

**Mariana M. Vidal, Erica Hasui, Marco A. Pizo, Jorge Y. Tamashiro, Wesley R. Silva, and Paulo R. Guimarães Jr. Frugivores at higher risk of extinction are the key elements of a mutualistic network.**

APPENDIX B. Computation of nestedness, modularity, and species-level network metrics ( $n_i$ ,  $z_i$  and  $c_i$ ). Values of network descriptors of the three interaction networks studied. Correlation coefficients for the species-level network metrics calculated for birds.

Below, we present the formulas used to compute nestedness (*NODF*); modularity (*M*); and species-level network metrics: contribution to nestedness ( $n_i$ ); standardized within-module degree ( $z_i$ ), and among-module connectivity ( $c_i$ ). These metrics were applied to binary matrices of interaction, represented as presence (1) or absence (0) of interaction between pairs of species.

*Nestedness*

We assessed nestedness of the studied interaction matrices by computing *NODF* - *Nestedness metric based on Overlap and Decreasing Fill* (Almeida-Neto et al. 2008), a metric that also permits estimation of contribution to nestedness ( $n_i$ ). *NODF* is calculated as follows:

$$NODF = \frac{\sum N_{paired}}{\left[ \frac{n(n-1)}{2} \right] + \left[ \frac{m(m-1)}{2} \right]} \quad (B.1)$$

where  $N_{paired}$  is a measure of nestedness among pairwise rows and columns (see Almeida-Neto et al. 2008 for further details);  $n$  is the number of rows; and  $m$  is the number of columns in the interaction matrix.

*Species contribution to nestedness*

The contribution of each matrix element (species) to nestedness ( $n_i$ ) is based on the metric *NODF* (Almeida-Neto et al. 2008), which considers the decreasing number of interactions (1's) between successive rows and columns in a binary matrix and the percentage of interactions that occur at identical positions between pairs of rows and columns. As with *NODF*, the metric used here ( $n_i$ ) was developed based on the concept that a nested matrix presents decreasing fill and paired overlap of presences (1's) and that its calculation accounts for pairs of rows and pairs of columns. We describe in detail the procedure for calculating  $n_i$  for the species represented in the rows, and the same is applied to columns.

First, assume a matrix of interactions with  $m$  rows and  $n$  columns. The number of presences (1's) in each row is contrasted to all other rows. If species  $i$  presents the same number of interactions as species  $j$  or fewer, then the value zero (0) is attributed to species  $i$  in relation to  $j$  to indicate that the pair  $ij$  does not contribute to nestedness, as there is no decreasing fill between them.

Then, this value is plotted in a square matrix ( $m \times m$ ), in which  $m$  species are represented in both rows and columns and the value zero is the element  $a_{ij}$ . On the other hand, if species  $i$  has more interactions than species  $j$ , it is necessary to calculate the proportion of 1's of the species  $j$  that is exactly at the same column position as the 1's attributed to species  $i$ . This proportion is the value attributed to species  $i$  in relation to  $j$ , representing the power of species  $i$  to predict the occurrence of 1's in the column of species  $j$ . In this case, element  $a_{ij}$  would be this proportion.

These pairwise comparisons generate an  $m \times m$  matrix in which each row contains the proportions of 1's of the species in the row that were correctly predicted by the other species and each column represents the proportions of correct predictions by the species in the column. The contribution to nestedness depends on both proportions, and the average of these proportions (Average1 and Average2) is calculated for each species:

**Columns:**

$$Average1 = \left( \sum_{i=1}^{i=m} a_{ij} \right) / (m-1) \quad (B.2)$$

**Rows:**

$$Average2 = \left( \sum_{j=1}^{j=m} a_{ij} \right) / (m-1) \quad (B.3)$$

Then, the contribution to nestedness ( $n_i$ ) is calculated as

$$n_i = Average1 + Average2$$

Therefore, the contribution to nestedness is the sum of *Average1* and *Average 2*, taking into account both the power of prediction and predictability of each species to quantify its overall importance to nestedness.

As mentioned above, the methods used for species in rows were applied to the species represented in columns, generating a square matrix of dimensions  $n \times n$  upon which all the other calculations must be made.

*Modularity*

The modularity ( $M$ ) of each studied network was estimated using a simulated annealing optimization procedure (Guimerà & Amaral 2005; Olesen et al. 2007). For a given division of network nodes into distinct modules, network modularity is computed as follows:

$$M = \sum_{s=1}^{N_M} \left[ I_s / I - (k_s / 2I)^2 \right] \quad (B.4)$$

where  $N_M$  is the number of modules in the network;  $I_s$  is the number of interactions among all the species within the module  $s$ ;  $I$  is the total number of interactions in the network; and  $k_s$  is the sum of the number of interactions of all the species inside module  $s$ .

Two topological properties associated to modularity of each node in the network were computed: the standardized within-module degree ( $z_i$ ), which is a standardized measure of the extent to which each species is connected to the others in its own module, and the inter-module connectivity ( $c_i$ ), which describes how well each species is connected to species in other modules. The formulas for computing  $z_i$  and  $c_i$  are below.

*Standardized within-module degree ( $z_i$ )*

$$z_i = \frac{k_{is} - \bar{k}_s}{SD_{ks}} \quad (\text{B.5})$$

where  $k_{is}$  is the number of interactions between  $i$  and the other species in its own module  $s$  and  $\bar{k}_s$  and  $SD_{ks}$  are the average and standard deviation of the number of within-module degrees of all species in module  $s$ .

*Among-module connectivity ( $c_i$ )*

$$c_i = 1 - \sum_{t=1}^{N_M} \left( \frac{k_{it}}{k_i} \right)^2 \quad (\text{B.6})$$

where  $k_i$  is the number of interactions of species  $i$  and  $k_{it}$  is the number of interactions between  $i$  and species in module  $t$  (including  $i$ 's own module).

We also present the correlation coefficients among the species-level network metrics calculated for birds and plants (Table B1).

TABLE B1. Pearson’s correlation coefficients among species-level network metrics calculated for birds and plants: number of interactions ( $k_i$ ), contribution to nestedness ( $n_i$ ), standardized within-module degree ( $z_i$ ), and among-module connectivity ( $c_i$ ).

Group	Variable	By variable	Correlation	Count	Significance probabilities
Birds	$c_i$	$k_i$	0.76	59	<0.0001
	$z_i$	$k_i$	0.85	59	<0.0001
	$z_i$	$c_i$	0.48	59	0.0001
	$n_i$	$k_i$	0.55	59	<0.0001
	$n_i$	$c_i$	0.58	59	<0.0001
	$n_i$	$z_i$	0.26	59	0.0504
Plants	$c_i$	$k_i$	0.75	88	<0.0001
	$z_i$	$k_i$	0.88	88	<0.0001
	$z_i$	$c_i$	0.63	88	<0.0001
	$n_i$	$k_i$	0.68	88	<0.0001
	$n_i$	$c_i$	0.70	88	<0.0001
	$n_i$	$z_i$	0.48	88	<0.0001

#### LITERATURE CITED

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