Supporting online material for

The Geographical Scaling of Biotic Interactions

by

Miguel B. Araújo and Alejandro Rozenfeld

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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 ρ_A and then Species B with ρ_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:

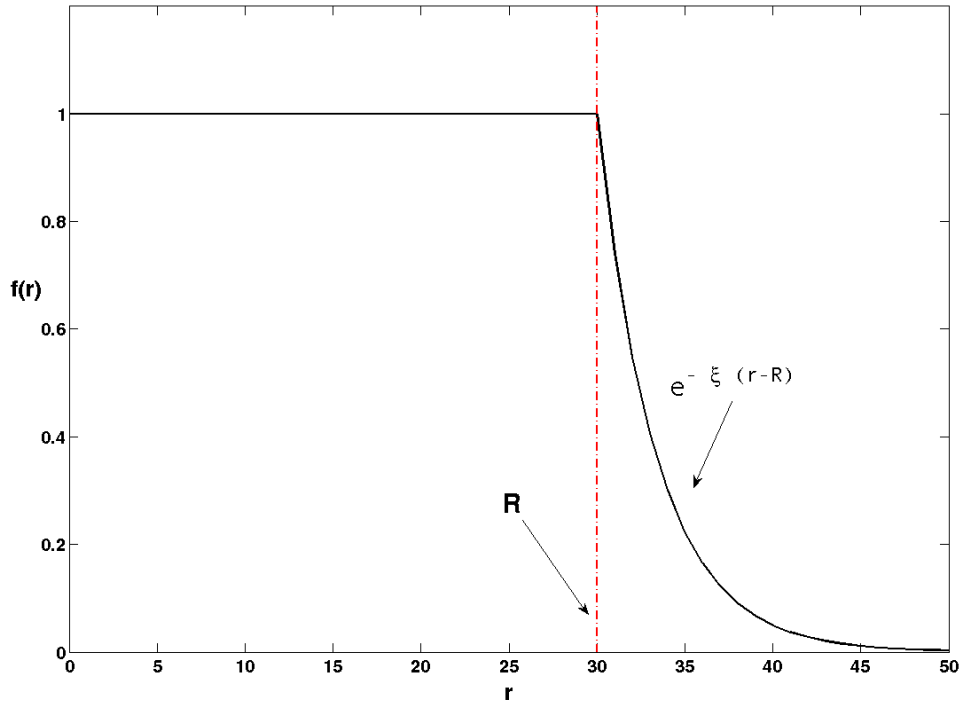
   a. Species A is expected to cover randomly a circular region with radius "R" around center G. Cell G is placed randomly elsewhere in the landscape.
   b. "R" is lower than "L" so that the region covered by A is completely included into the landscape.
   c. The probability of placing species A at distance r from G, decays exponentially beyond r=R as:

$$P(r) = exp(-\xi(r - R))$$

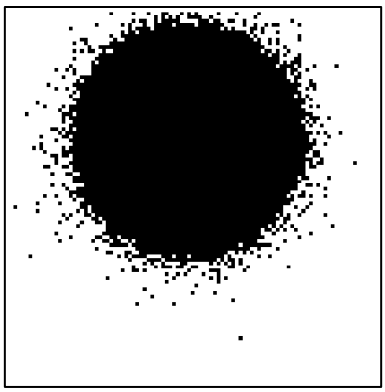
where ξ is a correlation decay parameter.

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 $f(r) = \begin{cases} 1, & r < R \\ P(r), & r \geq R \end{cases}$

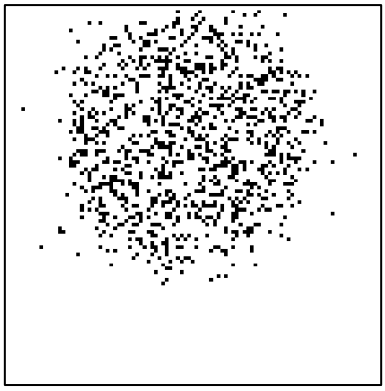


Then we get the following distribution:

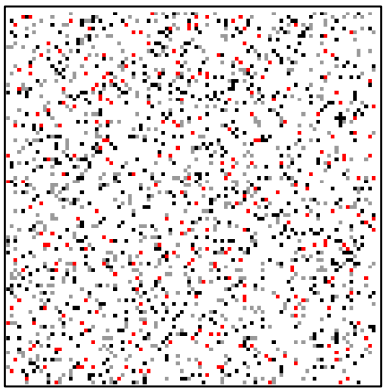


b) Since more than $N_A = \rho_A L^2$ cells were marked as being in 'state II', we counted the number of cells in 'state II' and chose randomly among them cells to mark back

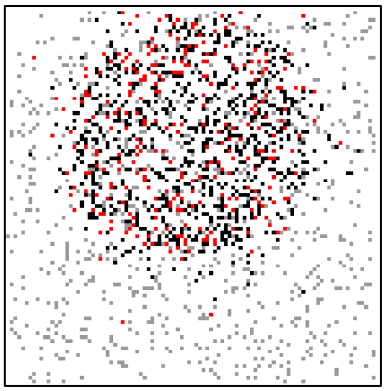
as ‘state I’ so as to get the required N_A cells occupied by species A,



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 $I^{+}_{A\to B}$=0.2 and $I^{+}_{B\to A}$=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 $L = 100$.

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.

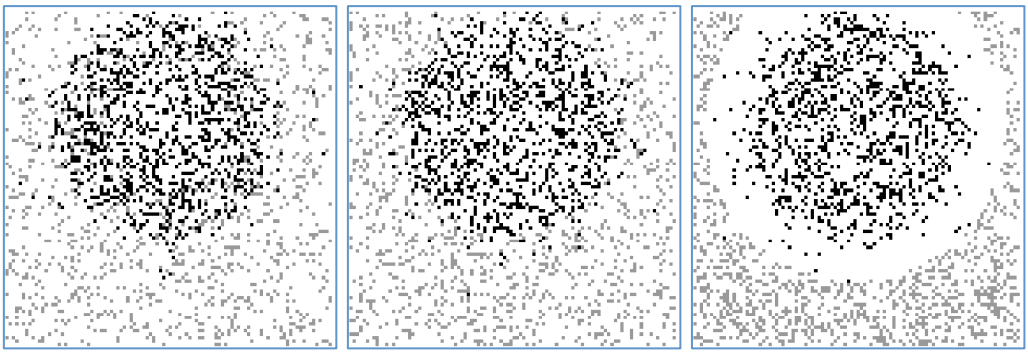
Finally, for each scale "l" we estimate the "actual" and "sampled" co-occurrence as the ratio between the numbers of blocks found to be in state IV to the number of occupied (state II or III or IV) blocks. These results are shown in the outer plots in figure 2.

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 ξ 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 μ_{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 $I^{-}_{A\to B}$=1 and $I^{-}_{B\to A}$=1 (i.e., extremely repulsion), with $\xi = 0.3$ and $R = 30$ is shown in the following



$\mu_{excl} = 0.6$ $\mu_{excl} = 1$

$\mu_{excl} = 1.5$

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

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)
```

```
%              Excl: < Exclusion Factor>         (for the
case of self-%                   correlated and exclusive
ranges)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%

    land=ones(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]*L;   % 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
            ixA=[ixA(1:iRand-1)' ixA(iRand+1:end)'];
%released cell removed from A 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;
```

```
            rhoAB=(rhoA*rhoB+(min(rhoA,rhoB)-
rhoA*rhoB)*Ib)*(1-Ia);
        else        %(-/-)
            Ia=-Ia;
            Ib=-Ib;
            rhoAB=rhoA*rhoB*(1-max(Ia,Ib));
        end
    end

    AB_Target=rhoAB*L^2;



    %reshufle list of A cells
    for i=1:A_curr,
        iRand=floor(rand*A_curr)+1;
        aux=ixA(i);
        ixA(i)=ixA(iRand);
        ixA(iRand)=aux;
    end
    %--------



    for i=1:AB_Target,
        land(ixA(i))=4;  % 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
     %reshufle 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
```

5. Supporting figures

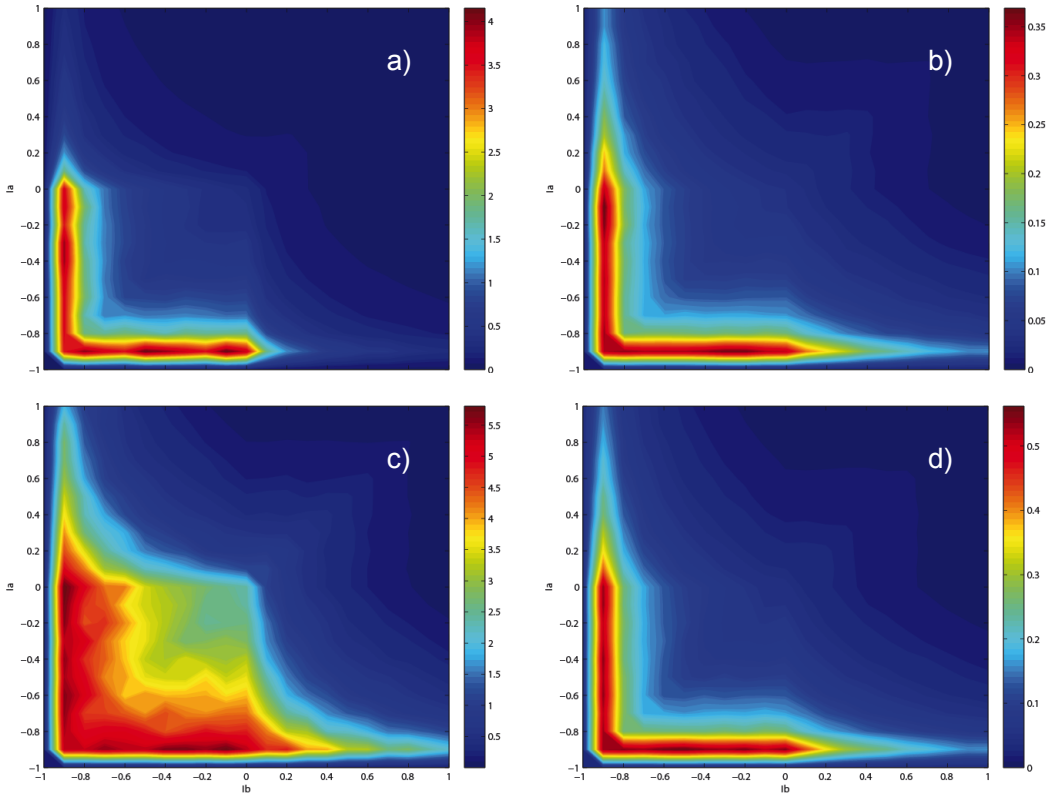


Figure S1. **Dispersion in scale dependence across biotic interaction space.** Increasing gradients of red indicate increased dispersion in estimates of scale dependence (i.e., increased SD in estimates of the area between red and black lines in figure 2), while increasing gradients of blue indicate decreased dispersion in estimates of scale dependence: a) random distributions with ρ=0.1; b) random distributions with ρ=0.3; c) spatially autocorrelated distributions with ρ=0.1; d) spatially correlated distributions with ρ=0.3. Underlying estimates of scale dependence were obtained by averaging across 1000 model runs.