

FROM STOCHASTIC, INDIVIDUAL-BASED MODELS TO THE CANONICAL EQUATION OF ADAPTIVE DYNAMICS IN ONE STEP

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We consider a model for Darwinian evolution in an asexual population with a large but nonconstant populations size characterized by a natural birth rate, a logistic death rate modeling competition and a probability of mutation at each birth event. In the present paper, we study the long-term behavior of the system in the limit of large population ($K \rightarrow \infty$) size, rare mutations ($u \rightarrow 0$) and small mutational effects ($\sigma \rightarrow 0$), proving convergence to the canonical equation of adaptive dynamics (CEAD). In contrast to earlier works, for example, by Champagnat and Méléard, we take the three limits simultaneously, that is, $u = u_K$ and $\sigma = \sigma_K$, tend to zero with K , subject to conditions that ensure that the time-scale of birth and death events remains separated from that of successful mutational events. This slows down the dynamics of the microscopic system and leads to serious technical difficulties that require the use of completely different methods. In particular, we cannot use the law of large numbers on the diverging time needed for fixation to approximate the stochastic system with the corresponding deterministic one. To solve this problem, we develop a “stochastic Euler scheme” based on coupling arguments that allows to control the time evolution of the stochastic system over time-scales that diverge with K .

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Received August 2015; revised February 2016.

¹Supported by the German Research Foundation through the Priority Programme 1590 “Probabilistic Structures in Evolution.”

²Supported in part by the German Research Foundation in the Collaborative Research Center 1060 “The Mathematics of Emergent Effects,” the Priority Programme 1590 “Probabilistic Structures in Evolution,” the Hausdorff Center for Mathematics (HCM), and the Cluster of Excellence “ImmunoSensation” at Bonn University.

³Supported by the project NON LOCAL ANR-14-CE25-0013 of the French National Research Agency.

MSC2010 subject classifications. Primary 60K35, 92D25; secondary 60J85.

Key words and phrases. Adaptive dynamics, canonical equation, large population limit, mutation-selection individual-based model.

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1. Introduction. In this paper, we study a microscopic model for evolution in a population characterized by a birth rate with a probability of mutation at each event and a logistic death rate, which has been studied in many works before [6–9, 13]. More precisely, it is a model for an asexual population in which each individual’s ability to survive and to reproduce is a function of a one-dimensional phenotypic trait, such as body size, the age at maturity or the rate of food intake. The evolution acts on the trait distribution and is the consequence of three basic mechanisms: heredity, mutation and selection. Heredity passes the traits through generations, mutation drives the variation of the trait values in the population and selection acts on individuals with different traits and is a consequence of competition between the individuals for limited resources or area.

The model is a generic stochastic individual-based model and belongs to the models of adaptive dynamics. In general, adaptive dynamic models aim to study the interplay between ecology (viewed as driving selection) and evolution, more precisely, the interplay between the three basic mechanisms mentioned above. It tries to develop general tools to study the long time evolution of a wide variety of ecological scenarios [10, 11, 21]. These tools are based on the assumption of separation of ecological and evolutionary time scales and on the notion of invasion fitness [19, 20]. While the biological theory of adaptive dynamics is based on partly heuristic derivations, various aspects of the theory have been derived rigorously over the last years in the context of stochastic, individual-based models [6–9,

15, 16]. All of them concern the limit when the population size, K , tends to infinity. They either study the separation of ecological and evolutionary time scales based on a limit of rare mutations, $u \rightarrow 0$, combined with a limit of large population [6, 9], the limit of small mutation effects, $\sigma \rightarrow 0$ [7, 9, 15], the stationary behavior of the system [16] or the links between individual-based and infinite-population models [8]. An important concept in the theory of adaptive dynamics is the canonical equation of adaptive dynamics (CEAD), introduced by Dieckmann and Law [10]. This is an ODE that describes the evolution in time of the expected trait value in a monomorphic population. The heuristics leading to the CEAD are based on the biological assumptions of large population and rare mutations with small effects and the assumption that no two different traits can coexist. (Note that we write sometimes mutation steps instead of effects.) There are mathematically rigorous papers that show that the limit of large population combined with rare mutations leads to a jump process, the Trait Substitution Sequence, [6] and that this jump process converges, in the limit of small mutation steps, to the CEAD [9]. Since these two limits are applied separately and on different time scales, they give no clue about how the biological parameters (population size K , probability of mutations u and size of mutation steps σ) should compare to ensure that the CEAD approximation of the individual-based model is correct.

The purpose of the present paper is to analyse the situation when the limits of large population size, $K \rightarrow \infty$, rare mutations, $u_K \rightarrow 0$ and small mutation steps, $\sigma_K \rightarrow 0$, are taken *simultaneously*. We consider populations with monomorphic initial condition, meaning that at time zero the population consists only of individuals with the same trait. Then we identify a time-scale where evolution can be described as a succession of mutant invasions. To prove convergence to the CEAD, we show that, if a mutation occurs, then the individuals with this mutant trait can either die out or invade the resident population on this time scale. Here, invasion means that the mutant trait supersedes the resident trait, that is, the individuals with the resident trait become extinct after some time. This implies that the population stays essentially monomorphic with a trait that evolves in time. We will impose conditions on the mutation rates that imply a separation of ecological and evolutionary time scales, in the sense that an invading mutant population converges to its ecological equilibrium before a new invading (successful) mutant appears. In order to avoid too restrictive hypothesis on the mutation rates, we do, however, allow noninvading (unsuccessful) mutation events during this time, in contrast to all earlier works.

We will see that the combination of the three limits simultaneously, and entails some considerable technical difficulties. The fact that the mutants have only a K -dependent small evolutionary advantage decelerates the dynamics of the microscopic process such that the time of any macroscopic change between resident and mutant diverges with K . This makes it impossible to use a law of large numbers as in [6] to approximate the stochastic system with the corresponding deterministic

system during the time of invasion. Showing that the stochastic system still follows in an appropriate sense the corresponding competition Lotka–Volterra system (with K -dependent coefficients) requires a completely new approach. Developing this approach, which can be seen as a rigorous “stochastic Euler-scheme,” is the main novelty of the present paper. The proof requires methods, based on couplings with discrete time Markov chains combined with some standard potential theory arguments for the “exit from a domain problem” in a moderate deviations regime, as well as comparison and convergence results of branching processes. Note that since the result of [6] is already different from classical time scales separations results (cf. [14]), our result differs from them a fortiori. Thus, our result can be seen as a rigorous justification of the biologically motivated, heuristic assumptions which lead to CEAD.

The remainder of this paper is organized as follows. In Sections 2 and 3, we introduce the model and give an overview on previous related results. In Section 4, we state our results and give a detailed outline of the proof. Full details of the proof are presented in Sections 6, 7 and 8. In the Appendix, we state and prove several elementary facts that are used throughout the proof.

2. The individual-based model. In this section, we introduce the model we analyze. We consider a population of a single asexual species that is composed of a finite number of individuals, each of them characterized by a one-dimensional phenotypic trait. The microscopic model is an individual-based model with nonlinear density-dependence, which has already been studied in ecological or evolutionary contexts by many authors [6, 8, 9, 13].

The *trait space* \mathcal{X} is assumed to be a compact interval of \mathbb{R} . We introduce the following biological parameters:

- (i) $b(x) \in \mathbb{R}_+$ is the *rate of birth* of an individual with trait $x \in \mathcal{X}$.
- (ii) $d(x) \in \mathbb{R}_+$ is the *rate of natural death* of an individual with trait $x \in \mathcal{X}$.
- (iii) $K \in \mathbb{N}$ is a parameter which scales the population size.
- (iv) $c(x, y)K^{-1} \in \mathbb{R}_+$ is the *competition kernel* which models the competition pressure felt by an individual with trait $x \in \mathcal{X}$ from an individual with trait $y \in \mathcal{X}$.
- (v) $u_K m(x)$ with $u_K, m(x) \in [0, 1]$ is the *probability that a mutation occurs at birth* from an individual with trait $x \in \mathcal{X}$, where $u_K \in [0, 1]$ is a scaling parameter.
- (vi) $M(x, dh)$ is the *mutation law* of the mutational jump h . If the mutant is born from an individual with trait x , then the mutant trait is given by $x + \sigma_K h \in \mathcal{X}$, where $\sigma_K \in [0, 1]$ is a parameter scaling the size of mutation and h is a random variable with law $M(x, dh)$. We restrict for simplicity the setting to mutation measures with support included in \mathbb{Z} .

The three scaling parameters of the model are the *population size*, controlled by the scaling parameter K , the *mutation probability*, controlled by the scaling parameter u_K , the *mutation size*, controlled by the scaling parameter σ_K . The novelty of our approach is that we consider the case where all these parameters tend

to their limit jointly, more precisely that both u_K and σ_K are functions of K and tend to zero as K tends to infinity (subject to certain constraints).

At any time t , we consider a finite number, N_t , of individuals, each of them having a trait value $x_i(t) \in \mathcal{X}$. It is convenient to represent the population state at time t by the rescaled point measure, v_t^K , which depends on K , u_K and σ_K

$$(2.1) \quad v_t^K = \frac{1}{K} \sum_{i=1}^{N_t} \delta_{x_i(t)}.$$

Let $\langle \mu, f \rangle$ denote the integral of a measurable function f with respect to the measure μ . Then $\langle v_t^K, \mathbb{1} \rangle = N_t K^{-1}$ and for any $x \in \mathcal{X}$, the positive number $\langle v_t^K, \mathbb{1}_{\{x\}} \rangle$ is called the *density of trait x at time t* . With this notation, an individual with trait x in the population v_t^K dies due to age or competition with rate

$$(2.2) \quad d(x) + \int_{\mathcal{X}} c(x, y) v_t^K(dy).$$

Let $\mathcal{M}(\mathcal{X})$ denote the set of finite nonnegative measures on \mathcal{X} , equipped with the weak topology, and define

$$(2.3) \quad \mathcal{M}^K(\mathcal{X}) \equiv \left\{ \frac{1}{K} \sum_{i=1}^n \delta_{x_i} : n \geq 0, x_1, \dots, x_n \in \mathcal{X} \right\}.$$

Similar as in [13], we obtain that the population process, $(v_t^K)_{t \geq 0}$, is a $\mathcal{M}^K(\mathcal{X})$ -valued Markov process with infinitesimal generator, \mathcal{L}^K , defined for any bounded measurable function f from $\mathcal{M}^K(\mathcal{X})$ to \mathbb{R} and for all $\mu^K \in \mathcal{M}^K(\mathcal{X})$ by

$$(2.4) \quad \begin{aligned} &\mathcal{L}^K f(\mu^K) \\ &= \int_{\mathcal{X}} \left(f\left(\mu^K + \frac{\delta_x}{K}\right) - f(\mu^K) \right) (1 - u_K m(x)) b(x) K \mu^K(dx) \\ &\quad + \int_{\mathcal{X}} \int_{\mathbb{Z}} \left(f\left(\mu^K + \frac{\delta_{x+\sigma_K h}}{K}\right) - f(\mu^K) \right) u_K m(x) b(x) M(x, dh) K \mu^K(dx) \\ &\quad + \int_{\mathcal{X}} \left(f\left(\mu^K - \frac{\delta_x}{K}\right) - f(\mu^K) \right) \left(d(x) + \int_{\mathcal{X}} c(x, y) \mu^K(dy) \right) K \mu^K(dx). \end{aligned}$$

The first and second terms are linear (in μ^K) and describe the births (without and with mutation), but the third term is nonlinear and describes the deaths due to age or competition. The density-dependent nonlinearity of the third term models the competition in the population, and hence drives the selection process.

ASSUMPTION 1. We will use the following assumptions on the parameters of the model:

- (i) b, d and c are measurable functions, and there exist $\bar{b}, \bar{d}, \bar{c} < \infty$ such that

$$b(\cdot) \leq \bar{b}, \quad d(\cdot) \leq \bar{d} \quad \text{and} \quad c(\cdot, \cdot) \leq \bar{c}.$$

- (ii) For all $x \in \mathcal{X}$, $b(x) - d(x) > 0$, and there exists $\underline{c} > 0$ such that $\underline{c} \leq c(x, x)$.
- (iii) The support of $M(x, \cdot)$ is a subset of $\mathbb{Z} \cap \mathcal{X} - x$ and uniformly bounded for all $x \in \mathcal{X}$. This means that there exists $A \in \mathbb{N}$ such that

$$M(x, dh) = \sum_{k=-A}^A p_k(x) \delta_k(dh), \quad \text{where } \sum_{k=-A}^A p_k(x) = 1 \text{ for any } x \in \mathcal{X}.$$

- (iv) $b, d, m \in C^2(\mathcal{X}, \mathbb{R})$ and $c \in C^2(\mathcal{X}^2, \mathbb{R})$.

Assumptions (i) and (iii) allow to deduce the existence and uniqueness in law of a process on $\mathbb{D}(\mathbb{R}_+, \mathcal{M}^K(\mathcal{X}))$ with infinitesimal generator \mathcal{L}^K (cf. [13]). Note that assumption (iii) differs from the assumptions in [13] because we restrict the setting to mutation measures with support included in \mathbb{Z} and that it ensures that a mutant trait remains in \mathcal{X} . Assumption (ii) prevents the population from exploding or becoming extinct too fast. Since \mathcal{X} is compact, assumption (iv) ensures that the derivatives of the functions b, c, d and m are uniformly Lipschitz-continuous.

Before we state the main result of the paper, Theorem 4.1, in Section 4, it will be helpful to recall some earlier results for this class of models and to fix some more notation. These results serve as a guideline to what behavior one should expect, even though on a technical level proofs have to be changed completely.

3. Some notation and previous results. We start with a theorem due to N. Fournier and S. Méléard [13] which describes the behavior of the population process, for fixed u and σ , when $K \rightarrow \infty$.

THEOREM 3.1 (Theorem 5.3 in [13]). *Fix u and σ . Let Assumption 1 hold and assume in addition that the initial conditions v_0^K converge for $K \rightarrow \infty$ in law and for the weak topology on $\mathcal{M}(\mathcal{X})$ to some deterministic finite measure $\xi_0 \in \mathcal{M}(\mathcal{X})$ and that $\sup_K \mathbb{E}[\langle v_0^K, \mathbb{1} \rangle^3] < \infty$.*

Then for all $T > 0$, the sequence v^K , generated by \mathcal{L}^K , converges for $K \rightarrow \infty$ in law, in $\mathbb{D}([0, T], \mathcal{M}(\mathcal{X}))$, to a deterministic continuous function $\xi \in C([0, T], \mathcal{M}(\mathcal{X}))$. This measure-valued function ξ is the unique solution, satisfying $\sup_{t \in [0, T]} \langle \xi_t, \mathbb{1} \rangle < \infty$, of the integro-differential equation written in its weak form: for all bounded and measurable functions, $f : \mathcal{X} \rightarrow \mathbb{R}$,

$$\begin{aligned}
 & \int_{\mathcal{X}} \xi_t(dx) f(x) \\
 (3.1) \quad &= \int_{\mathcal{X}} \xi_0(dx) f(x) \\
 &+ \int_0^t ds \int_{\mathcal{X}} \xi_s(dx) um(x)b(x) \int_{\mathbb{Z}} M(x, dh) f(x + \sigma h) \\
 &+ \int_0^t ds \int_{\mathcal{X}} \xi_s(dx) f(x) \left((1 - um(x))b(x) - d(x) - \int_{\mathcal{X}} \xi_s(dy)c(x, y) \right).
 \end{aligned}$$

Without mutation, one obtains convergence to the competitive system of Lotka–Volterra equations defined below (see [13]).

COROLLARY 3.2 (The special case $u = 0$ and ξ_0 is n -morphic). *If the same assumptions as in the theorem above with $u = 0$ hold and if in addition $\xi_0 = \sum_{i=1}^n z_i(0)\delta_{x_i}$, then ξ_t is given by $\xi_t = \sum_{i=1}^n z_i(t)\delta_{x_i}$, where z_i is the solution of the competitive system of Lotka–Volterra equations defined below.*

DEFINITION 3.3. For any $(x_1, \dots, x_n) \in \mathcal{X}^n$, we denote by $\text{LV}(n, (x_1, \dots, x_n))$ the competitive system of Lotka–Volterra equations defined by

$$(3.2) \quad \frac{dz_i(t)}{dt} = z_i \left(b(x_i) - d(x_i) - \sum_{j=1}^n c(x_i, x_j) z_j \right), \quad 1 \leq i \leq n.$$

Next, we introduce the notation of coexisting traits and of invasion fitness (see [9]).

DEFINITION 3.4. We say that the distinct traits x and y coexist if the system $\text{LV}(2, (x, y))$ admits a unique nontrivial equilibrium, named $\bar{z}(x, y) \in (0, \infty)^2$, which is locally strictly stable in the sense that the eigenvalues of the Jacobian matrix of the system $\text{LV}(2, (x, y))$ at $\bar{z}(x, y)$ are all strictly negative.

The invasion of a single mutant trait in a monomorphic population which is close to its equilibrium is governed by its initial growth rate. Therefore, it is convenient to define the fitness of a mutant trait by its initial growth rate.

DEFINITION 3.5. If the resident population has the trait $x \in \mathcal{X}$, then we call the following function *invasion fitness* of the mutant trait y

$$(3.3) \quad f(y, x) = b(y) - d(y) - c(y, x)\bar{z}(x).$$

REMARK 1. The unique strictly stable equilibrium of $\text{LV}(1, x)$ is $\bar{z}(x) = \frac{b(x)-d(x)}{c(x,x)}$, and hence $f(x, x) = 0$ for all $x \in \mathcal{X}$.

Coexistence and invasion fitness are closely related (cf. [17]).

PROPOSITION 3.6. *There is coexistence in the system $\text{LV}(2, (x, y))$ if and only if $f(x, y) \equiv b(x) - d(x) - c(x, y)\bar{z}(y) > 0$ and $f(y, x) \equiv b(y) - d(y) - c(y, x)\bar{z}(x) > 0$.*

The following convergence result from [6] describes the limit behavior of the populations process, for fixed σ , when $K \rightarrow \infty$ and $u_K \rightarrow 0$. More precisely, it says that the rescaled individual-based process converges in the sense of finite dimensional distributions to the “trait substitution sequence” (TSS), if one assumes in addition to Assumption 1 the following “Invasion implies fixation” condition.

ASSUMPTION 2. Given any $x \in \mathcal{X}$, Lebesgue almost any $y \in \mathcal{X}$ satisfies one of the following conditions:

- (i) $f(y, x) < 0$ or (ii) $f(y, x) > 0$ and $f(x, y) < 0$.

Note that by Proposition 3.6, this means that either a mutant cannot invade, or it cannot coexist with the resident.

THEOREM 3.7 (Corollary 1 in [6]). *Let Assumption 1 and 2 hold. Fix σ and assume that*

$$(3.4) \quad \forall V > 0, \quad \exp(-VK) \ll u_K \ll \frac{1}{K \ln(K)}, \quad \text{as } K \rightarrow \infty.$$

Fix also $x \in \mathcal{X}$ and let $(N_0^K)_{K \geq 1}$ be a sequence of \mathbb{N} -valued random variables such that (N_0^K/K) converges for $K \rightarrow \infty$ in law to $\bar{z}(x)$ and is bounded in \mathbb{L}^p for some $p > 1$. Consider the processes v^K generated by \mathcal{L}^K with monomorphic initial state $(N_0^K/K)\delta_{\{x\}}$.

Then the sequence of the rescaled processes v_{t/Ku_K}^K converges in the sense of finite dimensional distributions to the measure-valued process

$$(3.5) \quad \bar{z}(X_t)\delta_{X_t},$$

where the \mathcal{X} -valued Markov jump process X has initial state $X_0 = x$ and infinitesimal generator

$$(3.6) \quad \begin{aligned} A\phi(x) &= \int_{\mathbb{Z}} (\phi(x + \sigma h) - \phi(x))m(x)b(x)\bar{z}(x) \\ &\times \frac{[f(x + \sigma h, x)]_+}{b(x + \sigma h)}M(x, dh). \end{aligned}$$

Here, we write $f(K) \ll g(K)$ if $f(K)/g(K) \rightarrow 0$ when $K \rightarrow \infty$. Note that, for any $s < t$, the convergence does not hold in law for the Skorokhod topology on $\mathbb{D}([s, t], \mathcal{M}(\mathcal{X}))$, for any topology $\mathcal{M}(\mathcal{X})$ such that the total mass function $\nu \mapsto \langle \nu, \mathbb{1} \rangle$ is continuous, because the total mass of the limit process is a discontinuous function. The main part of the proof of this theorem is the study of the invasion of a mutant trait y that has just appeared in a monomorphic population with trait x . The invasion can be divided into three steps. First, as long as the mutant population size $\langle v_t^K, \mathbb{1}_{\{y\}} \rangle$ is smaller than some $\varepsilon > 0$ (independent of K), the resident population size $\langle v_t^K, \mathbb{1}_{\{x\}} \rangle$ stays close to $\bar{z}(x)$. Therefore, $\langle v_t^K, \mathbb{1}_{\{y\}} \rangle$ can be approximated by a branching process with birth rate $b(y)$ and death rate $d(y) + c(y, x)\bar{z}(x)$ until it goes extinct or reaches ε . Second, once $\langle v_t^K, \mathbb{1}_{\{y\}} \rangle$ has reached ε , for large K , v_t^K is close to the solution of LV(2, (x, y)) with initial state $(\bar{z}(x), \varepsilon)$, which reaches the ε -neighborhood of $(0, \bar{z}(y))$ in finite time. This is a consequence of Corollary 3.2. Finally, once $\langle v_t^K, \mathbb{1}_{\{y\}} \rangle$ is close to $\bar{z}(y)$ and $\langle v_t^K, \mathbb{1}_{\{x\}} \rangle$ is small, $\langle v_t^K, \mathbb{1}_{\{x\}} \rangle$ can be approximated by a subcritical process, which becomes extinct a.s. The time of

the first and third step are proportional to $\ln(K)$, whereas the time of the second step is bounded. Thus, the second inequality in (3.4) guarantees that, with high probability, the three steps of invasion are completed before a new mutation occurs.

Without Assumption 2, it is possible to construct the “polymorphic evolution sequence” (PES) under additional assumptions on the n -morphic logistic system. This is done in [9]. Finally, in [9], the convergence of the TSS with small mutation steps scaled by σ to the “canonical equation of adaptive dynamics” (CEAD) is proved. We indicate the dependence of the TSS of the previous Theorem on σ with the notation $(X_t^\sigma)_{t \geq 0}$.

THEOREM 3.8 (Remark 4.2 in [9]). *If Assumption 1 is satisfied and the family of initial states of the rescaled TSS, X_0^σ , is bounded in \mathbb{L}^2 and converges to a random variable X_0 , as $\sigma \rightarrow 0$, then, for each $T > 0$, the rescaled TSS X_{t/σ^2}^σ converges, as $\sigma \rightarrow 0$, in the Skorokhod topology on $\mathbb{D}([0, T], \mathcal{X})$ to the process $(x_t)_{t \leq T}$ with initial state X_0 and with deterministic sample path, which is the unique solution of an ordinary differential equation, known as CEAD:*

$$(3.7) \quad \frac{dx_t}{dt} = \int_{\mathbb{Z}} h[hm(x_t)\bar{z}(x_t)\partial_1 f(x_t, x_t)]_+ M(x_t, dh),$$

where $\partial_1 f$ denotes the partial derivative of the function $f(x, y)$ with respect to the first variable x .

REMARK 2. If $M(x, \cdot)$ is a symmetric measure on \mathbb{Z} for all $x \in \mathcal{X}$, then the equation (3.7) has the classical form; cf. [10],

$$(3.8) \quad \frac{dx_t}{dt} = \frac{1}{2} \int_{\mathbb{Z}} h^2 m(x_t)\bar{z}(x_t)\partial_1 f(x_t, x_t) M(x_t, dh),$$

Note that this result does not imply that, applying to the individual-based model first the limits $(K, u_K) \rightarrow (\infty, 0)$ and afterwards the limit $\sigma \rightarrow 0$ yields its convergence to the CEAD. One problem of these two successive limits is, for example, that the first convergence holds on a finite time interval, the second requires to look at the Trait Substitution Sequence on a time interval which diverges. Moreover, as already mentioned these two limits give no clue about how K , u and σ should be compared to ensure that the CEAD approximation is correct.

4. The main result. In this section, we present the main result of this paper, namely the convergence to the canonical equation of adaptive dynamics in one step. The time scale on which we control the population process is $t/(\sigma_K^2 u_K K)$ and corresponds to the combination of the two time scales of Theorems 3.7 and 3.8. Since we combine the limits we have to modify the assumptions to obtain the convergence. We use in this section the notation and definitions introduced in Section 3.

ASSUMPTION 3. For all $x \in \mathcal{X}$, $\partial_1 f(x, x) \neq 0$.

Assumption 3 implies that either $\forall x \in \mathcal{X}: \partial_1 f(x, x) > 0$ or $\forall x \in \mathcal{X}: \partial_1 f(x, x) < 0$. Therefore, coexistence of two traits is not possible. Without loss of generality, we can assume that, $\forall x \in \mathcal{X}$, $\partial_1 f(x, x) > 0$. In fact, a weaker assumption is sufficient, see Remark 3(iii).

THEOREM 4.1. Assume that Assumptions 1 and 3 hold and that there exists a small $\alpha > 0$ such that

$$(4.1) \quad K^{-\frac{1}{2}+\alpha} \ll \sigma_K \ll 1 \quad \text{and}$$

$$(4.2) \quad \exp(-K^\alpha) \ll u_K \ll \frac{\sigma_K^{1+\alpha}}{K \ln K}, \quad \text{as } K \rightarrow \infty.$$

Fix $x_0 \in \mathcal{X}$ and let $(N_0^K)_{K \geq 0}$ be a sequence of \mathbb{N} -valued random variables such that $N_0^K K^{-1}$ converges in law, as $K \rightarrow \infty$, to the positive constant $\bar{z}(x_0)$ and is bounded in \mathbb{L}^p , for some $p > 1$.

For each $K \geq 0$, let v_t^K be the process generated by \mathcal{L}^K with monomorphic initial state $N_0^K K^{-1} \delta_{\{x_0\}}$. Then, for all $T > 0$, the sequence of rescaled processes, $(v_{t/(Ku_K \sigma_K^2)}^K)_{0 \leq t \leq T}$, converges in probability, as $K \rightarrow \infty$, with respect to the Skorokhod topology on $\mathbb{D}([0, T], \mathcal{M}(\mathcal{X}))$ to the measure-valued process $\bar{z}(x_t) \delta_{x_t}$, where $(x_t)_{0 \leq t \leq T}$ is given as a solution of the CEAD,

$$(4.3) \quad \frac{dx_t}{dt} = \int_{\mathbb{Z}} h[hm(x_t) \bar{z}(x_t) \partial_1 f(x_t, x_t)]_+ M(x_t, dh),$$

with initial condition x_0 .

REMARK 3. (i) If $x_t \in \partial \mathcal{X}$ for $t > 0$, then (4.3) is $\frac{dx_t}{dt} = 0$, that is, the process stops.

(ii) We can prove convergence in a stronger topology. Namely, let us equip $\mathcal{M}_S(\mathcal{X})$, the vector space of signed finite Borel-measures on \mathcal{X} , with the following Kantorovich–Rubinstein norm:

$$(4.4) \quad \|\mu_t\|_0 \equiv \sup \left\{ \int_{\mathcal{X}} f d\mu_t : f \in \text{Lip}_1(\mathcal{X}) \text{ with } \sup_{x \in \mathcal{X}} |f(x)| \leq 1 \right\},$$

where $\text{Lip}_1(\mathcal{X})$ is the space of Lipschitz continuous functions from \mathcal{X} to \mathbb{R} with Lipschitz norm one (cf. [4] page 191). Then, for all $\delta > 0$, we will prove that

$$(4.5) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\sup_{0 \leq t \leq T} \|v_{t/(Ku_K \sigma_K^2)}^K - \bar{z}(x_t) \delta_{x_t}\|_0 > \delta \right] = 0.$$

By Proposition A.1, this implies convergence in probability with respect to the Skorokhod topology.

(iii) The main result of the paper actually holds under weaker assumptions. More precisely, Assumption 3 can be replaced by the following.

ASSUMPTION 3'. The initial state v_0^K has a.s. (deterministic) support $\{x_0\}$ with $x_0 \in \mathcal{X}$ satisfying $\partial_1 f(x_0, x_0) \neq 0$.

The reason is that, and since $x \mapsto \partial_1 f(x, x)$ is continuous, the Assumption 3(a) is satisfied locally and since $x \mapsto \partial_1 f(x, x)$ is Lipschitz-continuous, the CEAD never reaches an evolutionary singularity (i.e., a value $y \in \mathcal{X}$ such that $\partial_1 f(y, y) = 0$) in finite time. In particular, for a fixed $T > 0$, the CEAD only visits traits in some interval I of \mathcal{X} where $\partial_1 f(x, x) \neq 0$. By modifying the parameters of the model out of I in such a way that $\partial_1 f(x, x) \neq 0$ everywhere in \mathcal{X} , we can apply Theorem 4.1 to this modified process \tilde{v} and deduce that $\tilde{v}_{t/Ku_K\sigma_K^2}$ has support included in I for $t \in [0, T]$ with high probability, and hence coincides $v_{t/Ku_K\sigma_K^2}$ on this time interval.

(iv) The condition $u_K \ll \frac{\sigma_K^{1+\alpha}}{K \ln K}$ allows mutation events during an invasion phase of a mutant trait (see below), but ensures that there is no “successful” mutational event during this phase.

(v) The fluctuations of the resident population are of order $K^{-\frac{1}{2}}$, thus $K^{-\frac{1}{2}+\alpha} \ll \sigma_K$ ensures that the sign of the initial growth rate is not influenced by the fluctuations of the population size. We will see later that, if a mutant trait y appears in a monomorphic population with trait x , then its initial growth rate is $b(y) - d(y) - c(y, x)\langle v_t^K, \mathbb{1} \rangle = f(y, x) + o(\sigma_K) = (y - x)\partial_1 f(x, x) + o(\sigma_K)$ since $y - x = O(\sigma_K)$.

(vi) $\exp(K^\alpha)$ is the time the resident population stays with high probability in an $O(\varepsilon\sigma_K)$ -neighborhood of an attractive domain. This is a moderate deviation result. Thus, the condition $\exp(-K^\alpha) \ll u_K$ ensures that the resident population is still in this neighborhood when a mutant occurs.

(vii) The time scale is $(Ku_K\sigma_K^2)^{-1}$ since the expected time for a mutation event is $(Ku_K)^{-1}$, the probability that a mutant invades is of order σ_K and one needs $O(\sigma_K^{-1})$ mutant invasions to see an $O(1)$ change of the resident trait value. This is consistent with the combination of Theorems 3.7 and 3.8.

(viii) Note that the ε that we use in the proof of the theorem and in the main idea below will not depend on K , but it will converge to zero in the end of the proof of Theorem 4.1. The constant M introduced below will be fixed all the time. It depends only the parameters of the model, but not on K and ε .

(ix) The conditions on the initial states $N_0^K K^{-1}$ imply that $\mathbb{E}[\langle v_t^K, \mathbb{1} \rangle^p] < \infty$, uniformly in K and t and, therefore, since $p > 1$, the family of random variables $\{\langle v_t^K, \mathbb{1} \rangle\}_{K \geq 1, t \geq 0}$ is uniformly integrable (cf. [6] Lemma 1).

4.1. *The main idea and the structure of the proof of Theorem 4.1.* Under the conditions of the theorem, the evolution of the population will be described as a succession of *mutant invasions*.

We first control a single *invasion step*. Namely, we show that there is a time-scale that is long enough for exactly one mutant population to fixate and for the

resident trait to die out, but sufficiently short, such that no two successful mutant populations can exist during this time. We say the mutant trait fixates in the population. Note that this does not prevent the appearance of other mutant traits that do not invade.

Second, we consider a much longer time scale on which the single invasion steps aggregate and give rise to a *macroscopic evolution* that converges to the CEAD.

Study of a single invasion step. In order to analyze the invasion of a mutant, we divide the time until a mutant trait has fixated in the population into two phases (compare with Figure 1).

Phase 1 (Section 6). Here, we fix a small $\varepsilon > 0$ and prove the existence of a constant, $M < \infty$, independent of ε , such that, as long as all mutant densities are smaller than $\varepsilon\sigma_K$, the resident density stays in an $M\varepsilon\sigma_K$ -neighborhood of $\bar{z}(x)$. Note that, because mutations are rare and the population size is large, the monomorphic initial population has time to stabilize in an $M\varepsilon\sigma_K$ -neighborhood of this equilibrium $\bar{z}(x)$ before the first mutation occurs. [The time of stabilization is of order $\ln(K)\sigma_K^{-1}$ and the time where the first mutant occurs is of order $1/Ku_K$].

This allows us to approximate the density of one mutant trait y_1 by a branching process with birth rate $b(y_1)$ and death rate $d(y_1) - c(y_1, x)\bar{z}(x)$ such that we can compute the probability that the density of the mutant trait y_1 reaches $\varepsilon\sigma_K$, which is of order σ_K , as well as the time it takes to reach this level or to die out. Therefore, the process needs $O(\sigma_K^{-1})$ mutation events until there appears a mutant subpopulation which reaches a size $\varepsilon\sigma_K$. Such a mutant is called *successful mutant* and its trait will be the next resident trait. (In fact, we can calculate the distribution of the successful mutant trait only on an event with probability $1 - \varepsilon$, but we

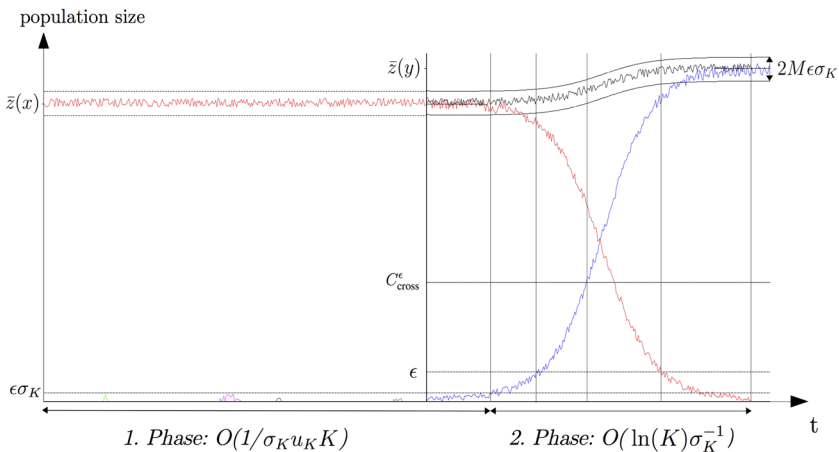


FIG. 1. Typical evolution of the population during a mutant invasion.

show that on an event of probability $1 - o(\sigma_K)$, this distribution has support in $\{x + \sigma_K h : 1 \leq h \leq A\}$. Therefore, the exact value of the mutant trait is unknown with probability ε , but the difference of the possible values is only of order σ_K .

We prove in this step also that there are never too many different mutants alive at the same time. From all this, we deduce that the subpopulation of the successful mutant reaches the density $\varepsilon\sigma_K$, before a different successful mutant appears. Note that we cannot use large deviation results on our time scale as used in [9] to prove this step. Instead, we use some standard potential theory and coupling arguments to obtain estimates of moderate deviations needed to prove that a successful mutant will appear before the resident density exists an $M\varepsilon\sigma_K$ -neighborhood of its equilibrium.

Phase 2 (Section 7). We prove that if a mutant population with trait y_s reaches the size $\varepsilon\sigma_K$, it will increase to an $M\varepsilon\sigma_K$ -neighborhood of its equilibrium density $\bar{z}(y_s)$. Simultaneously, the density of the resident trait decreases to $\varepsilon\sigma_K$ and finally dies out. Since the fitness advantage of the mutant trait is only of order σ_K , the dynamics of the population process and the corresponding deterministic system are very slow. Even if we would start at a macroscopic density ε , the deterministic system needs a time of order σ_K^{-1} to reach an ε -neighborhood of its equilibrium density.

The law of large numbers (see Theorem 3.1 or Chapter 11 of [12]) allows to control the distance between the stochastic process and its deterministic limit only on finite, K -independent time intervals. In the regime considered in [6] and [9], namely $\sigma > 0$ independent of K , this suffices to control the stochastic process during this transition phase, since the mutant population of trait y_s only needs a finite, K -independent time, to grow from size ε to the ε -neighborhood of $\bar{z}(y_s)$. In the regime we consider here, this is no longer possible and a new technique is needed. The method we develop to handle this situation can be seen as a rigorous stochastic “Euler-Scheme” and will be explained in detail in Section 7. Nevertheless, the proof contains an idea which is strongly connected with the properties of the deterministic dynamical system. Namely, the deterministic system of equations for the case $\sigma_K = 0$ has an invariant manifold of fixed points with a vector field independent of σ_K pointing toward this manifold. Turning on a small σ_K , we therefore expect the stochastic system to stay close to this invariant manifold and to move along it with speed of order σ_K .

With this method, we are able to prove that, in fact, the mutant density reaches the $M\varepsilon\sigma_K$ -neighborhood of $\bar{z}(y_s)$ and the resident trait dies out. Note that it is possible that an unsuccessful mutant is alive at this time. Therefore, we prove that after the resident trait has died out, there is a time when the population consists only of one trait, namely the one that had fixed, before the next successful mutant occurs.

Note that Figure 1 is only an artist’s sketch and not a “real” simulation.

Convergence to the CEAD (Section 8). The proof of convergence to the CEAD uses comparison of the measure valued process ν_t^K with two families of control processes, $\mu^{1,K,\varepsilon}$ and $\mu^{2,K,\varepsilon}$, which will converge to the CEAD as $K \rightarrow \infty$ and then $\varepsilon \rightarrow 0$. To make more precise statements, we need the following order relation \preceq for random variables. Roughly speaking, $X \preceq Y$ will mean that Y is larger than X in law.

NOTATION. (a) Let X and Y be real-valued random variables on a probability space $(\Omega, \mathcal{F}, \mathbb{P})$. We write $X \preceq Y$, if there is a random variable, \tilde{Y} on Ω , such that Y and \tilde{Y} have the same distribution, and that for all $\omega \in \Omega$, $X(\omega) \leq \tilde{Y}(\omega)$.

(b) For $\mu, \nu \in \mathcal{M}(\mathcal{X})$, we write $\nu \preceq \mu$, if:

- (i) $\langle \nu, \mathbb{1} \rangle \leq \langle \mu, \mathbb{1} \rangle$ and
- (ii) $\sup\{x \in \mathcal{X} : x \in \text{Supp}(\nu)\} \leq \inf\{x \in \mathcal{X} : x \in \text{Supp}(\mu)\}$.

Note that (i) and (ii) imply that, for all monotone increasing functions $f \in \text{Lip}_1(\mathcal{X}, [-1, 1])$ and for all $0 \leq t \leq T$,

$$(4.6) \quad \int_{\mathcal{X}} f(x) d\nu_t \leq \int_{\mathcal{X}} f(x) d\mu_t.$$

This notion of order between measures is not very informative, except for measures which are close to Dirac masses, where it means that the masses and the supports of the measures are ordered. This is in particular the case for the measures $\mu^{1,K,\varepsilon}$ and $\mu^{2,K,\varepsilon}$ defined below.

Given $T > 0$, with the results of the two invasion phases, we will define for all $\varepsilon > 0$ two measure-valued processes, in $\mathbb{D}([0, \infty), \mathcal{M}(\mathcal{X}))$, such that, for all $\varepsilon > 0$,

$$(4.7) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\forall t \leq \frac{T}{Ku_K \sigma_K^2} : \mu_t^{1,K,\varepsilon} \preceq \nu_t^K \preceq \mu_t^{2,K,\varepsilon} \right] = 1,$$

and, for all $\varepsilon > 0$ and $i \in \{1, 2\}$,

$$(4.8) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\sup_{0 \leq t \leq T/(Ku_K \sigma_K^2)} \left\| \mu_{t/(Ku_K \sigma_K^2)}^{i,K,\varepsilon} - \bar{z}(x_t) \delta_{x_t} \right\|_0 > \delta(\varepsilon) \right] = 0,$$

for some function δ such that $\delta(\varepsilon) \rightarrow 0$ when $\varepsilon \rightarrow 0$. This implies (4.5) and therefore the theorem.

The control processes, $\mu^{1,K,\varepsilon}$ and $\mu^{2,K,\varepsilon}$, are constructed as follows. Let θ_i^K be the random time of the i th invasion phase, that is, the first time after θ_{i-1}^K such that a mutant density is larger than $\varepsilon \sigma_K$, and let R_i^K be the trait of the i th successful mutant. Knowing the random variables θ_{i-1}^K and R_{i-1}^K , we are able to approximate θ_i^K and R_i^K : After the $(i - 1)$ th invasion phase (of the process ν^K), we define two

random times, $\theta_i^{K,1}$ and $\theta_i^{K,2}$, and two random variables $R_i^{K,1}$ and $R_i^{K,2}$ in \mathcal{X} , such that

$$\lim_{K \rightarrow \infty} \mathbb{P} \left[\forall i \leq \sup \left\{ j \in \mathbb{N} : \theta_j^K \leq \frac{T}{Ku_K \sigma_K^2} \right\} : R_i^{K,1} \preceq R_i^K \preceq R_i^{K,2} \text{ and } \theta_i^{K,2} \preceq \theta_i^K \preceq \theta_i^{K,1} \right] = 1.$$

Thus, we define $\mu^{1,K}$ and $\mu^{2,K}$ through

$$(4.9) \quad \mu_t^{1,K} \equiv z_t^1 \delta_{R_t^{K,1}}, \quad \text{for } t \in [\theta_i^{K,1}, \theta_{i+1}^{K,1}),$$

$$(4.10) \quad \mu_t^{2,K} \equiv z_t^2 \delta_{R_t^{K,2}}, \quad \text{for } t \in [\theta_i^{K,2}, \theta_{i+1}^{K,2}).$$

for some appropriate masses z_i^1 and z_i^2 . In fact, z_i^1 will be approximately $\bar{z}(R_i^{K,1})$ for $t \in [\theta_i^{K,1}, \theta_{i+1}^{K,1})$, and z_i^2 approximately $\bar{z}(R_i^{K,2})$ for $t \in [\theta_i^{K,2}, \theta_{i+1}^{K,2})$. We will prove that the times $\theta_i^{K,1}$ and $\theta_i^{K,2}$ are (approximately) exponentially distributed with parameters of order $Ku_K \sigma_K$, and that the difference of $R_i^K - R_{i-1}^K$ is of order σ_K . The processes $\mu^{1,K,\varepsilon}$ and $\mu^{2,K,\varepsilon}$ will be constructed by slightly modifying the two processes $\mu^{1,K}$ and $\mu^{2,K}$ in order to make them Markovian. This will imply by standard arguments from [12] that the processes $\mu_{t/Ku_K \sigma_K^2}^{1,K}$ and $\mu_{t/Ku_K \sigma_K^2}^{2,K}$ converge to $\bar{z}(x_t) \delta_{x_t}$ when $\sigma_K \rightarrow 0$, where x_t is the solution of the canonical equation of adaptive dynamics.

We have now prepared the setting to be able to perform the steps of the proof of Theorem 4.1 as indicated in the outline given in Section 4.1 in Sections 6, 7 and 8. Before this, we need a some more notation and preparatory results that we collect in Section 5. Four technical propositions are delegated to an [Appendix](#).

All the remaining sections are devoted to the proof of the Theorem 4.1.

5. An augmented process and some elementary properties. In the proof of Theorem 4.1, we need to construct an augmented process (\tilde{v}^K, L^K) that keeps track of part of the history of the population, namely L_t^K is the number of mutations that occurred before t . We first describe this process, then define it by a stochastic equation from which one finds that it is a Markov process with an explicitly given generator.

Let $\mathcal{M}_F^K(\mathbb{N}_0 \times \mathcal{X}) \equiv \{ \frac{1}{K} \sum_{i=1}^n \delta_{\xi(i)} : n \geq 0, \xi(1), \dots, \xi(n) \in \mathbb{N}_0 \times \mathcal{X} \}$ denote the set of finite nonnegative point measures on $\mathbb{N}_0 \times \mathcal{X}$ rescaled by K . We write $\xi(i) = (\xi_1(i), \xi_2(i))$, where $\xi_1(i) \in \mathbb{N}_0$ and $\xi_2(i) \in \mathcal{X}$. The augmented process, (\tilde{v}^K, L^K) , is a continuous time stochastic process with state space $\mathcal{M}_F^K(\mathbb{N}_0 \times \mathcal{X}) \times \mathbb{N}_0$. The label k of an individual with trait (k, x) denotes that there were $k - 1$ mutational events in the population before the trait (k, x) appeared for the first time in the population. As in [13], we give a path-wise description of (\tilde{v}^K, L^K) .

NOTATION. Let $\mu^K = \frac{1}{K} \sum_{i=1}^n \delta_{\xi(i)} \in \mathcal{M}_F^K(\mathbb{N}_0 \times \mathcal{X})$ and

$$(5.1) \quad \mathfrak{M}^k(\mu^K) \equiv K \int_{\mathbb{N}_0 \times \mathcal{X}} \mathbb{1}_{\{\xi_1=k\}} \mu^K(d\xi)$$

be the number of individuals holding a mutation of label k . Then we rewrite μ^K as follows:

$$(5.2) \quad \mu^K = \frac{1}{K} \sum_{k=1}^{\infty} \sum_{j=1}^{\mathfrak{M}^k(\mu^K)} \delta_{(k, x_j^k)}, \quad \text{where } \sum_{k=1}^{\infty} \mathfrak{M}^k(\mu^K) = n.$$

In fact, the $x_1^k, \dots, x_{\mathfrak{M}^k(\mu^K)}^k$ will be equal in our situation, because the only variation in the trait value is driven by mutational events. We need to define three functions. First, $H : \mathcal{M}_F^K(\mathbb{N}_0 \times \mathcal{X}) \mapsto (\mathbb{N}_0 \times \mathcal{X})^{\mathbb{N}_0^2}$ is defined as

$$(5.3) \quad H(\mu^K) \equiv \begin{pmatrix} (0, x_1^0) & (0, x_2^0) & \cdots & (0, x_{\mathfrak{M}^0(\mu)}^0) & (0, 0) & (0, 0) & \cdots \\ (1, x_1^1) & (1, x_2^1) & \cdots & \cdots & (1, x_{\mathfrak{M}^1(\mu)}^1) & (1, 0) & \cdots \\ (2, x_1^2) & (2, x_2^2) & \cdots & (2, x_{\mathfrak{M}^2(\mu)}^2) & (2, 0) & (2, 0) & \cdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \cdots & \ddots \end{pmatrix}.$$

Second, $h : \mathcal{M}_F^K(\mathbb{N} \times \mathcal{X}) \mapsto (\mathcal{X})^{\mathbb{N}_0^2}$ us given in terms of H by

$$(5.4) \quad h_{ij}(\mu^K) \equiv \text{the second component of } H_{ij}(\mu^K),$$

that is, if $H_{ij}(\mu^K) = (i, x)$, then $h_{ij} = x$. Third, $\tilde{H} : \mathcal{M}_F^K(\mathbb{N} \times \mathcal{X}) \mapsto \mathcal{X}^{\mathbb{N}_0}$ is defined as follows: if $\mu = \frac{1}{K} \sum_{i=1}^n \delta_{\xi(i)}$, then

$$(5.5) \quad \tilde{H}(\mu) \equiv (\xi_2(\sigma(1)), \xi_2(\sigma(2)), \dots, \xi_2(\sigma(n)), 0, \dots),$$

where $\xi_2(\sigma(1)) \leq \dots \leq \xi_2(\sigma(n))$.

DEFINITION 5.1. Let $(\Omega, \mathcal{F}, \mathbb{P})$ be an abstract probability space. On this space, we define the following independent random elements:

- (i) an \mathcal{X} -valued random variable X_0 (the random initial trait),
- (ii) a sequence of independent Poisson point measures, $(N_k^{\text{death}}(ds, di, d\theta))_{k \geq 0}$, on $\mathbb{R}_+ \times \mathbb{N} \times \mathbb{R}_+$ with intensity measure $ds \sum_{n \geq 0} \delta_n(di) dz$,
- (iii) a sequence of independent Poisson point measures, $(N_k^{\text{birth}}(ds, di, d\theta))_{k \geq 0}$, on $\mathbb{R}_+ \times \mathbb{N} \times \mathbb{R}_+$ with intensity measure $ds \sum_{n \geq 0} \delta_n(di) dz$,
- (vi) a Poisson point measures, $N^{\text{mutation}}(ds, di, d\theta, dh)$, on $\mathbb{R}_+ \times \mathbb{N} \times \mathbb{R}_+ \times \{-A, \dots, A\}$ with intensity measure $ds \sum_{n \geq 0} \delta_n(di) dz \sum_{j=-A}^A \delta_j(dh)$.

Moreover, we define the *augmented process* (\tilde{v}^K, L^K) by setting $L_0^K \equiv 0$, $\tilde{v}_0^K \equiv \frac{1}{K} N_0^K \delta_{X_0}$, and, for $t > 0$,

$$\begin{aligned}
 (\tilde{v}_t^K, L_t^K) &= (\tilde{v}_0^K, L_0^K) \\
 &+ \sum_{k \geq 0} \left(\int_0^t \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \mathfrak{M}^k(\tilde{v}_{s^-}^K), \theta \leq b(h_{k,i}(\tilde{v}_{s^-}^K))(1 - u_{Km}(h_{k,i}(\tilde{v}_{s^-}^K)))\}} \right. \\
 &\times \left. \left(\frac{1}{K} \delta_{H_{k,i}(\tilde{v}_{s^-}^K)}, 0 \right) N_k^{\text{birth}}(ds, di, d\theta) \right. \\
 (5.6) \quad &- \int_0^t \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \mathfrak{M}^k(\tilde{v}_{s^-}^K), \theta \leq d(h_{k,i}(\tilde{v}_{s^-}^K)) + \int_{\mathbb{N}_0 \times \mathcal{X}} c(h_{k,i}(\tilde{v}_{s^-}^K), \xi_2) \tilde{v}_{s^-}^K(d\xi)\}} \\
 &\times \left. \left(\frac{1}{K} \delta_{H_{k,i}(\tilde{v}_{s^-}^K)}, 0 \right) N_k^{\text{death}}(ds, di, d\theta) \right) \\
 &+ \int_0^t \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \int_{\{-A, \dots, A\}} \mathbb{1}_{\{i \leq K \langle \tilde{v}_{s^-}^K, \mathbb{1} \rangle, \theta \leq b(\tilde{H}_i(\tilde{v}_{s^-}^K)) u_{Km}(\tilde{H}_i(\tilde{v}_{s^-}^K)) M(\tilde{H}_i(\tilde{v}_{s^-}^K), h)\}} \\
 &\times \left. \left(\frac{1}{K} \delta_{(L(s^-)+1, \tilde{H}_{k,i}(\tilde{v}_{s^-}^K) + \sigma h)}, 1 \right) N^{\text{mutation}}(ds, di, d\theta, dh) \right)
 \end{aligned}$$

Note that the process $(\tilde{v}_t^K, L_t^K)_{t \geq 0}$ is a Markov process with generator

$$\begin{aligned}
 &\tilde{\mathcal{L}}^K f((\tilde{v}, L)) \\
 &= \sum_{k \geq 0} \left(\int_{\mathcal{X}} \left(f\left(\tilde{v} + \frac{\delta(k,x)}{K}, L\right) - f(\tilde{v}, L) \right) (1 - u_{Km}(x)) b(x) K \tilde{v}((k, dx)) \right. \\
 &\quad + \int_{\mathcal{X}} \left(f\left(\tilde{v} - \frac{\delta(k,x)}{K}, L\right) - f(\tilde{v}, L) \right) \\
 &\quad \times \left(d(x) + \int_{\mathbb{N}_0 \times \mathcal{X}} c(x, \xi_2) \tilde{v}(d\xi) \right) K \tilde{v}((k, dx)) \Big) \\
 &\quad + \int_{\mathbb{N}_0 \times \mathcal{X}} \int_{\mathbb{Z}} \left(f\left(\tilde{v} + \frac{\delta(L+1, x + \sigma_K h)}{K}, L + 1\right) \right. \\
 &\quad \left. - f(\tilde{v}, L) \right) u_{Km}(x) b(x) M(x, dh) K \tilde{v}(d(k, x)).
 \end{aligned}$$

Naturally, the process generated by \mathcal{L}^K defined in Section 2 is a projection of the process with generator $\tilde{\mathcal{L}}^K$.

The first elementary property we give is that there exists a rough upper bound for the total mass of the population.

LEMMA 5.2. *Under the same assumptions as in Theorem 4.1, there exists a constant, $V > 0$, such that*

$$(5.7) \quad \lim_{K \rightarrow \infty} \mathbb{P}[\inf\{t \geq 0 : \langle \tilde{v}_t^K, \mathbb{1} \rangle \geq 4\bar{b}/\underline{c}\} < \exp(VK)] = 0.$$

PROOF. Apply Theorem 2(a) and then Theorem 3(c) of [6]. \square

6. The first phase of an invasion. Our first task is to control the trait value (other than the resident trait) where the population first attains a density $\varepsilon\sigma_K$, as well as the time when this happens. Since we need to do this for $O(\sigma_K^{-1})$ steps, we need to control this with probability at least $1 - o(\sigma_K)$. Before stating the main result of this section as Theorem 6.2 below, we need to introduce some notation. We want to analyze such a step from a monomorphic initial condition that satisfies the following assumption that is stronger than what is assumed in Theorem 4.1.

ASSUMPTION 4. Fix $\varepsilon > 0$. Let $(R^K)_{K \geq 0}$ be a sequence random variables with values in \mathcal{X} . Then there exists a constant $\tilde{M} > 0$ (independent of ε and K) such that for all K large enough

$$(6.1) \quad L_0^K = 0 \quad \text{and} \quad \tilde{v}_0^K = N_{R^K}^K K^{-1} \delta_{(0, R^K)},$$

where $N_{R^K}^K \in \mathbb{N}$ is a sequence of random variable with $|\bar{z}(R^K) - N_{R^K}^K K^{-1}| < \tilde{M}\varepsilon\sigma_K$ a.s. We call R^K the resident trait.

The following proposition asserts that if we start with an initial condition as in Theorem 4.1, after a short time the state of the population satisfies the stronger conditions of Assumption 4.

PROPOSITION 6.1. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 4.1 hold. Then there exists a constant $\tilde{M} > 0$ (independent from ε and K), such that*

$$\begin{aligned} \lim_{K \rightarrow \infty} \mathbb{P}[\inf\{t \geq 0 : |\langle \tilde{v}_t^K, \mathbb{1} \rangle - \bar{z}(x)| < \tilde{M}\varepsilon\sigma_K\} \\ < \ln(K)\sigma_K^{-1} \wedge \inf\{t \geq 0 : L(t) \geq 1\}] = 1. \end{aligned}$$

Since we can assume for the moment that Assumption 4 hold, we do not state the proof here. In fact, it can be proven in similar way as Lemma 7.4(a). We begin with several notation, which we use in the lemmata below.

NOTATION. Fix $\varepsilon > 0$. Suppose that Assumptions 1, 3 and 4 hold. Let τ_k^K be the k th mutant time and let $Y_k^K \in \mathcal{X}$ be the trait of the k th mutant, that is,

$$(6.2) \quad \tau_k^K \equiv \inf\{t \geq 0 : L_t^K = k\} \quad \text{and} \quad Y_k^K \equiv h_{k,1}(\tilde{v}_{\tau_k^K}^K).$$

We denote by $\theta_{\text{invasion}}^K$ the first time such that a mutant density is larger than $\varepsilon\sigma_K$, that is,

$$(6.3) \quad \theta_{\text{invasion}}^K \equiv \inf\{t \geq 0 : \exists k \in \{1, \dots, L_t^K\} \text{ such that } \mathfrak{M}^k(\tilde{v}_t^K) > \varepsilon\sigma_K K\},$$

and let R_1^K be the trait value of the mutant which is larger than $\varepsilon\sigma_K K$ at time $\theta_{\text{invasion}}^K$, that is,

$$(6.4) \quad R_1^K \equiv h_{k_1,1}(\tilde{v}_{\theta_{\text{invasion}}^K}^K) \quad \text{with } k_1 = \inf\{k \geq 1 : \mathfrak{M}^k(\tilde{v}_{\theta_{\text{invasion}}^K}^K) > \varepsilon\sigma_K K\}.$$

Note that k_1 is the label of the first surviving mutant, that is, $k_1 - 1$ mutations happened before the first surviving mutant appeared. Furthermore, let $\theta_{\text{diversity}}^K$ be the first time such that $\lceil 3/\alpha \rceil$ different traits are present in the population, that is,

$$(6.5) \quad \theta_{\text{diversity}}^K \equiv \inf\left\{t \geq 0 : \sum_{k=0}^{L^K(t)} \mathbb{1}_{\{\mathfrak{M}^k(\tilde{v}_t^K) \geq 1\}} = \lceil 3/\alpha \rceil\right\},$$

and similarly let $\theta_{\text{mut. of mut.}}^K$ the first time such that a “2nd generation mutant” occurs, that is, a mutant which was born from a mutant that in turn was born from the resident trait R^K . Note that

$$(6.6) \quad \theta_{\text{mut. of mut.}}^K \leq \inf\{t \geq 0 : \exists k \in \{1, \dots, L_t^K\} \text{ such that } |R^K - Y_k^K| > A\sigma_K\}.$$

Then we define

$$(6.7) \quad \hat{\theta}^K \equiv \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K \wedge \exp(K^\alpha).$$

The following theorem collects the main results of this section.

THEOREM 6.2. *Fix $\varepsilon > 0$. Under the Assumptions 1, 3 and 4, there exists a constant $M > 0$ (independent of ε and K) such that for all K large enough:*

- (i) $\tilde{v}_0^K = N_{R^K}^K K^{-1} \delta_{(0,R^K)}$, where $|\bar{z}(R^K) - N_{R^K}^K K^{-1}| < (M/3)\varepsilon\sigma_K$ a.s.
- (ii) We can construct on $(\Omega, \mathcal{F}, \mathbb{P})$ two random variables, $R_1^{K,1}$ and $R_1^{K,2}$, such that

$$(6.8) \quad \mathbb{P}[R_1^{K,1} \leq R_1^K \leq R_1^{K,2} \text{ and } R_1^{K,2} - R_1^{K,1} \leq A\sigma_K] = 1 - o(\sigma_K), \quad \text{and}$$

$$(6.9) \quad \mathbb{P}[R_1^{K,1} = R_1^K = R_1^{K,2}] = 1 - O(\varepsilon).$$

The distributions of $R_1^{K,1}$ and $R_1^{K,2}$ are given in Corollary 6.10.

- (iii) We can construct on $(\Omega, \mathcal{F}, \mathbb{P})$ two exponential random variables, $E^{K,1}$ and $E^{K,2}$, with parameters of order $\sigma_K u_K K$, such that

$$(6.10) \quad \mathbb{P}[E^{K,2} \leq \theta_{\text{invasion}}^K \leq E^{K,1} + \ln(K)\sigma_K^{-1-\alpha/2}] = 1 - o(\sigma_K).$$

The distributions of $E^{K,1}$ and $E^{K,2}$ are given in Lemma 6.7.

Moreover, until the first time of invasion, $\theta_{\text{invasion}}^K$, the resident density stays in an $\varepsilon M \sigma_K$ -neighborhood of $\bar{z}(R^K)$, the number of different living mutant traits is bounded by $\lceil \alpha/3 \rceil$, and there is no mutant of a mutant, with probability $1 - o(\sigma_K)$. that is,

$$\begin{aligned} &\mathbb{P}[\theta_{\text{invasion}}^K < \inf\{t \geq 0 : |\mathfrak{M}^0(\tilde{v}_t^K) - \lceil K \bar{z}(R^K) \rceil| > \varepsilon M \sigma_K K\} \\ &\quad \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] \\ &= 1 - o(\sigma_K). \end{aligned}$$

REMARK 4. The constant $M > 0$ depends only on α and on the functions $b(\cdot), d(\cdot), c(\cdot, \cdot)$, and $m(\cdot)$, but not on K, R^K and ε .

6.1. Exit time from an attractive domain.

LEMMA 6.3. Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that

$$(6.11) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\inf\{t \geq 0 : |\mathfrak{M}^0(\tilde{v}_t^K) - \lceil K \bar{z}(R^K) \rceil| > \varepsilon M \sigma_K K\} < \hat{\theta}^K] = 0.$$

The statement is stronger than the corresponding one in [6], Theorem 3(c), since the diameter of the domain converges to zero, when K tends to infinity and since it gives control of the speed of convergence to 0 of the probabilities. Therefore, it does not follow from the classical results about the time of exit from an attractive domain (cf. [14]). Our proof is based on a coupling with a discrete Markov chain and some standard potential theoretical argument.

PROOF. Define

$$(6.12) \quad X_t \equiv |\mathfrak{M}_t^0 - \lceil K \bar{z}(R^K) \rceil|$$

and, for all $M \geq 0$,

$$(6.13) \quad \tau_0 \equiv \inf\{t > 0 : X_t = 0\} \quad \text{and} \quad \tau_{M\varepsilon\sigma_K K} \equiv \inf\{t > 0 : X_t \geq M\varepsilon\sigma_K K\}.$$

Note that τ_0 and $\tau_{M\varepsilon\sigma_K K}$ are stopping times with respect to the natural filtration of X_t , which is equal to $\sigma(\mathfrak{M}_s^0; s \leq t)$, and that the process $(\mathfrak{M}_t^0)_{t \geq 0}$ is not Markovian. We can associate with the continuous time process X_t a discrete time (non-Markovian) process Y_n , which records the sequence of values that X_t takes. (This can be formally defined by introducing the sequences T_k of the stopping times which record the instances when $X_t \neq X_{t-}$ and setting $Y_n = X_{T_n}$.) Now, we can compute

$$(6.14) \quad \mathbb{P}[\tau_{M\varepsilon\sigma_K K} < \tau_0 \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K]$$

with respect to the stopping times defined for the discrete time process Y_n and exploit the natural renewal structure on Y_n . Therefore, we prove the following claim.

CLAIM. For $1 \leq i \ll K$, and K large enough,

$$(6.15) \quad \begin{aligned} & \mathbb{P}[Y_{n+1} = i + 1 | Y_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] \\ & \leq \frac{1}{2} - (\underline{c}/4\bar{b})K^{-1}i + (\bar{c}/\underline{b})\varepsilon\sigma_K \equiv p_+^K(i), \end{aligned}$$

where \underline{c} , \underline{b} , \bar{c} and \bar{b} are the lower, respectively, upper bounds for birth and competition rates.

Recall from Remark 1 that the equilibrium $\bar{z}(R^K)$ is equal to $\frac{b(R^K) - d(R^K)}{c(R^K, R^K)}$ and observe that there are at most $\lceil 3/\alpha \rceil \varepsilon \sigma_K K$ mutant individuals alive at any time $t < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K$. Therefore, for $1 \leq i \ll K$ and K large enough,

$$(6.16) \quad \begin{aligned} & \mathbb{P}[Y_{n+1} = i + 1 | Y_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] \\ & \leq \frac{(1 - m(R^K)u_K)b(R^K)}{(1 - m(R^K)u_K)b(R^K) + d(R^K) + c(R^K, R^K)K^{-1}(\lceil K\bar{z}(R^K) \rceil + i)} \\ & \quad \vee \frac{d(R^K) + c(R^K, R^K)K^{-1}(\lceil K\bar{z}(R^K) \rceil - i) + \bar{c}\lceil 3/\alpha \rceil \varepsilon \sigma_K K}{(1 - m(R^K)u_K)b(R^K) + d(R^K) + c(R^K, R^K)K^{-1}(\lceil K\bar{z}(R^K) \rceil - i)} \\ & \leq \frac{b(R^K) - m(R^K)u_K b(R^K)}{2b(R^K) - m(R^K)u_K b(R^K) + c(R^K, R^K)K^{-1}i} \\ & \quad \vee \frac{b(R^K) - c(R^K, R^K)K^{-1}(i - 1) + \bar{c}\lceil 3/\alpha \rceil \varepsilon \sigma_K K}{2b(R^K) - m(R^K)u_K b(R^K) - c(R^K, R^K)K^{-1}i} \\ & \leq \frac{1}{2} - (\underline{c}/4\bar{b})K^{-1}i + (\bar{c}/\underline{b})\lceil 3/\alpha \rceil \varepsilon \sigma_K. \end{aligned}$$

This proves the claim. Next, we introduce a coupling, that is, we define a discrete time process Z_n with the following properties:

- (i) $Z_0 = Y_0$,
- (ii) $\mathbb{P}[Z_{n+1} = i + 1, Y_{n+1} = i + 1 | Y_n = Z_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] = \mathbb{P}[Y_{n+1} = i + 1 | Y_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K]$,
- (iii) $\mathbb{P}[Z_{n+1} = i + 1, Y_{n+1} = i - 1 | Y_n = Z_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] = p_+^K(i) - \mathbb{P}[Y_{n+1} = i + 1 | Y_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K]$,
- (iv) $\mathbb{P}[Z_{n+1} = i + 1 | Y_n < Z_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] = p_+^K(i)$,
- (v) $\mathbb{P}[Z_{n+1} = i - 1 | Y_n < Z_n = i, T_{n+1} < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] = 1 - p_+^K(i)$.

Note that by construction $Z_n \geq Y_n$ a.s. for all n such that $T_n < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K$ and the marginal distribution of Z_n is a Markov chain with transition probabilities

$$(6.17) \quad \mathbb{P}[Z_{n+1} = j | Z_n = i] = \begin{cases} 1, & \text{for } i = 0 \text{ and } j = 1, \\ p_+^K(i), & \text{for } i \geq 1 \text{ and } j = i + 1, \\ 1 - p_+^K(i), & \text{for } i \geq 1 \text{ and } j = i - 1, \\ 0, & \text{else.} \end{cases}$$

Now we define a continuous time process, \tilde{Z} , associated to Z_n . To do this, let $(\tilde{T}_j)_{j \in \mathbb{N}}$ be the sequence of jump times of \tilde{Z} , that is, $\tilde{Z}_t \equiv Z_n$ if $t \in [\tilde{T}_n, \tilde{T}_{n+1})$, defined for all $j \in \mathbb{N}$ as follows:

$$(6.18) \quad \tilde{T}_j - \tilde{T}_{j-1} = \begin{cases} T_j - T_{j-1}, & \text{if } T_j < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K, \\ W_j, & \text{else,} \end{cases}$$

where W_j are independent exponential distributed random variables with mean $(C_{\text{total rate}} K)^{-1}$ where $C_{\text{total rate}} = 4\bar{b}\underline{c}(\bar{b} + \bar{d} + \bar{c}(4\bar{b}\underline{c}))$. By Lemma 5.2, $C_{\text{total rate}} K$ is an upper bound for the total event rate of $\langle \tilde{v}_t^K, \mathbb{1} \rangle$ and, therefore, also for \mathfrak{M}_t^0 .

Define $\tau_{M\varepsilon\sigma_K K}^Z \equiv \inf\{n \geq 0 : Z_n \geq M\varepsilon\sigma_K K\}$ and $\tau_0^Z \equiv \inf\{n \geq 0 : Z_n = 0\}$. Then, since $\tilde{Z}_t \geq X_t$ a.s. for all $t < \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K$,

$$(6.19) \quad \mathbb{P}[\tau_{M\varepsilon\sigma_K K} < \tau_0 \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K] \leq \mathbb{P}[\tau_{M\varepsilon\sigma_K K}^Z < \tau_0^Z].$$

Applying Proposition A.2 yields that, for all $M \geq 32\lceil 3/\alpha \rceil (\bar{c}\bar{b})/(\underline{b}\underline{c})$ such that $Z_0 \leq \frac{1}{3}M\varepsilon\sigma_K K$ and large K large enough,

$$(6.20) \quad \mathbb{P}[\tau_{M\varepsilon\sigma_K K}^Z < \tau_0^Z] \leq \exp(-K^{2\alpha}).$$

Next, we prove that the process X_t returns many times to zero before it reaches for the first time the value $M\varepsilon\sigma_K K$. More precisely, we first prove a lower bound on the number of returns to zero of the discrete time process Z_n . Then we calculate the time for a return to zero. From now on, we assume that $M \geq 32\lceil 3/\alpha \rceil (\bar{c}\bar{b})/(\underline{b}\underline{c})$. We define the following stopping times with respect to the natural filtration of Z which records the number of jumps the process Z needs for m zero-returns:

$$(6.21) \quad \tau_m^Z \text{ returns} \equiv \inf \left\{ n \geq 1 : \sum_{i=1}^n \mathbb{1}_{Z_i=0} = m \right\}.$$

Let $Q^m \equiv \mathbb{P}[\tau_m^Z \text{ returns} < \tau_{M\varepsilon\sigma_K K}^Z < \tau_{(m+1) \text{ returns}}^Z]$ be the probability that the Markov chain Z_n returns exactly m times to zero before it reaches the value $M\varepsilon\sigma_K K$. We have

$$(6.22) \quad Q^0 = \mathbb{P}[\tau_{M\varepsilon\sigma_K K}^Z < \tau_0^Z] \leq \exp(-K^{2\alpha}),$$

and, due to the Markov property, for $m \geq 1$,

$$(6.23) \quad Q^m = \mathbb{P}[\tau_0^Z < \tau_{M\varepsilon\sigma_K K}^Z](1 - \mathbb{P}_1[\tau_{M\varepsilon\sigma_K K}^Z < \tau_0^Z])^{m-1} \mathbb{P}_1[\tau_{M\varepsilon\sigma_K K}^Z < \tau_0^Z],$$

where the last term in the product is smaller than $\exp(-K^{2\alpha})$. Thus,

$$(6.24) \quad Q^m \leq \exp(-K^{2\alpha}) \quad \text{for all } m \geq 0.$$

Let B be the random variable which records the number of zero returns of Z_n before Z_n reaches $M\varepsilon\sigma_K K$. With other words, $B = n$ if and only if $\tau_{n \text{ returns}}^Z < \tau_{M\varepsilon\sigma_K K}^Z < \tau_{n+1 \text{ returns}}^Z$, and we obtain that

$$(6.25) \quad \mathbb{P}[B \leq n] = \sum_{i=0}^n Q^i \leq (n + 1) \exp(-K^{2\alpha}).$$

Set $I_1 \equiv \tilde{T}_{\tau_1^Z}$ and $I_j \equiv \tilde{T}_{\tau_j^Z} - \tilde{T}_{\tau_{(j-1)}^Z}$ for $j \geq 2$. For any j , I_j is the random time between the $(j - 1)$ th and the j th zero return of the associated continuous time process \tilde{Z}_t and

$$(6.26) \quad \sum_{i=1}^B I_i \leq \inf\{t \geq 0 : \tilde{Z}_t \geq M\varepsilon\sigma_K K\} \leq \sum_{i=1}^{B+1} I_i.$$

We get an upper bound for the probability which we want to compute

$$(6.27) \quad \begin{aligned} & \mathbb{P}[\inf\{t \geq 0 : |\mathfrak{M}^0(\tilde{v}_t^K) - \lceil K\bar{z}(R^K) \rceil \rceil > \varepsilon M\varepsilon\sigma_K K\} < \hat{\theta}^K] \\ & \leq \sum_{l=n}^{\infty} \mathbb{P}[\inf\{t \geq 0 : \tilde{Z}_t \geq M\varepsilon\sigma_K K\} < \exp(K^\alpha), B = l] + \mathbb{P}[B \leq n]. \end{aligned}$$

According to (6.26), if $B = l$ and if in addition more than $l/2$ of the l random times I_j in the sum are larger than $2l^{-1} \exp(K^\alpha)$, then $\inf\{t \geq 0 : \tilde{Z}_t \geq M\varepsilon\sigma_K K\}$ is larger than $\exp(K^\alpha)$. Therefore, for all $l \geq n$,

$$(6.28) \quad \begin{aligned} & \mathbb{P}[\inf\{t \geq 0 : \tilde{Z}_t \geq M\varepsilon\sigma_K K\} < \exp(K^\alpha), B = l] \\ & \leq \mathbb{P}\left[\sum_{i=1}^l \mathbb{1}_{\{I_j < 2l^{-1} \exp(K^\alpha)\}} > \frac{l}{2}, B = l\right]. \end{aligned}$$

As mentioned before, $C_{\text{total rate}} K$ is an upper bound for the total event rate of $(\tilde{v}_t^K, \mathbb{1})$. Thus, we can bound the jump times by a sequence of independent, exponential random variables $(V_j)_{j \in \mathbb{N}}$ with mean $(C_{\text{total rate}} K)^{-1}$. Namely,

$$(6.29) \quad \tilde{T}_j - \tilde{T}_{j-1} \equiv T_j - T_{j-1} \succcurlyeq V_j \quad \text{if } T_j \leq \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K.$$

Otherwise, the random times $\tilde{T}_j - \tilde{T}_{j-1}$ are by definition independent and exponentially distributed with mean $(C_{\text{total rate}} K)^{-1}$. The process \tilde{Z} has to make at least two jumps to return to zero. Hence,

$$(6.30) \quad I_i \succcurlyeq \tilde{W}_i, \quad \text{for all } i \in \mathbb{N},$$

where $(\tilde{W}_i)_{i \in \mathbb{N}}$ is a sequence of independent, exponential random variables with mean $(C_{\text{total rate}} K)^{-1}$. Thus,

$$(6.31) \quad \mathbb{P} \left[\sum_{l=1}^l \mathbb{1}_{\{l_j < 2l^{-1} \exp(K^\alpha)\}} > \frac{l}{2}, B = l \right] \leq \mathbb{P} \left[\sum_{i=1}^l \mathbb{1}_{\{\tilde{W}_i < 2l^{-1} \exp(K^\alpha)\}} > \frac{l}{2} \right].$$

Since $\mathbb{P}[\tilde{W}_i < 2l^{-1} \exp(K^\alpha)] = 1 - \exp(-C_{\text{total rate}} K l^{-1} \exp(K^\alpha))$ and $(\tilde{W}_i)_{i \geq 1}$ are independent, we obtain that $\sum_{i=1}^l \mathbb{1}_{\{\tilde{W}_i < 2l^{-1} \exp(K^\alpha)\}}$ is binomially distributed with $n = l$ and $p = 1 - \exp(-C_{\text{total rate}} K l^{-1} \exp(K^\alpha))$. Therefore, the right-hand side of (6.31) is equal to

$$(6.32) \quad \sum_{i=\frac{l}{2}}^l \binom{l}{i} (1 - \exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^i (\exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^{l-i}.$$

For the following two computations, we use the elementary facts that $\binom{l}{i} < 2^l$ and $l < 2^l$, for all $l \in \mathbb{N}$ and $i \leq l$. We obtain that, for large K enough, the left-hand side of (6.27) is bounded from above by

$$(6.33) \quad \sum_{l=n}^\infty \sum_{i=\frac{l}{2}}^l \binom{l}{i} (1 - \exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^i (\exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^{l-i} + \mathbb{P}[B \leq n] \\ \leq \sum_{l=n}^\infty \frac{l}{2} 2^l (1 - \exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^{\frac{l}{2}} + \mathbb{P}[B \leq n].$$

By (6.25), we see that $\mathbb{P}[B \leq n] = o(\sigma_K)$ if the variable n fulfills the following condition:

$$(6.34) \quad n \ll \exp(K^{2\alpha}) \sigma_K.$$

Therefore, we choose $n = \lceil \exp(2K^\alpha) \rceil$ and get, for large K enough,

$$(6.35) \quad \mathbb{P}[\inf\{t \geq 0 : |\mathfrak{M}^0(\tilde{v}_t^K) - \lceil K \bar{z}(R^K) \rceil| > \varepsilon M \sigma_K K\} < \hat{\theta}^K] \\ \leq \sum_{l=\lceil \exp(2K^\alpha) \rceil}^\infty 4^l (1 - \exp(-C_{\text{total rate}} K l^{-1} e^{K^\alpha}))^{\frac{l}{2}} + o(\sigma_K) \\ \leq \sum_{l=\lceil \exp(2K^\alpha) \rceil}^\infty (4(1 - \exp(-C_{\text{total rate}} K e^{-K^\alpha}))^{\frac{1}{2}})^l + o(\sigma_K) \\ \leq 2(4^2(1 - \exp(-C_{\text{total rate}} K e^{-K^\alpha})))^{\frac{1}{2} \lceil \exp(2K^\alpha) \rceil} + o(\sigma_K) \\ \leq 2(4^2 C_{\text{total rate}} K e^{-K^\alpha})^{\frac{1}{2} \lceil \exp(2K^\alpha) \rceil} + o(\sigma_K) \\ \leq o(K e^{-K^\alpha}) + o(\sigma_K),$$

where we used that $\exp(-x) \geq 1 - x$ for $x \geq 0$ and $K \exp(K^{-\alpha}) \ll \sigma_K$. \square

6.2. Controlling the number L_t^K of mutations by Poisson processes.

LEMMA 6.4. Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then

$$(6.36) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} (1 - \mathbb{P}[\forall 0 \leq t \leq \hat{\theta}^K : A^{1,K}(t) \preceq L_t^K \preceq A^{2,K}(t)]) = 0,$$

where $A^{1,K}$ and $A^{2,K}$ are Poisson counting processes with parameter $a_1^K u_K K$ and $a_2^K u_K K$ with

$$(6.37) \quad a_1^K \equiv (\bar{z}(R^K) - \varepsilon M \sigma_K) b(R^K) m(R^K),$$

$$(6.38) \quad a_2^K \equiv (\bar{z}(R^K) + \varepsilon (M + \lceil 3/\alpha \rceil) \sigma_K) (b(R^K) m(R^K) + C_L^{b,m,M} A \sigma_K),$$

and $C_L^{b,m,M}$ is a constant depending only on the functions $b(\cdot)$, $m(\cdot)$ and $M(\cdot, h)$ for $h \in \{-A, \dots, A\}$.

PROOF. We obtain from the last lemma that

$$\begin{aligned} & \mathbb{P}\left[\forall 0 \leq t \leq \hat{\theta}^K : \bar{z}(R^K) - \varepsilon M \sigma_K \leq \langle \tilde{v}_t, \mathbb{1} \rangle \leq \bar{z}(R^K) + \varepsilon \left(M + \left\lceil \frac{3}{\alpha} \right\rceil\right) \sigma_K\right] \\ & = 1 - o(\sigma_K). \end{aligned}$$

Therefore, define

$$(6.39) \quad \begin{aligned} A^{1,K}(t) &= \int_0^t \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \int_{\{-A, \dots, A\}} \mathbb{1}_{\{i \leq K(\bar{z}(R^K) - \varepsilon M \sigma_K), \theta \leq b(R^K) u_K m(R^K) M(R^K, h)\}} \\ & \times N^{\text{mutation}}(ds, di, d\theta, dh) \end{aligned}$$

and similarly

$$(6.40) \quad \begin{aligned} A^{2,K}(t) &= \int_0^t \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \int_{\{-A, \dots, A\}} \mathbb{1}_{\{i \leq K(\bar{z}(R^K) + \varepsilon (M + \lceil 3/\alpha \rceil) \sigma_K)\}} \\ & \times \mathbb{1}_{\{\theta \leq u_K (b(R^K) m(R^K) M(R^K, h) + C_L^{b,m,M} A \sigma_K)\}} \\ & \times N^{\text{mutation}}(ds, di, d\theta, dh). \end{aligned}$$

Since $\hat{\theta}^K \leq \theta_{\text{mut. of mut.}}^K$, any mutant trait differs at most $A \sigma_K$ from the resident trait, R^K . Thus, we have that $u_K (b(R^K) m(R^K) M(R^K, h) + C_L^{b,m,M} A \sigma_K)$ is a rough upper bound for the mutation rate per individual for an appropriate choice of $C_L^{b,m,M}$. Note that $A^{i,K}$ are Poisson counting process with parameter $a_i^K u_K K$. By construction, we obtain (6.36). \square

6.3. *Controlling the number $\mathfrak{M}^k(\tilde{v}_t)$ of offspring of the k th mutant by birth–death processes.*

LEMMA 6.5. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant in Lemma 6.3. Then*

$$(6.41) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} (1 - \mathbb{P}[\forall 1 \leq k \leq L_{\hat{\theta}^K}^K, \forall t \leq \hat{\theta}^K : Z_k^{K,1}(t) \leq \mathfrak{M}^k(\tilde{v}_t) \leq Z_k^{K,2}(t)]) = 0,$$

where $Z_k^{K,1}(t)$, respectively, $Z_k^{K,2}(t)$ are \mathbb{N}_0 -valued processes, which are zero until time τ_k^K , the first time s.t. $\mathfrak{M}^k(\tilde{v}_t) \neq 0$, and afterwards linear, continuous time birth–death processes with initial state 1 at time τ_k^K , birth rates per individual

$$(6.42) \quad b_k^{K,1} = b_k^{K,2} = b(Y_k^K)(1 - u_K m(Y_k^K)),$$

and death rate per individual

$$(6.43) \quad d_k^{K,1} = d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) + M\varepsilon\sigma_K) + \bar{c}[3/\alpha]\varepsilon\sigma_K,$$

respectively,

$$(6.44) \quad d_k^{K,2} = d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) - M\varepsilon\sigma_K).$$

Furthermore, define $\tilde{Z}_k^{K,1}(t) \equiv Z_k^{K,1}(\tau_k + t)$ and $\tilde{Z}_k^{K,2}(t) \equiv Z_k^{K,2}(\tau_k + t)$, then the processes $\{(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2})\}_{k \geq 1}$ are independent and identically distributed.

PROOF. For any $t \leq \hat{\theta}^K$, any individual of $\mathfrak{M}^k(\tilde{v}_t)$ gives birth to a new individual with the same trait with rate $b(Y_k^K)(1 - u_K m(Y_k^K))$ and dies with rate $d(Y_k^K) + \int_{\mathbb{N} \times \mathcal{X}} c(Y_k^K, \xi_2) \tilde{v}_t^K(d\xi)$, which belongs to the following interval:

$$(6.45) \quad [d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) - M\varepsilon\sigma_K), \\ d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) + M\varepsilon\sigma_K) + \bar{c}[3/\alpha]\varepsilon\sigma_K].$$

Thus, let us define, for $k \leq L_{\hat{\theta}^K}$,

$$(6.46) \quad \begin{aligned} & \tilde{Z}_k^{K,1}(t) \\ & \equiv \int_{\tau_k}^{\tau_k+t} \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \tilde{Z}_k^{K,1}(s^-), \theta \leq b(Y_k^K)(1 - u_K m(Y_k^K))\}} N_k^{\text{birth}}(ds, di, d\theta) \\ & - \int_{\tau_k}^{\tau_k+t} \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \tilde{Z}_k^{K,1}(s^-), \theta \leq d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) + M\varepsilon\sigma_K) + \bar{c}[3/\alpha]\varepsilon\sigma_K\}} \\ & \times N_k^{\text{death}}(ds, di, d\theta) \end{aligned}$$

and similarly

$$\begin{aligned}
 \tilde{Z}_k^{K,2}(t) &\equiv \int_{\tau_k}^{\tau_k+t} \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \tilde{Z}_k^{K,1}(s^-), \theta \leq b(Y_k)(1-u_K m(Y_k))\}} N_k^{\text{birth}}(ds, di, d\theta) \\
 (6.47) \quad &- \int_{\tau_k}^{\tau_k+t} \int_{\mathbb{N}_0} \int_{\mathbb{R}_+} \mathbb{1}_{\{i \leq \tilde{Z}_k^{K,1}(s^-), \theta \leq d(Y_k^K) + c(Y_k^K, R^K)(\bar{z}(R^K) - M\varepsilon\sigma_K)\}} \\
 &\times N_k^{\text{death}}(ds, di, d\theta),
 \end{aligned}$$

and a similar construction for $k > L_{\hat{\theta}K}$, where the random variables Y_k^K are replaced by i.i.d. ones with distribution $f_K * M(R^K, \cdot)$, independent of all the previously introduced random variables, where f_K is the homothety of ratio σ_K . Note that, the Poisson point measures N_k^{birth} and N_k^{death} are independent of Y_k^K and τ_k , and that the processes $\tilde{Z}_k^{K,1}$ and $\tilde{Z}_k^{K,2}$ only depend on N_k^{birth} , N_k^{death} , Y_k^K and τ_k . By construction, conditionally on $Y_k^K = y$ and $\tau_k = s$, the process $\tilde{Z}_k^{K,1}$ is distributed as a linear birth–death processes with birth rate $b(y)(1 - u_K m(y))$ and death rate $d(y) + c(y, R^K)(\bar{z}(R^K) + M\varepsilon\sigma_K) + \bar{c}\lceil 3/\alpha \rceil \varepsilon\sigma_K$, and similarly for $\tilde{Z}_k^{K,2}$. In particular, the law of $(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2})$ does not depend on τ_k . Therefore, defining $\mathcal{G}_k \equiv \sigma(\tilde{v}_t, t \leq \tau_k, Y_k^K, N_\ell^{\text{birth}}, N_\ell^{\text{death}}, 1 \leq \ell \leq k - 1)$, for all bounded measurable functions F_1, \dots, F_k on $\mathbb{D}(\mathbb{R}_+, \mathbb{Z}_+^2)$,

$$\begin{aligned}
 &\mathbb{E}[F_1(\tilde{Z}_1^{K,1}, \tilde{Z}_1^{K,2}) \dots F_k(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2})] \\
 (6.48) \quad &= \mathbb{E}[F_1(\tilde{Z}_1^{K,1}, \tilde{Z}_1^{K,2}) \dots F_{k-1}(\tilde{Z}_{k-1}^{K,1}, \tilde{Z}_{k-1}^{K,2}) \mathbb{E}[F_k(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2}) | \mathcal{G}_k]] \\
 &= \mathbb{E}[F_1(\tilde{Z}_1^{K,1}, \tilde{Z}_1^{K,2}) \dots F_{k-1}(\tilde{Z}_{k-1}^{K,1}, \tilde{Z}_{k-1}^{K,2}) \mathbb{E}[F_k(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2}) | Y_k^K]] \\
 &= \mathbb{E}[F_1(\tilde{Z}_1^{K,1}, \tilde{Z}_1^{K,2}) \dots F_{k-1}(\tilde{Z}_{k-1}^{K,1}, \tilde{Z}_{k-1}^{K,2})] \mathbb{E}[F_k(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2})],
 \end{aligned}$$

where the last equality follows from the fact that the random variable Y_k^K is independent of $(\tilde{Z}_\ell^{K,1}, \tilde{Z}_\ell^{K,2})$ for $1 \leq \ell \leq k - 1$. Actually, $(Y_k^K)_{1 \leq k \leq L_{\hat{\theta}K}}$ are i.i.d. random variables, with law $f_K * M(R^K, \cdot)$. This implies by induction that the processes $\{(\tilde{Z}_k^{K,1}, \tilde{Z}_k^{K,2})\}_{k \geq 1}$ are i.i.d. \square

6.4. Controlling survival of the k th mutant population.

NOTATION. Let us define $B_k^K \equiv \mathbb{1}_{\{\inf\{t \geq \tau_k : \mathfrak{M}^k(\tilde{v}_t) \geq \varepsilon\sigma_K K\} < \inf\{t \geq \tau_k : \mathfrak{M}^k(\tilde{v}_t) = 0\}\}}$.

This random variable indicates whether or not the k th mutant population, which appeared at time τ_k , invades, that is, reaches $\varepsilon\sigma_K K$ individuals before dying out. The following lemma introduces a sequence of i.i.d. random variables $(B_k^{1,K}, B_k^{2,K})$ which are 2-tuples of Bernoulli random variables constructed from the processes $Z_k^{K,1}(t)$ and $Z_k^{K,2}(t)$ defined in Lemma 6.5, such that $(B_k^K)_{k \geq 0}$ is stochastically dominated by the sequences $(B_k^{i,K})_{k \geq 0}$.

LEMMA 6.6. Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then

$$(6.49) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} (1 - \mathbb{P}[\forall 1 \leq k \leq L_{\hat{\theta}^K}^K : B_k^{1,K} \preceq B_k^K \preceq B_k^{2,K}]) = 0,$$

where $((B_k^{1,K}, B_k^{2,K}))_{k \geq 1}$ is a sequence of i.i.d. 2-tuples of Bernoulli random variables such that $B_k^{1,K} \leq B_k^{2,K}$ a.s. Its distribution is characterized by

$$(6.50) \quad \begin{aligned} \sigma_K q_1^K(h) &\equiv \mathbb{P}[B_k^{1,K} = 1 | Y_k^K = R^K + h\sigma_K] \\ &= \begin{cases} \sigma_K \left(h \frac{\partial_1 f(R^K, R^K)}{b(R^K)} - \varepsilon C_{\text{Bernoulli}}^1 \right), & \text{if } 1 \leq h \leq A, \\ 0, & \text{otherwise} \end{cases} \end{aligned}$$

and

$$(6.51) \quad \begin{aligned} \sigma_K q_2^K(h) &\equiv \mathbb{P}[B_k^{2,K} = 1 | Y_k^K = R^K + h\sigma_K] \\ &= \begin{cases} \sigma_K \left(h \frac{\partial_1 f(R^K, R^K)}{b(R^K)} + \varepsilon C_{\text{Bernoulli}}^2 \right), & \text{if } 1 \leq h \leq A, \\ 0, & \text{otherwise,} \end{cases} \end{aligned}$$

where $C_{\text{Bernoulli}}^1$ and $C_{\text{Bernoulli}}^2$ depend only on α , M , and C_L (the Lipschitz constant of our parameters). Then, for $i = 1, 2$ and $k \geq 1$, $B_k^{i,K}$ is a Bernoulli random variable of parameter $\sigma_K p_i^K$, where

$$(6.52) \quad p_i^K \equiv \sum_{h=1}^A q_i^K(h) M(R^K, h).$$

REMARK 5. (i) For all $k \geq 1$, $\mathbb{P}[B_k^{1,K} = 0 | B_k^{2,K} = 1] = 1 - \frac{p_1^K}{p_2^K}$ and is thereby of order ε .

(ii) We use in here the assumption that $\partial_1 f(x, x) > 0$ for all $x \in \mathcal{X}$.

PROOF. Let $Z_k^{K,1}(t)$, respectively, $Z_k^{K,2}(t)$ as defined in Lemma 6.5 and define

$$(6.53) \quad \tilde{B}_k^{i,K} \equiv \mathbb{1}_{\inf\{t \geq \tau_k : Z_k^{K,i}(t) \geq \varepsilon \sigma_K K\} < \inf\{t \geq \tau_k : Z_k^{K,i}(t) = 0\}} \quad \text{for } i = 1, 2.$$

Then, due to the last lemma

$$(6.54) \quad \mathbb{P}[\forall 1 \leq k \leq L_{\hat{\theta}^K}^K : \tilde{B}_k^{1,K} \preceq B_k^K \preceq \tilde{B}_k^{2,K}] = 1 - o(\sigma_K).$$

For all $1 \leq k \leq L_{\hat{\theta}^K}^K$, we obtain with Proposition A.3, that

$$(6.55) \quad \begin{aligned} & \left| \mathbb{P}[\inf\{t \geq \tau_k : Z_k^{K,i}(t) \geq \varepsilon \sigma_K K\} < \inf\{t \geq \tau_k : Z_k^{K,i}(t) = 0\} | Y_k^K] \right. \\ & \left. - \frac{[b_k^{i,K} - d_k^{i,K}]_+}{b_k^{i,K}} \right| \\ & = o(\exp(-K^\alpha)), \end{aligned}$$

where, using that $f(x, x) = 0$ for all x , we have

$$(6.56) \quad \begin{aligned} & b_k^{1,K} - d_k^{1,K} \\ & = f(Y_k^K, R^K) - (c(Y_k^K, R^K)M + \bar{c}[3/\alpha])\varepsilon \sigma_K - u_K b(Y_k^K) m(Y_k^K) \\ & = \partial_1 f(R^K, R^K)(Y_k^{K,1} - R^K) - (c(Y_k^K, R^K)M + \bar{c}[3/\alpha])\varepsilon \sigma_K \\ & \quad + O(\sigma_K^2), \end{aligned}$$

and similarly

$$(6.57) \quad b_k^{2,K} - d_k^{2,K} = \partial_1 f(R^K, R^K)(Y_k^K - R^K) + c(Y_k^K, R^K)M\varepsilon \sigma_K + O(\sigma_K^2).$$

Recall that the sequence $(Y_k^K)_{k \geq 1}$ used to construct the processes $Z_k^{K,1}$ and $Z_k^{K,2}$ is a sequence of i.i.d. random variables with distribution $M(R^K, \cdot)$. Since $b_k^{i,K} - d_k^{i,K} < 0$ if $Y_k^K - R^K < 0$, we obtain

$$(6.58) \quad \begin{aligned} & \mathbb{P}[\tilde{B}_k^{1,K} = 1] \\ & = \mathbb{E}[\mathbb{P}[\tilde{B}_k^{1,K} | Y_k^K] = 1] \\ & \geq \sum_{h=1}^A \left(\frac{\partial_1 f(R^K, R^K)\sigma_K h - (c(Y_k^K, R^K)M + \bar{c}[3/\alpha])\varepsilon \sigma_K + O(\sigma_K^2)}{b(R^K)} \right) \\ & \quad \times M(R^K, h). \end{aligned}$$

Therefore, there exists a constant $C_{\text{Bernoulli}}^1 > 0$ (which depends only on α, M and C_L) such that the sum in the right-hand side of (6.58) is, term by term, bounded from below by

$$(6.59) \quad \sigma_K \sum_{h=1}^A \left(h \frac{\partial_1 f(R^K, R^K)}{b(R^K)} - \varepsilon C_{\text{Bernoulli}}^1 \right) M(R^K, h)$$

and similarly there exists a constant $C_{\text{Bernoulli}}^2 > 0$ such that

$$(6.60) \quad \mathbb{P}[\tilde{B}_k^{2,K} = 1] \leq \sigma_K \sum_{h=1}^A \left(h \frac{\partial_1 f(R^K, R^K)}{b(R^K)} + \varepsilon C_{\text{Bernoulli}}^2 \right) M(R^K, h).$$

Next, we introduces two couplings, that is, we define a sequences of i.i.d. 2-tuples of Bernoulli random variables $((B_k^{1,K}, B_k^{2,K}))_{k \geq 1}$ with the following properties:

- (i) $\mathbb{P}[B_k^{1,K} = 0, \tilde{B}_k^{1,K} = 0 | Y_k^K = R^K + h\sigma_K] = \mathbb{P}[\tilde{B}_k^{1,K} = 0 | Y_k^K = R^K + h\sigma_K]$
and $\mathbb{P}[B_k^{1,K} = 1, \tilde{B}_k^{1,K} = 1 | Y_k^K = R^K + h\sigma_K] = q_1^K(h)\sigma_K$,
- (ii) $\mathbb{P}[B_k^{2,K} = 1, \tilde{B}_k^{2,K} = 1 | Y_k^K = R^K + h\sigma_K] = \mathbb{P}[\tilde{B}_k^{2,K} = 1 | Y_k^K = R^K + h\sigma_K]$
and $\mathbb{P}[B_k^{2,K} = 1, \tilde{B}_k^{2,K} = 0 | Y_k^K = R^K + h\sigma_K] = 1 - q_2^K(h)\sigma_K$.

By construction, $B_k^{1,K} \leq \tilde{B}_k^{1,K}$, a.s., and $\tilde{B}_k^{2,K} \leq B_k^{2,K}$ a.s. for all $k \geq 1$ and these random variables satisfy (6.50) and (6.51). \square

6.5. *Controlling the time of the arrival of the first successful mutant.*

NOTATION. (a) For $i \in \{1, 2\}$, define

$$(6.61) \quad T_k^{K,i} \equiv \inf\{t \geq 0 : Z_k^{K,i}(\tau_k + t) = 0 \text{ or } Z_k^{K,i}(\tau_k + t) > \varepsilon\sigma_K K\}.$$

Obverse that $(T_k^{K,i})_{k \geq 1}$ are i.i.d. random variables that are independent of $A^{K,i}$.

(b) Define $I^K = k_1 \equiv \inf\{k \geq 1 : B_k^K = 1\}$ and $I^{K,i} \equiv \inf\{k \geq 1 : B_k^{K,i} = 1\}$. Then $I^{K,i}$ are independent of $A^{K,i}$, and we have

$$(6.62) \quad \mathbb{P}[\{I^{K,2} \preceq I^K \preceq I^{K,1}\} \cap \{\tau_{I^K} \leq \hat{\theta}^K\}] = \mathbb{P}[\tau_{I^K} \leq \hat{\theta}^K] - o(\sigma_K).$$

(c) Define $R_1^K \equiv Y_{\inf\{k \geq 1 : B_k^K = 1\}}^K$.

In fact, we prove at the end of this section that $\mathbb{P}[\tau_{I^K} \leq \hat{\theta}^K] = 1 - o(\sigma_K)$, that is, R_1^K is with high probability the random variable which gives the value of the next resident trait and τ_{I^K} , the first time where a successful mutant appears, is approximately exponential distributed as stated in lemma below. Note that this time is a random time, but not a stopping time.

LEMMA 6.7. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then*

$$(6.63) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} (\mathbb{P}[\tau_{I^K} \leq \hat{\theta}^K] - \mathbb{P}[\{E^{K,2} \preceq \tau_{I^K} \preceq E^{K,1}\} \cap \{\tau_{I^K} \leq \hat{\theta}^K\}]) = 0,$$

where $E^{K,1}$ and $E^{K,2}$ are exponential random variables with mean $a_1^K p_1^K \sigma_K u_K K$, respectively, $a_2^K p_2^K \sigma_K u_K K$.

With other words, we have $\mathbb{P}[E^{K,2} \preceq \tau_{I^K} \preceq E^{K,1} | \tau_{I^K} \leq \hat{\theta}^K] = 1 - o(\sigma_K)$, provided that $\liminf_{K \rightarrow \infty} \mathbb{P}[\tau_{I^K} \leq \hat{\theta}^K] > 0$.

PROOF. Let $A_t^{K,i}$ be defined as in Lemma 6.4 and observe that $\tau_{IK} = \inf\{t \geq 0 : L_t^K = I^K\}$. Then we obtain by construction,

$$(6.64) \quad \mathbb{P}[\{\inf\{t \geq 0 : A_t^{K,2} = I^{K,2}\} \preceq \tau_{IK} \preceq \inf\{t \geq 0 : A_t^{K,1} = I^{K,1}\}\} \cap \{\tau_{IK} \leq \hat{\theta}^K\}] = \mathbb{P}[\tau_{IK} \leq \hat{\theta}^K] - o(\sigma_K).$$

By definition, $I^{K,1}$ and $I^{K,2}$ are geometrically distributed with parameter $p_1^K \sigma_K$, resp. $p_2^K \sigma_K$. $A^{K,1}$ and $A^{K,2}$ are Poisson counting processes with parameter $a_1^K u_K K$, resp. $a_2^K u_K K$. Therefore, the times between each pair of successive events is exponential distributed with parameter $a_1^K u_K K$ resp. $a_2^K u_K K$. Since the random variables $I^{K,i}$ are independent of $A^{K,i}$ and the sum of a geometrically distributed number of independent exponentially distributed random variables is again exponentially distributed, we get that $\inf\{t \geq 0 : A_t^{K,1} = I^{K,1}\}$ and $\inf\{t \geq 0 : A_t^{K,2} = I^{K,2}\}$ are exponentially distributed with parameter $a_1^K u_K K p_1^K$, respectively, $a_2^K u_K K p_2^K$. \square

6.6. *No surprises happen before the successful mutant invades.* In the next lemma, we prove that a mutant invades with high probability before the resident population exits the neighborhood of this equilibrium, before too many different mutant traits are present and before a mutant of a mutant appears.

LEMMA 6.8. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then*

$$(6.65) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\theta_{\text{invasion}}^K \geq \theta_{\text{diversity}}^K \wedge \exp(K^\alpha) \wedge \theta_{\text{mut. of mut.}}^K] = 0.$$

PROOF. We start with proving the following:

$$(6.66) \quad \mathbb{P}[\theta_{\text{diversity}}^K < (K u_K \sigma_K^{1+\alpha})^{-1} \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{mut. of mut.}}^K] = o(\sigma_K).$$

Define

$$\hat{Z}_k^{K,2}(s) \equiv \begin{cases} 0, & \text{for } s < \inf\{t \geq 0 : A_t^{K,2} = k\}, \\ Z_k^{K,2}(\tau_k + s - \inf\{t \geq 0 : A_t^{K,2} = k\}), & \\ 0, & \text{for } s \geq \inf\{t \geq 0 : A_t^{K,2} = k\}. \end{cases}$$

By construction of $A^{K,2}$ and $\hat{Z}^{K,2}$, the left-hand side of (6.66) does not exceed

$$(6.67) \quad \mathbb{P}\left[\inf\left\{t \geq 0 : \sum_{k=1}^{A_t^{K,2}} \mathbb{1}_{\{1 \leq \hat{Z}_k^{K,2}(t) \leq \varepsilon \sigma_K K\}} \geq \left\lceil \frac{3}{\alpha} \right\rceil - 1\right\} < (K u_K \sigma_K^{1+\alpha})^{-1}\right] + o(\sigma_K).$$

Next, we compute an upper bound for the mutation events that happen before $(Ku_K \sigma_K^{1+\alpha})^{-1}$. Since $A^{K,2}$ is a Poisson counting process with parameter $a_2^K u_K K$, Chebychev’s inequality implies that

$$(6.68) \quad \mathbb{P}[A^{K,2}_{(Ku_K \sigma_K^{1+\alpha})^{-1}} \geq 2a_2^K \sigma_K^{-1-\alpha}] \leq \frac{\text{Var}(A^{K,2}_{(Ku_K \sigma_K^{1+\alpha})^{-1}})}{(2a_2^K \sigma_K^{-1-\alpha})^2} = \frac{1}{a_2^K \sigma_K^{-1-\alpha}}.$$

Next, we need an upper bound for the lifetimes of the mutant’s traits, $T_k^{K,2}$. First, observe that the probability that $Z_k^{K,2}$ goes extinct after it has reached the value $\lceil \varepsilon \sigma_K K \rceil$ converges to zero very fast. More precisely, Propositions A.3 and A.4(a) imply that

$$(6.69) \quad \begin{aligned} &\mathbb{P}[\inf\{t \geq 0 : Z_k^{K,2} = \lceil \varepsilon \sigma_K K \rceil\} < \inf\{t \geq \tau_k : Z_k^{K,2} = 0\} < \infty] \\ &= \mathbb{P}[\inf\{t \geq \tau_k : Z_k^{K,2} = 0\} < \infty] \\ &\quad - \mathbb{P}[\inf\{t \geq 0 : Z_k^{K,2} = \lceil \varepsilon \sigma_K K \rceil\} > \inf\{t \geq \tau_k : Z_k^{K,2} = 0\}] \\ &= o(\exp(-K^\alpha)). \end{aligned}$$

Note that, for each k , $Z_k^{K,2}$, conditioned on extinction, is a subcritical linear birth–death process (cf. [18]). Let $\check{Z}_k^{K,2}$ denote the conditioned process. If $Z_k^{K,2}$ is subcritical, then conditioning has no effect, otherwise the birth–death rates are exchanged. Denote by $\check{b}_k^{K,2}$ the birth rate and $\check{d}_k^{K,2}$ the death rate of $\check{Z}_k^{K,2}$. Then there exist uniform constants, $\check{C}_1 > 0$ and $\check{C}_2 > 0$, such that $\check{C}_1 \sigma_K \leq \check{d}_k^{K,2} - \check{b}_k^{K,2} \leq \check{C}_2 \sigma_K$, for all $k < I^{K,2}$. Thus, [2] page 109 entails, for all $k < I^{K,2}$,

$$(6.70) \quad \mathbb{P}[T_k^{K,2} \leq t] \geq \frac{\check{d}_k^{K,2} - e^{(\check{d}_k^{K,2} - \check{b}_k^{K,2})t} \check{d}_k^{K,2}}{\check{b}_k^{K,2} - e^{(\check{d}_k^{K,2} - \check{b}_k^{K,2})t} \check{d}_k^{K,2}} - o(\exp(-K^{-\alpha})).$$

The error term $o(\exp(-K^{-\alpha}))$ appears since $Z_k^{K,2}$, for $k < I^{K,2}$, is conditioned on extinction before reaching the value $\lceil \varepsilon \sigma_K K \rceil$ and not only on extinction. Choose $t = (\check{d}_k^{K,2} - \check{b}_k^{K,2})^{-1} \ln(K)$, Then

$$(6.71) \quad \begin{aligned} &\mathbb{P}[T_k^{K,2} \leq (\check{d}_k^{K,2} - \check{b}_k^{K,2})^{-1} \ln(K)] \\ &= \frac{\check{d}_k^{K,2} (1 - K)}{\check{b}_k^{K,2} (1 - K) - K(\check{d}_k^{K,2} - \check{b}_k^{K,2})} - o(\exp(-K^{-\alpha})) \\ &= 1 + \frac{\check{d}_k^{K,2} - \check{b}_k^{K,2}}{\check{b}_k^{K,2} (1 - K) - K(\check{d}_k^{K,2} - \check{b}_k^{K,2})} - o(\exp(-K^{-\alpha})) \\ &= 1 - O(\sigma_K K^{-1}) \end{aligned}$$

and hence

$$(6.72) \quad \mathbb{P}[\forall 1 \leq k < I^{K,2} : T_k^{K,2} \leq (\check{C}_1 \sigma_K)^{-1} \ln(K)] = 1 - o(\sigma_K).$$

Therefore, we can bound the first summand of (6.67) by $2a_2^K \sigma_K^{-1-\alpha}$ times the probability that more than $\lceil 3/\alpha \rceil - 1$ mutation events of $A^{K,2}$ take place in an interval of length $(\check{C}_1 \sigma_K)^{-1} \ln(K)$. More precisely, (6.67) is smaller than

$$(6.73) \quad 2a_2^K \sigma_K^{-1-\alpha} \mathbb{P}[A_{(\check{C}_1 \sigma_K)^{-1} \ln(K)}^{K,2} \geq \lceil 3/\alpha \rceil - 1] + o(\sigma_K).$$

Thus, for α small enough, the proof of (6.66) is concluded by the observation that

$$(6.74) \quad \begin{aligned} & \mathbb{P}[A_{(\check{C}_1 \sigma_K)^{-1} \ln(K)}^{K,2} \geq \lceil 3/\alpha \rceil - 1] \\ &= e^{-a_2^K u_K K (\check{C}_1 \sigma_K)^{-1} \ln(K)} \sum_{i=\lceil 3/\alpha \rceil - 1}^{\infty} \frac{(a_2^K u_K K (\check{C}_1 \sigma_K)^{-1} \ln(K))^i}{i!} \\ &\leq (a_2^K u_K K (\check{C}_1 \sigma_K)^{-1} \ln(K))^{\lceil 3/\alpha \rceil - 1} \\ &= o(\sigma_K^{3-\alpha}), \end{aligned}$$

where the last equality holds since $u_K K \sigma_K^{-1} \ln(K) \ll (\sigma_K)^\alpha$.

Next, we want to prove that

$$(6.75) \quad \mathbb{P}[\theta_{\text{mut. of mut.}}^K < (K u_K \sigma_K^{1+\alpha})^{-1} \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K] = o(\sigma_K).$$

Set, for all $\lambda \geq 0$,

$$(6.76) \quad G(\lambda) = \mathbb{E}\left[\exp\left(-\lambda \int_0^\infty Z_t dt\right) \middle| Z_0 = 1\right],$$

where $(Z_t, t \geq 0)$ is a linear birth–death process with individual birth rate b and individual death rate d . Applying the strong Markov property and the branching property at the first jump time of Z and using the facts that $G(\lambda)^2 = \mathbb{E}[\exp(-\lambda \int_0^\infty Z_t dt) | Z_0 = 2]$ and $\mathbb{E}[\exp(-\lambda \tau_{\text{first jump}}) | Z_0 = 1] = \frac{b+d}{b+d+\lambda}$, we obtain

$$(6.77) \quad bG(\lambda)^2 - (b + d + \lambda)G(\lambda) + d = 0.$$

Thus, since

$$(6.78) \quad \begin{aligned} \lim_{\lambda \downarrow 0} G(\lambda) &= \lim_{\lambda \downarrow 0} \mathbb{E}\left[\exp\left(-\lambda \int_0^\infty Z_t dt\right) \mathbb{1}_{\{\tau_{\text{extinction}} < \infty\}} \middle| Z_0 = 1\right] \\ &+ \lim_{\lambda \downarrow 0} \mathbb{E}\left[\exp\left(-\lambda \int_0^\infty Z_t dt\right) \mathbb{1}_{\{\tau_{\text{extinction}} = \infty\}} \middle| Z_0 = 1\right] \\ &= \mathbb{P}[\tau_{\text{extinction}} < \infty] + 0, \end{aligned}$$

which is 0 in the subcritical case and $1 - d/b$ in the super-critical case, it follows that

$$(6.79) \quad G(\lambda) = \frac{b + d + \lambda - \sqrt{(b + d + \lambda)^2 - 4bd}}{2b}.$$

Let $\tilde{Z}_k^{K,2}(t) \equiv Z_k^{K,2}(\tau_k + t)$, that is, a linear birth–death process with birth rate $b_k^{K,2}$ and death rate $d_k^{K,2}$. Observe that $\int_0^\infty \tilde{Z}_k^{K,2}(t) dt$ gives an upper bound for the sum of the lifetimes of all individuals with label k . Since the mutation rate of any individual in the population is smaller than $\bar{b}u_K$, the probability that a mutant appears, which was born from an unsuccessful mutant with label k , is bounded from above by

$$(6.80) \quad \begin{aligned} & 1 - \mathbb{E} \left[\exp \left(-u_K \bar{b} \int_0^\infty \tilde{Z}_k^{K,2}(t) dt \right) \middle| \tau_{\text{extinction}} < \inf \{ t \geq 0 : \tilde{Z}_k^{K,2}(t) > \varepsilon \sigma_K K \} \right] \\ & \leq 1 - \mathbb{E} \left[\exp \left(-u_K \bar{b} \int_0^\infty \tilde{Z}_k^{K,2}(t) dt \right) \middle| \tau_{\text{extinction}} < \infty \right] + o(\exp(-K^\alpha)). \end{aligned}$$

Since $\tilde{Z}_k^{K,2}(t)$, conditioned on extinction, is a subcritical linear birth–death process, the right-hand side of (6.80) is equal to $1 - G_{\mathbb{E}[\tilde{Z}_k^{K,2} | \tau_{\text{extinction}} < \infty]}(u_K \bar{b}) + o(\exp(-K^\alpha))$ and

$$\begin{aligned} & G_{\mathbb{E}[\tilde{Z}_k^{K,2} | \tau_{\text{extinction}} < \infty]}(u_K \bar{b}) \\ & = \begin{cases} \frac{b_k^{K,2} + d_k^{K,2} + u_K \bar{b} - \sqrt{(b_k^{K,2} + d_k^{K,2} + u_K \bar{b})^2 - 4b_k^{K,2} d_k^{K,2}}}{2b_k^{K,2}}, & \text{if } d_k^{K,2} > b_k^{K,2}, \\ \frac{d_k^{K,2} + b_k^{K,2} + u_K \bar{b} - \sqrt{(d_k^{K,2} + b_k^{K,2} + u_K \bar{b})^2 - 4d_k^{K,2} b_k^{K,2}}}{2d_k^{K,2}}, & \text{if } b_k^{K,2} > d_k^{K,2} \end{cases} \\ & = \begin{cases} \frac{2b_k^{K,2} + u_K \bar{b} - O(u_K \sigma_K^{-1})}{2b_k^{K,2}}, & \text{if } d_k^{K,2} > b_k^{K,2}, \\ \frac{2d_k^{K,2} + u_K \bar{b} - O(u_K \sigma_K^{-1})}{2d_k^{K,2}}, & \text{if } b_k^{K,2} > d_k^{K,2} \end{cases} \\ & = 1 - O(u_K \sigma_K^{-1}) = 1 - o(\sigma_k^{2+\alpha} K^{-2\alpha}). \end{aligned}$$

Note that we used for the second equality that $|b_k^{K,2} - d_k^{K,2}| = \xi \sigma_K$ for some $\xi > 0$. By (6.68), the total number of unsuccessful mutations until $(Ku_K \sigma_K^{1+\alpha})^{-1} \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K$ is with probability $1 - o(\sigma_K)$ smaller or equal $2d_2^K \sigma_K^{-1-\alpha}$. Therefore, we finally obtain that the probability to have one mutant of an unsuccessful mutant during that time is $o(\sigma_K)$. On the other hand, let P_t^K be a Poisson

counting process with parameter $\bar{b}u_K \varepsilon \sigma_K K$ and $(\tilde{Z}_t^{K,1}, t \geq 0)$ a linear birth–death process with initial state 1 and birth rate $b^{K,1}(Y_{I_K}^K)$ and death rate $d^{K,1}(Y_{I_K}^K)$, then the probability to have one mutant of the successful mutant until the time $(Ku_K \sigma_K^{1+\alpha})^{-1} \wedge \theta_{\text{invasion}}^K \wedge \theta_{\text{diversity}}^K$ is bounded from above by

$$\begin{aligned}
 & \mathbb{P}[P_{\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}}}^K \neq 0 | \tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} < \tau_0^{\tilde{Z}^{K,1}}] + o(\sigma_K) \\
 (6.81) \quad &= \mathbb{E}[\mathbb{1}_{\{P_{\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}}}^K \neq 0\}} (\mathbb{1}_{\{\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} \leq t_K\}} + \mathbb{1}_{\{\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} > t_K\}}) | \tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} < \tau_0^{\tilde{Z}^{K,1}}] + o(\sigma_K) \\
 &\leq (1 - \exp(-\bar{b}u_K \varepsilon \sigma_K K t_K)) + \mathbb{P}[\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} > t_K | \tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} < \tau_0^{\tilde{Z}^{K,1}}] + o(\sigma_K),
 \end{aligned}$$

for each t_K , because the mutation rate per individual is bounded by $\bar{b}u_K$ and there are at most $\varepsilon \sigma_K K$ successful mutant individuals alive until $\theta_{\text{invasion}}^K$. If we choose $t_K = \ln(K) \sigma_K^{-1-\alpha/2}$, then by Proposition A.4, all terms in the last line of (6.81) are $o(\sigma_K)$. This implies (6.75).

Note that we have $\theta_{\text{invasion}}^K = \tau_{I_K} + \inf\{t \geq 0 : \mathfrak{M}^{I_K}(\tilde{v}_{\tau_{I_K}+t}) > \varepsilon \sigma_K K\}$. Let $E^{K,1}$ be an exponential distributed random variable with mean $a_1^K p_1^K \sigma_K u_K K$. Then

$$\begin{aligned}
 (6.82) \quad & \mathbb{P}[\tau_{I_K} + \inf\{t \geq 0 : \mathfrak{M}^{I_K}(\tilde{v}_{\tau_{I_K}+t}) > \varepsilon \sigma_K K\} \geq \theta_{\text{diversity}}^K \wedge e^{K\alpha} \wedge \theta_{\text{mut. of mut.}}^K] \\
 &\geq \mathbb{P}[E^{K,1} + T_{I_K}^{K,1} \geq (Ku_K \sigma_K^{1+\alpha})^{-1}] - o(\sigma_K).
 \end{aligned}$$

Let $\tilde{Z}^{K,1}$ as defined before, then again by Proposition A.4,

$$\begin{aligned}
 (6.83) \quad & \mathbb{P}[T_{I_K}^{K,1} > \ln(K) \sigma_K^{-1-\alpha/2}] = \mathbb{P}[\tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} > \ln(K) \sigma_K^{-1-\alpha/2} | \tau_{\varepsilon \sigma_K K}^{\tilde{Z}^{K,1}} < \tau_0^{\tilde{Z}^{K,1}}] \\
 &= o(\sigma_K).
 \end{aligned}$$

Since $\ln(K) \sigma_K^{-1-\alpha/2} \ll (Ku_K \sigma_K^{1+\alpha})^{-1}$, the Markov inequality for the function $f(x) = x^n$, where n is smallest even number which is larger than $2/\alpha$, yields

$$\begin{aligned}
 (6.84) \quad & \mathbb{P}[E^{K,1} + T_{I_K} > (Ku_K \sigma_K^{1+\alpha})^{-1}] \\
 &\leq \mathbb{P}[E^{K,1} > (2Ku_K \sigma_K^{1+\alpha})^{-1}] + o(\sigma_K) \\
 &\leq \frac{(2Ku_K \sigma_K^{1+\alpha})^n n!}{(a_1^K p_1^K u_K K \sigma_K)^n} = O(\sigma_K^2). \quad \square
 \end{aligned}$$

The following lemma shows that there are no two successful mutants during the first phase of an invasion.

LEMMA 6.9. Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\text{there is a successful mutation in time interval } [\tau_{I_K}, \theta_{\text{invasion}}^K]] = 0.$$

PROOF. Let $P_{\text{succ. mut.}}^K(t)$ the process which recodes the number of successful mutants born after τ_{I^K} until $\tau_{I^K} + t$. Then

$$(6.85) \quad \mathbb{P}[\text{for all } t \geq 0 \text{ such that } \tau_{I^K} + t < \hat{\theta}^K : P_{\text{succ. mut.}}^K(t) \leq P_t^K] = 1 - o(\sigma_K),$$

where P_t^K is Poisson process with parameter $a_2^K p_2^K \sigma_K u_K K$. Define $Z_{I^K}^{K,2}(t)$ as in Lemma 6.5. Then $\mathbb{P}[\forall t \leq \hat{\theta}^K : \mathfrak{M}^{I^K}(\tilde{v}_t) \leq Z_{I^K}^{K,2}(t)] \geq 1 - o(\sigma_K)$. Note that P_t^K and $Z^{K,2}$ are independent by construction. Therefore, as in the last lemma, or each t_K ,

$$(6.86) \quad \begin{aligned} & \mathbb{P}[\text{there is a successful mutation in } [\tau_{I^K}, \theta_{\text{invasion}}^K]] \\ & \leq \mathbb{P}[P_{\tau_{\varepsilon\sigma_K K}^{Z^{K,2}}}^K \neq 0 | \tau_{\varepsilon\sigma_K K}^{Z^{K,2}} < \tau_0^{Z^{K,2}}] + o(\sigma_K) \\ & \leq (1 - \exp(-a_2^K p_2^K \sigma_K u_K K t_K)) + \mathbb{P}[\tau_{\varepsilon\sigma_K K}^{Z^{K,2}} > t_K | \tau_{\varepsilon\sigma_K K}^{Z^{K,2}} < \tau_0^{Z^{K,2}}] \\ & \quad + o(\sigma_K). \end{aligned}$$

With $t_K = \ln(K)\sigma_K^{-1-\alpha/2}$, by Proposition A.4, all terms in the last line of (6.86) are $o(\sigma_K)$. \square

6.7. *Finishing up: Control of the distribution of the next resident trait.*

COROLLARY 6.10. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 6.2 hold and let M be the constant of Lemma 6.3. Then there exist two \mathcal{X} -valued random variables $R_1^{K,1}$ and $R_1^{K,2}$ with distribution*

$$(6.87) \quad \begin{aligned} & \mathbb{P}[R_1^{K,1} = R^K + \sigma_K h] \\ & = \begin{cases} \frac{M(R^K, 1)q_1^K(1)}{p_2^K} + 1 - \frac{p_1^K}{p_2^K}, & \text{if } h = 1, \\ \frac{M(R^K, h)q_1^K(h)}{p_2^K}, & \text{if } h \in \{2, \dots, A\}, \end{cases} \end{aligned}$$

and

$$(6.88) \quad \begin{aligned} & \mathbb{P}[R_1^{K,2} = R^K + \sigma_K h] \\ & = \begin{cases} \frac{M(R^K, h)q_1^K(h)}{p_2^K}, & \text{if } h \in \{1, \dots, A - 1\}, \\ \frac{M(R^K, A)q_1^K(A)}{p_2^K} + 1 - \frac{p_1^K}{p_2^K}, & \text{if } h = A, \end{cases} \end{aligned}$$

such that

$$(6.89) \quad \begin{aligned} & \lim_{K \rightarrow \infty} \sigma_K^{-1} (1 - \mathbb{P}[R_1^{K,1} \leq R_1^K \leq R_1^{K,2} | \theta_{\text{invasion}}^K < \theta_{\text{diversity}}^K \wedge \theta_{\text{mut. of mut.}}^K \wedge e^{K^\alpha}]) \\ & = 0. \end{aligned}$$

PROOF. Define

$$R_1^{K,1} \equiv \begin{cases} Y_{I^K}^K, & \text{if } I^{K,1} = I^{K,2}, \\ R^K + \sigma_K, & \text{otherwise,} \end{cases}$$

and

$$R_1^{K,2} \equiv \begin{cases} Y_{I^K}^K, & \text{if } I^{K,1} = I^{K,2}, \\ R^K + A\sigma_K, & \text{otherwise.} \end{cases}$$

By construction of $B_k^{K,i}$ and $Y_k^{K,i}$, we have that (6.89) holds. Next, we compute

$$\begin{aligned} & \mathbb{P}[Y_{I^K,2}^K = R^K + \sigma_K h, I^{K,1} = I^{K,2}] \\ (6.90) \quad &= \mathbb{P}[Y_1^K = R^K + \sigma_K h, B_1^{K,1} = 1 | B_1^{K,2} = 1] \\ &= \frac{\mathbb{P}[Y_1^K = R^K + \sigma_K h, B_1^{K,1} = 1]}{\mathbb{P}[B_1^{K,2} = 1]} \\ &= \frac{M(R^K, h)q_1^K(h)}{p_2^K} \end{aligned}$$

and $\mathbb{P}[I^{K,1} \neq I^{K,2}] = 1 - \sum_{h=1}^A \frac{M(R^K, h)q_1^K(h)}{p_2^K} = 1 - p_1^K/p_2^K$. Since $\mathbb{P}[R_1^{K,1} = R^K + \sigma_K h] = \mathbb{P}[Y_{I^K,2}^K = R^K + \sigma_K h, I^{K,1} = I^{K,2}] + \mathbb{1}_{\{h=1\}}\mathbb{P}[I^{K,1} \neq I^{K,2}]$ and similarly for $R_1^{K,2}$, we deduce (6.87) and (6.89). \square

7. The second phase of an invasion. Theorem 7.1 below describes precisely how the invading mutant replaces the resident population. This section is the central piece of the entire paper.

NOTATION. Let us denote

$$\theta_{\text{fixation}}^K = \inf\{t \geq \theta_{\text{invasion}}^K : |\text{Supp}(\tilde{v}_t^K)| = 1 \text{ and } |\langle \tilde{v}_t, \mathbb{1} \rangle - \bar{z}(R_1^K)| < (M/3)\varepsilon\sigma_K\}$$

that is, the first time after $\theta_{\text{invasion}}^K$ such that the population is monomorphic and in the $(M/3)\varepsilon\sigma_K$ -neighborhood of the corresponding equilibrium.

THEOREM 7.1. Fix $\varepsilon > 0$. Under the Assumptions 1, 3 and 4, there exists a constant, $M > 0$, such that, for all K large enough:

- (i) $\tilde{v}_0^K = N_{R^K}^K K^{-1} \delta_{(0, R^K)}$, where $|\bar{z}(R^K) - N_{R^K}^K K^{-1}| < (M/3)\varepsilon\sigma_K$ a.s.
- (ii) At the first time of invasion, $\theta_{\text{invasion}}^K$, the resident density is in an $\varepsilon M \sigma_K$ -neighborhood of $\bar{z}(R^K)$, the number of different living mutant traits is bounded by $\lceil \alpha/3 \rceil$ and there is no mutant of a mutant, with probability $1 - o(\sigma_K)$. (cf. Theorem 6.2).

(iii) The time between $\theta_{\text{invasion}}^K$ and $\theta_{\text{fixation}}^K$ is smaller than $5 \ln(K) \sigma_K^{-1-\alpha/2}$, with probability $1 - o(\sigma_K)$.

(iv) The trait of the population at time $\theta_{\text{fixation}}^K$ is the trait of the mutant whose density was larger than $\varepsilon \sigma_K$ at time $\theta_{\text{invasion}}^K$, that is, $\text{Supp}(\tilde{\nu}_{\theta_{\text{fixation}}^K}^K) = (I^K, R_1^K)$, with probability $1 - o(\sigma_K)$. The distribution of R_1^K can be approximated as in Corollary 6.10.

Moreover, until time $\theta_{\text{fixation}}^K$, the total mass of the population stays in the $O(\sigma_K)$ -neighborhood of $\bar{z}(R^K)$, the number of different living mutant traits is bounded by $\lceil \alpha/3 \rceil$, and there is no second successful mutant, with probability $1 - o(\sigma_K)$.

To prove this theorem, we divide this phase into five steps, as illustrated in Figure 2.

Step 1. From $\theta_{\text{invasion}}^K$ to $\theta_{\text{mut. size } \varepsilon}^K$, the first time when a mutant’s density reaches the value ε . During this period, we approximate the mutant density by a continuous time branching process, which is super-critical (of order σ_K). Thus, we obtain that $\theta_{\text{mut. size } \varepsilon}^K - \theta_{\text{invasion}}^K$ is of order $(\ln(K) \sigma_K^{-1})$.

Step 2. From $\theta_{\text{mut. size } \varepsilon}^K$ to $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K$, the first time when the mutant density reaches a value $C_{\text{cross}}^\varepsilon$ [defined in equation (7.1) below]. This step can be seen as the “stochastic Euler scheme.” The idea is that the total mass of the population stays close to a function which depends only on the density of the successful mutant. This allows to approximate the number of mutants by a discrete time Markov chain until the mutant density has increased by ε . Furthermore, we control the number of jumps needed to increase by ε and use upper and lower bounds for one jump time

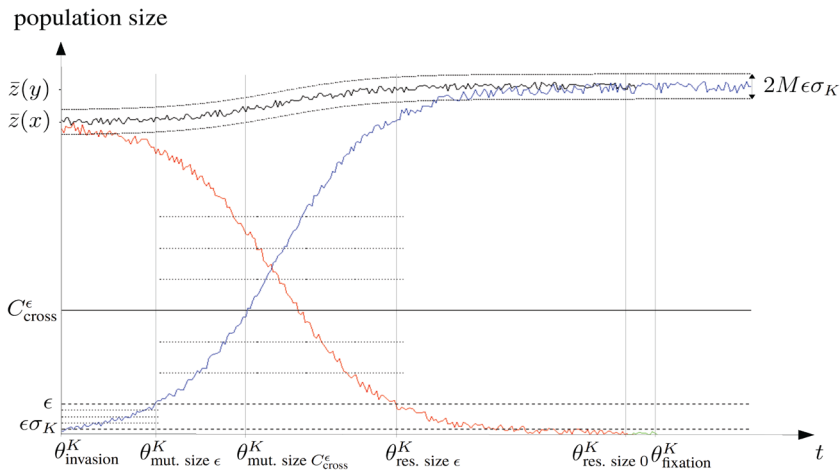


FIG. 2. Evolution of the population after the density of the successful mutant has reached the value $\varepsilon \sigma_K$.

of the associated continuous time process to control the time of this step. Then we recompute the parameters and start again. Iterating, we obtain that $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K - \theta_{\text{mut. size } \varepsilon}^K$ is also of order $\ln(K)\sigma_K^{-1}$.

Step 3. From $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K$ until $\theta_{\text{res. size } \varepsilon}^K$, the first time when the density of the resident trait R^K decreases to the value ε . The proof is very similar to the proof of Step 2, the only difference is that we approximate the number of resident individuals by a discrete Markov chain, which decreases slowly.

Step 4. From $\theta_{\text{res. size } \varepsilon}^K$ until $\theta_{\text{res. size } 0}^K$, the first time when the resident trait R^K goes extinct. We approximate the dynamics of the resident trait by a continuous time branching process which is subcritical (of order σ_K) and, therefore, goes extinct, a.s., after a time of order $\ln(K)\sigma_K^{-1}$.

Step 5. From $\theta_{\text{res. size } 0}^K$ until $\theta_{\text{fixation}}^K$, even if it is unlikely that this time period is larger than 0, we have to obtain an upper bound for this time.

NOTATION. Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 7.1 hold. Set

$$(7.1) \quad C_{\text{cross}}^\varepsilon \equiv \left\lceil \left(\inf_{x \in \mathcal{X}} \frac{b(x) - d(x)}{c(x, x)} \right) \varepsilon^{-1} \right\rceil \frac{\varepsilon}{2}, \quad \text{and}$$

$$(7.2) \quad \theta_{2 \text{ succ. mut.}}^K \equiv \inf \left\{ t \geq 0 : \sum_{k=0}^\infty \mathbb{1}_{\mathfrak{M}^k(\tilde{v}_t) \geq \varepsilon \sigma_K K} \geq 3 \right\}.$$

Moreover, for any $\xi \geq 0$,

$$(7.3) \quad \theta_{\text{mut. size } \xi}^K \equiv \inf \{ t \geq 0 : \exists k \geq 1 : \mathfrak{M}^k(\tilde{v}_t) = \lceil \xi K \rceil \},$$

$$(7.4) \quad \theta_{\text{res. size } \xi}^K \equiv \inf \{ t \geq 0 : \mathfrak{M}^0(\tilde{v}_t) = \lceil \xi K \rceil \},$$

and let S_K be a sequence in K such that $1 \ll S_K \ll \varepsilon \sigma_K^{-1}$.

REMARK 6. Using similar arguments as in the proofs of Lemmas 6.3, 6.8 and 6.9, we obtain

$$(7.5) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\theta_{\text{invasion}}^K + 5\sigma_K^{-1-\alpha/2} \ln(K) > \theta_{\text{diversity}}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge e^{K^\alpha}] = 0.$$

More precisely, until the time $\theta_{\text{diversity}}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \exp(K^\alpha)$ the total mass of the population stays with high probability in the $O(\sigma_K)$ neighborhood of $\bar{z}(R^K)$. This can be proved similarly as Lemmas 6.3 or 7.2. Since we have only an approximation of order σ_K (not $\varepsilon \sigma_K$), we have less precise bounds for the rates of the mutants and for their success probability. Nevertheless, we can bound the mutant subpopulations from above by linear branching processes which are slightly super-critical of order σ_K .

7.1. *Step 1: A mutant’s density reaches the value ε .* The following lemma shows that the total mass stays from the beginning (including the first phase) until $\theta_{\text{mut. size } \varepsilon}^K$ in the $M\varepsilon\sigma_K$ neighborhood of $\bar{z}(x)$.

LEMMA 7.2. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that*

$$(7.6) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\inf\{t \geq 0 : |\langle \tilde{v}_t, \mathbb{1} \rangle - \bar{z}(R^K)| > M\varepsilon\sigma_K\} < \theta_{\text{mut. size } \varepsilon}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \wedge \exp(K^\alpha)] = 0.$$

PROOF. The proof of this lemma is very similar to the one of Lemma 6.3, therefore, we omit some details. Define

$$(7.7) \quad X_t \equiv |\langle \tilde{v}_t, \mathbb{1} \rangle K - \lceil K\bar{z}(R^K) \rceil.$$

We associate with the continuous time process X_t a discrete time (non-Markov) process Y_n which records the sequence of values that X_t takes on.

CLAIM. *For $1 \leq i \leq \varepsilon K$ and K large enough,*

$$(7.8) \quad \mathbb{P}[Y_{n+1} = i + 1 | Y_n = i, T_{n+1} < \theta_{\text{mut. size } \varepsilon}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K] \leq \frac{1}{2} - (\underline{c}/4\bar{b})K^{-1}i + (2C_L^{b,d,c}A/\underline{b})\varepsilon\sigma_K \equiv p_+^K(i),$$

where $C_L^{b,d,c}$ is the sum of the Lipschitz constants for the birth, death and competition rate.

This can be proven exactly as in Lemma 6.3, using the facts that $b(R^K) = d(R^K) + c(R^K, R^K)\bar{z}(R^K)$ and that all mutant traits are at a distance of at most $2A\sigma_K$ from R^K , and hence, $|b(x) - b(R^K)| < C_L^b\sigma_K 2A$, $|d(x) - d(R^K)| < C_L^d\sigma_K 2A$ and $|c(x, y) - c(R^K, R^K)| < C_L^c\sigma_K 2A$ for all traits x and y alive in the population. By continuing as in Lemma 6.3, we obtain (7.6). \square

Next, we prove that $\theta_{\text{invasion}}^K - \theta_{\text{mut. size } \varepsilon}^K$ is smaller than $\ln(K)\sigma_K^{-1-\alpha/2}$. We use the following notation.

NOTATION.

$$\tilde{\theta}^K \equiv \inf\{t \geq 0 : |\langle \tilde{v}_t, \mathbb{1} \rangle - \bar{z}(R^K)| > M\varepsilon\sigma_K\} \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K.$$

LEMMA 7.3. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 7.1 hold. Let M be the constant from Lemma 7.2. Then*

$$(7.9) \quad \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\theta_{\text{mut. size } \varepsilon}^K > (\theta_{\text{invasion}}^K + \ln(K)\sigma_K^{-1-\alpha/2}) \wedge \tilde{\theta}^K] = 0.$$

PROOF. To prove this lemma, we use a coupling with a linear continuous time birth–death process. From the results on Phase 1 and Lemma 7.3, we know that $\theta_{\text{invasion}}^K$ is, with probability $1 - o(\sigma_K)$, smaller than $\tilde{\theta}^K$. Recall $I^K \equiv k_1$, the label of the first successful mutation [see (6.4)]. For any $t \in (\theta_{\text{invasion}}^K, \tilde{\theta}^K]$, any individual of $\mathfrak{M}^{k_1}(\tilde{\nu}_t)$ gives birth to a new individual with the same trait, R_1^K , with rate

$$(7.10) \quad (1 - u_K m(R_1^K))b(R_1^K) \in [b(R_1^K) - u_K \bar{b}, b(R_1^K)],$$

and dies with rate

$$(7.11) \quad d(R_1^K) + \int_{\mathcal{X} \times \mathbb{N}_0} c(R_1^K, \xi) d\tilde{\nu}_t(\xi),$$

which is smaller than $d_Z \equiv d(R_1^K) + c(R_1^K, R^K)(\bar{z}(R^K) + M\varepsilon\sigma_K) + \bar{c}(\varepsilon + \lceil 3/\alpha \rceil \sigma_K)A\sigma_K$. Similarly as in Lemma 6.5 we construct, by using a standard coupling argument, a processes Z_t such that

$$(7.12) \quad Z_t \leq \mathfrak{M}^{k_1}(\tilde{\nu}_{\theta_{\text{invasion}}^K + t})$$

for all t such that $\theta_{\text{invasion}}^K + t \leq \tilde{\theta}^K \wedge \inf\{t \geq 0 : \mathfrak{M}^{k_1}(\tilde{\nu}_t) \geq \varepsilon K\}$. The processes Z_t is a branching process starting at $\lceil \varepsilon\sigma_K K \rceil$, with birth rate per individual $b_Z = b(R_1^K) - \bar{b}u_K$ and with death rate per individual d_Z . For all $\varepsilon < \inf_{x \in \mathcal{X}} \frac{\partial_1 f(x, x)}{2(M+A+1)}$, we have

$$(7.13) \quad \begin{aligned} b_Z - d_Z &\geq f(R_1^K, R^K) - \bar{c}\sigma_K(M\varepsilon + A(\varepsilon + \lceil 3/\alpha \rceil \sigma_K)) \\ &\geq \sigma_K \inf_{x \in \mathcal{X}} \frac{\partial_1 f(x, x)}{2}. \end{aligned}$$

Thus, Z_t is super-critical of order σ_K . Let τ_i^Z be the first hitting time of level i by Z_t , then by Proposition A.4

$$(7.14) \quad \mathbb{P}[\tau_{\lceil \varepsilon K \rceil}^Z > \tau_0^Z] \leq \exp(-K^\alpha).$$

Furthermore, we have the following exponential tail bound (see [1] page 41):

$$(7.15) \quad \begin{aligned} &\mathbb{P}[\tau_{\lceil \varepsilon K \rceil}^Z \geq \ln(K)\sigma_K^{-1-\alpha/2} | \tau_{\lceil \varepsilon K \rceil}^Z < \tau_0^Z] \\ &\leq \exp\left(-\left\lfloor \frac{\ln(K)\sigma_K^{-1-\alpha/2}}{e \max_{n \leq \lceil \varepsilon K \rceil} \mathbb{E}_n[\tau_{\lceil \varepsilon K \rceil}^Z | \tau_{\lceil \varepsilon K \rceil}^Z < \tau_0^Z]} \right\rfloor\right), \end{aligned}$$

and $\max_{n \leq \lceil \varepsilon K \rceil} \mathbb{E}_n[\tau_{\lceil \varepsilon K \rceil}^Z | \tau_{\lceil \varepsilon K \rceil}^Z < \tau_0^Z] \leq O(\ln(K)\sigma_K)$ (compare with Proposition A.3). Therefore,

$$(7.16) \quad \mathbb{P}[\tau_{\lceil \varepsilon K \rceil}^Z < \ln(K)\sigma_K^{-1-\alpha/2}] \geq (1 - e^{-\sigma_K^{-\alpha/3}})(1 - e^{-K^\alpha}) = 1 - o(\sigma_K),$$

which implies the claim. \square

7.2. *Step 2: The mutant density reaches a value $C_{\text{cross}}^\varepsilon$ (stochastic Euler scheme).* Recall that the trait of the successful mutant is $R^K + \sigma_K h$ where $h \in \{1, \dots, A\}$. Due to the regularity assumptions (iv) in Assumption 1, we have the following estimates:

$$\begin{aligned}
 b(R^K + \sigma_K h) &= b(R^K) + b'(R^K)\sigma_K h + O((\sigma_K h)^2), \\
 d(R^K + \sigma_K h) &= d(R^K) + d'(R^K)\sigma_K h + O((\sigma_K h)^2), \\
 r(R^K + \sigma_K h) &= r(R^K) + r'(R^K)\sigma_K h + O((\sigma_K h)^2), \\
 (7.17) \quad c(R^K + \sigma_K h, R^K) &= c(R^K, R^K) + \partial_1 c(R^K, R^K)\sigma_K h + O((\sigma_K h)^2), \\
 c(R^K, R^K + \sigma_K h) &= c(R^K, R^K) + \partial_2 c(R^K, R^K)\sigma_K h + O((\sigma_K h)^2), \\
 c(R^K + \sigma_K h, R^K + \sigma_K h) &= c(R^K, R^K) + (\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K))\sigma_K h \\
 &\quad + O((\sigma_K h)^2).
 \end{aligned}$$

The deterministic system. Although we cannot use a law of large numbers, to understand the behavior of the stochastic system it is useful to look at the properties of the corresponding deterministic Lotka–Volterra system. The limiting system when $K \rightarrow \infty$, with $\sigma_K = 0$, takes the simple form

$$(7.18) \quad \frac{dm_t^0}{dt} = m_t^0(r(R^K) - c(R^K, R^K)(m_t^0 + m_t^{k_1})),$$

$$(7.19) \quad \frac{dm_t^{k_1}}{dt} = m_t^{k_1}(r(R^K) - c(R^K, R^K)(m_t^0 + m_t^{k_1})).$$

The corresponding vector field is depicted in Figure 3. This system has an invariant manifold made of fixed points given by the roots of the equation

$$(7.20) \quad m^0 + m^{k_1} = r(R^K)/c(R^K, R^K) = \bar{z}(R^K),$$

with $m^0, m^{k_1} \geq 0$. This manifold connects the fixed points of the monomorphic equations, $(\bar{z}(R^K), 0)$ and $(0, \bar{z}(R^K))$. Note that $\bar{z}(R^K)$ has the interpretation of the total mass of the population in equilibrium. A simple computation shows that the Hessian matrix on the invariant manifold is given by

$$(7.21) \quad H(m^0, m^{k_1}) = -c(R^K, R^K) \begin{pmatrix} m^0 & m^0 \\ m^{k_1} & m^{k_1} \end{pmatrix}.$$

The corresponding eigenvectors are $(1, -1)$ with eigenvalue 0, and $(m^0, \bar{z}(R^K) - m^0)$ with eigenvalue $-c(R^K, R^K)\bar{z}(R^K)$.

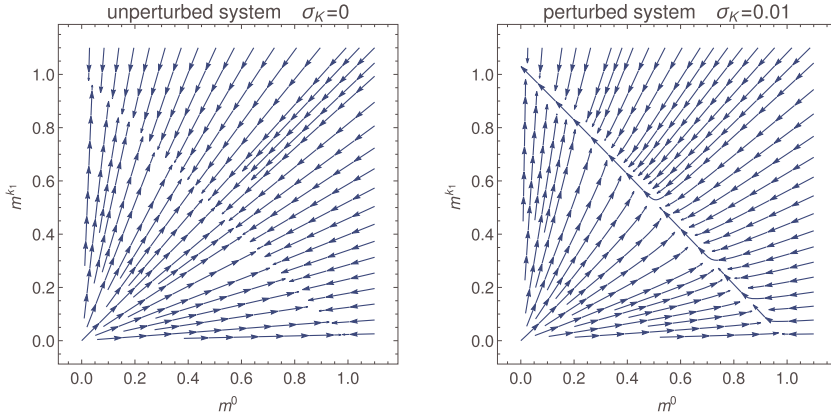


FIG. 3. Right: Vector field of the unperturbed system ($\sigma_K = 0$), Left: Vector field of the perturbed system ($\sigma_K = 0.01$). Parameters are given in Table 1.

It follows that the perturbed system

$$(7.22) \quad \frac{dm_t^0}{dt} = m_t^0(r(R^K) - c(R^K, R^K)m_t^0 - c(R^K, R^K + \sigma_K h)m_t^{k_1}),$$

$$(7.23) \quad \frac{dm_t^{k_1}}{dt} = m_t^{k_1}(r(R^K + \sigma_K h) - c(R^K + \sigma_K h, R^K)m_t^0 - c(R^K + \sigma_K h, R^K + \sigma_K h)m_t^{k_1}),$$

has an invariant manifold connecting its fixed points $(\bar{z}(R^K), 0)$ and $(0, \bar{z}(R^K + \sigma_K h))$, where $\bar{z}(R^K + \sigma_K h) = r(R^K + \sigma_K h)/c(R^K + \sigma_K h, R^K + \sigma_K h)$ in a σ_K -neighborhood of the unperturbed invariant manifold (see Figure 3). Thus, the perturbed deterministic system will move quickly toward a small neighborhood of this invariant manifold and then move slowly with speed $O(\sigma_K)$ along it. Since the invariant manifold is close to the curve $m^0 + m^{k_1} = \bar{z}(R^K)$, it is reasonable to choose as variables $M_t = m_t^0 + m_t^{k_1}$. The motion of the system will then be close to the curve $\tilde{\phi}(m_t^{k_1})$ defined by the condition that the derivative of M_t vanishes for $M_t = \tilde{\phi}(m_t^{k_1})$.

TABLE 1
Parameters of the Figures 3

$b(R^K) = 2$	$d(R^K) = 1$	$c(R^K, R^K) = 1$	$c(R^K, R^K + \sigma_K h) = 1 - 2\sigma_K$
$b(R^K + \sigma_K h) = 2 + \sigma_K$	$d(R^K + \sigma_K h) = 1 - \sigma_K$	$c(R^K + \sigma_K h, R^K) = 1 - 2\sigma_K$	$c(R^K + \sigma_K h, R^K + \sigma_K h) = 1 - \sigma_K$

Since

$$\begin{aligned}
 \frac{dM_t}{dt} &= M_t(r(R^K) - c(R^K, R^K)M_t) \\
 (7.24) \quad &- [(\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K))M_t - r'(R^K)]\sigma_K h m_t^{k_1} \\
 &+ O(\sigma_K^2).
 \end{aligned}$$

Setting the right-hand side to zero yields the leading orders in σ_K

$$\begin{aligned}
 \tilde{\phi}(m_t^{k_1}) &= \bar{z}(R^K) + \sigma_K h m_t^{k_1} \left(\frac{r'(R^K)}{r(R^K)} - \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{c(R^K, R^K)} \right) \\
 (7.25) \quad &+ O(\sigma_K^2).
 \end{aligned}$$

We expect that the stochastic system also evolves along this curve, that is, we will show that m^{k_1} increases while the total mass stays close to the curve defined in (7.25).

Define the function

$$(7.26) \quad \phi(y) \equiv \bar{z}(R^K) + \sigma_K h y \left(\frac{r'(R^K)}{r(R^K)} - \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{c(R^K, R^K)} \right),$$

and the stopping time

$$(7.27) \quad \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K \equiv \inf \{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \phi(i(\varepsilon/2))| < (M/3)\varepsilon\sigma_K \}.$$

The dependence of ϕ with respect to the mutant density allows us to decompose the increase of the mutant density into successive steps during which the total mass does not move more than $M\varepsilon\sigma_K$.

LEMMA 7.4. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε, K and i) such that and for all $2 \leq i \leq 2\varepsilon^{-1}C_{\text{cross}}^\varepsilon$:*

(a) *Soon after $\theta_{\text{mut. size } i(\varepsilon/2)}^K$, the total population size is close to $\phi(i \frac{\varepsilon}{2})$:*

$$\begin{aligned}
 \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K > (\theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K) \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\
 \left. \wedge \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \exists k \geq 1 : \mathfrak{N}^k(\tilde{v}_t) = \left[\left(i \pm \frac{1}{2} \right) (\varepsilon/2) K \right] \right\} \right] = 0.
 \end{aligned}$$

(b) *A change of order ε for the mutant density takes more than $o(\sigma_K^{-1})$ time:*

$$\begin{aligned}
 \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \exists k \geq 1 : \mathfrak{N}^k(\tilde{v}_t) = \left[\left(i \pm \frac{1}{2} \right) (\varepsilon/2) K \right] \right\} \right. \\
 \left. < (\theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K) \wedge \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] = 0.
 \end{aligned}$$

(c) *At the time when the mutant density has changed of order ε the total population size is still close to $\phi(i \frac{\varepsilon}{2})$:*

$$\begin{aligned} & \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi \left(i \frac{\varepsilon}{2} \right) \right| > M \varepsilon \sigma_K \right\} \right. \\ & \quad < \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \\ & \quad \left. \wedge \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \exists k \geq 1 : \mathfrak{M}^k(\tilde{v}_t) = \lceil (i \pm 1)(\varepsilon/2)K \rceil \right\} \right] = 0. \end{aligned}$$

(d) *A change of order ε for the mutant density takes no more than $(i\sigma_K)^{-1-\alpha/2}$ time:*

$$\begin{aligned} & \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{mut. size } (i+1)(\varepsilon/2)}^K > (\theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K + (i\sigma_K)^{-1-\alpha/2}) \wedge \theta_{2 \text{ succ. mut.}}^K \right. \\ & \quad \left. \wedge \theta_{\text{diversity}}^K \wedge \inf \left\{ t \geq \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi(i(\varepsilon/2)) \right| > M \varepsilon \sigma_K \right\} \right] = 0. \end{aligned}$$

REMARK 7. For each $\varepsilon > 0$, Lemma 7.4 implies that the mutant density reaches the value $C_{\text{cross}}^\varepsilon$ with high probability, since ε is independent of K . Moreover, for all $\varepsilon > 0$,

$$\begin{aligned} & \mathbb{P} \left[\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K > \left(\theta_{\text{mut. size } \varepsilon}^K + \frac{\ln(K)}{\sigma_K^{1+\alpha/2}} \right) \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] \\ (7.28) \quad & = o(\sigma_K) \end{aligned}$$

and

$$(7.29) \quad \mathbb{P} \left[\left| \langle \tilde{v}_{\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K}, \mathbb{1} \rangle - \phi(C_{\text{cross}}^\varepsilon) \right| > M \varepsilon \sigma_K \right] = o(\sigma_K).$$

PROOF. We will prove the lemma by induction over i . Base clause: Compare with Lemmas 7.2 and 7.3 that there exists a constant $M > 0$ such that $|\langle \tilde{v}_{\theta_{\text{mut. size } \varepsilon}^K}, \mathbb{1} \rangle - \phi(0)|$ is smaller than $M \varepsilon \sigma_K$ and that $\theta_{\text{mut. size } \varepsilon}^K < \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K$ both with probability $1 - o(\sigma_K)$.

Induction step from $i - 1$ to i : Assume that the lemma holds true for $i - 1$, then be prove separately that (a)–(d) are true for i , as long as $i < 2\varepsilon^{-1}C_{\text{cross}}^\varepsilon$. \square

PROOF OF (a) FOR i BY ASSUMING THAT THE LEMMA HOLDS FOR $i - 1$. In the proof, we use the following notation:

$$\begin{aligned} \tilde{\theta}_i^K & \equiv \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \\ & \wedge \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \exists k \geq 1 : \mathfrak{M}^k(\tilde{v}_t) = \left\lceil \left(i \pm \frac{1}{2} \right) \frac{\varepsilon}{2} K \right\rceil \right\}. \end{aligned}$$

Note that $\tilde{\theta}_i^K$ differs from $\tilde{\theta}^K$ defined in Lemma 7.3. We will prove (a) provided it happens before $\tilde{\theta}_i^K$ and we use the estimates of step (b) for i to prove that it indeed happens before $\tilde{\theta}_i^K$ with high probability.

If the lemma is true for $i - 1$, we know that [with (d)],

$$(7.30) \quad \mathbb{P} \left[\left| \langle \tilde{v}_{\theta_{\text{mut. size } i(\varepsilon/2)}^K}, \mathbb{1} \rangle - \phi \left((i-1) \frac{\varepsilon}{2} \right) \right| < M\varepsilon\sigma_K \right] = 1 - o(\sigma_K).$$

Since $\phi(x) - \phi(y) = O(h(x-y)\sigma_K)$, we have with probability $1 - o(\sigma_K)$ either

$$(7.31) \quad \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi \left(i \frac{\varepsilon}{2} \right) \right| < (M/3)\varepsilon\sigma_K \right\} = \theta_{\text{mut. size } i(\varepsilon/2)}^K,$$

which implies (a) for i , or at least

$$(7.32) \quad \left| \langle \tilde{v}_{\theta_{\text{mut. size } i(\varepsilon/2)}^K}, \mathbb{1} \rangle - \phi \left(i \frac{\varepsilon}{2} \right) \right| < \left(M + \left| h \left(\frac{r'(R^K)}{r(R^K)} - \frac{(\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K))}{c(R^K, R^K)} \right) \right| \right) \varepsilon\sigma_K.$$

Similarly, as in many previous lemmata, we want to couple $K \langle \tilde{v}_t, \mathbb{1} \rangle$ with a discrete time Markov chain. Therefore, let

$$(7.33) \quad X_t^i = \left| K \langle \tilde{v}_t, \mathbb{1} \rangle - \left\lceil \phi \left(i \frac{\varepsilon}{2} \right) K \right\rceil \right|,$$

and $T_0^i = \theta_{\text{mut. size } i(\varepsilon/2)}^K$ and $(T_k^i)_{k \geq 1}$ be the sequences of the jump times of $\langle \tilde{v}_t, \mathbb{1} \rangle$ after $\theta_{\text{mut. size } i(\varepsilon/2)}^K$. Then let Y_k^i be the associated discrete time process which records the values that X_t^i takes after time $\theta_{\text{mut. size } i(\varepsilon/2)}^K$.

CLAIM. *There exists a constant, $C_{\text{derivative}}^{b,d,c} > 0$, such that for all $\lceil C_{\text{derivative}}^{b,d,c} \varepsilon\sigma_K K \rceil \leq j < \lceil \varepsilon K \rceil$ and K large enough,*

$$(7.34) \quad \mathbb{P}[Y_{n+1}^i = j + 1 | Y_n^i = j, T_{n+1} < \tilde{\theta}_i^K] \leq \frac{1}{2} - \varepsilon\sigma_K =: p_+^K.$$

Moreover, we can choose

$$(7.35) \quad C_{\text{derivative}}^{b,d,c} = \sup_{x \in \mathcal{X}} \frac{1}{c(x, x)} \left(4b(x) + A \left| \frac{r'(x)c(x, x)}{r(x)} - \partial_1 c(x, x) - \partial_2 c(x, x) \right| \right).$$

If $\langle \tilde{v}_t, \mathbb{1} \rangle K > \lceil \phi(i(\varepsilon/2))K \rceil$ at time $t = T_n^i$, then $\langle \tilde{v}_{T_n^i}, \mathbb{1} \rangle K = \lceil \phi(i(\varepsilon/2))K \rceil + Y_n^i$ and, conditionally on $\mathcal{F}_{T_n^i}$, the left-hand side of (7.34) is equal to the probability

that the next event is a birth. Namely,

$$\begin{aligned}
 & \frac{\sum_{k \geq 0} b(h_{k,1}(\tilde{v}_{T_n^i})) \mathfrak{M}^k(\tilde{v}_{T_n^i})}{\sum_{k \geq 0} (b(h_{k,1}(\tilde{v}_{T_n^i})) + d(h_{k,1}(\tilde{v}_{T_n^i})) + \int_{\mathbb{N} \times \mathcal{X}} c(h_{k,1}(\tilde{v}_{T_n^i}), \xi) d\tilde{v}_{T_n^i}(\xi)) \mathfrak{M}^k(\tilde{v}_{T_n^i})} \\
 & \leq \left(b(R^K) \sum_{k \geq 0} \mathfrak{M}^k(\tilde{v}_{T_n^i}) + \sigma_K h b'(R^K) \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i}) \right. \\
 & \quad \left. + C_L^b 2A\sigma_K \left\lceil \frac{3}{\alpha} \right\rceil \sigma_K \varepsilon K + O(\sigma_K^2 K) \right) \\
 (7.36) \quad & \times \left(\sum_{k \geq 0} \left(b(R^K) + d(R^K) + \sum_{k \geq 0} \frac{c(R^K, R^K)}{K} \mathfrak{M}^k(\tilde{v}_{T_n^i}) \right) \mathfrak{M}^k(\tilde{v}_{T_n^i}) \right. \\
 & \quad \left. + \sigma_K h \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i}) \left(b'(R^K) + d'(R^K) \right. \right. \\
 & \quad \left. \left. + \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{K} (\mathfrak{M}^0(\tilde{v}_{T_n^i}) + \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})) \right) \right) \\
 & \quad - \left(C_L^{b,d,c} 2A\sigma_K \lceil 3/\alpha \rceil \sigma_K \varepsilon K - O(\sigma_K^2 K) \right)^{-1}.
 \end{aligned}$$

For the inequality, we have used the fact that, conditioned on $T_n < \tilde{\theta}_i^K$, there at most $\sigma_K \varepsilon \lceil 3/\alpha \rceil$ many unsuccessful mutant individuals which differ at most $2A\sigma_K$ from the resident trait R^K . Since $\sum_{k \geq 0} \mathfrak{M}^k(\tilde{v}_{T_n^i}) = \langle \tilde{v}_{T_n^i}, \mathbb{1} \rangle K$ which equals $\lceil \phi(i(\varepsilon/2))K \rceil + j$ conditioned on $j = Y_n^i$, the right-hand side of the last inequality is smaller or equals

$$\begin{aligned}
 & \left(b(R^K) + \sigma_K h b'(R^K) \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{\lceil \phi(i(\varepsilon/2))K \rceil + j} + O(\sigma_K^2) \right) \\
 & \quad \times \left(b(R^K) + d(R^K) + c(R^K, R^K) \frac{\lceil \phi(i(\varepsilon/2))K \rceil + j}{K} \right. \\
 & \quad \left. + \sigma_K \frac{h \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{\lceil \phi(i(\varepsilon/2))K \rceil + j} \left(b'(R^K) + d'(R^K) \right. \right. \\
 & \quad \left. \left. + \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{K} (\mathfrak{M}^0(\tilde{v}_{T_n^i}) + \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})) \right) \right) - O(\sigma_K^2) \Big)^{-1}
 \end{aligned}$$

and by definition of ϕ the denominator equals

$$\begin{aligned}
 & 2b(R^K)\sigma_K + 2\sigma_K h b'(R^K) \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{\lceil \phi(i(\varepsilon/2))K \rceil + j} + c(R^K, R^K) \frac{j}{K} - O(\sigma_K^2) \\
 & \quad + \sigma_K h \left[i \frac{\varepsilon}{2} \left(\frac{r'(R^K)}{\bar{z}(R^K)} + \partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K) \right) \right]
 \end{aligned}$$

$$\begin{aligned}
 & + \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{\lceil \phi(i(\varepsilon/2))K \rceil + j} \left(d'(R^K) - b'(R^K) \right. \\
 & \left. + \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{K} (\mathfrak{M}^0(\tilde{v}_{T_n^i}) + \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})) \right) \Big].
 \end{aligned}$$

Thus, we obtain that the right-hand side of (7.36) is bounded from above by

$$\begin{aligned}
 & \frac{1}{2} - \frac{c(R^K, R^K)}{3b(R^K)} j K^{-1} \\
 & - \frac{\sigma_K h}{4b(R^K)} \left[i \frac{\varepsilon}{2} \left(\frac{r'(R^K)}{\bar{z}(R^K)} - \partial_1 c(R^K, R^K) - \partial_2 c(R^K, R^K) \right) \right. \\
 & + \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{\lceil \phi(i(\varepsilon/2))K \rceil + j} \left(-r'(R^K) \right. \\
 & \left. \left. + \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{K} (\mathfrak{M}^0(\tilde{v}_{T_n^i}) + \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})) \right) \right] + O(\sigma_K^2).
 \end{aligned}$$

In the case where $\langle \tilde{v}_t, \mathbb{1} \rangle K < \lceil \phi(i(\varepsilon/2))K \rceil$ at time $t = T_n^i$, we obtain the same inequality but with an opposite sign in front of the third term. Since

$$\begin{aligned}
 & \left| \frac{i\varepsilon r'(R^K)}{2 \bar{z}(R^K)} - \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{K} \frac{r'(R^K)K}{\lceil \phi(i(\varepsilon/2))K \rceil \pm j} \right. \\
 & \left. - (\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)) \left(\frac{i\varepsilon}{2} - \frac{\mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})}{K} \right) \right| \\
 & < (\varepsilon/2) \left| \frac{r'(R^K)}{\bar{z}(R^K)} - \partial_1 c(R^K, R^K) - \partial_2 c(R^K, R^K) \right|,
 \end{aligned}$$

we deduce the claim. Since we choose M such that $M \geq 3C_{\text{derivative}}^{b,d,c}$, we can construct a Markov chain Z_n^i such that $Z_n^i \geq Y_n^i$, a.s., for all n such that $T_n^i < \tilde{\theta}_i^K \wedge \inf\{t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \phi(i(\varepsilon/2))| < \frac{1}{3}M\varepsilon\sigma_K\}$ and the marginal distribution of Z_n is a Markov chain with $Z_0^i = Y_0^i$ and transition probabilities

$$(7.37) \quad \mathbb{P}[Z_{n+1}^i = j_2 | Z_n^i = j_1] = \begin{cases} p_+^K, & \text{for } j_1 \geq 1 \text{ and } j_2 = j_1 + 1, \\ 1 - p_+^K, & \text{for } j_1 \geq 1 \text{ and } j_2 = j_1, \\ 0, & \text{else.} \end{cases}$$

Let $C_{\text{exit}} = \sup_{x \in \mathcal{X}} 2A \left| \frac{r'(x)}{r(x)} - \frac{(\partial_1 c(x,x) + \partial_2 c(x,x))}{c(x,x)} \right|$. Then, by applying Proposition A.5(b), we obtain, for all $a \leq (M + C_{\text{exit}})\varepsilon\sigma_K K$ and K large enough,

$$(7.38) \quad \mathbb{P}_a \left[\inf\{n \geq 0 : Z_n^i \geq 2(M + C_{\text{exit}})\varepsilon\sigma_K K\} < \inf\left\{n \geq 0 : Z_n^i \leq \left(\frac{M}{3}\right)\varepsilon\sigma_K K\right\} \right] \leq \exp(-K^\alpha).$$

Next, define $B^i \equiv \inf\{n \geq 0 : Z_n^i \leq \frac{1}{3}M\varepsilon\sigma_K K\}$. This is the random variable, which counts the number of jumps Z^i makes until it is smaller than $\varepsilon\sigma_K K$. Note that $(T_{n+1}^i - T_n^i)$, the times between two jumps of X_t^i , are exponential distributed with a parameter $(b(R^K) + d(R^K) + c(R^K, R^K)\bar{z}(R^K))\bar{z}(R^K)K + O(\sigma_K K)$, if T_{n+1}^i is smaller than $\tilde{\theta}_i^K$. Thus,

$$(7.39) \quad (T_{l+1}^i - T_l^i) \preceq E_l^i,$$

where $(E_l^i)_{l \geq 0}$ is a sequence of i.i.d. exponential random variables with parameter $\inf_{x \in \mathcal{X}} b(x)\bar{z}(x)K$. Therefore,

$$(7.40) \quad \begin{aligned} &\mathbb{P}[\theta_{\text{near } \phi(i\frac{\varepsilon}{2})}^K > \theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K \wedge \tilde{\theta}_i^K] \\ &\leq \mathbb{P}\left[\sum_{l=0}^{B^i} E_l^i > S_K\right] + \mathbb{P}[\tilde{\theta}_i^K < \theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K \wedge \theta_{\text{near } \phi(i\frac{\varepsilon}{2})}^K]. \end{aligned}$$

Our next goal is to find a number, n_i , such that $\mathbb{P}[B^i > n_i]$ is $o(\sigma_K)$. Since the transition probabilities of Z^i do not depend on the present state, we have that $Z_n^i - Z_0^i$ has the same law as $\sum_{k=1}^n V_k^i$, where $(V_k^i)_{k \in \mathbb{N}}$ is a sequence of i.i.d. random variables with

$$(7.41) \quad \mathbb{P}[V_k^i = 1] = p_+^K \quad \text{and} \quad \mathbb{P}[V_k^i = -1] = 1 - p_+^K$$

and $\mathbb{E}[V_k^i] = -2\varepsilon\sigma_K$ and $|V_k^i| = 1$. Furthermore, we get

$$(7.42) \quad \begin{aligned} \mathbb{P}[B^i \leq n_i] &\geq \mathbb{P}\left[\inf\left\{j \geq 0 : Z_j - Z_0 \leq -\left[\left(\frac{3}{2}M + C_{\text{exit}}\right)\varepsilon\sigma_K K\right]\right\} \leq n_i\right] \\ &\geq \mathbb{P}\left[\sum_{k=1}^{n_i} V_k^i \leq -\left[\left(\frac{3}{2}M + C_{\text{exit}}\right)\varepsilon\sigma_K K\right]\right] \end{aligned}$$

and by applying the following.

HOEFFDING’S INEQUALITY (Appendix 2 in [22]). Let Y_1, \dots, Y_n be independent random variables such that, for all $j \in \mathbb{N}$, $a_j \leq Y_j - \mathbb{E}[Y_j] \leq b_j$ for some real constants a_j, b_j . Then, for $x > 0$,

$$(7.43) \quad \mathbb{P}\left[\sum_{j=1}^n Y_j - \mathbb{E}[Y_j] \geq x\right] \leq \exp\left(-2x^2\left(\sum_{j=1}^n (a_j - b_j)^2\right)^{-1}\right)$$

we obtain

$$(7.44) \quad \mathbb{P}\left[\sum_{k=1}^{n_i} V_k^i \geq -2\varepsilon\sigma_K n_i + (n_i)^{\frac{1}{2} + \alpha/2}\right] \leq 2 \exp(-(n_i)^\alpha).$$

With $n_i \equiv \lceil K(\frac{3}{2}M + C_{\text{exit}}) \rceil$, we get $-2\varepsilon\sigma_K n_i + (n_i)^{\frac{1}{2}+\alpha/2} \leq -\lceil(\frac{3}{2}M + C_{\text{exit}})\varepsilon\sigma_K K \rceil$, since $K^{-\frac{1}{2}+\alpha} \ll \sigma_K$. Applying the exponential Chebychev inequality (with $\lambda = K^\alpha$)

$$\begin{aligned}
 & \mathbb{P} \left[\sum_{l=0}^{\lceil K(\frac{3}{2}M + C_{\text{exit}}) \rceil} E_l^i > S_K \right] \\
 & \leq \exp(-\lambda S_K) \mathbb{E} \left[\exp \left(\lambda \sum_{l=0}^{\lceil K(\frac{3}{2}M + C_{\text{exit}}) \rceil} E_l^i \right) \right] \\
 & \leq \exp(-\lambda S_K) \left(\frac{\inf_{x \in \mathcal{X}} b(x) \bar{z}(x) K}{\inf_{x \in \mathcal{X}} b(x) \bar{z}(x) K - \lambda} \right)^{\lceil K(\frac{3}{2}M + C_{\text{exit}}) \rceil + 1} \\
 (7.45) \quad & \leq \exp \left(-\lambda S_K + \left(\left\lceil K \left(\frac{3}{2}M + C_{\text{exit}} \right) \right\rceil + 1 \right) \right. \\
 & \quad \left. \times \ln \left(1 + \frac{\lambda}{\inf_{x \in \mathcal{X}} b(x) \bar{z}(x) K - \lambda} \right) \right) \\
 & \leq \exp \left(-\lambda S_K + \lambda \frac{\frac{3}{2}M + C_{\text{exit}} + 1}{\inf_{x \in \mathcal{X}} b(x) \bar{z}(x)} + O(\lambda^2 K^{-1}) \right) \leq \exp(-K^\alpha).
 \end{aligned}$$

Hence, the left-hand side of (7.40) is bounded from above by

$$\begin{aligned}
 & \exp(-K^\alpha) + 2 \exp \left(- \left(K \left(\frac{3}{2}M + C_{\text{exit}} \right) \right)^\alpha \right) \\
 (7.46) \quad & \quad + \mathbb{P}[\tilde{\theta}_i^K < (\theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K) \wedge \theta_{\text{near } \phi(i\frac{\varepsilon}{2})}^K].
 \end{aligned}$$

This proves the lemma, if we can show that

$$(7.47) \quad \mathbb{P}[\tilde{\theta}_i^K < (\theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K) \wedge \theta_{\text{near } \phi(i\frac{\varepsilon}{2})}^K] = o(\sigma_K).$$

According to Remark 6 and Lemma 7.3, we have that

$$(7.48) \quad \mathbb{P}[\theta_{\text{succ. mut.}}^K \wedge \theta_{\text{diversity}}^K < \theta_{\text{mut. size } i(\varepsilon/2)}^K + S_K] = o(\sigma_K).$$

Therefore, the following proof of (b) for i implies (a) for i . \square

PROOF OF (b) FOR i BY ASSUMING THAT THE LEMMA HOLDS FOR $i - 1$. Note that the random elements $B^i, T^i, V^i, W^i, X^i, Y^i$ and Z^i are not the ones of the last proof. They will be defined during this proof. In fact, the structure of the proof is similar to the one of (a), except that we prove a lower bound for the time of a change of order ε for the mutant density instead of upper bound for the time of a change of order $\varepsilon\sigma_K$ of the total mass. We couple $\mathfrak{M}_t^{k_1}$, for $t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K$, with a discrete time Markov chain (depending on i). Therefore, let $T_0^i = \theta_{\text{mut. size } i(\varepsilon/2)}^K$

and $(T_k^i)_{k \geq 1}$ be the sequences of jump times of $\mathfrak{M}_t^{k_1}$ after $\theta_{\text{mut. size } i(\varepsilon/2)}^K$. Furthermore, let $(Y_n^i)_{n \geq 0}$ be the discrete time process which records the values that $\mathfrak{M}_t^{k_1}$ takes, that is, $Y_0^i = \mathfrak{M}_0^{k_1}(\tilde{v}_{T_0^i}) = \lceil Ki(\varepsilon/2) \rceil$ and $Y_n^i = \mathfrak{M}_t^{k_1}(\tilde{v}_{T_n^i})$. Observe that if

$$\tilde{\theta}_i^K > \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K$$

$$\wedge \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi\left(i \frac{\varepsilon}{2}\right) \right| \geq 2(M + C_{\text{exit}})\varepsilon\sigma_K K \right\},$$

we know from the inequality (7.38) that the probability that $\theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K$ is larger than $\inf\{t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \phi(i(\varepsilon/2))| \geq 2(M + C_{\text{exit}})\varepsilon\sigma_K K\}$ is smaller than $\exp(-K^\alpha)$. Define

$$\hat{\theta}_i^K \equiv \inf \left\{ t \geq \theta_{\text{mut. size } i(\varepsilon/2)}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi\left(i \frac{\varepsilon}{2}\right) \right| \geq 2(M + C_{\text{exit}})\varepsilon\sigma_K K \right\}$$

$$(7.49) \quad \wedge \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K$$

and

$$(7.50) \quad \tilde{C}_{\text{fitness}} \equiv \inf_{x \in \mathcal{X}} \partial_1 f(x, x) / \bar{b}.$$

Note that $\hat{\theta}_i^K \neq \hat{\theta}^K$. Then, for all $-\lceil \frac{\varepsilon}{4}K \rceil \leq j \leq \lceil \frac{\varepsilon}{4}K \rceil$, for K large enough and for ε small enough, we have that

$$\mathbb{P} \left[Y_{n+1}^i = \left\lceil i \frac{\varepsilon}{2} K \right\rceil + j + 1 \mid Y_n^i = \left\lceil i \frac{\varepsilon}{2} K \right\rceil + j, T_{n+1}^i < \hat{\theta}_i^K \right]$$

$$(7.51) \quad \in \left[\frac{1}{2} + \frac{1}{2} \tilde{C}_{\text{fitness}} \sigma_K, \frac{1}{2} + 2A \tilde{C}_{\text{fitness}} \sigma_K \right],$$

since the left-hand side of (7.51) is equal to the expectation of the probability that the next event is a birth without mutation conditioned on $\mathcal{F}_{T_n^i}$. Namely,

$$\frac{b(R^K + \sigma_K h)(1 - u_K m(R^K - \sigma_K h))}{(b(R^K + \sigma_K h) + d(R^K + \sigma_K h) + \int_{\mathbb{N} \times \mathcal{X}} c(R^K + \sigma_K h, \xi) d\tilde{v}_{T_n}(\xi))}$$

$$= b(R^K + \sigma_K h) \left[b(R^K + \sigma_K h) + d(R^K + \sigma_K h) \right.$$

$$+ c(R^K + \sigma_K h, R^K) \left(\phi\left(i \frac{\varepsilon}{2}\right) - \frac{\lceil i \frac{\varepsilon}{2} K \rceil + j}{K} \right)$$

$$+ c(R^K + \sigma_K h, R^K + h\sigma_K) \left(\frac{\lceil i \frac{\varepsilon}{2} K \rceil + j}{K} \right)$$

$$(7.52) \quad \left. + \xi_1 \left(\varepsilon \sigma_K C_L^c \left(\left\lceil \frac{3}{\alpha} \right\rceil + 2(M + C_{\text{exit}}) \right) \right) \right]^{-1} + O(u_K)$$

$$\begin{aligned}
 &= b(R^K + \sigma_K h) \left[2b(R^K + \sigma_K h) - f(R^K + \sigma_K h, R^K) \right. \\
 &\quad + c(R^K + \sigma_K h, R^K) \left(\phi\left(i \frac{\varepsilon}{2}\right) - \frac{r(R^K)}{c(R^K, R^K)} \right) \\
 &\quad + \sigma_K h \partial_2 c(R^K, R^K) \left(\frac{\lceil i \frac{\varepsilon}{2} K \rceil + j}{K} \right) \\
 &\quad \left. + \xi_1 \left(\varepsilon \sigma_K C_L^c \left(\left\lceil \frac{3}{\alpha} \right\rceil + 2(M + C_{\text{exit}}) \right) \right) \right]^{-1} + O(u_K)
 \end{aligned}$$

for some $\xi_1 \in (-1, 1)$. By definition of ϕ of (7.52) is equal to

$$\begin{aligned}
 &b(R^K + \sigma_K h) \left[2b(R^K + \sigma_K h) - \partial_1 f(R^K, R^K) \sigma_K h + c(R^K + \sigma_K h, R^K) \sigma_K h \right. \\
 &\quad \times \left(i \frac{\varepsilon}{2} \right) \left(\frac{r'(R^K)}{r(R^K)} - \frac{\partial_1 c(R^K, R^K)}{c(R^K, R^K)} \right) \\
 &\quad \left. + \xi_1 \left(\varepsilon \sigma_K C_L^c \left(\left\lceil \frac{3}{\alpha} \right\rceil + 2(M + C_{\text{exit}}) \right) \right) \right]^{-1} \\
 &\quad + O\left(\frac{\sigma_K j}{K} + \sigma_K^2 + u_K\right) \\
 &= b(R^K + \sigma_K h) \left[2b(R^K + \sigma_K h) \right. \\
 &\quad - \sigma_K h \left(1 - i \frac{\varepsilon}{2} \frac{c(R^K, R^K)}{r(R^K)} \right) \partial_1 f(R^K, R^K) \\
 &\quad \left. + \xi_1 \left(\varepsilon \sigma_K C_L^c \left(\left\lceil \frac{3}{\alpha} \right\rceil + 2(M + C_{\text{exit}}) \right) \right) \right]^{-1} + O\left(\frac{\sigma_K j}{K} + \sigma_K^2 + u_K\right) \\
 &= \frac{1}{2} + \sigma_K h \left(1 - i \frac{\varepsilon}{2} \frac{c(R^K, R^K)}{r(R^K)} \right) \frac{\partial_1 f(R^K, R^K)}{b(R^K)} \\
 &\quad + \varepsilon \sigma_K \xi_1 \frac{C_L^c(\lceil \frac{3}{\alpha} \rceil + 2(M + C_{\text{exit}}))}{b(R^K)} \\
 &\quad + O\left(\frac{\sigma_K j}{K} + \sigma_K^2 + u_K\right).
 \end{aligned}$$

Then, because $i < 2\varepsilon^{-1} C_{\text{cross}}^\varepsilon$ implies that $1 - i \frac{\varepsilon}{2} \frac{c(R^K, R^K)}{r(R^K)} > 0$, we obtain (7.51). Thus, we can construct a Markov chain Z_n^i such that $Z_n^i \geq Y_n^i$, a.s., for all n such that $T_n^i < \hat{\theta}^K$ and such that the marginal distribution of Z_n^i is a Markov chain with

transition probabilities

$$(7.53) \quad \mathbb{P}[Z_{n+1}^i = j_2 | Z_n^i = j_1] = \begin{cases} \frac{1}{2} + 2A\tilde{C}_{\text{fitness}}\sigma_K, & \text{for } j_2 = j_1 + 1, \\ \frac{1}{2} - 2A\tilde{C}_{\text{fitness}}\sigma_K, & \text{for } j_2 = j_1 - 1, \\ 0, & \text{else.} \end{cases}$$

We define a continuous time process, \tilde{Z}^i , associate to Z_n^i . To do this, we define first $(\tilde{T}_j^i)_{j \in \mathbb{N}}$, the sequence of jump times, by $\tilde{T}_0^i = 0$ and

$$(7.54) \quad \tilde{T}_j^i - \tilde{T}_{j-1}^i = \begin{cases} T_j^i - T_{j-1}^i, & \text{if } T_j^i < \tilde{\theta}^K, \\ W_j^i, & \text{else,} \end{cases}$$

where W_j^i are exponential random variables with mean $(\lceil K(i + \frac{1}{2})(\varepsilon/2) \rceil (\bar{b} + \bar{d} + \bar{c}(4\bar{b}/\underline{c})))^{-1}$. We set $\tilde{Z}_t^i = Z_n^i$ if $t \in [\tilde{T}_n^i, \tilde{T}_{n+1}^i)$. Obverse that we obtain by construction $\tilde{Z}_t^i \geq \mathfrak{M}^{k_1}(\tilde{v}_{\theta_{\text{mut. size } i(\varepsilon/2)}^K}^i + t)$, for all t such that $\theta_{\text{mut. size } i(\varepsilon/2)}^K + t \leq \hat{\theta}_i^K$. Next, we want to show that

$$(7.55) \quad \mathbb{P}\left[\inf\left\{t \geq 0 : \tilde{Z}_t^i \geq \left\lceil K\left(i + \frac{1}{2}\right)(\varepsilon/2) \right\rceil\right\} > S_K\right] = 1 - o(\sigma_K).$$

Therefore, let $B_i^Z = \inf\{n \geq 0 : Z_n^i = \lceil K(i + \frac{1}{2})(\varepsilon/2) \rceil\}$. We can construct $(X_j^i)_{j \geq 1}$ a sequence of independent, exponential random variables with parameter $x_i^K \equiv \lceil K(i + \frac{1}{2})(\varepsilon/2) \rceil (\bar{b} + \bar{d} + \bar{c}(4\bar{b}/\underline{c}))$ such that

$$(7.56) \quad (\tilde{T}_{j+1}^i - \tilde{T}_j^i) \succcurlyeq X_j^i \quad \text{for all } 1 \leq j \leq B_i^Z.$$

Our next goal is to find a barrier, n_i , such that B_i^Z is smaller than n_i only with very small probability. Since the transition probabilities of Z^i do not depend on the present state, $Z_{B_i^Z}^i - Z_0$ is stochastically equivalent to $\sum_{k=1}^j V_k^i$, where $(V_k^i)_{k \in \mathbb{N}}$ are i.i.d. random variables taking values ± 1 with probabilities

$$(7.57) \quad \mathbb{P}[V_k^i = 1] = \frac{1}{2} + 2A\tilde{C}_{\text{fitness}}\sigma_K \quad \text{and} \quad \mathbb{P}[V_k^i = -1] = \frac{1}{2} - 2A\tilde{C}_{\text{fitness}}\sigma_K.$$

Note that $\mathbb{E}[V_k^i] = 4A\tilde{C}_{\text{fitness}}\sigma_K$ and $|V_k^i| = 1$. Furthermore, we get

$$(7.58) \quad \mathbb{P}[B_i^Z \leq n_i] = \mathbb{P}\left[\exists \lceil (\varepsilon/4)K \rceil \leq j \leq n_i : \sum_{k=1}^j V_k^i \geq \lceil (\varepsilon/4)K \rceil\right].$$

Hoeffding’s inequality implies that, for $j \geq \lceil (\varepsilon/4)K \rceil$,

$$(7.59) \quad \mathbb{P}\left[\sum_{k=1}^j V_k^i \geq 4A\tilde{C}_{\text{fitness}}\sigma_K j + j^{\frac{1}{2} + \alpha/2}\right] \leq 2 \exp(-j^\alpha).$$

We take $n_i \equiv \varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}$ and get for all $\lceil(\varepsilon/4)K\rceil \leq j \leq n_i$,

$$(7.60) \quad 4A\tilde{C}_{\text{fitness}}\sigma_K j + j^{\frac{1}{2}+\alpha/2} \leq \lceil(\varepsilon/4)K\rceil,$$

since $K^{-\frac{1}{2}+\alpha} \ll \sigma_K$. Then, the probability that $B_i^Z \leq \varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}$ is bounded from above by $2 \exp(-K^\alpha)$. Therefore, the left- hand side of equation (7.55) is larger than

$$(7.61) \quad \mathbb{P} \left[\sum_{j=1}^{\varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}} X_j^i > S_K \right] - 2 \exp(-K^\alpha),$$

By applying the exponential Chebychev inequality, we get, similarly as in (a),

$$\begin{aligned} & \mathbb{P} \left[\sum_{j=1}^{\varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}} X_j^i \leq S_K \right] \\ &= \mathbb{P} \left[- \sum_{j=1}^{\varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}} X_j^i \geq -S_K \right] \\ &\leq \exp(K^\alpha S_K) \mathbb{E}[\exp(-K^\alpha X_j^i)]^{\varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1}} \\ (7.62) \quad &\leq \exp(K^\alpha S_K) \exp\left(\varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1} \ln\left(\frac{x_i^K}{x_i^K + K^\alpha}\right)\right) \\ &\leq \exp(K^\alpha S_K - \varepsilon K (8A\tilde{C}_{\text{fitness}}\sigma_K)^{-1} C K^{-1+\alpha}), \\ &\hspace{15em} \text{for some small } C > 0, \\ &\leq \exp(-K^\alpha). \end{aligned}$$

This proves that $\mathbb{P}[\inf\{t \geq 0 : \tilde{Z}_t^i \geq \lceil K(i + \frac{1}{2})(\varepsilon/2) \rceil\} > S_K] \geq 1 - 3 \exp(-K^\alpha)$ and, therefore, (b) and (a) for i , provided that the lemma holds for $i - 1$. \square

PROOF OF (c) FOR i BY ASSUMING THAT THE LEMMA HOLDS FOR $i - 1$. Note that the random elements T^i, X^i , and Y^i are not the ones of the last proof. As in (a), we couple $K \langle \tilde{v}_t, \mathbb{1} \rangle$ with a discrete time Markov chain. Therefore, let

$$(7.63) \quad X_t^i = |K \langle \tilde{v}_t, \mathbb{1} \rangle - \lceil \phi(i(\varepsilon/2))K \rceil|$$

and $T_0^i = \theta_{\text{mut. size } i(\varepsilon/2)}^K$ and $(T_k^i)_{k \geq 1}$ be the sequences of the jump times of $\langle \tilde{v}_t, \mathbb{1} \rangle$ after $\theta_{\text{mut. size } i(\varepsilon/2)}^K$. Then let Y_k^i be the associated discrete time process which records the values that X_t^i takes after time $\theta_{\text{mut. size } i(\varepsilon/2)}^K$.

CLAIM. *There exists a constant $\tilde{C}_{\text{derivative}}^{b,d,c}$ such that for all $j < \lceil \varepsilon K \rceil$ and K large enough,*

$$(7.64) \quad \begin{aligned} \mathbb{P}[Y_{n+1}^i = j + 1 | Y_n^i = j, T_{n+1} < \tilde{\theta}_i^K] \\ \leq \frac{1}{2} - \frac{c}{3b} j K^{-1} + \varepsilon \sigma_K \tilde{C}_{\text{derivative}}^{b,d,c} \equiv p_+^K(j). \end{aligned}$$

Moreover, we can choose $\tilde{C}_{\text{derivative}}^{b,d,c} \equiv \sup_{x \in \mathcal{X}} \frac{A}{4b(x)} \left| \frac{r'(x)}{\bar{z}(x)} - \partial_1 c(x, x) - \partial_2 c(x, x) \right|$.

From (a), we know that the left-hand side of (7.64) is smaller or equals

$$(7.65) \quad \begin{aligned} \frac{1}{2} - \frac{c(R^K, R^K)}{3b(R^K)} j K^{-1} \\ + \frac{\varepsilon \sigma_K h}{8b(R^K)} \left| \frac{r'(R^K)}{\bar{z}(R^K)} - \partial_1 c(R^K, R^K) - \partial_2 c(R^K, R^K) \right| + O(\sigma_K^2). \end{aligned}$$

This proves the claim. Note that $p_+^K(j)$ depends on j . Since we can choose $M \geq 8\tilde{C}_{\text{derivative}}^{b,d,c} \frac{3\bar{b}}{c}$, continuing as in Lemma 6.3 implies that (c) is true for i , provided that the lemma holds for $i - 1$. \square

PROOF OF (d) FOR i BY ASSUMING THAT THE LEMMA HOLDS FOR $i - 1$. Again we couple $\mathfrak{M}_t^{k_1}$, for $t \geq \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K$, with a discrete time Markov chain. Let $T_0^i = \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K$ and $(T_k^i)_{k \geq 1}$ be the sequences of the jump times of $\mathfrak{M}_t^{k_1}$ after $\theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K$. Then let $(Y_n^i)_{n \geq 0}$ be the discrete time process which records the values that $\mathfrak{M}_t^{k_1}$, that is,

$$(7.66) \quad Y_0^i = \mathfrak{M}^{k_1}(\tilde{v}_{T_0^i}) \in \left[K \left(\frac{i\varepsilon}{2} - \frac{\varepsilon}{4} \right) - 1, K \left(\frac{i\varepsilon}{2} + \frac{\varepsilon}{4} \right) + 1 \right],$$

and $Y_n^i = \mathfrak{M}^{k_1}(\tilde{v}_{T_n^i})$. Define

$$(7.67) \quad \begin{aligned} \hat{\theta}_i^K \equiv \inf \left\{ t \geq \theta_{\text{near } \phi(i \frac{\varepsilon}{2})}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \phi \left(i \frac{\varepsilon}{2} \right) \right| > M\varepsilon \sigma_K \right\} \\ \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K. \end{aligned}$$

Note that this $\hat{\theta}_i^K$ differs only a bit from the one defined in (b). From the proof of (b), we know that the density of the mutant trait has the tendency to increase. More precisely, since $i \leq C_{\text{cross}}^\varepsilon (2/\varepsilon)$, we have, for all $-\lceil \frac{\varepsilon}{4} K \rceil \leq j \leq \lceil \frac{\varepsilon}{2} K \rceil$, for K large enough and ε small enough,

$$(7.68) \quad \begin{aligned} \mathbb{P} \left[Y_{n+1}^i = \left\lceil i \frac{\varepsilon}{2} K \right\rceil + j + 1 \mid Y_n^i = \left\lceil i \frac{\varepsilon}{2} K \right\rceil + j, T_{n+1}^i < \hat{\theta}_i^K \right] \\ \geq \frac{1}{2} + \sigma_K \frac{\inf_{x \in \mathcal{X}} \partial_1 f(x, x)}{2b}. \end{aligned}$$

By continuing in a similar way as in (b) with bounding the random variables in the other direction [as in (a)], implies that (d) is true for i , provided that the lemma holds for $i - 1$. \square

7.3. *Step 3: The density of the resident trait R^K decreases to ε .* Similarly, as in Step 2, we define a function which allows us to approximate the total mass of the population for a given density of the resident trait.

NOTATION. Let us define

$$(7.69) \quad \begin{aligned} \psi(x) &\equiv \bar{z}(R^K) + \sigma_K h(\bar{z}(R^K) - x) \\ &\times \left(\frac{r'(R^K)}{r(R^K)} + \frac{\partial_1 c(R^K, R^K) + \partial_2 c(R^K, R^K)}{c(R^K, R^K)} \right). \end{aligned}$$

Note that $\phi(y) = \psi(\phi(y) - y) + O(\sigma_K^2)$. Therefore, and since $|\langle \tilde{\nu}_{\theta^K}^{\text{mut. size } C_{\text{cross}}^\varepsilon}, \mathbb{1} \rangle - \phi(C_{\text{cross}}^\varepsilon)| < M\varepsilon\sigma_K$ with probability $1 - o(\sigma_K)$, we get that at time $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K$ the density of the resident population belongs to an interval centered at $\phi(C_{\text{cross}}^\varepsilon) - C_{\text{cross}}^\varepsilon$ with diameter $2(M + \lceil 3/\alpha \rceil)\varepsilon\sigma_K$ with probability $1 - o(\sigma_K)$, and hence

$$(7.70) \quad \begin{aligned} \psi(\mathfrak{M}^0(\tilde{\nu}_{\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K})K^{-1}) &= \psi(\phi(C_{\text{cross}}^\varepsilon) - C_{\text{cross}}^\varepsilon) + O(\varepsilon\sigma_K^2) \\ &= \phi(C_{\text{cross}}^\varepsilon) + O(\sigma_K^2) \end{aligned}$$

with probability $1 - o(\sigma_K)$. Thus, the total mass of the population also belongs to an interval centered at $\psi(\phi(C_{\text{cross}}^\varepsilon) - C_{\text{cross}}^\varepsilon)$ with diameter $2(M\varepsilon\sigma_K + O(\sigma_K^2)) < 2(M + 1)\varepsilon\sigma_K$.

NOTATION. Let us define

$$\tilde{C}_{\text{cross}}^K \equiv \lceil (\phi(C_{\text{cross}}^\varepsilon) - C_{\text{cross}}^\varepsilon - \varepsilon)2/\varepsilon \rceil (\varepsilon/2)$$

and

$$\begin{aligned} &\theta_{\text{near}} \psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2}) \\ &\equiv \inf \left\{ t \geq \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K : \left| \langle \tilde{\nu}_t, \mathbb{1} \rangle - \psi\left(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2}\right) \right| < (M/3)\varepsilon\sigma_K \right\}. \end{aligned}$$

Note that the term $-\varepsilon$ in the definition of $\tilde{C}_{\text{cross}}^K$ ensures that resident population is larger than $\tilde{C}_{\text{cross}}^K$ at time $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K$.

First, we need a lemma to connect Step 2 and Step 3.

LEMMA 7.5. *Fix $\varepsilon > 0$. Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that:*

(a) *Soon after* $\theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K$, *the total population size is close to* $\psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})$:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{near } \psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})}^K > \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K + S_K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \{ t \geq \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K : \mathfrak{M}^0(\tilde{v}_t) = \lceil (\tilde{C}_{\text{cross}}^\varepsilon \pm 3\varepsilon/4)K \rceil \} \right] = 0.$$

(b) *A change of order* ε *for the resident density takes more than* $o(\sigma_K^{-1})$ *time:*

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \{ t \geq \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K : \mathfrak{M}^0(\tilde{v}_t) = \lceil (\tilde{C}_{\text{cross}}^\varepsilon \pm 3\varepsilon/4)K \rceil \} \right. \\ \left. < \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K + S_K \wedge \theta_{\text{near } \psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] = 0.$$

(c) *At the time when the resident density has changed of order* ε , *the total population size is still close to* $\psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})$:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{near } \psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \psi \left(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2} \right) \right| > M\varepsilon\sigma_K \right\} \right. \\ \left. < \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \{ t \geq \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K : \mathfrak{M}^0(\tilde{v}_t) = \lceil (\tilde{C}_{\text{cross}}^\varepsilon \pm \varepsilon)K \rceil \} \right] = 0.$$

(d) *A change of order* ε *for the resident density takes no more than* $(i\sigma_K)^{-1-\alpha/2}$ *time:*

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{res. size } \tilde{C}_{\text{cross}}^\varepsilon - \varepsilon}^K > \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K + (i\sigma_K)^{-1-\alpha/2} \right. \\ \left. \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \left\{ t \geq \theta_{\text{near } \psi(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2})}^K : \left| \langle \tilde{v}_t, \mathbb{1} \rangle - \psi \left(\tilde{C}_{\text{cross}}^\varepsilon - \frac{\varepsilon}{2} \right) \right| > M\varepsilon\sigma_K \right\} \right] = 0.$$

PROOF. Apply the methods of (a) to (d) from Lemma 7.4. \square

Next, we have the following similar lemmata as in Step 2. For them, let us define

$$(7.71) \quad \theta_{\text{near } \psi(i\frac{\varepsilon}{2})}^K \equiv \inf \{ t \geq \theta_{\text{res. size } i(\varepsilon/2)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(i(\varepsilon/2))| < (M/3)\varepsilon\sigma_K \}.$$

LEMMA 7.6. *Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant* $M > 0$ *(independent of* ε , K , *and* i) *such that, for all* $\varepsilon > 0$ *and for all* $(\tilde{C}_{\text{cross}}^\varepsilon - \varepsilon)(2/\varepsilon) \geq i \geq 2$:

(a) *Soon after* $\theta_{\text{res. size } i(\varepsilon/2)}^K$, *the total population size is close to* $\psi(i\frac{\varepsilon}{2})$:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{near } \psi(i\frac{\varepsilon}{2})}^K > \theta_{\text{res. size } i(\varepsilon/2)}^K + S_K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \left\{ t \geq \theta_{\text{res. size } i(\varepsilon/2)}^K : \mathfrak{M}^0(\tilde{v}_t) = \left\lceil \left(i \pm \frac{1}{2} \right) (\varepsilon/2) K \right\rceil \right\} \right] = 0.$$

(b) A change of order ε for the resident density takes more than $o(\sigma_K^{-1})$ time:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{res. size } i(\varepsilon/2)}^K : \mathfrak{M}^0(\tilde{v}_t) = \left[\left(i \pm \frac{1}{2} \right) (\varepsilon/2) K \right] \right\} < \theta_{\text{res. size } i(\varepsilon/2)}^K + S_K \wedge \theta_{\text{near } \psi(i \frac{\varepsilon}{2})}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] = 0.$$

(c) At the time when the resident density has changed of order ε , the total population size is still close to $\psi(i \frac{\varepsilon}{2})$:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{near } \psi(i \frac{\varepsilon}{2})}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(i(\varepsilon/2))| > M\varepsilon\sigma_K \right\} < \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \wedge \inf \left\{ t \geq \theta_{\text{res. size } i(\varepsilon/2)}^K : \mathfrak{M}^0(\tilde{v}_t) = \left[(i \pm 1)(\varepsilon/2) K \right] \right\} \right] = 0.$$

(d) A change of order ε for the resident density takes no more than $(i\sigma_K)^{-1-\alpha/2}$ time:

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{res. size } (i-1)(\varepsilon/2)}^K > (\theta_{\text{near } \psi(i \frac{\varepsilon}{2})}^K + (i\sigma_K)^{-1-\alpha/2}) \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \wedge \inf \left\{ t \geq \theta_{\text{near } \psi(i \frac{\varepsilon}{2})}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(i(\varepsilon/2))| > M\varepsilon\sigma_K \right\} \right] = 0.$$

PROOF. Apply the methods of (a) to (d) from Lemma 7.4. \square

REMARK 8. Lemmas 7.5 and 7.6 imply that the density of the resident trait decreases to the value ε . Moreover,

$$(7.72) \quad \mathbb{P} \left[\theta_{\text{res. size } \varepsilon}^K > \theta_{\text{mut. size } C_{\text{cross}}^\varepsilon}^K + \frac{\ln(K)}{\sigma_K^{1+\alpha/2}} \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] = o(\sigma_K)$$

and

$$(7.73) \quad \mathbb{P} \left[|\langle \tilde{v}_{\theta_{\text{res. size } \varepsilon}^K}, \mathbb{1} \rangle - \psi(\varepsilon)| > M\varepsilon\sigma_K \right] = o(\sigma_K).$$

7.4. Step 4: The resident trait R^K goes extinct. After the time $\theta_{\text{res. size } \varepsilon}^K$, we have to wait less than $\ln(K)\sigma_K^{1+\alpha/2}$ time to know that the resident trait is extinct with high probability.

NOTATION. Define

$$\theta_{\text{near } \psi(0)}^K \equiv \inf \left\{ t \geq \theta_{\text{res. size } \varepsilon}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| < (M/3)\varepsilon\sigma_K \right\}.$$

LEMMA 7.7. Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that, for all $\varepsilon > 0$:

(a) *Soon after $\theta_{\text{res. size } \varepsilon}^K$, the total population size is close to $\psi(0)$:*

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{near } \psi(0)}^K > \theta_{\text{res. size } \varepsilon}^K + S_K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \left\{ t \geq \theta_{\text{res. size } \varepsilon}^K : \mathfrak{M}^0(\tilde{v}_t) = \left[\left(1 \pm \frac{1}{4} \right) \varepsilon K \right] \right\} \right] = 0.$$

(b) *A change of order ε for the resident density takes more than $o(\sigma_K^{-1})$ time:*

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\inf \left\{ t \geq \theta_{\text{res. size } \varepsilon}^K : \mathfrak{M}^0(\tilde{v}_t) = \left[\left(1 \pm \frac{1}{4} \right) \varepsilon K \right] \right\} \right. \\ \left. < \theta_{\text{res. size } \varepsilon}^K + S_K \wedge \theta_{\text{near } \psi(0)}^K \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right] = 0.$$

PROOF. See proof of Lemma 7.4 \square

LEMMA 7.8. *Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that, for all $\varepsilon > 0$*

$$\lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P} \left[\theta_{\text{res. size } 0}^K > (\theta_{\text{near } \psi(0)}^K + \ln(K) \sigma_K^{-1-\alpha/2}) \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \right. \\ \left. \wedge \inf \{ t \geq \theta_{\text{near } \psi(0)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| > M \varepsilon \sigma_K \} \right] = 0.$$

PROOF. To prove this lemma, we use a coupling with a continuous time branching process as in the proof of Lemma 7.3. For any $\theta_{\text{near } \psi(0)}^K \leq t \leq \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \wedge \inf \{ t \geq \theta_{\text{near } \psi(0)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| > M \varepsilon \sigma_K \}$, any individual of $\mathfrak{M}^0(\tilde{v}_t)$ gives birth to a new individual with trait R^K with rate

$$(7.74) \quad (1 - u_K m(R^K)) b(R^K) \in [b(R^K) - u_K \bar{b}, b(R^K)],$$

and dies with rate

$$(7.75) \quad d(R^K) + c(R^K, R^K) \mathfrak{M}^0(\tilde{v}_t) + \int_{\mathcal{X} \times \mathbb{N}} c(R^K, \xi) \tilde{d}v_t(\xi),$$

which is larger than $d_Z \equiv d(R^K) + c(R^K, R^K + \sigma_K h) \bar{z}(R^K + \sigma_K h) - C_{\text{total death}}^M \varepsilon \sigma_K$ where $C_{\text{total death}}^M \equiv M + \bar{c} \lceil 3/\alpha \rceil - 2h \partial_2 c(R^K, R^K)$. Therefore, we construct, by using a standard coupling argument, a process Z_t such that

$$(7.76) \quad Z_t \geq \mathfrak{M}^0(\tilde{v}_t)$$

for all $\theta_{\text{near } \psi(0)}^K \leq t \leq \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \wedge \inf \{ t \geq \theta_{\text{near } \psi(0)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| > M \varepsilon \sigma_K \}$. The process Z_t is a linear birth–death process starting at $\lceil \frac{5}{4} \varepsilon K \rceil$, with birth rate per individual $b_Z = b(R^K)$ and with death rate per individual d_Z . Since

$$(7.77) \quad b_Z - d_Z = f(R^K, R^K + \sigma_K h) + C_{\text{total death}}^M \varepsilon \sigma_K \\ = -\sigma_K h \partial_1 f(R^K + \sigma_K h, R^K + \sigma_K h) + C_{\text{total death}}^M \varepsilon \sigma_K + O((\sigma_K h)^2) \\ \equiv -\sigma_K \xi_K$$

is negative and of order σ_K , the process Z_t is subcritical.

Note that $\xi_K \geq \inf_{x \in \mathcal{X}} \frac{\partial_1 f(x,x)}{2} > 0$. Let τ_i^Z be the first hitting time of level i by Z_t , then we have

$$(7.78) \quad \mathbb{P}[\tau_{\lfloor 2\varepsilon K \rfloor}^Z < \tau_0^Z] \leq \exp(-K^\alpha)$$

compare with the proof of Proposition A.5. Since $Z_t \geq \mathfrak{M}^0(\tilde{v}_t)$, we obtain also that, with high probability, $\mathfrak{M}^0(\tilde{v}_t)$ stays smaller than $\lfloor 2\varepsilon K \rfloor$ before it dies out. For any $t \geq 0$ and $n \in \mathbb{N}$, the distribution of the extinction time of Z_t for $b_Z \neq d_Z$ is given by

$$(7.79) \quad \mathbb{P}_n(\tau_0^Z \leq t) = \left(\frac{d_Z - d_Z \exp((d_Z - b_Z)t)}{b_Z - d_Z \exp((d_Z - b_Z)t)} \right)^n$$

(cf. [2] page 109 and [6]). Therefore, we can compute in our case where $d_Z - b_Z = \sigma_K \xi_K$ with ξ_K uniformly positive

$$(7.80) \quad \begin{aligned} \mathbb{P}[\tau_0^Z \leq \ln(K)\sigma_K^{-1-\alpha/2}] &= \left(\frac{d_Z - d_Z \exp((d_Z - b_Z) \ln(K)\sigma_K^{-1-\alpha/2})}{b_Z - d_Z \exp((d_Z - b_Z) \ln(K)\sigma_K^{-1-\alpha/2})} \right)^{\frac{5}{4}\varepsilon K} \\ &= \left(\frac{d_Z - d_Z K^{\xi_K \sigma_K^{-\alpha/2}}}{d_Z - \sigma_K \xi_K - d_Z K^{\xi_K \sigma_K^{-\alpha/2}}} \right)^{\frac{5}{4}\varepsilon K} \\ &= \left(1 - \frac{\xi_K \sigma_K}{d_Z (K^{\xi_K \sigma_K^{-\alpha/2}} - 1) + \sigma_K \xi_K} \right)^{\frac{5}{4}\varepsilon K} \\ &\geq \left(1 - \sigma_K \left(\frac{5}{4} \varepsilon K \right)^{-1} K^{-1} \right)^{\frac{5}{4}\varepsilon K} \\ &\geq 1 - O(\sigma_K K^{-1}) \geq 1 - o(\sigma_K), \end{aligned}$$

which proves the lemma. \square

7.5. Step 5: The population becomes monomorphic and stays close to its equilibrium. After the extinction time of the resident trait, we have to wait at most $\ln(K)\sigma_K^{-1-\alpha/2}$ time until the population is monomorphic with trait $R^K + \sigma_K h$.

LEMMA 7.9. Suppose that the assumptions of Theorem 7.1 hold. Then there exists a constant $M > 0$ (independent of ε and K) such that, for all $\varepsilon > 0$:

$$\begin{aligned} \lim_{K \rightarrow \infty} \sigma_K^{-1} \mathbb{P}[\theta_{\text{fixation}}^K > (\theta_{\text{res. size } 0}^K + \ln(K)\sigma_K^{-1-\alpha/2}) \wedge \theta_{2 \text{ succ. mut.}}^K \wedge \theta_{\text{diversity}}^K \\ \wedge \inf\{t \geq \theta_{\text{near } \phi(0)}^K : |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| > M\varepsilon\sigma_K\}] = 0. \end{aligned}$$

PROOF. By the last lemmata, we have $\theta_{\text{fixation}}^K = \inf\{t \geq \theta_{\text{res. size } 0}^K : |\text{Supp}(\tilde{v}_t^K)| = 1, |\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| < (M/3)\varepsilon\sigma_K\}$ with probability $1 - o(\sigma_K)$. Set $D \equiv \{k \in \mathbb{N} : 1 \leq \mathfrak{M}^k(\tilde{v}_{\theta_{\text{res. size } 0}^K}) < \varepsilon\sigma_K K\}$. Then $|D| \leq \lceil 3/\alpha \rceil$, and none of these traits are successful since we have seen that $\theta_{\text{res. size } 0}^K$ is smaller than $\theta_{2 \text{ succ. mut.}}^K$ and $\theta_{\text{diversity}}^K$ with probability of order $1 - o(\sigma_K)$. By applying Proposition A.3 and using the Markov inequality, we obtain that the life time of each of these subpopulations is with probability $1 - o(\sigma_K)$ smaller than $\ln(K)\sigma_K^{-1-\alpha/4}$. Therefore, if no new mutant is born between $\theta_{\text{res. size } 0}^K$ and $\theta_{\text{res. size } 0}^K + \ln(K)\sigma_K^{-1-\alpha/4}$, we obtain the claim. On the other hand, as in Lemma 6.4, the number of mutants born in the time interval $[\theta_{\text{res. size } 0}^K, \theta_{\text{res. size } 0}^K + \ln(K)\sigma_K^{-1-\alpha/2}]$ is stochastically dominated by a Poisson point process, $A^K(t)$, with parameter $au_K K$, where $a \equiv \sup_{x \in \mathcal{X}} \bar{z}(x)b(x)m(x) + 1$. Hence, the probability to have no new mutant in this interval is

$$\begin{aligned} \mathbb{P}[A^K(\ln(K)\sigma_K^{-1-\alpha/2}) = 0] &= \exp(-\ln(K)\sigma_K^{-1-\alpha/2} au_K K) \\ (7.81) \qquad \qquad \qquad &\geq \exp(-\sigma_K^{\alpha/2}) \geq 1 - o(1). \end{aligned}$$

Because the probability that a mutant is successful is of order σ_K , the probability that a successful mutant is born between times $\theta_{\text{res. size } 0}^K$ and $\theta_{\text{res. size } 0}^K + \ln(K)\sigma_K^{-1-\alpha/2}$ is $o(\sigma_K)$. Since

$$\begin{aligned} \mathbb{P}[A^K(\ln(K)\sigma_K^{-1-\alpha/2}) \leq \lceil 3/\alpha \rceil] &= \exp(-\ln(K)\sigma_K^{-1-\alpha/2} au_K K) \sum_{i=0}^{\lceil 3/\alpha \rceil} \frac{\ln(K)\sigma_K^{-1-\alpha/2} au_K K}{i} \\ (7.82) \qquad \qquad \qquad &\geq 1 - (\ln(K)\sigma_K^{-1-\alpha/2} au_K K)^{\lceil 3/\alpha \rceil + 1} \\ &\geq 1 - \sigma_K^{3/2} = 1 - o(\sigma_K), \end{aligned}$$

there are maximal $\lceil 3/\alpha \rceil$ unsuccessful mutations in this interval. With the same argument as before the life time of each of these subpopulations is with probability $1 - o(\sigma_K)$ smaller than $\ln(K)\sigma_K^{-1-\alpha/4}$. Therefore, with probability $1 - o(\sigma_K)$ the maximal possible time interval where at least one mutant individual is alive is smaller or equal $\ln(K)\sigma_K^{-1-\alpha/4} + \lceil 3/\alpha \rceil \ln(K)\sigma_K^{-1-\alpha/4} \ll \ln(K)\sigma_K^{-1-\alpha/2}$. Recall from Lemma 7.7 that if $|\langle \tilde{v}_t, \mathbb{1} \rangle - \psi(0)| > (M/3)\varepsilon\sigma_K$ at the first time when the population is again monomorphic, then the time the process needs to enter the $(M/3)\varepsilon\sigma_K$ -neighborhood of $\psi(0)$ is smaller than S_K , which can be chosen smaller than $\sigma_K^{1+\alpha}/(Ku_K)$. This proves the lemma. \square

This ends Step 5 and the second invasion phase. Note that the estimates of the two phases do not depend on the exact trait value of the resident trait, especially

the a priori different constants M . In fact, we can use in all lemmata the same constant M , namely the largest. Therefore, we can apply our results for the successful mutant trait $R_1^K = R^K + \sigma_K h$, which is the next resident trait by using the strong Markov property for (\tilde{v}, L) at the stopping time $\theta_{\text{fixation}}^K$.

8. Convergence to the CEAD. Our goal is to find $T_0 > 0$ and to construct, for all $\varepsilon > 0$, two measure valued processes, $(\mu_t^{1,K,\varepsilon}, t \geq 0)$ and $(\mu_t^{2,K,\varepsilon}, t \geq 0)$, in $\mathbb{D}([0, \infty), \mathcal{M}(\mathcal{X}))$ such that

$$(8.1) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\forall t \leq \frac{T_0}{Ku_K \sigma_K^2} : \mu_t^{1,K,\varepsilon} \preceq \nu_t^K \preceq \mu_t^{2,K,\varepsilon} \right] = 1,$$

and for $j \in \{1, 2\}$

$$(8.2) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\sup_{0 \leq t \leq T_0} \|\mu_{t/(Ku_K \sigma_K^2)}^{i,K,\varepsilon} - \bar{z}(x_t) \delta_{x_t}\|_0 > \delta(\varepsilon) \right] = 0,$$

for some function δ independent of x, K such that $\delta(\varepsilon) \rightarrow 0$ when $\varepsilon \rightarrow 0$. This easily implies (4.5) for all $T \leq T_0$.

The result for all $T > 0$ then follows from the strong Markov property. Indeed, the construction below implies that there exists a stopping time:

$$(8.3) \quad \tau \in [T_0/2Ku_K \sigma_K^2, T_0/Ku_K \sigma_K^2]$$

(a fixation time) such that, with probability converging to 1, ν_τ^K has a unique (random) point Y as support and a total mass belonging to $[\bar{z}(Y) - M\sigma_K, \bar{z}(Y) + M\sigma_K]$. Hence, (8.1) and (8.2) also hold for the process $(\nu_{\tau+t}^K, t \geq 0)$, and (4.5) is thus true for all $T \leq 3T_0/2$. We obtain (4.5) for any fixed $T > 0$ by induction.

8.1. *Construction of two processes $\mu^{K,1}$ and $\mu^{K,2}$ such that $\mu_t^{1,K} \preceq \nu_t^K \preceq \mu_t^{2,K}$.* Fix $T > 0$. Let θ_i^K denote the random time of i th invasion (i.e., $\theta_i^K = \theta_{i,\text{invasion}}^K$), $\theta_{i,\text{fixation}}^K$ the time of i th fixation and R_i^K the trait of the i th successful mutant. Let us fix the following initial conditions $R_0^{K,1} = R_0^K - A\sigma_K$, $R_0^{K,2} = R_0^K + A\sigma_K$ and $\theta_0^{K,1} = \theta_0^{K,2} = 0$. Assume that we have constructed $\theta_i^{K,1}$ and $\theta_i^{K,2}$, and $R_i^{K,1}$ and $R_i^{K,2}$. By Theorem 6.2 and the Markov property, we can construct two random variables $R_{i+1}^{K,1}$ and $R_{i+1}^{K,2}$ such that

$$(8.4) \quad R_{i+1}^{K,1} - R_i^{K,1} \leq R_{i+1}^K - R_i^K \leq R_{i+1}^{K,2} - R_i^{K,2}$$

with probability $1 - o(\sigma_K)$. Moreover, $R_{i+1}^{K,1} - R_i^{K,1} = R_{i+1}^K - R_i^K = R_{i+1}^{K,2} - R_i^{K,2}$ with probability $1 - O(\varepsilon)$ and $R_{i+1}^{K,2} - R_{i+1}^{K,1} \leq A\sigma_K$. The distributions of $R_{i+1}^{K,1} -$

$R_i^{K,1}$ and $R_{i+1}^{K,2} - R_i^{K,2}$ are (cf. Corollary 6.10)

$$(8.5) \quad \begin{aligned} r_1^\varepsilon(R_i^K, h) &\equiv \mathbb{P}[R_{i+1}^{K,1} = R_i^K + \sigma_k h] \\ &= \begin{cases} \frac{M(R_i^K, 1)q_1^\varepsilon(R_i^K, 1)}{p_2^\varepsilon(R_i^K)} + 1 - \frac{p_1^\varepsilon(R_i^K)}{p_2^\varepsilon(R_i^K)}, & \text{if } h = 1, \\ \frac{M(R_i^K, h)q_1^\varepsilon(R_i^K, h)}{p_2^\varepsilon(R_i^K)}, & \text{if } h \in \{2, \dots, A\} \end{cases} \end{aligned}$$

and

$$(8.6) \quad \begin{aligned} r_2^\varepsilon(R_i^K, h) &\equiv \mathbb{P}[R_{i+1}^{K,2} = R_i^K + \sigma_k h] \\ &= \begin{cases} \frac{M(R_i^K, h)q_1^\varepsilon(R_i^K, h)}{p_2^\varepsilon(R_i^K)}, & \text{if } h \in \{1, \dots, A - 1\}, \\ \frac{M(R_i^K, A)q_1^\varepsilon(R_i^K, A)}{p_2^\varepsilon(R_i^K)} + 1 - \frac{p_1^\varepsilon(R_i^K)}{p_2^\varepsilon(R_i^K)}, & \text{if } h = A, \end{cases} \end{aligned}$$

where

$$(8.7) \quad \begin{aligned} q_1^\varepsilon(x, h) &= h \frac{\partial_1 f(x, x)}{b(x)} - C_{\text{Bernoulli}}^1 \varepsilon, \\ q_2^\varepsilon(x, h) &= h \frac{\partial_1 f(x, x)}{b(x)} + C_{\text{Bernoulli}}^2 \varepsilon \end{aligned}$$

and $p_j^\varepsilon(x) = \sum_{h=1}^A q_j^\varepsilon(x, h)M(x, h)$ for $j = 1, 2$. (Note that we changed a bit the notation of Corollary 6.10 to make explicit the dependence on ε and R_i^K .) Since we assumed that the fitness gradient $\partial_1 f(x, x)$ is positive and uniformly lower bounded on \mathcal{X} , the transition probabilities $r_j^\varepsilon(x, h)$, $j = 1, 2$ are uniformly Lipschitz-continuous functions of x with some Lipschitz constant C_{Lip}^r .

By Theorem 6.2 and Lemmata 6.7 and 6.4, we can construct two exponential random variables, $E_{i+1}^{K,1}$ and $E_{i+1}^{K,2}$, with parameters $a_1^{K,\varepsilon}(R_i^K)p_1^\varepsilon(R_i^K)\sigma_K u_K K$ and $a_2^{K,\varepsilon}(R_i^K)p_2^\varepsilon(R_i^K)\sigma_K u_K K$ given by

$$(8.8) \quad a_1^{K,\varepsilon}(x) = (\bar{z}(x) - \varepsilon\sigma_K M)b(x)m(x),$$

$$(8.9) \quad a_2^{K,\varepsilon}(x) = (\bar{z}(x) + \varepsilon\sigma_K (M + \lceil 3/\alpha \rceil))(b(x)m(x) + C_L^{b,m,M} A\sigma_K),$$

such that

$$(8.10) \quad \mathbb{P}[E_{i+1}^{K,2} \leq \theta_{i+1}^K - \theta_{i,\text{fixation}}^K \leq E_{i+1}^{K,1} + \ln(K)\sigma_K^{-1-\alpha/2}] = 1 - o(\sigma_K).$$

Note that this inequality involves $\theta_{i,\text{fixation}}^K$ instead of θ_i^K since we apply the Markov property at the fixation time of Lemma 7.9 before we can apply Theorem 6.2. However, Lemma 7.9 entails that we also have

$$(8.11) \quad \mathbb{P}[E_{i+1}^{K,2} \leq \theta_{i+1}^K - \theta_i^K \leq E_{i+1}^{K,1} + 6\ln(K)\sigma_K^{-1-\alpha/2}] = 1 - o(\sigma_K).$$

We then define

$$(8.12) \quad \theta_{i+1}^{K,1} - \theta_i^{K,1} \equiv E_{i+1}^{K,1} + 6 \ln(K) \sigma_K^{-1-\alpha/2} \quad \text{and} \quad \theta_{i+1}^{K,2} - \theta_i^{K,2} \equiv E_{i+1}^{K,2}.$$

In addition, by their construction in Section 6, it is clear that the random vectors $\{(E_{i+1}^{K,1}, E_{i+1}^{K,2}, R_{i+1}^{K,1} - R_i^{K,1}, R_{i+1}^{K,2} - R_i^{K,2})\}_{i \geq 0}$ are independent conditionally on $(R_j^K)_{j \geq 0}$.

LEMMA 8.1. *With the previous notation, the stochastic processes $\mu^{K,1}$ and $\mu^{K,2}$ in $\mathbb{D}([0, \infty), \mathcal{M}(\mathcal{X}))$ defined for all $t \geq 0$ by*

$$(8.13) \quad \mu_t^{1,K} = (\bar{z}(R_j^K) - (M\varepsilon + \bar{C})\sigma_K)\delta_{R_i^{K,1}},$$

for $t \in [\theta_i^{K,1}, \theta_{i+1}^{K,1}) \cap [\theta_j^K, \theta_{j+1}^K)$,

$$(8.14) \quad \mu_t^{2,K} = \left(\bar{z}(R_j^K) + \left(M\varepsilon + \left\lceil \frac{3}{\alpha} \right\rceil \varepsilon + \bar{C} \right) \sigma_K \right) \delta_{R_i^{K,2}},$$

for $t \in [\theta_i^{K,2}, \theta_{i+1}^{K,2}) \cap [\theta_j^K, \theta_{j+1}^K)$,

for some constant \bar{C} independent of K, x, ε , satisfy for all $T > 0$

$$(8.15) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\forall t \leq \frac{T}{Ku_K \sigma_K^2} : \mu_t^{1,K} \preceq \nu_t^K \preceq \mu_t^{2,K} \right] = 1.$$

Note that the support of $\mu^{j,K}$, $j = 1, 2$, is defined from the sequences $(R_i^{K,j})_{i \geq 0}$ and $(\theta_i^{K,j})_{i \geq 1}$ but the mass of $\mu^{j,K}$ is defined from the sequences $(R_i^K)_{i \geq 0}$ and $(\theta_i^K)_{i \geq 1}$.

PROOF. Let us fix $T > 0$ and $\Gamma > 0$. Since each of the steps previously described holds with probability $1 - o(\sigma_K)$, we deduce that the above construction can be done on a *good event* of probability $1 - o(1)$, for all integers $i \leq \Gamma/\sigma_K$. Since in addition, on \mathcal{X} , $a_2^{K,\varepsilon}(x)p_2^\varepsilon(x)$ is uniformly bounded from below by a positive constant \underline{a} , the random variables $E_i^{K,2}$ can be coupled with i.i.d. exponential ones of parameter $\underline{a}Ku_K\sigma_K$, and hence $\mathbb{P}[\theta_{\lfloor \Gamma/\sigma_K \rfloor}^{K,2} < T/(Ku_K\sigma_K^2)]$ is smaller than the probability that a Poisson process with parameter $\underline{a}Ku_K\sigma_K$ is larger than $\lfloor \Gamma/\sigma_K \rfloor$ at time $T/(Ku_K\sigma_K^2)$. By the law of large numbers for Poisson processes, we deduce that, if $\Gamma > T\underline{a}$ (which we assume true in the sequel),

$$(8.16) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\theta_{\lfloor \Gamma/\sigma_K \rfloor}^{K,2} < \frac{T}{Ku_K\sigma_K^2} \right] = 0.$$

Let us recall that, on the previous good event of probability $1 - o(1)$, the number, the trait and the size of the living mutant populations and the size of the resident population are controlled at any time in the i th first phase (Lemmata 6.3 and 6.9).

In addition, during the i th second phase, the number, trait, and size of living mutant populations are controlled (see all the lemmas of Section 7), the total mass of the population stays within the $M\varepsilon\sigma_K$ -neighborhood of $\phi(y)$ or $\psi(y)$ for some $y \in [0, \bar{z}(R_i^K)]$ (Lemmata 7.4 and 7.6). Since $|\phi(y) - \bar{z}(R_i^K)| \leq \bar{C}\sigma_K$ and $|\psi(y) - \bar{z}(R_i^K)| \leq \bar{C}\sigma_K$ for some constant \bar{C} , as seen in (7.26) and (7.69), and since the sequences $(R_i^{j,K})_{i \geq 0}$ for $j = 1, 2$ and $(R_i^K)_{i \geq 0}$ are all increasing on the good event, we deduce the required comparison between the supports of $\mu_t^{1,K}$, ν_t^K , and $\mu_t^{2,K}$ for $t \leq \frac{T}{Ku_K\sigma_K^2}$, on the good event. Since we used $\bar{z}(R_j^K)$ to define the masses of $\mu_t^{1,K}$ and $\mu_t^{2,K}$, the required comparison between the masses is also clear. \square

Note that, since the function \bar{z} may not be nondecreasing, replacing $\bar{z}(R_j^K)$ by $\bar{z}(R_j^{K,1})$ in the definition of $\mu_t^{1,K}$ may not imply the required comparison between the masses of $\mu_t^{1,K}$, ν_t^K and $\mu_t^{2,K}$.

The next goal is now to prove the convergence of both processes $\mu_{t/Ku_K\sigma_K^2}^{K,j}$ for $j = 1, 2$ to $\bar{z}(x_t)\delta_{x_t}$ in probability in $L^\infty(\mathcal{M}(\mathcal{X}), \|\cdot\|_0)$. For this, we will use standard convergence results of Markov jump processes. However, the two processes $\mu^{K,j}$, $j = 1, 2$ are not Markov because the i th jump rates and transition probabilities defined above depend on R_i^K which is close, but different from $R_i^{K,j}$. Therefore, we introduce a small parameter, $\eta > 0$, and we construct two Markov processes $\mu^{K,j,\varepsilon,\eta}$, $j = 1, 2$ in $\mathbb{D}([0, \infty), \mathcal{M}(\mathcal{X}))$ such that

$$(8.17) \quad \lim_{K \rightarrow +\infty} \mathbb{P} \left[\mu_{(t-1)/(Ku_K\sigma_K)}^{K,1,\varepsilon,\eta} \preceq \mu_t^{1,K} \preceq \nu_t^K \preceq \mu_t^{2,K} \preceq \mu_t^{K,2,\varepsilon,\eta}, \right. \\ \left. \forall t \leq \frac{T}{Ku_K\sigma_K^2} \wedge S_\eta^K \right] = 1,$$

where S_η^K is the first time where the distance between the support of $\mu_t^{K,1,\varepsilon,\eta}$, and $\mu_t^{K,2,\varepsilon,\eta}$ is larger than η . The last equation will be proved below in Section 8.2. The time-shift of $-1/(Ku_K\sigma_K)$ in $\mu^{K,1,\varepsilon,\eta}$ is due to the terms $6 \ln(K)\sigma_K^{-1-\alpha/2}$ in (8.12). We will next study the convergence of these two Markov processes when $K \rightarrow \infty$ and prove in Section 8.3 that, for a convenient choice of η , there exists some $T_0 > 0$ independent of K, x, ε, η such that

$$(8.18) \quad \lim_{K \rightarrow +\infty} \mathbb{P} \left[S_\eta^K < \frac{T_0}{Ku_K\sigma_K^2} \right] = 0.$$

8.2. *Proof of (8.17).* For all $x \in \mathcal{X}$, we define $(\bar{r}_1^{\varepsilon,\eta}(x, h), 1 \leq h \leq A)$, and $(\bar{r}_2^{\varepsilon,\eta}(x, h), 1 \leq h \leq A)$ by, for all $1 \leq \ell \leq A$,

$$(8.19) \quad \sum_{h=1}^\ell \bar{r}_1^{\varepsilon,\eta}(x, h) \equiv \left[\sum_{h=1}^\ell (r_1^\varepsilon(x, h) + C_{\text{Lip}}^\varepsilon \eta) \right] \wedge 1 \geq \sup_{y \in [x, x+\eta]} \sum_{h=1}^\ell r_1^\varepsilon(y, h)$$

and

$$(8.20) \quad \sum_{h=1}^{\ell} \bar{r}_2^{\varepsilon, \eta}(x, h) \equiv \left[\sum_{h=1}^{\ell} (r_2^{\varepsilon}(x, h) - C_{\text{Lip}}^r \eta) \right] \vee 0 \leq \inf_{y \in [x, x+\eta]} \sum_{h=1}^{\ell} r_1^{\varepsilon}(y, h).$$

Note that $\bar{r}_1^{\varepsilon, \eta}(x, \cdot)$ and $\bar{r}_2^{\varepsilon, \eta}(x, \cdot)$ are probability distributions on $\{1, \dots, A\}$ for all $x \in \mathcal{X}$ and that, by standard coupling arguments, for all $x < y$ such that $y - x \leq \eta$, the distribution $\bar{r}_1^{\varepsilon, \eta}(x, \cdot)$ is stochastically dominated by the distribution $r_1^{\varepsilon}(y, \cdot)$ and the distribution $r_2^{\varepsilon}(x, \cdot)$ is stochastically dominated by the distribution $\bar{r}_2^{\varepsilon, \eta}(y, \cdot)$. We define similarly

$$(8.21) \quad \bar{a}_1^{K, \varepsilon, \eta}(x) \equiv a_1^{K, \varepsilon}(x) p_1^{\varepsilon}(x) - C_{\text{Lip}}^a \eta \leq \inf_{y \in [x, x+\eta] \cap \mathcal{X}} a_1^{K, \varepsilon}(y) p_1^{\varepsilon}(y),$$

and

$$(8.22) \quad \bar{a}_2^{K, \varepsilon, \eta}(x) \equiv a_2^{K, \varepsilon}(x) p_2^{\varepsilon}(x) + C_{\text{Lip}}^a \eta \geq \sup_{y \in [x-\eta, x] \cap \mathcal{X}} a_2^{K, \varepsilon}(y) p_2(y),$$

where C_{Lip}^a is a uniform Lipschitz constant for the functions $a_j^{K, \varepsilon} p_j^{\varepsilon}$, $j = 1, 2$. Note that $a_1^{K, \varepsilon, \eta}(x) > 0$ for all $x \in \mathcal{X}$ if η is small enough.

It is then clear that there exist two Markov chains $(\bar{R}_i^{K, j, \eta})_{i \geq 0}$, $j = 1, 2$, with initial condition $\bar{R}_0^{K, j, \eta} = R_0^{K, j}$ and with transition probabilities $\bar{r}_j^{K, \varepsilon, \eta}(x, h)$ from x to $x + h$, such that, for all $i \geq 0$ satisfying $\bar{R}_i^{K, 2, \eta} - \bar{R}_i^{K, 1, \eta} \leq \eta$,

$$(8.23) \quad \begin{aligned} \bar{R}_{i+1}^{K, 1, \eta} - \bar{R}_i^{K, 1, \eta} &\leq R_{i+1}^{K, 1} - R_i^{K, 1} \quad \text{and} \\ R_{i+1}^{K, 2} - R_i^{K, 2} &\leq \bar{R}_{i+1}^{K, 2, \eta} - \bar{R}_i^{K, 2, \eta} \leq R_{i+1}^{K, 1} - R_i^{K, 1}. \end{aligned}$$

Similarly, there are random variables $\bar{E}_{i+1}^{K, j, \eta}$, $j = 1, 2$, independent and exponentially distributed with parameters $\bar{a}_j^{K, \varepsilon, \eta}(\bar{R}_i^{K, j, \eta})$ conditionally on $(\bar{R}_i^{K, j, \eta})_{i \geq 0}$, such that $\bar{E}_{i+1}^{K, 2, \eta} \leq E_{i+1}^{K, 2}$ and $E_{i+1}^{K, 1} \leq \bar{E}_{i+1}^{K, 1, \eta}$. We then define $\bar{\theta}_{i+1}^{K, j, \eta} - \bar{\theta}_i^{K, j, \eta} = E_{i+1}^{K, j, \theta}$ with $\bar{\theta}_0^{K, j, \eta} = 0$.

Since the function \bar{z} is $C_{\text{Lip}}^{\bar{z}}$ -Lipschitz, it is clear that (8.17) is satisfied for the processes:

$$(8.24) \quad \bar{\mu}_t^{K, 1, \varepsilon, \eta} = (\bar{z}(\bar{X}_t^{K, 1, \eta}) - (M\varepsilon + \bar{C})\sigma_K - C_{\text{Lip}}^{\bar{z}}\eta)\delta_{\bar{X}_t^{K, 1, \eta}} \quad \text{and}$$

$$(8.25) \quad \mu_t^{K, 2, \varepsilon, \eta} = (\bar{z}(X_t^{K, 2, \eta}) + (M\varepsilon + \lceil 3/\alpha \rceil \varepsilon + \bar{C})\sigma_K + C_{\text{Lip}}^{\bar{z}}\eta)\delta_{X_t^{K, 2, \eta}},$$

where

$$\begin{aligned} \bar{X}_t^{K, 1, \eta} &= \bar{R}_i^{K, 1, \eta}, \\ \text{for } t \in [\bar{\theta}_i^{K, 1, \eta} + 6i \ln(K)\sigma_K^{-1-\alpha/2}, \bar{\theta}_{i+1}^{K, 1, \eta} + 6(i+1) \ln(K)\sigma_K^{-1-\alpha/2}), \end{aligned}$$

and

$$(8.26) \quad X_t^{K,2,\eta} = \bar{R}_i^{K,2,\eta}, \quad \text{for } t \in [\bar{\theta}_i^{K,2,\eta}, \bar{\theta}_{i+1}^{K,2,\eta}).$$

By construction, the processes $X^{K,2,\eta}$ and $\mu^{K,2,\eta}$ are Markov jump processes, but the process $\bar{X}^{K,1,\eta}$ is not because of the terms $6 \ln(K)\sigma_K^{-1-\alpha/2}$ involved in its definition. However, the process $\mu_t^{K,1,\varepsilon,\eta} = (\bar{z}(X_t^{K,1,\eta}) - \varepsilon\sigma_K M - C_{\text{Lip}}^{\bar{z}}\eta)\delta_{X_t^{K,1,\eta}}$ is Markov, where

$$(8.27) \quad X_t^{K,1,\eta} = \bar{R}_i^{K,1,\eta}, \quad \text{for } t \in [\bar{\theta}_i^{K,1,\eta}, \bar{\theta}_{i+1}^{K,1,\eta}).$$

The proof of (8.16) above also applies to the processes $\mu^{K,1,\varepsilon,\eta}$, and $\bar{\mu}^{K,1,\varepsilon,\eta}$. Since in addition the support of $\mu_t^{K,1,\varepsilon,\eta}$ is nondecreasing, it follows that

$$(8.28) \quad \mu_{(t-6\Gamma \ln(K)\sigma_K^{-2-\alpha/2}) \vee 0}^{K,1,\varepsilon,\eta} \preceq \bar{\mu}_t^{K,1,\varepsilon,\eta} \quad \text{for all } t \leq T/(Ku_K\sigma_K^2)$$

with probability $1 + o(1)$. Our assumption (4.2) entails (8.17).

8.3. *Convergence of $X^{K,j,\eta}$ when $K \rightarrow +\infty$ and proof of (8.18).* The two Markov processes $X_{t/(Ku_K\sigma_K)}^{K,1,\eta}$, and $X_{t/(Ku_K\sigma_K)}^{K,2,\eta}$ fit exactly to the framework and assumptions of Theorem 2.1 of Chapter 11 of [12]: their state spaces are (up to a translation) a subset of $\sigma_K\mathbb{Z}$, and their transition rates from z to $z + h\sigma_K$ have the form $\sigma_K^{-1}[\beta_h(z) + O(\sigma_K)]$ for some Lipschitz functions β_h . For such a process X , provided X_0 converges a.s. to x_0 , the process $(X_{t/\sigma_K}, t \geq 0)$ converges when $\sigma_K \rightarrow 0$ almost surely in $L^\infty([0, T])$ for all $T > 0$ to the unique deterministic solution of the ODE $dx(t)/dt = \sum_h h\beta_h(x)$ with $x(0) = x_0$. In our situation, we obtain, for $j = 1, 2$, that

$$(8.29) \quad \lim_{K \rightarrow +\infty} \sup_{t \in [0, T]} |X_{t/(Ku_K\sigma_K^2)}^{K,j,\eta} - x_j(t)| = 0 \quad \text{a.s.,}$$

where x_1 and x_2 are the unique solutions such that $x_1(0) = x_2(0) = x$ of the ODEs

$$(8.30) \quad \begin{aligned} \frac{dx_1(t)}{dt} &= (\bar{z}(x_1(t))b(x_1(t))m(x_1(t))p_1^\varepsilon(x_1(t)) - C_{\text{Lip}}^a\eta) \\ &\quad \times \sum_{h=1}^A h\bar{r}_1^{\varepsilon,\eta}(x_1(t), h) \end{aligned}$$

and

$$(8.31) \quad \begin{aligned} \frac{dx_2(t)}{dt} &= (\bar{z}(x_2(t))b(x_2(t))m(x_2(t))p_2^\varepsilon(x_2(t)) + C_{\text{Lip}}^a\eta) \\ &\quad \times \sum_{h=1}^A h\bar{r}_2^{\varepsilon,\eta}(x_2(t), h). \end{aligned}$$

LEMMA 8.2. For all $T > 0$, and for $j = 1, 2$,

$$(8.32) \quad \sup_{t \in [0, T]} |x_j(t) - x_t| \leq CT e^{CT} (\eta + \varepsilon),$$

for a constant C independent of x, T, ε and η , where x_t is the solution of the CEAD (4.3) with initial condition $x_0 = x$.

PROOF. We only write the proof for $j = 1$, the case $j = 2$ being similar. Since the functions $\bar{r}_j^{\varepsilon, \eta}, j = 1, 2, \bar{z}, b, m$ and p_1 are bounded by constants independent of K, ε, η , we have for all $t \in [0, T]$ and for a constant $C > 0$ that may change from line to line,

$$(8.33) \quad \begin{aligned} |x_t - x_1(t)| &\leq CC_{\text{Lip}}^a \eta T + \int_0^t \left| (\bar{z} b m p_1^\varepsilon)(x_1(s)) \sum_{h=1}^A h \bar{r}_1^{\varepsilon, \eta}(x_1(s), h) \right. \\ &\quad \left. - (\bar{z} b m p_1^\varepsilon)(x_s) \sum_{h=1}^A \frac{h^2 M(x_s, h) \partial_1 f(x_s, x_s)}{b(x_s) p_1^\varepsilon(x_s)} \right| ds \\ &\leq C(C_{\text{Lip}}^a + AC_{\text{Lip}}^r) T \eta + C \int_0^t |x_s - x_1(s)| ds \\ &\quad + C \int_0^t \sum_{h=1}^A \left| r_1^\varepsilon(x_s, h) - \frac{h M(x_s, h) \partial_1 f(x_s, x_s)}{b(x_s) p_1^\varepsilon(x_s)} \right| ds, \end{aligned}$$

where the last inequality follows from the uniform Lipschitz-continuity of all functions involved in the computation. Now, $|p_2^\varepsilon(x) - p_1^\varepsilon(x)| \leq C\varepsilon$ and $p_j^\varepsilon(x) \geq c > 0$ for $j = 1, 2$, for some constants $C, c > 0$ independent of ε and x . Hence, there exists a constant C such that

$$(8.34) \quad \begin{aligned} |x_t - x_1(t)| &\leq CT(\eta + \varepsilon) + C \int_0^t |x_s - x_1(s)| ds \\ &\quad + C \int_0^t \sum_{h=1}^A \left| q_1^\varepsilon(x_s, h) - h \frac{\partial_1 f(x_s, x_s)}{b(x_s)} \right| M(x_s, h) ds. \end{aligned}$$

In view of (8.7), we obtain $|x_t - x_1(t)| \leq CT(\eta + \varepsilon) + C \int_0^t |x_s - x_1(s)| ds$. Gronwall’s lemma ends the proof of Lemma 8.2. \square

In view of Lemma 8.2, there exists $T_0 > 0$ independent of x, ε, η such that, for all $\eta \geq \varepsilon$, $\sup_{t \in [0, T_0]} |x_j(t) - x_t| \leq \eta/4$. Let us fix $\eta = \varepsilon$. Combining (8.29) with the last inequality entails (8.18).

8.4. *End of the proof.*

PROOF OF THEOREM 4.1. Defining $\bar{\mu}^{K,1,\varepsilon} = \mu^{K,1,\varepsilon,\varepsilon}$ and $\mu^{K,2,\varepsilon} = \mu^{K,2,\varepsilon,\varepsilon}$, and combining (8.17) and (8.18), we see that we have defined a constant, $T_0 > 0$, such that

$$(8.35) \quad \lim_{K \rightarrow +\infty} \mathbb{P} \left[\bar{\mu}_{(t-1/(Ku_K\sigma_K)) \vee 0}^{K,1,\varepsilon} \preceq \mu_t^{1,K} \preceq v_t^K \preceq \mu_t^{2,K} \preceq \mu_t^{K,2,\varepsilon}, \right. \\ \left. \forall t \leq \frac{T_0}{Ku_K\sigma_K^2} \right] = 1.$$

This is (8.1) with $\mu_t^{K,1,\varepsilon} = \bar{\mu}_{(t-1/(Ku_K\sigma_K)) \vee 0}^{K,1,\varepsilon}$. It only remains to check (8.2).

Using that $\eta = \varepsilon$, we get

$$(8.36) \quad \begin{aligned} & \left\| \mu_{t/Ku_K\sigma_K^2}^{K,1,\varepsilon} - \bar{z}(x(t))\delta_{x(t)} \right\|_0 \\ & \leq C(\varepsilon + \sigma_K + |\bar{z}(x_t) - \bar{z}(X_{(t-\sigma_K) \vee 0}^{K,1,\eta}/Ku_K\sigma_K^2)| + |x_t - x_1((t - \sigma_K) \vee 0)|) \\ & \quad + |X_{(t-\sigma_K) \vee 0}^{K,1,\eta}/Ku_K\sigma_K^2 - x_1((t - \sigma_K) \vee 0)| \\ & \leq C'(\varepsilon + \sigma_K \\ & \quad + \sup_{t \in [0, T]} (|x_{(t-\sigma_K) \vee 0} - x_t| + |x_t - x_1(t)| + |X_{t/Ku_K\sigma_K^2}^{K,1,\eta} - x_1(t)|)), \end{aligned}$$

for some finite constants $C, C' > 0$. The analogous estimate holds for $\mu_{t/Ku_K\sigma_K^2}^{2,K,\eta}$. Setting, for example, $\delta(\varepsilon) = \sqrt{\varepsilon}$, (8.2) follows from (8.29), Lemma 8.2 and the uniform continuity of x_t . This completes the proof of Theorem 4.1. \square

APPENDIX

In this section, we state and prove several elementary results, which we used in the proof of our main theorem. Recall that $\|\cdot\|_0$ is the Kantorovich–Rubinstein norm on the vector space of finite, signed measures on \mathcal{X} , that is,

$$(A.1) \quad \|\mu_t\|_0 \equiv \sup \left\{ \int_{\mathcal{X}} f d\mu_t : f \in \text{Lip}_1(\mathcal{X}) \text{ with } \sup_{x \in \mathcal{X}} |f(x)| \leq 1 \right\},$$

where $\text{Lip}_1(\mathcal{X})$ is the space of Lipschitz continuous functions from \mathcal{X} to \mathbb{R} . Let $\mathcal{M}_F(\mathcal{X})$ be the set of nonnegative finite Borel-measures on \mathcal{X} .

PROPOSITION A.1. *Let $\{v^K, K \geq 0\}$ and μ be random elements in $\mathbb{D}([0, T], \mathcal{M}_F(\mathcal{X}))$. If, for all $\delta > 0$,*

$$(A.2) \quad \lim_{K \rightarrow \infty} \mathbb{P} \left[\sup_{0 \leq t \leq T} \|v_t^K - \mu_t\|_0 > \delta \right] = 0,$$

then ν^K converges in probability, as $K \rightarrow \infty$, with respect to the Skorokhod topology on $\mathbb{D}([0, T], \mathcal{M}(\mathcal{X}))$ to μ .

PROOF. Let us equip $\mathcal{M}_F(\mathcal{X})$ with the topology of weak convergence. Observe that this topology is metrizable with the Kantorovich–Rubinstein norm; see [4] Volume II, page 193. Let Λ be the class of strictly increasing, continuous mapping of $[0, T]$ onto itself. If $\lambda \in \Lambda$, then $\lambda(0) = 0$ and $\lambda(T) = T$. The Skorokhod topology on $\mathbb{D}([0, T], (\mathcal{M}_F(\mathcal{X}), \|\cdot\|_0))$ is generated by the distance

$$(A.3) \quad d(\mu, \nu) = \inf_{\lambda \in \Lambda} \left\{ \max \left\{ \sup_{t \in [0, T]} |\lambda(t) - t|, \sup_{t \in [0, T]} \|\mu_t - \nu_{\lambda t}\|_0 \right\} \right\},$$

on $\mathbb{D}([0, T], (\mathcal{M}_F(\mathcal{X}), \|\cdot\|_0))$; see, for example, [3], Chapter 3. Since the identity lies in Λ , it is clear that $d(\mu, \nu) \leq \sup_{t \in [0, T]} \|\mu_t - \nu_t\|_0$. Therefore, if a sequence of random elements with state space $\mathbb{D}([0, T], \mathcal{M}_F(\mathcal{X}))$ equipped with the metric induced by the norm $\sup_{t \in [0, T]} \|\mu_t\|_0$ converges in probability to μ , it also converges in probability to μ if $\mathbb{D}([0, T], \mathcal{M}_F(\mathcal{X}))$ is equipped with the metric d . \square

PROPOSITION A.2. Fix $\varepsilon > 0$ and let σ_K a sequence in K with $K^{-\frac{1}{2} + \alpha} \ll \sigma_K \ll 1$. Let Z_n be a Markov chain with state space \mathbb{N}_0 and with the following transition probabilities:

$$(A.4) \quad \begin{aligned} &\mathbb{P}[Z_{n+1} = j | Z_n = i] \\ &= p(i, j) = \begin{cases} 1, & \text{for } i = 0 \text{ and } j = 1, \\ \frac{1}{2} - C_1 i K^{-1} + C_2 \varepsilon \sigma_K, & \text{for } i \geq 1 \text{ and } j = i + 1, \\ \frac{1}{2} + C_1 i K^{-1} - C_2 \varepsilon \sigma_K, & \text{for } i \geq 1 \text{ and } j = i - 1, \end{cases} \end{aligned}$$

for some constants $C_1 > 0$ and $C_2 \geq 0$. Let τ_i be the first hitting time of level i by Z and let \mathbb{P}_a denote the law of Z conditioned on $Z_0 = a$. Then, for all $M \geq \frac{8C_2}{C_1}$ and for all $a \leq \frac{1}{3} M \varepsilon \sigma_K K$

$$(A.5) \quad \lim_{K \rightarrow \infty} e^{K^{2\alpha}} \mathbb{P}_a[\tau_{\lceil M \varepsilon \sigma_K K \rceil} < \tau_0] = 0.$$

REMARK 9. The proposition can be seen as a moderate deviation result for this particular Markov chain. More precisely, we can prove that there exist two constants $M > 0$ and $C_3 > 0$ which depend only on C_1 and C_2 such that for $a < \frac{1}{3} M \varepsilon \sigma_K K$

$$(A.6) \quad \mathbb{P}_a[\tau_{\lceil M \varepsilon \sigma_K K \rceil} < \tau_0] \leq \exp\left(-C_3 K^{-1} \left(\left(\frac{1}{3} M \varepsilon \sigma_K K\right)^2 - a^2\right)\right),$$

for all K large enough.

PROOF. We calculate this probability with some standard potential theory arguments. Let $h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(a)$ be the solution of the Dirichlet problem with $\lambda = 0$, that is,

$$\begin{aligned}
 \mathcal{L}h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(x) &= 0, & \text{for } 0 < x < \lceil M\varepsilon\sigma_K K \rceil, \\
 h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(x) &= 1, & \text{for } x \geq \lceil M\varepsilon\sigma_K K \rceil, \\
 h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(x) &= 0, & \text{for } x = 0.
 \end{aligned}
 \tag{A.7}$$

Therefore, we obtain for $0 < a < \lceil M\varepsilon\sigma_K K \rceil$ (cf. [5] page 188)

$$\mathbb{P}_a[\tau_{\lceil M\varepsilon\sigma_K K \rceil} < \tau_0] = h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(a) = \frac{\sum_{i=1}^a \frac{1}{\pi(i)} \frac{1}{p(i, i-1)}}{\sum_{i=1}^{\lceil M\varepsilon\sigma_K K \rceil} \frac{1}{\pi(i)} \frac{1}{p(i, i-1)}},
 \tag{A.8}$$

where $\pi = (\pi(0), \pi(1), \pi(2), \dots)$ is an invariant measure of the one-dimensional Markov chain Z_n . In our case, any invariant measure π has to satisfy, for all $i \geq 1$,

$$\begin{aligned}
 \pi(0) &= p(1, 0)\pi(1) \quad \text{and} \\
 \pi(i) &= p(i-1, i)\pi(i-1) + p(i+1, i)\pi(i+1).
 \end{aligned}
 \tag{A.9}$$

Therefore, π with $\pi(0) = 1$, $\pi(1) = \frac{1}{p(1, 0)}$ and $\pi(i) = \prod_{j=1}^{i-1} \frac{p(j, j+1)}{p(j, j-1)} \frac{1}{p(i, i-1)}$ is the unique invariant measure for the Markov chain Z_n . Thus, we get from (A.8) that

$$\begin{aligned}
 h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(a) &= \frac{\sum_{i=1}^a \prod_{j=1}^{i-1} \frac{p(j, j-1)}{p(j, j+1)}}{\sum_{i=1}^{\lceil M\varepsilon\sigma_K K \rceil} \prod_{j=1}^{i-1} \frac{p(j, j-1)}{p(j, j+1)}} \\
 &= \frac{\sum_{i=1}^a \exp(\sum_{j=1}^{i-1} \ln(\frac{1+2C_1K^{-1}j-2C_2\varepsilon\sigma_K}{1-2C_1K^{-1}j+2C_2\varepsilon\sigma_K}))}{\sum_{i=1}^{\lceil M\varepsilon\sigma_K K \rceil} \underbrace{\exp(\sum_{j=1}^{i-1} \ln(\frac{1+2C_1K^{-1}j-2C_2\varepsilon\sigma_K}{1-2C_1K^{-1}j+2C_2\varepsilon\sigma_K}))}_{=: f(j)}}.
 \end{aligned}
 \tag{A.10}$$

For all $j \leq M\varepsilon\sigma_K K$, we can approximate $f(j)$ as follows:

$$\begin{aligned}
 f(j) &= \ln\left(1 + \frac{4C_1K^{-1}j - 4C_2\varepsilon\sigma_K}{1 - 2C_1K^{-1}j + 2C_2\varepsilon\sigma_K}\right) \\
 &= \frac{4C_1K^{-1}j - 4C_2\varepsilon\sigma_K}{1 - 2C_1K^{-1}j + 2C_2\varepsilon\sigma_K} - O\left(\left(\frac{4C_1K^{-1}j - 4C_2\varepsilon\sigma_K}{1 - 2C_1K^{-1}j + 2C_2\varepsilon\sigma_K}\right)^2\right) \\
 &= 4C_1\frac{j}{K} - 4C_2\varepsilon\sigma_K + O\left(\left(\frac{j}{K}\right)^2 + \varepsilon\sigma_K\frac{j}{K} + \varepsilon^2\sigma_K^2\right) \\
 &= 4C_1\frac{j}{K} - 4C_2\varepsilon\sigma_K + O((M\varepsilon\sigma_K)^2).
 \end{aligned}
 \tag{A.11}$$

Therefore,

$$\begin{aligned}
 & h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(a) \\
 & \leq \frac{\sum_{i=1}^a \exp(\sum_{j=1}^{i-1} 4C_1 \frac{j}{K} + O((M\varepsilon\sigma_K)^2))}{\sum_{i=1}^{\lceil M\varepsilon\sigma_K K \rceil} \exp(\sum_{j=1}^{i-1} 4C_1 \frac{j}{K} - 4C_2\varepsilon\sigma_K - O((M\varepsilon\sigma_K)^2))} \\
 \text{(A.12)} \quad & \leq \frac{a \exp(2C_1 a^2 K^{-1} + O(a(M\varepsilon\sigma_K)^2))}{\sum_{i=1}^{\lceil M\varepsilon\sigma_K K \rceil} \exp(2C_1 K^{-1}(i^2 - i) - 4C_2\varepsilon\sigma_K i - O((i-1)(M\varepsilon\sigma_K)^2))} \\
 & \leq \frac{a \exp(2C_1 a^2 K^{-1} + O(a(M\varepsilon\sigma_K)^2))}{\sum_{i=\frac{1}{2}\lceil M\varepsilon\sigma_K K \rceil}^{\lceil M\varepsilon\sigma_K K \rceil} \exp(2C_1 K^{-1} i^2 - (2C_1 K^{-1} + 4C_2\varepsilon\sigma_K) i - O(i(M\varepsilon\sigma_K)^2))}.
 \end{aligned}$$

Choosing $M \geq \frac{8C_2}{C_1}$, if $a < \frac{M\varepsilon\sigma_K K}{3}$, then

$$\begin{aligned}
 & h_{\lceil M\varepsilon\sigma_K K \rceil, 0}(a) \\
 & \leq \frac{a \exp(2C_1 a^2 K^{-1} + O(a(M\varepsilon\sigma_K)^2))}{\frac{1}{2}\lceil M\varepsilon\sigma_K K \rceil \exp((\frac{1}{2}C_1 M - 2C_2)M\varepsilon^2\sigma_K^2 K - O((\varepsilon\sigma_K M)^3 K + \varepsilon\sigma_K M))} \\
 \text{(A.13)} \quad & \leq 2a(\lceil M\varepsilon\sigma_K K \rceil)^{-1} \exp\left(C_1 K^{-1} \left(2a^2 - \frac{1}{4}(\lceil M\varepsilon\sigma_K K \rceil)^2\right)\right) \\
 & \leq \exp\left(-C_3 K^{-1} \left(\left(\frac{1}{3}\lceil M\varepsilon\sigma_K K \rceil\right)^2 - a^2\right)\right).
 \end{aligned}$$

Since $K^{-\frac{1}{2}+\alpha} \ll \sigma_K$ when K tends to infinity, (A.5) follows. \square

PROPOSITION A.3. *Let $(Z_t)_{t \geq 0}$ be a branching process with birth rate per individual b and death rate per individual d . Let τ_i be the first hitting time of level i by Z and let \mathbb{P}_j denote the law of Z conditioned on $Z_0 = j$, and \mathbb{E}_j the corresponding expectation. Then*

$$\text{(A.14)} \quad \mathbb{P}_j[\tau_k < \tau_0] = \frac{(d/b)^j - 1}{(d/b)^k - 1} \quad \text{for all } 1 \leq j \leq k - 1,$$

$$\text{(A.15)} \quad \left| \mathbb{P}_1[\tau_k < \tau_0] - \frac{[b-d]_+}{b} \right| \leq k^{-1} \quad \text{and}$$

$$\text{(A.16)} \quad \mathbb{E}_1[\tau_k \wedge \tau_0] \leq \frac{1 + \ln(k)}{b},$$

where $[b-d]_+ \equiv \max\{b-d, 0\}$. Moreover, if Z_t is slightly super-critical, that is, $b = d + \varepsilon$, then

$$\text{(A.17)} \quad \max_{n \leq k} \frac{\mathbb{E}_n[\tau_k \wedge \tau_0]}{\mathbb{P}_n[\tau_k < \tau_0]} \leq \frac{1 + \ln(k)}{\varepsilon}.$$

PROOF. Let $p_j \equiv \mathbb{P}_j[\tau_k < \tau_0]$. Then $p_0 = 0$, $p_k = 1$, and $p_j = \frac{b}{b+d}p_{j+1} + \frac{d}{b+d}p_{j-1}$ for all $1 \leq j \leq k - 1$ by the Markov property. From this recursion, we obtain the characteristic polynomial:

$$(A.18) \quad P(x) = bx^2 - (b + d)x + d.$$

With its roots 1 and d/b , we obtain the following general solution for the recursion:

$$(A.19) \quad p_n = \kappa_0 \cdot 1^n + \kappa_1 \left(\frac{d}{b}\right)^n,$$

where κ_0 and κ_1 are constants. From the initial condition $p_0 = 0$ and $p_k = 1$, we obtain $\kappa_0 = -((\frac{d}{b})^k - 1)^{-1}$ and $\kappa_1 = ((\frac{d}{b})^k - 1)^{-1}$. Therefore,

$$(A.20) \quad p_n = \frac{(\frac{d}{b})^n - 1}{(\frac{d}{b})^k - 1} \quad \text{and} \quad p_1 = \frac{\frac{d}{b} - 1}{(\frac{d}{b})^k - 1} = \frac{1}{1 + \frac{d}{b} + \dots + (\frac{d}{b})^{k-1}}.$$

If $d \geq b$, this computation implies that $p_1 \equiv \mathbb{P}_1[\tau_k < \tau_0] \leq 1/k$ and $[b - d]_+ = 0$. If $d < b$,

$$(A.21) \quad \begin{aligned} & \mathbb{P}_1[\tau_k < \tau_0] - \frac{b - d}{b} \\ &= \frac{\frac{d}{b} - 1}{(\frac{d}{b})^k - 1} - \left(1 - \frac{d}{b}\right) \frac{(\frac{d}{b})^k - 1}{(\frac{d}{b})^k - 1} = \frac{(\frac{d}{b} - 1)(\frac{d}{b})^k}{(\frac{d}{b})^k - 1} = \frac{\frac{d}{b} - 1}{1 - (\frac{b}{d})^k} \\ &= \frac{\frac{d}{b}(1 - \frac{b}{d})}{1 - (\frac{b}{d})^k} = \frac{1}{\frac{b}{d}(1 + \frac{b}{d} + \dots + (\frac{b}{d})^{k-1})} = \frac{1}{\frac{b}{d} + \dots + (\frac{b}{d})^k} \\ &\leq \frac{1}{k}. \end{aligned}$$

Similarly, if $e_n \equiv \mathbb{E}_n[\tau_k \wedge \tau_0]$, then e_n is the solution of the following nonhomogeneous Dirichlet problem:

$$(A.22) \quad \begin{aligned} \mathcal{L}e_n &= -1, & \text{for } n \in \{1, \dots, k - 1\}, \\ e_n &= 0, & \text{for } n \in \mathbb{N}_0 \setminus \{1, \dots, k - 1\}, \end{aligned}$$

where $(\mathcal{L}f)(x) = x(b[f(x + 1) - f(x)] + d[f(x - 1) - f(x)])$ is the generator of the branching process Z . Therefore, we have to solve the following nonhomogeneous recurrence:

$$(A.23) \quad e_{n+2} - \frac{b + d}{b}e_{n+1} + \frac{d}{b}e_n = \frac{-1}{b(n + 1)} \quad \text{and} \quad e_0 = e_k = 0.$$

We solve this by variation of parameters. Thus, we first solve the associated linear homogeneous recurrence relation:

$$(A.24) \quad h_{n+2} - \frac{b + d}{b}h_{n+1} + \frac{d}{b}h_n = 0.$$

As we have seen before $h_n = \kappa_2 1 + \kappa_3 \left(\frac{d}{b}\right)^j$ for any $\kappa_2, \kappa_3 \in \mathbb{R}$ solves the equation. Obverse that these functions are the harmonic functions of \mathcal{L} . Second, we have to find a particular solution. Let (x_{1j}, x_{2j}) the solution of the system of linear equations

$$(A.25) \quad x_{1j} + \left(\frac{d}{b}\right)^{j+1} x_{2j} = 0,$$

$$(A.26) \quad x_{1j} + \left(\frac{d}{b}\right)^{j+2} x_{2j} = -\frac{1}{b(j+1)},$$

then

$$(A.27) \quad \begin{aligned} e_n^p &= \sum_{j=0}^{n-1} x_{1j} 1^n + \sum_{j=0}^{n-1} x_{2j} \left(\frac{d}{b}\right)^n \\ &= \frac{-1}{b-d} \sum_{j=1}^n \frac{1}{j} + \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \left(\frac{b}{d}\right)^j \left(\frac{d}{b}\right)^n \\ &= \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \left(\left(\frac{d}{b}\right)^{n-j} - 1 \right) \end{aligned}$$

is a particular solution. Now, we obtain we obtain the following general solution for the recurrence:

$$(A.28) \quad e_n = h_n + e_n^p = \kappa_2 + \kappa_3 \left(\frac{d}{b}\right)^n + \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \left(\left(\frac{d}{b}\right)^{n-j} - 1 \right).$$

We have the boundary condition $e_0 = e_k = 0$, therefore, κ_2 and κ_3 are given by the solution of the following system of linear equations:

$$(A.29) \quad \kappa_2 + \kappa_3 \left(\frac{d}{b}\right)^0 + \frac{1}{b-d} \sum_{j=1}^0 \frac{1}{j} \left(\left(\frac{d}{b}\right)^{0-j} - 1 \right) = 0,$$

$$(A.30) \quad \kappa_2 + \kappa_3 \left(\frac{d}{b}\right)^k + \frac{1}{b-d} \sum_{j=1}^k \frac{1}{j} \left(\left(\frac{d}{b}\right)^{k-j} - 1 \right) = 0,$$

and we obtain that

$$(A.31) \quad \begin{aligned} e_n &= \frac{1}{b-d} \sum_{j=1}^k \frac{1}{j} \frac{\left(\frac{d}{b}\right)^{k-j} - 1}{\left(\frac{d}{b}\right)^k - 1} - \frac{1}{b-d} \sum_{j=1}^k \frac{1}{j} \frac{\left(\frac{d}{b}\right)^{k-j} - 1}{\left(\frac{d}{b}\right)^k - 1} \left(\frac{d}{b}\right)^n \\ &\quad + \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \left(\left(\frac{d}{b}\right)^{n-j} - 1 \right) \\ &= \frac{1}{b-d} \sum_{j=1}^k \frac{1}{j} \frac{\left(\frac{d}{b}\right)^{k-j} - 1}{\left(\frac{d}{b}\right)^k - 1} \frac{(1 - \left(\frac{d}{b}\right)^n)}{\left(\frac{d}{b}\right)^k - 1} + \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \left(\left(\frac{d}{b}\right)^{n-j} - 1 \right). \end{aligned}$$

With this formula, we can easily prove the second inequality of the proposition,

$$(A.32) \quad e_1 = \frac{1}{b-d} \sum_{n=1}^k \frac{1}{n} \frac{\left(\frac{d}{b}\right)^{k-n} - 1}{\left(\frac{d}{b}\right)^k - 1} \left(1 - \frac{d}{b}\right) + 0 \leq \frac{1}{b} \sum_{n=1}^k \frac{1}{n} \leq \frac{1 + \ln(k)}{b}.$$

Finally, we obtain for slightly super-critical Z_t , that is, with $b = d + \varepsilon$,

$$(A.33) \quad \begin{aligned} \frac{\mathbb{E}_n[\tau_k \wedge \tau_0]}{\mathbb{P}_n[\tau_k < \tau_0]} &= \frac{e_n}{p_n} = \frac{1}{b-d} \sum_{j=1}^k \frac{1}{j} \underbrace{\left(\left(\frac{d}{b}\right)^{k-j} - 1 \right)}_{\leq 1} (-1) \\ &+ \frac{1}{b-d} \sum_{j=1}^n \frac{1}{j} \underbrace{\frac{\left(\frac{d}{b}\right)^{n-j} - 1}{1 - \left(\frac{d}{b}\right)^n} \left(1 - \left(\frac{d}{b}\right)^k\right)}_{\leq 0} \\ &\leq \frac{1}{\varepsilon} \sum_{j=1}^k \frac{1}{j} \leq \frac{1 + \ln(k)}{\varepsilon}, \end{aligned}$$

which proves (A.17). \square

PROPOSITION A.4. *Let $(Z_t^K)_{t \geq 0}$ be a sequence branching process with birth rate per individual $b \geq 0$ and death rate per individual $d \geq 0$ and $|b - d| = O(\sigma_K)$, where $K^{-1/2+\alpha} \ll \sigma_K \ll 1$. Let τ_i be the first hitting time of level i by Z and let \mathbb{P}_j denote the law of Z conditioned on $Z_0 = j$.*

(a) *The invasion probability can be approximated up to an error of order $\exp(-K^\alpha)$:*

$$(A.34) \quad \lim_{K \rightarrow \infty} \exp(K^\alpha) \left| \mathbb{P}_1[\tau_{\lceil \varepsilon \sigma_K K \rceil} < \tau_0] - \frac{[b-d]_+}{b} \right| = 0.$$

(b) *If $b > d$ (super-critical case), we have exponential tails, that is,*

$$(A.35) \quad \lim_{K \rightarrow \infty} \exp(\sigma_K^{-\alpha/3}) \mathbb{P}_1[\tau_{\lceil \varepsilon \sigma_K K \rceil} > \ln(K) \sigma_K^{-1-\alpha/2} | \tau_{\lceil \varepsilon \sigma_K K \rceil} < \tau_0] = 0$$

and

$$(A.36) \quad \lim_{K \rightarrow \infty} \exp(K^\alpha) \mathbb{P}_{\lceil \varepsilon \sigma_K K \rceil}[\tau_{\lceil \varepsilon K \rceil} > \tau_0] = 0.$$

PROOF. (a) Compare with (A.14) that

$$(A.37) \quad \mathbb{P}_1[\tau_{\lceil \varepsilon \sigma_K K \rceil} < \tau_0] = \frac{(d/b) - 1}{(d/b)^{\lceil \varepsilon \sigma_K K \rceil} - 1}.$$

If $b > d$ (subcritical case), there exist two constants $\underline{C}^{\text{sub}} > 0$ and $\bar{C}^{\text{sub}} > 0$ such that $1 + \underline{C}^{\text{sub}} \sigma_K \leq d/b \leq 1 + \bar{C}^{\text{sub}} \sigma_K$. Therefore, the left-hand side of (A.37) does

not exceed

$$(A.38) \quad \frac{\bar{C}^{\text{sub}}\sigma_K}{(1 + \underline{C}^{\text{sub}}\sigma_K)^{\lceil \varepsilon\sigma_K K \rceil} - 1} \leq \frac{\bar{C}^{\text{sub}}\sigma_K}{\exp(\underline{C}^{\text{sub}}\sigma_K \lceil \varepsilon\sigma_K K \rceil) - O(\sigma_K^3 \varepsilon K)} - 1 = o(e^{-K^\alpha}).$$

The last equality holds, since $K^{2\alpha} \ll \sigma_K^2 K$. If $b > d$ (super-critical case), we obtain similarly

$$(A.39) \quad \left| \mathbb{P}_1[\tau_k < \tau_0] - \frac{b-d}{b} \right| = \left| \frac{\frac{d}{b} - 1}{1 - (\frac{b}{d})^k} \right| = o(\exp(-K^\alpha)).$$

(b) Compare with [1] page 41, that

$$(A.40) \quad \begin{aligned} & \mathbb{P}_1[\tau_{\lceil \varepsilon\sigma_K K \rceil} > \ln(K)\sigma_K^{-1-\alpha/2} | \tau_{\lceil \varepsilon\sigma_K K \rceil} < \tau_0] \\ & \leq \exp\left(-\left\lfloor \frac{\ln(K)\sigma_K^{-1-\alpha/2}}{e \max_{n \leq \lceil \varepsilon\sigma_K K \rceil} \mathbb{E}_n[\tau_{\lceil \varepsilon\sigma_K K \rceil} | \tau_{\lceil \varepsilon\sigma_K K \rceil} < \tau_0]} \right\rfloor\right) \\ & \leq \exp(-\sigma_K^{-\alpha/3}), \end{aligned}$$

where the last inequality holds, because we can apply Proposition A.3:

$$(A.41) \quad \begin{aligned} & \max_{n \leq \lceil \varepsilon\sigma_K K \rceil} \mathbb{E}_n[\tau_{\lceil \varepsilon\sigma_K K \rceil} | \tau_{\lceil \varepsilon\sigma_K K \rceil} < \tau_0] \\ & = \max_{n \leq \lceil \varepsilon\sigma_K K \rceil} \frac{\mathbb{E}_n[\tau_{\lceil \varepsilon\sigma_K K \rceil} \wedge \tau_0 \mathbb{1}_{\tau_0 > \tau_{\lceil \varepsilon\sigma_K K \rceil}}]}{\mathbb{P}_n[\tau_0 > \tau_{\lceil \varepsilon\sigma_K K \rceil}]} \\ & \leq O(\ln(K)\sigma_K^{-1}). \end{aligned}$$

On the other hand, we have

$$(A.42) \quad \mathbb{P}_{\lceil \varepsilon\sigma_K K \rceil}[\tau_{\lceil \varepsilon K \rceil} > \tau_0] = 1 - \frac{(d/b)^{\lceil \varepsilon\sigma_K K \rceil} - 1}{(d/b)^{\lceil \varepsilon K \rceil} - 1} \leq \exp(-K^{2\alpha})$$

since $d/b = 1 - O(\sigma_K)$ and $K^{2\alpha} \ll \sigma_K \varepsilon K$. \square

PROPOSITION A.5. Let $(Z_n^K)_{n \geq 0}$ a sequence of discrete time Markov chain with state space \mathbb{Z} and with transition probabilities:

$$(A.43) \quad \mathbb{P}[Z_{n+1}^K = j | Z_n^K = i] = p(i, j) = \begin{cases} \frac{1}{2} + C\sigma_K, & \text{if } j = i + 1, \\ \frac{1}{2} - C\sigma_K, & \text{if } j = i - 1, \\ 0, & \text{else,} \end{cases}$$

for some constant $C \neq 0$. Let τ_i be the first hitting time of level i by Z^K and let \mathbb{P}_j denote the law of Z^K conditioned on $Z_0^K = j$ and let σ_K a zero sequence such that $K^{-\frac{1}{2}+\alpha} \ll \sigma_K \ll 1$.

(a) If Z^K is slightly super-critical, that is, $C > 0$, then, for all $i \geq 1$

$$(A.44) \quad \lim_{K \rightarrow \infty} \exp(K^\alpha) \mathbb{P}_{i \lceil (\varepsilon/2)\sigma_K K \rceil} [\tau_{(i-1) \lceil (\varepsilon/2)\sigma_K K \rceil} < \tau_{(i+1) \lceil (\varepsilon/2)\sigma_K K \rceil}] = 0.$$

(b) If Z^K is slightly subcritical, that is, $C < 0$, then, for all constants $C_1, C_2, C_3 > 0$

$$(A.45) \quad \lim_{K \rightarrow \infty} \exp(K^\alpha) \mathbb{P}_{(C_1+C_2) \lceil \varepsilon \sigma_K K \rceil} [\tau_{(C_1+C_2+C_3) \lceil \varepsilon \sigma_K K \rceil} < \tau_{C_1 \lceil \varepsilon \sigma_K K \rceil}] = 0.$$

PROOF. Since the transition probabilities of Z^K do not depend on the state of Z^K , we have that

$$(A.46) \quad \begin{aligned} & \mathbb{P}_{i \lceil (\varepsilon/2)\sigma_K K \rceil} [\tau_{(i-1) \lceil (\varepsilon/2)\sigma_K K \rceil} > \tau_{(i+1) \lceil (\varepsilon/2)\sigma_K K \rceil}] \\ &= \mathbb{P}_{\lceil (\varepsilon/2)\sigma_K K \rceil} [\tau_0 > \tau_2 \lceil (\varepsilon/2)\sigma_K K \rceil]. \end{aligned}$$

By (A.14), the left-hand side of (A.46) is equal

$$(A.47) \quad \frac{1 - (1 - 2C\sigma_K + O(\sigma_K^2))^{\lceil (\varepsilon/2)\sigma_K K \rceil}}{1 - (1 - 2C\sigma_K + O(\sigma_K^2))^{2 \lceil (\varepsilon/2)\sigma_K K \rceil}} \geq 1 - \exp(-K^2\alpha),$$

since $\sigma_K^2 K \gg K^{2\alpha}$. With the same arguments, we obtain also (A.45). \square

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