

Comparative study between discrete and continuum models for the evolution of competing phenotype-structured cell populations in dynamical environments

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Deterministic continuum models formulated as nonlocal partial differential equations for the evolutionary dynamics of populations structured by phenotypic traits have been used recently to address open questions concerning the adaptation of asexual species to periodically fluctuating environmental conditions. These models are usually defined on the basis of population-scale phenomenological assumptions and cannot capture adaptive phenomena that are driven by stochastic variability in the evolutionary paths of single individuals. In light of these considerations, in this paper we develop a stochastic individual-based model for the coevolution of two competing phenotype-structured cell populations that are exposed to time-varying nutrient levels and undergo spontaneous, heritable phenotypic changes with different probabilities. Here, the evolution of every cell is described by a set of rules that result in a discrete-time branching random walk on the space of phenotypic states, and nutrient levels are governed by a difference equation in which a sink term models nutrient consumption by the cells. We formally show that the deterministic continuum counterpart of this model comprises a system of nonlocal partial differential equations for the cell population density functions coupled with an ordinary differential equation for the nutrient concentration. We compare the individual-based model and its continuum analog, focusing on scenarios whereby the predictions of the two models differ. The results obtained clarify the conditions under which significant differences between the two models can emerge due to bottleneck effects that bring about both lower regularity of the density functions of the two populations and more pronounced demographic stochasticity. In particular, bottleneck effects emerge in the presence of lower probabilities of phenotypic variation and are more apparent when the two populations are characterized by lower fitness initial mean phenotypes and smaller initial levels of phenotypic heterogeneity. The emergence of these effects, and thus the agreement between the two modeling approaches, is also dependent on the initial proportions of the two populations. As an illustrative example, we demonstrate the implications of these results in the context of the mathematical modeling of the early stage of metastatic colonization of distant organs.

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I. INTRODUCTION

Adaptation to dynamically changing environments occurs in a variety of biological and ecological contexts [1–4]. In particular, when changes in nutrient availability occur, individuals in a population can either adopt a highly plastic phenotype [5], which enables them to acquire different traits based on environmental cues, or a risk-spreading strategy (e.g., bet-hedging), which allows at least some fraction of the population to survive in the face of sudden environmental changes by producing offspring adapted to the new conditions [6–8].

Mathematical modeling of evolutionary dynamics in time-varying environments has received considerable attention from mathematicians and physicists over the past 50 years—see, for instance, Refs. [9–20] and references therein. Re-

cently, deterministic continuum models formulated in terms of nonlocal partial differential equations (PDEs) for the evolutionary dynamics of populations, structured by phenotypic traits, have been used to address open questions concerning the adaptation of asexual species to periodically fluctuating environments [21–28].

Although more amenable to analytical and numerical approaches, which allow for a more in-depth theoretical understanding of the underlying dynamics, these deterministic continuum models are usually defined on the basis of population-scale phenomenological assumptions. This makes it more difficult to incorporate the finer details of phenotypic adaptation by single individuals. Moreover, such models cannot capture adaptive phenomena that are driven by stochastic effects in the evolutionary paths of single individuals. This will be particularly relevant at low population levels, which are commonly observed when risk-spreading adaptive strategies occur [29]. Ideally, we want to derive deterministic continuum models from first principles (i.e., as the appropriate limit of discrete stochastic models that track the

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evolution of single individuals), which permit the representation of individual-scale adaptive mechanisms, and account for possible stochastic interindividual variability in evolutionary trajectories [30–33].

In light of these considerations, we develop a stochastic individual-based (IB) model for the evolutionary dynamics of two competing phenotype-structured cell populations that are exposed to time-varying nutrient levels and undergo spontaneous, heritable phenotypic changes with different probabilities. In this model, every cell is viewed as an individual agent whose phenotypic state is modeled by a discrete variable, which represents the normalized level of expression of a gene that allows cells to cope with nutrient scarcity. For instance, activation of hypoxia-inducible factors allows mammalian cells to adapt to oxygen deprivation [34]. In the model, cells proliferate, die and undergo phenotypic changes according to a set of rules that correspond to a discrete-time branching random walk on the space of phenotypic states [32,35]. We assume that the cell proliferation rate depends on nutrient levels, and that nutrient concentration is governed by a difference equation in which a sink term models nutrient consumption by the cells.

This work builds on our earlier analytical and numerical studies of deterministic continuum models for the evolutionary dynamics of competing phenotype-structured asexual populations exposed to periodically oscillating nutrient levels [22,23]. In [22], we focused on a scenario where the evolution of nutrient levels was independent from the dynamics of the populations, and we analyzed the long-time behavior of the solutions to the model equations, to dissect the role of spontaneous, heritable phenotypic changes in the adaptation of asexual species to fluctuating environments. In Ref. [23], we extended the original model by letting the nutrient levels coevolve with the competing populations and carried out simulation-assisted analysis of the long-time behavior of the solutions to the model equations to investigate how negative feedback mechanisms, which regulate population growth through nutrient consumption, may shape the evolutionary dynamics of cell populations under oscillating environmental conditions. In this paper, we show that the models considered in Refs. [22,23] can be formally obtained as the deterministic continuum limit of the stochastic IB model presented here. Moreover, we conduct a comparative study between the IB model and its continuum analog, our aim being to explore scenarios in which differences between the outcomes of the two models may emerge.

The paper is organized as follows. In Sec. II, we introduce the stochastic IB model. In Sec. III, we present its deterministic continuum counterpart (a formal derivation is provided in Appendix A), which comprises a system of nonlocal PDEs for the population density functions (i.e., the cell distribution over the space of phenotypic states) coupled with an ordinary differential equation (ODE) for the nutrient concentration. In Sec. IV, we present the main results of the comparative study between the two models. As an illustrative example, in Sec. V we interpret our results in the context of the early stage of metastatic colonization of distant organs by cancer cells. In Sec. VI, we summarize the main findings and outline directions for future research.

II. STOCHASTIC INDIVIDUAL-BASED MODEL

We model the evolutionary dynamics of two competing cell populations in a well-mixed system. Cells in the two populations proliferate (i.e., divide), die and undergo spontaneous, heritable phenotypic changes. We assume that the two populations differ only in their probability of phenotypic variation. The population undergoing phenotypic changes with a higher probability is labeled by the letter H , while the other population is labeled by the letter L . The phenotypic state of every cell at time $t \in [0, t_f] \subset \mathbb{R}^+$ is characterized by a variable $x \in [0, 1] \subset \mathbb{R}^+$, which represents the normalized level of expression of a gene that allows cells to cope with nutrient deprivation. In particular, we assume that cells in the phenotypic state $x = 0$ are best adapted to nutrient-rich environments, whereas cells in the phenotypic state $x = 1$ are best adapted to nutrient-scarce environments.

We represent each cell as an agent that occupies a position on a lattice. We discretize the time variable and the phenotypic state via $t_h = h\tau \in [0, t_f]$ and $x_j = j\chi \in [0, 1]$, respectively, where $h, j \in \mathbb{N}_0$, and $\tau \in \mathbb{R}_*^+$ and $\chi \in \mathbb{R}_*^+$ are the time- and phenotype-step, respectively. We introduce the dependent variable $N_{i,j}^h \in \mathbb{N}_0$ to represent the number of cells of population $i \in \{H, L\}$ on lattice site j (i.e., in the j th phenotypic state) at time-step h . The density (i.e., the phenotype distribution) of population i , the size of population i , and the total number of cells are defined, respectively, as follows

$$n_i(t_h, x_j) = n_{i,j}^h := N_{i,j}^h \chi^{-1}, \quad (1)$$

$$\rho_i(t_h) = \rho_i^h := \sum_j N_{i,j}^h \quad \text{and} \quad \rho(t_h) = \rho^h := \sum_i \rho_i^h. \quad (2)$$

We further define the mean phenotype of population i and the related standard deviation, respectively, as

$$\mu_i(t_h) = \mu_i^h := \frac{1}{\rho_i^h} \sum_j x_j N_{i,j}^h \quad (3)$$

and

$$\sigma_i(t_h) = \sigma_i^h := \left(\frac{1}{\rho_i^h} \sum_j x_j^2 N_{i,j}^h - (\mu_i^h)^2 \right)^{\frac{1}{2}}. \quad (4)$$

Finally, the nutrient concentration at time-step h is modeled by the discrete, nonnegative function $S(t_h) = S^h$.

A. Mathematical modeling of phenotypic changes

We account for spontaneous, heritable phenotypic changes by allowing cells to update their phenotypic states according to a random walk. More precisely, between the time-steps h and $h + 1$, every cell in population $i \in \{H, L\}$ either enters a new phenotypic state, with probability $\lambda_i \in [0, 1]$, or remains in its current phenotypic state, with probability $1 - \lambda_i$. Since we assume that phenotypic changes occur randomly due to nongenetic instability, rather than selective pressures [36], then a cell of population i in phenotypic state x_j that undergoes a phenotypic change enters into either of the phenotypic states $x_{j\pm 1} = x_j \pm \chi$ with probabilities $\lambda_i/2$. No-flux boundary conditions are implemented by aborting any attempted

phenotypic variation of a cell if it requires moving into a phenotypic state outside the interval $[0,1]$.

B. Mathematical modeling of cell division and death

Cells divide, die, or remain quiescent with probabilities that depend on their phenotypic states, the total number of cells and the nutrient concentration. We assume that a dividing cell is replaced by two identical cells that inherit the phenotypic state of the parent cell (i.e., the progenies are placed on the same lattice site as their parent), while a dying cell is removed from the population.

To translate into mathematical terms the idea that larger population sizes correspond to more intense competition between cells, at every time-step h we allow cells to die due to intrapopulation and interpopulation competition at a rate proportional to the total cell number ρ^h , with constant of proportionality $d > 0$.

We denote by $p(x_j, S^h)$ the division rate of a cell in the j th phenotypic state, where S^h is the nutrient concentration. Since x_j represents the normalized expression level of a gene that allows cells to cope with nutrient scarcity, we assume that phenotypic variants with $x_j \rightarrow 0$ are characterized by the maximal division rate when nutrient is abundant (i.e., if $S^h \rightarrow \infty$), whereas phenotypic variants with $x_j \rightarrow 1$ are characterized by the maximal division rate when nutrient is scarce (i.e., if $S^h \rightarrow 0$). Our implicit assumption here is that cells in the phenotypic state $x_j = 1$ switch to other nutrients that are abundant, and therefore they are no longer dependent on the specific nutrient we are modeling. (We refer the interested reader to Sec. V for a specific biological application of this modeling approach.) Under these assumptions, and following the modeling strategies that we proposed in Refs. [22,23], we define the cell division rate $p(x_j, S^h)$ as follows:

$$p(x_j, S^h) := \gamma \frac{S^h}{\kappa + S^h} (1 - x_j^2) + \zeta \left(1 - \frac{S^h}{\kappa + S^h} \right) [1 - (1 - x_j)^2]. \quad (5)$$

In Eq. (5), the parameters $\gamma > 0$ and $\zeta > 0$ model, respectively, the maximum cell division rate of the phenotypic variants best adapted to nutrient-rich and nutrient-scarce environments (i.e., cells in the phenotypic states $x_j = 0$ and $x_j = 1$, respectively). To incorporate into the model the possible fitness cost associated with the ability to survive in nutrient-scarce environments [37,38], we make the additional assumption that $\zeta \leq \gamma$. Moreover, $\kappa > 0$ is the Michaelis constant of the nutrient, i.e. the nutrient concentration at which the proliferation rate is half maximal. After a little algebra, Eq. (5) can be rewritten as

$$p(x_j, S^h) = \gamma g(S^h) - h(S^h)[x_j - \varphi(S^h)]^2, \quad (6)$$

where

$$g(S^h) := \frac{S^h}{\kappa + S^h} + \frac{\zeta^2 \kappa^2}{\gamma(\kappa + S^h)(\gamma S^h + \zeta \kappa)},$$

$$\varphi(S^h) := \frac{\zeta \kappa}{\gamma S^h + \zeta \kappa} \quad \text{and} \quad h(S^h) := \frac{\gamma S^h + \zeta \kappa}{\kappa + S^h}. \quad (7)$$

Here, $\gamma g(S^h)$ is the maximum fitness, $\varphi(S^h)$ is the fittest phenotypic state and $h(S^h)$ is a selection gradient. Consistent with our modeling assumptions, we have

$$\varphi : [0, \infty) \rightarrow [0, 1], \quad \lim_{S \rightarrow 0} \varphi(S) = 1 \quad \text{and} \quad \lim_{S \rightarrow \infty} \varphi(S) = 0.$$

Under these assumptions, between time-steps h and $h + 1$, a cell in the j th phenotypic state may divide with probability

$$\mathcal{P}_b := \tau p(x_j, S^h), \quad (8)$$

die with probability

$$\mathcal{P}_d := \tau d \rho^h, \quad (9)$$

or remain quiescent (i.e., do not divide nor die) with probability

$$\mathcal{P}_q := 1 - \tau (p(x_j, S^h) + d \rho^h). \quad (10)$$

Notice that we are implicitly assuming that the time-step τ is sufficiently small that $0 < \mathcal{P}_i < 1$ for all $i \in \{b, d, q\}$.

C. Mathematical modeling of nutrient dynamics

Following Ardaševa *et al.* [23], we describe the nutrient dynamics via the following difference equation for S^h

$$S^{h+1} = S^h + \tau \left[I^h - \eta S^h - \theta \gamma \frac{S^h}{\kappa + S^h} \sum_j (1 - x_j)^2 (N_{H,j}^h + N_{L,j}^h) \right], \quad (11)$$

complemented with a suitable initial nutrient concentration S^0 . Since we consider a well-mixed system, there is no diffusion of the nutrient. In the difference Eq. (11), the parameter $\eta > 0$ represents the rate of natural decay of the nutrient, while the last term on the right-hand side of the difference Eq. (11) models the rate of nutrient consumption by the cells and is based on the following argument. Cells in the phenotypic state $x_j = 1$ do not rely on the nutrient we are modeling for their survival—these cells might produce energy via different metabolic pathways that do not require the nutrient under consideration—and, as such, they do not consume any nutrient. By contrast, cells in the phenotypic state $x_j = 0$ consume the nutrient at a rate proportional to their cell division rate, with constant of proportionality $\theta > 0$. Finally, the rate at which the nutrient is consumed by cells in phenotypic states $x_j \in (0, 1)$ is a fraction of the consumption rate of cells in the phenotypic state $x_j = 0$, with higher values of x_j correlating with lower rates of nutrient consumption. The discrete, nonnegative function I^h on the right-hand side of the difference Eq. (11) models the rate at which the nutrient is supplied to the system. When the nutrient inflow is constant we fix

$$I^h \equiv \bar{I} \geq 0; \quad (12)$$

when the nutrient inflow undergoes periodic oscillations we prescribe

$$I^h := \max \left[0, A \sin \left(\frac{2\pi t_h}{T} \right) \right], \quad (13)$$

with the parameters $T > 0$ and $A > 0$ modeling, respectively, the period and the amplitude of the oscillations.

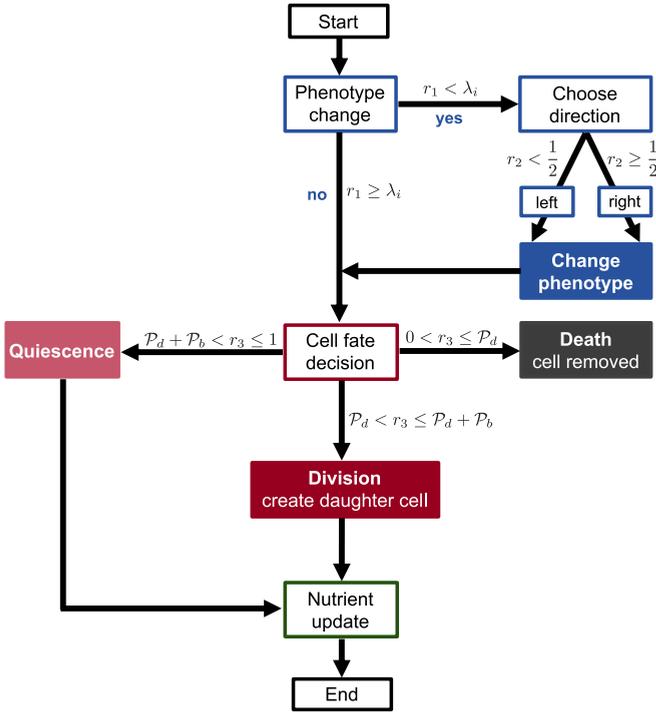


FIG. 1. Flowchart illustrating the procedure underlying the computational implementation of the stochastic IB model for each cell at every time-step. Once all cells have undergone both the phenotype-change step and the fate-decision step, the total number of cells is computed and the nutrient level is updated.

D. Computational implementation

Numerical simulations of the IB model are performed using the open-source Java library Hybrid Automata Library (HAL) [39]. At each time-step, we follow the procedures summarized in Fig. 1 and described hereafter to simulate phenotypic changes as well as cell division and death. All random numbers mentioned below are real numbers drawn from the standard uniform distribution on the interval (0,1) using the Java function `Rand.Double()`.

a. Computational implementation of spontaneous, heritable phenotypic changes. For each cell in population i , a random number, r_1 , is generated and used to determine whether the cell undergoes a phenotypic change (i.e., $0 < r_1 < \lambda_i$) or not (i.e., $\lambda_i \leq r_1 < 1$). If the cell undergoes a phenotypic change, then a second random number, r_2 , is generated. If $0 < r_2 < 1/2$, then the cell moves into the phenotypic state to the left of its current state, i.e., a cell in the phenotypic state x_j will move into the phenotypic state $x_{j-1} = x_j - \chi$, whereas if $1/2 \leq r_2 < 1$ then the cell moves into the phenotypic state to the right of its current state, i.e. a cell in the phenotypic state x_j will move into the phenotypic state $x_{j+1} = x_j + \chi$. No-flux boundary conditions are implemented by aborting attempted phenotypic changes that would move a cell into a phenotypic state outside the unit interval.

b. Computational implementation of cell division and death. For each population, the number of cells in each phenotypic state is counted. The size of each cell population and the total number of cells are then computed via Eq. (2). Definition Eqs. (8)–(10) are used to calculate the probabilities of cell

division, death and quiescence for every phenotypic state. For each cell, a random number, r_3 , is generated and the cells' fate is determined by comparing this number with the probabilities of division, death and quiescence corresponding to the phenotypic state of the cell. If $0 < r_3 < \mathcal{P}_d$, then the cell is considered dead and is removed from the population. If $\mathcal{P}_d \leq r_3 < \mathcal{P}_d + \mathcal{P}_b$, then the cell undergoes division and an identical daughter cell is created. Finally, if $\mathcal{P}_d + \mathcal{P}_b \leq r_3 < 1$, then the cell remains quiescent (i.e., does not divide nor die).

c. Computational implementation of nutrient dynamic. At each time-step, the number of cells of the two populations in each phenotypic state is counted to evaluate the last term on the right-hand side of the difference Eq. (11). The nutrient concentration is then updated via the difference Eq. (11).

III. CORRESPONDING DETERMINISTIC CONTINUUM MODEL

Using the formal method presented in Refs. [32,33], we let the time-step $\tau \rightarrow 0$ and the phenotype-step $\chi \rightarrow 0$ in such a way that

$$\frac{\lambda_i \chi^2}{2\tau} \rightarrow \beta_i \in \mathbb{R}_*^+ \quad \text{for } i \in \{H, L\}. \quad (14)$$

Here, the parameter β_i is the rate of spontaneous, heritable phenotypic changes of cells in population i . It is then possible to formally show (see Appendix A) that the deterministic continuum counterpart of the stochastic IB model is given by the following system of nonlocal PDEs for the cell population density functions $n_H(x, t)$ and $n_L(x, t)$:

$$\begin{aligned} \frac{\partial n_H}{\partial t} &= \beta_H \frac{\partial^2 n_H}{\partial x^2} + \{p[x, S(t)] - d \rho(t)\} n_H, \\ \frac{\partial n_L}{\partial t} &= \beta_L \frac{\partial^2 n_L}{\partial x^2} + \{p[x, S(t)] - d \rho(t)\} n_L, \\ \rho(t) &:= \rho_H(t) + \rho_L(t), \quad \rho_i(t) := \int_0^1 n_i(x, t) dx, \end{aligned} \quad (15)$$

posed on $(0, 1) \times (0, t_f]$ and subject to no-flux boundary conditions, i.e.,

$$\frac{\partial n_i(0, t)}{\partial x} = 0, \quad \frac{\partial n_i(1, t)}{\partial x} = 0 \quad \text{for all } t \in (0, t_f]. \quad (16)$$

In the system of nonlocal PDEs (15), the nutrient concentration $S(t)$ is governed by the continuum counterpart of the difference Eq. (11), i.e., the following ODE posed on $(0, t_f]$:

$$\frac{dS}{dt} = I(t) - \eta S - \theta \gamma \frac{S}{\kappa + S} \int_0^1 (1 - x^2) (n_H + n_L) dx, \quad (17)$$

which can be easily obtained in a formal way by letting $\tau \rightarrow 0$ and $h \rightarrow 0$ in the ODE (11). In the continuum modeling framework given by the system of nonlocal PDEs (15), the mean phenotype of population i and the related standard deviation are defined, respectively, as

$$\mu_i(t) := \frac{1}{\rho_i(t)} \int_0^1 x n_i(x, t) dx \quad (18)$$

TABLE I. Parameter values used in numerical simulations.

	Description	Values
λ_H	Probability of phenotypic variation of population H	{0.05, 0.4, 1}
λ_L	Probability of phenotypic variation of population L	{0.02, 0.2}
γ	Maximum cell division rate of phenotypic variants $x = 0$	100
ζ	Maximum cell division rate of phenotypic variants $x = 1$	50
κ	Michaelis constant of nutrient	1
d	Death rate due to inter- and intrapopulation competition	{0.01, 0.1, 0.2, 0.4, 1.0}
θ	Consumption rate of nutrient	{ 10^{-5} , 10^{-4} , 2×10^{-4} , 10^{-3} }
η	Rate of natural decay of nutrient	10^{-3}
S^0	Initial nutrient concentration	{0, 10}
a_i	Initial size of population i	800
c	Initial mean phenotype of both populations	{0, 0.5, 1}
b	Initial inverse variance of both populations	{10, 1000}
\bar{I}	Constant rate of oxygen supply	10
A	Amplitude of fluctuations in oxygen supply	{30, 200}
T	Period of fluctuations in oxygen supply	5
ε	Scaling factor for the rate of phenotypic variation (Sec. IV B)	{1, 2, ..., 10}
ν	Initial proportion of population H (Sec. IV D)	{0.1, 0.2, 0.3, 0.7, 0.8, 0.9}
Z	Initial total number of cells (Sec. IV D)	800
χ	Phenotype-step	0.032
τ	Time-step	10^{-3}
t_f	Final time	{10, 20, 40}

and

$$\sigma_i(t) := \left(\frac{1}{\rho_i(t)} \int_0^1 x^2 n_i(x, t) dx - \mu_i^2(t) \right)^{\frac{1}{2}}, \quad (19)$$

for $i \in \{H, L\}$.

IV. MAIN RESULTS

In this section, we compare the results of numerical simulations of the stochastic IB model introduced in Sec. II and numerical solutions of the corresponding deterministic continuum model presented in Sec. III.

For consistency with previous mathematical studies of the evolutionary dynamics of phenotype-structured populations, which rely on the prima facie assumption that population densities are Gaussians [40], simulations are carried out under the assumption that the initial phenotype distribution of population i for the IB model is of the form

$$n_{i,j}^0 = a_i \left(\frac{b}{2\pi} \right)^{\frac{1}{2}} \exp \left[-\frac{b}{2} (x_j - c)^2 \right], \quad (20)$$

with $i \in \{H, L\}$. In Eq. (20), the parameter a_i is related to the initial size of population i , while the parameters b and c are related, respectively, to the inverse of the initial standard deviation and the initial mean phenotype of the two populations. The initial population density $n_i(x, 0)$ for the continuum model is defined as the continuum analog of Eq. (20) (see Appendix B).

First, we present a sample of base-case results that demonstrate excellent quantitative agreement between the stochastic IB model and its deterministic continuum counterpart. Then, we perform a systematic sensitivity analysis of some key parameters. In particular, we investigate how the base-case results change as we vary the values of the probabilities of

phenotypic variation λ_H and λ_L (see Sec. IV B), the parameters b and c in Eq. (20) (see Sec. IV C)—i.e., the inverse of the initial standard deviation and the initial mean phenotype of the two populations—and the parameters a_H and a_L in Eq. (20) (see Sec. IV D)—i.e., the initial sizes of the two populations.

We consider the nutrient concentration to be nondimensionalized and use the dimensionless parameter values listed in Table I to carry out numerical simulations of the IB model. The methods employed to numerically solve the equations of the related continuum model are described in Appendix B.

A. Base-case results

We first assume that the supply rate of nutrient is constant [i.e., we define the term I^h via Eq. (12)] and consider different values of the nutrient consumption rate θ . The results displayed in Fig. 2 show excellent quantitative agreement between numerical simulations of the IB and continuum models, both for relatively low and relatively high values of θ . As expected, based on the results we presented in Ref. [23], population L outcompetes population H , which eventually goes extinct. Moreover, since the nutrient concentration converges to smaller equilibrium values for larger values of the nutrient consumption rate, higher values of θ correspond to decreasing equilibrium sizes of population L and equilibrium values of the mean phenotype which are closer to 1 (i.e., the fittest phenotypic state in nutrient-scarce environments). In all cases, the phenotype distribution of the surviving population is unimodal and attains its maximum at the mean phenotype [see Figs. 10(a) and 10(b) in Appendix C].

We then let the supply rate of nutrient undergo periodic oscillations [i.e., we define the term I^h via Eq. (13)] and, informed by numerical results presented in Ref. [23], we consider different values of the consumption rate θ that lead to the emergence of either mild (i.e., small-amplitude) or severe (i.e.,

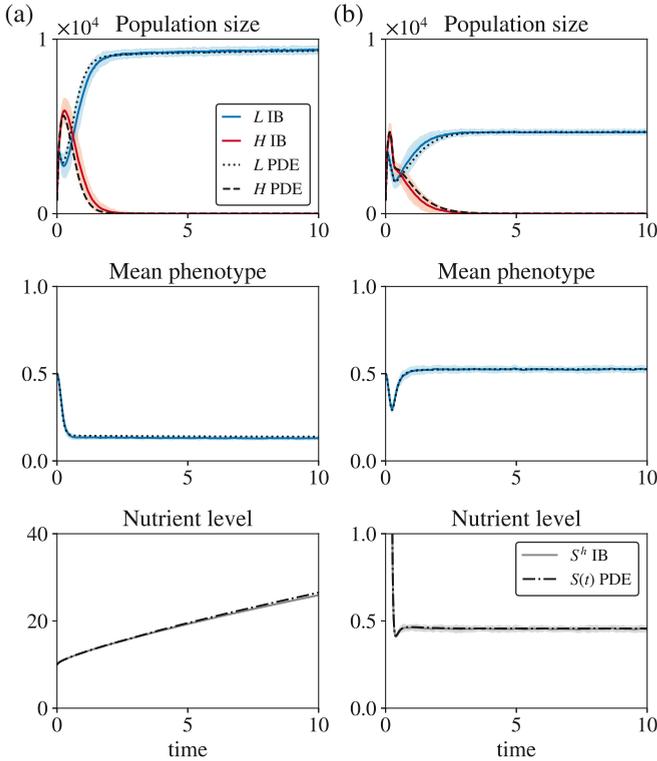


FIG. 2. Base-case results when the nutrient inflow is constant. Comparison between numerical simulations of the IB (solid, colored lines) and continuum (broken, black lines) models in the case where the evolution of the nutrient concentration is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (12) with $\bar{I} = 10$. (a) Dynamics of the population sizes (top panel), mean phenotype of the surviving population (central panel), and nutrient level (bottom panel) in the case where $\theta = 10^{-5}$. Here, $a_H = a_L = 800$, $b = 1000$, and $c = 0.5$ in Eq. (20), and the values of the other parameters are those listed in Table I with $\lambda_H = 1$ and $\lambda_L = 0.2$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b) Same as panel (a) but for larger nutrient consumption, i.e., $\theta = 10^{-4}$.

large-amplitude) fluctuations in the nutrient concentration S^h . The results displayed in Fig. 3 demonstrate that, both for mild and severe fluctuations in the nutrient concentration, the size and the mean phenotype of the surviving population converge to positive T -periodic functions. Furthermore, in agreement with the analytical results we presented in Ref. [22], the numerical results in Fig. 3 indicate that, when nutrient levels undergo smaller fluctuations, population L survives [see Fig. 3(b)]. However, when nutrient levels undergo larger fluctuations, population H ultimately outcompetes population L [see Fig. 3(a)]. In both cases, the phenotype distribution of the surviving population is unimodal and attains its maximum at the mean phenotype [see Figs. 10(c) and 10(d) in Appendix C]. Moreover, excellent agreement between numerical simulations of the IB and continuum models is observed.

The numerical results presented in Appendix D show that analogous conclusions hold in the simplified scenario where the concentration of nutrient is prescribed and does not coevolve with the cells.

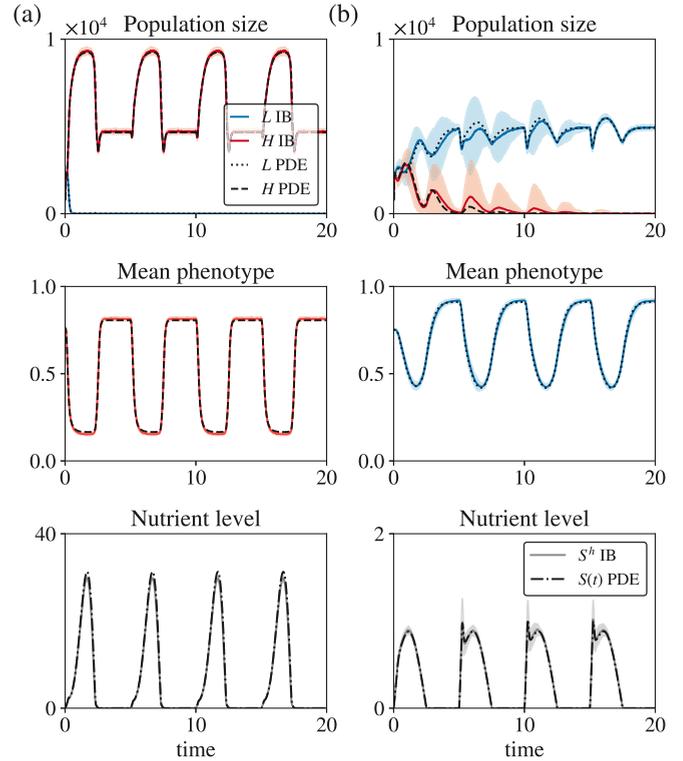


FIG. 3. Base-case results when the nutrient inflow is periodic. Comparison between numerical simulations of the IB (solid, colored lines) and continuum (broken, black lines) models in the case where the evolution of the nutrient concentration is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (13) with $A = 200$ and $T = 5$. (a) Dynamics of the population sizes (top panel), mean phenotype of the surviving population (central panel), and nutrient level (bottom panel) in the case where $\theta = 2 \times 10^{-4}$. Here, $a_H = a_L = 800$, $b = 1000$, and $c = 0.5$ in Eq. (20), and the values of the other parameters are those listed in Table I with $\lambda_H = 0.4$ and $\lambda_L = 0.02$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b) Same as panel (a) but for larger nutrient consumption, i.e., $\theta = 10^{-3}$.

B. Sensitivity analysis of the probabilities of phenotypic variation

Based on the analytical results presented in Ref. [22] for a simplified continuum model, we expect smaller values of λ_H and λ_L (i.e., the probabilities of phenotypic variation) to correlate with longer transient intervals in the dynamics of the sizes of the two cell populations. To test this hypothesis, we focus on the case where the supply rate of nutrient is constant [i.e., when the term I^h is defined via Eq. (12)]. We carry out numerical simulations of the IB model assuming

$$\lambda_i = \varepsilon \Lambda_i, \quad (21)$$

with Λ_i fixed and $\varepsilon \in \{1, \dots, 10\}$. As summarized by the plots in Fig. 4, smaller values of ε bring about longer transient intervals [i.e., larger values of t_{tr} in Fig. 4(d)] during which the two populations coexist before population L ultimately outcompetes population H .

The results displayed in Figs. 4(a)–4(c) indicate that the size of population L decreases during the transient, defined as

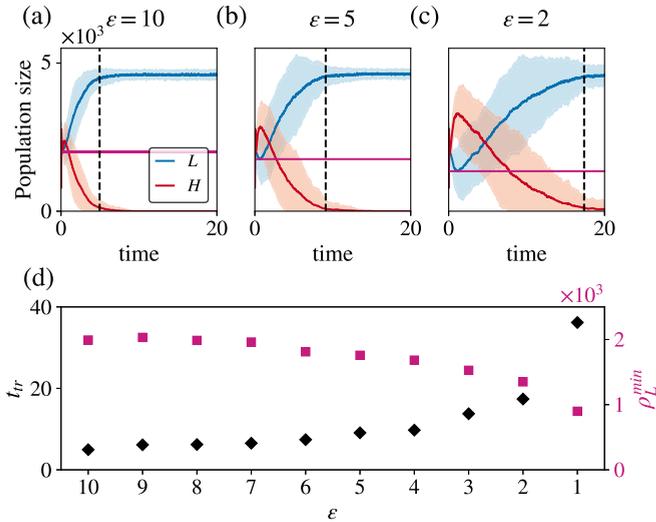


FIG. 4. Emergence of longer transient intervals for lower probabilities of phenotypic variation. (a–c) Numerical simulations of the IB model in the case where the probabilities of phenotypic variation λ_H and λ_L are defined via Eq. (21) with $\Lambda_H = 0.05$, $\Lambda_L = 0.02$, and $\varepsilon = 10$ (a) or $\varepsilon = 5$ (b) or $\varepsilon = 2$ (c). The black dashed lines highlight the time t_{tr} such that $\rho_L(t_f) - \rho_L(t_{tr}) < 100$, while the solid pink lines highlight the value of $\rho_L^{\min} := \min_h \rho_L^h$. These results correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (d) Plots of t_{tr} (black diamonds) and ρ_L^{\min} (pink squares) as functions of $\varepsilon \in \{1, \dots, 10\}$. The evolution of the nutrient concentration is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (12) with $\bar{I} = 10$. Here, $a_H = a_L = 800$, $b = 1000$ and $c = 0.5$ in Eq. (20), and the values of the other parameters are those listed in Table I with $\theta = 10^{-3}$.

the early part of the population trajectory, before approaching steady-state. Moreover, longer transients correlate with sharper drops in the size of population L , and thus smaller minimum values of ρ_L [i.e., smaller ρ_L^{\min} in Fig. 4(d)], which makes bottleneck effects that bring about both lower regularity of the density functions of the two populations, and more pronounced demographic stochasticity more likely to come into play. This suggests that lower probabilities of phenotypic variation may create conditions for the emergence of differences between predictions of the IB and continuum models.

To investigate this further, we compare numerical simulations of the IB model with numerical solutions of the continuum model in the setting of Fig. 2 [i.e., defining the nutrient supply term I^h via Eq. (12) and considering different values of nutrient consumption rate θ] but using lower values of the probabilities of phenotypic variation λ_H and λ_L . The results, summarized in Fig. 5, demonstrate that while excellent quantitative agreement between numerical simulations of the IB model and numerical solutions of the continuum model is obtained for relatively large values of θ [see Fig. 5(b)], significant differences in the behavior of the two models can be observed for relatively low values of θ [see Fig. 5(a)]. Such differences persist when smaller values of the time-step τ and the phenotype-step χ are considered. More specifically, lower time- and phenotype-steps correlate with a more drastic decay

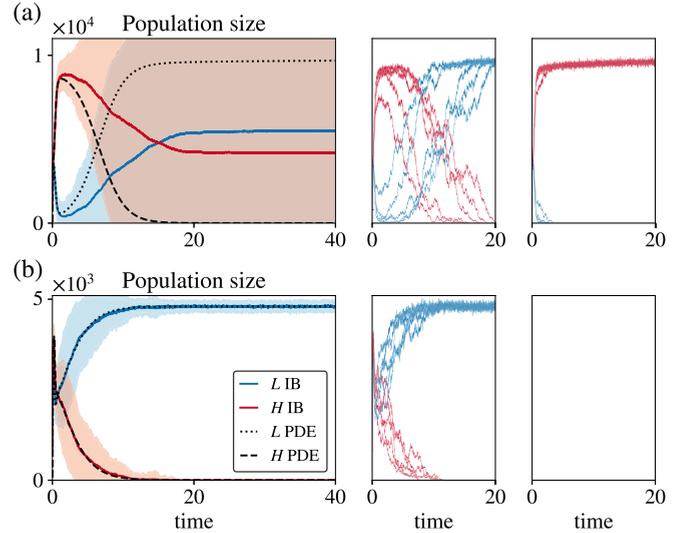


FIG. 5. Sensitivity analysis of the probabilities of phenotypic variation. (a) Comparison between numerical simulations of the IB (solid, colored lines in the left panel) and continuum (broken, black lines in the left panel) models under the parameter setting of Fig. 2(a) but with $\lambda_H = 0.05$ and $\lambda_L = 0.02$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. The plots in the central and right panels show the dynamics of the sizes of the two populations for single realizations of the IB model that match with (central panel) or differ from (right panel) numerical solutions of the continuum model. (b) Same as panel (a) for the parameter setting of Fig. 2(b) but with $\lambda_H = 0.05$ and $\lambda_L = 0.02$.

in the size of population L , which then becomes more prone to extinction due to demographic stochasticity.

This is because, when lower values of λ_H and λ_L are considered, a relatively small nutrient consumption rate θ corresponds to a longer initial phase of cell dynamics during which the size of population L decays and the size of population H grows. After this initial phase, the numerical solutions of the continuum model exhibit trend inversion, with the size of population L converging to a stable positive value and the size of population H decaying to zero. Numerical simulations of the IB model, however, demonstrate that there are realizations whereby, due to stochastic effects, the aftermath of the initial phase of cell dynamics is the extinction of population L and the survival of population H [see right panel of Fig. 5(a)].

Differences between the discrete and the continuum models are also observed when the supply rate of nutrient undergoes periodic oscillations [i.e., when the term I^h is defined via Eq. (13)] and different values of θ are considered, provided that lower values of λ_H and λ_L are chosen (results not shown). In this case, for values of nutrient consumption rate θ leading to the emergence of severe fluctuations in the nutrient level (i.e., when population H is ultimately selected according to the continuum model), there is an excellent quantitative agreement between the two models. However, for values of θ leading to the emergence of mild fluctuations in nutrient levels (i.e., when the continuum model predicts that population L will ultimately be selected after an initial phase of population

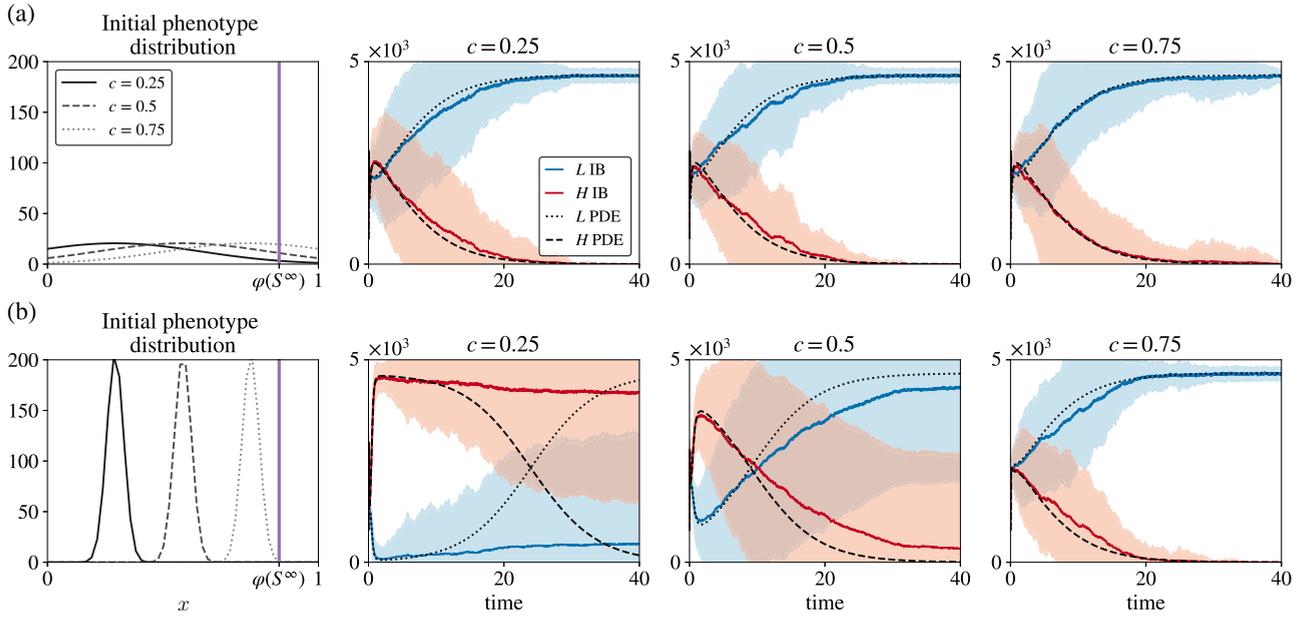


FIG. 6. Sensitivity analysis of the initial mean phenotype and the initial standard deviation when the nutrient inflow is constant. (a) Comparison between numerical simulations of the IB (solid, colored lines in panels 2–4) and continuum (broken, black lines in panels 2–4) models in the case where the initial phenotype distributions of the two populations are defined as shown by the plots in the first panel, corresponding to different values of c in Eq. (20). The purple line in the first panel highlights the equilibrium value of the fittest phenotypic state $\varphi(S^\infty)$, which is computed by substituting into Eq. (7) the long-time limit S^∞ that is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (12) with $\bar{I} = 10$. Here, $a_H = a_L = 800$ and $b = 10$ in Eq. (20), and the values of the other parameters are those listed in Table I with $\lambda_H = 0.05$, $\lambda_L = 0.02$ and $\theta = 10^{-3}$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b) Same as panel (a) but for $b = 1000$.

size contraction), there are realizations of the IB model in which population L is outcompeted by population H .

C. Sensitivity analysis of the initial standard deviation and the initial mean phenotype

Based on analytical results presented in Ref. [22] for a simplified continuum model, in the case where the nutrient concentration coevolves with the cells according to the difference Eq. (11) and the supply rate I^h is defined via Eq. (12), we anticipate stronger bottleneck effects in the presence of both small initial standard deviations, $\sigma_{H,L}^0$, and large distances between the initial mean phenotypes, $\mu_{H,L}^0$, and the equilibrium value of the fittest phenotypic state, $\varphi(S^\infty)$, which is computed by substituting the long-time limit S^∞ of the nutrient concentration into Eq. (7). Since the results presented in Sec. IV B demonstrate that stronger bottleneck effects may promote the emergence of differences between the predictions of the two models, we expect that larger values of $|\mu_H^0 - \varphi(S^\infty)|$ and $|\mu_L^0 - \varphi(S^\infty)|$, along with smaller values of σ_H^0 and σ_L^0 , will increase the likelihood of observing differences between numerical simulations of the IB and continuum models.

To test this hypothesis, we first suppose the nutrient supply rate to be constant and we carry out numerical simulations for different values of the parameters b and c in Eq. (20). We recall that larger values of b correlate with lower σ_H^0 and σ_L^0 ; moreover. Moreover, in the setting considered here, lower values of c correspond to higher $|\mu_H^0 - \varphi(S^\infty)|$ and $|\mu_L^0 - \varphi(S^\infty)|$ (i.e., less fit initial mean phenotypes). The plots

presented in Fig. 6(a) reveal excellent quantitative agreement between numerical simulations of the IB and continuum models for sufficiently large values of σ_H^0 and σ_L^0 , regardless of the values of $|\mu_H^0 - \varphi(S^\infty)|$ and $|\mu_L^0 - \varphi(S^\infty)|$ (i.e., independently of the value of c). However, and consistent with our expectations, the numerical results presented in Fig. 6(b) show that, for sufficiently small values of σ_H^0 and σ_L^0 , higher $|\mu_H^0 - \varphi(S^\infty)|$ and $|\mu_L^0 - \varphi(S^\infty)|$ (i.e., lower values of c) correlate with stronger bottleneck effects leading to the emergence of differences between the cell dynamics produced by the two models.

We now suppose that the nutrient supply rate undergoes periodic oscillations and perform numerical simulations for different values of the parameter c (i.e., the initial mean phenotype of the two populations), which correspond to different values of the quantities $|\mu_H^0 - \langle \varphi \rangle|$ and $|\mu_L^0 - \langle \varphi \rangle|$, where

$$\langle \varphi \rangle := \frac{1}{2} \left[\min_{t^h \in [0, T]} \tilde{S}(t^h) + \max_{t^h \in [0, T]} \tilde{S}(t^h) \right], \quad (22)$$

with $\tilde{S}(t^h) = \tilde{S}^h$ being the positive T -periodic function to which S^h converges as $h \rightarrow \infty$. In the setting considered here, smaller values of c correspond to higher $|\mu_H^0 - \langle \varphi \rangle|$ and $|\mu_L^0 - \langle \varphi \rangle|$ (i.e., less fit initial mean phenotypes). The results presented in Fig. 7(b) indicate that excellent quantitative agreement is observed between numerical simulations of the IB and continuum models when the consumption rate θ is such that the nutrient level undergoes severe fluctuations (i.e., when population H is ultimately selected according to the continuum model), regardless of the values

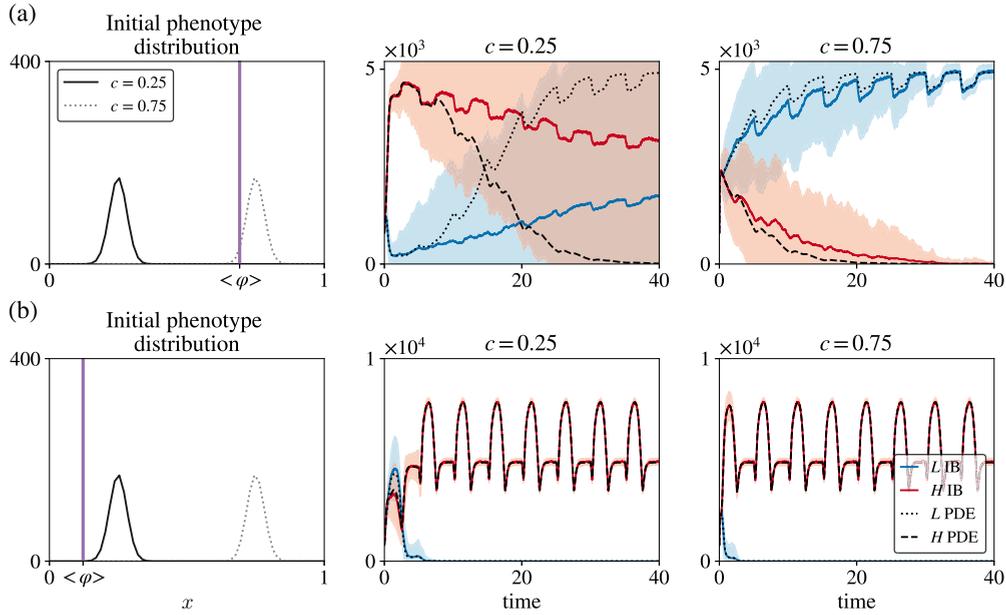


FIG. 7. Sensitivity analysis of the initial mean phenotype when the nutrient inflow is periodic. (a) Comparison between numerical simulations of the IB (solid, colored lines in the central and right panel) and continuum (broken, black lines in the central and right panel) models in the case where the initial phenotype distributions of the two populations are the same and both defined as shown by the plots in the left panel, which correspond to different values of the parameter c in Eq. (20). The purple line in the first panel highlights the value of the quantity $\langle \varphi \rangle$ defined according to Eq. (22). The evolution of S^h is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (13) with $A = 30$ and $T = 5$. Numerical simulations are carried out assuming $a_H = a_L = 800$ and $b = 1000$ in Eq. (20), and using the parameter values listed in Table I with $\lambda_H = 0.05$, $\lambda_L = 0.02$, and $\theta = 10^{-3}$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b) Same as panel (a) but for $\theta = 5 \times 10^{-5}$.

of $|\mu_H^0 - \langle \varphi \rangle|$ and $|\mu_L^0 - \langle \varphi \rangle|$ (i.e., independently of the value of c). However, the results presented in Fig. 7(a) show that, when θ is such that the nutrient level undergoes mild fluctuations (i.e., when the continuum model predicts population L to be ultimately selected after an initial phase of population size contraction), good quantitative agreement between numerical simulations of the IB and continuum models is observed only if $|\mu_L^0 - \langle \varphi \rangle|$ and $|\mu_H^0 - \langle \varphi \rangle|$ are sufficiently small (i.e., only if c is sufficiently large). Indeed, larger values of these distances correlate with stronger bottleneck effects that may drive discrepancies between the cell dynamics of the two models.

D. Sensitivity analysis of the initial population sizes

Motivated by the numerical results presented in Sec. IV C, we hypothesize that differences between numerical simulations of the IB and continuum models, which are observed for sufficiently large values of $|\mu_i^0 - \langle \varphi \rangle|$ (i.e., sufficiently small c) and sufficiently small values of σ_i^0 (i.e., sufficiently high b), will be amplified when smaller initial sizes of population L are considered and the initial total number of cells is held fixed. Indeed, lower values of ρ_L^0 may exaggerate stochastic effects associated with small population sizes in the course of the population bottleneck that occurs in the initial phase of the cell dynamics (i.e., when the size of population L decays). To test this hypothesis, we focus on the case where the nutrient inflow rate is constant and carry out numerical simulations for which the parameters a_H and a_L (i.e., the parameters linked to

the initial population sizes) in Eq. (20) are related as follows:

$$a_H = \nu Z \quad \text{and} \quad a_L = (1 - \nu)Z, \quad (23)$$

with Z fixed and for increasing values of $0 < \nu < 1$.

The results presented in Fig. 8 show that higher values of ν lead to a sharper bottleneck in population L and longer transient intervals during which the two populations coexist. For all admissible values of ν , the solutions of the continuum model are such that the size of population L evolves to a stable positive value and population H becomes extinct. By contrast, for ν sufficiently large there are realizations of the IB model whereby population H outcompetes population L . Moreover, the size of population H may undergo small stochastic fluctuations about a stable positive value that is larger than that about which the size of population L fluctuates—i.e., the mean size of population H is larger than the mean size of population L .

Analogous results pertain when a periodic nutrient inflow defined via Eq. (13) is considered, provided that values of θ leading to the emergence of mild fluctuations in the nutrient level are chosen (i.e., when the continuum model predicts population L to be ultimately selected after an initial phase of population size contraction) along with sufficiently high $|\mu_L^0 - \langle \varphi \rangle|$ and $|\mu_H^0 - \langle \varphi \rangle|$ (results not shown).

V. APPLICATION TO THE MATHEMATICAL MODELING OF METASTATIC COLONIZATION

The results presented in Sec. IV lead us to conclude that significant differences between the predictions made by the

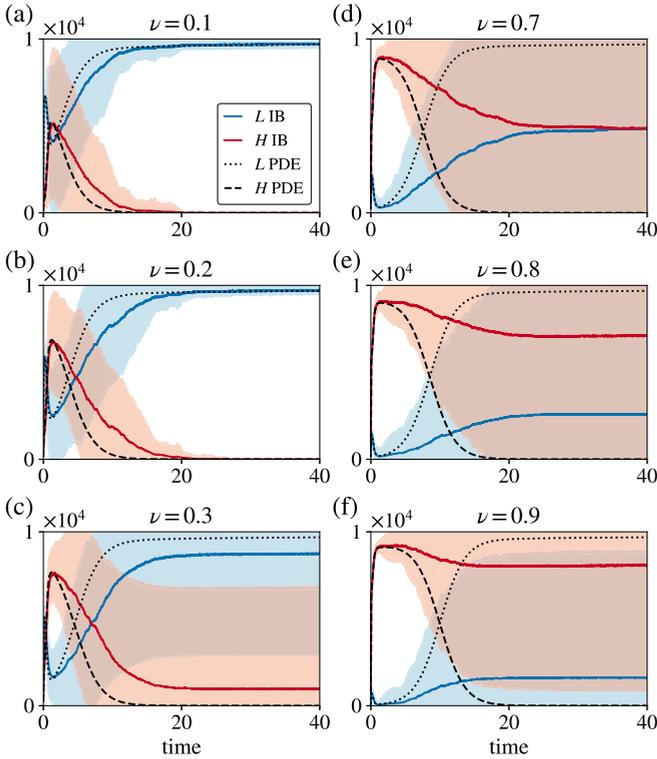


FIG. 8. Sensitivity analysis of the initial population sizes. (a) Comparison between numerical simulations of the IB (solid, colored lines) and continuum (broken, black lines) models in the case where a_i in Eq. (20) is defined via Eq. (23) with $Z = 800$ and $\nu = 0.1$. The evolution of the nutrient concentration is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (12) with $\bar{I} = 10$. Numerical simulations are carried out assuming $b = 1000$ and $c = 0.5$ in Eq. (20), and using the parameter values listed in Table I with $\lambda_H = 0.05$, $\lambda_L = 0.02$, and $\theta = 10^{-3}$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b)–(f) Same as (a) but for $\nu = 0.2$ (b), $\nu = 0.3$ (c), $\nu = 0.7$ (d), $\nu = 0.8$ (e), $\nu = 0.9$ (f).

stochastic IB model and the corresponding deterministic continuum model can arise due to the occurrence of bottleneck effects, which may be encountered during the early stage of colonization of new habitats by invasive species across a wide range of ecological scenarios. As an illustrative example, here we demonstrate the implications of such differences between the two modeling approaches when studying *in silico* the metastatic colonization of distant organs by cancer cells.

A. Essentials of the biological problem

Metastasis is a multistep process that requires cancer cells to leave the primary tumour site, survive in the blood circulation, extravasate and proliferate at distant sites. During the course of such a multifaceted process, cancer cells need to sequentially acquire different phenotypic characteristics and ultimately adapt to the environmental conditions of distant organs, which may be significantly different from those of the primary tumour [41–43].

TABLE II. Parameter values used in numerical simulations.

Parameter	Value	Units
γ	0.66	day ⁻¹
ζ	0.5	day ⁻¹
d	5.2×10^{-4}	day ⁻¹ cells ⁻¹
K	1.25×10^5	cells
θ	8.2×10^{-9}	mmol cells ⁻¹
κ	2.1×10^{-3}	mmol
η	0.24	day ⁻¹
I_v	1.5×10^{-4}	mmol day ⁻¹
α	{0.01, 1, 10}	–
λ_H	0.02	–
λ_L	0.002	–
a_H, a_L	25	cells
b	1000	–
c	0	–
τ	10^{-3}	day
t_f	365	day
χ	0.032	–

Cancer cells have been reported to undergo spontaneous, heritable phenotypic variation [44], which may facilitate adaptation to unpredictable environmental changes, such as those faced during the colonization of a new niche following extravasation [45]. Since metastases are seeded by single cancer cells or small cell clusters, which originate from the primary site, the adaptive process undergone by cancer cells during the early stage of colonization may be strongly impacted by demographic stochasticity.

B. Definition and calibration of the model

We use the stochastic IB model presented in Sec. II and its deterministic continuum analog provided in Sec. III to investigate the role that spontaneous, heritable phenotypic changes play in the evolutionary dynamics of cancer cells during the early stage of colonization of a distant organ upon extravasation. In particular, we model the dynamics of cancer cells within a small metastatic lesion that is embedded in a 1 mm³ portion of tissue and we assume the metastatic lesion to consist of two competing populations of cancer cells which undergo spontaneous, heritable phenotypic changes with different probabilities.

As before, the population with the lower probability of phenotypic variation is labeled by the index L , while the other population is labeled by the index H . Coherently with the existing literature [46], we choose the value of the probability of phenotypic variation λ_H reported in Table II and we estimate the probability of phenotypic variation λ_L to be one order of magnitude smaller than λ_H (i.e., $\lambda_L = 0.1\lambda_H$).

In this case, the phenotypic state of every cell at any time t_h is characterized by the discrete variable $x_j \in [0, 1]$, which models the normalized level of expression of a gene that controls the cell metabolic state, for example, the GLUT-1 gene [47]. In this scenario, cells in the phenotypic state $x_j = 0$ have a fully oxidative metabolism and produce energy through oxygen consumption only; cells in the phenotypic state $x_j = 1$ express a fully glycolytic metabolism and produce energy

through glucose consumption only; cells in other phenotypic states $x_j \in (0, 1)$ produce energy via both oxygen and glucose consumption, and higher values of x correlate with a less oxidative and more glycolytic metabolism [23]. Cells in the phenotypic state $x_j = 0$ are best adapted to oxygen-rich environments (i.e., normoxic conditions), while cells in the phenotypic state $x_j = 1$ are best adapted to oxygen-poor environments (i.e., hypoxic conditions), since they rely on glucose as their primary source of energy and do not require oxygen for their survival. We assume that glucose is not a limiting factor in cancer cell proliferation, since its level remains constantly high [48].

Under the biological scenario corresponding to these assumptions, the parameter γ in our model represents the maximum proliferation rate of fully oxidative phenotypic variants, while the parameter ζ is the maximum proliferation rate of fully glycolytic phenotypic variants. Based on the existing literature [49], we estimate the values of these parameters to be those reported in Table II. Notice that since glucose is an inefficient energy source compared to oxygen, we have that $\zeta < \gamma$ [50].

In particular, letting the average diameter of a cell be about $20 \mu\text{m}$, we estimate the maximum number of cells that can be accommodated in 1 mm^3 of tissue to be $K = 1.25 \times 10^5$ [51], and we assume that only 1% of them can be cancer cells since, during the early stage of metastatic colonization, other cells that are present in the tissue prior to cancer cell extravasation will leave very limited amount of space available for cancer cells to invade. Hence, using the fact that the approximate carrying capacity for our model in oxygen-rich environments is γ/d [23], we estimate the value of the death rate due intra- and interpopulation competition d as follows:

$$\frac{\gamma}{d} \approx \frac{K}{100} \implies d \approx 100 \frac{\gamma}{K}.$$

We assume the phenotype distributions of the two cell populations at time $t_h = 0$ to be of the form given by Eq. (20) with the values of the parameters a_H , a_L , b and c corresponding to a biological scenario whereby the two cell populations are both small and mainly composed of cells in the fully oxidative phenotypic state $x_j = 0$ (cf. the values of the parameters a_H , a_L , b , and c reported in Table II).

We let the function S^h represent the concentration of oxygen available to cancer cells at time t_h . The dynamic of S^h is governed by the difference Eq. (11), whereby the term I^h models the rate at which cancer cells are supplied with oxygen by blood vessels found in the tissue. Here, the parameter η is the rate of natural decay of oxygen, the value of which is estimated based on Ref. [52], κ is the Michaelis constant of oxygen and θ is a conversion factor for cell consumption of oxygen, the values of which are chosen consistent with those reported in Ref. [49]. Making the simplifying assumption that oxygen supply from blood vessels is constant over time, we define I^h via Eq. (12). Furthermore, denoting by I_v the average amount of oxygen released from a single healthy blood vessel, the value of which is chosen based on experimental measurements reported in Ref. [53], we use the following definition of the term \bar{I} in Eq. (12):

$$\bar{I} := \alpha I_v. \quad (24)$$

The parameter $\alpha > 0$ in Eq. (24) models the level of tissue oxygenation, which is known to be organ-specific—viz. lungs and bones are, respectively, highly and poorly oxygenated organs [54].

In summary, the parameter values used to carry out numerical simulations of the IB model are those reported in Table II and the parameter values of the corresponding continuum model are defined accordingly.

C. Results

We expect lower values of α in Eq. (24) (i.e., lower levels of tissue vascularisation) to correlate with a lower saturation value of the oxygen concentration. On the basis of the simulation-assisted analysis carried out in Ref. [23], we can foresee that lower saturation values of the oxygen concentration will bring about cancer cell populations of smaller size and will favour glycolytic phenotypic variants (i.e., cells in phenotypic states $x_j \rightarrow 1$) over oxidative phenotypic variants (i.e., cells in phenotypic states $x_j \rightarrow 0$). Under the biological conditions corresponding to the initial phenotype distributions considered here (cf. the values of the parameters b and c reported in Table II), the initial mean phenotype of the two cancer cell populations is the fully oxidative phenotypic state $x_j = 0$ and, therefore, lower values of α will correspond to initial mean phenotype of lower fitness. Hence, based on the results of the sensitivity analysis presented in Sec. IV, we expect smaller α to make it more likely that differences between the IB model and its continuum counterpart will emerge. This is confirmed by the results presented in Fig. 9.

The sample dynamics of the size of the cell populations H and L displayed in Fig. 9 demonstrate that when α is sufficiently high there is excellent quantitative agreement between the discrete and continuum models [see Fig. 9(a)]. However, the match between the two models deteriorates as the value of α decreases. This discrepancy arises because, in contrast with the deterministic continuum model, the IB model predicts that population L may be driven to extinction by demographic stochasticity, resulting in the survival of population H [see Figs. 9(b) and 9(c)].

These results communicate the biological notion that higher probabilities of spontaneous, heritable phenotypic changes may constitute a competitive advantage for cancer cells during the early stage of metastatic colonization of poorly oxygenated distant organs. The same results act also as a proof of concept for the idea that whilst stochastic effects associated with small cell numbers, which cannot be captured by deterministic continuum models formulated as nonlocal PDEs, can be, in a first approximation, neglected when modeling the metastatic colonization of highly oxygenated distant organs, such as the lungs, they become particularly relevant when considering poorly oxygenated organs, such as the bones. This supports the idea that particular care should be taken when selecting the mathematical modeling approach employed to describe such a process of biological colonization of new habitats.

VI. CONCLUSIONS

We developed a stochastic IB model for the evolutionary dynamics of two competing phenotype-structured cell

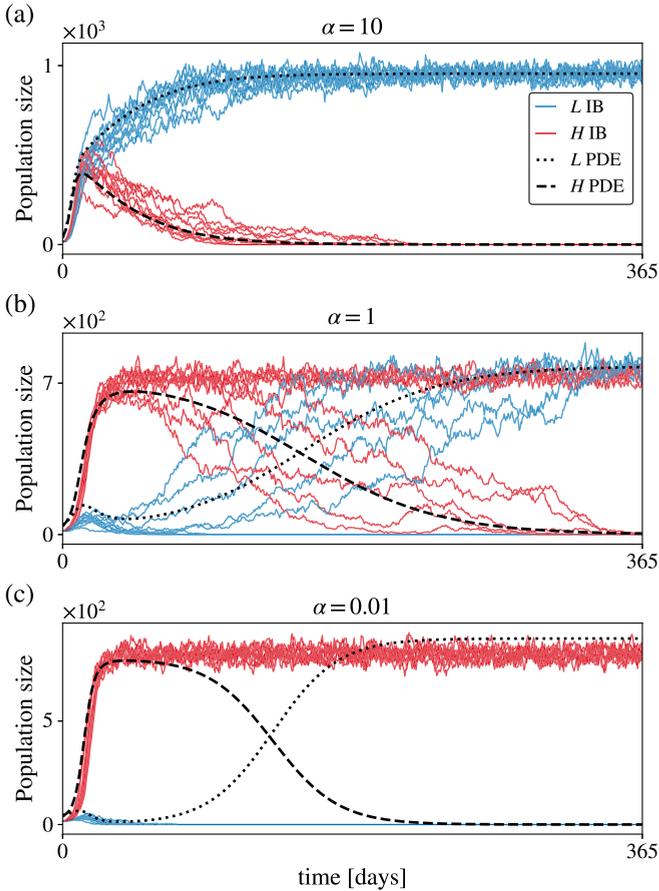


FIG. 9. Application to the mathematical modeling of metastasis. (a) Comparison between numerical simulations of the IB (solid, colored lines) and continuum (broken, black lines) models, in the case where realistic parameter values corresponding to the early stage of metastatic colonization of distant organs by cancer cells are considered (cf. parameter values reported in Table II). The evolution of the oxygen concentration is governed by the difference Eq. (11), whereby the term I^h is defined via Eq. (12) and the term \bar{I} in Eq. (12) is defined according to Eq. (24) with $\alpha = 10$. (b, c) Same as panel (a) but for $\alpha = 1$ and $\alpha = 0.01$, respectively.

populations that are exposed to time-varying nutrient levels and undergo spontaneous, heritable phenotypic changes with different probabilities. We formally derived the deterministic continuum counterpart of this model and carried out a systematic comparison between numerical simulations of the IB and continuum models.

We presented base-case results that demonstrate an excellent quantitative match between the outcomes of the two models. These results agree with our previously published analytical and numerical results for related deterministic continuum models [22,23]. Moreover, we investigated the importance of stochastic effects in driving differences between the predictions made by the two models and how these cannot be captured by the deterministic continuum model. Finally, considering suitably parameterised versions of the IB and continuum models, we demonstrated how such differences may impact on the mathematical modeling of the early stage of metastatic colonization of distant organs by cancer cells.

The results obtained indicate that bottleneck effects, which are crucial during the colonization of new habitats by invasive species, can lead to significant differences between the two models. In fact, more prominent population bottlenecks bring about sharper drops in cell numbers. This correlates with both lower regularity of the density functions of the two populations and more pronounced demographic stochasticity, which cause a reduction in the quality of the approximations employed in the formal derivation of the deterministic continuum model from the stochastic IB model [cf. the approximations given by Eqs. (A2)–(A5) and (A7)]. In particular, bottleneck effects emerge in the presence of lower probabilities of phenotypic variation, and are more apparent when the two populations are characterized by less fit initial mean phenotypes and smaller initial levels of phenotypic heterogeneity. The emergence of these effects, and thus the agreement between the two modeling approaches, is also dependent on the initial proportions of the two populations.

The generality of our assumptions make the discrete modeling framework considered here applicable to a broad range of asexual organisms exposed to dynamically changing environments. Such a modeling framework, along with the related method to formally derive corresponding continuum models, can be easily extended to incorporate the effects of additional biological aspects related to spatial structure, such as cell movement, inter-cellular spatial interactions, nutrient diffusion and the presence of multiple sources of nutrient distributed across the spatial domain. These extensions will enable a more biologically relevant exploration of the scenarios under which stochastic effects may result in discrepancies between the predictions made by discrete stochastic models and those made by their deterministic continuum limits. This will ultimately help disentangle the impact of, different sources of, stochasticity on the emergence of spatiotemporal evolutionary patterns in a variety of living systems [55,56].

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APPENDIX A: FORMAL DERIVATION OF THE DETERMINISTIC CONTINUUM MODEL GIVEN BY THE SYSTEM OF NONLOCAL PDES (15)

Using a method analogous to that employed in Refs. [32,33], we show that the coupled system of nonlocal

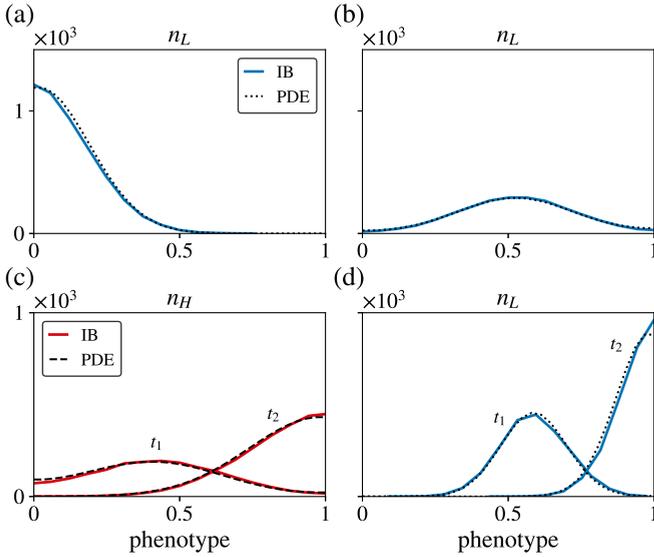


FIG. 10. Sample phenotype distributions for base-case results. Comparison between the phenotype distributions of the surviving population for the IB (solid, colored lines) and continuum (broken, black lines) models in the case where the evolution of the nutrient concentration is governed by the difference Eq. (11). The results from the IB model correspond to the average over 30 realizations. (a) Phenotype distribution at numerical equilibrium (i.e., at time $t_f = 10$) under the simulation set-up of Fig. 2(a). (b) Phenotype distribution at numerical equilibrium (i.e., at time $t_f = 10$) under the simulation set-up of Fig. 2(b). (c) Phenotype distribution at the time instants $t_1 = 17.5$ and $t_2 = 20$ under the simulation set-up of Fig. 3(a). (d) Phenotype distribution at the time instants $t_1 = 17.5$ and $t_2 = 20$ under the simulation set-up of Fig. 3(b).

PDEs (15) can be formally derived as the appropriate continuum limit of our discrete model.

In the case where the dynamics of the cells is governed by the rules described in Sec. II, the principle of mass balance gives the following difference equations

$$n_{i,j}^{h+1} = \{2\tau p(x_j, S^h) + [1 - \tau(p(x_j, S^h) + d\rho^h)]\} \times \left[\frac{\lambda_i}{2} n_{i,j+1}^h + \frac{\lambda_i}{2} n_{i,j-1}^h + (1 - \lambda_i) n_{i,j}^h \right],$$

for $i \in \{H, L\}$, which can be rewritten as

$$n_{i,j}^{h+1} = (1 + \tau p(x_j, S^h) - \tau d \rho^h) \left[\frac{\lambda_i}{2} n_{i,j+1}^h + \frac{\lambda_i}{2} n_{i,j-1}^h + (1 - \lambda_i) n_{i,j}^h \right]. \quad (\text{A1})$$

Using the fact that the following relations hold for τ and χ sufficiently small

$$t_h \approx t, \quad t_{h+1} \approx t + \tau, \quad x_j \approx x, \quad x_{j\pm 1} \approx x \pm \chi, \quad n_{i,j}^h \approx n_i(x, t), \quad S^h \approx S(t), \quad (\text{A2})$$

$$n_{i,j}^{h+1} \approx n_i(x, t + \tau), \quad n_{i,j\pm 1}^h \approx n_i(x \pm \chi, t), \quad (\text{A3})$$

$$\rho_i^h \approx \rho_i(t) := \int_0^1 n_i(x, t) dx, \quad (\text{A4})$$

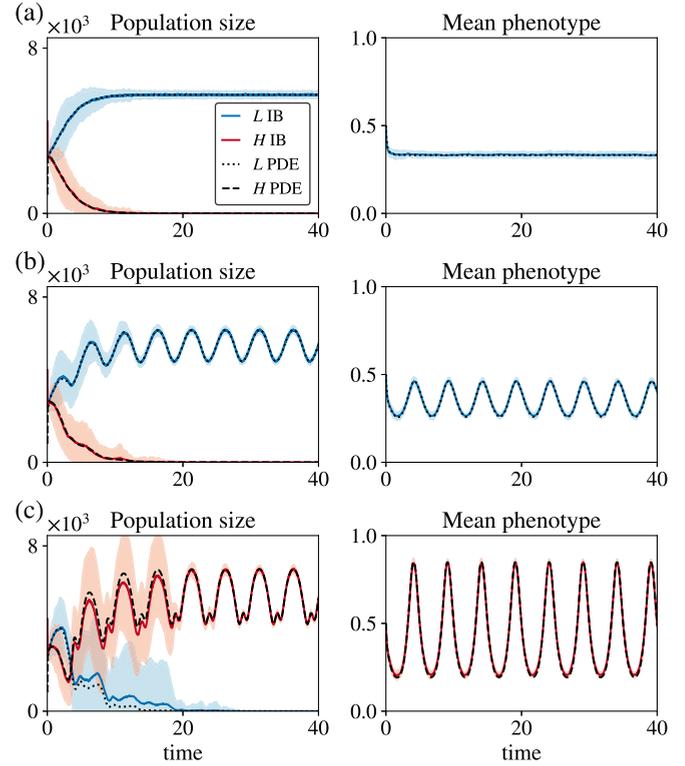


FIG. 11. Base-case results when the nutrient concentration is prescribed. Comparison between numerical simulations of the IB (solid, colored lines) and continuum (broken, black lines) models in the case where the nutrient concentration is prescribed and defined via Eq. (D1). (a) Dynamics of the population sizes (left column) and the mean phenotype of the surviving population (right column) in the case where $M = 1$, $T = 5$ and $A = 0$ in Eq. (D1). Here, $a_H = a_L = 800$, $b = 10$ and $c = 0.5$ in Eq. (20), and the values of the other parameters are those listed in Table I with $\lambda_H = 0.05$ and $\lambda_L = 0.02$. The results from the IB model correspond to the average over 30 realizations and the related variance is displayed by the colored areas surrounding the curves. (b, c) Same as panel (a) but for $A = 0.5$ [row (b)] and $A = 1$ [row (c)].

and

$$\rho^h \approx \rho(t) := \int_0^1 n_H(x, t) dx + \int_0^1 n_L(x, t) dx. \quad (\text{A5})$$

Equation (A1) can be formally rewritten in the approximate form

$$n_i(x, t + \tau) = \{1 + \tau R[x, S(t), \rho(t)]\} \left[\frac{\lambda_i}{2} n_i(x + \chi, t) + \frac{\lambda_i}{2} n_i(x - \chi, t) + (1 - \lambda_i) n_i(x, t) \right], \quad (\text{A6})$$

with $R[x, S(t), \rho(t)] := p[x, S(t)] - d\rho(t)$. If the function $n_i(x, t)$ is twice continuously differentiable with respect to the variable x , then for χ sufficiently small we can use the Taylor expansions

$$n_i(x \pm \chi, t) = n_i \pm \chi \frac{\partial n_i}{\partial x} + \frac{\chi^2}{2} \frac{\partial^2 n_i}{\partial x^2} + \text{h.o.t.}, \quad (\text{A7})$$

where $n_i \equiv n_i(x, t)$. Substituting Eq. (A7) into Eq. (A6) and dividing both sides of the resulting equation by τ , after a little

algebra we find

$$\begin{aligned} & \frac{n_i(x, t + \tau) - n_i(x, t)}{\tau} \\ &= R[x, S(t), \rho(t)]n_i(x, t) + \frac{\lambda_i \chi^2}{2\tau} \frac{\partial^2 n_i(x, t)}{\partial x^2} \\ & \quad + R[x, S(t), \rho(t)] \frac{\lambda_i \chi^2}{2} \frac{\partial^2 n_i(x, t)}{\partial x^2} + \text{h.o.t.} \end{aligned}$$

If, in addition, the function $n_i(x, t)$ is continuously differentiable with respect to the variable t , letting $\tau \rightarrow 0$ and $\chi \rightarrow 0$ in such a way that the condition given by Eq. (14) is met, then from the latter equation we formally obtain

$$\frac{\partial n_i(x, t)}{\partial t} = \beta_i \frac{\partial^2 n_i(x, t)}{\partial x^2} + R[x, S(t), \rho(t)] n_i(x, t),$$

which gives the system of nonlocal PDEs (15). Finally, the no-flux boundary condition Eqs. (16) follow from the fact that the attempted phenotypic variation of a cell is aborted if it requires moving into a phenotypic state that does not belong to the interval $[0, 1]$.

APPENDIX B: DETAILS OF NUMERICAL SIMULATIONS OF THE CONTINUUM MODEL

To construct numerical solutions of the system of nonlocal PDEs (15) posed on $(0, 1) \times (0, t_f]$, and subject both to the no-flux boundary condition Eqs. (16) and to the continuum analog of the initial condition Eq. (20), i.e.,

$$n_i(x, 0) = a_i \left(\frac{b}{2\pi} \right)^{\frac{1}{2}} \exp \left[-\frac{b}{2} (x - c)^2 \right], \quad (\text{B1})$$

with $i \in \{H, L\}$, we use a uniform discretization of the interval $(0, 1)$ as the computational domain of the independent variable x , and we discretize the time interval $(0, t_f]$ with the uniform step $\Delta t = 0.0001$. The method for constructing numerical solutions is based on a three-point finite difference explicit scheme for the diffusion terms and an explicit finite difference scheme for the reaction term [57]. Moreover, the ODE (17), which is subject to the initial condition $S(0) = 10$ and complemented with the continuum analogues of the alternative definitions of the term I^h that are specified in the main body of the paper, is solved numerically by using an explicit Euler method with step Δt . Given the values of the parameter τ , χ , λ_H and λ_L of the IB model, the values of the parameters β_H and β_L are defined so that the condition given by Eq. (14)

is met. The other parameter values are chosen to be coherent with those used to carry out numerical simulations of the IB model, which are specified in the main body of the paper.

APPENDIX C: SAMPLE PHENOTYPE DISTRIBUTIONS FOR THE BASE-CASE RESULTS PRESENTED IN SECTION IV A

Figure 10 shows the phenotype distribution of the surviving population when the supply rate of nutrient is constant [(a)–(b)] and when the nutrient supply undergoes periodic oscillations [(c)–(d)].

APPENDIX D: BASE-CASE RESULTS IN THE CASE WHERE THE NUTRIENT CONCENTRATION IS PRESCRIBED

We carried out preliminary numerical simulations in the case where, instead of being the solution of the difference Eq. (11), the nutrient concentration is prescribed and given by

$$S^h := M + A \sin \left(\frac{2\pi t_h}{T} \right), \quad (\text{D1})$$

where $M > 0$ is the mean nutrient level, and the parameter $0 \leq A \leq M$ models the semi-amplitude of possible oscillations of the nutrient level, which have period $T > 0$. We fix the values of M and T and consider three different values of A that correspond to distinct environmental regimes: constant nutrient level (i.e., no oscillations), mild nutrient fluctuations (i.e., small-amplitude oscillations) and severe nutrient fluctuations (i.e., large-amplitude oscillations).

The results presented in Fig. 11 show that, for all values of A considered, there is an excellent quantitative match between the numerical simulations of the IB and continuum models. In agreement with the analytical results that we presented in Ref. [22], when the nutrient concentration is constant, population L outcompetes population H [see Fig. 11(a)]. The same outcome is observed in the presence of mild nutrient fluctuations [see Fig. 11(b)]. By contrast, population L is outcompeted by population H when severe nutrient fluctuations occur [see Fig. 11(c)]. In all cases, the phenotype distribution of the surviving population is unimodal and attains its maximum at the mean phenotype (results not shown). Moreover, when the nutrient level is constant, the size and the mean phenotype of the surviving population converge to stable values. However, in the presence of T -periodic nutrient fluctuations, the size and mean phenotype of the surviving population converge to T -periodic functions.

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