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Origin of compartmentalization in food webs

(Digital Appendices)

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A Homogeneity calculations

A.1 Niche homogeneity

Recall from the manuscript that we define the niche homogeneity H_n as

$$H_n = \frac{\langle B \rangle - B^*}{\sigma_B}, \quad (\text{A.1})$$

where B^* is the number of boundaries, in the niche space, between the observed compartments, $\langle B \rangle$ is the average number of boundaries between compartments for the ensemble of all partitions of the species (with the same number of compartments and the same compartment sizes as the observed partitions), and σ_B is the standard deviation of the same quantity (Fig. A1).

For a given partition of a network with N_C compartments of sizes $\{n_1, n_2, \dots, n_{N_C}\}$, both $\langle B \rangle$ and σ_B can be calculated analytically by realizing that averaging over partitions is equivalent to averaging over random re-orderings of the species in the niche space (and keeping each species' actual compartment).

Let m_j be the compartment of species j , and \mathcal{O}_i the species in position i in a given ordering \mathcal{O} of the species, so that $m_{\mathcal{O}_i}$ is the compartment of the species in position i . Then, the number of boundaries between compartments for ordering \mathcal{O} is $\sum_{i=1}^{S-1} (1 - \delta(m_{\mathcal{O}_i}, m_{\mathcal{O}_{i+1}}))$, where S is the total number of species, and the average is

$$\langle B \rangle = \frac{1}{S!} \sum_{\{\mathcal{O}\}} \sum_{i=1}^{S-1} (1 - \delta(m_{\mathcal{O}_i}, m_{\mathcal{O}_{i+1}})) , \quad (\text{A.2})$$

where the first sum is over all possible orderings of the species. Similarly, σ_B can be calculated as

$$\sigma_B = \left(\langle B^2 \rangle - \langle B \rangle^2 \right)^{1/2}, \quad (\text{A.3})$$

with

$$\langle B^2 \rangle = \frac{1}{S!} \sum_{\{\mathcal{O}\}} \left[\sum_{i=1}^{S-1} (1 - \delta(m_{\mathcal{O}_i}, m_{\mathcal{O}_{i+1}})) \right]^2. \quad (\text{A.4})$$

After some algebra, we obtain

$$\langle B \rangle = S - \frac{1}{S} \sum_{m=1}^{N_C} s_m^2 \quad (\text{A.5})$$

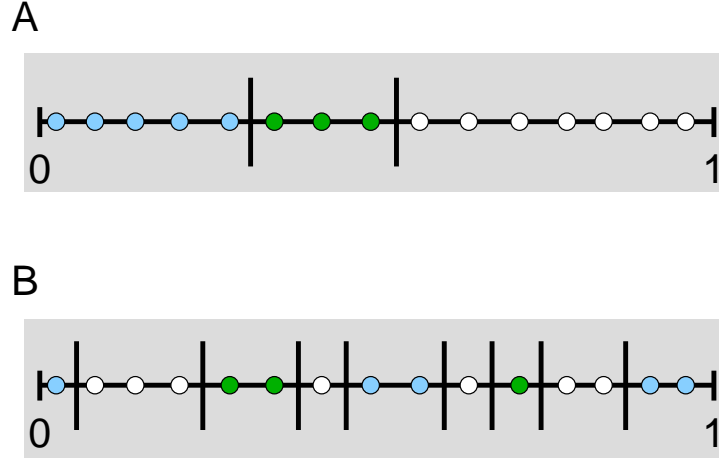


Figure A1: Boundaries in niche space between hypothetical compartments. The horizontal axis represents the niche space and each circle represents a species, with colors indicating compartments. Boundaries are indicated with vertical lines. A, For very niche-homogeneous compartments, all species in a compartment occupy contiguous positions in the niche space, so the number of “boundaries” between compartments (a boundary separates each pair of contiguous species with different color) is low. When compartments are perfectly homogeneous, the number of boundaries is simply the number of compartments minus 1. B, For less homogeneous compartments, the number of boundaries is larger.

$$\sigma_B = \left\{ \frac{1}{S(S-1)} \left[(S+1) \sum_{m=1}^{N_C} s_m^2 - 2 \sum_{m=1}^{N_C} s_m^3 + \frac{1}{S} \left(\sum_{m=1}^{N_C} s_m^2 \right)^2 - S^2 \right] \right\}^{1/2}. \quad (\text{A.6})$$

where s_m is the number of species in compartment m , and N_c is the number of compartments.

A.2 Trophic homogeneity

Again, recall from the manuscript that we define trophic homogeneity H_t in the same way as niche homogeneity, but counting the boundaries in the trophic space, rather than the niche space. The trophic level l_i of species i is (Levine, 1980)

$$l_i = 1 + \sum_{j \in P_i} \frac{l_j}{k_i^{\text{in}}}, \quad (\text{A.7})$$

where P_i is the set of i 's prey, and k_i^{in} is the number of prey (Levine, 1980).

This definition of trophic level raises an important issue about the structure of model food webs. In principle, nothing precludes the generalized niche model (or the niche model) from generating food webs that are “trophically inconsistent.” For example, a species could have no other prey than itself, so that Eq. A.7 does not have a solution. Since these inconsistencies are not observed in real food webs, we discard all trophically inconsistent model food webs for all the calculations reported in the manuscript.

A.3 Sink homogeneity

For each species i in a food web, we find the set T_i of species that belong to i 's sink food web, that is, the species on which i preys directly and indirectly (i 's prey, the prey of i 's prey, the prey of the prey of i 's prey, and so on). For convenience, we always exclude i from T_i .

We then count the number o_i^* of species that belong to both T_i and species i 's compartment C_i . We define sink homogeneity as

$$H_s = \sum_{i=1}^S \frac{o_i^* - \langle o_i \rangle}{\sigma_{o_i}}, \quad (\text{A.8})$$

where the sum is over all species, and $\langle o_i \rangle$ and σ_{o_i} are the average and standard deviation, respectively, of the null expectation for the overlap between T_i and C_i .

The simplest null model is one in which nodes in T_i are randomly selected from the actual compartments. Let us call t_i the number of nodes in T_i and s_i the number of nodes in C_i . In the null model, the probability $p_i(k)$ that T_i contains exactly k nodes from C_i is

$$p_i(k) = \frac{\binom{s_i-1}{k} \binom{S-s_i}{t_i-k}}{\binom{S-1}{t_i}} \quad k \leq s_i - 1, k \leq t_i. \quad (\text{A.9})$$

The denominator is the total number of ways in which one can pick t_i elements among a set of $S - 1$ (all the nodes in the network except i). The numerator is the number of ways in which those elements can be selected so that exactly k of them come from compartment C_i ; that is, the number of ways one can select k elements among the $s_i - 1$ in C_i (excluding i), times the number of ways one can select the remaining $t_i - k$ among the $S - s_i$ nodes in compartments other than C_i .

With this, one can calculate the expected overlap $\langle o_i \rangle$ between T_i and M_i , as well as the standard deviation σ_{o_i}

$$\langle o_i \rangle = \sum_k k p_i(k) = t_i \frac{s_i - 1}{S - 1} \quad (\text{A.10})$$

$$\langle o_i^2 \rangle = \sum_k k^2 p_i(k) \quad (\text{A.11})$$

$$\begin{aligned} &= t_i(s_i - 1) \frac{(S - s_i)!(S - t_i - 1)!}{(S - 1)!(S - t_i - s_i + 1)!} {}_3F_2(2, 2 - s_i, 1 - t_i; 1, S - t_i - s_i + 2; 1) \\ \sigma_{o_i} &= \sqrt{\langle o_i^2 \rangle - \langle o_i \rangle^2} \end{aligned} \quad (\text{A.12})$$

where ${}_3F_2(a_1, a_2, a_3; b_1, b_2; z)$ is the generalized hypergeometric function (Weisstein, 2008).

References

- Levine, S. 1980. Several measures of trophic structure applicable to complex food webs. *J. Theor. Biol.* **83**:195–207.
- Weisstein, E. W., 2008. Regularized Hypergeometric Function. From MathWorld—A Wolfram Web Resource. URL <http://mathworld.wolfram.com/RegularizedHypergeometricFunction.html>.