Important, Unique, Central, the Distribution of Species’ Food-Web Relevance.

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## The Random Dot Product Graph model

More in the detail, chosen a model dimension , we compute a singular value decomposition of into three matrices , satisfying . and are real, orthogonal matrices, and is an diagonal matrix whose entries are the singular values of , in a non-decreasing order. Chosen a model dimension , we define three new matrices 1) , an matrix given by the first columns of ; 2) , an matrix given by the first columns of ; 3) , an diagonal matrix defined by the square root of the first entries of , i.e., the square root of the first greatest singular values of . From the truncated matrices we define as and as . The three matrices so defined capture the leading traits for the community of species as predators and as prey: the rows of define the species’ vulnerability functional traits and the rows of define the foraging functional traits of the species in . The species’ relative position and the induced pairwise distance structure in the abstract functional space are uniquely defined.

Different approaches are available for the choice of a suitable dimension range: a dimensionality reduction problem, discussed for the Principal Component Analysis scenario in (Jolliffe 2002). These include selection procedures, such as the visual analysis of the singular values scree plot, the maximization of a profile likelihood function (Zhu & Ghodsi 2006), and the maximization of a goodness-of-fit criterion. Here we rely on the results of (Dalla Riva & Stouffer 2015).

We will make use of some notation. Let denote a matrix: we denote the matrix obtained by dropping the -th column and row from ; we denote the matrix obtained by removing just the -th row from . Let denote another, suitable dimensioned, matrix, we denote a Procrustes transformation of of minimal distance to —we drop from the notation whenever it is clear. Finally, we denote the squared sum of ’s entries, i.e., the Frobenius norm of the matrix .

Then, matrix is defined as the Procrustes transformation of of minimal distance to , that is . We define the rank of the species as the sum of squared differences between and . Being the matrix of either the in, ou’ or all dimensional functional traits, we will speak of species’ , or strain, respectively.

This is equivalent to the ordinary Procrustes sum of squares of the matrices and , for which computation we used the function in the R package (Dryden 2013,R Core Team (2014)).

We computate the species’ strain using the function in the R package .

which we computed using Qhull(Barber *et al.* 1996), through the package (Habel *et al.* 2014).

The above centralities are all implemented in the package (Csardi & Nepusz 2006).

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