

A continuous model of MERA — intra- and interspecific resource distributions

Jade, June 8

In this generalized model, the resource amount allocated to an individual can be any continuous positive value smaller than the resource constraint, in contrast to being limited to discrete levels $(0, \theta, 2\theta)$ as in the original model. The continuous intra- and interspecific resource distributions that maximize resource allocation entropy can be derived. Here I will not assert any demographic outcome of the resource distributions but leave it as an open question for future exploration.

1 A generalized expression of W_{total}

In this model I relax the assumption on the number of resource units an individual could get (originally limited to 0, θ or 2θ) so that it can be any positive value smaller than R . Under the updated assumption, W_{total} is still:

$$W_{total} = W_{grouping} \times W_{across} \times \prod_i^{S_0} W_{within,i}^{D_{r,i}} \quad (1)$$

But the expressions for $W_{grouping}$, W_{across} and $W_{within,i}$ have changed into:

$$W_{grouping} = \prod_i^{S_0} \frac{N_i!}{1!1!\dots} = \prod_i^{S_0} N_i! = C \quad (2)$$

$$W_{across} = \frac{R_0!}{\prod_i^{S_0} R_i!} \quad (3)$$

$$W_{within,i} = \frac{R_i!}{\prod_j^{N_i} r_{i,j}!} \quad (4)$$

R_i is the total resource amount allocated to species i and $r_{i,j}$ is the amount allocated to individual j of the species.

Notice that under the updated assumption, the definition of “demographic group” becomes trivial since the amount allocated to an individual can be any value, which means that there are as many demographic groups as the number of individuals (one individual in each demographic group) and $W_{grouping}$ is a constant ($C = \prod_i^{S_0} N_i!$) given the current species abundances regardless of the resource allocation pattern. It is the maximization of W_{across} and W_{within} that determines the R_i and $r_{i,j}$ distributions.

Log-transforming Eq. 1 we get:

$$\begin{aligned} \log W_{total} &= \log W_{grouping} + \log W_{across} + \sum_i^{S_0} D_{r,i} \log W_{within,i} \\ &= \log C + \log W_{across} + \sum_i^{S_0} D_{r,i} \log W_{within,i} \end{aligned} \quad (5)$$

Log-transforming Eqs. 3-4 we get:

$$\begin{aligned}\log W_{across} &= R_0 \log R_0 - \sum_i^{S_0} R_i \log R_i \\ &= -R_0 \sum_i^{S_0} P_i \log P_i\end{aligned}\tag{6}$$

$$\begin{aligned}\log W_{within,i} &= R_i \log R_i - \sum_j^{N_i} r_j \log r_j \\ &= -R_i \sum_j^{N_i} p_{ij} \log p_{ij}\end{aligned}\tag{7}$$

Where $P_i = R_i/R_0$ is the relative resource abundance of species i in the community and $p_{ij} = r_j/R_i$ is the relative resource abundance of individual j in species i . For the current model, there are no other constraints than the normalization rule: $\sum_i^{S_0} P_i = 1$ and $\sum_j^{N_i} p_{ij} = 1$ for all i .

In the following section, W_{total} will be maximized subject to the normalization constraints in a step-wise manner: 1) maximize the $W_{within,i}$ given species level measures, based on which 2) maximize W_{total} given that $W_{within,i}$ s are maximized.

2 Step-wise maximization of W_{total}

With the normalization constraint as the only constraint, maximizing $W_{within,i}$ yields a uniform distribution for p_{ij} :

$$p_{ij} = \frac{1}{N_i}\tag{8}$$

Substituting Eq. 8 into Eq. 7 we get

$$\log W_{within,i} = R_i \log N_i \quad (9)$$

(Please notice that there is no constraint on $\sum_i r_j p_{ij}$ since $p_{ij} = r_j/R_i$ is NOT the probability for a individual j to have r_i resource units, but the probability for a resource unit to be allocated to individual j .)

Substituting Eqs. 6 and 9 into Eq. 5 we get

$$\begin{aligned} \log W_{total} &= \log C - R_0 \sum_i^{S_0} P_i \log P_i \\ &\quad + \sum_i^{S_0} D_{r,i} R_i \log N_i \\ &= \log C - R_0 \sum_i^{S_0} P_i (\log P_i - D_{r,i} \log N_i) \end{aligned} \quad (10)$$

Next I define an objective function S as:

$$\begin{aligned} S(W, \lambda) &= \log W_{total} - \lambda(1 - \sum_i^{S_0} P_i) \\ &= \log C - R_0 \sum_i^{S_0} P_i (\log P_i - D_{r,i} \log N_i) - \lambda(1 - \sum_i^{S_0} P_i) \end{aligned} \quad (11)$$

Equaling the derivative of S over P_i to zero gives:

$$\frac{\partial S(W, \lambda)}{\partial P_i} = \log C - R_0 \sum_i^{S_0} P_i (\log P_i - D_{r,i} \log N_i) - \lambda(1 - \sum_i^{S_0} P_i) = 0 \quad (12)$$

From which we can solve for the expression of P_i :

$$P_i = e^{\frac{\lambda}{R_0} - 1} N_i^{D_{r,i}} \quad (13)$$

Since $e^{\frac{\lambda}{R_0}-1}$ is a constant for all species, the species relative resource abundance P_i is solely determined by its abundance N_i and individual distinguishability $D_{r,i}$. More specifically, if $D_{r,i} = 0$ for all species, cross species resource distribution will be uniform $P_i = 1/S_0$ regardless of the initial abundance, leading to permanent coexistence for all species. On the other hand, $D_{r,i} = 1$ for all species leads to maximum density dependence for resource allocation, or the more abundant species (higher N_i) is allocated proportionally more resource than less abundant species, reducing the chance of coexistence. Scenarios with one or more species having $0 < D_{r,i} < 1$ generates patterns in between these extremes. This result is consistent with those obtained from the discrete MERA model, even without specific assumptions on the demographic outcome of resource allocation.

3 Future extensions

Here I have only used the normalization rule as constraints to derive p_{ij} and P_i . Although it is not yet apparent to me how to do so, more constraints could potentially be applied, e.g. on the variation of p_{ij} (can be related to $D_{r,i}$), in which case the within-species resource allocation will not be uniform any more.

With P_i and p_{ij} solved for all species, the community and population

dynamics can be modeled with further assumptions on the demographic outcome of resource allocation. Separating the resource allocation outcomes from the demographic outcomes makes the model much more flexible. First, instead of using a single parameter such as θ in the original model, we can set up more flexible and realistic connection between resource allocation and maintenance, growth and reproduction, as well as allowing species to have differential growth period and accumulate resource through time. It also makes it easier to model the multiple resource scenarios, where distributions from different resource types can be added or multiplied to generate certain demographic outcomes, without the odd definition of “resource specified sub-communities”.