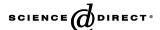


Available online at www.sciencedirect.com



Environmental Modelling & Software

Environmental Modelling & Software 21 (2006) 1512-1513

www.elsevier.com/locate/envsoft

Software data news

Improving the analyses of nestedness for large sets of matrices

Paulo R. Guimarães Jr. a,b,*, Paulo Guimarães c

^a Instituto de Biologia, UNICAMP, CP 6109, 13083-970, Campinas, SP, Brazil
 ^b Integrative Ecology Group, Estación Biológica de Doñana, CSIC, Sevilla, Spain
 ^c Daitan Labs, Galleria Office, Campinas, SP, Brazil

Received 24 November 2005; received in revised form 10 April 2006; accepted 10 April 2006 Available online 13 June 2006

Abstract

Nestedness is a property of binary matrices of ecological data and quantified by the matrix's temperature, T. The program widely used to calculate T is Nestedness Temperature Calculator (NTC). NTC analyses matrices individually, turning the analysis of large sets time-consuming. We introduce ANINHADO, a program developed to perform rapid and automatic calculation of T over 10,000 matrices. ANINHADO can be useful to minimize the time spent in analysis and to compare real data against a variety of null models that typically generate a large number of replicates.

© 2006 Elsevier Ltd. All rights reserved.

Keywords: Biogeography; Community assembly; Ecological networks

Software availability

Name of software: ANINHADO

Developers: Paulo Guimarães and Paulo R. Guimarães Jr.

Platform: MS-DOS under Windows.

Contact address: Instituto de Biologia, UNICAMP, CP 6109,

Campinas, SP, Brazil Telephone: +55 19 97861978 E-mail address: prguima@gmail.com Availability: http://www.guimaraes.bio.br

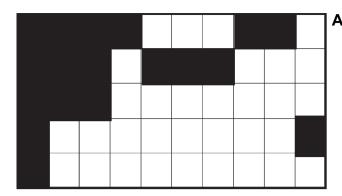
Environmental scientists have been studying systems to discover for the patterns of the underlying processes. Many of these patterns are described in binary or presence/absence matrices (Bascompte et al., 2003). Nestedness is a pattern (Fig. 1), which characterizes distributions of species within a habitat (Atmar and Patterson, 1993), parasites among hosts (Worthen and Rohde, 1996), and interactions in ecological networks (Bascompte et al., 2003).

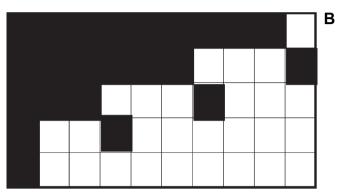
E-mail address: prguima@gmail.com (P.R. Guimarães).

The degree of nestedness of a matrix can be quantified by the matrix's temperature (*T*), a measure of how the presence/ absence pattern departs from perfect nestedness (calculated by NESTEDNESS TEMPERATURE CALCULATOR (NTC), see Atmar and Patterson, 1993). Nevertheless, as the studies about nestedness have increased, some analyses cannot be optimally performed using NTC, leading to the necessity of new tools. Here we introduce ANINHADO, a program developed to attend to one of these needs: the rapid, automatic calculation of *T* for many matrices.

NTC is a Visual Basic package downloadable at http://aicsresearch.com/nestedness/tempcalc.html. It implements a good graphical user interface, intuitive menus, it includes background information about the nestedness theory and it also allows hypothesis testing: the observed value of T can be compared with the expected one under the assumption that presences were randomly assigned to any cell within the matrix. The graphical user interface and the supporting documentation about nestedness theory make NTC a convenient tool for users willing to analyze a limited number of matrices. However, the user needs to load and calculate T from each matrix individually, making the calculation of T time-consuming when there are many matrices to examine.

^{*} Corresponding author. Instituto de Biologia, UNICAMP, CP 6109, 13083-970, Campinas, SP, Brazil.





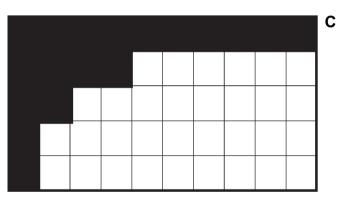


Fig. 1. Hypothetical matrices describing presences (black squares) of species (rows) in locations (columns). Nestedness occurs when presences in a row/column is often a subset of presences recorded in rows/columns with more presences. The matrices vary in their degree of nestedness: low (A), high (B), and perfect (C).

The C++ software ANINHADO was developed to perform rapid, automatic calculation of T of many matrices (Table 1). ANINHADO analyzes a set of user-specified matrices and generates a file containing their names and respective T values.

Table 1
Performance of NTC and ANINHADO using a Mobile Intel Pentium 4, 2.8 GHz CPU processor

	NTC	ANINHADO
Matrices/run	One	10,000
Matrices/min	~8	>80
Automatic processing	No	Full

Moreover ANINHADO does not require the user's interaction during its execution, and it is therefore possible to perform other tasks in the computer during the analysis.

The automatic processing capabilities and speed of ANIN-HADO are also an asset when the user is interested in analyzing sets of real matrices or when testing null models other than the one implemented in NTC (Bascompte et al., 2003). The null model approach is based on the comparison of real data with an empirical distribution obtained from the analysis of thousands of algorithm-generated matrices that deliberately exclude an influence (Gotelli and Graves, 1996). As a consequence, the rigorous characterization of the expected *T* for an alternative null model will consume hours of continuous work in NTC, but only few minutes in ANINHADO. Additionally, ANINHADO generates empirical distributions for four pre-determined null models, allowing users not familiarized with programming to compare their data against alternative hypotheses.

Acknowledgements

We are indebted to W. Atmar for providing the VB code of NTC; A.E. Rizzoli, J. Bascompte, M. Fortuna, M.A. Mello, P. Jordano, P.P. Coltri, S.F. dos Reis, W. Atmar and two anonymous reviewers for criticisms on the manuscript; and FAPESP for support.

References

Atmar, W., Patterson, B.D., 1993. The measure of order and disorder in the distribution of species in fragmented habitat. Oecologia 96, 373–382.

Bascompte, J., Jordano, P., Melián, C.J., Olesen, J.M., 2003. The nested assembly of plant-animal mutualistic networks. Proceedings of the National Academy of Sciences of the United States of America 100, 9383–9387.

Gotelli, N.J., Graves, G.R., 1996. Null Models in Ecology. Smithsonian Institution Press, Washington.

Worthen, W.B., Rohde, K., 1996. Nested subset analyses of colonization-dominated communities: Metazoan ectoparasites of marine fishes. Oikos 75 (3), 471–478.