Ecography

Supplementary material

Appendix 1

Supplementary Text

Derivation of a distance-based conspecific-encounter index

To effectively incorporate distance information of sequentially sampled neighboring organisms, inspired from the unification of the original index v and Moran's I index (see Eqs. 1-4 in the main text), we develop a distance-based conspecific-encounter index as follows:

$$v_d = \frac{\sum_{i \in S} \sum_{k \geq 2} e^{-d_{k,k-1}} I(Z_k = Z_{k-1} = i)}{\sum_{k \geq 2} e^{-d_{k,k-1}}}, \tag{A1}$$

where $d_{k,k-1}$ denotes the distance between the k-th and $(k-1)$-th organisms. One important purpose of introducing the denominator $\sum_{k \geq 2} e^{-d_{k,k-1}}$ in Eq. A1 is to normalize the distance-based index to make it bounded between 0 and 1. When $d_{2,1} = d_{3,2} = \cdots = d_{m,m-1}$, the above equation actually is identical to the original conspecific-encounter index v. Another important consideration of formulating the distance-based index v_d as Eq. A1 above is because it could have a similar relationship with Moran's I index as proved below.

Firstly, like the partitioning of the original index v into species-specific components (Eq. 1 in the main text), we can also partition the above distance-based index v_d into separated components for different species (i.e., species-specific distance-based index $v_d(i)$) found within the sampling line transect as

$$v_d = \sum_{i \in S} v_d(i).$$

Here,

$$v_d(i) = \frac{\sum_{k \geq 2} e^{-d_{k,k-1}} I(Z_k = Z_{k-1} = i)}{\sum_{k \geq 2} e^{-d_{k,k-1}}}.$$

For Moran's I index with a specific species i, we have

$$I_d(i) = \left(\frac{m}{\sum_{k=1}^{m} q_k} \right) \left(\frac{\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j} q_k q_j}{\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j}} \right), \tag{A2}$$

where we let $q_k = I(Z_k = i)$ and $w_{k,j} = e^{-d_{k,j}}$ for $|k-j| = 1$ and $w_{k,j} = 0$ otherwise. Clearly, we have $\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j} = 2 \sum_{k \geq 2} e^{-d_{k,k-1}}$ and $\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j} q_k q_j = 2 \sum_{k \geq 2} e^{-d_{k,k-1}} I(Z_k = Z_{k-1} = i)$. Moreover, $n_i = \sum_{k=1}^{m} q_k$ is the observed abundance of species i within the line transect.

Consequently, we obtain a simple relationship between the species-specific Moran's I index and the species-specific distance-based v_d index as

$$I_d(i) = \left(\frac{m}{n_i} \right) v_d(i).$$

As such, when conducting line-transect sampling, the distance-based conspecific-encounter index v_d can be computed as the sum of abundance-weighted Moran's I index for each single species along the line transect as follows:

$$v_d = \sum_{i \in S} \left(\frac{n_i}{m} \right) I_d(i). \tag{A3}$$

This distance-based conspecific-encounter index is an extension of the original index but effectively accounts for the potential influence of spatial distance when measuring multi-species distributional aggregation level for line-transect sampling.

Derivation of a functional conspecific-encounter index

We define the functional conspecific-encounter index as

$$v_F = \frac{\sum_{i \in S} \sum_{k \geq 2} I(Z_k = Z_{k-1} = i) e^{-|X_k - X_{k-1}|}}{\sum_{k \geq 2} e^{-|X_k - X_{k-1}|}},$$ (A4)

where X_k is the value of the targeted functional trait of the k-th encountered organism along a line transect. The denominator $\sum_{k \geq 2} e^{-|X_k - X_{k-1}|}$ in the index v_F is to normalize the index to have a range between 0 and 1; moreover, it stands for the functional trait difference between sequentially encountered neighboring organisms, irrespective of their species-level identity. The introduction of the indicator function $I(Z_k = Z_{k-1} = i)$ in the numerator confines the index v_F to focus on the functional trait distance or difference between two sequentially encountered organisms from the same species. If all X_k's are the same or missing, the functional conspecific-encounter index v_F is identical to the original index v.

Being analogous to the partition of the original conspecific-encounter index into species-specific components presented in the main text, we can partition the index v_F into species-specific components as

$$v_F = \sum_{i \in S} v_F(i).$$

Here,

$$v_F(i) = \frac{\sum_{k \geq 2} I(Z_k = Z_{k-1} = i) e^{-|X_k - X_{k-1}|}}{\sum_{k \geq 2} e^{-|X_k - X_{k-1}|}}.$$

For the form of the species-specific Moran's I index, the calculation formula again follows Eq. A2 (or Eq. 2 in the main text). However, for the functional conspecific-encounter index here, the weight is different: we set $q_k = I(Z_k = i)$ and $w_{k,j} = e^{-|X_k - X_j|}$ for $|k - j| = 1$ and $w_{k,j} = 0$ otherwise. Then, we have $\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j} = 2 \sum_{k \geq 2} e^{-|X_k - X_{k-1}|}$ and $\sum_{k=1}^{m} \sum_{j=1}^{m} w_{k,j} q_k q_j = 2 \sum_{k \geq 2} e^{-|X_k - X_{k-1}|} I(Z_k = Z_{k-1} = i)$. Again, $n_i = \sum_{k=1}^{m} q_k$ represents the observed abundance of species i within the line transect.

Consequently, a simple relationship between the species-specific Moran's I index and the species-specific index $v_F(i)$ can be established as follows:

$$I_F(i) = \left(\frac{m}{n_i}\right) v_F(i).$$

Accordingly, when conducting line-transect sampling, the functional trait-based conspecific-encounter index v_F can be computed as the sum of the abundance-weighted Moran's I index for each single species along the line transect as follows:

$$v_F = \sum_{i \in S} \left(\frac{n_i}{m}\right) I_F(i).$$ (A5)