

When does gene flow facilitate evolutionary rescue? –

Supplemental Material

Matteo Tomasini^{*,†,‡} and Stephan Peischl^{*, ‡,1}

^{*}Interfaculty Bioinformatics Unit, University of Bern, 3012 Bern, Switzerland

[†]Computational and Molecular Population Genetics Laboratory, Institute of Ecology and Evolution, University of Bern, 3012 Bern, Switzerland

[‡]Swiss Institute for Bioinformatics, 1015 Lausanne, Switzerland

¹Corresponding author: stephan.peischl@bioinformatics.unibe.ch

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Appendix A: probability of rescue

We calculate the probability of rescue from beneficial mutations in a two-deme model in which habitats deteriorate over time. A mutation has selective coefficient $z > 0$ in a deteriorated region and coefficient $s < 0$ in a non-deteriorated region. We distinguish three different temporal phases: (phase 0) at $t < t_0$, both demes are not deteriorated; (phase 1) at t_0 we deteriorate deme 1; (phase 2) at time $t = t_0 + \theta$ we deteriorated deme 2.

To evaluate equations (5)–(8) (at end of phase 0 and during phase 1) we use the probabilities of establishment of mutations experiencing divergent selection in a two-deme model [Tomasini and Peischl, 2018]:

$$p^{(1)} = z(1 + \sigma - \Delta) - s\mu_{12} , \quad (\text{S1})$$

$$p^{(2)} = z\mu_{21} - s(1 - \sigma + \Delta) , \quad (\text{S2})$$

where

$$\sigma = \frac{z + s}{\lambda} , \quad \mu_{ij} = \frac{2m_{ij}}{\lambda} , \quad \Delta = \frac{\mu_{12} - \mu_{21}}{2} \quad (\text{S3})$$

and $\lambda = \sqrt{(m_{12} + m_{21})^2 + (z + s)^2 - 2(m_{12} - m_{21})(z + s)}$. Note that these equations do not account for the temporal in-homogeneity in selection coefficients at time $t = \theta$, which should be a good approximation if $\theta \gg 0$.

24 **Probability of rescue for *de novo* mutations**

25 In order to calculate formula (7) we need to solve equations (9) and (10). During phase 1 ($t < t_0 + \theta$),
 26 $N_2(t) = \kappa$. Solving (9) yields

$$N_1(t) = [(m_{12} + r)\kappa_1 + (e^{(m_{12}+r)t} - 1)m_{21}\kappa_2] \frac{e^{-(m_{12}+r)t}}{m_{12} + r} \quad (\text{S4})$$

27 During phase 2, when both demes are deteriorated, $N_1(t)$ and $N_2(t)$ follow equation (10) with
 28 corresponding initial conditions. The solutions $N_1(t)$ and $N_2(t)$ can be obtained straightforwardly
 29 for $t > t_0 + \theta$ but are very long and it does not bear any use to write them explicitly here. Plugging
 30 everything into (7) and (8), we obtain a straightforward analytical formula for the probability of
 31 rescue from *de novo* mutations during phase 1. All calculations can be easily carried out with
 32 software such as *Mathematica*.

33 **Appendix B: when does gene flow facilitate rescue?**

34 We want to know for which set of parameters intermediate migration increases the chance for
 35 evolutionary rescue, as compared to no migration. This is equivalent to the set of parameters for
 36 which

$$\left. \frac{\partial P_{\text{res}}}{\partial m} \right|_{m=0} > 0. \quad (\text{S5})$$

37 We first re-scale all parameters with respect to z ($s = z\xi$, $m_{ij} = z\chi_{ij}$) and then linearize (2) with
 38 respect to z . Switching back to the original variables, we find that condition (S5) is satisfied when

$$\frac{s}{z} < \tilde{\beta}\tilde{\zeta} \frac{e^{r\theta}r(f_0 + u\theta)}{e^{r\theta}(f_0r + u) - u}. \quad (\text{S6})$$

39 If we set $f_0 = 0$ (hence no standing genetic variation), we find that the condition reads

$$\frac{s}{z} < \tilde{\beta}\tilde{\zeta} \frac{e^{r\theta}r\theta}{e^{r\theta} - 1}. \quad (\text{S7})$$

40 Because the function $xe^x/(e^x - 1) \approx x$ if x is large enough (approximately for $x \gtrsim 4$), we obtain
 41 equation (16).

42 **Appendix C: the role of density regulation and local growth**
 43 **rates**

44 Figure 5 shows examples for the probability of evolutionary rescue when the density of the non-
 45 deteriorated deme is regulated following a Beverton-Holt model of logistic growth:

$$N_2(t+1) = N_2(t) \frac{\rho}{(1 + (\rho - 1)N_{\text{tot}}(t)/\kappa)}. \quad (\text{S8})$$

46 We find that the probability of rescue in this case can deviate strongly from the regime of
 47 instantaneous growth, where the population in the non-deteriorated deme always remains at car-
 48 rying capacity. The latter should be a good approximation to the former if the growth rate ρ is
 49 large enough relatively to the migration rate.

50 Here, we explore this intuition quantitatively. We calculate the loss of individuals from deme
 51 2 during one generation, neglecting individuals coming in from deme 1. This works in particular
 52 for t large, since deme 1 is almost depleted after a few generations and we can ignore the influx of
 53 immigrants from deme 1 into deme 2. Hence, we solve

$$N_2(t+1) = N_2(t) \left(1 - \frac{m}{2}\right) \frac{\rho}{1 + (\rho - 1)N_2(t)/\kappa}, \quad (\text{S9})$$

54 with initial condition $N_2(t=0) = \kappa$. We find

$$N_2(t) = \frac{\kappa(2 - 2\rho + m\rho)}{2 - 2\rho + 2^t m\rho \left(\frac{1}{2\rho - m\rho}\right)^t}. \quad (\text{S10})$$

55 Now, gene flow should be detrimental to evolutionary rescue if the interplay of m (causing loss of
 56 individuals from deme 2) and ρ (causing gain of individuals in deme 2) causes deme 2 to eventually
 57 go extinct. We find that $N_2(t) \rightarrow 0$ if $t \rightarrow \infty$ if

$$\rho \left(1 - \frac{m}{2}\right) \leq 1. \quad (\text{S11})$$

58 In particular, condition (S11) is very accurate for large m , as rescue for that range of migration
 59 is ensured exclusively by mutations arising during phase 2 (see figure 1). Figure 5 shows that this
 60 rule of thumb remains accurate over the whole range of m when other kind of density regulation
 61 are at play.

62 Appendix D: figures

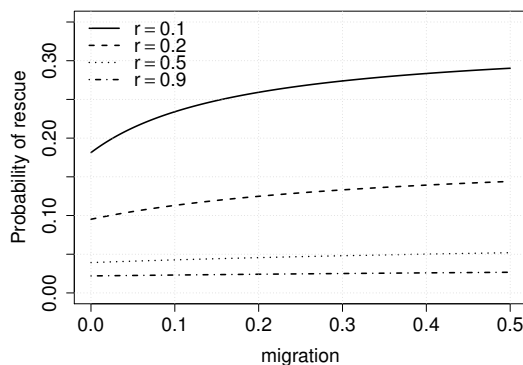


Figure S1: **Symmetric model:** contribution of mutations arising during phase 2 to evolutionary rescue for different r , $z = 0.02$, $s = 1$, $\theta = 200$. All curves increase with m .

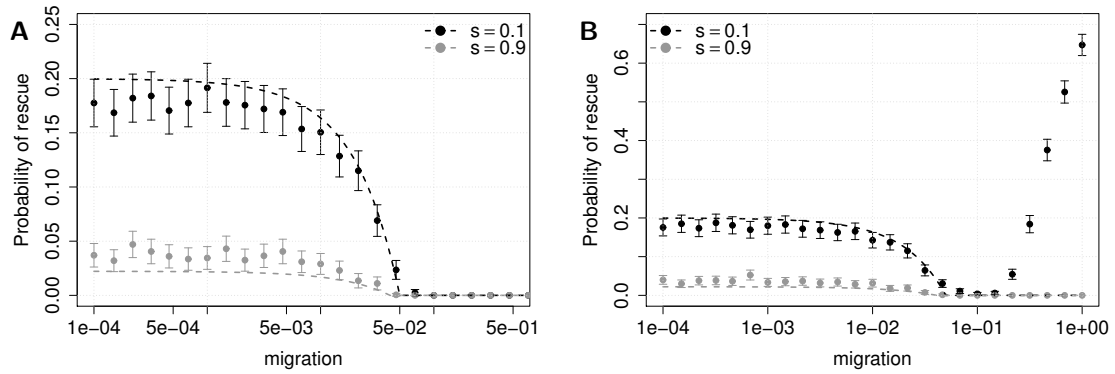


Figure S2: **Standing genetic variation:** contribution to evolutionary rescue by standing genetic variation in the symmetric model, simulations with analytical expectations (see equation (5)). Parameters are $z = 0.02$, $\theta = 500$, $r = 0.3$. Black points show $s = 0.1$, gray points $s = 0.9$. (A) After density up-regulation, mutants are not replaced according to mutant frequencies preceding the regulation. (B) Mutants are replaced according to mutant frequencies. We can notice the effect of relaxed competition for mildly deleterious mutations (see main text).

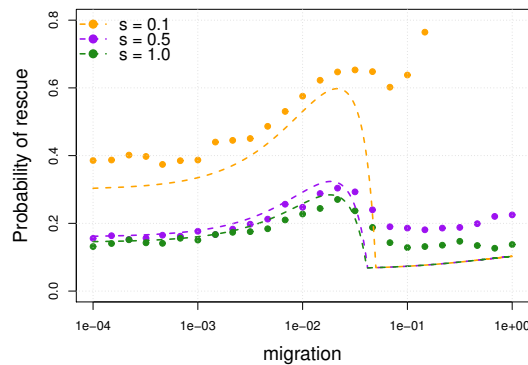


Figure S3: **Symmetric model:** evolutionary rescue as a function of m for different selective coefficients s (cost in the unperturbed deme). Comparison between theoretical calculations and simulations, for $z = 0.02$, $\theta = 500$ and $r = 0.3$, $s = 0.1$ (orange), $s = 0.5$ (purple), $s = 1.0$ (green). We observe that our model is unable to correctly account for mildly deleterious mutations (see orange line).

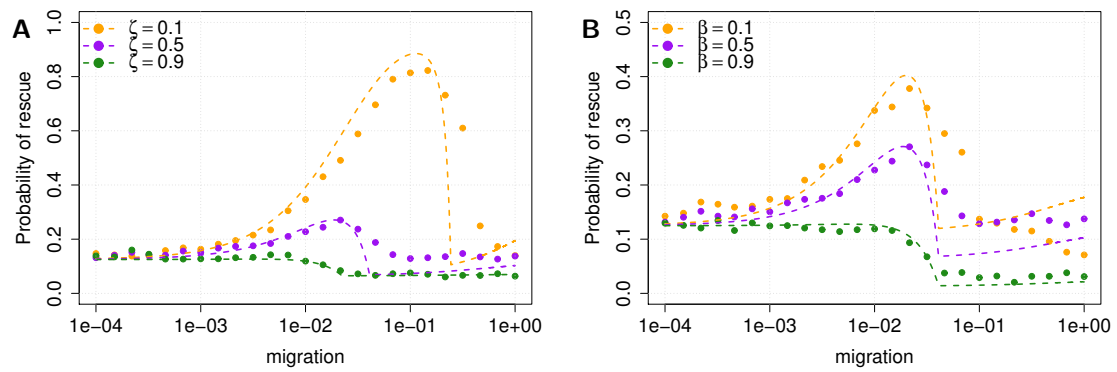


Figure S4: **Asymmetric models for lethal mutations:** comparison between theoretical calculations and simulations, for $z = 0.02$, $\theta = 500$, $r = 0.3$, $s = 1.0$. (A) Asymmetric migration rates. In orange, $\zeta = 0.1$, in purple $\zeta = 0.5$, in green $\zeta = 0.9$. (B) Asymmetric carrying capacities. In orange, $\beta = 0.1$, in purple $\beta = 0.5$, in green $\beta = 0.9$.

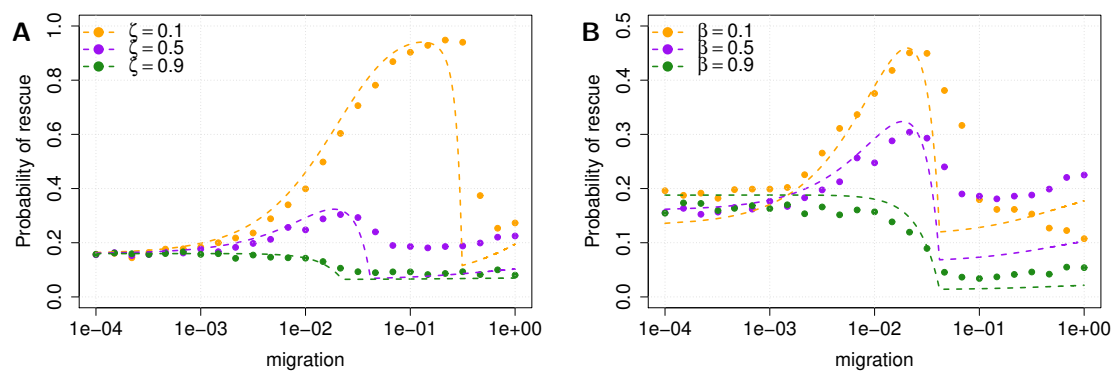


Figure S5: **Asymmetric models with standing genetic variation:** comparison between theoretical calculations and simulations, for $z = 0.02$, $\theta = 500$, $r = 0.3$, $s = 0.5$. (A) Asymmetric migration rates. In orange, $\zeta = 0.1$, in purple $\zeta = 0.5$, in green $\zeta = 0.9$. (B) Asymmetric carrying capacities. In orange, $\beta = 0.1$, in purple $\beta = 0.5$, in green $\beta = 0.9$. We can see that at $m = 0$ expectations are different than simulations (see Appendix A).

63 References

- 64 M. Tomasini and S. Peischl. Establishment of locally adapted mutations under divergent selection.
 65 *Genetics*, 209(3):885–895, 2018. doi: 10.1534/genetics.118.301104.