Supplementary material
Appendix 1

1 - Generating geographical distributions

We develop our analysis of geographic distribution of interacting species A and B across a lattice landscape of “LxL” cells. Each cell admits one of the following states:

I. No species present.
II. Only species A present.
III. Only species B present.
IV. Both species are present simultaneously.

The cell is assumed to represent geographical unit in which individuals of species A and B interact.

In order to build co-occurrence maps, we proceed in two steps. First, we distribute species A with prevalence $\rho_A$ and then Species B with $\rho_B$.

Initially, all cells are in state (I).

Species A is located in the landscape by setting $\rho_A L^2$ cells into state (II). Those cells are selected following two approaches:

1. Randomly. The species is distributed randomly across whole available landscape.
2. With auto-correlation. The species is distributed as if constrained by localized factors that emulate patch-type distribution, namely:

   a. Species A is expected to cover randomly a circular region with radius “R” around center G. Cell G is placed randomly elsewhere in the landscape.

   b. “R” is lower than “L” so that the region covered by A is completely included into the landscape.

   c. The probability of placing species A at distance r from G, decays exponentially beyond r=R as:

   \[ P(r) = \exp(-\xi(r - R)) \]

   where \( \xi \) is a correlation decay parameter.

To achieve the auto-correlated distribution pattern we proceeded in two steps:

   a) We first mark cells around G as “state II”, following a profile

   \[ f(r) = \begin{cases} 
   1, & r < R \\
   P(r), & r \geq R 
   \end{cases} \]
Then we get the following distribution:

b) Since more than $N_A = \rho_A L^2$ cells were marked as being in 'state II', we counted the number of cells in 'state II' and chose randomly among them cells to mark back as 'state I' so as to get the required $N_A$ cells occupied by species A,
Once species A has been distributed across the landscape, Species B is located by randomly selecting $\rho_B L^2$ cells and change their states either from (I) to (III) or from (II) to (IV) until we satisfy equations 3-5 in the main text of the manuscript. As an example, the resulting distribution of species A and B with $\rho_A = 0.1$ and $\rho_B = 0.1$, for $I_{A\rightarrow B}^+=0.2$ and $I_{B\rightarrow A}^+=0.2$ has the following pattern

for the case of random distribution, and
for the case of auto-correlated distribution of species A with $R = 30$ and $\xi = 0.3$

Our simulations were performed on lattices of $L = 100$.

Appendix 2

2. Assessing overlaps across scales

Once the landscape has been populated by species A and B following the procedure described above, we measured changes in species co-occurrence across scales. We first fix a scale length $1 \leq l \leq L$, and fragment the landscape into blocks of $lxl$ cells.

Then, each block is labeled with two properties:

1. Actual state.
2. Sampled state

Each of them consists of one between (I-IV) states. They only differ on how we estimate whether they are or not on
state IV. In the case of “actual state”, the block is set to be in state IV only if at least one of their constitutive cells is in state IV. In the case of “sampled state”, the block is estimated to be in state IV if at least one of its cells is in state II and at least one of its cells is in state III.

Finally, for each scale "1" we estimate the “actual” and “sampled” co-occurrence as the ratio between the numbers of blocks found to be in state IV to the number of occupied (state II or III or IV) blocks. These results are shown in the outer plots in figure 2.

Appendix 3

3. Competitive Exclusion

In the case of extreme competitive interaction $I_{A\to B} = 1$ and $I_{B\to A} = 1$, co-occurrence is forbidden. However, species ranges can be interlaced. In order to explore how interlace impacts on co-occurrence across scales we produced full range of interlace as follows.

We first locate species A on $N_A = \rho_A L^2$ cells, with auto-correlation $\xi$ up to a radius $R$ around a center $G$, as explained above. Then, we focus on vacuum cells at distance $r > \mu_{excl} R$ from $G$, where $\mu_{excl}$ is the “exclusion factor”.
Finally, we randomly choose $N_B = \rho_B L^2$ cells among them to be marked as occupied by species B. The resulting distribution for the case of $\rho_A = 0.1$ and $\rho_B = 0.1$, for $I_{A \rightarrow B} = 1$ and $I_{B \rightarrow A} = 1$ (i.e., extremely repulsion), with $\xi = 0.3$ and $R = 30$ is shown in the following

\[ \mu_{\text{excl}} = 0.6 \quad \mu_{\text{excl}} = 1 \quad \mu_{\text{excl}} = 1.5 \]

Notice that for $\mu_{\text{excl}} < 1$ species B (grey) invades the region occupied by species A (black) towards $G$, and for $\mu_{\text{excl}} > 1$ species B is allowed to occupy cells beyond distance $R$ from $G$. 
Appendix 4

4. MATLAB code to estimate co-occurrences with different interactions

function land=CreateLand(L,rhoA,rhoB,Ia,Ib,xi,R,Excl)

%% Developed by Alejandro Rozenfeld (2012)
%% Email: alejandro.rozenfeld@gmail.com
%% This function creates a square matrix for the landscape of cells.
%% Then, cells are labeled with states I to IV according to species occupancy
%% Co-occurrence of cells is assessed according to eq. 3-5 of manuscript Araújo & Rozenfeld (in review).

%% Parameters: L: <side of matrix>
%% rhoA: <Prevalence of A>
%% rhoB: <Prevalence of B>
%% Ia: <Interaction strength A --> B>
%% Ib: <Interaction strength %A --> B>
%% xi: <correlation strength > (this is for the case of self-correlated distribution)
%% R: <Expected Radius of species range> (also for the self-correlated case)
land=zeros(L,L); %all cells marked as vacuum (State I)
A_curr=0;
A_Target=rhoA*L^2;

if xi>0,
    G=[1/2,1/3]; % Center of species A, in the case of self-correlated distribution
    for x=1:L,
        for y=1:L,
            r=sqrt((x-G(1))^2+(y-G(2))^2); %distance to G
            if rand<=exp(-xi*(r-R))
                land(x,y)=2; %occupied by A - step I
                A_curr=A_curr+1;
            end
        end
    end
end
ixa=find(land==2);
ixVacuum=find(land==1);

A_toTarget=A_Target-A_curr;
% occupy or release as required - step II
if A_toTarget < 0, % If too much A, release A cells randomly
    for i=A_toTarget:-1,  
        iRand=floor(rand*length(ixA))+1; %randomly selected A cell
        land(ixA(iRand))=1; %released
        A_curr=A_curr-1;
        ixVacuum(end+1)=ixa(iRand); %add released cell to the list of vacuum cells
    end
else % If too few A, occupy randomly as many vacuum cells as required
    for i=1:A_toTarget,
        iRand=floor(rand*length(ixVacuum))+1; %random cell selected
        land(ixVacuum(iRand))=2; %occupy
        A_curr=A_curr+1;
        ixa(end+1)=ixVacuum(iRand); %updating tables
ixVacuum=[ixVacuum(1:iRand-1)'
ixVacuum(iRand+1:end)']; % updating tables
end
end

% Now is the turn for species B
B_curr=0;
B_Target=rhoB*L^2;

% Calculate the amount of co-occurrence cells according to interactions (eq. 3 - 5)
rhoAB_null=rhoA*rhoB;

if Ia>=0,
    if Ib>=0,  % (+/+)
rhoAB=rhoA*rhoB*(1-max(Pa,Pb))+min(rhoA,rhoB)*max(Pa,Pb);
    else      % (+/-)
        Ib=-Ib;
        rhoAB=(rhoA*rhoB+(min(rhoA,rhoB)-rhoA*rhoB)*Ia)*(1-Ib);
    end
else
    if Ib>=0,  % (-/+)
        Ia=-Ia;
    else
        % (-/-)
    end
end

\[ \rho_{AB} = (\rho_A \rho_B + (\min(\rho_A, \rho_B) - \rho_A \rho_B) I_b) (1 - I_a); \]

else
\[
\begin{align*}
I_a &= -I_a; \\
I_b &= -I_b; \\
\rho_{AB} &= \rho_A \rho_B (1 - \max(I_a, I_b));
\end{align*}
\]

end

end

\[ \text{AB\_Target} = \rho_{AB} L^2; \]

% reshuffle list of A cells
for i = 1:A\_curr,
\[
\begin{align*}
iRand &= \text{floor}(\text{rand} \times A\_curr) + 1; \\
aux &= ixA(i); \\
ixA(i) &= ixA(iRand); \\
ixA(iRand) &= aux;
\end{align*}
\]
end

\[ \%---------- \]

for i = 1:AB\_Target,
\[
\text{land}(ixA(i)) = 4; \quad \% \text{cell marked as co-occurrence AB}
\]

B\_curr = B\_curr + 1;
end
B_toTarget=B_Target-B_curr;

vacuum=length(ixVacuum);
if vacuum && B_toTarget, %need more B and there are
still vacuum cells
%reshuffle vacuum cell list
    for i=1:vacuum,
        iRand=floor(rand*vacuum)+1;
        aux=ixVacuum(i);
        ixVacuum(i)=ixVacuum(iRand);
        ixVacuum(iRand)=aux;
    end
%--------

    for i=1:min(B_toTarget,vacuum),
        land(ixVacuum(i))=3; % mark cell as
occupied by B
        B_curr=B_curr+1;
    end
end
end
Appendix 5

5. Supporting figures

Figure A1. Dispersion in scale dependence across biotic interaction space. Increasing gradients of red indicate increased dispersion in estimates of scale dependence (i.e., increased SD in estimates of the area between red and black lines in figure 2), while increasing gradients of blue indicate decreased dispersion in estimates of scale dependence: a) random distributions with $\rho=0.1$; b) random distributions with $\rho=0.3$; c) spatially autocorrelated distributions with $\rho=0.1$; d) spatially correlated distributions with $\rho=0.3$. Underlying estimates of scale
dependence were obtained by averaging across 1000 model runs.