

Supplementary Information: “How does habitat choice affect evolutionary rescue in subdivided populations?”

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S1 Deriving the model dynamics

In this section we provide the mathematical description of the verbally described model in the main text. We start by deriving the population dynamics of the wild type in both patch types. This will allow us to compute the local growth rate of the mutant in old-habitat patches, s_{old} .

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

$$m_w^{\text{old} \rightarrow \text{new}} = m \frac{1 - f_{\text{old}}}{1 - f_{\text{old}} + \pi_w f_{\text{old}}}. \quad (\text{S1})$$

Analogously, the probability for a wild-type individual in a new-habitat patch to move to an old-habitat patch reads

$$m_w^{\text{new} \rightarrow \text{old}} = m \frac{\pi_w f_{\text{old}}}{1 - f_{\text{old}} + \pi_w f_{\text{old}}}. \quad (\text{S2})$$

All the subsequent computations can be checked with a symbolic programming language (e.g. *Mathematica*). A *Mathematica* notebook is deposited on Gitlab¹.

Stationary wild-type population sizes

We start by deriving the (deterministic) stationary population size of the wild-type. These values are denoted by \widehat{N}_w^k , where k denotes the patch type (old or new). In old-patch habitats we assume that the population is always at carrying capacity. Therefore, we have $\widehat{N}_w^{\text{old}} = K$.

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

$$\begin{aligned} \widehat{N}_w^{\text{new}} &= \left(1 - m + m \frac{(1 - f_{\text{old}})}{(1 - f_{\text{old}} + \pi_w f_{\text{old}})} \frac{(1 - f_{\text{old}})M}{(1 - f_{\text{old}})M} \right) (1 - r) \widehat{N}_w^{\text{new}} \\ &\quad + m_w^{\text{old} \rightarrow \text{new}} \frac{f_{\text{old}}M}{(1 - f_{\text{old}})M} (1 - r) \widehat{N}_w^{\text{old}} \quad (\text{S3}) \\ &= (1 - m + m_w^{\text{old} \rightarrow \text{new}}) (1 - r) \widehat{N}_w^{\text{new}} + m_w^{\text{old} \rightarrow \text{new}} \left(\frac{f_{\text{old}}}{1 - f_{\text{old}}} \right) (1 - r) K, \end{aligned}$$

which gives

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

¹https://gitlab.com/pczuppon/evolutionary_rescue_and_dispersal

Since we assume density regulation, this value cannot be larger than K , the carrying capacity of patches. Hence, we find

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

Wild-type population sizes after dispersal

In order to explicitly compute the growth rate of the mutant in old-habitat patches, we need to compute the number of wild-type individuals after the dispersal event. 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 \widetilde{N}_w^k , where k denotes the habitat type (old or new). These are given as the solutions to the following equations

$$\begin{aligned} \widetilde{N}_w^{\text{old}} &= \left(1 - m + m \frac{\pi_w f_{\text{old}}}{(1 - f_{\text{old}} + \pi_w f_{\text{old}})} \frac{f_{\text{old}} M}{f_{\text{old}} M} \right) \widehat{N}_w^{\text{old}} + m_w^{\text{new} \rightarrow \text{old}} \frac{(1 - f_{\text{old}}) M}{f_{\text{old}} M} \widehat{N}_w^{\text{new}}, \\ \widetilde{N}_w^{\text{new}} &= \left(1 - m + m \frac{(1 - f_{\text{old}})}{1 - f_{\text{old}} + \pi_w f_{\text{old}}} \frac{(1 - f_{\text{old}}) M}{(1 - f_{\text{old}}) M} \right) \widehat{N}_w^{\text{new}} + m_w^{\text{old} \rightarrow \text{new}} \frac{f_{\text{old}} M}{(1 - f_{\text{old}}) M} \widehat{N}_w^{\text{old}}. \end{aligned} \quad (\text{S6})$$

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

$$\begin{aligned} \widetilde{N}_w^{\text{old}} &= \left(1 - m + m_w^{\text{new} \rightarrow \text{old}} + m_w^{\text{new} \rightarrow \text{old}} \frac{(1 - f)}{f} \right) K \\ &= \left(1 - \frac{m(1 - \pi_w)(1 - f_{\text{old}})}{1 - f + \pi_w f} \right) K, \\ \widetilde{N}_w^{\text{new}} &= \left(1 - m + m_w^{\text{old} \rightarrow \text{new}} + m_w^{\text{old} \rightarrow \text{new}} \frac{f_{\text{old}}}{(1 - f_{\text{old}})} \right) K \\ &= \left(1 + \frac{mf_{\text{old}}(1 - \pi_w)}{1 - f_{\text{old}} + \pi_w f_{\text{old}}} \right) K. \end{aligned} \quad (\text{S7})$$

Plugging in the values for $\widehat{N}_w^{\text{new}} < K$ we obtain

$$\begin{aligned}
\widetilde{N}_w^{\text{old}} &= (1 - m + m_w^{\text{new} \rightarrow \text{old}}) K \\
&\quad + \left(m_w^{\text{new} \rightarrow \text{old}} \frac{m(1-r)f_{\text{old}}}{mf_{\text{old}}\pi_w + r(1-f_{\text{old}} + f_{\text{old}}\pi_w - m\pi_w f_{\text{old}})} \left(\frac{1-f}{f} \right) \right) K \\
&= \left(1 - \frac{rm(1-f)}{fm\pi + r(1-f + \pi f(1-m))} \right) K, \\
\widetilde{N}_w^{\text{new}} &= (1 - m + m_w^{\text{old} \rightarrow \text{new}}) \frac{m(1-r)f_{\text{old}}}{mf_{\text{old}}\pi_w + r(1-f_{\text{old}} + f_{\text{old}}\pi_w - m\pi_w f_{\text{old}})} K \\
&\quad + m_w^{\text{old} \rightarrow \text{new}} \frac{f_{\text{old}}}{(1-f_{\text{old}})} K \\
&= \frac{mf_{\text{old}}}{f_{\text{old}}m\pi_w + r(1-f_{\text{old}} + f_{\text{old}}\pi_w(1-m))} K.
\end{aligned} \tag{S8}$$

We note that for $r = 0$ and $\pi = 1$ all equations in (S7) and (S8) give $\widetilde{N}_w^{\text{old,new}} = K$.

The local growth rate s_{old}

As stated in equation (3) in the main text, we define the growth rate of a single mutant in the old habitat by

$$1 + s_{\text{old}} = K \frac{\omega_m}{\omega_w \widetilde{N}_w^{\text{old}}}. \tag{S9}$$

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

$$s_{\text{old}} = \begin{cases} \frac{\omega_m}{\omega_w \left(1 - \frac{m(1-\pi_w)(1-f_{\text{old}})}{1-f+\pi f} \right)} - 1, & \text{if } \widehat{N}_w^{\text{new}} = K; \\ \frac{\omega_m}{\omega_w \left(1 - \frac{rm(1-f)}{fm\pi+r(1-f+\pi f(1-m))} \right)} - 1, & \text{otherwise.} \end{cases} \tag{S10}$$

We recall that the mutant growth rate in the new habitat, s_{new} , is not affected by the different dispersal schemes. This holds because in our following analysis we do not assume density regulation in those patches.

S2 Approximation of the establishment probability

We compute the survival probability of a single mutant starting either in 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-population. It is denoted by φ_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) and is based on the theory of multi-type branching processes. For a detailed explanation of the theory we refer to the Supplementary Information of Tomasini and Peischl (2018).

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 mutant resides. It is given as (see also equation (5) in the main text)

$$M = \begin{array}{cc} & \begin{array}{c} \text{old patch} \\ \text{new patch} \end{array} \\ \begin{array}{c} \text{old patch} \\ \text{new patch} \end{array} & \left(\begin{array}{cc} (1 - m_m^{\text{old} \rightarrow \text{new}})(1 + s_{\text{old}}) & m_m^{\text{old} \rightarrow \text{new}}(1 + s_{\text{new}}) \\ m_m^{\text{new} \rightarrow \text{old}}(1 + s_{\text{old}}) & (1 - m_m^{\text{new} \rightarrow \text{old}})(1 + s_{\text{new}}) \end{array} \right), \quad (\text{S11}) \end{array}$$

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

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

$$\varphi_i = \frac{2(\rho - 1)}{B} v_i + O(\varepsilon), \quad (\text{S12})$$

with

$$B = \sum_{i=1}^2 u_i \sum_{j=1}^2 v_j M_{ij} + \rho(1 - \rho) \sum_{j=1}^2 u_j v_j^2. \quad (\text{S13})$$

Computing the largest eigenvalue

We start by approximating the largest eigenvalue of M denoted by ρ . It is given by (see *Mathematica* notebook)

$$\rho = \frac{1}{2} \left(2 + s_{\text{old}} + s_{\text{new}} - m - m_m^{\text{old} \rightarrow \text{new}} s_{\text{old}} - m_m^{\text{new} \rightarrow \text{old}} s_{\text{new}} + \sqrt{4(m-1)(1+s_{\text{old}})(1+s_{\text{new}}) + (2+s_{\text{old}}+s_{\text{new}}-m-m_m^{\text{old} \rightarrow \text{new}} s_{\text{old}}-m_m^{\text{new} \rightarrow \text{old}} s_{\text{new}})^2} \right) \quad (\text{S14})$$

In order to make 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 ε . We write $s_{\text{old}} = \varepsilon$, $s_{\text{new}} = \varepsilon\xi$ and $m = \varepsilon\mu$. Assuming that ε is small enough, i.e. effectively a weak selection assumption in old-habitat patches, we can neglect higher orders of ε and find

$$\begin{aligned}\rho &= 1 + \frac{1}{2}\varepsilon \left(1 + \xi - \mu + \sqrt{(\xi - 1 + \mu_m^{\text{old} \rightarrow \text{new}})^2 + 2(1 - \xi + \mu_m^{\text{old} \rightarrow \text{new}})\mu_m^{\text{new} \rightarrow \text{old}} + (\mu_m^{\text{new} \rightarrow \text{old}})^2} \right) \\ &= 1 + \frac{1}{2}\varepsilon \left(1 + \xi - \mu + \sqrt{\frac{\gamma}{1 - f_{\text{old}} + \pi_m f_{\text{old}}}} \right),\end{aligned}\tag{S15}$$

where γ is the rescaled version of the constant C in the main text (equation (8)), i.e.

$$\gamma = (1 - f_{\text{old}})(\xi - 1 + \mu)^2 + \pi_m f_{\text{old}}(\xi - 1 - \mu)^2.\tag{S16}$$

For $\varepsilon \rightarrow 0$ we find that $\rho \rightarrow 1$. It therefore remains to show that the branching process is slightly super-critical. We find that $\rho > 1$ and real if

$$1 + \xi - \mu > 0.\tag{S17}$$

This translates to the growth rates $s_{\text{old}} + s_{\text{new}}$ being larger than the dispersal rate m .

Computing the establishment probability

For the solution of equation (S12) it remains to compute the normalized eigenvectors. Their precise form is of not much insight. We therefore omit stating them explicitly (see the *Mathematica* notebook for the explicit expressions). Solving equation (S12) to the first order of ε we then find

$$\begin{aligned}\varphi_{\text{old}} &= \varepsilon + \frac{\varepsilon(1 - \xi)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}}} + \frac{\varepsilon(\mu_m^{\text{new} \rightarrow \text{old}} - \mu_m^{\text{old} \rightarrow \text{new}} + 2\mu_m^{\text{old} \rightarrow \text{new}}\xi)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}}}, \\ \varphi_{\text{new}} &= \varepsilon\xi + \frac{\varepsilon\xi(\xi - 1)}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}}} + \frac{\varepsilon(\xi\mu_m^{\text{old} \rightarrow \text{new}} - \xi\mu_m^{\text{new} \rightarrow \text{old}} + 2\mu_m^{\text{new} \rightarrow \text{old}})}{\sqrt{\frac{\gamma}{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}}}.\end{aligned}\tag{S18}$$

Transforming back to the original variables and replacing γ by the constant C from the main text (equation (8)), we obtain

$$\begin{aligned}\varphi_{\text{old}} &= s_{\text{old}} + \frac{(1 - f_{\text{old}} + \pi_m f_{\text{old}})s_{\text{old}}(s_{\text{old}} - s_{\text{new}})}{\sqrt{C}} + \\ &\quad m \frac{(\pi_m f_{\text{old}}s_{\text{old}} - (1 - f_{\text{old}})s_{\text{old}} + 2(1 - f_{\text{old}})s_{\text{new}})}{\sqrt{C}}, \\ \varphi_{\text{new}} &= s_{\text{new}} + \frac{(1 - f_{\text{old}} + \pi_m f_{\text{old}})s_{\text{new}}(s_{\text{new}} - s_{\text{old}})}{\sqrt{C}} \\ &\quad + m \frac{(s_{\text{new}}(1 - f_{\text{old}}) - s_{\text{new}}\pi_m f_{\text{old}} + 2s_{\text{old}}\pi_m f_{\text{old}})}{\sqrt{C}}.\end{aligned}\tag{S19}$$

Slightly re-ordering the terms, this gives the establishment probability of a single mutant individual, equation (7) in the main text:

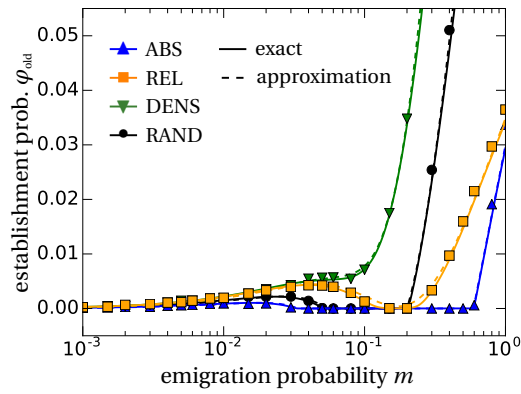
$$\begin{aligned}
\varphi_{\text{old}} &\approx s_{\text{old}} + s_{\text{old}} \frac{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}{\sqrt{C}} (s_{\text{old}} - s_{\text{new}}) \\
&\quad + \frac{m}{\sqrt{C}} (s_{\text{new}}(1 - f_{\text{old}}) + s_{\text{old}}\pi_m f_{\text{old}} - (s_{\text{old}} - s_{\text{new}})(1 - f_{\text{old}})) , \\
\varphi_{\text{new}} &\approx \underbrace{s_{\text{new}}}_{\text{(1) local growth parameter}} + \underbrace{s_{\text{new}} \frac{(1 - f_{\text{old}} + \pi_m f_{\text{old}})}{\sqrt{C}} (s_{\text{new}} - s_{\text{old}})}_{\text{(2) effect of the heterogeneous environment}} \\
&\quad + \underbrace{\frac{m}{\sqrt{C}} (s_{\text{new}}(1 - f_{\text{old}}) + s_{\text{old}}\pi_m f_{\text{old}} - (s_{\text{new}} - s_{\text{old}})\pi_m f_{\text{old}})}_{\text{(3) effect of dispersal: new patches + old patches - loss to the other patch type}} .
\end{aligned} \tag{S20}$$

S2.1 Disentangling the contributions to the establishment probability

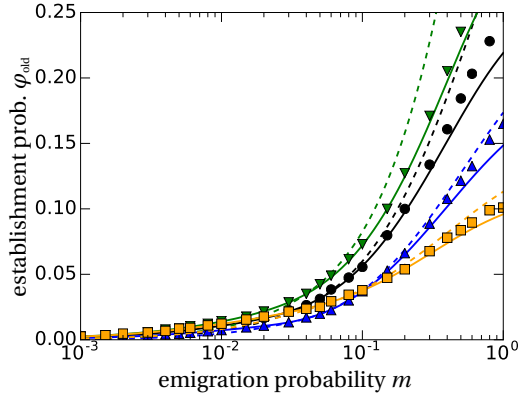
We now proceed explaining the three regions of the establishment probability from Figure 2(a) in the main text. These were defined by: (i) an initial increase of the establishment probability at low dispersal rates m ; (ii) a local maximum with a subsequent decrease of the establishment probability;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

For clarity, we re-plot Figures 2(a,c) in Figure S1(a,b), respectively. Using equation (S20) we are able to identify the dominant term for each of the three regions, see also Figure S1(c,d).

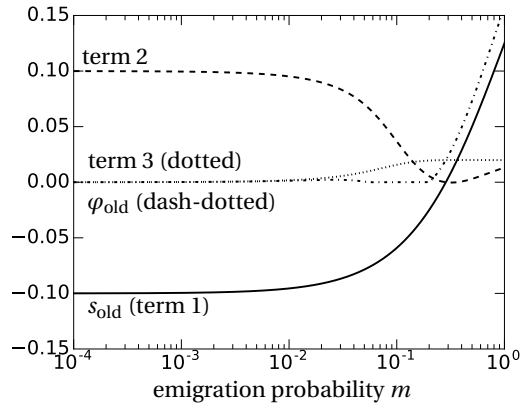
Region (i) is explained by the positive effect of dispersal. Mutants disperse from old- to new-habitat patches where they are advantageous when compared to the wild-type. This effect is mediated through the third term of the establishment probability in eq. (S20). While this term increases with increasing emigration rate m , the second term in eq. (S20) decreases, cf. Figure S1. The intuition is that habitat differences become less important under stronger population mixing – recall that the dispersal rate m appears in the constant C in the denominator. This alone would explain the decreasing curve of the second term. Additionally though, the local growth rate in old-habitat patches, s_{old} , is linked to the population demography which changes for varying m . With larger dispersal rates, more individuals leave the densely populated old habitats. This results in alleviated competition pressure for the remaining individuals, thus increasing the local growth rate s_{old} . This decreases the difference of growth rates $s_{\text{old}} - s_{\text{new}}$. Therefore, the local maximum can be explained by the decreasing environmental influence and the increasing dispersal effect, the second and the third term in eq. (S20), respectively. Hence, region (ii), beginning with the local maximum, is dominated by the decreasing effect of the environment on the establishment probability. Finally, in region (iii) dispersal is so large that the population homogenizes. This culminates in even less competitive pressure in old-habitat patches. Eventually, this yields a positive growth rate s_{old} (first term in eq. (S20)). Therefore, this region is driven by the local growth rate in old habitats.



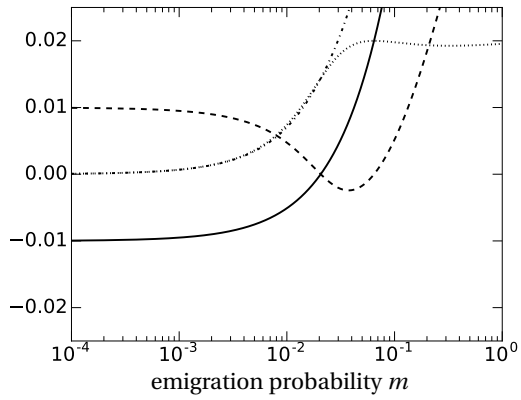
(a) $\omega_m = 9$ (large fecundity difference)



(b) $\omega_m = 9.9$ (small fecundity difference)



(c) $\omega_m = 9$ (large fecundity difference)



(d) $\omega_m = 9.9$ (small fecundity difference)

Figure S1: **Contribution of the different terms in eq. (S20) to the establishment probability φ_{old} .** Subfigures (a,b) are the same as Figures 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. (S20) separately ($\pi_m = \pi_w = 1$). Term 1, the local growth rate (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.

S2.2 Low fecundity values of the mutant in the old habitat

We set the fecundity parameter of the mutant in the old habitat to $\omega_m = 6.5$. For these large fecundity differences, we see that region (iii) disappears since the mutant is, even under relaxed competition in old habitats, not able to successfully establish a mutant population, cf. Figure S2.

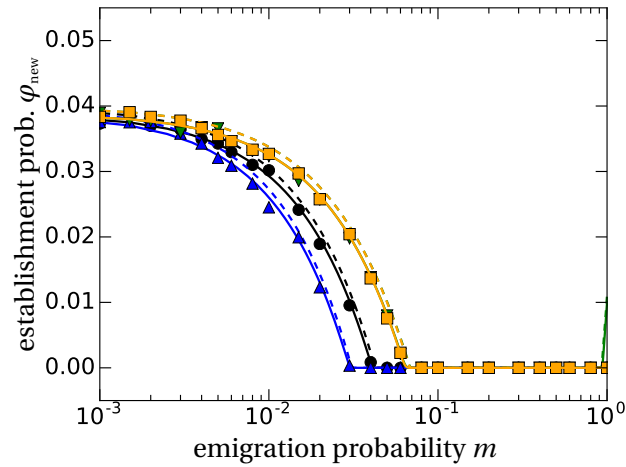


Figure S2: **Disappearance of region (iii) for large fecundity differences in the old habitat.** If the mutant fecundity in old-habitat patches is too low, here $\omega_m = 6.5$, the effect of relaxed competition is not strong enough to have an impact on the establishment probability for high dispersal rates. The establishment probability stays at zero.

S3 Habitat of origin of the adaptive mutation

We investigate the habitat type of the origin of the adaptive mutations for low fecundity values of the mutant in the old habitat. We see that the contribution of new-habitat mutants can indeed exceed the number of successful mutant lineages arising from old-habitat patches. In the subsequent figure, besides the default parameters as stated in Table 1 in the main text, we chose $\omega_m = 5$ and $\theta = 10/(MK)$. The plot corresponding to Figure 4 in the main text then looks as follows:

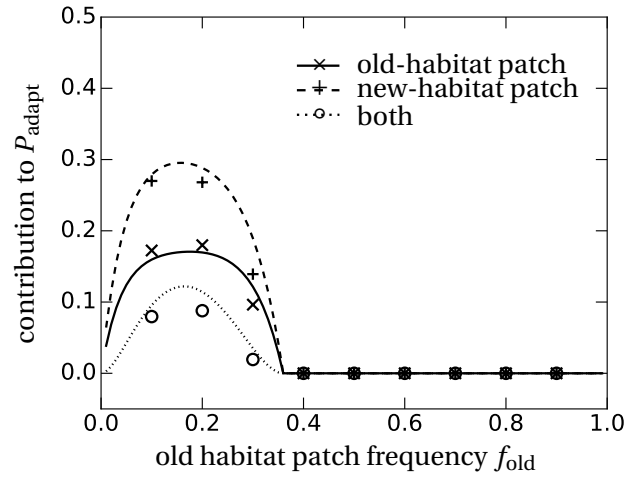


Figure S3: **Habitat type of the origin for strong fecundity differences in the old habitat ($\omega_m = 5$).**

S4 Establishment probability when varying the frequency of old-habitat patches

We plot the establishment probability of a single mutant individual, either starting in an old- or in a new-habitat patch, when varying the frequency of old-habitat patches. Apart from the default parameters as given in Table 1 in the main text, we have set the dispersal probability to $m = 0.5$ and the fecundity of the mutant in the old habitat to $\omega_m = 9.9$. As visible in Figure S4 below, for high frequencies of old-habitat patches the establishment probability becomes very small, if not 0. This supports the explanation that homogenizing the population reduces the impact of standing genetic variation on the probability of evolutionary rescue, see Figure 6(b) in the main text.

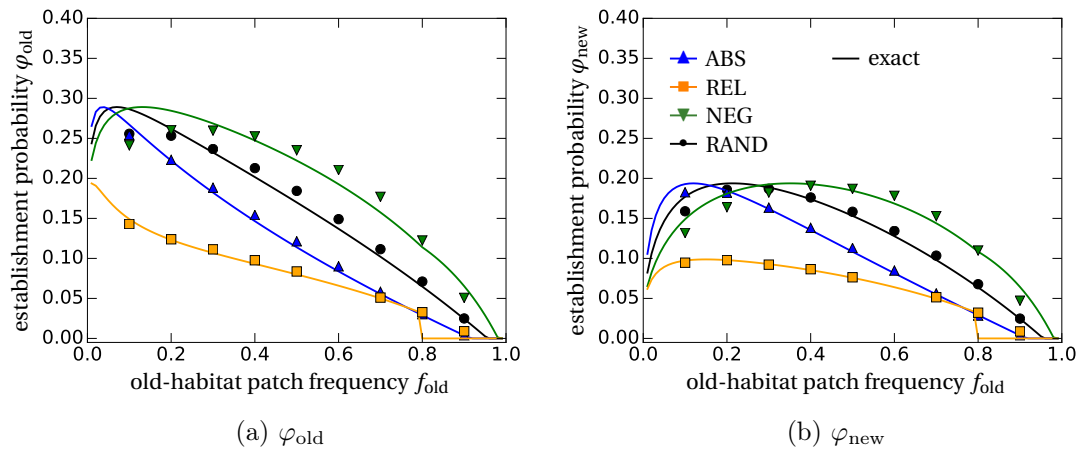


Figure S4: **Establishment probability when varying the old-habitat patch frequency.**

S5 Establishment probability in a model without demography

Here, we consider a variation of our original model. The dispersal process and 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 declining wild-type population. 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. For simplicity, we assume that the fecundity values are given as

$$\omega_w^{\text{old}} = \omega_m^{\text{new}} \quad \text{and} \quad \omega_w^{\text{new}} = \omega_m^{\text{old}}. \quad (\text{S21})$$

This means that the local growth rate s_{old} in equation (S10) takes the form for $\widehat{N}_w^{\text{new}} = K$. Additionally, we now also need to adjust the local growth rate s_{new} . It can be computed by solving

$$1 + s_{\text{new}} = K \frac{\omega_m^{\text{new}}}{\omega_w^{\text{new}} \widehat{N}_w^{\text{new}}}, \quad (\text{S22})$$

which with help of equation (S7) yields

$$s_{\text{new}} = \frac{\omega_m^{\text{new}}}{\omega_w^{\text{new}} \left(1 + \frac{m f_{\text{old}} (1 - \pi_w)}{1 - f_{\text{old}} + \pi_w f_{\text{old}}} \right)}. \quad (\text{S23})$$

Plugging this in the approximation of the establishment probability from equation (S20) we find the curves in Figure S5.

We see that, as highlighted in the main text, region (iii) of the establishment probability disappears in these type of models except for the relative habitat choice dispersal scheme (orange). The reason for the disappearance of the region is that relaxed competition only plays a subordinate role for the symmetric dispersal schemes (absolute habitat choice (blue), random dispersal (black) and negative density-dependent (green)). In other words, these dispersal schemes maintain the local frequencies of the mutant at the same level as before the dispersal step and by that do not change the population dynamics. In contrast, the relative habitat choice scheme strongly increases the frequency of mutants in new-habitat patches and by that increases the establishment probability. It is worth mentioning though, that this is not a effect of relaxed competition but rather a biased dispersal of the mutant into the habitat where it is favored.

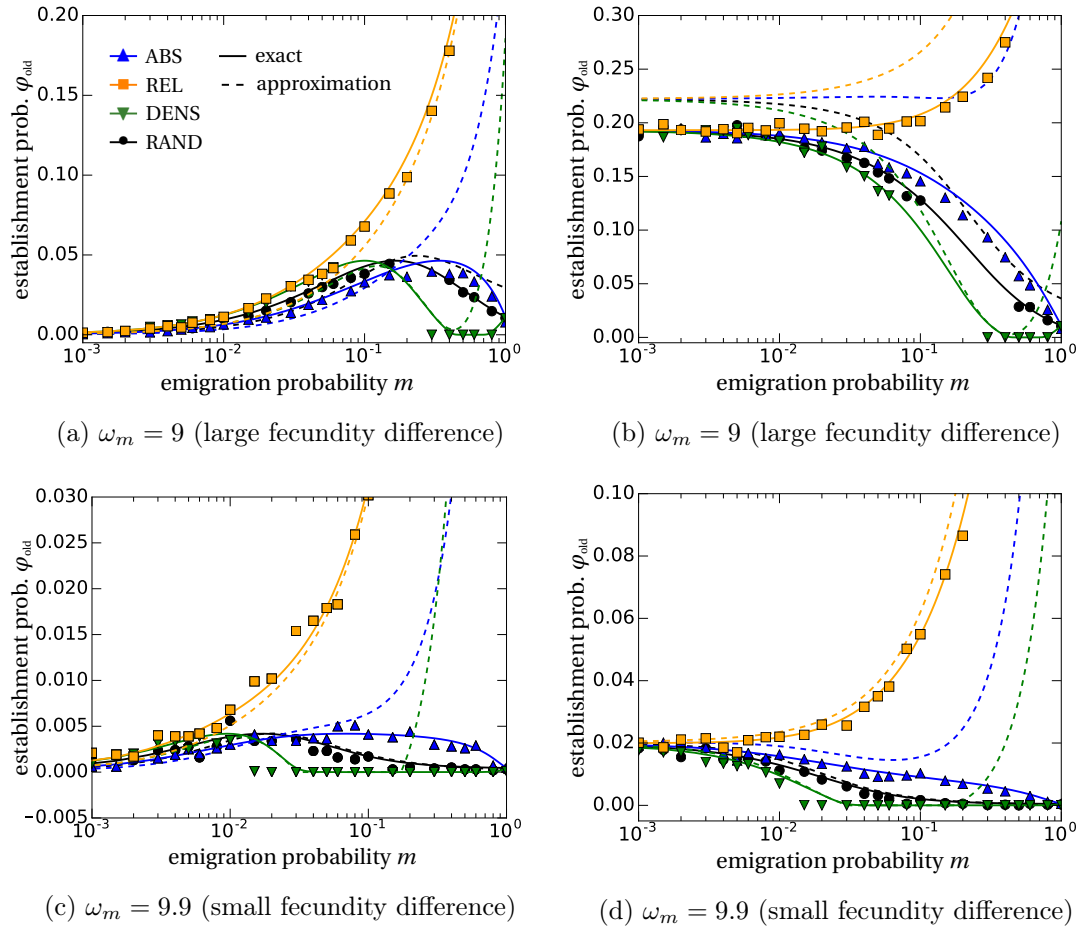


Figure S5: **Establishment probability when populations in both habitats are at carrying capacity.** We plot the establishment probability for a single mutant either initially in an old-habitat patch (a,c) or in a new-habitat patch (b,d). The numerical solution (solid lines) still approximates the simulated data reasonably well. The analytical approximation (dashed lines) however deviates strongly from the data due to large growth rates ($s_{\text{new}} \approx 0.2$) so that the conditions for the approximation to hold are violated. In this case, in eq. (S20) higher order corrections would need to be taken into account. Missing data points are due to too large computation times. All data points are averages from 10^4 independent runs. Note the varying y-axes scales.

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 $\omega_m = 9$ we have plotted the relative contribution of the each natal habitat type to the probability of evolutionary rescue, Figure S6. We do not see large differences between the four dispersal schemes. Solely, for relative habitat choice we observe a slightly higher contribution of old-habitat patches to the rescue process. A possible explanation are the high population sizes in old-habitat patches before reproduction and mutation and the increased tendency for potentially produced mutants to disperse to new-habitat patches.

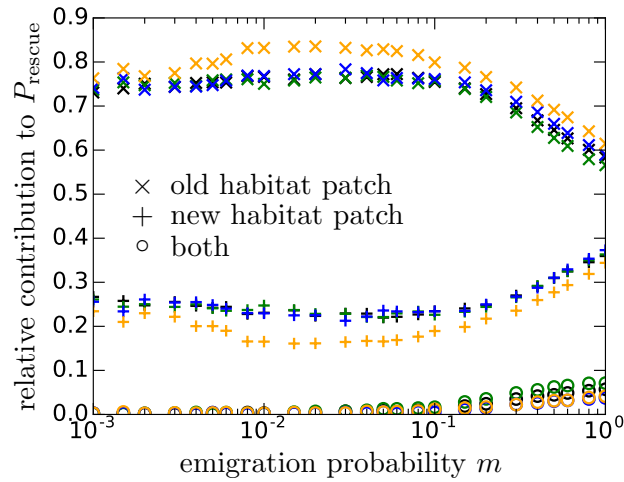


Figure S6: **Habitat type of the origin of the rescue mutant dependent on the dispersal scheme.** Varying the emigration probability m we plot the relative contributions of each habitat type to the probability of evolutionary rescue. The color-coding is the same as in the main text: blue for absolute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

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