Evolution of Species' Range and Niche in Changing Environments

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What causes species' niche and range margins to shift is not only a fundamental theoretical question, but also directly affects how we assess the resilience of natural populations in current and future environments. Yet, despite the urgent need for theory that can predict evolutionary and ecological responses in times of accelerated climate change, the assumptions of eco-evolutionary theory currently remain restrictive, relying on theory that neglects important interactions between ecological and evolutionary forces. In this study, I provide testable predictions on limits to adaptation in changing environments, which arise from the feedback between selection, genetic drift and population dynamics. This eco-evolutionary feedback creates a tipping point where genetic drift overwhelms selection, and species' range contracts from the margins or fragments abruptly – even under gradual environmental change. This tipping point is determined by three parameters: two quantifying the effects of spatial and temporal variability on fitness, and one capturing the impact of genetic drift (the reduction of local genetic diversity across generations in finite populations). Importantly, I show that by increasing the "neighbourhood size", dispersal can counteract the loss of genetic variation, which would otherwise limit evolvability and increase extinction risk. This suggests that increasing local dispersal, possibly via assisted migration, can facilitate evolutionary rescue when local population size is small. While standard ecological niche models assume that species' ranges simply shift with environmental change, this study shows that eco-evolutionary feedback can lead to a sudden range fragmentation into disjunct subpopulations with depleted genetic variance, increasing the probability of extinction.

eco-evolutionary dynamics | gene flow | range margin | adaptation | ecological niche modelling

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Introduction. As environments change over time, species' ranges may shift, expand, or contract. These ecological changes are profoundly influenced by evolutionary processes: changes in mean fitness drive changes in population size, while variance in fitness drives adaptation (1–4). Although theoretical progress has been made in understanding range shifts, this progress has come at a cost of significant simplification. In particular, most current theory assumes fixed genetic variance (5–8), even though the evolution of genetic variance can profoundly change the expected species' range limits.

When environments vary through both time and space, their effects on fitness and genetic variation interact, influencing adaptation rates and the probability of evolutionary rescue (9–14). In spatially structured populations, a substantial proportion of genetic variance can be maintained by gene flow (15–17) – and spatial subdivision can substantially extend the time scales over which the recurrent sweeps elevate local genetic variance, relative to well-mixed populations (18, 19). To date, however, eco-evolutionary studies with evolving genetic variation in jointly spatially and temporally varying environments have only rarely been attempted (see (20–23)) and we lack a framework for predictive quantitative results of species' range and niche evolution in realistic, spatially and temporally changing environments, which includes the effects of genetic drift.

Critical to developing such theoretical framework is accurate accounting for the effect of dispersal of individuals through space, long recognised as a an important factor for species' range limits as well as limits to adaptation in general (24, 25). Population subdivision and dispersal play a central role in Wright's (26) shifting balance theory. However, dispersal can fundamentally affect adaptation even on smooth fitness landscapes. Already Haldane (27) introduced the idea that asymmetric gene flow from the centre to the edges of a species' range could swamp local adaptation at the margin, confining the species to a defined range, an example of migrational meltdown (28). On the other hand, dispersal can promote expansion of species' ranges, through elevating adaptive genetic variance (29, 30), which enables adaptation (31, 32). The conflicting qualitative predictions (15, 24, 33) imply a need for explicit models which include the feedback between population size and adaptation as well as evolution of genetic variance.

Dispersal also has an important effect on demographic fluctuations and genetic stochasticity. By enlarging the neighbourhood size, which can be thought of as a local mating pool, dispersal reduces genetic drift, i.e., stochastic fluctuations in allele frequencies. Neighbourhood size was first defined by Wright (34) as the size of a single panmictic population that would give the same probability of identity-by-descent in the previous generation, and quantifies the strength of genetic drift in populations distributed across continuous space. More generally, it can be defined as the ratio of the rate at which individuals spread through space to the per-generation rate of coalescence (35). In two dimensions with diffusive dispersal, the neighbourhood size then corresponds to $\mathcal{N} = 4\pi\,\sigma^2\,N$, a population within the area of a circle with a diameter σ and local (effective) population density N. In a haploid population, we get $\mathcal{N} = 2\pi\,\sigma^2\,N$. Neighbourhood size reflects the local strength of genetic drift, which is particularly relevant for diversifying selection. In two-dimensional habitats, it is dimensionless. In contrast, effective population size has units of time and reflects the speed of genetic drift population-wide.

Increasing dispersal tends to increase neighbourhood size, while effective population size N_e may either increase or decrease. N_e decreases with dispersal when local population density fluctuations are low or absent, but can increase if dispersal dampens large demographic fluctuations (16, 36, 37). Interestingly, although a sufficiently large neighbourhood size is critical for the maintenance of adaptive diversity across space (16, 38, 39), it is – unlike effective population size or census size – currently almost never explicitly considered in conservation guidelines [though see (40–42)]. Despite a growing understanding that higher dispersal and gene flow may enhance population resilience, especially under changing environments (43), the importance of population structure, and neighbourhood size in particular, remains neglected.

Here, I develop a framework for predictive quantitative results of range and niche evolution in realistic, spatially and temporally changing environments. This model incorporates five dimensionless parameters capturing rates of environmental change in space and time, population size and dispersal distances, as well as selection and mutation, allowing predictions of species' range collapse or expansion. These predictions highlight an important feedback between ecological and evolutionary processes, leading to a tipping point where genetic drift overwhelms adaptation.

Model and methodology summary. The core features of the model are eco-evolutionary feedback through the coupling between fitness and population growth, the inclusion of both genetic and demographic stochasticity, and a quantitative genetic model in which both the trait mean and its variance evolve. The effect of environment (biotic and abiotic) is represented by a gradient in the optimum value of a trait of the focal species. The optimum changes through time along one spatial coordinate: an example could be a spatial gradient in optimal flowering time, changing with altitude (but not along the contours of a hill) and time. Both range and niche shifts are possible, as suitable habitats can be accessed through dispersal, while the selected trait – including its variance – evolves in response to environmental change.

Individual fitness depends on both the local density and the distance of the trait from the environmental optimum. The population growth is given by the mean fitness, which reflects the local density and phenotypic distance from the optimum. Selection is hard, i.e., the locally attainable density ("carrying capacity") declines with maladaptation. If selection were acting on relative fitness only (soft selection *sensu* Christiansen (44)) and the carrying capacity were fixed, there would be no range margins unless they were *a priori* imposed by niche vacancies to be filled. Note that Christiansen's definition differs from how hard and soft selection were originally defined by Wallace (45), motivated by the problem of the maintenance of adaptive variation when selection carries a demographic cost (4, 46). In this model, the allele-frequency clines of the polygenic trait are under frequency-dependent selection but there is no density-dependent selection, while population growth is reduced due to maladaptation, and the regulation of local population size is density-dependent.

The additive quantitative trait that determines adaptation to the environment is determined by a large number of loci with exponentially distributed effects α_i. There is free recombination but there are no differences between sexes; for simplicity, individuals are assumed to be hermaphroditic and haploid. Thus, there are no dominance effects; yet there is epistasis as the fitness effect of each allele depends on other allele frequencies via the trait mean. The dispersal distances are normally distributed, independent of fitness and do not evolve through time. The model is written as both an individual-based discrete-time model (IBM) on a spatial lattice and, as an approximation, as a system of coupled stochastic partial differential equations (SPDE) in continuous time and space. The dynamics of this complex model is elucidated with the help of the following steps. First, the SPDE formalisation in continuous time provides a rescaling in terms of dimensionless parameters. This reduces the apparent dimensionality of the system, and the robustness of the non-dimensionalisation is then tested using the IBM. Second, the outcomes of the IBM are compared to known analytical expectations of simpler systems: namely to the deterministic equilibria and the predictions of a phenotypic model with fixed genetic variance. An illustrative example of the simulated IBM is given at Fig. S1.

Results.

Scale-free parameters of the model. This model of species' range and niche dynamics has over ten parameters, which arise from coupling the classic formalizations of evolutionary and ecological dynamics. Fortunately, there is a rescaling which both reduces the apparent dimensionality of the problem and facilitates interpretation. Upon nondimensionalization, we obtain five dimensionless parameters that describe the core system – see Table 1, extending from (6, 47, 48)). The first parameter measures the effective rate of change of the optimum through time: the rate of temporal change k is scaled as $k^* = k\,/\sqrt{V_s\, r^{*3}}$, relative to the strength of stabilising selection V_s and the rate $r^* \equiv -N\,\partial\overline{r}/\partial N|_{N\to\hat{N}}$ at which the population returns to its demographic equilibrium $\hat{N}$. The second parameter $B = b\,\sigma/(\sqrt{2V_s}\,r^*)$ describes the effective steepness of the environmental gradient b across space x in terms of the expected reduction in fitness due to dispersal σ. The third parameter is the neighbourhood size $\mathcal{N} = 2\pi\,\sigma^2\,N$, which describes the population attainable within a generation's dispersal and measures the weakness of genetic drift on local scales; N is the local population density. The fourth parameter is the strength of selection $s \equiv \alpha^2/V_s$ relative to the rate of return of population to a demographic equilibrium s/r^* and finally the fifth is the scaled mutation rate μ/r^*. Further details on the model and its scaling are provided in the Methods.

Known predictions: fixed variance or no temporal change. The rate of adaptation increases with the product of selection gradient and additive genetic variance (49, 50). The genetic variance itself increases with the effective environmental gradient B such that in the absence of stochastic and demographic effects, the scaled genetic variance is $A = V_G/(r^*\,V_s) = \sqrt{2}B$ (51). We might thus expect that with increasing heterogeneity of the environment, measured by the effective environmental gradient B, genetic variance will steadily rise and thus support adaptation to ever-increasing temporal change k^*: yet, this would only be true in infinitely large populations. Increasing spatial heterogeneity aids adaptation until the load

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due to genetic variance becomes too large. As the proportion of population sufficiently adapted to the local environment declines, the elimination of maladapted combinations will eventually drive the population to extinction. Furthermore, long before the deterministic extinction, genetic and demographic stochasticity reshape the dynamics.

The influence of the effective environmental gradient B and the effective rate of temporal change k^* on the rate of species' range and niche expansion is demonstrated in Fig. 1. It shows that there is a fundamental bound to species' range expansion at $k^*_{e,det} = \sqrt{2}A = 2B$ (red dashed line), which extends from the threshold derived by (32) for a given genetic variance in the absence of spatial structure. The depicted line uses the predicted deterministic genetic variance maintained by gene flow across heterogeneous environments. Yet, adaptation to temporal change fails considerably before this upper bound is reached. This is because genetic drift depletes genetic variance when neighbourhood size $\mathcal{N}$ is small, which hinders adaptation. In the absence of temporal change, the limit where continuous adaptation to environmental gradients is possible is given by $\mathcal{N} \gtrapprox 6.3\,B + 0.56$. This limit is derived using scaling arguments complemented by a numerical approximation (48). Beyond this limit, genetic drift is too strong relative to selection for stable clines to form. This threshold is depicted by a green diamond ♦ in Fig. 1.

Expansion threshold. When the optimum changes through time, the above limit to adaptation changes. A moving optimum induces a lag load, which imposes a demographic cost that further lowers the neighbourhood size, thereby depleting genetic variance as genetic drift increases. In changing environments, the expansion threshold is jointly determined by the effective environmental gradient B, the neighbourhood size $\mathcal{N}$, and the effective rate of temporal change k^*. Its approximate form, expressed for the critical effective rate of temporal change k^*_e, is given by $k^*_e = 2B\,(1 - 8/\mathcal{N})\sqrt{1 - (6.3B + 0.56)(\sqrt{2}B + 2h^2)/(2h^2\mathcal{N})}$, and is shown as the green curve in Fig. 1. Here $h^2 \equiv V_G/V_P$ denotes the narrow-sense heritability of the additive trait. The derivation of the threshold is partly heuristic: while it utilises the analytical non-dimensionalization and approximates the effects of genetic drift on genetic variance, it neglects some interdependencies (e.g., genetic variance also evolves in response to selection imposed by the lag).

This approximate threshold marks the transition between expanding, well-adapted populations, in which variance is maintained by staggered clines in allele frequencies and collapsing populations in which genetic drift overwhelms selection and variance is depleted. Notably, it only depends on the balance between k^*, B, and $\mathcal{N}$. In contrast, rates of adaptation and range expansion are also influenced by the mutational input μ/r^* and by the selection strength per locus, s/r^*. The robustness of the threshold to selection per locus $s \equiv \alpha^2/V_s$ is demonstrated in Fig. S3. When selection per locus is weak, the effect of genetic drift on the clines in two dimensional habitats is negligible (52).

Genetic variance is maintained by gene flow across the environment and reduced by genetic drift. In the absence of genetic drift, the tension between local adaptation and gene

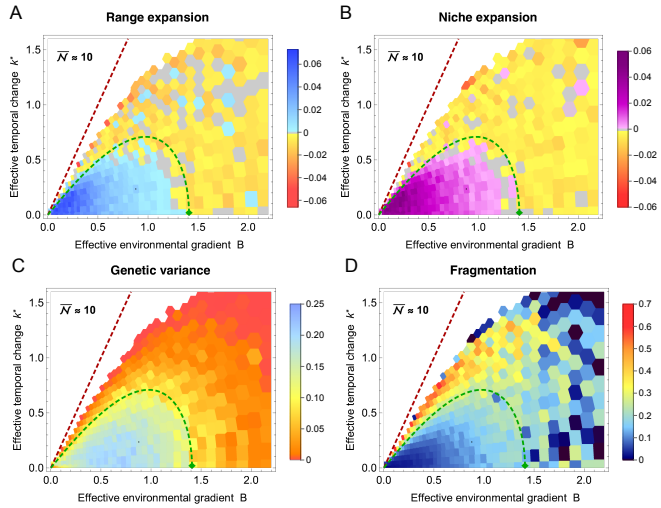

Fig. 1. Evolution of species' range, ecological niche and local genetic under spatial and temporal change. Species' range and niche expand when sufficient variance is maintained by the gene flow across the environmental gradient and contract or fragment otherwise. Each rectangle represents an independent simulation from an array of changing environmental gradients b and rates of temporal change k. The expansion threshold is shown in a green dashed curve, approximated by $k^*_e = 2B\,(1-8/\mathcal{N})\sqrt{1-(6.3B+0.56)(\sqrt{2}B+2h^2)/(2h^2\mathcal{N})}$. The deterministic extinction limit $k^*_{e,det} = 2B$ is depicted in a red dashed line. (A) The rate of range (defined as the maximum width of the occupied habitat) expansion relative to the initial range size is shown in blue, while the rate of niche (defined as width of the trait space) expansion, is shown in purple in (B). The rates of range and niche contraction are shown in orange and red hues. Grey indicates no significant change (95% CI) and white space represents extinctions within 500 generations. (C) Local genetic variance initially increases with both spatial and temporal variability but collapses abruptly at the expansion threshold where the effect of genetic drift overwhelms selection. Variance is estimated as the mean local variance in the central quarter of the habitat x, averaged over the neutral space y. (D) Species' range and niche fragment abruptly as temporal change increases. Fragmentation is measured as the proportion of unoccupied space within the species' range. Fragmentation correlates with an increased probability of local extinction, resulting in high stochasticity in fragmentation on very steep gradients because fragmentation of the last subpopulation is zero. Median neighbourhood size $\overline{\mathcal{N}} = 2\pi\sigma^2 N \approx 10$ ranges between 8 and 17 (and is higher for lower B and k^*, where the overall demographic load is lower); median total population size is about $3.2 \cdot 10^3$ for all surviving populations, ranging from 450 for expanding populations to $3 \cdot 10^5$ at $T = 500$ generations. See Methods for parameters.

flow across heterogeneous environments leads to staggered clines, with local genetic variance of $V_{G,det} = b\,\sigma\sqrt{V_s} + V_m$ (51). Mutational variance is given by $V_m = 2\mu\, n_l V_s$, where n_l denotes the number of loci – and in this context, it is small relative to the variance maintained by gene flow. When genetic drift increases relative to selection, these clines become increasingly rugged, shift in position, and steepen (38, 53, 54). The rugged allele frequencies may still contribute to adaptation even when they do not resemble a conventional cline (55, 56).

There is no exact analytical expression for the effect of genetic drift on a cline, and thus on genetic variance in two-dimensional habitats, but we can approximate the decrease of genetic variance with drift as $V_G \approx V_{G,det}(1-8/\mathcal{N})$ for $\mathcal{N} > 8$ – see Fig. 2. This estimate assumes that the reduction in genetic variance in two dimensions takes the same form as in one dimension (39), using the dimension-appropriate neighbourhood size, and with the constant of 8 numerically fitted. When the optimum changes in both time and space, the selection arising from the distance between the trait mean and the optimum drives

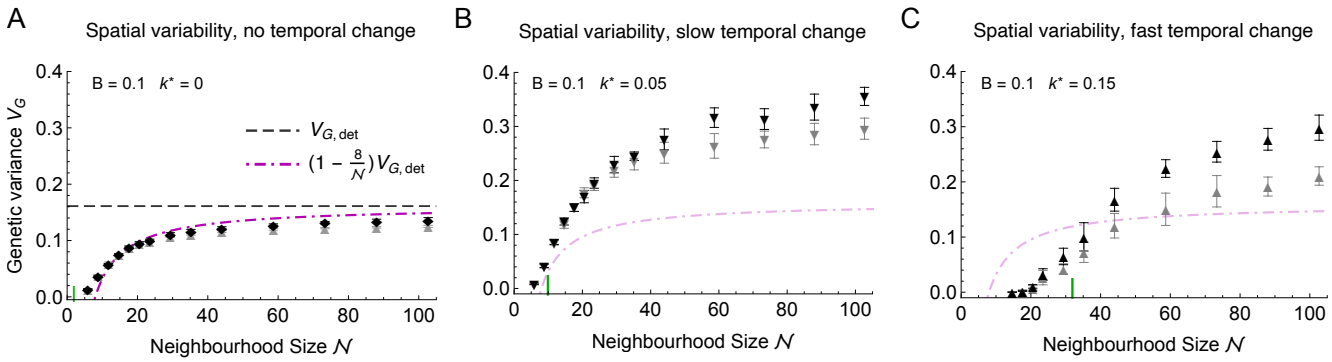

Fig. 2. Genetic variance is significantly reduced when neighbourhood size $\mathcal{N}$ is low. As the effective rate of temporal change k^* increases, larger neighbourhood size is necessary so that the population can sustain itself: the expansion threshold (in terms of $\mathcal{N}(k^*, B)$), illustrated by **|**, is roughly at the inflection point for the increase of genetic variance with $\mathcal{N}$. (A) In stable environments, the decrease in genetic variance due to drift in two-dimensional habitats approximately follows $V_G \approx V_{G,det}(1 - 8/\mathcal{N})$, shown as a dash-dotted magenta curve. Deterministic variance (dashed line) is given by $V_{G,det} = b\,\sigma\sqrt{V_s} + V_m$ (see text). (B) When the environment changes slowly through time (at $k^* \ll k_e^*$), genetic variance can increase substantially as newly selected alleles spread through the population.The increase of genetic variance with k^* is non-monotonic – with fast temporal change (C), increasing genetic drift suppresses the increase in variance. Black symbols: neutral habitat width is fixed at $y_d = 100$, so that total population increases with $\mathcal{N}$ and the habitat remains truly two-dimensional. Gray symbols represent simulations where neutral habitat width scales inversely with carrying capacity ($y_d = 600/K$), ensuring similar census sizes as $\mathcal{N}$ increases ($N_{tot} \approx 1.5 \cdot 10^5$). When the neutral habitat width y_d becomes too narrow due to this scaling, genetic variance increases less than expected (gray, $y_d \lessapprox 50$ for $\mathcal{N} \gtrapprox 60$). This is largely because in the limit of a one-dimensional habitat ($y_d = 1$), the strength of genetic drift scales with $1/(\sqrt{s}\,\mathcal{N}_{1D})$ (39, 57, 58), where the one-dimensional neighbourhood size is $\mathcal{N}_{1D} = 2\sqrt{\pi}N\sigma$ (34). Error bars show standard deviations for 10 replicates. Parameters as in Fig. 1 with $b = 0.225$, $k = 0$ (A), $k = 0.06 \equiv k^* = 0.05$ (B) and $k = 0.18 \equiv k^* = 0.15$ (C), run time $T = 300$ generations and neighbourhood size $\mathcal{N} = 2\pi\sigma^2 N \approx 2\pi\sigma^2 K(1 - B/\sqrt{2})$, where local carrying capacity ranges from $K = 2$ to $K = 35$.

the emergence of further clines in allele frequencies, which, locally, bring the trait closer to the optimum. This drives an increase in genetic variance which is stable over longer time scales relative to well-mixed populations (18) because these clines can shift through space. More generally, Fig. 2 demonstrates that neighbourhood size, rather than total (effective) population size, fundamentally drives the increase in genetic variance. Quantitative analysis of the evolution of variance in both spatially and temporally variable environments will be the subject of a forthcoming paper.

Fragmentation. When the strength of genetic drift and the rate of temporal change are high, species' range may fragment abruptly: see Fig. 3. Fragmentation can occur abruptly across the entire geographic range, and it is underlined by fragmentation in the trait (ecological niche) space and depleted genetic variance: see Fig. 4 and Movie S1. Genetic variance drops because clines spanning multiple subpopulations cannot be maintained, and the remnants of heterozygosity within the population fragments only support a fraction of the variance which was present prior to the fragmentation: see Fig. 5.

Fragmentation readily occurs under rapid temporal change, which generates a large lag load as the trait mean lags behind the moving optimum. Eventually, as the rate of temporal change increases, the fitness cost due to the combined lag, dispersal, and standing load becomes so high that the remaining Malthusian fitness is close to zero, and the population cannot maintain clinal adaptation. However, the population may still (temporarily) survive as a metapopulation with locally depleted variance, adapted to a series of distinct niches. Note that the classic phenotypic model (6) predicts two distinct modes of adaptation to an environmental gradient. In the first mode, there is sufficient genetic variance, and the population can adapt uniformly to the spatial gradient. In the second mode, genetic variance is too low, and each subpopulation is adapted only to a single optimum. This mode is represented in the fragmented populations, which lack adaptive variance – and therefore the population survives purely by tracking the old optimum through space, as long as it remains available (47). Fragmented populations are also subject to large demographic fluctuations, further reducing population resilience. Note that fragmentation can be reversed upon an increase in local dispersal: see Fig. 5 B *vs.* C. Under larger dispersal, both the deterministic genetic variance and the neighbourhood size increase, reducing genetic drift and restoring stable clinal adaptation.

Species' range can also fragment in the absence of temporal change when the neighbourhood size is small, particularly beyond the expansion threshold: see (48) and Fig. S4 under $k^* = 0$. Due to strong genetic drift, clines in allele frequencies become increasingly rugged, steep and unstable. As clines steepen and variation in allele frequencies is lost, genetic variance is depleted and becomes too low to support a continuous adaptation (59, Fig. 4). Demographic fluctuations, while not a primary driver, contribute to fragmentation and accelerate population collapse, as maladaptation increases due to higher genetic drift at low population sizes, which in turn drives even greater demographic stochasticity.

Dispersal and neighbourhood size. Larger neighbourhood size promotes adaptation by mitigating genetic drift and supporting adaptation to steeper environmental gradients B and faster temporal change k^*. Supplementary Figs. S4 ($\overline{\mathcal{N}} = 8$) *vs.* S5 ($\overline{\mathcal{N}} = 14$) show that the expansion threshold k_e^* increases with neighbourhood size $\mathcal{N}$ – despite scaling of the neutral width of the habitat, which keeps census population size is kept approximately constant.

Neighbourhood size also increases with dispersal, but so does the effective environmental gradient B. However, in two dimensions, neighbourhood size $\mathcal{N} = 2\pi\sigma^2 N$ increases with the square of dispersal distance σ^2, while the effective gradient

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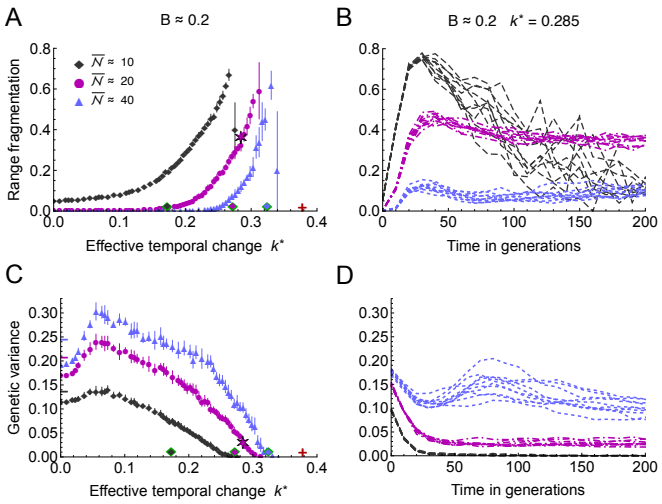

Fig. 3. Species' range fragments under rapid temporal change and small neighbourhood size. (A) Range fragmentation increases with the effective rate of temporal change k^* and decreasing neighbourhood size $\mathcal{N}$. The expansion threshold $k_e^*(B, \mathcal{N})$ is shown as green-outlined diamonds with coloured centres matching the respective neighbourhood sizes (and roughly corresponds to fragmentation above 0.2). The deterministic extinction threshold $k_{e,det}^* = 2B$ is marked with a red cross. (B) Beyond the expansion threshold, the onset of fragmentation is rapid and associated with a loss of genetic variance. The apparent decrease in fragmentation for $\mathcal{N} \approx 10$ is due to only a few fragments remaining in fast-collapsing populations. (C) Genetic variance decreases with genetic drift (i.e., decreasing neighbourhood size $\mathcal{N}$) and is highest for intermediate rates of temporal change before declining again. Dashes at $k^* = 0$ represent the predicted genetic variance in stable environments, accounting for genetic drift. (D) Genetic variance drops as populations fragment when neighbourhood size is small. Only for $\mathcal{N} = 40$ (above the expansion threshold), there is a temporary recovery, as local selective sweeps bringing the trait mean closer to the optimum elevate genetic variance – before the variance stabilizes at about $V_G = 0.1$. Parameters as in Fig. 1 with $b = 0.4$ (and $k = 0.31 \equiv k^* = 0.285$ for B, D); the magenta star marks an illustration shown in Fig. 4. Neighbourhood sizes correspond to local carrying capacities $K = 5, 10, 20$, and are slightly below the maximum attainable neighbourhood size $\mathcal{N} = 2\pi\sigma^2 K$. Error bars show standard deviations for 10 replicates. Runtime 500 generations with first 200 generations shown in (B, D).

$B = b\,\sigma/(\sqrt{2V_s}\,r^*)$ increases only linearly. Therefore, when genetic drift is strong, increasing local dispersal aids adaptation Fig. S6 demonstrates that the benefits of reducing genetic drift *via* increased dispersal outweigh the costs associated with increasing dispersal load: when both the effective environmental gradient B and the neighbourhood size $\mathcal{N}$ increase with local dispersal, the drift-induced expansion threshold is approximately replaced by the deterministic limit, $k_{e,det}^* = 2B$.

So far, we have assumed diffusive dispersal with a Gaussian dispersal kernel. However, dispersal kernels may have heavier tails than implied by local diffusion. I illustrate the effect of a leptokurtic dispersal kernel represented by a mixture of two Gaussians, where the one of the dispersal kernel has a substantially higher variance. Fig. S7 (B) shows an example where 10% of migrants disperse, on average, 10× further than the baseline dispersal distance of the remaining 90% of the population. Such fat-tailed dispersal (example kurtosis $\kappa = 25.3$) has little effect in facilitating adaptation to steep gradients, relative to the baseline with just local diffusion (Fig. S7 (A)). Yet, the fat-tailed dispersal kernel can facilitate adaptation to temporal change when the spatial gradient is shallow: this makes sense, as the increased mixing brings in further variants which may be beneficial under fast temporal change, while the cost of dispersing far across a shallow gradients is low.

Quantitative generalizations beyond diffusive dispersal are not trivial: both the effective environmental gradient B and the neighbourhood size $\mathcal{N}$ change. Under diffusive dispersal, neighbourhood size is given by the ratio of the effective area of spread per generation, $2\pi\sigma^2$, to the per-generation coalescence rate, $1/(2N)$, yielding $\mathcal{N} = 4\pi\,N\sigma^2$ (35, 52). Wright (34) defined neighbourhood size as the inverse of identity-by-descent of nearby individuals, yielding the same $\mathcal{N}$ under Gaussian dispersal. While Wright generalized the neighbourhood size to non-Gaussian dispersal kernels (60, p. 302-310), the inverse of generalized Wright's $\mathcal{N}$ may no longer robustly measure the strength of genetic drift. Under fat-tailed dispersal, the identity in state over local scales is dominated by local dispersal, and over wide scales by long-distance dispersal (35, 61). Thus, rare long-distance events have little effect locally (on the scales of cline widths in this model). Only when the kurtosis of the dispersal kernel is moderate so that the diffusion approximation is not strongly violated, do simple generalizations of both the effective environmental gradient B and Wright's neighbourhood size provide an accurate prediction: see Fig. S7 (C, D). Note that there is no simple approximate generalization of Wright's neighbourhood size to arbitrary dispersal kernels using only their variance and kurtosis (*cf.* (42, Box 2)); see S7 for details.

Adaptive phenotypic plasticity. Last, I briefly explore the effects of adaptive phenotypic plasticity. Fig. S8 demonstrates that adaptive phenotypic plasticity does not extend the range of survivable rates of temporal change in the same manner as it does for spatial variability. Adaptive phenotypic plasticity implies that the expressed trait z is closer to the optimum θ than expected based on its genetic basis alone, $(z - \theta) \to (1 - \mathfrak{p})\,(z - \theta)$, where $\mathfrak{p}$ denotes adaptive plasticity. This means that the spatial gradient B appears shallower by $1 - \mathfrak{p}$. While this reduces the demographic load and lowers the impact of genetic drift, it also diminishes the increase in genetic variance due to spatial variability. Thus, when genetic variance evolves in response to the effective environmental gradient, the effects of plasticity on adaptation to a steady temporal change largely cancel out. This finding contrasts with predictions assuming fixed genetic variance in the selected trait, where the benefits of plasticity in response to variation in time and space are equivalent (7, 62).

Discussion. There is an urgent need for predictive theory to forecast adaptive responses and population resilience in changing environments (20, 63–67). Existing ecological niche modelling (ENM) framework typically considers multidimensional niche space that includes both biotic and abiotic components but accounts neither for adaptive potential (68, 69) nor genetic drift, with only recent advances incorporating adaptive genetic diversity (70, 71). Yet, already for predictions over time scales longer than a few generations, species' range dynamics may change qualitatively when eco-evolutionary feedback is included, particularly the feedback between genetic variance and population dynamics.

Adaptation typically involves changes across many loci, and predicting the trajectory of each of them is not feasible (72). In contrast, predictions based on higher-order parameters

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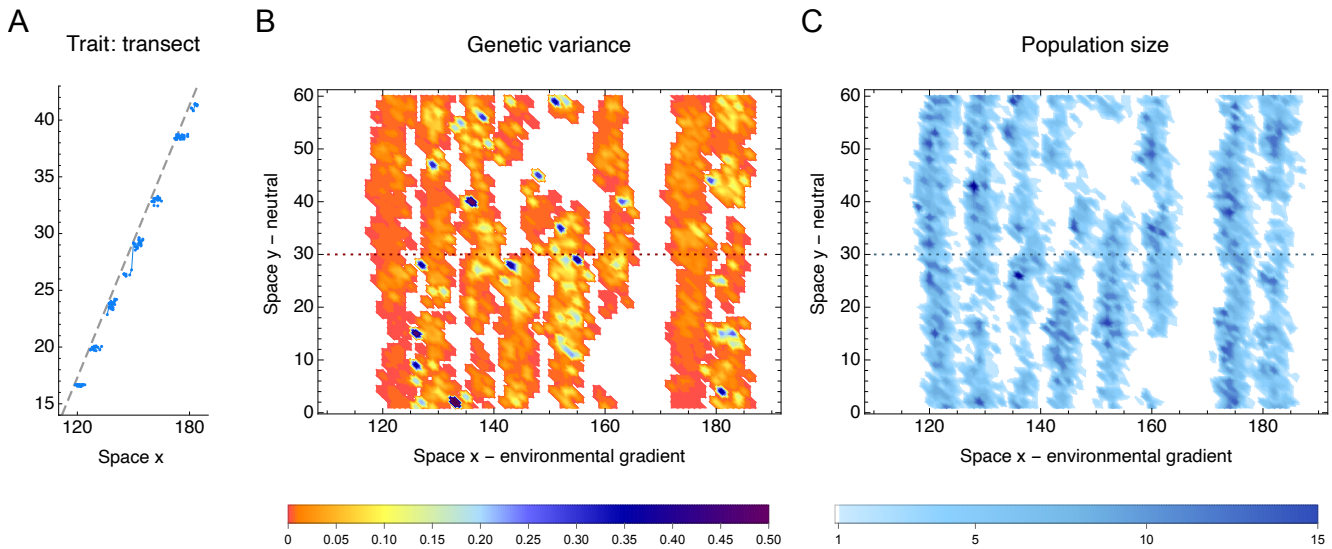

Fig. 4. Example of species' range fragmentation due to a fast temporal change. (A) In fragmented populations, trait mean (blue line) no longer tracks the optimum (grey dashed line) but instead, disjunct subpopulations are each adapted to a single optimum and move through space tracking their niche. Blue dots show individual trait values. The subfigure (A) shows a transect at the central neutral habitat ($y = 30$), marked by the dotted line in (B, C). (B) Genetic variance is depleted considerably below the expected value of $V_G \approx (b\,\sigma\sqrt{V_s} + V_m)(1 - 8/\mathcal{N}) = 0.21$, although local spikes of high variance (blue hues) persist. (C) Local population density (population size contained in a single deme) is close to the carrying capacity $K = 10$, yet 40% of the space is unoccupied, and the population gradually contracts over time. Subpopulations are connected *via* gene flow along the neutral habitat (y) but largely isolated along the environmental gradient (x). Parameters are the same as in Fig. 3 (K = 10, magenta), with $k^* = 0.285$, with this example indicated by a magenta star there. This example is chosen just beyond the expansion threshold $k_e^*(B, \mathcal{N}) \approx 0.273$, where some clines in allele frequencies still persist (see Fig. 5) and therefore genetic variance is not uniformly low. The dynamics of fragmentation is illustrated in Supplementary Movie S1, demonstrating that fragmentation occurs abruptly and follows a marked increase in lag (and thus lag load) behind the moving optimum.

derived from fundamental quantitative genetics (based additive genetic variance in the selected trait) are considerably more robust: particularly in controlled settings and over shorter time scales (73–77).

By explicitly integrating key eco-evolutionary processes and the feedback between them, this theory provides novel quantitative predictions concerning species' range limits, adaptation, and resilience. It explains that a gradual increase in the rate of temporal change, as well as a decrease in neighbourhood size $\mathcal{N}$, can lead to a tipping point where adaptation collapses. Neighbourhood size, the population accessible by dispersal within a generation, can decrease when dispersal decreases, reducing connectivity across space, or due to a reduction in local density. Beyond this eco-evolutionary tipping point, genetic drift becomes too strong relative to the strength of environmental change, leading to the collapse of clinal adaptation. The population may decline gradually, when the species' range contracts from the margins, or fragment abruptly. When the loss of fitness due to temporal change (k^*) is high, fragmentation can occur rapidly even when genetic drift is not particularly strong. In contrast, fragmentation due to spatial variation alone only occurs when the neighbourhood size is low (48). Since fragmentation is associated with both local and global a loss of genetic variance, recovery when conditions later improve is slower than the fragmentation.

Importantly, the predictive parameters are measurable: thus, the theory can be tested and offers applications in conservation genetics. Neighbourhood size $\mathcal{N}$ can be estimated from ecological parameters of local density and dispersal as well as from population-genetic parameters – specifically, the rate of increase in neutral F_{ST} with distance (78, Eq. 11). However, F_{ST} will be affected by population dynamics as well as long-range migration: see (41, 79) for estimates and discussion of assumptions. With diffusive dispersal, neighbourhood size is the number of individuals within a circle of diameter σ: $\mathcal{N} = 4\pi\sigma^2 N$ for a diploid organism, where N gives the local density and σ^2 is the average axis-projected squared distance between parent and offspring. Generalizations beyond diffusive dispersal are discussed in section *Dispersal and neighbourhood size*: roughly speaking, rare long range dispersal can significantly facilitate adaptation to temporal change across shallow spatial gradients, but has little beneficial affect when the effective spatial gradient is steep – and with increasing frequency, will eventually swamp adaptation; see also (80) with only spatial gradients.

Parameters B and k^* quantify the fitness loss (demographic load) due to spatial and temporal environmental variability. The dispersal load can be estimated from transplant experiments: moving a well-adapted population by a distance σ reduces fitness by $B^2 r^{*2}$. The fitness cost of a temporal change $k^{*2} r^*/2$, over a characteristic time $1/r^*$, is more challenging to infer: in some cases, past generations' fitness can be assessed using seeds or diapausing animals, or more commonly, by substituting space for time (66, 81, 82) in spatial transplant experiments – see also the Discussion in (47). The rate of this characteristic time, $1/r^*$, can be estimated from the demographic dynamics: (83, 84), where the reported measure D is approximately equivalent to r^* (47, Appendix D).

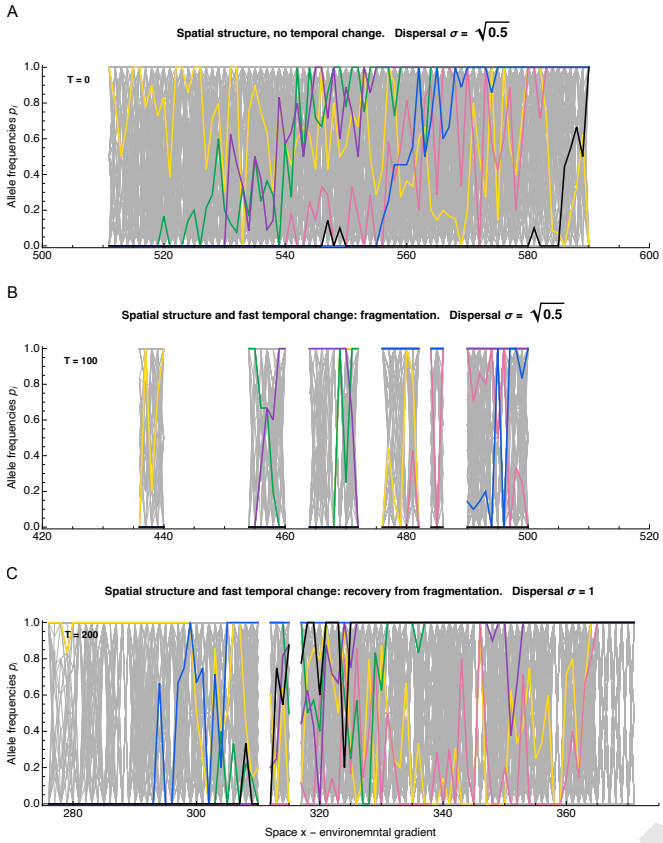

Fig. 5. Clinal variation is substantially reduced in fragmented populations. Subfigures (A–C) depict in colour six illustrative loci over a grey background showing all polymorphic loci. (A) Continuous adaptation to an environmental gradient is maintained by a series of staggered clines. These clines are rugged due to strong genetic drift, yet together maintain a smoothly changing trait adapted to the environmental gradient. (B) Upon a fast temporal change with an effective rate of $k^* = 0.285$ over 100 generations (marginally beyond the expansion threshold $k_e^*(B, \mathcal{N}) \approx 0.273$), the population fragments and most of the clinal variation is lost. (C) An increase in local dispersal σ reverses fragmentation under the same rate temporal change. With a wider dispersal kernel (σ changes from $\sqrt{0.5}$ to 1), genetic variance maintained by dispersal across the environment increases while genetic drift decreases. After 200 generations with broader dispersal (and thus weaker genetic drift), most of the variation is restored. Clines appear more rugged than in the absence of temporal change (A). Even at the limit of low stochasticity, cline shape is no longer necessarily monotonic – this is because local selective sweeps bring the trait closer to the moving optimum. Parameters are the same as in Fig. 4. The corresponding selection per locus for illustrative clines is $s = \alpha^2/(2V_s)$: $s \approx 0.03$ (black), $s \approx 0.016$ (blue), $s \approx 0.009$ (purple), $s \approx 0.007$ (green), $s \approx 0.0046$ (pink), $s \approx 1.5 \times 10^{-6}$ (yellow). Darker colours indicate stronger selection, with the yellow cline effectively neutral. In the absence of temporal change (A), the neighbourhood size calculated from ecological parameters using the mean local deme size and parent-offspring dispersal distance σ, is approximately $\mathcal{N} \approx 25$; while for the recovered population with a wider dispersal kernel (C), it is $\mathcal{N} \approx 31$, despite local density decreasing from 8 to 5 due to elevated dispersal load. Census size drops from 39079 individuals (A) to 13079 individuals (B) and then recovers to 31767 individuals in (C).

There are three major limitations to this theory. First, it considers a single trait under stabilising selection and assumes no rigid genetic trade-off, which could further constrain adaptation (85). Second, it considers gradual spatial and temporal change in continuous environments. Habitat fragmentation driven by local environmental heterogeneity will generally hinder adaptation and shifts of the species' range through space. While a full analysis of the effects of local habitat heterogeneity and habitat fragmentation would warrant a dedicated paper, Fig. S9 illustrates that extrinsic habitat fragmentation (30% of empty patches) has a significant negative effect, preventing adaptation to steep gradients and rapid temporal change. Selection also fluctuates through time, with extremes potentially incurring a higher fitness costs than the mean steady change (86, 87). Third, the theory considers a single focal species. Although the environmental optimum can include both abiotic and biotic components (88), the theory neglects the coevolution of species over similar time scales (89, 90). While none of these concerns invalidate the scale-free parameters, they imply that the numerical value of the expansion threshold should be considered an approximate baseline, rather than a definitive value.

When dispersal is predominantly local, eco-evolutionary dynamics is determined over local scales. Therefore, the theory does not require spatial gradients to be linear and also applies to other forms of gradual change, such as environmental gradient gradually steepening across the species' range (48, 91–93) or when neighbourhood size gradually decreases. As conditions deteriorate across space (and time), the expansion threshold may be exceeded locally. Then the part of the species' range beyond the expansion threshold is predicted to fragment or contract toward the new range margin. Because the dynamics operates over local scales and the predicted range margin is abrupt, the theory makes no claims regarding the abundant center of a species' range (94, 95).

Conservation genetics and predictions from eco-evolutionary theory have been increasingly incorporated into conservation practice and while there is still a notable separation of the fields (96), low or rapidly declining heterozygosity or effective population size N_e represents a clear cause for concern (97). Yet, the utility of any cut-off value for effective population size N_e remains contested (98–100). At the same time, assisted migration (43, 101) is increasingly advocated as a strategy to facilitate adaptation under climate change. To date, no comprehensive predictive theory has incorporated the effects of gene flow across variable environments on local polygenic adaptation and species' range dynamics under temporal change. This theory provides a framework for predicting when an increase in local dispersal, for example via assisted migration, can aid adaptation and identifies a critical tipping point beyond which populations may be at risk of collapse or abrupt fragmentation.

Materials and Methods

The model is of evolution of a species' range in two dimensions, where both population dynamics and evolution are considered jointly. The eco-evo coupling occurs through the mean (absolute) fitness $\overline{r}(\overline{z}, N)$, which gives the growth rate of the population, decreasing with population density and maladaptation: $\overline{r}(\overline{z}, N) = r_e(N) + \overline{r}_g(\overline{z})$. The ecological component of growth rate, r_e, can take various forms. Here, we assume logistic regulation, so that fitness declines linearly with density N: $r_e = r_m(1 - N/K)$, where r_m is the maximum per capita growth rate in the limit of the local population density $N \to 0$. The maximum carrying capacity K is assumed to be uniform across space and the attainable population density is $\hat{N} = Kr^*/r_m = K(1 - V_P/(2r_m V_s))$.

The second term, $r_g(\overline{z}) \leq 0$, represents the reduction in growth rate due to deviation from the optimum. Selection is stabilising around the optimum $\theta = b\,x - kt$, which changes smoothly (with a

gradient b) along one spatial dimension (x), and through time t at a constant rate k. For any individual with a trait value of z, the drop in fitness due to maladaptation is $r_g(z) = -(z-\theta)^2/(2V_s)$, where $1/V_s$ gives the strength of stabilising selection. A population with a mean phenotype $\overline{z}$ has its fitness reduced by $\overline{r}_g(\overline{z}) = -(\overline{z}-\theta)^2/(2V_s) - V_P/(2V_s)$.

The phenotype z is determined by many di-allelic loci with allelic effects α_i; the model is haploid, hence $\overline{z} = \sum_i \alpha_i p_i$, where p_i is the allele frequency at locus i. Phenotypic variance is $V_P = V_G + V_E$. The loss of fitness due to environmental variance V_E can be included in $r^*_m = r_m - V_E/(2V_s)$; V_E is a redundant parameter (and thus we can use $V_P = V_G$). In the absence of genetic drift and no temporal change, genetic variance is largely maintained by gene flow and the contribution of mutation is relatively small. Variance maintained by mutation-selection balance, $V_{G,\mu/s} = 2\mu V_s n_l$ (where μ gives the mutation rate per locus and n_l the number of loci), is typically much smaller than variance generated by gene flow across environments, $V_G = b\,\sigma\sqrt{V_s}$ (51).

Evolution of trait mean with joint population dynamics; unscaled. For any given additive genetic variance V_G (assuming a Gaussian distribution of breeding values), the change in the trait mean $\overline{z}$ over time satisfies:

$$\frac{\partial \overline{z}}{\partial t} = \frac{\sigma^2}{2}\left(\frac{\partial^2 \overline{z}}{\partial x^2} + \frac{\partial^2 \overline{z}}{\partial y^2}\right) + \sigma^2\left(\frac{\partial \ln(N)}{\partial x}\frac{\partial \overline{z}}{\partial x} + \frac{\partial \ln(N)}{\partial y}\frac{\partial \overline{z}}{\partial y}\right) + V_G\frac{\partial \overline{r}}{\partial \overline{z}} + \zeta \quad [1]$$

The first term gives the change in the trait mean due to migration, with a mean displacement of σ; the second term describes the effect of the asymmetric flow from nearby areas of higher density; the third term gives the change due to selection, given by the product of genetic variance and gradient in mean fitness (5, Eq. 2). The last term ζ gives the fluctuations in the trait variance due to genetic drift: $\zeta = \sqrt{V_{G,LE}/N}\,W_\zeta(x,y,t)$, where W_* represents white noise in space and time (38, 52). $V_{G,LE} = \sum_i \alpha_i^2 p_i q_i$ denotes genetic variance assuming linkage equilibrium.

Note that the diffusion approximation breaks down over very local scales in two dimensions because in a continuous two-dimensional habitat, two independent Brownian motions will, with probability one, never be in the same place at the same time (and thus, there would be no coalescence). The simulation avoids this problem by considering a discrete lattice; an analytical approach would require the introduction of a local scale of population interactions (52).

The trait mean is $\overline{z} = \sum_i \alpha_i p_i$ for a haploid model, where p_i is the i-th allele frequency, $q_i = 1 - p_i$ and α_i is the effect of the allele on the trait – the change of the trait mean $\overline{z}$ as frequency of locus i changes from 0 to 1. For both haploid and diploid models, the allele frequencies p_i change as:

$$\begin{aligned}\frac{\partial p_i}{\partial t} &= \frac{\sigma^2}{2}\left(\frac{\partial^2 p_i}{\partial x^2} + \frac{\partial^2 p_i}{\partial y^2}\right) + \sigma^2\left(\frac{\partial p_i}{\partial x}\frac{\partial \ln(N)}{\partial x} + \frac{\partial p_i}{\partial y}\frac{\partial \ln(N)}{\partial y}\right) + \\ &+ p_i q_i \frac{\partial \overline{r}}{\partial p_i} - \mu(p_i - q_i) + \epsilon \quad [2]\end{aligned}$$

The expected change of allele frequency due to a gradient in fitness and local heterozygosity is $p_i q_i \frac{\partial \overline{r}}{\partial p_i} = s_i\, p_i q_i (p_i - q_i - 2\Delta_i)$, where selection at locus i is $s_i \equiv \alpha_i^2/(2V_s)$ and $\Delta_i = (\overline{z} - bx - kt)/\alpha_i$ (51, Appendix 3). Here, the fourth term describes the change due to (symmetric) mutation at rate μ. The last term ϵ describes genetic drift (52, Eq. 7): $\epsilon = \sqrt{\frac{p_i q_i}{N}}\,W_\epsilon(x,y,t)$; where N is the haploid population density.

Population dynamics reflects diffusive migration in two dimensions, growth due to the mean Malthusian fitness $\overline{r}$, and stochastic fluctuations. The number of offspring follows a Poisson distribution with mean and variance of N, fluctuations in population numbers are given by (102): $\xi = \sqrt{N}\,W_\xi(x,y,t)$:

$$\frac{\partial N}{\partial t} = \frac{\sigma^2}{2}\left(\frac{\partial^2 N}{\partial x^2} + \frac{\partial^2 N}{\partial y^2}\right) + \overline{r}N + \xi \quad [3]$$

Rescaling and formalising in terms of allele frequencies, with evolution of variance. Following (6, 51), the model can be simplified by rescaling time t with the characteristic rate r^* of return to the equilibrium population size, distances x and y relative to dispersal σ, trait z relative to strength of stabilising selection $1/(2V_s)$ and local population density N relative to equilibrium population density with perfect adaptation: $\hat{N} = Kr^*/r_m,\ T = r^*t,\ X = x\sqrt{\frac{2r^*}{\sigma^2}},\ Y = y\sqrt{\frac{2r^*}{\sigma^2}},\ Z = \frac{z}{\sqrt{r^* V_s}}$.

The characteristic time scales with the rate of return to the equilibrium population density, defined as its negative elasticity: $r^* \equiv -N\,\partial\overline{r}/\partial N|_{N\to\hat{N}}$; see also (83, 103). When the trait mean matches the optimum, we get $r^* = r_m - V_G/(2V_s) \to r_m - b\,\sigma/(2\sqrt{V_s})$. In addition, we normalise density as $\tilde{N} = N/\hat{N}$ such that near the equilibrium of a well-adapted population, $\tilde{N} \approx 1$. White noise is rescaled as $W_{\tilde{\epsilon},\tilde{\zeta}}(X,Y,T) = \sqrt{J}\,W_{\epsilon,\zeta}(x,y,t)$, where $J = dx\,dy\,dt/dX\,dY\,dT = \sigma^2/(2r^{*2})$; see also (38).

Assuming linkage equilibrium, the rescaled equations for evolution of allele frequencies and for demographic dynamics are:

$$\begin{aligned}\frac{\partial \tilde{N}}{\partial T} &= \frac{\partial^2 \tilde{N}}{\partial X^2} + \frac{\partial^2 \tilde{N}}{\partial Y^2} + \overline{R}\tilde{N} + \sqrt{\frac{2\tilde{N}}{\hat{N}\sigma^2}}\,W_{\tilde{\xi}(X,Y,T)} \\ \frac{\partial p_i}{\partial T} &= \frac{\partial^2 p_i}{\partial X^2} + \frac{\partial^2 p_i}{\partial Y^2} + 2\left(\frac{\partial p_i}{\partial X}\frac{\partial \ln(\tilde{N})}{\partial X} + \frac{\partial p_i}{\partial Y}\frac{\partial \ln(\tilde{N})}{\partial Y}\right) + \\ &+ \frac{s}{r^*}\left(p_i q_i - 2\frac{\overline{Z} - BX - k^*T}{\alpha^*}\right) - \frac{\mu}{r^*}(p_i - q_i) + \\ &+ \sqrt{\frac{2p_i q_i}{\tilde{N}\hat{N}\sigma^2}}\,W_{\tilde{\epsilon}(X,Y,T)} \quad [4]\end{aligned}$$

where $\overline{R} \equiv \overline{r}/r^* = 1 - \tilde{N} - (BX - k^*T - Z)^2/2$.

The rescaled equations show that four parameters fully describe the system. First, the effective rate of temporal change, $k^* = k/\sqrt{V_s\, r^{*3}}$. Second, the effective environmental gradient, $B \equiv b\sigma/(r^*\sqrt{2V_s})$. Third, the strength of genetic drift $1/\hat{\mathcal{N}} = 1/(2\pi\hat{N}\sigma^2)$. The parameter $\hat{\mathcal{N}}$ gives the neighbourhood size of a well-adapted population at equilibrium. The fourth parameter is the strength of selection relative to the strength of density dependence, s/r^*; the scaled effect of a single substitution α^* also scales with s/r^*: $\alpha^* \equiv \alpha/\sqrt{r^* V_s} = \sqrt{2s/r^*}$. The effect of this fourth parameter s/r^* is expected to be small, because typically, $s \lll r^*$. The fifth parameter, μ/r^*, is small and can be neglected for the purpose of finding threshold conditions for range expansion *vs.* collapse; we fix the mutation rate μ to 10^{-5}.

It can be shown that in the absence of genetic drift, allele frequencies are approximately at linkage equilibrium (LE): positive linkage disequilibrium (LD) generated by dispersal approximately cancels out with negative linkage disequilibrium generated by stabilizing selection, to the first-order of the pairwise LD (59, Supplementary Information). Genetic drift would however generate positive linkage disequilibrium. At the infinitesimal limit (104), each allele has a such small effect that due to genetic drift, changes in each locus are almost random, and selection operates by changing LD between loci. In general, therefore, linkage disequilibrium may develop, particularly when genetic drift is strong: we will assess the evolution of LD in a separate paper concerned with details of evolution of genetic variance and genetic architecture.

Individual-based simulations. Discrete-time individual based simulations are set to correspond to the model with continuous time and space. The life cycle is selection → mutation → recombination → birth → migration. Generations are non-overlapping and selfing is allowed at no cost. Every generation, each individual mates with a partner drawn from the same deme, with probability proportional to its fitness, to produce a number of offspring drawn from a Poisson distribution with mean of $\exp[r(z,N)]$. Because the probability that a given individual is the parent of a particular offspring is small, Poisson distribution corresponds well to the binomial distribution of Wright-Fisher model (3), which can be

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Table 1. Five scale-free parameters: B, k^*, $\mathcal{N}$, $s/r^*$and μ/r^* describe the system. The middle column gives the dimensions of the parameters, where T stands for time, D for distance and Z for trait.

param.	dim.	description
k^*	–	effective rate of temporal change $k^* = k/\sqrt{V_s\, r^{*3}}$
B	–	effective environmental gradient $B = b\sigma/(r^*\sqrt{2V_s})$
$\mathcal{N}$	–	neighbourhood size $\mathcal{N} = 4\pi N_e \sigma^2 = 2\pi N \sigma^2$
s/r^*	–	strength of selection per locus relative to r^*
μ/r^*	–	mutation rate relative to r^*
s	$1/T$	selection per locus: $s \equiv \alpha^2/(2V_s)$
r^*	$1/T$	rate of return to equilibrium population size: $r^* \equiv -N\, \partial\overline{r}/\partial N\|_{N\to\hat{N}}$
b	Z/D	gradient in the environmental optimum
V_s	Z^2T	variance of stabilising selection
σ	$D/\sqrt{T}$	dispersal per generation
K	T/D^2	max. carrying capacity (haploid) K = N when all phenotypes are perfectly adapted
r_m	$1/T$	max. intrinsic rate of increase
α	Z	allelic effect
μ	$1/T$	mutation rate, $\mu \equiv 10^{-5}$

passed to the diffusion limit (57, 105). The population density N thus corresponds to population size within a single deme.

The space is represented by two-dimensional lattice with spacing between demes $\delta x = 1$, and is wide enough along both spatial dimensions x_d and y_d so that species' range does not reach the edges and that the random processes (genetic drift) occur in a truly two-dimensional habitat. Migration is assumed to be diffusive with a Gaussian dispersal kernel: in the IBM which runs on a lattice, individuals migrate according to the distribution of a discretised Gaussian. Due to the discretisation of the space, the tails of the dispersal kernel need to be truncated: truncation is set to three standard deviations of the dispersal kernel 3σ throughout, and dispersal probabilities are adjusted so that the discretised dispersal kernel sums to 1 while ensuring the correct variance (see (106, p. 1209)). Note that truncation at 2σ would give the nearest-neighbour migration, where the probability of staying in place is $1/4$, the probability of migrating to perpendicular neighbours is $1/8$ and to diagonal neighbours is $1/16$.

The genome is haploid with 1000 unlinked loci, so the probability of recombination between any two loci is $1/2$. The additive trait is determined by the sum of allelic effects α_i, exponentially distributed with mean of $\alpha = 0.07$ unless stated otherwise. This gives the mean strength of selection per locus $s = \alpha^2/(2V_s) \approx 0.005$. Mutation is set to $\mu = 10^{-5}$. Burn-in time (no temporal change) is 200 generations; run time 500 generations (unless stated otherwise). Simulations were written in Mathematica (Wolfram) and executed on the Vienna Scientific Cluster (VSC); the code will be available on Dryad upon acceptance.

Parameters (unless stated otherwise): Gaussian dispersal per generation with variance $\sigma^2 = 0.5$, width of stabilising selection $V_s = 1$, maximum growth rate $r_m = 1.2$, maximum local carrying capacity $K = 6$, mutation rate $\mu = 10^{-5}$, $n_l = 1000$ loci with exponentially distributed effects with mean $\overline{\alpha} = 0.07$. Initially, a third of all loci form clines that contribute to the adaptation to the environmental gradient so that in the central part of the range, trait mean matches the environmental optimum. The habitat is wide enough ($x_d \geq 600$) so that species' range does not reach the edges along the dimension of spatial change and that the stochastic fluctuations of allele frequencies occur in truly two-dimensional habitat: the number of demes along the neutral dimension is $y_d = 600/K = 100$.

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Supplementary Materials. Supplementary Figures S1 to S9
Supplementary Movie S1

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