

# Supplementary Information: “The effect of habitat choice on evolutionary rescue in subdivided populations”

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## S1 Deriving the model dynamics

s2 In this section we provide the mathematical **details** of the model that is verbally described  
 in the main text. We start by deriving the population dynamics of the wild type **when**  
 s4 **alone** in both patch types. This will allow us to compute the local growth rate of the  
 mutant **when rare** in old-habitat patches,  $a_{\text{old}}$ .

s6 Before we go into the details of the computation, we recall the form of the dispersal  
 rates. For a wild-type individual to disperse to a new-habitat patch, this probability is  
 s8 given by

$$m_w^{\text{new}} = m \frac{1 - f_{\text{old}}}{1 - f_{\text{old}} + \hat{\pi}_w f_{\text{old}}}, \quad (\text{S1}) \quad \{\text{Seq:dispersal\_}$$

with  $m$  denoting the emigration probability,  $f_{\text{old}}$  the frequency of old-habitat patches  
 s10 and  $\hat{\pi}_w$  the transformed wild-type bias towards old-habitat patches. Analogously, the  
 probability for a wild-type individual **to emigrate and** to move to an old-habitat patch  
 s12 reads

$$m_w^{\text{old}} = m \frac{\hat{\pi}_w f_{\text{old}}}{1 - f_{\text{old}} + \hat{\pi}_w f_{\text{old}}}. \quad (\text{S2}) \quad \{\text{Seq:dispersal\_}$$

s14 All the subsequent computations can be checked with a symbolic programming language  
 s16 (e.g. *Mathematica*). A *Mathematica* notebook is deposited on Gitlab<sup>1</sup>.

### Stationary wild-type population sizes

s18 We derive the (deterministic) stationary population sizes of the wild-type in both patch  
 types. These values are denoted by  $\hat{N}_w^k$ , where  $k$  corresponds to the patch type (old  
 s20 or new). In old-patch habitats we assume that the population is always at its carrying  
 capacity. Therefore, we have  $\hat{N}_w^{\text{old}} = K_{\text{old}}$ .

s22 In new-habitat patches, the stationary value is given by the solution of the following  
 equation:

$$\begin{aligned} \hat{N}_w^{\text{new}} &= \left( 1 - m + m \frac{(1 - f_{\text{old}})}{(1 - f_{\text{old}} + \hat{\pi}_w f_{\text{old}})} \frac{(1 - f_{\text{old}})M}{(1 - f_{\text{old}})M} \right) (1 - r) \hat{N}_w^{\text{new}} \\ &\quad + m_w^{\text{new}} \frac{f_{\text{old}} M}{(1 - f_{\text{old}})M} (1 - r) \hat{N}_w^{\text{old}} \quad (\text{S3}) \quad \{\text{Seq:wt\_deme2}\} \\ &= (1 - m + m_w^{\text{new}}) (1 - r) \hat{N}_w^{\text{new}} + m_w^{\text{new}} \left( \frac{f_{\text{old}}}{1 - f_{\text{old}}} \right) (1 - r) K_{\text{old}}, \end{aligned}$$

s24 which simplifies to

$$\hat{N}_w^{\text{new}} = \frac{m(1 - r)f_{\text{old}}K_{\text{old}}}{mf_{\text{old}}\hat{\pi}_w + r(1 - f_{\text{old}} + f_{\text{old}}\hat{\pi}_w - m\hat{\pi}_w f_{\text{old}})}. \quad (\text{S4})$$

<sup>1</sup>[https://gitlab.com/pczuppon/evolutionary\\_rescue\\_and\\_dispersal](https://gitlab.com/pczuppon/evolutionary_rescue_and_dispersal)

Since we assume density regulation, this value cannot be larger than  $K_{\text{new}}$ , the carrying capacity of new-habitat patches. Hence, we find

$$\hat{N}_w^{\text{new}} = \begin{cases} K_{\text{new}}, & \text{if } \frac{m(1-r)f_{\text{old}}K_{\text{old}}}{mf_{\text{old}}\hat{\pi}_w + r(1-f_{\text{old}} + f_{\text{old}}\hat{\pi}_w - m\hat{\pi}_wf_{\text{old}})} \geq K_{\text{new}}; \\ \frac{m(1-r)f_{\text{old}}K_{\text{old}}}{mf_{\text{old}}\hat{\pi}_w + r(1-f_{\text{old}} + f_{\text{old}}\hat{\pi}_w - m\hat{\pi}_wf_{\text{old}})}, & \text{otherwise.} \end{cases} \quad (\text{S5})$$

### Wild-type population sizes after dispersal

In order to explicitly compute the growth rate of the mutant in old-habitat patches, we need an analytical expression for the number of wild-type individuals after the dispersal step. Later on, in the approximation of the probability of adaptation, we also use the number of wild-type individuals in new-habitat patches before reproduction. We denote these values by  $\tilde{N}_w^k$ , where  $k$  corresponds to the habitat type (old or new). These are given as the solutions to the following equations

$$\begin{aligned} \tilde{N}_w^{\text{old}} &= \left(1 - m + m \frac{\hat{\pi}_wf_{\text{old}}}{(1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}})} \frac{f_{\text{old}}M}{f_{\text{old}}M}\right) \hat{N}_w^{\text{old}} + m_w^{\text{old}} \frac{(1-f_{\text{old}})M}{f_{\text{old}}M} \hat{N}_w^{\text{new}}, \\ \tilde{N}_w^{\text{new}} &= \left(1 - m + m \frac{(1-f_{\text{old}})}{1-f_{\text{old}} + \pi f_{\text{old}}} \frac{(1-f_{\text{old}})M}{(1-f_{\text{old}})M}\right) \hat{N}_w^{\text{new}} + m_w^{\text{new}} \frac{f_{\text{old}}M}{(1-f_{\text{old}})M} \hat{N}_w^{\text{old}}. \end{aligned} \quad (\text{S6})$$

Using  $\hat{N}_w^{\text{old}} = K_{\text{old}}$  and in the case of  $\hat{N}_w^{\text{new}} = K_{\text{new}}$  this reduces to

$$\begin{aligned} \tilde{N}_w^{\text{old}} &= \frac{(1-f_{\text{old}})m\hat{\pi}_wK_{\text{new}} + (1-m-f_{\text{old}}(1-m-\hat{\pi}_w))K_{\text{old}}}{1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}}} \\ \tilde{N}_w^{\text{new}} &= \frac{(1-f_{\text{old}} + f_{\text{old}}\hat{\pi}_w(1-m))K_{\text{new}} + mf_{\text{old}}K_{\text{old}}}{1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}}}. \end{aligned} \quad (\text{S7}) \quad \{\text{Seq:wt\_eq1}\}$$

If on the other hand  $\hat{N}_w^{\text{new}} < K_{\text{new}}$  holds, we obtain

$$\begin{aligned} \tilde{N}_w^{\text{old}} &= (1-m+m_w^{\text{old}})K_{\text{old}} \\ &\quad + \left(m_w^{\text{old}} \frac{m(1-r)f_{\text{old}}}{mf_{\text{old}}\hat{\pi}_w + r(1-f_{\text{old}} + f_{\text{old}}\hat{\pi}_w - m\hat{\pi}_wf_{\text{old}})} \left(\frac{1-f_{\text{old}}}{f_{\text{old}}}\right)\right) K_{\text{old}} \\ &= \frac{m\hat{\pi}_wf_{\text{old}} + r(1-m)(1-f_{\text{old}}(1-\hat{\pi}_w))}{m\hat{\pi}_wf_{\text{old}} + r(1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}}(1-m))} K_{\text{old}} \\ &= \left(1 - \frac{rm(1-f_{\text{old}})}{m\hat{\pi}_wf_{\text{old}} + r(1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}}(1-m))}\right) K_{\text{old}}, \\ \tilde{N}_w^{\text{new}} &= (1-m+m_w^{\text{new}}) \frac{m(1-r)f_{\text{old}}}{mf_{\text{old}}\hat{\pi}_w + r(1-f_{\text{old}} + f_{\text{old}}\hat{\pi}_w - m\hat{\pi}_wf_{\text{old}})} K_{\text{old}} \\ &\quad + m_w^{\text{new}} \frac{f_{\text{old}}}{(1-f_{\text{old}})} K_{\text{old}} \\ &= \frac{mf_{\text{old}}}{m\hat{\pi}_wf_{\text{old}} + r(1-f_{\text{old}} + \hat{\pi}_wf_{\text{old}}(1-m))} K_{\text{old}}. \end{aligned} \quad (\text{S8}) \quad \{\text{Seq:wt\_eq2}\}$$

### S36 Wild-type population sizes during the environmental change

S38 Lastly, compute the (deterministic) wild-type population size over time during the  
 S38 environmental change. This value is used in the approximation of the probability of  
 evolutionary rescue in eq. (9) in the main text, more precisely to estimate the number of  
 S40 rescue mutants that appear during the deterioration of patches.

S42 If a patch deteriorates its current population size is given by the carrying capacity of  
 the old habitat,  $K_{\text{old}}$ . Subsequently, it is reduced by  $(1 - r)$ , the fecundity of a single  
 wild-type individual in a new-habitat patch. That is, neglecting dispersal for the moment,  
 S44 in generation  $j$  after the degradation of a patch, we would have

$$N_w^{\text{new}}(j) = K_{\text{old}}(1 - r)^j \quad (\text{S9})$$

wild-type individuals in this patch. Including dispersal between the patches then results  
 S46 in the following number of wild-type individuals in a patch  $i$  at time  $j$ , given that there  
 are  $k - 1$  other new-habitat patches

$$N_w^{i,k}(j) = (1 - r) \left( (1 - m)N_w^{i,k}(j - 1) + \frac{m_w^{\text{new}}}{k}(M - k)K_{\text{old}} + \frac{m_w^{\text{new}}}{k} \sum_{l=1}^k N_w^{l,k}(j - 1) \right). \quad (\text{S10})$$

S48 The first term represents the remaining individuals after emigration,  $(1 - m)$ , the second  
 and third term are immigrants from old- and new-habitat patches (distributed equally  
 S50 among the  $k$  new-habitat patches), respectively.

### The local growth rate $a_{\text{old}}$

S52 As stated in eq. (1) in the main text, we define the growth rate of a single mutant in the  
 old habitat by

$$1 + a_{\text{old}} = K_{\text{old}} \frac{\omega_m}{\omega_w \tilde{N}_w^{\text{old}}}. \quad (\text{S11})$$

S54 Having computed the number of wild-type individuals after dispersal in an old-habitat  
 patch,  $\tilde{N}_w^{\text{old}}$ , we can write the growth rate as follows

$$a_{\text{old}} = \begin{cases} \frac{\omega_m K_{\text{old}}}{\omega_w \left( \frac{(1-f_{\text{old}})m\hat{\pi}_w K_{\text{new}} + (1-m-f_{\text{old}}(1-m-\hat{\pi}_w))K_{\text{old}}}{1-f_{\text{old}}+\hat{\pi}_w f_{\text{old}}} \right)} - 1, & \text{if } \hat{N}_w^{\text{new}} = K_{\text{new}}; \\ \frac{\omega_m}{\omega_w \left( 1 - \frac{rm(1-f_{\text{old}})}{f_{\text{old}}m\hat{\pi}_w + r(1-f_{\text{old}}+\hat{\pi}_w f_{\text{old}}(1-m))} \right)} - 1, & \text{otherwise.} \end{cases} \quad (\text{S12}) \quad \{\text{Seq:s\_old}\}$$

### S56 The local growth rate $a_{\text{new}}$

S58 In new-habitat patches we assume that during the relevant phase of establishment of  
 a rare mutant the carrying capacity  $K_{\text{new}}$  is not reached. Then the growth rate of the  
 mutant in these patches,  $a_{\text{new}}$ , is not affected by the different dispersal schemes.

S60 Of course there may be parameter configurations, typically high emigration rates  $m$   
 and a bias of the wild type towards the new habitat ( $\pi_w < 0$ ), where our assumption of

S62 density-independent reproduction is violated. Then our approximation and the numerical  
solution of eq. (4) in the main text strongly deviate from the simulation results (e.g. the  
S64 New-New dispersal scheme in Fig. 2(d)).

## S2 Approximation of the establishment probability

s66 We compute the survival probability of the lineage of a single mutant starting either in  
s68 an old- or in a new-habitat patch. We call this probability the establishment probability  
because it implies the successful establishment of a mutant population within the meta-  
s70 population. It is denoted by  $\varphi_k$  where the index  $k$  indicates the initial habitat type of  
the mutant (old or new).

Our method is the same as used in Tomasini and Peischl (2018) with the exception  
s72 that our growth rate in old-habitat patches,  $a_{\text{old}}$ , depends on the demography of the  
population. The method in general is based on the theory of multi-type branching  
s74 processes, cf. Chapter 5.5 in Haccou et al. (2005). For a detailed application of the theory  
we refer to the Supplementary Information of Tomasini and Peischl (2018).

s76 We start by recalling the mean reproduction matrix of a mutant that gives the average  
number of offspring in a certain habitat, dependent on the habitat type in which the  
s78 mutant resides. It is given as (see also eq. (3) in the main text)

$$\mathcal{M} = \begin{array}{cc} & \begin{array}{c} \text{old patch} \\ \text{new patch} \end{array} \\ \begin{array}{c} \text{old patch} \\ \text{new patch} \end{array} & \begin{pmatrix} (1 - m_m^{\text{new}})(1 + a_{\text{old}}) & m_m^{\text{new}}(1 + a_{\text{new}}) \\ m_m^{\text{old}}(1 + a_{\text{old}}) & (1 - m_m^{\text{old}})(1 + a_{\text{new}}) \end{pmatrix} \end{array}, \quad (\text{S13}) \quad \{\text{Seq:mean\_repro}\}$$

where the rows denote the parent locations, and the columns the patch type of the  
s80 offspring.

Our goal is to apply Theorem 5.6 from Haccou et al. (2005) which states that for a  
s82 slightly super-critical branching process, i.e. where the survival probability is slightly above  
zero, the establishment probability can be expressed in terms of the largest eigenvalue  $\rho$   
s84 and the corresponding left- and right-eigenvectors of the mean reproduction matrix  $\mathcal{M}$ ,  
denoted by  $u$  and  $v$ , respectively. The eigenvectors should be normalized in the following  
s86 way:  $u_1 + u_2 = 1$  and  $\sum_{i=1}^2 u_i v_i = 1$ . The establishment probabilities are then given by

$$\varphi_i = \frac{2(\rho - 1)}{B} v_i + O(\varepsilon), \quad (\text{S14}) \quad \{\text{Seq:theory}\}$$

with

$$B = \sum_{i=1}^2 u_i \sum_{j=1}^2 v_j \mathcal{M}_{ij} + \rho(1 - \rho) \sum_{j=1}^2 u_j v_j^2. \quad (\text{S15})$$

### s88 Computing the largest eigenvalue

We first approximate the largest eigenvalue of  $\mathcal{M}$  denoted by  $\rho$ . It is given by (see  
s90 *Mathematica* notebook)

$$\rho = \frac{1}{2} \left( 2 + a_{\text{old}} + a_{\text{new}} - m - m_m^{\text{new}} a_{\text{old}} - m_m^{\text{old}} a_{\text{new}} \right. \\ \left. + \sqrt{4(m - 1)(1 + a_{\text{old}})(1 + a_{\text{new}}) + (2 + a_{\text{old}} + a_{\text{new}} - m - m_m^{\text{new}} a_{\text{old}} - m_m^{\text{old}} a_{\text{new}})^2} \right) \quad (\text{S16})$$

In order to make analytical progress and to identify under which conditions the process is slightly super-critical, i.e.  $\rho > 1$ , we rescale the parameters by a small parameter  $\varepsilon$ . We set  $a_{\text{old}} = \varepsilon$ ,  $a_{\text{new}} = \varepsilon\xi$  and  $m = \varepsilon\mu$ . Assuming that  $\varepsilon$  is small enough, i.e. effectively a weak selection assumption in old-habitat patches, we can neglect higher orders of  $\varepsilon$  and find

$$\begin{aligned}\rho &\approx 1 + \frac{1}{2}\varepsilon \left( 1 + \xi - \mu + \sqrt{(\xi - 1 + \mu_m^{\text{new}})^2 + 2(1 - \xi + \mu_m^{\text{new}})\mu_m^{\text{old}} + (\mu_m^{\text{old}})^2} \right) \\ &= 1 + \frac{1}{2}\varepsilon \left( 1 + \xi - \mu + \sqrt{\frac{\gamma}{1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}}}} \right),\end{aligned}\tag{S17} \quad \{\text{eq:eigenvalue}\}$$

where  $\gamma$  is the rescaled version of the constant  $C$  in the main text (eq. (6)), i.e.

$$\gamma = (1 - f_{\text{old}})(\xi - 1 + \mu)^2 + \hat{\pi}_m f_{\text{old}}(\xi - 1 - \mu)^2.\tag{S18}$$

For  $\varepsilon \rightarrow 0$  we find that  $\rho \rightarrow 1$  (eq. (S17)) which means that the branching is slightly super-critical if  $\rho > 1$  and real. A sufficient condition for this to be true is

$$1 + \xi - \mu > 0 \quad \Leftrightarrow \quad a_{\text{old}} + a_{\text{new}} - m > 0\tag{S19}$$

In case that the branching process is not super-critical the establishment probability in eq. (S14) becomes negative and as such is not a probability anymore. Hence, we can simply reject negative solutions of the establishment probability and by that implicitly justify that our approximation is valid.

### Computing the establishment probability

For the solution of eq. (S14) it remains to compute the normalized eigenvectors. Their precise form is of not much insight. We therefore omit stating them explicitly but refer to the *Mathematica* notebook. Solving eq. (S14) to the first order of  $\varepsilon$  we find

$$\begin{aligned}\varphi_{\text{old}} &= \varepsilon + \frac{\varepsilon(1 - \xi)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}}} + \frac{\varepsilon(\mu_m^{\text{old}} - \mu_m^{\text{new}} + 2\mu_m^{\text{new}}\xi)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}}}, \\ \varphi_{\text{new}} &= \varepsilon\xi + \frac{\varepsilon\xi(\xi - 1)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}}} + \frac{\varepsilon(\xi\mu_m^{\text{new}} - \xi\mu_m^{\text{old}} + 2\mu_m^{\text{old}})}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}}}.\end{aligned}\tag{S20}$$

Transforming back to the original variables and replacing  $\gamma$  by the constant  $C$  from the main text (eq. (6))

$$C = (1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}}) \left( (1 - f_{\text{old}})(a_{\text{new}} - a_{\text{old}} + m)^2 + \hat{\pi}_m f_{\text{old}}(a_{\text{new}} - a_{\text{old}} - m)^2 \right),\tag{S21}$$

we obtain

$$\begin{aligned}
\varphi_{\text{old}} &= a_{\text{old}} + \frac{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})a_{\text{old}}(a_{\text{old}} - a_{\text{new}})}{\sqrt{C}} + \\
&\quad m \frac{(\hat{\pi}_m f_{\text{old}} a_{\text{old}} - (1 - f_{\text{old}})a_{\text{old}} + 2(1 - f_{\text{old}})a_{\text{new}})}{\sqrt{C}}, \\
\varphi_{\text{new}} &= a_{\text{new}} + \frac{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})a_{\text{new}}(a_{\text{new}} - a_{\text{old}})}{\sqrt{C}} \\
&\quad + m \frac{(a_{\text{new}}(1 - f_{\text{old}}) - a_{\text{new}}\hat{\pi}_m f_{\text{old}} + 2a_{\text{old}}\hat{\pi}_m f_{\text{old}})}{\sqrt{C}}.
\end{aligned} \tag{S22}$$

Slightly re-ordering the terms, this gives the establishment probability of a single mutant individual, eq. (5) in the main text:

$$\begin{aligned}
\varphi_{\text{old}} &\approx a_{\text{old}} + a_{\text{old}} \frac{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}{\sqrt{C}} (a_{\text{old}} - a_{\text{new}}) \\
&\quad + \frac{m}{\sqrt{C}} (a_{\text{new}}(1 - f_{\text{old}}) + a_{\text{old}}\hat{\pi}_m f_{\text{old}} - (a_{\text{old}} - a_{\text{new}})(1 - f_{\text{old}})), \\
\varphi_{\text{new}} &\approx \underbrace{a_{\text{new}}}_{(1) \text{ local growth parameter}} + \underbrace{a_{\text{new}} \frac{(1 - f_{\text{old}} + \hat{\pi}_m f_{\text{old}})}{\sqrt{C}} (a_{\text{new}} - a_{\text{old}})}_{(2) \text{ effect of the heterogeneous environment}} \\
&\quad + \underbrace{\frac{m}{\sqrt{C}} (a_{\text{new}}(1 - f_{\text{old}}) + a_{\text{old}}\hat{\pi}_m f_{\text{old}} - (a_{\text{new}} - a_{\text{old}})\hat{\pi}_m f_{\text{old}})}_{(3) \text{ effect of dispersal: new patches} + \text{old patches} - \text{loss to the other patch type}}.
\end{aligned} \tag{S23}$$

For  $m = 0$  we see that  $\varphi_{\text{old}} = 0$ , i.e. terms (1) and (2) cancel out. For the establishment probability in the new habitat we recover Haldane's result for the establishment probability of a slightly advantageous mutant:  $\varphi_{\text{new}} = 2a_{\text{new}}$  (Haldane, 1927).

## S2.1 Disentangling the contributions to the establishment probability

We now proceed to explain the three regions of the establishment probability from Fig. 2(a) in the main text. These were defined by: (i) an initial increase of the establishment probability at low dispersal rates  $m$ ; (ii) a local maximum with a subsequent decrease of the establishment probability; (iii) an increase of the establishment probability for high dispersal rates.

For clarity, we re-plot Figs. 2(a,c) in Fig. S1(a,b), respectively. We try to explain the ongoing processes for each of the regions through the approximations of the establishment probabilities in eq. (S23), see also Fig. S1(c,d). Note that these explanations are only valid for the establishment probability of a mutant initially in an old-habitat patch,  $\varphi_{\text{old}}$ . For the intuition behind the shape of  $\varphi_{\text{new}}$  we refer to the corresponding section in the main text.

Region (i) is explained by the positive effect of dispersal. Mutants disperse from old- to new-habitat patches where they have a higher growth rate. This effect is mediated



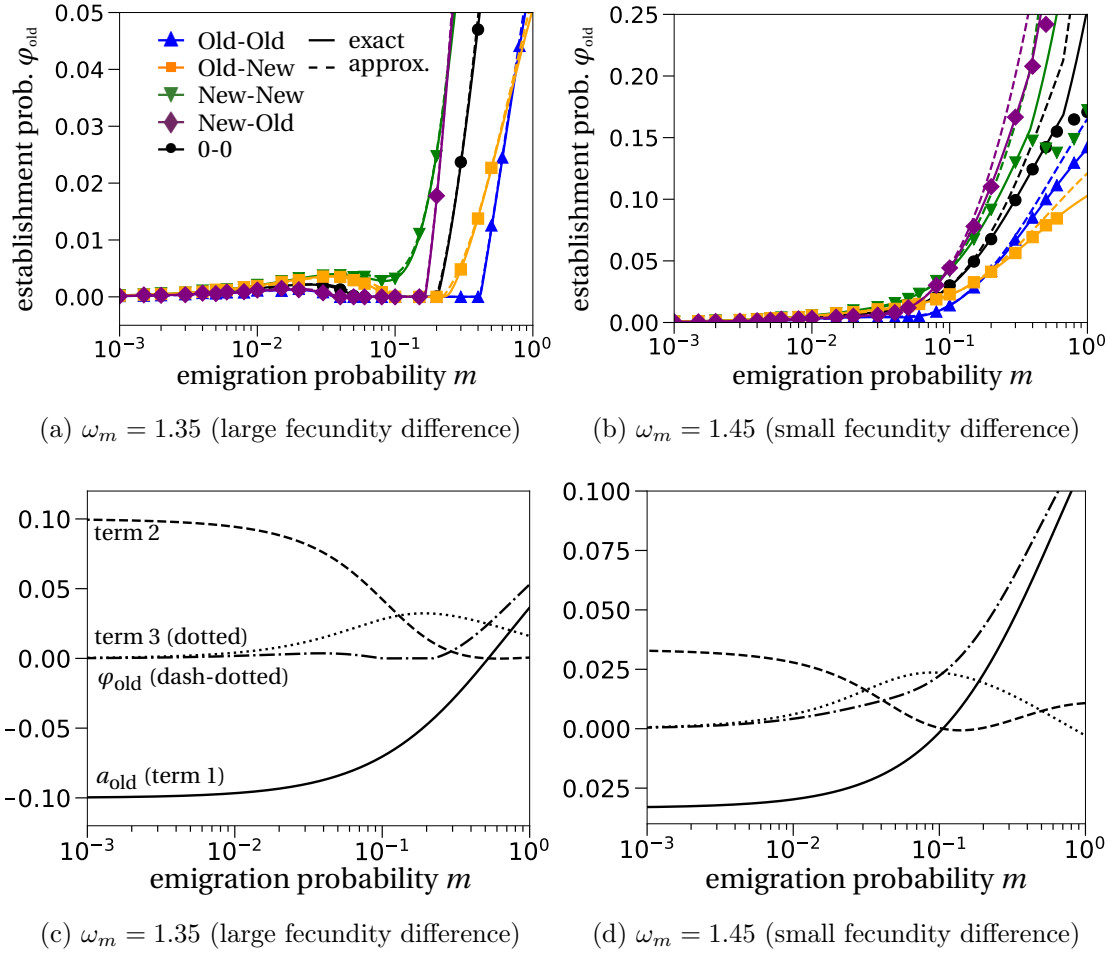


Figure S1: **Contribution of the different terms in eq. (S23) to the establishment probability  $\varphi_{\text{old}}$ .** Subfigures (a,b) are the same as Figs. 2(a,c) in the main text. They show the establishment probability for a single mutant individual arising in an old-habitat patch for varying emigration probabilities  $m$ . In subfigures (c,d) we plot the terms from eq. (S23) separately ( $\pi_w = 0.5, \pi_m = -0.5$ ). Term 1, the mutant growth rate in old habitats (solid), increases with increasing dispersal rates as a consequence of relaxed competition. Term 2, the environmental effect (dashed), captures the differences between the growth rates in the habitats. The larger the difference, the larger its contribution to the overall establishment probability. Term 3, the effect of dispersal (dotted), (largely) increases with increasing dispersal rates  $m$ . The sum of the three terms is plotted as a dash-dotted line.

{Sfig:contribut

through the third term of the establishment probability in eq. (S23). Note that the first two terms of the approximation cancel out for small emigration probabilities  $m$ . While

S130

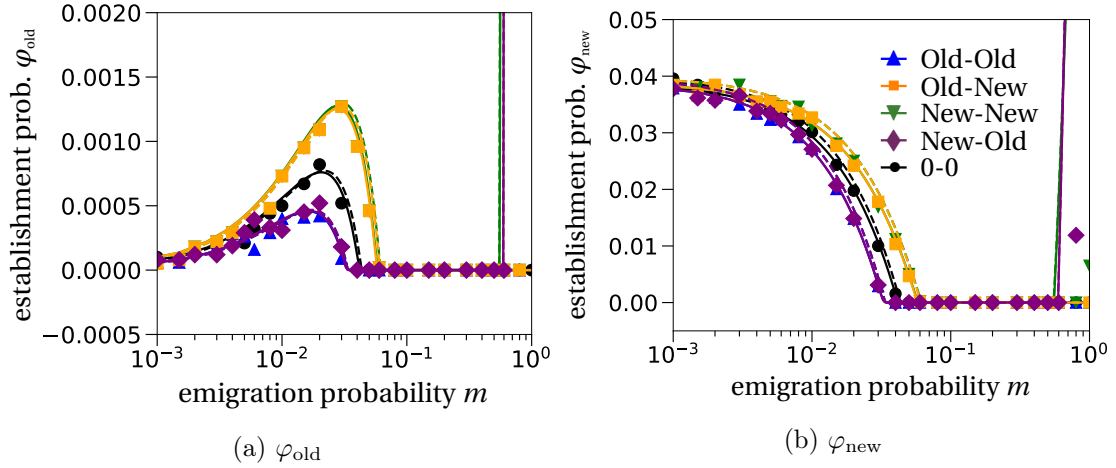


Figure S2: **Disappearance of region (iii) for large fecundity differences in the old habitat.** If the mutant fecundity in old-habitat patches is too low, here  $\omega_m = 1.1$ , the effect of relaxed competition is not strong enough to have an impact on the establishment probability for high dispersal rates. The establishment probability remains at zero.

{Sfig:weak\_fecu

the third term increases with increasing emigration rate  $m$ , the second term in eq. (S23) decreases, cf. Fig. S1. In the formula this is mediated through the increase of the local growth rate in the old-habitat,  $a_{\text{old}}$ , i.e. it becomes less negative. Then both factors of the second term,  $a_{\text{old}}$  and the difference  $(a_{\text{old}} - a_{\text{new}})$ , increase (which in turn decreases term two). The intuitive reason is that due to larger emigration probabilities  $m$ , more individuals leave old habitats before the reproductive event. This relaxes competition in these patches and therefore increases the local growth rate of mutants in old-habitat patches. Finally, in region (iii) dispersal is so large that the population homogenizes. This results in even less competitive pressure in old-habitat patches. Eventually, this yields a positive growth rate  $a_{\text{old}}$  (first term in eq. (S23)). Therefore, this region is driven by the local growth rate in old habitats.

Note that region (iii) can be shifted to the left by increasing the absolute number of offspring of mutants in old-habitat patches,  $\omega_m$ , and therefore decreasing the local disadvantage of the mutant. If shifted sufficiently to the left, like in Fig. S1(d), region (ii) might vanish due to this effect.

Contrarily, if we set the fecundity parameter of the mutant in the old habitat to  $\omega_m = 1.1$ , we see that region (iii) disappears for most dispersal schemes, cf. Fig. S2. Due to the low fecundity of the mutant, even under relaxed competition in old habitats, establishment of a mutant population is very unlikely. The final increase of our approximation in the dispersal schemes New-New and New-Old is due to our density-independence assumption in new habitats. For these large values of  $m$  and the bias of the wild type towards new-habitat patches, this assumption is violated in the simulations explaining the deviation from the simulation results and our prediction.

### S154 S3 Habitat of origin of the adaptive mutation

S156 Here, we provide further insight into the origin of the adaptive mutation. Therefore we  
 S158 plot the establishment probabilities  $\varphi_{\text{old}}$  and  $\varphi_{\text{new}}$  when varying the frequency of old  
 S160 habitats,  $f_{\text{old}}$ . In Fig. 4 in the main text we have seen that most successful adaptive  
 mutations arise in old-habitat patches. Here, we show that this is explained mostly due to  
 the large mutational input that is provided by the much larger wild-type population sizes  
 in old habitats, see Fig. S3(b). The establishment probability though is always larger for  
 mutants that arise in new habitats than in old habitats (Fig. S3(a)).

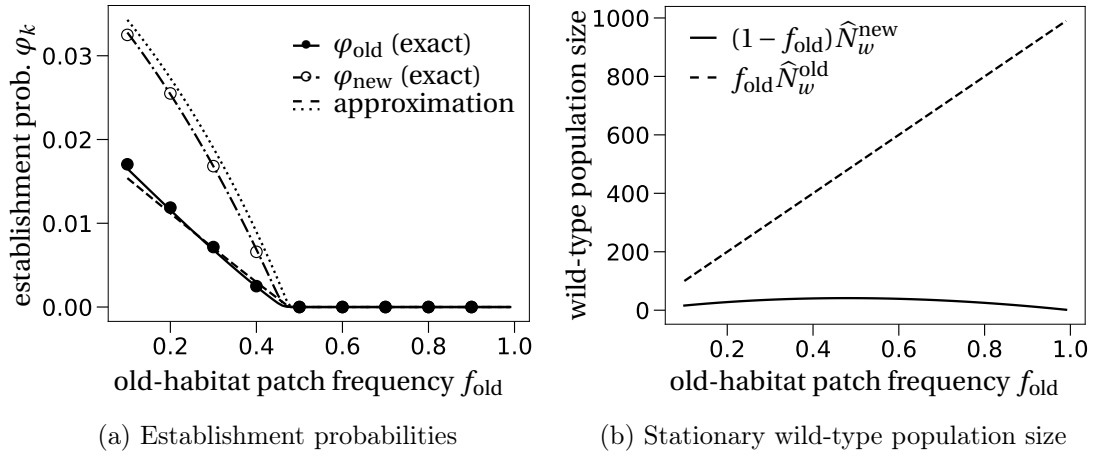


Figure S3: **Establishment probability and stationary wild-type population size when varying the old-habitat frequency.** In the simulations we have used the standard set of parameters as given in Table 1 and the unbiased dispersal scheme ( $\pi_w = \pi_m = 0$ ). In (a) we additionally chose the large fecundity difference scenario ( $\omega_m = 1.35$ ).

{Sfig:vary\_f\_or

S162 (There was a figure where the contribution from new habitats was larger than from  
 S164 old habitats. With the changed fecundities, I only get this behavior if the fecundity of  
 S166 the mutant is larger in the new patches than in the old patches, i.e.  $\omega_m < a_{\text{new}}$ . Also,  
 for some reason the approximations do not work that well in these scenarios (I did not  
 investigate why the estimated lines are bad – soft sweeps still work fine but the other  
 approximations don't.))

## S168 S4 Probability of establishment for large frequencies of S170 old-habitat patches

S170 We plot the probability of establishment for a large frequency of old-habitat patches,  $f_{\text{old}}$ .  
S172 As visible in Fig. S4 below, for high frequencies of old-habitat patches the probability of  
S174 adaptation becomes very small, if not zero, for large emigration probabilities  $m$ . These  
S176 high frequency of old-habitat patches are the patch configurations which mutants that  
S178 were present before the first patch degrades, i.e. standing genetic variation mutants,  
experience. Therefore, it is very unlikely that the mutant, which will eventually rescue  
the population, was already present before the first degradation event. This supports the  
explanation that homogenizing the population (large  $m$ ) reduces the impact of standing  
genetic variation on the probability of evolutionary rescue, see Fig. 6(b) in the main text  
where  $\pi_w = \pi_m = 0$  was plotted.

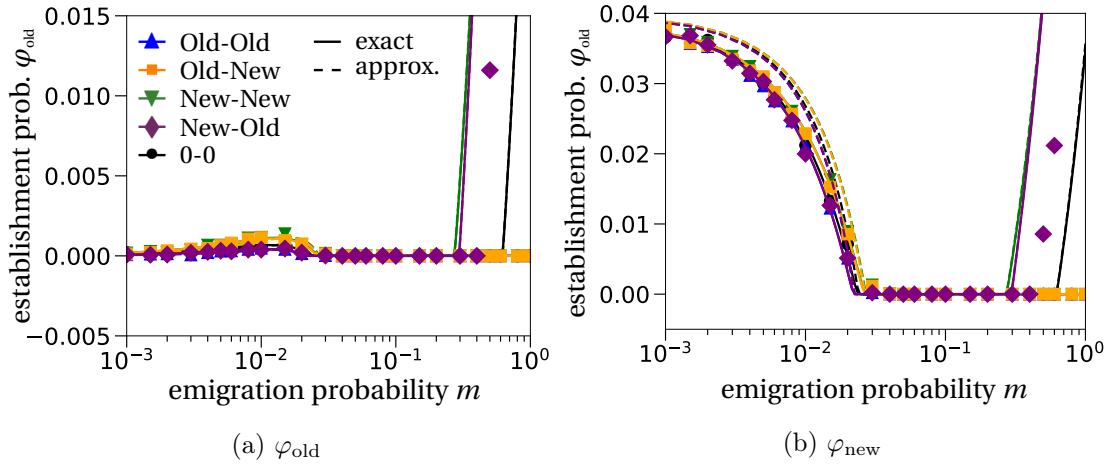


Figure S4: **Probability of adaptation for a large frequency of old-habitat patches** ( $f_{\text{old}} = 0.9$ ). The fecundity of the mutant in old-habitat patches is set to  $\omega_m = 1.45$ . Note also the difference between the scales of the y-axes in the two panels.

{Sfig:vary\_f}

## S180 S5 Establishment probability in a model without demography

S182 Here, we consider a variation of our original model in order to investigate the impact of  
demography on the establishment probabilities  $\varphi_{\text{old}}$  and  $\varphi_{\text{new}}$ . The dispersal process and  
S184 the dynamics in old-habitat patches remain as studied before. In new-habitat patches we  
now assume that the population remains at carrying capacity, i.e. there is no longer a  
S186 declining wild-type population. This means that the local growth rate  $a_{\text{old}}$  in eq. (S12)  
takes the form for  $\hat{N}_w^{\text{new}} = K_{\text{new}}$ . For simplicity we will also assume that  $K_{\text{new}} = K_{\text{old}} = K$ .  
S188 In order to maintain the divergent selection assumption, we assume that the fecundity  
of the wild-type in the new habitat is below the fecundity of the mutant. Therefore, we  
S190 need to adjust the local growth rate of a single mutant,  $a_{\text{new}}$ . The local growth rate in  
old habitats,  $a_{\text{old}}$ , remains as outlined in eq. (S12). We have

$$1 + a_{\text{new}} = K \frac{\omega_m^{\text{new}}}{\omega_w^{\text{new}} \tilde{N}_w^{\text{new}} + \omega_m^{\text{new}}} \approx K \frac{\omega_m^{\text{new}}}{\omega_w^{\text{new}} \tilde{N}_w^{\text{new}}}, \quad (\text{S24})$$

S192 which with the help of eq. (S7) yields

$$a_{\text{new}} \approx \frac{\omega_m^{\text{new}}}{\omega_w^{\text{new}} \left( 1 + \frac{mf_{\text{old}}(1 - \hat{\pi}_w)}{1 - f_{\text{old}} + \hat{\pi}_w f_{\text{old}}} \right)}. \quad (\text{S25})$$

Note, that we again used that during the establishment phase the wild type is much  
S194 more abundant than the mutant which explains the approximation in the two equations.  
Plugging this in the approximation of the establishment probability from eq. (S23) we  
S196 find the curves in Fig. S5.

We see that, as briefly mentioned in the main text, region (iii) of the establishment  
S198 probability disappears in these type of models except for the Old-New and the New-  
Old dispersal schemes. The reason for the disappearance of the region is that relaxed  
S200 competition only plays a subordinate role for the symmetric dispersal schemes (Old-Old,  
New-New and 0-0). In other words, these dispersal schemes maintain the local frequencies  
S202 of the mutant at the same level as before the dispersal step and by that do not change  
the population dynamics. In contrast, the Old-New dispersal scheme strongly increases  
S204 the frequency of mutants in new-habitat patches and by that increases the establishment  
probability. It is worth mentioning though, that this is not an effect of relaxed competition  
S206 but rather a biased dispersal of the mutant into the habitat where it is favored. Solely for  
the New-Old dispersal scheme where individuals prefer the habitat they are relatively  
S208 less fit, we see a relaxed competition scenario in old-habitat patches. For high dispersal  
rates  $m$  the majority of the wild-type individuals emigrate to new habitats and by that  
S210 leave space for the rare mutants in old-habitat patches to reproduce. This explains why  
this dispersal scheme still shows the characteristic pattern of a three-stage establishment  
S212 probability.

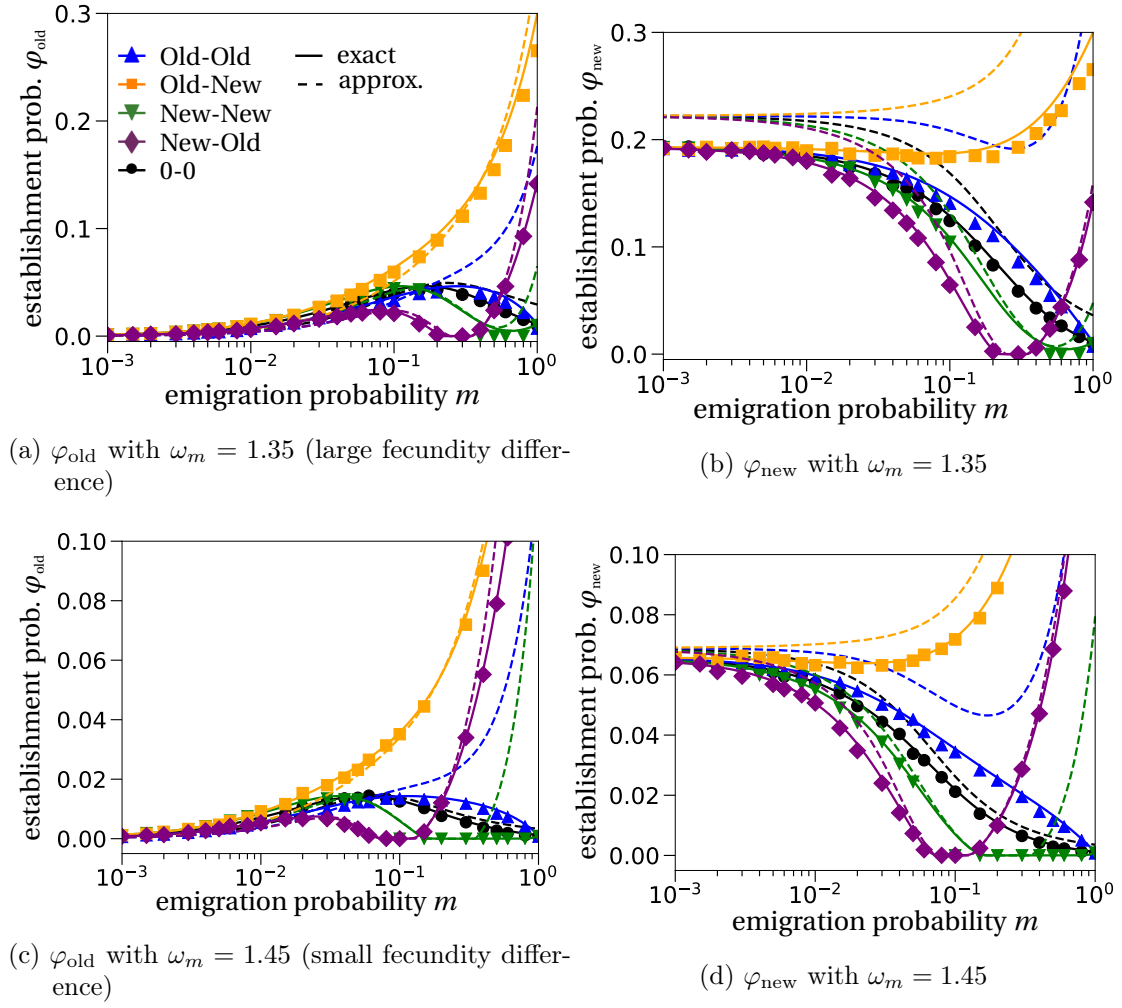


Figure S5: **Establishment probability when populations in both habitats are at carrying capacity.** We plot the establishment probability for a single mutant either initially in an old-habitat patch (a,c) or in a new-habitat patch (b,d). The numerical solution (solid lines) still approximates the simulated data reasonably well. The analytical approximation (dashed lines) however deviates strongly from the data due to large growth rates ( $a_{\text{new}} \approx 0.2$ ) so that the conditions for the approximation to hold are violated. In this case, in eq. (S23) higher order corrections would need to be taken into account. The fecundity values in the new habitat are given by  $\omega_w^{\text{new}} = \omega_m^{\text{old}}$  and  $\omega_m^{\text{new}} = \omega_w^{\text{old}}$  and the carrying capacity is  $K_{\text{new}} = K_{\text{old}} = K = 500$ . Missing data points (mostly for the negative density-dependent dispersal scheme – green triangles) are explained by too large computation times. All data points are averages from  $10^4$  independent runs. Note the varying y-axes scales.

{Sfig:pop\_gen}

## S6 Habitat of origin dependent on the dispersal scheme

The habitat type of the origin of the rescue mutation is largely independent of the considered dispersal scheme. For  $\omega_m = 1.35$  we have plotted the relative contribution of each natal habitat type to the probability of evolutionary rescue, Fig. S6. We do not see large differences between the three symmetric dispersal schemes (0-0, Old-Old, and New-New) and the Old-New dispersal scheme. Only for the New-Old dispersal schemes we see an increase in the contribution of mutants emerging from old-habitat patches for very high emigration probabilities  $m$ . A possible explanation is the large probability of establishment for a mutant emerging in old-habitat patches for this parameter set (cf. Fig. S1(a)).

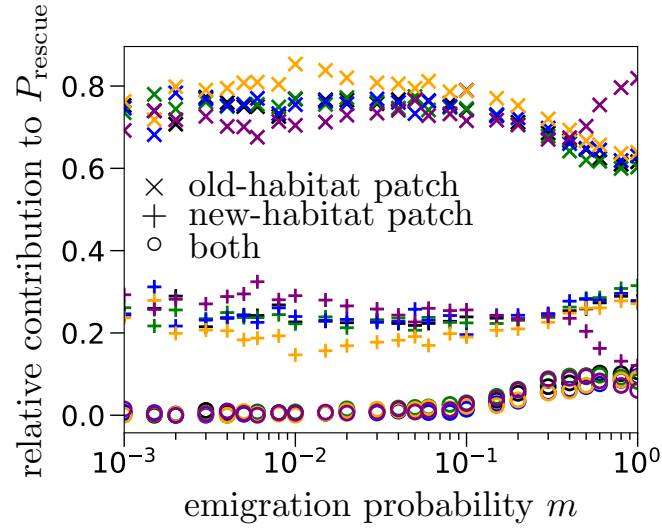


Figure S6: **Habitat type of the origin of the rescue mutant dependent on the dispersal scheme.** Varying the emigration probability  $m$  we plot the relative contributions of each habitat type to the probability of evolutionary rescue. The color-coding is as in the main text: black for 0-0, blue for the Old-Old, green for the New-New, orange for the Old-New, and purple for the New-Old dispersal scheme.

{Sfig:natal\_hab

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