

Our proof strategy consists in introducing a spinal decomposition. It amounts to distinguishing a particular line of descent in the population, constructed from a size-biased tree [15], and to prove that the dynamics of the trait along this particular lineage is representative of the dynamics of the trait of a typical individual in the population, *i.e.* an individual picked uniformly at random. We refer to [11, 12, 6, 9, 16, 17] for general results on these topics in the continuous-time setting.

The paper is structured as follows. In Section 1, we define the population process and give assumptions ensuring its existence and uniqueness as the strong solution to a SDE. Sections 2 and 3 are dedicated to the study of the asymptotic behaviour of the mean number of cells alive in the population for various dynamics for the parasites. In particular, we compare different strategies for the sharing of the parasites at division and give explicit conditions ensuring extinction or survival of the cell population. In Section 4, we focus on the case of a parasites dynamics without stable positive jumps and study the asymptotic behaviour of the proportion of infected cells. Sections 5 and 6 are dedicated to the proofs.

In the sequel $\mathbb{N} := \{0, 1, 2, ...\}$ will denote the set of nonnegative integers, $\mathbb{R}_+ := [0, \infty)$ the real line, $\overline{\mathbb{R}}_+ := \mathbb{R}_+ \cup \{+\infty\}$, and $\mathbb{R}_+^* := (0, \infty)$. We will denote by $\mathcal{C}_0^2(\mathbb{R}_+)$ the set of twice continuously differentiable functions on $\mathbb{R}_+$ vanishing at 0 and infinity. Finally, for any stochastic process X on $\overline{\mathbb{R}}_+$ or Z on the set of point measures on $\overline{\mathbb{R}}_+$, we will denote by $\mathbb{E}_x[f(X_t)] = \mathbb{E}\left[f(X_t)\middle|X_0 = x\right]$ and $\mathbb{E}_{\delta_x}[f(Z_t)] = \mathbb{E}\left[f(Z_t)\middle|Z_0 = \delta_x\right]$.

1. Definition of the population process

1.1. **Parasites dynamics in a cell.** Each cell contains parasites whose quantity evolves as a diffusion with positive jumps. More precisely, we consider the SDE

$$\mathfrak{X}_t = x + \int_0^t g(\mathfrak{X}_s)ds + \int_0^t \sqrt{2\sigma^2(\mathfrak{X}_s)}dB_s + \int_0^t \int_0^{p(\mathfrak{X}_{s-})} \int_{\mathbb{R}_+} z\widetilde{Q}(ds, dx, dz) + \int_0^t \int_0^{\mathfrak{X}_{s-}} \int_{\mathbb{R}_+} zR(ds, dx, dz), \tag{1.1}$$

where x is nonnegative, g, $\sigma \geq 0$ and $p \geq 0$ are real functions on $\overline{\mathbb{R}}_+$, B is a standard Brownian motion, $\widetilde{Q}$ is a compensated Poisson point measure (PPM) with intensity $ds \otimes dx \otimes \pi(dz)$, π is a nonnegative measure on $\mathbb{R}_+$, R is a PPM with intensity $ds \otimes dx \otimes \rho(dz)$, with

$$\rho(dz) = \frac{c_{\mathfrak{b}}\mathfrak{b}(\mathfrak{b}+1)}{\Gamma(1-\mathfrak{b})}\frac{1}{z^{2+\mathfrak{b}}}\mathrm{d}z, \quad z \in \mathbb{R}_+$$

where $\mathfrak{b} \in (-1, 0)$ and $c_{\mathfrak{b}} < 0$ (see [14, Section 1.2.6] for details on stable distributions and processes). Finally, B, Q and R are independent.

We will provide later on conditions under which the SDE (1.1) has a unique nonnegative strong solution. In this case, it is a Markov process with infinitesimal generator $\mathcal{G}$, satisfying for all $f \in C_0^2(\mathbb{R}_+)$,

$$\mathcal{G}f(x) = g(x)f'(x) + \sigma^2(x)f''(x) + p(x)\int_{\mathbb{R}_+} \left(f(x+z) - f(x) - zf'(x)\right)\pi(dz) + x\int_{\mathbb{R}_+} \left(f(x+z) - f(x)\right)\rho(dz), \tag{1.2}$$

and 0 and $+\infty$ are two absorbing states. Following [16], we denote by $(\Phi(x, s, t), s \leq t)$ the corresponding stochastic flow *i.e.* the unique strong solution to (1.1) satisfying $\mathfrak{X}_s = x$ and the dynamics of the trait between division events is well-defined.

1.2. **Cell division.** Each cell carrying a quantity x of parasites divides at rate r and is replaced by two daughter cells with quantity of parasites $\Theta(x, \zeta)x$ and $(1 - \Theta(x, \zeta))x$, where $\Theta(x, \zeta)$ is a symmetrical random variable on $(0, 1)$, with associated distribution $\kappa(x, \cdot)$, Θ is a measurable function from $\mathbb{R}_+ \times [0, 1]$ to $(0, 1)$ and ζ is a uniform random variable on $[0, 1]$. This formalism will prove useful for the use of Poisson point measures. However, for the sake of simplicity, we will often omit the dependence in ζ and write $\Theta(x)$ for the random variable corresponding to the proportion of parasites at birth, instead of $\Theta(x, \zeta)$. Finally, we assume that $\sup_{x\in\mathbb{R}_+} |\mathbb{E}[\ln \Theta(x)]| < \infty$.

1.3. **Cell death.** Cells can die because of two mechanisms. First, they have a natural death rate $q(x)$ which depends on the quantity of parasites x they carry. Second, cells die when the quantity of parasites they carry explodes (*i.e.*, reaches infinity in finite time), as a proper functioning of the cell is not possible anymore. Notice that to model this case, we do not 'kill the cell' strictly speaking. As infinity is an absorbing state for the quantity of parasites in a cell, and as a cell with an infinite quantity of parasites transmits an infinite quantity of parasites to both its daughter cells, we let the process evolve and decide that a cell is dead if it contains an infinite quantity of parasites.

1.4. **Existence and uniqueness.** We use the classical Ulam-Harris-Neveu notation to identify each individual. Let us denote by

$$\mathcal{U} := \bigcup_{n\in\mathbb{N}} \{0,1\}^n$$

the set of possible labels, $\mathcal{M}_P(\overline{\mathbb{R}}_+)$ the set of point measures on $\overline{\mathbb{R}}_+$, and $\mathbb{D}(\mathbb{R}_+, \mathcal{M}_P(\overline{\mathbb{R}}_+))$, the set of càdlàg measure-valued processes. For any $Z \in \mathbb{D}(\mathbb{R}_+, \mathcal{M}_P(\overline{\mathbb{R}}_+))$, $t \geq 0$, we write

$$Z_t = \sum_{u\in V_t} \delta_{X_t^u}, \tag{1.3}$$

where $V_t \subset \mathcal{U}$ denotes the set of individuals alive at time t and X_t^u the quantity of parasites at time t of cell u. By convention, Z_t is the null measure if $V_t = \emptyset$. By extension, for $u \in V_t$ and any $s \leq t$, X_s^u denotes the quantity of parasites in the ancestor of u in the population at time s. Thus, $(X_s^u, s \leq \sup(\mathfrak{t} \geq 0 \text{ s.t. } u \neq V_{\mathfrak{t}}))$ follows (1.1) between events of division impacting the lineage under consideration.

Let $\left(\Phi^u(x,s,t), u \in \mathcal{U}, x \in \overline{\mathbb{R}}_+, s \leq t\right)$ be a family of independent stochastic flows satisfying (1.1) describing the individual-based dynamics. Let $E = \mathcal{U} \times (0,1) \times \overline{\mathbb{R}}_+$ and $M(ds, du, d\zeta, dz)$ be a PPM on $\mathbb{R}_+ \times E$ with intensity $ds \otimes n(du) \otimes d\zeta \otimes dz$, where $n(du)$ denotes the counting measure on $\mathcal{U}$. We assume that M and $(\Phi^u, u \in \mathcal{U})$ are independent. We denote by $\mathcal{F}_t$ the filtration generated by the restriction of the PPM M to $[0,t] \times E$ and the family of stochastic processes $(\Phi^u(x,s,t), u \in \mathcal{U}, x \in \overline{\mathbb{R}}_+, s \leq t)$ up to time t.

We now introduce assumptions to ensure the strong existence and uniqueness of the process. They are simpler than those of the companion paper [19] because the cells' division rate does not depend on the quantity of parasites they carry.

Assumption EU. *i) The function p is locally Lipschitz on $\mathbb{R}_+$, non-decreasing and $p(0) = 0$. The function g is continuous on $\mathbb{R}_+$, $g(0) = 0$ and for any $n \in \mathbb{N}$ there exists a finite constant B_n such that for any $0 \leq x \leq y \leq n$*

$$|g(y) - g(x)| \leq B_n \phi(y-x), \quad \textit{where} \quad \phi(x) = \begin{cases} x\,(1 - \ln x) & \textit{if } x \leq 1, \\ 1 & \textit{if } x > 1. \end{cases}$$

ii) The function σ is Hölder continuous with index $1/2$ on compact sets and $\sigma(0) = 0$.
iii) The measure π satisfies

$$\int_0^\infty \left(z \wedge z^2\right) \pi(dz) < \infty.$$

Recall the definition of $\mathcal{G}$ in (1.2). Then, the structured population process may be defined as the strong solution to a SDE.

Proposition 1.1. *Under Assumption* **EU**, *there exists a strongly unique $\mathcal{F}_t$-adapted càdlàg process $(Z_t, t \geq 0)$ taking values in $\mathcal{M}_P(\overline{\mathbb{R}}_+)$ such that for all $f \in C_0^2(\overline{\mathbb{R}}_+)$ and $x_0, t \geq 0$,*

$$\begin{aligned}\langle Z_t, f\rangle =& f(x_0) + \int_0^t \int_{\mathbb{R}_+} \mathcal{G}f(x) Z_s(dx)\, ds + M_t^f(x_0) \\ &+ \int_0^t \int_E \mathbf{1}_{\{u\in V_{s^-}\}} \Big(\mathbf{1}_{\{z\leq r\}} \left(f\left(\Theta(X_{s^-}^u, \zeta) X_{s^-}^u\right) + f\left((1-\Theta(X_{s^-}^u,\zeta))X_{s^-}^u\right) - f\left(X_{s^-}^u\right)\right) \\ &\qquad - \mathbf{1}_{\left\{0<z-r\leq q(X_{s^-}^u)\right\}} f\left(X_{s^-}^u\right)\Big) M(ds, du, d\zeta, dz),\end{aligned}$$

where for all $x \geq 0$, $M_t^f(x)$ is a $\mathcal{F}_t$-martingale.

The proof is a combination of [21, Proposition 1] and [16, Theorem 2.1] (see [19, Appendix A] for details). For the sake of readability, we will assume that all the processes under consideration in the sequel satisfy Assumption **EU**, but we will not indicate it.

We will now investigate the long time behaviour of the infection in the cell population. As we explained above, the strategy to obtain information at the population level is to introduce an auxiliary process providing information on the behaviour of a 'typical individual'. We will provide a general expression for this auxiliary process in Section 5.

2. Mean number of cells alive: General results

We denote by $\mathfrak{C}_t$ the number of cells alive at time t. We give here results on the asymptotic behaviour of $\mathfrak{C}_t$. For general parasites dynamics, we give sufficient conditions for the cell population to survive with positive probability (see Proposition 2.1 below). Moreover, for specific dynamics of the parasites population, we give the asymptotic order of magnitude of the mean number of cells alive in the population. As in [22, Proposition 2.1], we exhibit three different regimes, depending on the parameters of both the cells and the parasites dynamics (see Proposition 2.2 below). It allows us to study the effects of parasites growth rate and diffusion parameter, and cells division and death rates. The next section will be devoted to the study of the effect of the partitioning kernel on the average number of cells alive in large time.

Let us introduce a random variable Θ on $(0,1)$ with symmetrical distribution κ satisfying

$$\mathbb{E}\left[|\ln\Theta|\right] = \int_0^1 |\ln\theta|\kappa(d\theta) < \infty, \tag{2.1}$$

as well as the function

$$\phi(\lambda) := \lambda(g-\sigma^2) + \lambda^2\sigma^2 + 2r\left(\mathbb{E}[\Theta^\lambda] - 1\right), \tag{2.2}$$

for any $\lambda \in (\lambda^-, \infty)$, where

$$\lambda^- := \inf\{\lambda < 0 : \phi(\lambda) < \infty\}.$$

The function ϕ is the Laplace exponent of a Lévy process (see the proof of Proposition 2.1), and is thus convex on (λ^-, ∞). Let

$$\mathfrak{m} := \phi'(0+) = g - \sigma^2 + 2r\mathbb{E}\left[\ln\Theta\right] \tag{2.3}$$

and denote by $\hat{\tau} = \operatorname{argmin}_{(\lambda^-,0)}\phi(\lambda)$ which is well-defined if $\lambda^- < 0 < \mathfrak{m}$ because ϕ' is an increasing function. We also define

$$\mathfrak{d} := \phi(\hat{\tau}) + r - q = \hat{\tau}(g-\sigma^2) + \hat{\tau}^2\sigma^2 + r\left[2\int_0^1 \theta^{\hat{\tau}}\kappa(d\theta) - 1\right] - q. \tag{2.4}$$

We have the following sufficient condition for the mean number of cells to go to infinity.

Proposition 2.1. *Assume that the dynamics of the quantity of parasites in a cell follows* (1.1)*, with $p(x) = x$, and $\sigma(x)^2 = \mathfrak{s}^2(x)x + \sigma^2x^2$ for any $x \in \overline{\mathbb{R}}_+$ with $\sigma \in \mathbb{R}_+$.*

Suppose that

- *$q(x) \le q < r$ and $g(x) \le gx$ for any $x \in \overline{\mathbb{R}}_+$ with $g \in \mathbb{R}_+$.*
- *the function $\mathfrak{s}$ is Hölder continuous with index $1/2$ on compact sets and there exists a finite constant $\mathfrak{c}$ such that for $x \ge 0$, $\mathfrak{s}(x)\sqrt{x} \le \mathfrak{c} \vee x^{\mathfrak{c}}$*
- *for $x \ge 0$ the random variable $\Theta(x)$ is stochastically dominated by a random variable Θ satisfying* (2.1)*.*

Then, if $\mathfrak{m} \le 0$ or ($\mathfrak{m} > 0$ and $\mathfrak{d} > 0$), then for any $x > 0$

$$\lim_{t\to\infty}\mathbb{E}_{\delta_x}[\mathfrak{C}_t] = \infty.$$

Hence, for a large class of models, the cell population survives the infection with positive probability if the strategy for repartition of the parasites at division is well-chosen. The sign of $\mathfrak{m}$ indicates if the quantity of parasites stays finite with a positive probability in a typical cell line. If it is the case ($\mathfrak{m} \leq 0$), then the expected number of cells alive goes to infinity as time goes to infinity because the cell population grows exponentially at a rate larger than $r - q > 0$. If $\mathfrak{m} > 0$, then the probability that the quantity of parasites is infinite in a typical cell line goes to 1 as time goes to infinity. In that case, the speed of convergence of this probability has to be compared with the growth of the population. And if the growth of the population is strong enough ($\mathfrak{d} > 0$), the expected number of cells that are alive still goes to infinity as time goes to infinity.

Focusing on the role of the partitioning kernel, Proposition 2.1 shows that if the cell population manages to adapt its partitioning strategy to make it more asymmetrical, it can save the cell population (in the sense of making the mean number of cells alive tend to infinity for large time). Indeed, for any choice of the triplet (g, σ, r), we can find a kernel κ satisfying (2.1) such that

$$\mathbb{E}\left[\ln \Theta\right] \leq \frac{\sigma^2 - g}{2r},$$

and thus $\mathfrak{m} \leq 0$.

If we specify a bit more the dynamics of the quantity of parasites, we can give more precise results on the asymptotic behaviour of $\mathfrak{C}_t$. To that end, we consider that the quantity of parasites in a cell follows the SDE:

$$\mathfrak{X}_t = x + g\int_0^t \mathfrak{X}_s ds + \int_0^t \sqrt{2\sigma^2 \mathfrak{X}_s^2} dB_s + \int_0^t \int_0^{\mathfrak{X}_{s^-}} \int_{\mathbb{R}_+} zR(ds, dx, dz), \tag{2.5}$$

where $g \geq 0, \sigma \geq 0$, $x \geq 0$, B is a standard Brownian motion and the Poisson measure R has been defined in (1.1). In this case, we are able to obtain an equivalent of the mean number of cells alive at a large time t. It emphasizes how crucial is the choice of repartition of the parasites at division between daughter cells.

Proposition 2.2. *Assume that the dynamics of the quantity of parasites in a cell follows* (2.5)*, that* $\Theta(x) \overset{\mathcal{L}}{=} \Theta$ *and satisfies* (2.1)*, and that* $q(x) \equiv q \geq 0$ *with* $q \neq r$*.*

i) If $\mathfrak{m} < 0$*, then for every* $x > 0$ *there exists* $0 < c_1(x) < 1$ *such that*

$$\lim_{t\to\infty} e^{(q-r)t}\mathbb{E}_{\delta_x}\left[\mathfrak{C}_t\right] = c_1(x).$$

ii) If $\mathfrak{m} = 0$ *and* $\lambda^- < 0$*, then for every* $x > 0$ *there exists* $c_2(x) > 0$ *such that*

$$\lim_{t\to\infty} \sqrt{t}e^{(q-r)t}\mathbb{E}_{\delta_x}\left[\mathfrak{C}_t\right] = c_2(x).$$

iii) If $\mathfrak{m} > 0$*, then for every* $x > 0$ *there exists* $c_3(x) > 0$ *such that*

$$\lim_{t\to\infty} t^{\frac{3}{2}} e^{-\mathfrak{d}t}\mathbb{E}_{\delta_x}\left[\mathfrak{C}_t\right] = c_3(x).$$

Note that the dependency on $\mathfrak{b}$ (parameter of the law of positive jumps for the parasites) is hidden in the limiting functions c_1, c_2, c_3. We refer the reader to the proof for details.

In absence of parasites, if $r > q$, the cell population evolves as a supercritical Galton-Watson process and survives with probability $1 - q/r$ [3]. In the presence of parasites, the condition $r > q$ does not ensure that the cell population survives with a positive probability, as it goes extinct almost surely if $\mathfrak{m} > 0$ and $\mathfrak{d} \leq 0$. More generally, from the previous proposition, we deduce the following corollary on the asymptotic behaviour of $\mathfrak{C}_t$.

Corollary 2.3. *Under the assumptions of Proposition 2.2, for any* $x > 0$*,*

i) If $q \geq r$ *or if* ($\mathfrak{m} > 0$ *and* $\mathfrak{d} \leq 0$)*, then* $\lim_{t\to\infty} \mathbb{E}_{\delta_x}[\mathfrak{C}_t] = 0$*.*

ii) If ($\mathfrak{m} \leq 0$ *and* $r > q$) *or if* ($\mathfrak{m} > 0$ *and* $\mathfrak{d} > 0$)*, then* $\lim_{t\to\infty} \mathbb{E}_{\delta_x}[\mathfrak{C}_t] = \infty$*.*

Notice that the case $r = q$ is not taken into account in Proposition 2.2 for the simplicity of its statement as it corresponds to a critical birth and death process for the cell population dynamics. However, we know that in this case the number of cells (with a finite or infinite quantity of parasites) reaches 0 in finite time, hence the number of cells alive also reaches 0 in finite time.

We now study the asymptotic qualitative behaviour (0 or ∞) of $\mathbb{E}_{\delta_x}[\mathfrak{C}_t]$ as a function of g, r, q and σ. The dependence on κ will be the subject of Section 3 and will thus not be indicated here. For the sake of readability and only for Lemma 2.4, we denote by

$$\mathbb{E}_{\delta_x}^{(g,\sigma,r,q)}[\mathfrak{C}_t]$$

the mean number of cells alive at time t when there is initially one cell with a quantity x of parasites, and that the dynamics of the infected cell population follows the assumptions of Proposition 2.2 with parameters (g, σ, r, q). We also introduce its limit when t goes to infinity via

$$\mathfrak{A}_x(g, \sigma, r, q) := \lim_{t\to\infty} \mathbb{E}_{\delta_x}^{(g,\sigma,r,q)}[\mathfrak{C}_t]$$

Then, we prove that for each parameter of the model, fixing all the other parameters, there exists a limiting value corresponding to a change of asymptotic behaviour of $\mathfrak{A}_x(g, \sigma, r, q)$.

Lemma 2.4. *Under the assumptions of Proposition 2.2, for any $x > 0$,*

i) There exists $q_{\lim}(g, \sigma, r) \in \mathbb{R}_+$ such that

$$q \geq q_{\lim}(g, \sigma, r) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = 0 \text{ and } q < q_{\lim}(g, \sigma, r) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = \infty.$$

ii) There exists $r_{\lim}(g, \sigma, r, q) \in \mathbb{R}_+$ such that

$$r \leq r_{\lim}(g, \sigma, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = 0 \text{ and } r > r_{\lim}(g, \sigma, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = \infty.$$

iii) There exists $g_{\lim}(\sigma, r, q) \in \mathbb{R}_+$ such that

$$g \geq g_{\lim}(\sigma, r, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = 0 \text{ and } g < g_{\lim}(\sigma, r, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = \infty.$$

iv) There exists $\sigma_{\lim}(g, r, q) \in \bar{\mathbb{R}}_+$ such that

$$\sigma < \sigma_{\lim}(g, r, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = 0 \text{ and } \sigma > \sigma_{\lim}(g, r, q) \Rightarrow \mathfrak{A}_x(g, \sigma, r, q) = \infty.$$

Moreover, $\mathfrak{A}_x(g, \sigma_{\lim}(g, r, q), r, q) = \begin{cases} \infty, & \text{if } \sigma_{\lim}(g, r, q) = 0, \\ 0, & \text{otherwise.} \end{cases}$

The effect of κ, which describes the sharing of the parasites at division, is less intuitive and explicit computations are not always feasible. We nevertheless are able to study some particular cases and to compare some classes of partitioning kernels κ.

3. Mean number of cells alive: Role of the partitioning kernel

For the sake of simplicity, we assume in this section that the quantity of parasites in a cell follows the SDE (2.5) with $\sigma = 0$. We make this simplification to obtain simple expressions as the focus is here on the role of κ on the mean number of cells alive.

3.1. Deterministic vs random partitioning: a numerical study.

Focusing on two families of measures for the partitioning of the parasites at division, we first explore via numerical computations the optimality of the different strategies in terms of survival of the cell population. Note that those families have also been considered in [10] to study the effect of the partitioning kernels on the cell size distributions.

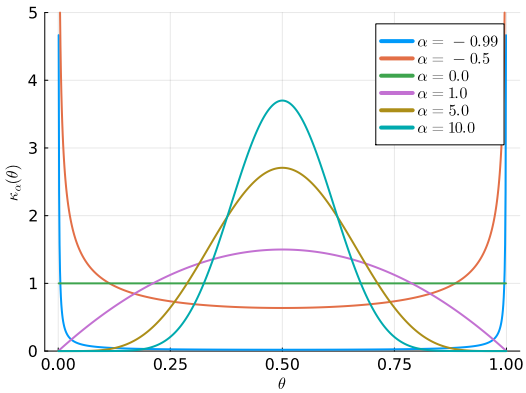

FIGURE 1. The density functions of the partitioning kernels κ_α for various values of α

The first family (also considered in [7]) corresponds to deterministic partitioning, with associated measures on $[0,1]$ denoted by κ_z, and given for all $z \in [0,1/2]$ by

$$\kappa_z(d\theta) = \frac{1}{2}(\delta_z(d\theta) + \delta_{1-z}(d\theta)).$$

The bigger z is, the more the partitioning is asymmetrical: $z = 1/2$ corresponds to symmetric partitioning and $z = 0$ to the case of all parasites going to one daughter cell. For this family, $\mathfrak{m}_z = g + r\ln(z(1-z))$, where $\mathfrak{m}$ is defined in (2.3) and the subscript z refers to the partitioning kernel κ_z.

The second family of measures that we consider corresponds to random partitioning. The associated partitioning measures on $[0,1]$, denoted by κ_α, are given for all $\alpha > -1$ by

$$\kappa_\alpha(d\theta) = c_\alpha \theta^\alpha (1-\theta)^\alpha d\theta, \tag{3.1}$$

where $c_\alpha = \Gamma(2\alpha+2)/\Gamma(\alpha+1)^2$, and Γ is the Gamma function. In Figure 1, the shapes of the kernels for various values of α are represented. The bigger α is, the more the partitioning is asymmetrical. Note that $\alpha = 0$ corresponds to the uniform sharing $\kappa(d\theta) = d\theta$, and will be studied in details below. For any $\alpha > -1$, $\mathfrak{m}_\alpha = g + 2r(\psi_0(\alpha) - \psi_0(2\alpha+1))$, where ψ_0 is the digamma function and the subscript α refers to the partitioning kernel κ_α.

We will now compare the two partitioning strategies, deterministic or random, represented by the two families of partitioning kernels $(\kappa_z,\ z \in\ (0,1/2])$ and $(\kappa_\alpha,\ \alpha > -1)$. We denote by Θ_z and Θ_α the random variables with distribution κ_z and κ_α respectively.

First, we define $\vartheta_z := \mathbb{E}[\min(\Theta_z, 1-\Theta_z)]$ and $\vartheta_\alpha := \mathbb{E}[\min(\Theta_\alpha, 1-\Theta_\alpha)]$. This quantity corresponds to the expectation of the minimal fraction of parasites inherited by one of the daughter cells. To each random partitioning κ_α, we associate the deterministic partitioning kernel κ_z such that $\vartheta_z = \vartheta_\alpha$. Notice that the choice of z, for a given ϑ_α is unique, as $\vartheta_z = z$. As a consequence, we denote by $(\alpha, z_\alpha) = (\alpha, \vartheta_\alpha)$ such couples of parameters. Simple computations give

$$\vartheta_\alpha = 2c_\alpha \mathrm{B}(1/2; \alpha+2, \alpha+1),$$

where $\mathrm{B}(x;a,b) := \int_0^x \theta^{a-1}(1-\theta)^{b-1}d\theta$ is the incomplete Beta function ($x \in [0,1], a, b > -1$). Then,

$$z_\alpha = 2c_\alpha \mathrm{B}(1/2; \alpha+2, \alpha+1).$$

Using this correspondence between the two families of kernels, we compare the two partitioning strategies (random or deterministic) for various values of ϑ. In Figure 2, we show the correspondence between the long time behaviour of the mean cell population size and the values of $(g/r, \alpha)$ for κ_α, and the values of $(g/r, z_\alpha)$ for κ_{z_α}. We fixed $q = 0$, but we

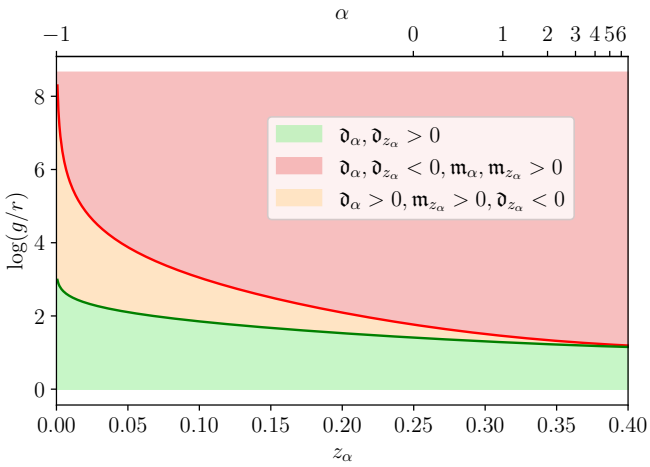

FIGURE 2. Classification of the couples of parameters $(g/r, z_\alpha)$ and $(g/r, \alpha)$ in the case of deterministic or random partitioning with $q = 0$.

get similar behaviours for all values of $q < r$. Interestingly, the two families of partitioning kernels exhibit the same qualitative behaviour in terms of proliferation of the infection. We observe that strategies with larger variances (small values of z and α) are more efficient in terms of survival of the cell population. For a given strength of proliferation of the infection g relative to the growth of the population r, the fate of the cell population depends on the value of α or z: parameters

- in the green area lead to survival of the cell population, for both partitioning kernels,
- in the red area lead to extinction of the cell population for both partitioning kernels,
- in the orange area lead to extinction of the cell population for deterministic partitioning strategies, and survival of the cell population for random partitioning strategies.

Therefore, for any infection level and a given ϑ, the random partitioning strategy is always better in terms of asymptotic mean number of cells alive in the population than deterministic partitioning ($\mathfrak{d}_{z_\alpha} < \mathfrak{d}_\alpha$). Moreover, there exist parameters g, r (*e.g.* $\log(g/r) = 4$ in Figure 2) such that a population with deterministic partitioning gets extinct (in the sense of asymptotic mean number of cells alive) whatever the value of z, whereas a population with random partitioning can survive, if the division is sufficiently asymmetrical. Note that to simplify the figure, we did no plot the curves $\mathfrak{m}_{z_\alpha} = 0$ and $m_\alpha = 0$, but they behave similarly to the curves $\mathfrak{d}_{z_\alpha} = 0$ and $\mathfrak{d}_\alpha = 0$.

Finally, for high levels of the proliferation, neither the random nor the deterministic strategies considered here can overcome the infection, or with an extreme asymmetrical distribution ($\vartheta \approx 0$). In Proposition 3.4 below, we prove that for any value of ϑ, there exists a partitioning strategy ensuring the survival of the population.

3.2. **Analytical comparison of partitioning strategies.** The most simple examples of partitioning strategies are the uniform law and the symmetrical sharing, belonging respectively to the family of random and deterministic partitioning studied above. For those laws, we can explicit the bounds of Corollary 2.3.

Corollary 3.1. *Assume that the quantity of parasites in a cell follows the SDE* (2.5) *with* $\sigma = 0$, *that* $r > q(x) \equiv q \geq 0$. *Recall the definition of* $g_{\lim}(\sigma, r, q)$ *in Lemma 2.4.*

- *If* $\kappa(d\theta) = d\theta$,

$$g_{\lim}(0, r, q) = 3r - q + 2\sqrt{2r(r-q)}.$$

- *If* $\kappa(d\theta) = \delta_{1/2}(d\theta)$,

$$g_{\lim}(0, r, q) = r x_0(q/r) \ln 2$$

where $x_0(q/r) > 2$ is the unique value such that

$$x_0(q/r) = \left(1 + \frac{q}{r}\right)(1 + \ln 2 - \ln(x_0(q/r)))^{-1}. \tag{3.2}$$

From this result, one can prove with a few more computations that the 'uniform sharing' strategy is always better than the 'equal sharing' strategy in terms of survival of the cell population. In fact, the symmetrical sharing is the worst strategy, as stated in the next proposition.

Proposition 3.2. *Assume that the quantity of parasites in a cell follows the SDE* (2.5) *with $\sigma = 0$, that $r > q(x) \equiv q \geq 0$. For any partitioning kernel κ, if $g/r < x_0(q/r)\ln 2$, where $x_0(q/r)$ is defined in* (3.2)*, we have for all $x \geq 0$,*

$$\lim_{t\to+\infty} \mathbb{E}_{\delta_x}[\mathfrak{C}_t] = \infty.$$

As $x_0(q/r)\ln 2$ is the limiting value corresponding to the case of an equal sharing, Proposition 3.2 proves that any other sharing strategy is better than the symmetric partitioning.

More generally, we expect that a more unequal strategy is beneficial for the cell population: it amounts to 'sacrificing' some lineages in order to save the other ones. We were not able to prove such a general statement, but we will try to understand better the effect of unequal sharing in the next two propositions. Recall that $\vartheta = \mathbb{E}[\min(\Theta, 1-\Theta)]$. First, as explained above and in Figure 2, for a fixed value of ϑ, random partitioning is always better than deterministic partitioning in terms of survival of the population. For a fixed value of ϑ, is the deterministic partitioning the worst strategy in general? Second, does there exist, for any level of infection and for a fixed value of ϑ, a partitioning distribution that leads to survival of the cell population?

To approach these questions, we first consider finite points partitioning distributions for illustrative purposes. Let $n \geq 1$ be the number of possible modes $z_1, \ldots, z_n \in (0, 1/2]$, which are independent and identically distributed according to a uniform law on $(0, 1/2]$. Then, the associated partitioning distribution has $2n$ modes, $z_1, \ldots, z_n, 1-z_1, \ldots, 1-z_n$. Next, we define $p_i := \mathbb{P}(\Theta = z_i)$ and $\mathbf{p} = (p_1, \ldots, p_n)$. For those multimodal distributions, we have

$$\vartheta = \mathbb{E}[\min(\Theta, 1-\Theta)] = 2\sum_{i=1}^{n} z_i p_i.$$

In Figure 3, we plot the logarithm of the limiting value g/r at which $\mathfrak{d} = 0$ for various multimodal distributions as a function of ϑ. The green and red curves represent the limiting value for the kernels κ_z and κ_α respectively, studied in the previous section. We observe that for a fixed value of ϑ, the worst scenario seems to be the case of a deterministic partitioning κ_z. We will prove this result analytically for any symmetric distribution on $[0, 1]$.

Proposition 3.3. *Assume that the quantity of parasites in a cell follows the SDE* (2.5) *with $\sigma = 0$, and that $r > q(x) \equiv q \geq 0$. Let $\vartheta \in (0, 1/2]$ and let κ be a symmetric distribution on $[0, 1]$ such that*

$$\int_0^1 \min(\theta, (1-\theta))\kappa(d\theta) = \vartheta.$$

Finally, let

$$\kappa_\vartheta(d\theta) = 1/2\,(\delta_\vartheta + \delta_{1-\vartheta}),$$

be the associated deterministic partitioning kernel. Then, for any $x > 0$,

$$\lim_{t\to+\infty} \mathbb{E}^{(\kappa)}_{\delta_x}[\mathfrak{C}_t] \geq \lim_{t\to+\infty} \mathbb{E}^{(\kappa_\vartheta)}_{\delta_x}[\mathfrak{C}_t],$$

where $\mathbb{E}^{(\kappa)}$ (resp. $\mathbb{E}^{(\kappa_\vartheta)}$) denotes the expectation for the population process with partitioning kernel κ (resp. κ_ϑ).

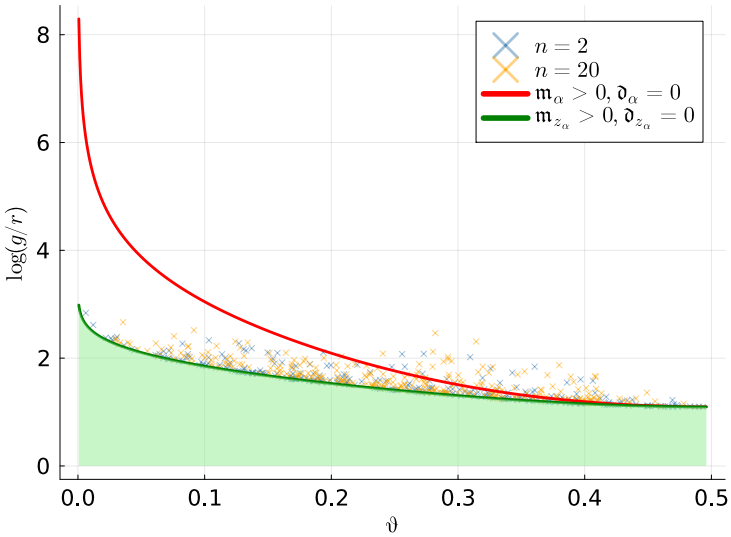

FIGURE 3. Classification of the couples of parameters $(g/r, z_\alpha)$ and $(g/r, \alpha)$ in the case of finite point partitioning distributions with $q = 0$. Parameters in the green area lead to survival of the cell population for any finite point partitioning kernel. Each cross corresponds to the limit for a finite point distribution with a given value of ϑ above which the cell population go to extinction. The orange crosses (resp. blue) correspond to distributions with 20 (resp. 2) modes below 1/2. The red curve corresponds to the limit above which a cell population with a random partitioning strategy (see (3.1)) goes to extinction.

On the other hand, there is no upper bound: for any value of $\vartheta \in (0, 1/2)$, and any value of $y \geq 0$, one can find a finite point measure (with $n = 2$ for example) such that for all $g/r < y$, the mean number of cells alive goes to infinity when time goes to infinity. This can be achieved by taking very small values for z_1, which is the smallest atom of the partitioning distribution. This is formally stated in the following proposition.

Proposition 3.4. *Let $g, r, q \in \mathbb{R}_+$ with $q < r$ and $\vartheta \in (0, 1/2)$. Then, there exists a multimodal distribution*

$$\kappa_2(d\theta) = \sum_{i=1}^{2} \left(\delta_{z_i}(d\theta) + \delta_{1-z_i}(d\theta)\right) p_i,$$

with $2(p_1 + p_2) = 1$, and $(z_1, z_2) \in (0, 1/2)^2$, such that if $\Theta \sim \kappa_2$,

$$\mathbb{E}\left[\min(\Theta, 1 - \Theta)\right] = \vartheta \quad \textit{and} \quad \lim_{t\to\infty} \mathbb{E}_{\delta_x}[\mathfrak{C}_t] = \infty \quad \textit{for any} \quad x > 0.$$

4. QUANTITY OF PARASITES IN THE CELLS

We now consider that the dynamics of the parasites in a cell follows the SDE (1.1) without the stable positive jumps, that is to say

$$\mathfrak{X}_t = x + \int_0^t g(\mathfrak{X}_s)ds + \int_0^t \sqrt{2\sigma^2(\mathfrak{X}_s)}dB_s + \int_0^t \int_0^{p(\mathfrak{X}_{s-})} \int_{\mathbb{R}_+} z\widetilde{Q}(ds, dx, dz). \tag{4.1}$$

In this case we can observe moderate infections, extinctions of the parasites in the cell population, but also cases where the quantity of parasites goes to infinity with an exponential growth in a positive fraction of the cells.

In order to state the next result, we need to introduce three assumptions. The first one is a technical assumption allowing to make couplings, that could probably be weakened.

Assumption A. *The measure π satisfies $\int_{\mathbb{R}_+} z\pi(dz) < \infty$.*

Note that the weaker condition $\int_{\mathbb{R}_+} \ln(1+z)\pi(dz) < \infty$, which is required in [18], is therefore satisfied under Assumption A. The second assumption provides a condition under which the quantity of parasites may reach 0. It is almost a necessary and sufficient condition (see [18, Remark 3.2 and Theorem 3.3]).

(LN0) There exist $0 < a < 1$, $\eta > 0$ and $x_0 > 0$ such that for all $x \leq x_0$

$$\frac{g(x)}{x} - a\frac{\sigma^2(x)}{x^2} - 2r\frac{1-\mathbb{E}\left[\Theta^{1-a}(x)\right]}{1-a} \leq -\ln(x^{-1})\left(\ln\ln(x^{-1})\right)^{1+\eta}.$$

The third assumption ensures that the process does not explode in finite time almost surely (see [18, Theorem 4.1]).

(SN∞) There exist $0 < a < 1$, and a nonnegative function f on $\mathbb{R}_+$ such that

$$\frac{g(x)}{x} - a\frac{\sigma^2(x)}{x^2} - 2r\frac{1-\mathbb{E}\left[\Theta^{1-a}(x)\right]}{1-a} - p(x)I_a(x) = -f(x) + o(\ln x), \quad (x \to +\infty),$$

where

$$I_a(x) = \frac{a}{x^2}\int_{\mathbb{R}_+} z^2 \left(\int_0^1 \frac{(1-v)}{(1+zvx^{-1})^{1+a}}dv\right)\pi(dz).$$

Note that the term $-2r\big(1-\mathbb{E}\left[\Theta(x)^{1-a}\right]\big)(1-a)^{-1}$ is not present in **(LN0)** and **(SN∞)** in [18] as it is a constant when the law of $\Theta(x)$ does not depend on x. However, the extension of the proofs of [18] to this case is possible under the additional assumption **LB** (Lower Bound) on the partitioning kernel.

Assumption LB. *There exists a symmetrical random variable Θ on $[0,1]$ and a constant $c > 0$ such that*

$$\inf_{x\geq 0}\Theta(x) \geq c\Theta.$$

Recall that the total number of cells is given by a continuous-time birth and death process with individual birth rate r and individual death rate q. From classical results on branching processes (see for instance [3]), we know that the cell population survives with probability $0 \vee (1-q/r)$. The long time behaviour for the quantity of parasites in the cells is described in the next proposition. We denote by N_t the cardinality of V_t.

Proposition 4.1. *Assume that the quantity of parasites in a cell follows the SDE* (4.1)*, that Assumption A holds, that $r > q \equiv q(x) \geq 0$.*

i) If $\sup_{x\geq 0}\mathbb{E}[\ln^2\Theta(x)] < \infty$, and there exists $\eta > 0$ such that for $x \geq 0$,

$$\frac{g(x)}{x} + 2r\mathbb{E}[\ln\Theta(x)] > \eta,$$

and if the function $x \mapsto (\sigma^2(x)+p(x))/x$ is bounded and there exists $\varepsilon_1 > 0$ such that

$$\int_{\mathbb{R}_+} z\ln^{1+\varepsilon_1}(1+z)\pi(dz) < \infty,$$

then for $\varepsilon > 0$,

$$\liminf_{t\to\infty}\mathbb{E}\left[\mathbf{1}_{\{N_t\geq 1\}}\frac{\#\{u\in V_t : X_t^u > e^{(\eta/2r-\varepsilon)t}\}}{N_t}\right] > 0.$$

ii) If Assumption **LB** *and* **(LN0)** *hold, and if there exists $\eta > 0$ such that for all $x \geq 0$,*

$$\frac{g(x)}{x} + 2r\mathbb{E}[\ln \Theta(x)] < -\eta,$$

then for $\varepsilon > 0$

$$\lim_{t\to\infty} \mathbf{1}_{\{N_t \geq 1\}} \frac{\#\{u \in V_t : X_t^u > \varepsilon\}}{N_t} = 0 \quad \textit{in probability.}$$

iii) If Assumption **LB**, **(LN0)** *and* **(SN∞)** *hold, and if there exist $\eta > 0$ and $x_0 \geq 0$ such that for $x \geq x_0$,*

$$\frac{g(x)}{x} - \frac{\sigma^2(x)}{x^2} + 2r\mathbb{E}[\ln \Theta(x)] - p(x) \int_0^\infty \left(\frac{z}{x} - \ln\left(1 + \frac{z}{x}\right)\right) \pi(dz) < -\eta,$$

then

$$\lim_{t\to\infty} \mathbf{1}_{\{N_t \geq 1\}} \frac{\#\{u \in V_t : X_t^u > 0\}}{N_t} = 0 \quad a.s.$$

Proposition 4.1 extends [8, Theorem 4.2] allowing for non constant drift for the quantity of parasites, a general class of diffusive functions, positive jumps, a parasites repartition kernel depending on the number of parasites carried by the mother, as well as the possibility for the cells to die at a constant rate.

Again, from Proposition 4.1 we see that in some sense an equal sharing is the worst strategy at the population level. Indeed, from the concavity of the functions $x \mapsto \ln x$ and $x \mapsto x^{1-a}$ for $0 \leq a < 1$, we can prove that if the proportion of highly infected cells is positive for large time (Proposition 4.1*i)*) with a given partitioning strategy, then the equal sharing strategy would have led to the same result. Conversely, if the equal sharing strategy guarantees the healing of the cell population for large time, then it would have been the case for any partitioning strategy.

Lemma 4.2. *Under the assumptions of Proposition 4.1, we have the following:*

i) If there exists a real function $(x, \zeta) \mapsto \Theta(x, \zeta)$ such that the assumptions of Proposition 4.1i) hold, then they also hold for the equal sharing (corresponding to $\Theta \equiv 1/2$).

ii) If the assumptions of point ii) (resp. iii)) of Proposition 4.1 hold for the equal sharing ($\Theta \equiv 1/2$), then they also hold for any real function $(x, \zeta) \mapsto \Theta(x, \zeta)$ such that $\mathbb{E}[\Theta(x)] = 1/2$ and $|\mathbb{E}[\ln \Theta(x)]| < \infty$.

The rest of the paper is dedicated to the proofs of the results presented in previous sections. As mentioned before, the proofs rely on the construction of an auxiliary process, which gives information on the dynamics of the quantity of parasites in a 'typical' cell, that is to say a cell chosen uniformly at random among the cells alive.

5. Many-to-One formula

Recall from (1.3) that the population state Z_t at time t can be represented by a sum of Dirac masses. We denote by $(M_t, t \geq 0)$ the first-moment semi-group associated with the population process Z given for all measurable functions f and $x, t \geq 0$ by

$$M_t f(x) = \mathbb{E}_{\delta_x}\left[\sum_{u \in V_t} f(X_t^u)\right].$$

The trait of a typical individual in the population is characterized by the so-called auxiliary process Y (see [16, Theorem 3.1] for detailed computations and proofs). In our case, for constant birth and death rate, Y is a time-homogeneous Markov process and for all measurable

bounded functions $F : \mathbb{D}([0,t],\mathbb{R}_+) \to \mathbb{R}$, we have:

$$\mathbb{E}_{\delta_x}\left[\sum_{u\in V_t} F\left(X_s^u, s\le t\right)\right] = e^{(r-q)t}\mathbb{E}_x\left[F\left(Y_s^{(t)}, s\le t\right)\right]. \tag{5.1}$$

Here $(Y_t, t\ge 0)$ is a Markov process with associated infinitesimal generator $\mathcal{A}$ given for $f\in\mathcal{C}_b^2(\mathbb{R}_+)$ and $x\ge 0$ by:

$$\mathcal{A}f(x) = \mathcal{G}f(x) + 2r\int_0^1 \left(f(\theta x) - f(x)\right)\kappa(x,d\theta),$$

We refer the reader [19, Section 4.2] for details on the role of the death rate in the auxiliary process.

6. Proofs

6.1. Proofs of Section 2.

Proof of Proposition 2.2. Let us consider the auxiliary process introduced in Section 5 as the unique strong solution to the following SDE:

$$\begin{aligned} Y_t = x + g\int_0^t Y_s ds + \int_0^t \sqrt{2\sigma^2 Y_s^2}dB_s + \int_0^t\int_0^{Y_{s^-}}\int_{\mathbb{R}_+} zR(ds,dx,dz) \\ + \int_0^t\int_0^1 (\theta-1)Y_{s^-}P(ds,d\theta), \end{aligned} \tag{6.1}$$

where P is a Poisson point measure on $\mathbb{R}_+\times[0,1]$ with intensity $2rds\otimes\kappa(d\theta)$. We can thus apply (5.1) to the function

$$F((X_s^u, s\le t)) = \mathbf{1}_{\{X_t^u<\infty\}},$$

and obtain

$$\mathbb{E}_{\delta_x}\left[\mathfrak{C}_t\right] = e^{(r-q)t}\mathbb{P}_x\left(Y_t<\infty\right),$$

where we recall that $\mathfrak{C}_t$ is the number of cells alive at time t (that is to say containing a finite quantity of parasites). The study of the asymptotic behaviour of $\mathbb{E}\left[\mathfrak{C}_t\right]$ is thus reduced to the study of the asymptotics of the non-explosion probability of Y. Following [22], the long time behaviour of $\mathbb{P}_x\left(Y_t<\infty\right)$ depends on the properties of the Lévy process L given by:

$$L_t := (g-\sigma^2)t + \sqrt{2\sigma^2}B_t + \int_0^t\int_0^1 \ln\theta P(ds,d\theta), \tag{6.2}$$

where B and N are the same as in (6.1). Its Laplace exponent ϕ is

$$\phi(\lambda) := \ln\mathbb{E}[e^{\lambda L_1}] = \lambda(g-\sigma^2) + \lambda^2\sigma^2 + 2r\left[\int_0^1 \theta^\lambda\kappa(d\theta) - 1\right],$$

for any $\lambda\in(\lambda^-,\infty)$. Recall that λ^- and $\mathfrak{m}$ have been defined on page 5. Then an application of [22, Proposition 2.1] gives the three following regimes:

i) If $\mathfrak{m}<0$, then for every $x>0$ there exists $0<c_1(x)<1$ such that
$$\lim_{t\to\infty}\mathbb{P}_x(Y_t<\infty) = c_1(x).$$

ii) If $\mathfrak{m}=0$ and $\lambda^-<0$, then for every $x>0$ there exists $c_2(x)>0$ such that
$$\lim_{t\to\infty}\sqrt{t}\mathbb{P}_x(Y_t<\infty) = c_2(x).$$

iii) If $\mathfrak{m}>0$, then for every $x>0$ there exists $c_3(x)>0$ such that
$$\lim_{t\to\infty} t^{\frac{3}{2}}e^{-\phi(\hat{\tau})}\mathbb{P}_x(Y_t<\infty) = c_3(x).$$

It ends the proof. □

Proof of Proposition 2.1. First, we consider the case $g(x) = gx$ and $q(x) \equiv q$. The process $\mathfrak{X}$ solution to (1.1) has the same law as the unique solution to the SDE

$$\tilde{\mathfrak{X}}_t = x + g\int_0^t \tilde{\mathfrak{X}}_s ds + \int_0^t \sqrt{2\sigma^2 \tilde{\mathfrak{X}}_s^2} dB_s + \int_0^t \sqrt{2\mathfrak{s}^2(\tilde{\mathfrak{X}}_s)\tilde{\mathfrak{X}}_s} dW_s$$
$$+ \int_0^t \int_0^{\tilde{\mathfrak{X}}_{s^-}} \int_{\mathbb{R}_+} z\widetilde{Q}(ds, dx, dz) + \int_0^t \int_0^{\tilde{\mathfrak{X}}_{s^-}} \int_{\mathbb{R}_+} zR(ds, dx, dz),$$

where W is a Brownian motion independent of B, Q and R. Notice that under the assumptions of Proposition 2.1, $y \mapsto \mathfrak{s}(y)\sqrt{y}$ satisfies point *ii)* of Assumption **EU**. As in the previous case, explicit computations are possible, and if we keep the notation Y for the auxiliary process associated to $\tilde{\mathfrak{X}}$ for the sake of simplicity, we obtain that Y is solution to:

$$Y_t = x + g\int_0^t Y_s ds + \int_0^t \sqrt{2\sigma^2 Y_s^2} dB_s + \int_0^t \sqrt{2\mathfrak{s}^2(Y_s)Y_s} dW_s + \int_0^t \int_0^{Y_{s^-}} \int_{\mathbb{R}_+} z\widetilde{Q}(ds, dx, dz)$$
$$+ \int_0^t \int_0^{Y_{s^-}} \int_{\mathbb{R}_+} zR(ds, dx, dz) + \int_0^t \int_0^1 (\Theta(Y_{s^-}, \zeta) - 1)Y_{s^-} N(ds, d\zeta), \tag{6.3}$$

where $Y_0 = x \geq 0$ and N is PPM on $\mathbb{R}_+ \times [0, 1]$ with intensity $2r ds \otimes d\zeta$.

Let us introduce the process $(\tilde{L}_t, t \geq 0)$ via

$$\tilde{L}_t := (g - \sigma^2)t + \sqrt{2\sigma^2} B_t + \int_0^t \int_0^1 \ln \Theta(Y_{s^-}, \zeta) N(ds, d\zeta). \tag{6.4}$$

Then by an application of Itô's formula with jumps similarly as in [21] we can show that for any $x, \lambda, 0 \leq s \leq t$,

$$e^{-Y_s e^{-\tilde{L}_s} v_t(s,\lambda,\tilde{L})} = \int_0^s e^{-Y_u e^{-\tilde{L}_u} v_t(u,\lambda,\tilde{L})} e^{-2\tilde{L}_u} v_t^2(u, \lambda, \tilde{L})\mathfrak{s}^2(Y_u)Y_u du + \mathfrak{M}_s, \tag{6.5}$$

where $(\mathfrak{M}_s, 0 \leq s \leq t)$ is a local martingale conditionally on $(\tilde{L}_s, 0 \leq s \leq t)$ and $v_t(., \lambda, \tilde{L})$ is the unique solution to

$$\partial_s v_t(s, \lambda, \tilde{L}) = e^{\tilde{L}_s} \psi_0 \left(e^{-\tilde{L}_s} v_t(s, \lambda, \tilde{L}) \right), \quad v_t(t, \lambda, \tilde{L}) = \lambda,$$

where

$$\psi_0(\lambda) = c_{\mathfrak{b}} \lambda^{1+\mathfrak{b}} + \int_0^\infty \left(e^{-\lambda z} - 1 + \lambda z \right) \pi(dz).$$

With our assumptions on the function $\mathfrak{s}$, the process

$$\left(\exp\left(-Y_u e^{-\tilde{L}_u} v_t(u, \lambda, \tilde{L}) \right) e^{-2\tilde{L}_u} v_t^2(u, \lambda, \tilde{L})\mathfrak{s}^2(Y_u)Y_u, 0 \leq u \leq t \right)$$

is bounded by a finite quantity depending only on $(\tilde{L}_u, 0 \leq u \leq t)$ (using that $x \mapsto e^{-x}$ and $x \mapsto e^{-x}x^{\mathfrak{c}}$ are bounded on $\mathbb{R}_+$, where $\mathfrak{c}$ is defined in the assumptions of Proposition 2.1). Hence $(\mathfrak{M}_s, 0 \leq s \leq t)$ is a true martingale conditionally on $(\tilde{L}_s, 0 \leq s \leq t)$, and from (6.5) we get

$$\mathbb{E}_x \left[e^{-\lambda Y_t e^{-\tilde{L}_t}} \right] = \mathbb{E}_x \left[e^{-Y_t e^{-\tilde{L}_t} v_t(t,\lambda,\tilde{L})} \right] \geq \mathbb{E} \left[e^{-x v_t(0,\lambda,\tilde{L})} \right]. \tag{6.6}$$

Using that $\psi_0(\lambda) > c_{\mathfrak{b}} \lambda^{1+\mathfrak{b}}$, we obtain

$$\partial_s v_t(s, \lambda, \tilde{L}) \geq c_{\mathfrak{b}} e^{\tilde{L}_s} \left(e^{-\tilde{L}_s} v_t(s, \lambda, \tilde{L}) \right)^{1+\mathfrak{b}}, \quad v_t(t, \lambda, \tilde{L}) = \lambda,$$

which entails

$$v_t(0, \lambda, \tilde{L}) \leq \left(\lambda^{-\mathfrak{b}} + \mathfrak{b} c_{\mathfrak{b}} \int_0^t e^{-\mathfrak{b}\tilde{L}_s} ds \right)^{-1/\mathfrak{b}}.$$

Combining this latter with (6.6), we obtain

$$\mathbb{E}_x\left[e^{-\lambda Y_t e^{-\tilde{L}_t}}\right] \geq \mathbb{E}\left[e^{-x\left(\lambda^{-\mathfrak{b}}+\mathfrak{b}c_{\mathfrak{b}}\int_0^t e^{-\mathfrak{b}\tilde{L}_s}ds\right)^{-1/\mathfrak{b}}}\right],$$

and letting λ tend to 0, we finally get:

$$\mathbb{P}_x\left(Y_t<\infty\right) \geq \mathbb{E}\left[e^{-x\left(\mathfrak{b}c_{\mathfrak{b}}\int_0^t e^{-\mathfrak{b}\tilde{L}_s}ds\right)^{-1/\mathfrak{b}}}\right].$$

From the assumptions of Proposition 2.1 we see that we can couple the processes L and $\tilde{L}$, defined in (6.2) and (6.4), respectively, in such a way that

$$\tilde{L}_t \leq L_t \quad \text{a.s. for all } t \geq 0.$$

We thus deduce that

$$\mathbb{P}_x\left(Y_t<\infty\right) \geq \mathbb{E}\left[e^{-x\left(\mathfrak{b}c_{\mathfrak{b}}\int_0^t e^{-\mathfrak{b}L_s}ds\right)^{-1/\mathfrak{b}}}\right].$$

As stated in [22], the right-hand side of the last inequality is equal to the probability of non-explosion before time t for a self-similar continuous state branching process in a Lévy random environment. Therefore, by [22, Proposition 2.1], we get

$$\liminf_{t\to+\infty} v(\mathfrak{m},t)\mathbb{P}_x\left(Y_t<\infty\right) =: \mathfrak{a}(x) > 0, \tag{6.7}$$

where

$$\begin{cases} v(\mathfrak{m},t)=1, & \text{for } \mathfrak{m}<0,\\ v(0,t)=\sqrt{t}, & \\ v(\mathfrak{m},t)=t^{3/2}e^{t\phi(\hat{\tau})}, & \text{for } \mathfrak{m}>0.\end{cases}$$

Next, we consider the auxiliary process $\tilde{Y}$ in the case where the quantity of parasites is described by (1.1), with $p(x)=x$, $\sigma^2(x)=\mathfrak{s}^2(x)x+\sigma^2x^2$ and $g(x)\leq gx$. In this case $\tilde{Y}$ has the same law as a process satisfying (6.3) replacing $g\int_0^t Y_s ds$ by $\int_0^t g(Y_s)ds \leq g\int_0^t Y_s ds$. Hence if we choose this version of $\tilde{Y}$, $\tilde{Y}_t \leq Y_t$ for all $t\geq 0$ using that both SDEs have a unique strong solution and that $\tilde{Y}_0 = Y_0$. Therefore,

$$\mathbb{P}_x(\tilde{Y}_t<\infty) \geq \mathbb{P}_x(Y_t<\infty).$$

As a consequence, from the Many-to-One formula (5.1) and the assumption that $q(\cdot)\equiv q$, we obtain for any $x>0$ and t large enough:

$$\begin{aligned}\mathbb{E}_{\delta_x}[\mathfrak{C}_t] = e^{(r-q)t}\mathbb{P}_x(\tilde{Y}_t<\infty) &\geq e^{(r-q)t}\mathbb{P}_x(Y_t<\infty)\\ &= e^{(r-q)t}v^{-1}(\mathfrak{m},t)\left(v(\mathfrak{m},t)\mathbb{P}_x\left(Y_t<\infty\right)\right)\\ &\geq e^{(r-q)t}v^{-1}(\mathfrak{m},t)\mathfrak{a}(x)/2,\end{aligned}$$

where we recall that $\mathfrak{a}(x)$ has been defined in (6.7). Adding that either ($\mathfrak{m}>0$ and $\mathfrak{d}>0$) or $\mathfrak{m}\leq 0$ holds under the assumptions of Proposition 2.1, we obtain that

$$\lim_{t\to\infty}\mathbb{E}_{\delta_x}[\mathfrak{C}_t]=\infty.$$

Now let us come back to the general case where for any $x\geq 0$, $q(x)\leq q$ for some $q\geq 0$. Then for any $x>0$ we can couple the process X with a process $X^{(q)}$ with death rate q and number of cells alive at time t given by $\mathfrak{C}_t^{(q)}$, and such that

$$\mathbb{E}_{\delta_x}[\mathfrak{C}_t] \geq \mathbb{E}_{\delta_x}[\mathfrak{C}_t^{(q)}].$$

Such a coupling may be obtained for instance by first realizing X and then obtaining $X^{(q)}$ by killing additional cells at rate $q - q(x)$ for a cell containing a quantity x of parasites. It ends the proof. □

Proof of Lemma 2.4. i) Let $\mathfrak{c} := \hat{\tau}(g - \sigma^2) + \hat{\tau}^2\sigma^2 + r\left[2\mathbb{E}[\Theta^{\hat{\tau}}] - 1\right]$, so that $\mathfrak{d} = \mathfrak{c} - q$. The value of $\mathfrak{m}$ does not depend on q. Hence, we distinguish three cases:

(1) If $\mathfrak{m} > 0$ and $\mathfrak{c} \leq 0$, then for all $q \geq 0$, $\mathfrak{d} \leq 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = 0$: we thus choose $q_{\lim}(g, \sigma, r) = 0$.
(2) If $\mathfrak{m} > 0$ and $\mathfrak{c} > 0$, then there is a unique $q_{\lim}(g, \sigma, r) = \mathfrak{c} > 0$ such that $\mathfrak{d} \leq 0$ for $q \geq q_{\lim}(g, \sigma, r)$ and $\mathfrak{d} > 0$ for $q < q_{\lim}(g, \sigma, r)$.
(3) If $\mathfrak{m} \leq 0$, we choose $q_{\lim}(g, \sigma, r, q) = r$.

We conclude the proof of *i)* using Corollary 2.3.
ii) Let $\eta := (g - \sigma^2)/(2\mathbb{E}[\ln(1/\Theta)])$.

(1) First assume that $\eta < q$. In this case, if $q < r$, we get $\mathfrak{m} < 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = \infty$ according to Corollary 2.3. Moreover, $q \geq r$ implies $\mathfrak{A}_x(g, \sigma, r, q) = 0$ according to Corollary 2.3. We thus choose $r_{\lim}(g, \sigma, q) = q$ in this case.
(2) Next, assume that $q \leq \eta$. Then,
- If $r \leq q$, we obtain $\mathfrak{A}_x(g, \sigma, r, q) = 0$ according to Corollary 2.3.
- If $r > \eta$, then $r > q$ and $\mathfrak{m} \leq 0$. According to Corollary 2.3, $\mathfrak{A}_x(g, \sigma, r, q) = \infty$.
- If $q < r = \eta$, then $\mathfrak{m} = 0$. According to Corollary 2.3, $\mathfrak{A}_x(g, \sigma, r, q) = \infty$.
- If $q < r < \eta$, then $\mathfrak{m} > 0$. Thus, the value of $\mathfrak{A}_x(g, \sigma, r, q)$ depends on the sign of $\mathfrak{d}$. From (2.2), we see that for any $\lambda \in \mathbb{R}$ the value of $\phi(\lambda)$ increases when r increases. This implies that it is also the case for the value of $\phi(\hat{\tau})$, by definition of $\hat{\tau}$ as the argument of the minimum of ϕ. As a consequence $\mathfrak{d} = \phi(\hat{\tau}) + r - q$ is strictly increasing with r. Next, for $r = q$,

$$\mathfrak{d} = \phi(\hat{\tau}) + q - q < 0,$$

and, when r tends to η, $\hat{\tau}$ tends to 0 and thus, $\phi(\hat{\tau})$ tends to 0. As $r > q$, $\mathfrak{d}$ tends to a positive value as r tends to η. We deduce that there exists a unique $r_{\lim}(g, \sigma, q) \in (q, \eta)$ such that $\mathfrak{d} = 0$ and that $\mathfrak{d} < 0$ when $r < r_{\lim}(g, \sigma, q)$ (resp. $\mathfrak{d} > 0$ when $r > r_{\lim}(g, \sigma, q)$). We conclude again by an application of Corollary 2.3.

iii)

(1) If $r \leq q$, $\mathfrak{A}_x(g, \sigma, r, q) = 0$ and $g_{\lim}(\sigma, r, q) = 0$ satisfies the needed property.
(2) If $q < r$ and $g \leq \sigma^2 - 2r\mathbb{E}[\ln \Theta]$, then $\mathfrak{m} \leq 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = \infty$.
(3) If $q < r$ and $g > \sigma^2 - 2r\mathbb{E}[\ln \Theta]$, then $\mathfrak{m} > 0$ and we have to study the sign of $\mathfrak{d}$. As $r > q$, $\mathfrak{d}$ is positive when g tends to $\sigma^2 - 2r\mathbb{E}[\ln \Theta]$, because $\hat{\tau}$ tends to 0. Moreover, from the equality

$$g = \sigma^2 - 2\hat{\tau}\sigma^2 - 2r\mathbb{E}[\Theta^{\hat{\tau}} \ln \Theta] \tag{6.8}$$

characterizing $\hat{\tau}$, we see that $\hat{\tau}$ goes to $-\infty$ when g goes to $+\infty$. Combining the definition of $\mathfrak{d}$ in (2.4) with (6.8), we obtain

$$\begin{aligned}\mathfrak{d} &= \frac{\hat{\tau}}{2}(g - \sigma^2) + r\left[\mathbb{E}[\Theta^{\hat{\tau}}(2 - \ln \Theta^{\hat{\tau}})] - 1\right] - q \\ &\leq \frac{\hat{\tau}}{2}(g - \sigma^2) + r\left[\mathbb{E}[\Theta^{\hat{\tau}}](2 - \ln \mathbb{E}[\Theta^{\hat{\tau}}]) - 1\right] - q\end{aligned}$$

where the inequality is a consequence of the concavity of the function $x \mapsto x(2-\ln x)$. Therefore, when g goes to ∞, $\hat{\tau}$ goes to $-\infty$, and $\mathfrak{d}$ goes to $-\infty$. Moreover, we have

$$\begin{aligned}\frac{d\mathfrak{d}}{dg} &= \frac{d\hat{\tau}}{2dg}(g-\sigma^2) + \frac{\hat{\tau}}{2} + r\frac{d\mathbb{E}[\Theta^{\hat{\tau}}(2-\ln\Theta^{\hat{\tau}})]}{d\hat{\tau}}\frac{d\hat{\tau}}{dg} \\ &= \frac{d\hat{\tau}}{2dg}(g-\sigma^2) + \frac{\hat{\tau}}{2} + r\mathbb{E}[\Theta^{\hat{\tau}}\ln\Theta(1-\ln\Theta^{\hat{\tau}})]\frac{d\hat{\tau}}{dg},\end{aligned}$$

which is negative as a sum of negative terms, as from (6.8), we see that $\hat{\tau}$ decreases when g increases. Thus, $\mathfrak{d}$ is decreasing with g. We deduce that there exists a unique $g_{\lim}(\sigma, r, q) \in (\sigma^2 - 2r\mathbb{E}[\ln\Theta], \infty)$ such that $\mathfrak{d} = 0$, and that $\mathfrak{d} > 0$ when $g < g_{\lim}(\sigma, r, q)$ (resp. $\mathfrak{d} < 0$ when $g > g_{\lim}(\sigma, r, q)$). We conclude again by an application of Corollary 2.3.

iv)

(1) If $r \leq q$, $\mathfrak{A}_x(g, \sigma, r, q) = 0$ and $\sigma_{\lim}(g, r, q) = \infty$ satisfies the needed property.
(2) If $q < r$ and $g \leq -2r\mathbb{E}[\ln\Theta]$, then $\mathfrak{m} \leq 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = \infty$, and $\sigma_{\lim}(g, r, q) = 0$ satisfies the needed property.
(3) If $q < r$ and $g > -2r\mathbb{E}[\ln\Theta]$
   - If $\sigma^2 \geq g + 2r\mathbb{E}[\ln\Theta]$, then $\mathfrak{m} \leq 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = \infty$.
   - If $\sigma^2 < g + 2r\mathbb{E}[\ln\Theta]$, then $\mathfrak{m} > 0$ and we have to study the sign of $\mathfrak{d}$. From (2.2) and (2.4), we have

$$\frac{\partial\mathfrak{d}}{\partial\sigma^2} = \frac{\partial\hat{\tau}}{\partial\sigma^2}\phi'(\hat{\tau}) + \hat{\tau}(\hat{\tau}-1) = \hat{\tau}(\hat{\tau}-1),$$

   where we used that $\phi'(\hat{\tau}) = 0$ because $\hat{\tau}$ is the argument of the minimum of ϕ. As $\hat{\tau} < 0$, we obtain that $\mathfrak{d}$ is increasing with σ^2. Moreover, when σ^2 tends to $g + 2r\mathbb{E}[\ln\Theta]$,

$$\mathfrak{d} \longrightarrow \hat{\tau}^2 g + r - q + 2r\mathbb{E}[\Theta^{\hat{\tau}} - 1 + (\hat{\tau}-1)\ln\Theta^{\hat{\tau}}] > 0.$$

   For $\sigma^2 = 0$, combining (6.8) and the definition of $\mathfrak{d}$, we have

$$\mathfrak{d} = 2r\mathbb{E}[\Theta^{\hat{\tau}}(1-\ln(\Theta^{\hat{\tau}}))] - r - q,$$

   which can be positive or negative, depending on g, r and the law of Θ. Then, if for $\sigma^2 = 0$, $\mathfrak{d} < 0$, there exists $\sigma_{\lim} > 0$ such that $\mathfrak{d} = 0$ for $\sigma = \sigma_{\lim}$. Else, $\mathfrak{d} > 0$ for all $\sigma \geq 0$ and $\mathfrak{A}_x(g, \sigma, r, q) = \infty$.

We conclude as for the previous points.

□

6.2. **Proof of Section 3.** We now explore how the long time behaviour of the infection depends on the parasites repartition kernel at division. We focus in particular on the uniform and the equal sharings, two cases where explicit computations are doable.

Proof of Corollary 3.1. We first consider $\kappa(d\theta) = d\theta$. We get $\lambda^- = -1$ and for $\lambda > -1$,

$$\phi(\lambda) = \lambda g + 2r\left[\frac{1}{\lambda+1} - 1\right], \quad \phi'(\lambda) = g - 2r\frac{1}{(\lambda+1)^2}, \quad \mathfrak{m} = g + 2r\int_0^1 \ln\theta d\theta = g - 2r.$$

The minimum of ϕ on $(-1, \infty)$ is reached at $\hat{\tau} = \sqrt{2rg^{-1}} - 1$ and equals

$$\phi(\hat{\tau}) = \left(\sqrt{\frac{2r}{g}} - 1\right)g + 2r\left[\sqrt{\frac{g}{2r}} - 1\right] = 2\sqrt{2rg} - g - 2r.$$

Let us look at the sign of $\phi(\hat{\tau}) + r - q = 2\sqrt{2rg} - g - r - q$. This quantity is nonpositive if and only if $8rg \leq g^2 + (r+q)^2 + 2g(r+q)$. Therefore, setting $X = g$, we have to solve the second degree polynomial equation

$$X^2 + 2X(q - 3r) + (r+q)^2 = 0.$$

Recall that $r > q$. In this case, the two solutions are given by

$$X_1 = 3r - q - 2\sqrt{2r(r-q)},\ X_2 = 3r - q + 2\sqrt{2r(r-q)},$$

so that $\phi(\hat{\tau}) + r - q$ is negative for $g < X_1$ or $g > X_2$. Notice that $X_1 - 2r = r - q - 2\sqrt{2r(r-q)} = \sqrt{r-q}(\sqrt{r-q} - 2\sqrt{2r}) < 0$ and $X_2 > 2r$. Then, the condition ($\mathfrak{m} > 0$ and $\phi(\hat{\tau}) + r - q \leq 0$) is equivalent to $g \geq 3r - q + 2\sqrt{2r(r-q)}$, and the first point is proved using Corollary 2.3 *i)*.

For the proof of *ii)*, we have $g < 3r - q + 2\sqrt{2r(r-q)}$ and we distinguish two cases: if $g \leq 2r$ then $\mathfrak{m} \leq 0$ and if $2r < g < 3r - q + 2\sqrt{2r(r-q)}$, then ($\mathfrak{m} > 0$ and $\phi(\hat{\tau}) + r - q > 0$) so that the second point is proved using Corollary 2.3 *ii)*.

Let us now consider the case where the cells share equally their parasites between their two daughters ($\Theta \equiv 1/2$). In this case we have $\lambda^- = -\infty$ and for $\lambda \in \mathbb{R}$,

$$\phi(\lambda) = \lambda g + 2r\left[2^{-\lambda} - 1\right], \quad \phi'(\lambda) = g - 2^{1-\lambda} r \ln 2, \quad \mathfrak{m} = g - 2r\ln 2.$$

The minimum of ϕ on $\mathbb{R}$ is reached at $\hat{\tau} = (\ln 2)^{-1} \ln\left(2r \ln 2 g^{-1}\right)$ and $\phi(\hat{\tau}) = g\hat{\tau} + g(\ln 2)^{-1} - 2r$. Thus to have almost sure extinction of the cell population, the two following conditions must be satisfied:

$$2r\ln 2 < g \quad \text{and} \quad \frac{g}{r\ln 2}\left(1 + \ln 2 - \ln\left(\frac{g}{r\ln 2}\right)\right) - 1 - \frac{q}{r} \leq 0.$$

Let

$$\varphi(x) = x\left(1 + \ln 2 - \ln(x)\right) - 1 - \frac{q}{r}.$$

We are looking for the sign of φ on $[2, +\infty)$, interval on which the first condition $\mathfrak{m} > 0$ is satisfied. On this interval, φ is decreasing from $1 - q/r > 0$ to $-\infty$. Thus, there exists $x_0(q/r) > 2$ such that $\varphi(x_0(q/r)) = 0$ and

$$\begin{aligned} \text{if } 2r\ln(2) < g < rx_0(q/r)\ln(2), &\quad \text{then } (\mathfrak{m} > 0 \text{ and } \phi(\hat{\tau}) + r - q > 0), \\ \text{if } g \geq rx_0(q/r)\ln(2), &\quad \text{then } (\mathfrak{m} > 0 \text{ and } \phi(\hat{\tau}) + r - q \leq 0). \end{aligned}$$

Finally, applying Corollary 2.3, we get

$$\begin{array}{lll} \text{if} & g \geq rx_0(q/r)\ln(2), & \text{then } \lim_{t\to\infty} \mathbb{E}[\mathfrak{C}_t] = 0, \\ \text{if } 2r\ln(2) < & g < rx_0(q/r)\ln(2) \text{ or } g \leq 2r\ln 2, & \text{then } \lim_{t\to\infty} \mathbb{E}[\mathfrak{C}_t] = \infty, \end{array}$$

which yields the result.

□

Proof of Proposition 3.2. Let κ be a partitioning kernel and Θ a random variable with distribution κ. Then, let us define $\mathfrak{m}(y) = y + 2\mathbb{E}[\ln\Theta]$. For any $y \leq -2\mathbb{E}[\ln\Theta]$, $\mathfrak{m}(y) \leq 0$ so that by Corollary 2.3, $\lim_{t\to+\infty} \mathbb{E}_{\delta_x}[\mathfrak{C}_t] = \infty$. By Jensen's inequality, $-\mathbb{E}[\ln\Theta] > \ln 2$. Then, for $g/r < 2\ln 2$, we proved the result.

For all $y > 2\ln 2$, let us define $\hat{\tau}(y)$ as the solution of

$$2\mathbb{E}[\ln(\Theta)\Theta^{\hat{\tau}(y)}] = -y. \tag{6.9}$$

Let $y_0 > 2\ln 2$ be such that

$$y_0\hat{\tau}(y_0) + 2\mathbb{E}[\Theta^{\hat{\tau}(y_0)}] - 1 - q/r = 0. \tag{6.10}$$

We want to prove that $y_0 > \ln(2)x_0(q/r)$, where $x_0(q/r)$ is defined in (3.2). By definition, x_0 is such that $\varphi(x_0) = x_0(1 + \ln(2) - \ln(x_0)) - 1 - q/r = 0$. As φ is a decreasing function on

$(2,+\infty)$ from $1-q/r$ to $-\infty$, we proved that $y_0 > \ln(2)x_0(q/r)$ if $\varphi(y_0/\ln(2)) < \varphi(x_0) = 0$. Therefore, we need to prove that that $y_0/\ln(2)(1+\ln(2\ln(2)) - \ln(y_0)) - 1 - q/r < 0$. Combining the latter with (6.10), we need to prove that

$$y_0/\ln(2)(1+\ln(2\ln(2) - \ln(y_0)) - y_0\hat{\tau}(y_0) - 2\mathbb{E}[\Theta^{\hat{\tau}(y_0)}] < 0.$$

For $y > 2\ln 2$, let us define $F(y) = y/\ln(2)(1+\ln(2\ln(2)) - \ln(y)) - y\hat{\tau}(y) - 2\mathbb{E}[\Theta^{\hat{\tau}(y)}]$. We have

$$F'(y) = \frac{1}{\ln(2)}(1+\ln(2\ln(2)) - \ln(y)) - \frac{1}{\ln(2)} - \hat{\tau}(y) - \frac{d\hat{\tau}}{dy}(y)\left(y + 2\mathbb{E}[\ln(\Theta)\Theta^{\hat{\tau}(y)}]\right).$$

By definition of $\hat{\tau}(y)$ in (6.9), we obtain

$$F'(y) = \frac{\ln(2\ln(2)) - \ln(y)}{\ln(2)} - \hat{\tau}(y).$$

Next, $x \mapsto \ln(x)x^\tau$ is concave for $\tau < 0$, and $x \in (0,1)$. Therefore,

$$\mathbb{E}[\ln(\Theta)\Theta^{\hat{\tau}(y)}] \leq \frac{-\ln(2)}{2^{\hat{\tau}(y)}},$$

so that by (6.9) again, $y \geq 2\ln(2)2^{-\hat{\tau}(y)}$ and

$$\hat{\tau}(y) \geq \frac{\ln(2\ln(2)) - \ln(y)}{\ln(2)},$$

and F is decreasing on $(2\ln(2),\infty)$. Moreover, if $X = -\hat{\tau}(2\ln(2))$,

$$F(2\ln(2)) = 2 + 2\ln(2)X - 2\mathbb{E}[\Theta^{-X}] \leq 2(1+\ln(2)X - 2^X) \leq 0,$$

where we used again Jensen's inequality. Then $F(y) \leq 0$ for all $y \geq 2\ln(2)$, and in particular, $F(y_0) < 0$, which ends the proof. □

Proof of Proposition 3.3. Let $\vartheta \in (0,1/2)$ and Θ_ϑ be a random variable with distribution

$$\kappa_\vartheta(d\theta) = \frac{1}{2}\left(\delta_\vartheta(d\theta) + \delta_{1-\vartheta}(d\theta)\right).$$

Let Θ be a symmetric random variable on $(0,1)$ with distribution κ and with expectation $1/2$, such that

$$\mathbb{E}[\min(\Theta,(1-\Theta))] = \vartheta.$$

Let

$$y^\star_\vartheta = \sup\left\{y \geq 0 \text{ s.t. if } g/r < y, \forall x \geq 0, \lim_{t\to+\infty} \mathbb{E}^{(\kappa_\vartheta)}_{\delta_x}[\mathfrak{C}_t] = \infty\right\}.$$

and

$$y^\star = \sup\left\{y \geq 0 \text{ s.t. if } g/r < y, \forall x \geq 0, \lim_{t\to+\infty} \mathbb{E}^{(\kappa)}_{\delta_x}[\mathfrak{C}_t] = \infty\right\}.$$

Let us define

$$\mathfrak{m}(y) := y + 2\mathbb{E}[\ln\Theta] = y + 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}\ln(\Theta(1-\Theta))]$$

and

$$y_0 := -2\mathbb{E}[\ln(\Theta)] = -2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}\ln(\Theta(1-\Theta))],$$

where the two rewritings of the expectation are a consequence of the symmetry of the random variable Θ. If $y \leq y_0$, then $\mathfrak{m}(y) \leq 0$ so that $y^\star \geq y_0$ by Corollary 2.3. Similarly, $y^\star_\vartheta \geq -\ln(\vartheta(1-\vartheta))$.

First, if $y^\star_\vartheta < y_0$, then , $y^\star_\vartheta < y^\star$ and the result is proved. Next, assume that $y^\star_\vartheta \geq y_0$. For all $y \geq y_0$, let $\hat{\tau}(y), \hat{\tau}_\vartheta(y) \leq 0$ be such that

$$2\mathbb{E}\left[\Theta^{\hat{\tau}(y)}\ln\Theta\right] = -y, \quad 2\mathbb{E}\left[\Theta_\vartheta^{\hat{\tau}_\vartheta(y)}\ln\Theta_\vartheta\right] = -y. \tag{6.11}$$

Then, by definition of $y^\star$, according to Corollary 2.3,

$$y^\star\hat{\tau}(y^\star) + 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\Theta^{\hat{\tau}(y^\star)} + (1-\Theta)^{\hat{\tau}(y^\star)})] = 1 + q/r. \tag{6.12}$$

Next, for all $y \geq y_0$, let $\varphi_\vartheta(y) = y\hat{\tau}_\vartheta(y) + \vartheta^{\hat{\tau}_\vartheta(y)} + (1-\vartheta)^{\hat{\tau}_\vartheta(y)} - 1 - q/r$. Using (6.11), we obtain that $\varphi_\vartheta'(y) = \hat{\tau}_\vartheta(y) < 0$, so that φ_ϑ is decreasing on $[y_0, +\infty)$. Moreover, $\varphi_\vartheta(y_\vartheta^\star) = 0$. Therefore, to show that $y^\star \geq y_\vartheta^\star$, we need to prove that $\varphi_\vartheta(y^\star) \leq 0$. Combining the definition of φ_ϑ with (6.12), we obtain

$$\begin{aligned}\varphi_\vartheta(y^\star) &= y^\star\hat{\tau}_\vartheta(y^\star) + \vartheta^{\hat{\tau}_\vartheta(y^\star)} + (1-\vartheta)^{\hat{\tau}_\vartheta(y^\star)} - y^\star\hat{\tau}(y^\star) - 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\Theta^{\hat{\tau}(y^\star)} + (1-\Theta)^{\hat{\tau}(y^\star)})] \\ &= \varphi_\vartheta(y^\star) - \varphi(y^\star),\end{aligned}$$

where for all $y \geq y_0$, $\varphi(y) = y\hat{\tau}(y) + 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\Theta^{\hat{\tau}(y)} + (1-\Theta)^{\hat{\tau}(y)})] - 1 - q/r$.

To prove that $\varphi_\vartheta(y^\star)$ is negative, let us define $F(y) = \varphi_\vartheta(y) - \varphi(y)$, for all $y \geq y_0$. Using (6.11), we have $F'(y) = \hat{\tau}_\vartheta(y) - \hat{\tau}(y)$. To find the sign of this latter, we study the convexity of $\varphi_1 : z \in (0,1) \mapsto \ln(z)z^\tau + \ln(1-z)(1-z)^\tau$, for any $\tau < 0$. We have

$$\begin{aligned}\varphi_1'(z) &= z^{\tau-1}\left(1 + \tau\ln(z)\right) - (1-z)^{\tau-1}\left(1 + \tau\ln(1-z)\right) \\ \varphi_1''(z) &= z^{\tau-2}\left((\tau-1)\left(1+\tau\ln(z)\right) + \tau\right) + (1-z)^{\tau-2}\left((\tau-1)\left(1+\tau\ln(1-z)\right) + \tau\right) < 0,\end{aligned}$$

as $\tau < 0$ and $z \in (0,1)$. Therefore, φ_1 is concave on $(0,1)$. Then, for all $y \geq y_0$, by Jensen's inequality we obtain

$$2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\ln\Theta\Theta^{\hat{\tau}(y)} + \ln(1-\Theta)(1-\Theta)^{\hat{\tau}(y)})] \leq \ln(\vartheta)\vartheta^{\hat{\tau}(y)} + \ln(1-\vartheta)(1-\vartheta)^{\hat{\tau}(y)},$$

where we used that $\vartheta = 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}\Theta]$. Combining the last inequality with (6.11), we have

$$\ln(\vartheta)\vartheta^{\hat{\tau}_\vartheta(y)} + \ln(1-\vartheta)(1-\vartheta)^{\hat{\tau}_\vartheta(y)} \leq \ln(\vartheta)\vartheta^{\hat{\tau}(y)} + \ln(1-\vartheta)(1-\vartheta)^{\hat{\tau}(y)}.$$

As $\tau \mapsto \ln(z)z^\tau + \ln(1-z)(1-z)^\tau$ is non-decreasing on $\mathbb{R}_-$, we get that

$$\hat{\tau}_\vartheta(y) \leq \hat{\tau}(y), \text{ for all } y \geq y_0. \tag{6.13}$$

Therefore, F is non-increasing on $[y_0, \infty)$. Finally, as $F(y^\star) = \varphi_\vartheta(y^\star) \leq F(y_0)$, we will now prove that $F(y_0) \leq 0$. We have

$$F(y_0) = y_0\left(\hat{\tau}_\vartheta(y_0) - \hat{\tau}(y_0)\right) + \vartheta^{\hat{\tau}_\vartheta(y_0)} + (1-\vartheta)^{\hat{\tau}_\vartheta(y_0)} - 2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\Theta^{\hat{\tau}(y_0)} + (1-\Theta)^{\hat{\tau}(y_0)})].$$

As $z \mapsto z^\tau + (1-z)^\tau$ is convex on $(0,1)$ for any $\tau < 0$, we have by Jensen's inequality

$$2\mathbb{E}[\mathbf{1}_{\Theta\leq 1/2}(\Theta^{\hat{\tau}(y_0)} + (1-\Theta)^{\hat{\tau}(y_0)})] \geq \vartheta^{\hat{\tau}(y_0)} + (1-\vartheta)^{\hat{\tau}(y_0)}.$$

Then,

$$F(y_0) \leq y_0\left(\tau_\vartheta - \tau\right) + \psi(\tau_\vartheta) - \psi(\tau),$$

where $\tau_\vartheta = \hat{\tau}_\vartheta(y_0)$, $\tau = \hat{\tau}(y_0)$, and $\psi(\tau) = \vartheta^\tau + (1-\vartheta)^\tau$. Recall that $\tau_\vartheta \leq \tau$ according to (6.13). By Taylor formula with integral remainder, we have

$$\psi(\tau) - \psi(\tau_\vartheta) = \psi'(\tau_\vartheta)(\tau - \tau_\vartheta) + \int_{\tau_\vartheta}^{\tau} \psi''(z)(\tau - z)dz.$$

First, note that $\psi'(\tau_\vartheta) = \ln\vartheta\vartheta^{\tau_\vartheta} + \ln(1-\vartheta)(1-\vartheta)^{\tau_\vartheta} = -y_0$ according to (6.11). Then,

$$F(y_0) \leq -\int_{\tau_\vartheta}^{\tau} \psi''(z)(\tau - z)dz \leq 0,$$

which ends the proof. □

Proof of Proposition 3.4. Let us first assume that

$$g \leq -r \ln \vartheta(1-\vartheta)$$

In this case, we choose $p_1 = 0, p_2 = 1/2$ and $z_2 = \vartheta$. This choice entails

$$\mathfrak{m} = g + r \ln \vartheta(1-\vartheta) \leq 0$$

and we conclude by an application of Corollary 2.3.

Let us now assume that

$$g > -r \ln \vartheta(1-\vartheta).$$

In this case, we choose

$$z_1 \in (0, \vartheta/4),\ p_1 = z_1^{(\ln\ln(1/z_1))^{-1}}, p_2 = 1/2 - z_1^{(\ln\ln(1/z_1))^{-1}}$$

and

$$z_2 = \frac{\vartheta - 2z_1^{1+(\ln\ln(1/z_1))^{-1}}}{1 - 2z_1^{(\ln\ln(1/z_1))^{-1}}}$$

This choice entails

$$\mathbb{E}\left[\min(\Theta, 1-\Theta)\right] = \vartheta$$

and

$$\begin{aligned}\mathfrak{m}(z_1) &= g + 2rz_1^{(\ln\ln(1/z_1))^{-1}} \ln(z_1(1-z_1)) \\ &\quad + 2r\left(\frac{1}{2} - z_1^{(\ln\ln(1/z_1))^{-1}}\right) \ln\left(\frac{\vartheta - 2z_1^{1+(\ln\ln(1/z_1))^{-1}}}{1 - 2z_1^{(\ln\ln(1/z_1))^{-1}}} \frac{1-\vartheta-(1-z_1)2z_1^{(\ln\ln(1/z_1))^{-1}}}{1-2z_1^{(\ln\ln(1/z_1))^{-1}}}\right)\end{aligned}$$

where we indicated explicitely the dependence on z_1 for the sake of readability. We will make z_1 tend to 0 and prove that for z_1 small enough the distribution of Θ meets the required properties. First we notice that

$$\lim_{z_1 \to 0} z_1^{(\ln\ln(1/z_1))^{-1}} \ln(z_1(1-z_1)) = 0$$

and

$$\begin{aligned}&\lim_{z_1 \to 0} \left(\frac{1}{2} - z_1^{(\ln\ln(1/z_1))^{-1}}\right) \ln\left(\frac{\vartheta - 2z_1^{1+(\ln\ln(1/z_1))^{-1}}}{1 - 2z_1^{(\ln\ln(1/z_1))^{-1}}} \frac{1-\vartheta-(1-z_1)2z_1^{(\ln\ln(1/z_1))^{-1}}}{1-2z_1^{(\ln\ln(1/z_1))^{-1}}}\right) \\ &\qquad = \frac{\ln\vartheta(1-\vartheta)}{2}.\end{aligned}$$

We deduce that

$$\lim_{z_1 \to 0} \mathfrak{m}(z_1) = g + r \ln \vartheta(1-\vartheta) > 0$$

and thus there exists $\mathfrak{z} > 0$ such that for all $z_1 < \mathfrak{z}$, $\mathfrak{m}(z_1) > 0$. Therefore, according to Corollary 2.3, to prove the result, we need to prove that there exists $z_1 < \mathfrak{z}$ such that $\mathfrak{d}(z_1) > 0$.

First, we know that for all $z_1 < \mathfrak{z}$, as $\mathfrak{m}(z_1) > 0$, the argument of the minimum of ϕ is negative, *i.e.* there exists $\tau(z_1) < 0$ such that

$$g = -2r\mathbb{E}[\Theta^{\tau(z_1)} \ln \Theta]. \tag{6.14}$$

We now prove by a reductio ad absurdum that for all $z_1 < \mathfrak{z} \wedge e^{-g/r}$,

$$\tau(z_1) > -\frac{1}{\ln\ln(1/z_1)}. \tag{6.15}$$

Let $z_1 < \mathfrak{z} \wedge e^{-g/r}$. If $\tau(z_1) \leq -1/\ln\ln(1/z_1)$ we have

$$\begin{aligned}\frac{g}{r} &\geq p_1 z_1^{\tau(z_1)} \ln(1/z_1) = z_1^{(\ln\ln(1/z_1))^{-1}} z_1^{\tau(z_1)} \ln(1/z_1) \\ &\geq z_1^{(\ln\ln(1/z_1))^{-1}} z_1^{-(\ln\ln(1/z_1))^{-1}} \ln(1/z_1) = \ln(1/z_1),\end{aligned}$$

so that $z_1 \geq e^{-g/r}$ which is absurd. We deduce that (6.15) holds for all $z_1 < \mathfrak{z} \wedge e^{-g/r}$, and as $\tau(z_1) < 0$, we obtain that $\tau(z_1)$ goes to 0 when z_1 goes to 0.

Finally, with our choice of parameters we have

$$\mathfrak{d}(z_1) = \tau(z_1)g + 2r\left(p_1\left(z_1^{\tau(z_1)} + (1-z_1)^{\tau(z_1)}\right) + p_2\left(z_2^{\tau(z_1)} + (1-z_2)^{\tau(z_1)}\right)\right) - r - q,$$

and

$$\lim_{z_1\to 0}\tau(z_1) = \lim_{z_1\to 0} p_1 = 0, \quad \lim_{z_1\to 0}(1-z_1)^{\tau(z_1)} = 1, \quad \lim_{z_1\to 0} p_2 = \frac{1}{2} \quad \text{and} \quad \lim_{z_1\to 0} z_2 = \vartheta.$$

Moreover, by (6.14),

$$\lim_{z_1\to 0} z_1^{\tau(z_1)} \ln(z_1) p_1 = -\frac{g}{2r} + \frac{1}{2}\ln(\vartheta(1-\vartheta)),$$

so that $\lim_{z_1\to 0} z_1^{\tau(z_1)} p_1 = 0$. Finally,

$$\lim_{z_1\to 0}\mathfrak{d}(z_1) = r - q > 0.$$

This ends the proof. □

6.3. **Proof of Section 4.** We now turn to the proof of the results on the asymptotic behaviour of the quantity of parasites in the cells. Hence, we consider that the dynamics of the parasites follows (4.1).

Proof of Proposition 4.1. From Section 5, we know that the auxiliary process Y is the unique strong solution to the SDE

$$\begin{aligned}Y_t = x &+ \int_0^t g(Y_s)ds + \int_0^t \sqrt{2\sigma^2(Y_s)}dB_s + \int_0^t\int_0^{p(Y_{s-})}\int_{\mathbb{R}_+} z\widetilde{Q}(ds,dx,dz) \\ &+ \int_0^t\int_0^1 (\Theta(Y_{s-},\zeta)-1)Y_{s-}N(ds,d\zeta),\end{aligned}$$

where N is as in (6.3). Let us begin with the proof of point *ii)*. Note that as $g(x)/x + 2r\mathbb{E}[\ln\Theta(x)] < -\eta$ for all $x > 0$, **(SN∞)** is satisfied. We plan to apply (6.3) of [18, Theorem 6.2]. This result still holds with $\Theta(x)$ instead of Θ. Indeed the proof of this result require two properties on the partitioning kernel. First, we need that $Y_t\exp(-\int_0^t g(Y_s)/Y_s ds - \int_0^t\int_0^1 \ln\Theta(Y_{s-},\zeta)N(ds,d\zeta))$ is a local martingale, which still holds. Second, we need a (possibly stochastic) lower bound on the proportion $\Theta(x)$ of the quantity of parasites that goes to one of the daughter cells at division, uniform in x. This is ensured by our assumptions. Thus, from (6.3) of [18, Theorem 6.2], we have

$$\lim_{t\to+\infty} Y_t = 0 \quad \text{almost surely,}$$

and combining (5.1) with the fact that $\mathbb{E}_{\delta_x}[N_t] = e^{(r-q)t}$, we obtain that

$$\mathbb{E}_{\delta_x}\left[\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u>\varepsilon\}}}{e^{(r-q)t}}\right] \xrightarrow[t\to\infty]{} 0.$$

Moreover, the fact that $(N_t, t\geq 0)$ is a birth and death process with individual death rate q and individual birth rate r also entails that $N_t e^{-(r-q)t}$ converges in probability to

an exponential random variable with parameter 1 on the event of survival, when t goes to infinity. Hence, we have

$$\mathbf{1}_{\{N_t\geq 1\}}\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u>\varepsilon\}}}{N_t}=\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u>\varepsilon\}}}{e^{(r-q)t}}\times\frac{\mathbf{1}_{\{N_t\geq 1\}}}{N_te^{-(r-q)t}}\xrightarrow[t\to\infty]{}0\quad\text{in probability.}$$

It ends the proof of point *ii)*.

We now prove point *iii)*. Applying again (6.3) of [18, Theorem 6.2] to Y, we obtain that

$$\mathbb{P}\left(Y_t\neq 0\right)\to 0,\quad (t\to\infty).$$

From this, similarly as for the proof of point *ii)* we obtain that

$$\mathbf{1}_{\{N_t\geq 1\}}\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u>0\}}}{N_t}\to 0\quad\text{in probability,}\quad (t\to\infty).$$

To end the proof of point *iii)*, we need to prove that the aforementioned convergence holds almost surely. We cannot follow directly the proof of [8, Theorem 4.2(i)] because their Lemma 4.3 concerns Yule processes and does not hold when we take into account the death of cells. However, we can prove a result similar to this lemma (see Lemma A.1 in the Appendix) which is sufficient to get our result. Except from this lemma the proof is exactly the same and we thus refer to [8] for details of the proof.

We end with the proof of point *i)*. Applying [18, Corollary 6.4.*iii)*] to Y, we obtain that

$$\liminf_{t\to\infty}Y_te^{-\Lambda_t}=W, \tag{6.16}$$

with $\mathbb{P}(W>0)>0$ and where Λ is defined by

$$\Lambda_t:=\int_0^t\frac{g(Y_s)}{Y_s}ds+\int_0^t\int_0^1\ln\Theta(Y_{s^-},\zeta)N(ds,d\zeta),$$

where N is PPM on $\mathbb{R}_+\times[0,1]$ with intensity $2rds\otimes d\zeta$. Notice that Λ may be rewritten as

$$\begin{aligned}\Lambda_t&=\int_0^t\left(\frac{g(Y_s)}{Y_s}+2r\mathbb{E}\left[\ln\Theta(Y_{s^-})\right]\right)ds+\int_0^t\int_0^1\ln\Theta(Y_{s^-},\zeta)N(ds,d\zeta)-2r\int_0^t\mathbb{E}\left[\ln\Theta(Y_{s^-})\right]ds\\&=:\int_0^t\left(\frac{g(Y_s)}{Y_s}+2r\mathbb{E}\left[\ln\Theta(Y_{s^-})\right]\right)ds+\mathscr{M}_t,\end{aligned}$$

where $\mathscr{M}$ is a martingale, as by assumption it has a finite variance. To be more precise, we have

$$Var(\mathscr{M}_t)=2r\int_0^t\int_0^1\mathbb{E}\left[\ln^2\Theta(Y_{s^-},\zeta)\right]dsd\zeta\leq 2r\sup_{x\geq 0}\mathbb{E}\left[\ln^2\Theta(x)\right]t=Ct,$$

where C is a finite constant under the assumptions of point i). Hence for $\varepsilon>0$,

$$\lim_{t\to\infty}\{\varepsilon t+\mathscr{M}_t\}=\infty,\ \text{almost surely,}$$

which implies

$$\Lambda_t-(\eta-\varepsilon)t\geq\varepsilon t+\mathscr{M}_t\underset{t\to\infty}{\to}\infty\ \text{almost surely.} \tag{6.17}$$

We thus get

$$\liminf_{t\to\infty}\mathbb{P}_x\left(Y_te^{-(\eta-\varepsilon)t}>0\right)\geq\mathbb{P}_x\left(\liminf_{t\to\infty}Y_te^{-(\eta-\varepsilon)t}>0\right)=\mathbb{P}_x\left(\liminf_{t\to\infty}Y_te^{-\Lambda_t}e^{\Lambda_t-(\eta-\varepsilon)t}>0\right)>0,$$

where we used Fatou's Lemma, (6.16) and (6.17). Hence, using (5.1) we obtain

$$\liminf_{t\to\infty}\mathbb{E}_{\delta_x}\left[\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^ue^{-(\eta-\varepsilon)t}>0\}}}{e^{(r-q)t}}\right]>0.$$

Now notice that the Cauchy-Schwarz inequality yields

$$\mathbb{E}_{\delta_x}^2\left[\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u e^{-(\eta-\varepsilon)t}>0\}}}{e^{(r-q)t}}\right] \le \mathbb{E}_{\delta_x}\left[\mathbf{1}_{\{N_t\ge 1\}}\left(\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u e^{-(\eta-\varepsilon)t}>0\}}}{N_t}\right)^2\right]\mathbb{E}_{\delta_x}\left[\left(\frac{N_t}{e^{(r-q)t}}\right)^2\right]$$
$$\le \mathbb{E}_{\delta_x}\left[\mathbf{1}_{\{N_t\ge 1\}}\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u e^{-(\eta-\varepsilon)t}>0\}}}{N_t}\right]\mathbb{E}_{\delta_x}\left[\left(\frac{N_t}{e^{(r-q)t}}\right)^2\right],$$

where the last inequality comes from the fact that the term in the first expectation in the right-hand side is smaller than one. The last expectation converges to $C := 1+(r+q)/(r-q)$ as t goes to infinity (see Lemma 5.3 in [19] in the case $\alpha = 0$). Hence we get

$$0 < C^{-1}\liminf_{t\to\infty}\mathbb{E}_{\delta_x}^2\left[\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u e^{-(\eta-\varepsilon)t}>0\}}}{e^{(r-q)t}}\right] \le \liminf_{t\to\infty}\mathbb{E}_{\delta_x}\left[\mathbf{1}_{\{N_t\ge 1\}}\frac{\sum_{u\in V_t}\mathbf{1}_{\{X_t^u e^{-(\eta-\varepsilon)t}>0\}}}{N_t}\right],$$

and it ends the proof of point *i)*. □

Appendix A. Technical lemma for the proof of Proposition 4.1*iii)*

This appendix is dedicated to the statement and proof of a lemma, which is a slightly weaker version of [8, Lemma 4.3]. The only difference is that they considered a Yule process instead of a birth and death process, and that the finite sets I and J could be arbitrary, whereas we impose the condition $J \subset I$. The statement and proof are deliberately very close to that of [8, Lemma 4.3]. We give the proof in its entirety for the sake of readability.

Lemma A.1. *Let V be a denumerable subset and $(N_t(i) : t \ge 0)$ be i.i.d. birth and death processes with birth and death rates r and $q < r$ for $i \in V$. Then there exist $\delta > 0$ and a nonnegative nonincreasing function G on $\mathbb{R}_+$ such that $G(y) \to 0$ as $y \to \infty$ and for all $J \subset I$ finite subsets of V and $x \ge 0$:*

$$\mathfrak{P}(x, \#J, \#I) := \mathbb{P}\Big(\sup_{t\ge 0}\mathbf{1}_{\{\sum_{i\in I}N_t(i)>0\}}\frac{\sum_{i\in J}N_t(i)}{\sum_{i\in I}N_t(i)} \ge x\Big) \le G\left(\frac{\#I}{\#J}x\right) + e^{-2\delta\#I}.$$

Proof. From classical results on birth and death processes (see [3] for instance), we know that for $i \in V$ the process $(N_t(i)e^{-(r-q)t})$ is a non negative martingale which converges to a random variable W which is positive on the survival event (occurring with probability $(r-q)/r$). Let us introduce the random variables,

$$M(i) := \sup_{t\ge 0}N_t(i)e^{-(r-q)t} \quad \text{and} \quad m(i) = \inf_{t\ge 0}N_t(i)e^{-(r-q)t}.$$

$(M(i) : i \in V)$ and $(m(i) : i \in V)$ are both sequences of finite nonnegative i.i.d. random variables with finite expectation. Moreover, if we introduce, for $i \in V$, the events:

$$V_\infty(i) := \{N_t(i) \ge 1, \forall t \ge 0\} \quad \text{and} \quad M_\infty(i) := \{\exists t < \infty, N_t(i) = 0\},$$

and the set

$$V_\infty := \{i \in I, V_\infty(i) \text{ holds}\},$$

we have that $0 = m(i) \le M(i)$ on the event $M_\infty(i)$, and $0 < m(i) \le M(i)$ on the event $V_\infty(i)$. As a consequence, for any $\varepsilon \in (0,1)$ and $t \ge 0$, using also that $J \subset I$, we have

$$\mathbf{1}_{\{\sum_{i\in I}N_t(i)>0\}}\frac{\sum_{i\in J}N_t(i)}{\sum_{i\in I}N_t(i)} \le \mathbf{1}_{\{\#V_\infty>\varepsilon\#I\}}\frac{\sum_{i\in J}M(i)}{\sum_{i\in I}m(i)} + \mathbf{1}_{\{\#V_\infty\le\varepsilon\#I\}}$$
$$= \frac{\#J}{\#I}\left(\mathbf{1}_{\{\#V_\infty>\varepsilon\#I\}}\frac{\sum_{i\in J}M(i)}{\#J}\frac{\#I}{\sum_{i\in I}m(i)} + \mathbf{1}_{\{\#V_\infty\le\varepsilon\#I\}}\frac{\#I}{\#J}\right).$$

Hence, we can bound $\mathfrak{P}$ as follows:

$$\begin{aligned}\mathfrak{P}(x,\#J,\#I) \leq & \mathbb{P}\left(\mathbf{1}_{\{\#V_\infty>\varepsilon\#I\}}\frac{\sum_{i\in J}M(i)}{\#J}\frac{\#I}{\sum_{i\in I}m(i)} \geq \frac{\#I}{\#J}\frac{x}{2}\right)\\ & + \mathbb{P}\left(\mathbf{1}_{\{\#V_\infty\leq\varepsilon\#I\}}\frac{\#I}{\#J} \geq \frac{\#I}{\#J}\frac{x}{2}\right). \end{aligned} \tag{A.1}$$

To handle the first term on the right-hand side of (A.1), we define for $y \geq 0$

$$G(y) = \sup\left\{\mathbb{P}\Big(\mathbf{1}_{\{\#V_\infty>\varepsilon\#I\}}\frac{\sum_{i\in J}M(i)}{\#J}\frac{\#I}{\sum_{i\in I}m(i)} \geq y\Big) : J,I \subset V; \#I < \infty\right\}.$$

By the law of large numbers, the sequence

$$\mathbf{1}_{\{\#V_\infty>\varepsilon\#I\}}\frac{\sum_{i\in J}M(i)}{\#J}\frac{\#I}{\sum_{i\in I}m(i)}$$

is uniformly tight. So $G(y) \to 0$ as $y \to \infty$.

For the second term on the right-hand side of (A.1), Markov's inequality yields

$$\mathbb{P}\left(\mathbf{1}_{\{\#V_\infty\leq\varepsilon\#I\}}\frac{\#I}{\#J} \geq \frac{\#I}{\#J}\frac{x}{2}\right) \leq \mathbb{P}\left(\#V_\infty \leq \varepsilon\#I\right)\frac{2}{x}.$$

To bound the last term, we recall that $\#V_\infty$ is a sum of $\#I$ independent Bernoulli random variables with parameter $1-q/r$. Hence, for $\varepsilon \leq 1-q/r$, using Hoeffding's inequality, we obtain

$$\mathbb{P}\left(\#V_\infty \leq \varepsilon\#I\right) \leq \exp\left(-2\#I\left(1-\frac{q}{r}-\varepsilon\right)^2\right)$$

and it concludes the proof. □

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References

[1] G. Alsmeyer and S. Gröttrup. A host-parasite model for a two-type cell population. Adv. in Appl. Probab., 45(3):719–741, 09 2013.
[2] G. Alsmeyer and S. Gröttrup. Branching within branching: A model for host–parasite co-evolution. Stoch. Proc. Appl., 126(6):1839 – 1883, 2016.
[3] K. B. Athreya and P. E. Ney. Branching processes. Springer-Verlag Berlin, Mineola, NY, 1972.
[4] V. Bansaye. Proliferating parasites in dividing cells: Kimmel's branching model revisited. Ann. Appl. Probab., 18(3):967–996, 2008.
[5] V. Bansaye. Cell contamination and branching processes in a random environment with immigration. Adv. Appl. Probab., 41(4):1059–1081, 2009.
[6] V. Bansaye, J.-F. Delmas, L. Marsalle, V. C. Tran, et al. Limit theorems for Markov processes indexed by continuous time Galton–Watson trees. Ann. Appl. Probab., 21(6):2263–2314, 2011.
[7] V. Bansaye, J. C. Pardo, and C. Smadi. On the extinction of continuous state branching processes with catastrophes. Electron. J. Probab., 18:no. 106, 31, 2013.
[8] V. Bansaye and V. Tran. Branching feller diffusion for cell division with parasite infection. ALEA, Lat. Am. J. Probab. Math. Stat, 2011.
[9] B. Cloez. Limit theorems for some branching measure-valued processes. Adv. Appl. Probab., 49(2):549–580, 2017.
[10] A. Genthon. Analytical cell size distribution: lineage-population bias and parameter inference. J R Soc Interface, 19(196):20220405, 2022.

[11] H.-O. Georgii and E. Baake. Supercritical multitype branching processes: the ancestral types of typical individuals. Adv. Appl. Probab., 35(4):1090–1110, 2003.
[12] R. Hardy and S. C. Harris. A spine approach to branching diffusions with applications to L_p-convergence of martingales. In Séminaire de probabilités XLII, pages 281–330. Springer, 2009.
[13] M. Kimmel. Quasistationarity in a Branching Model of Division-Within-Division, pages 157–164. Springer New York, 1997.
[14] A. E. Kyprianou. Introductory lectures on fluctuations of Lévy processes with applications. Springer Science & Business Media, 2006.
[15] R. Lyons, R. Pemantle, and Y. Peres. Conceptual proofs of $L \log L$ criteria for mean behavior of branching processes. Ann. Probab., 23(3):1125–1138, 1995.
[16] A. Marguet. Uniform sampling in a structured branching population. Bernoulli, 25, 2016.
[17] A. Marguet. A law of large numbers for branching Markov processes by the ergodicity of ancestral lineages. ESAIM: PS, 23:638–661, 2019.
[18] A. Marguet and C. Smadi. Long time behaviour of continuous-state nonlinear branching processes with catastrophes. Electron. J. Probab., 26:1–32, 2021.
[19] A. Marguet and C. Smadi. Spread of parasites affecting death and division rates in a cell population. Preprint arXiv:2211.08265, 2022.
[20] L. Osorio and A. Winter. Two level branching model for virus population under cell division. Preprint, arXiv:2004.14352, 2020.
[21] S. Palau and J. Pardo. Branching processes in a Lévy random environment. Acta Appl. Math., 153(1):55–79, 2018.
[22] S. Palau, J. C. Pardo, and C. Smadi. Asymptotic behaviour of exponential functionals of Lévy processes with applications to random processes in random environment. ALEA, Lat. Am. J. Probab. Math. Stat, 2016.

Aline Marguet, Univ. Grenoble Alpes, INRIA, 38000 Grenoble, France
Email address: aline.marguet@inria.fr

Charline Smadi, Univ. Grenoble Alpes, INRAE, LESSEM, 38000 Grenoble, France and Univ. Grenoble Alpes, CNRS, Institut Fourier, 38000 Grenoble, France
Email address: charline.smadi@inrae.fr