Fixation in Populations: Diffusion and Strategies for Survival

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How should dispersal strategies be chosen to increase the likelihood of survival of a species? We obtain the answer for the spatially extended versions of three well-known models of two competing species with unequal diffusivities. Though identical at the mean-field level, the three models exhibit drastically different behaviour leading to different optimal strategies for survival. When intra-species competition is present, faster dispersal is advantageous. With conserved total particle number, dispersal has no effect on survival probability, while with birth-death fluctuations present, moving slower is the optimal strategy for the weaker species: it is imperative to include fluctuations to properly formulate survival strategies.

Biological dispersal refers to the movement of individuals and is a key feature of population dynamics. Dispersal has consequences not only for species distribution but also for individual survival, thereby influencing many different aspects of evolutionary dynamics, from epidemic outbreaks to the evolution of language [1–7]. The importance of dispersal rates for ultimate survival stems from the fact that two individuals need to be in the same locality in order to interact. Evidently, the nature of interactions is also crucial, both within species and across species, and can affect the likelihood that a particular species eventually prevails [8–10]. Indeed, when intra-species interactions dominate, the optimal strategy for choosing dispersal rates has been explored earlier. In the presence of logistic-type competition for resources between members of the same species, the survival probability of a species increases as the dispersal rate increases [11], while in the presence of cooperation between members of the same species, the survival probability increases as the dispersal rate decreases [12]. In general, how should dispersal strategies be chosen so as to increase the likelihood of survival of a species?

In this Letter, we address this broad and important question by focusing on the dispersal properties of two competing species in a spatially extended system. The dynamics involves random diffusive motion and may also include stochastic birth and death of competing individuals. We will see below that choosing an optimal strategy to maximize survival probability needs a nuanced understanding of factors which arise from the dynamics.

To understand these factors, we carry out a parallel study of three simple well-studied models with different reaction dynamics [13–17]. The models show very different behavior, as evidenced by Fig. 2 which shows the time evolution for the three, with equal (top panels) and unequal (bottom panels) dispersal rates for the two species. This happens, as we show later, even though the mean field descriptions of all three are identical. The primary aim of this paper is to understand the origin of these differences, and to use the insight gained to formulate optimal dispersal strategies. We investigate both the neutral case in which the interspecies interactions are symmetric, as well as the case when one of the species has an advantage.

![FIG. 1. Space-time plots for three models, namely Voter Model with Diffusion (VMD), Fluctuating Voter Model with Diffusion (FVMD), and Competitive Lotka-Volterra Model with Diffusion (CLVMD), with equal (top panels) and unequal (bottom panels) diffusivities.](image)

We focus on the fixation probability $F$ which is the likelihood that a certain species would prevail over the
other. Here is a summary of our main results: (i) If the total number of individuals is strictly conserved, $\mathcal{F}$ is invariant with respect to change in diffusivity, implying that variation of dispersal rate is ineffective as a strategy to enhance $\mathcal{F}$ in this case. However, the dynamics is not symmetric as illustrated in the lower VMD panel in Fig. 2. (ii) If birth and death lead to fluctuations of the total number of individuals around an average value, $\mathcal{F}$ continues to be independent of diffusivity in the neutral case (lower FVMD panel in Fig. 2). However, there is a new effect in the non-neutral case, when there is a bias or selective advantage for one of the species: the optimal strategy for weaker individuals is then to move slower. (iii) Only when one allows for intra-species competition, does a difference in dispersal rates matter in the neutral case. In that case, the best strategy to enhance $\mathcal{F}$ is to move faster.

Our studies are carried out on three well-known lattice models involving two competing species (say $A$ and $B$), generalized to include diffusion in one dimension. Interactions are local and involve two individuals at a time on the same lattice site. We assume that the initial number of $A$ and $B$ particles is $N/2$. The onsite interactions in the three models of interest are defined below; in every case, these are supplemented by the diffusive moves given in Eq. (4).

**Voter-type Model with Diffusion (VMD):** In a single microstep, the inter-species reactions on each site follow Moran dynamics with rates $\lambda(1+\frac{s}{2})$ and $\lambda(1-\frac{s}{2})$:

$$A + B \xrightarrow{\lambda(1+\frac{s}{2})} A + A; \quad B + A \xrightarrow{\lambda(1-\frac{s}{2})} B + B$$

Here $s$ is the selective advantage, which gives a preference to either $A$ or $B$ in the competition, with $s = 0$ being the neutral case. For $s > 0$ ($s < 0$), species $A$ ($B$) has a selective advantage.

This is supplemented by the diffusive move Eq. (4).

Evidently the total number of particles in the full system is strictly conserved, but on each site the evolution differs from the strict Moran process as the number of particles fluctuates owing to diffusion. The dynamics on each site resembles that of the voter model [18–19], which has been used as a model of evolution of opinion [20–21], and disease spreading [22].

**Fluctuating Voter-type Model with diffusion (FVMD):** In addition to the Moran moves Eq. (1), we allow individuals to give birth or die, at equal rates $\mu$ [13].

$$A \xrightarrow{\mu} 2A; \quad B \xrightarrow{\mu} 0; \quad A + B \xrightarrow{\lambda(1+\frac{s}{2})} A + A; \quad B + A \xrightarrow{\lambda(1-\frac{s}{2})} B + B$$

In our numerical work, we choose $\mu = \lambda = 1$. Thus the total number of particles fluctuates around an average number. This is a model of various biological systems in which environments vary stochastically, thereby inducing fluctuations in the total number of individuals [23–24]. The long time dynamics involves two distinct outcomes, namely fixation of one of the two species, followed by overall extinction at longer times. We are interested only in the earlier fixation event.

**Competitive Lotka-Volterra Model with Diffusion (CLVMD):** In this model, individuals can give birth at rate $\lambda$ but death occurs because of intra-species and inter-species competition, at rates $\gamma$ and $\gamma (1 \pm s)$ respectively. The reactions are

$$A \xrightarrow{\mu} 2A; \quad A + A \xrightarrow{\gamma_1} A; \quad A + B \xrightarrow{\gamma_2(1+s)} A; \quad B \xrightarrow{\mu} 2B; \quad B + B \xrightarrow{\gamma_1} B; \quad B + A \xrightarrow{\gamma_2(1-s)} B$$

In steady state the mean concentration or carrying capacity $\rho$ is given by $\mu/\gamma$. This model is widely used in population ecology and genetics [14, 15].

In addition to the reactions of Eqs. (1), (2) or (3), individuals can move stochastically to neighboring sites but with different hopping rates for $A$ and for $B$, reflecting different dispersal rates:

$$\{\cdots; n_i^A, n_i^B; n_j^A, n_j^B; \cdots\} \xrightarrow{D_{AB}} \{\cdots; n_i^A - 1, n_i^B; n_j^A + 1, n_j^B; \cdots\}$$

Here $n_i^A, n_i^B (= 0, 1, 2, \ldots)$ are the $A$ and $B$ particle occupancies on site $i$ and $j = i \pm 1$ and $n_i^3 \rightarrow n_i^{A-1}$ moves occur only if $n_i^A > 0$, with a similar condition for $B$. Note that unlike the stepping stone model [20–21], the number of individuals on a site can fluctuate.

![FIG. 2. Fixation probability with respect to relative diffusivity of two species for three models in the neutral case. $\mathcal{F}(B)$ does not vary with $\Delta D$ for VMD and FVMD whereas $\mathcal{F}(B)$ for CLVMD shows a variation with respect to relative diffusivity. We used $D = 1$.](image-url)

The mean-field descriptions of the three models is similar as shown in the Supplemental Material. Therefore for investigating the non-trivial effects that we highlighted in the introduction, we performed agent-based simulations for these models.

**Methodology:** We devise a novel algorithm to carry out the reaction along with the diffusion dynamics, by splitting the two processes. A single time step is broken into many substeps, each of duration $\Delta t$. At the first substep, for reactions, we implement the event-based variant of
configuration, we display some moves and reactions, with the faster and stronger individuals $A$ and $B$ and varies from one history to another. As a result, the VMD reaction steps depend on the dynamic evolution of $\Delta D$. The result of each reaction step involves diffusion (with $D$ understood as follows. The full dynamics of the process are given in Supplemental Material. In what follows, we denote the fixation probability for the $A$ ($B$) species by $\mathcal{F}(A)$ ($\mathcal{F}(B)$), where $\mathcal{F}(A) + \mathcal{F}(B) = 1$.

Neutral Case ($s = 0$): In this case the rates of reactions are $A-B$ symmetric, while the diffusivities of the $A$ and $B$ species are unequal, with $D_A = D$, and $D_B = D - \Delta D$. Numerical simulations show that the variation of $\mathcal{F}(B)$ with $\Delta D$ is quite different for the three models (Fig. 2). While it is immune to change of $\Delta D$ for the VMD and FVMD, for the CLVMD $\mathcal{F}(B)$ is very sensitive to $\Delta D$. These pronounced differences occur although the mean-field equations for the concentration of species are the same for all three models, pointing to the inability of mean field theory to pick out subtle differences that arise from fluctuation effects.

The result $\mathcal{F}(A) = \mathcal{F}(B) = \frac{1}{2}$ for the VMD may be understood as follows. The full dynamics of the process involves diffusion (with $D_B < D_A$) along with $A-B$ symmetric reaction kinetics. The result of each reaction step is $2A$ or $2B$ with equal probability. Evidently, every reaction step can be mapped onto the corresponding step in a reference Moran process for the overall numbers of $A$ and $B$ particles, although the time between successive VMD reaction steps depends on the dynamic evolution and varies from one history to another. As a result, $\mathcal{F}(B)$ takes on the Moran value $\frac{1}{2}$ even though fixation times for each species are different because of the difference in dispersal dynamics. The inclusion of birth-death fluctuations in the FVMD does not change the conclusion $\mathcal{F}(B) = \frac{1}{2}$, even when $D_A = 1$ and $D_B = 0$.

The strong effect of $\Delta D$ on $\mathcal{F}(B)$ in the CLVMD (Fig. 3) may be understood as follows. The intra-species death terms in Eq. 3 have strong effects on sites with several particles of the same species. For $A$ particles, fluctuations spread out quickly as $D_A > D_B$, thus minimizing the effects of intra-species death. Dispersal of $B$ particles is slower making them more prone to intra-species death. A depleted $B$ population on a given site is then easier to convert to all $A$’s. The outcome of neutral inter-species competition is $A-B$ symmetric, and unaffected by dispersal rates. Thus overall, the optimal survival strategy with CLVMD is to move fast.

With Selective Advantage ($s > 0$): Going beyond the neutral case, we study the effects of unequal diffusivity with applied selective advantage by monitoring the change of fixation probability $\Delta \mathcal{F} = \mathcal{F}(B) - \mathcal{F}^*(B)$ where $\mathcal{F}(B)$ and $\mathcal{F}^*(B)$ are the probabilities when the diffusivities are unequal and equal, respectively. Figure 3 illustrates how different dynamical moves in the three processes influence the occurrence and likely outcomes of $A-B$ interactions.

For the VMD, $\mathcal{F}(B)$ remains unchanged from its equal diffusivity value even when $s$ is not zero. Hence $\Delta \mathcal{F} = 0$ irrespective of $\Delta D$.

For the FVMD, the best dispersal strategy depends on the strength of the species. For the weaker $B$ species, moving slowly is a better strategy than moving fast. To see why, consider $A$ and $B$ particles with initial separation $R$ as illustrated in Fig. 3. Under diffusion, they would meet after a typical time $\tau_{\text{diff}} \approx R^2/D_{\text{eff}}$ where the effective diffusion constant $D_{\text{eff}}$ is $D_{\text{eff}} = (D_A + D_B)$. Further, owing to the birth-death process, the typical time of survival of an $A$ particle is $1/\mu$, imply-
is strongly depleted, which lengthens the time before the next A particle arrives. This effect, which slows down the process, is absent while reaching an A-fixed state, which has a uniform A concentration.

For the CLVMD, we find \( t_A < t_B \). Recall that the dynamics is dominated by intra-species interactions which lead on average to the B population falling owing to slower spreading of B concentration fluctuations. Thus in the minority of cases in which the B species does achieve fixation, it must be before the intra-species terms have had much effect. Thus B fixation would occur at early times.

It is possible to obtain analytic results for \( \langle t_A \rangle \) and \( \langle t_B \rangle \) in the limit of the VMD dynamics in which one species (say B) has zero diffusivity, and the reactions on each site happen infinitely fast. Consider the neutral case with an initial condition with \( N_0 = N/2 \) A’s and an equal number of B’s, the latter all being at a single site \( i \). At each time step, a single A particle reaches the site; on-site reactions being completed before the next A arrives. We now compute \( F(B) \) for both species and show that the mean times \( \langle t_A \rangle \) and \( \langle t_B \rangle \) for A and B fixation, satisfy \( \langle t_A \rangle < \langle t_B \rangle \), while \( F(B) = \frac{1}{2} \).

Let us compute the probability that there is a global A fixation at the \( n \)’th step. A particles arriving earlier at the site would have converted to B, so that the number of B particles after the \( (n-1) \)th step is \( N_0 + n - 1 \). The probability \( Q(n-1) \) of this event is \( g_0 \times g_1 \times \cdots \times g_{n-1} \) where \( g_i = N_0 + i/(N_0 + i + 1) \) is the probability that an A particle arriving at the \( i \)th step is converted to B. Thus \( Q(n-1) = N_0/(N_0 + n - 1) \). Now consider the arrival of the next A particle. The reactions result in the \( N_0 + n \) particles becoming all A’s (with probability \( 1/N_0 + n \)). If this happens, the system would have fixated globally to all A’s. Thus the probability \( P_A(n) \) that A fixation happens at the \( n \)th time step is \( Q(n-1) \times 1/(N_0 + n) \). The mean time of A fixation is then straightforwardly found to be

\[
\langle t_A \rangle = 2N_0 \left[ H(2N_0) - H(N_0) \right] - (N_0 - 1) \tag{5}
\]

where \( H(M) = \sum_{m=1}^{M-1} \frac{1}{m} \). For large \( N_0 \), it then follows that \( \langle t_A \rangle \approx C N_0 \), with \( C = (2 \ln 2 - 1) \approx 0.386 N_0 \). On the other hand, in order for B fixation to occur, the B’s must have survived at each of the earlier steps. The corresponding probability is \( Q(N_0) = \frac{1}{2} \), and the corresponding survival time is \( \langle t_B \rangle = N_0 \). Evidently, \( \langle t_A \rangle < \langle t_B \rangle \) holds. This result accords with the qualitative point that the faster species fixes earlier on average, brought out by our numerical simulations of the VMD process (Fig. [5]).

In order to quantify the effects of unequal diffusion constants for the A and B species, we study the Time-sliced fixation probability, defined as the fractional number of A-fixations which occur at time \( t \), i.e., \( f(t) = m_A(t)/[m_A(t) + m_B(t)] \) where \( m_A(t) \) and \( m_B(t) \) are the number of histories in which A (B) fixations occur at time \( t \). For the neutral case with \( D_A > D_B \), we find that although the overall fixation probability \( F(A) = F(B) = \)
1/2 for the VMD and FVMD, the corresponding time-sliced fixation probability is not equal, as illustrated in Fig. 5. A fixes in time, but the reverse is true at later times. This result is in consonance with \( \langle t_A \rangle < \langle t_B \rangle \) and the explanation thereof, as discussed earlier, and with \( F = \frac{1}{2} \).

For the CLVMD, recall that the nonlinear terms associated with the reaction \( A + A \rightarrow A \) and \( B + B \rightarrow B \) lead to preferential fixation of fast-moving \( A \) particles when \( D_A > D_B \). The study of \( f(t) \) helps to see how the effects of a very small nonlinearity plays out in time (Fig. 6). At small times, the variation is very similar to that of the FVMD, but at longer times \( f(t) \) shows a nonmonotonic rise as the preference for the faster species is manifest, ultimately consistent with \( F > \frac{1}{2} \).

In conclusion, our results for three well known models of competing populations with unequal diffusivity show that it is crucial to account for fluctuations beyond mean field theory to understand their behavior and formulate dispersal strategies. The fixation probability is maximized by increasing the dispersal rate if interspecies competition is present; but in a situation where the species is disadvantaged and subject to fluctuations due to birth and death, fixation probability is maximized by moving slowly; and it is unaffected by dispersal if competing interactions are described by number-conserving dynamics that can be mapped onto a Moran process. It would be interesting to explore the effects of fluctuations in broader contexts, such as competing populations in compressible flows, or with clustered initial conditions.

![Graph showing time-sliced f(t) for A species in the FVMD with and without nonlinear intraspecies competitive interactions. The curve with black dots indicates that A fixation occurs preferentially at shorter times even though \( F(A) = F(B) = 1/2 \). A very small competitive nonlinear term changes both \( F \) and \( f(t) \).](image)

\[ f(t) = \begin{cases} 0 & \text{for the VMD and FVMD, the corresponding time-sliced probability is not equal, as illustrated in Fig. 5.} \\ \langle t_A \rangle < \langle t_B \rangle & \text{and the explanation thereof, as discussed earlier, and with } F = \frac{1}{2}. \end{cases} \]

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Supplemental Material to “Fixation in Populations: Diffusion and Strategies for Survival”

MEAN FIELD EQUATIONS

The mean field equations for the models discussed in the main text can be derived from the corresponding master equation [1–4]. Below we present the mean field equation for the concentration of the two species ($c_A$ and $c_B$) for each of models and from it derive the equation for the total concentration $c = c_A + c_B$ and the fraction $f = c_A/c$.

A. Mean field equation for VMD and FVMD

Note that because the birth-rate and death-rate in FVMD are the same, the mean field equation for VMD and FVMD are identical. The equations for the concentration of $A$ and $B$ species are:

$$\frac{dc_A}{dt} = \frac{\lambda s}{2} c_A c_B + D_A \frac{\partial^2 c_A}{\partial x^2},$$  \hspace{1cm} (1)

$$\frac{dc_B}{dt} = -\frac{\lambda s}{2} c_A c_B + D_B \frac{\partial^2 c_B}{\partial x^2}. \hspace{1cm} (2)$$

Using the above equations for $c_A$ and $c_B$, we obtain the following equations for $c$ and $f$:

$$\frac{dc}{dt} = (D_A - D_B) \frac{\partial^2 f c}{\partial x^2} + D_B \frac{\partial^2 c}{\partial x^2}, \hspace{1cm} (3)$$

$$\frac{df}{dt} = \lambda s f (1 - f) + D_A \frac{\partial^2 f}{\partial x^2} + 2 \frac{D_A}{c} \frac{\partial c}{\partial x} \frac{\partial f}{\partial x} + f \frac{D_A - D_B}{c} \frac{\partial^2 c}{\partial x^2} - f \frac{D_A - D_B}{c} \frac{\partial^2 f c}{\partial x^2}. \hspace{1cm} (4)$$

For $D_A = D_B$, Eq. (4) reduces to the Fisher equation [5, 6]

Mean field equation for CLVMD

For the CLVMD, we set $\gamma_2 = \gamma$ and obtain the following reaction-diffusion equations:

$$\frac{dc_A}{dt} = \mu c_A + \gamma c_A (c_A + c_B) - \gamma s c_A c_B + D_A \frac{\partial^2 c_A}{\partial x^2}, \hspace{1cm} (5)$$

$$\frac{dc_B}{dt} = \mu c_B + \gamma c_B (c_A + c_B) + \gamma s c_A c_B + D_B \frac{\partial^2 c_B}{\partial x^2}. \hspace{1cm} (6)$$

Again, from the above equations we get the following equations for the evolution of $c$ and $f$:

$$\frac{dc}{dt} = \mu c \left(1 - \frac{\gamma}{\mu} c\right) + (D_A - D_B) \frac{\partial^2 f c}{\partial x^2} + D_B \frac{\partial^2 c}{\partial x^2}, \hspace{1cm} (7)$$

$$\frac{df}{dt} = \gamma s f (1 - f) + D_A \frac{\partial^2 f}{\partial x^2} + 2 \frac{D_A}{c} \frac{\partial c}{\partial x} \frac{\partial f}{\partial x} + f \frac{D_A - D_B}{c} \frac{\partial^2 c}{\partial x^2} - f \frac{D_A - D_B}{c} \frac{\partial^2 f c}{\partial x^2}. \hspace{1cm} (8)$$

The homogeneous stable solution for the concentration equation is $c = \mu / \gamma$. Around this homogenous initial state, it is easy to see that the equations for CLVMD and VMD model are identical.

METHODOLOGY

In our numerical simulations, we start with $N/2$ individuals of type $A$ and an equal number of type $B$, placed randomly on a 1D lattice with $L$ sites. The total number $N$ is taken to be $> L$, implying that the average density of individuals $\rho_0 = N/L > 1$. In each of the three models of population dynamics under study, there are two physical processes (i) reactions, namely birth, death, intra- and inter-species competition, and (ii) movement of individuals via diffusion. In our lattice model, reactions are on-site processes and diffusive moves happen between nearest-neighbour lattice sites. We split the reaction and diffusion processes, i.e., only reactions occur for a time interval $\Delta t$, followed...
by only diffusive moves for time $\Delta t$. The time interval $\Delta t$ is chosen to be much smaller than one Monte-Carlo step yet large enough that many reactions occur in $\Delta t$.

For reactions, we implement the event-based Gillespie algorithm \[7\] at each site. To do so, we first calculate the propensity of all possible reactions on that site. A particular reaction would occur with a probability that is proportional to its rate. Let us consider a site $i$ containing $n_A$ individuals of type $A$ and $n_B$ number of type $B$. At this site, the total number of possible reactions due to birth, death, intra-species and inter-species reactions is

\[ R = (\mu^A_{\text{birth}} + \mu^A_{\text{death}}) n_A + (\mu^B_{\text{birth}} + \mu^B_{\text{death}}) n_B + \gamma_1 [n_A (n_A - 1) + n_B (n_B - 1)] + 2 (\lambda + \gamma_2) n_A n_B. \]

We choose $\mu^A_{\text{birth}} = \mu^B_{\text{birth}} = \mu^A_{\text{death}} = \mu^B_{\text{death}} = \mu$ in our numerical simulation. The probability of a particular reaction event occurring is the ratio of the rate of the event to the total rate $R$. For instance, $A$ would become 2$A$ with probability $\frac{n_A \mu}{R}$. If the reaction happens, the next step is to increase the time by $\ln(1/r)/R$ where $r \in (0, 1]$ is a random number chosen from uniform distribution. The number of $A$’s and $B$’s change after each successive reaction, thereby affecting the total rate $R$ at the site. Quite a few reactions occur until the sum of the reaction time-steps just crosses the chosen $\Delta t$. We follow the same procedure for all other sites. Recall that during this time step $\Delta t$, we solely do the reaction, and inter-site diffusive hops are not allowed.

Once the reactions are completed on every site of the system up to time $\Delta t$, we move a randomly chosen set of $ND\Delta t$ individuals to one of the nearest neighbor sites, where $D$ is the hopping rate of the species.

The time evolution is averaged over a number $N_{\text{hist}}$ of histories, each starting from a new initial condition, a typical value of $N_{\text{hist}}$ being 30,000. The values of the parameters that we have used for numerical simulations of the different models are given in Table I. To check that our results do not depend on $\Delta t$, we varied it by a factor 4 and found that there is no appreciable change in our numerical estimates of the fixation probability (Fig. 1).

![Figure 1](image_url)
### Table I

| Parameters | VMD | FVMD | CLVMD |
|------------|-----|------|-------|
| Reactions: | Eq. (1) | Eq. (2) | Eq. (3) |
| $\mu$      | 0   | 2    | 4     |
| $\lambda$  | 2   | 2    | 0     |
| $\gamma_1 = \gamma_2 = \gamma$ | 0 | 0 | 1/8 |
| $D_A = D$  | 1   | 1    | 1     |
| $D_B = D - \Delta D$ | 0 | 0, 0.25 | 0.96, 0.98 |

TABLE I. The chosen parameters for three models. The equations refer to the main text. In most cases, we took $L = 128$, $\rho_0 = 64$, and $\Delta t = \frac{1}{512}$.

### Table II

| System size | VMD | FVMD | CLVMD |
|-------------|-----|------|-------|
| $\langle t_A \rangle$ | $\langle t_B \rangle$ | $\langle t_A \rangle$ | $\langle t_B \rangle$ |
| 32          | 146 | 955  | 118   | 232  | 172  | 110  |
| 64          | 587 | 4102 | 380   | 625  | 527  | 213  |
| 128         | 2328 | 17721 | 1101  | 159  | 1904 | 1804 |

TABLE II. Fixation time with unequal diffusivities for different system sizes where $\rho = 64$. We consider $D_B = 0$ for the VMD and FVMD and $D_B = 0.98$ for CLVMD.

### Fixation of Different Species

**FIG. 2.** Space-time plots for the three models, namely VMD, FVMD, and CLVMD, with unequal diffusivities when $A$ wins (top panels) and unequal diffusivities when $B$ wins (bottom panels). Yellow indicates empty space. The slower species has diffusion constant zero for the VMD and FVMD, resulting in pillar-like structures localized at sites. It is evident that the dynamics of fluctuations is very different in the three cases.
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