The conflict between adaptation and dispersal for maintaining biodiversity in changing environments

Patrick L. Thompson and Emanuel A. Fronhofer

Supplementary materials
Tables

Table S1: Important model parameters, definitions and tested values. Standard values are underlined. A sensitivity analysis including all other values is shown in Figures S1 and S2.

| Parameter	Values	Meaning
d	0, 1e-05, 5e-05, 1e-04, 5e-04, 1e-03, 5e-03, 1e-02, 5e-02, 1e-01, 2e-01, 5e-01	**dispersal rate**: probability of emigrating for individuals of a given patch
m	0, 0.005, 0.01, 0.03, 0.1	**mutation rate**: probability of a random change (Gaussian with σ_{mut}) of a local adaptation allele
λ_0	1.5, 2, 4	**fecundity**: maximal mean number of offspring
μ	0.05, 0.1, 0.2	**dispersal cost**: probability of surviving a dispersal event
σ_{niche}	0.5, 1, 2	**niche width**: width of the local adaptation function (Gaussian)
σ_{mut}	0.02, 0.04, 0.06, 0.08	**mutation width**: width of the mutation function (Gaussian)
$\alpha_{j,j}$	0.001, 0.002, 0.004	**mean intraspecific competition coefficient**: intraspecific competition coefficients (i.e., the diagonal of the community matrix) are drawn from a log-normal distribution with mean $\alpha_{j,j}$ and variance 0.1
$\alpha_{j,k}$	0.0005, 0.001, 0.002	**mean interspecific competition coefficient**: intraspecific competition coefficients (i.e., off-diagonal elements in a symmetric community matrix) are drawn from a log-normal distribution with mean α_{ij} and variance 0.1
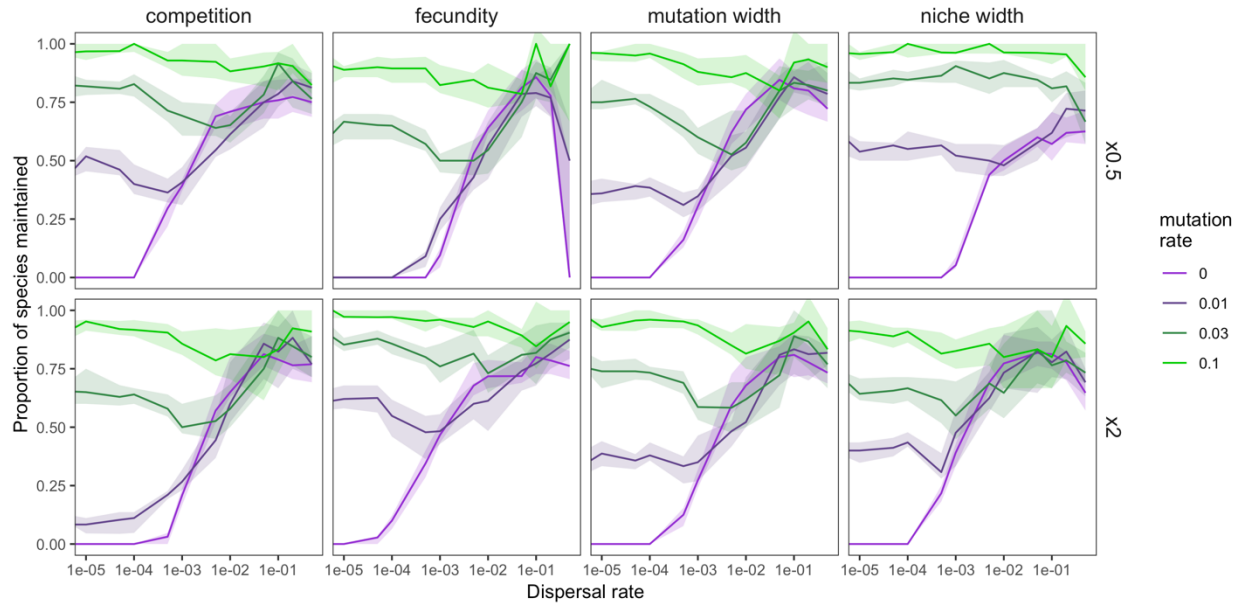
Figure S1. Sensitivity analysis showing the proportion of species maintained in analogue environments when fixed parameters are halved (top row) or doubled (bottom row). Each column shows the results when a single parameter is varied, keeping all of the others standard as outlined in Table S1. These are, from left to right, competition, fecundity, mutation width, and niche width. One exception is that the reduction in fecundity is x0.75 (1.5 vs 2). The lines show the median value across 25 replicate simulations with standard parameter values (Table S1) and the bands show the interquartile range.
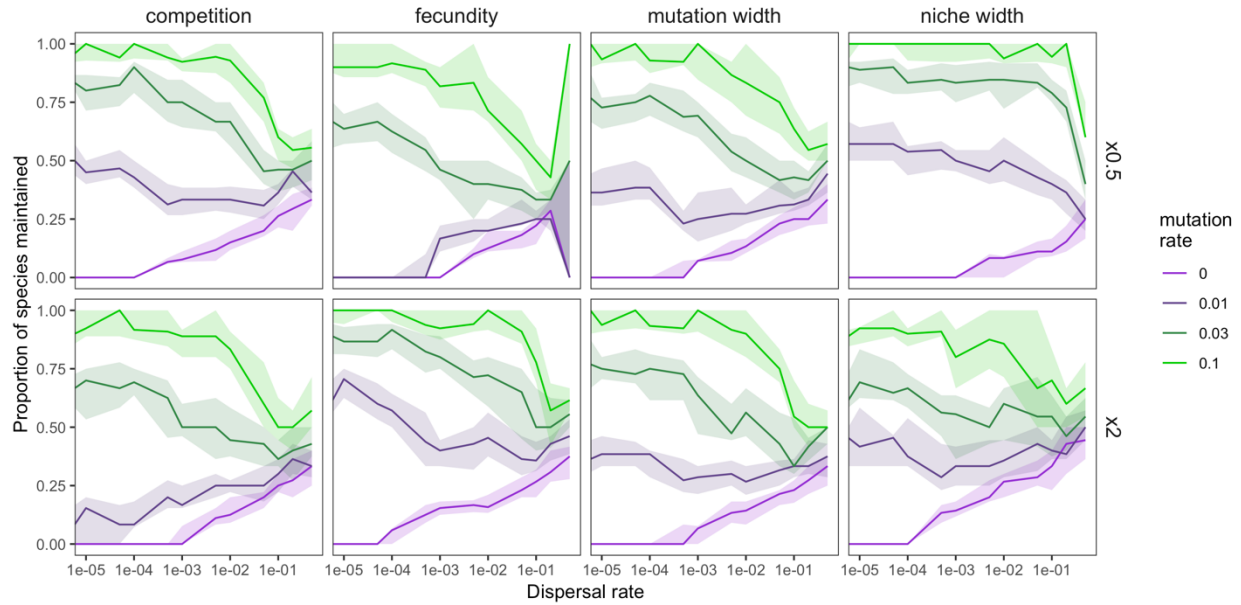
Figure S2. Sensitivity analysis showing the proportion of species maintained in non-analogue environments when fixed parameters are halved (top row) or doubled (bottom row). Each column shows the results when a single parameter is varied, keeping all of the others standard as outlined in Table S1. These are, from left to right, competition, fecundity, mutation width, and niche width. One exception is that the reduction in fecundity is x0.75 (1.5 vs 2). The lines show the median value across 25 replicate simulations with standard parameter values (Table S1) and the bands show the interquartile range.
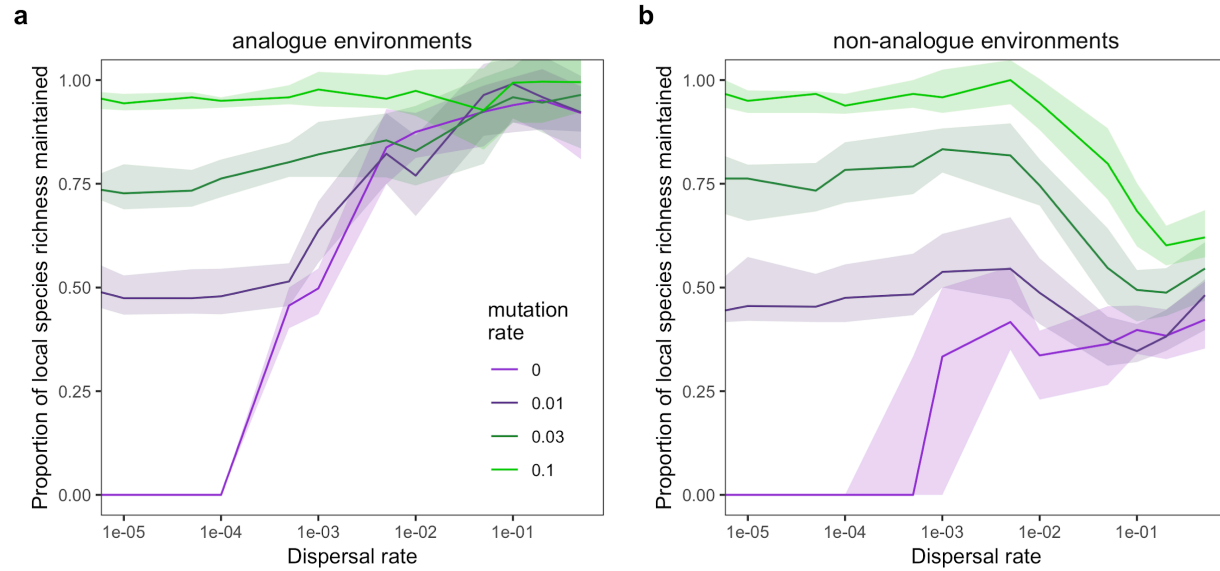
a

analogue environments

b

non-analogue environments

Figure S3. The proportion of species that are maintained in each patch (local scale richness) following environmental change depending on dispersal and mutation rates (colour). The proportion of species maintained was calculated as the number of species that were present in each patch (a - analogue or b - non-analogue) after environmental change, divided by the number of species that were present before. The lines show the median value across 50 replicate simulations with standard parameter values (Table S1) and the bands show the interquartile range.
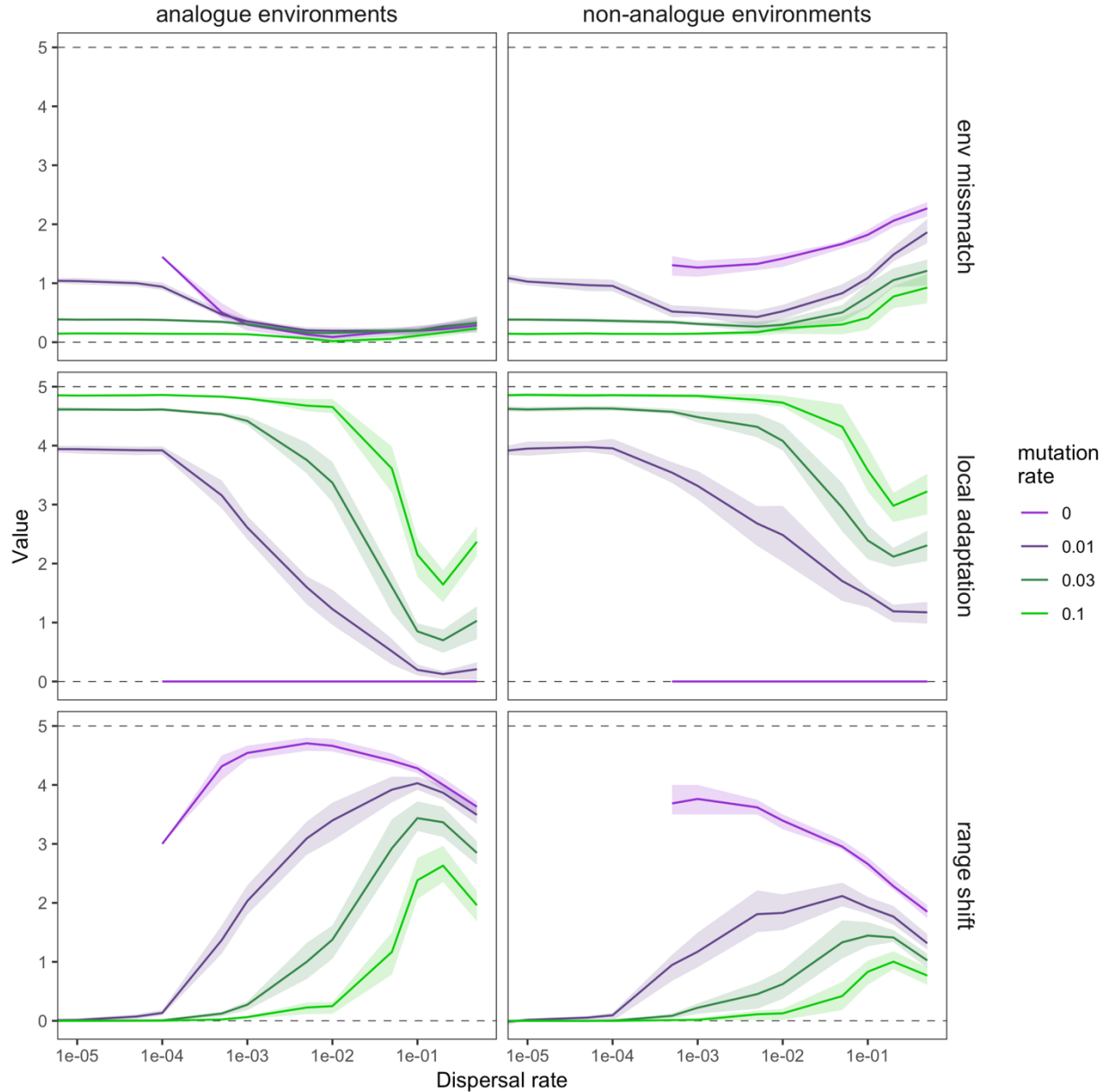
Figure S4. The degree of mismatch between individuals and their local environmental conditions at the end of the simulations (top row), the average magnitude of trait change that surviving lineages have undergone over the course of environmental change (middle row), and the magnitude of the range shift that surviving lineages have undergone (bottom row) depending on dispersal and mutation (colour) rates. We separate these results based on whether the final environmental conditions in each patch fall within the pre-environmental change range of conditions (analogue; left column) or not (non-analogue; right column). The lines show the median value across 50 replicate simulations with standard parameter values (Table S1) and the bands show the interquartile range.
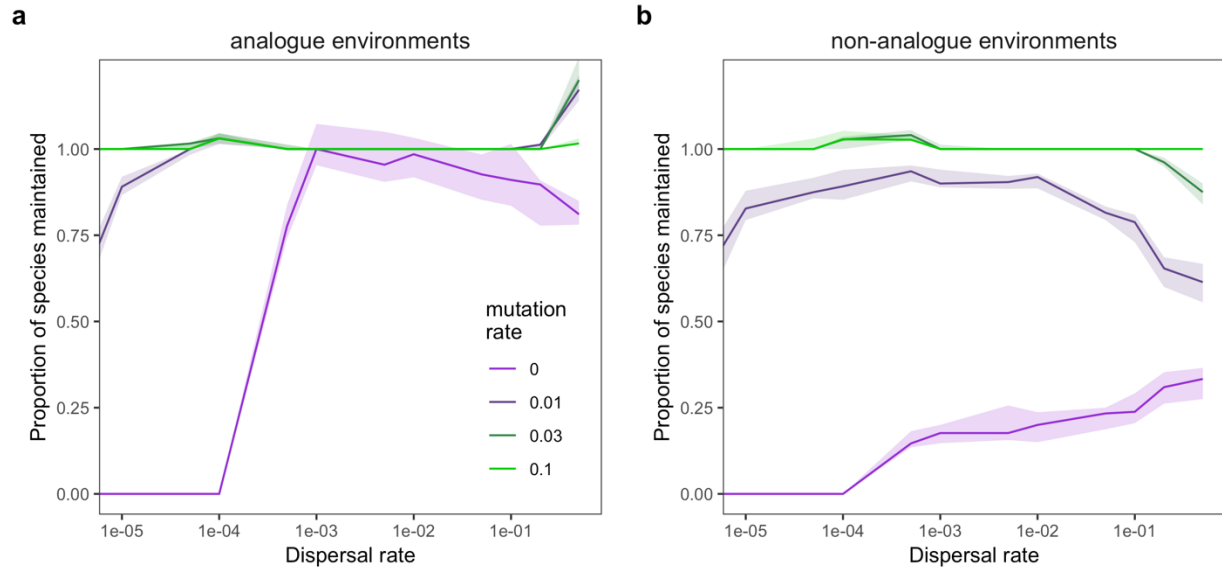
Figure S5. The proportion of species that are maintained following environmental change depending on dispersal and mutation rates (colour) when all interspecific competition $\alpha_{j,k}$ is set to 0. We separate these results based on whether the final environmental conditions in each patch fall within the pre-environmental change range of conditions (a, analogue) or not (b, non-analogue). The lines show the median value across 25 replicate simulations with standard parameter values (Table S1) and the bands show the interquartile range.
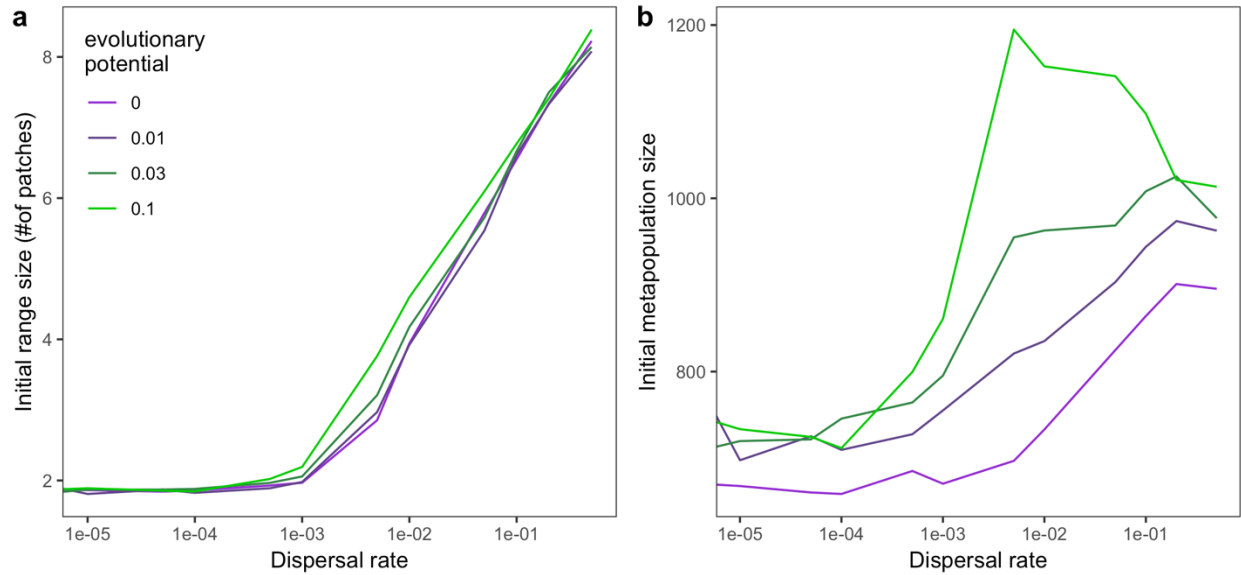
Figure S6. The average range size (a) and total metapopulation size (b) of species prior to environmental change, depending on dispersal and mutation (color) rates. Metapopulation size is the average number of individuals of each species across all patches. The lines show the median value across 50 replicate simulations with standard parameter values (Table S1).
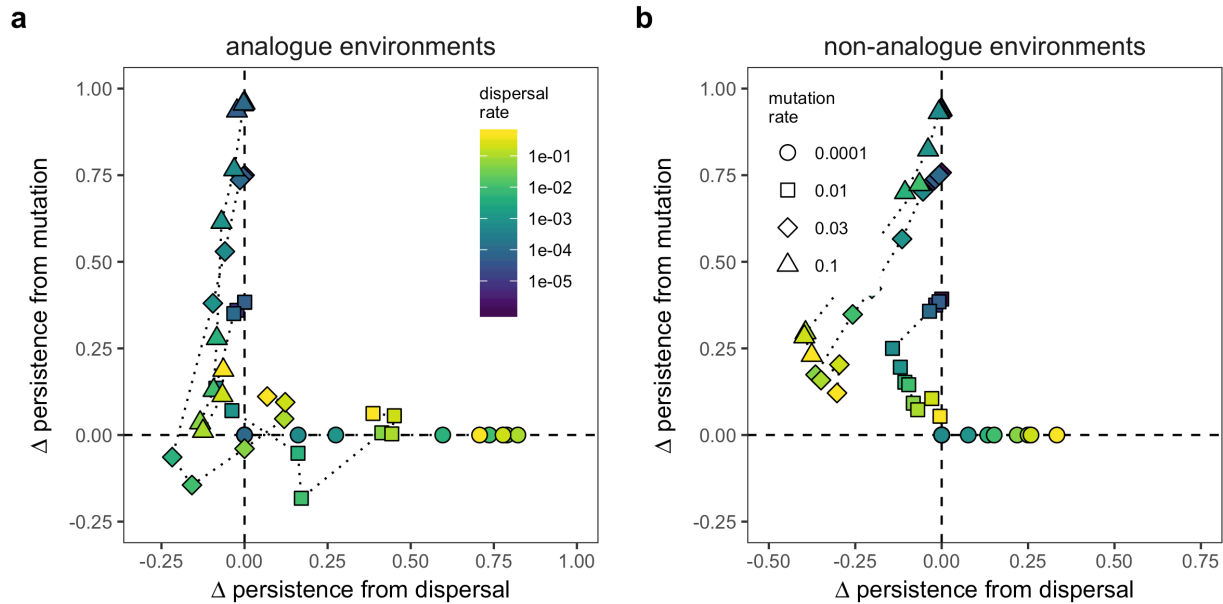
Figure S7. The proportion of species maintained in each combination of dispersal and mutation rates compared to if dispersal were 0 (x-axis) or if the mutation rate was 0.0001 (y-axis) in analogue (a) and non-analogue environments (b). This indicates the degree to which the combination of dispersal and mutation rates alters the persistence of species compared to if dispersal or mutations were to operate in isolation. Points that fall below zero on the x-axis indicate cases where dispersal reduces the number of species that could persist with that mutation rate in the absence of dispersal. The y-axis shows the same information but for mutation rates. The dispersal and mutation rates are shown by the colour and shape of the points, respectively. The dotted lines connect points with the same mutation rates in increasing dispersal rate. Median values across all 50 replicates with standard parameter values (Table S1) are shown.