Ecography

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Supplementary material

Appendix 1: Supplementary methods

Effect of including some locations that are unsuitable to some species.

In the main text p represents environments that are suitable to both species. Let the number of locations unsuitable either to one species, or both species be r. As a result, the total number of sites is now $p+r$. This makes little change to several of the results in the main text, in the absence of species interactions we should still expect to find $2p$ presences, in the absence of coexistence we should still find p presences and when coexistence is possible, we should still expect to find $p+q$ presences. As in the main text q represents the number of sites where coexistence is possible.

We have to be more careful when we consider the proportion of sites where we observe a given outcome, but our qualitative conclusions remain similar. The total number of presences that are possible in the absence of any constraints on species distributions is two times the number of sites $2(p+r)$. As result, the fraction of presences remaining given species interactions is:

$$\frac{p+q}{2(p+r)} \quad . \qquad \text{(S1)}$$

This still reaches a maximum when the two species coexist at all p sites that are suitable to both species. This maximum is now $\frac{p}{(p+r)}$. Equation S1 reaches a minimum when the number of sites supporting coexistence is 0 this minimum is now $\frac{p}{2(p+r)}$. Increasing the proportion of sites at which species coexist still decreases the importance of competition on species' distributions. However, the higher the proportion of sites that are unsuitable to one or both species (the larger r is relative to p) the less influence q will have on the total number of presences i.e. $2(p+r)$.

Equation 1 in the main text and Equation S1 here represent subtly different metrics to measure the effect of species interactions on species' distributions. As with ecological distance metrics, we suspect that there are several potential ways to quantify the effects of species interactions on species' distributions and that different metrics may be appropriate depending on nuances of the question being asked.

Rescaling

We start by noting the expression for the carrying capacity of each species ($K_i = m_i x + b_i$). By solving for $K_i = 0$ we find that the boundary of the fundamental niche of species i will be at $x = -b_i/m_i$. We can set $b_i = 0$ (eliminating one parameter) by measuring distances along x starting at the boundary of species 1's fundamental niche ($x = -b_1/m_1$). We can eliminate another parameter by setting m_1=0. To do this, we define the maximum carrying capacity of species 1 to be 1 and set our coordinate system so that $x = 1$ when we reach this point.

It is valuable to simplify Equations 4a and 4b further to ensure that all the locations suitable to both species are on the interval $0 < x < 1$. If the boundary of species 2's fundamental niche occurs outside this interval, all environments between 0 and 1 will be suitable to both species. If, on the other hand the boundary of species 2's fundamental niche is between 0 and 1, re-label species 1 as 2 and species 2 as species 1. Set the carrying capacity for the "new" species 1 to reach a maximum at the boundary of the "new" species 2's fundamental niche ($x = -b_2/m_2$) then repeat the re-scaling described in the previous paragraph.

Simulations presented in main text:

We manipulated species 2's response to the abiotic environment by simulating data using all combinations of 60 values for b_2 ranging from (-10 to 10) and 60 values for m_2 ranging from (-10 to 10). To calculate the influence of biotic interactions on species' distributions we summed the proportion of the environmental gradient that was occupied by species 1 and the portion occupied by species 2. When dispersal is present in our model, species' abundances can be very small, but they will never be 0. As a result, we deemed species to be present when their abundance was at least $1/20^{th}$ of the maximum carrying capacity for species 1 (0.05). We implemented simulations in R using the DeSolve package that employs a method of lines approximation of partial differential equations. In our case, for each species, we simulated a system of 4000 ordinary differential equations each representing site along the environmental gradient for 1000 time steps. To set the initial abundance of each species, we grouped sites into pairs (site 1 with 2, site 3 with 4 etc.), then chose the initial density of each pair of sites at random from an exponential distribution with a mean of 0.25. We paired sites to reduce the sensitivity of our conclusions to the number of sites we used to represent our environmental gradient. We assumed reflecting boundary conditions, but to reduce boundary effects, we simulated both species on a broad environmental gradient where half the abiotic environments were suitable for species 1 and half were too harsh (-1<x<1). To avoid convergence problems we assumed that the carrying capacity reached a minimum value that was small (0.001) rather than 0.

Robustness of simulations:

We tested if adding fine-scale environmental heterogeneity changed our conclusions. To do this we ran 800 additional simulations (10 m_2 values * 10 b_2 values * 2 values of α * 2 values of D_a* presence/absence of additional heterogeneity). We added periodic heterogeneity to the carrying capacity of species 2 using the equation:

$$K_2 = m_2 x + b_2 + 0.05\sin(100\pi x + z)$$

An example of the result is illustrated in Figure A1. The variable z randomized the starting position of the sin wave. This variable selected from a random uniform distribution ranging from $0 < z < \tau$, where $\tau = 2\pi$.

There was a strong correlation between the number of simulated presences with and without environmental heterogeneity ($R^2 > 0.99$), indicating that our conclusions are robust to the addition of a small amount of heterogeneity. We observed a similarly strong correlation whether we measured observed presences at a large grain size or a small grain size.

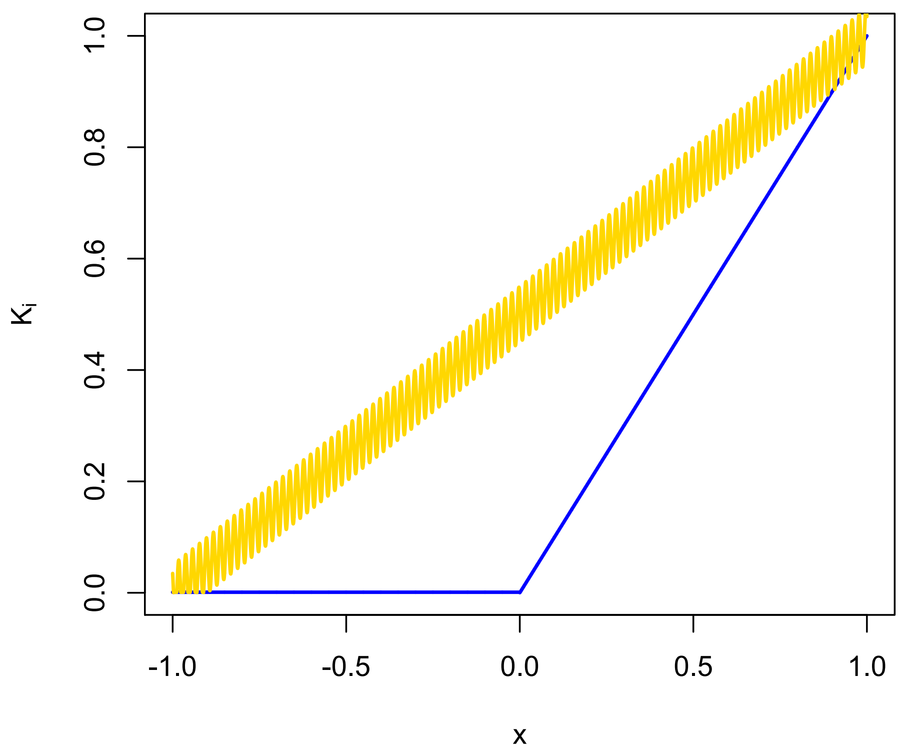

Figure A1 a plot of the K_1 and K_2 across a simulated environmental gradient showing the environmental heterogeneity in K_2.