

DIVORD 1.60. DIVERSITY ORDERING: FINITE AND INFINITE SAMPLES

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Abstract. Changes in the 1.60 release of DivOrd program are discussed. The main improvement is that it is possible now, to choose between the finite and infinite sample versions of rarefaction diversities. The arrangement of the menu system also has changed a little.

Keywords: diversity index families, diversity ordering, rarefaction diversity

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Introduction

Different diversity indices may rank inconsistently a given pair of communities (Hurlbert, 1971). This is related to the different sensitivities of diversity indices. A solution is to use parametric families of diversity indices instead of a numerical-valued diversity index. An important property of the family of diversity indices is their variable sensitivity to rare and abundant species. This means that communities can be compared for different "dominance levels" as a scale parameter changes. The family may be portrayed graphically by plotting diversities D_α against the scale parameter α ; this curve is the diversity profile of the community (Patil and Taillie, 1979, 1982). In fact, α serves as a scale parameter; members of the D_α family have varying sensitivities to the rare and abundant species as α changes.

Using diversity profiles the diversity ordering of communities is defined in the following way: Community A is more diverse than community B when the diversity profile of A is above or equal to the diversity profile of B on the whole range of the scale parameter. Curves of two diversity profiles may intersect. This means that one of the communities is more diverse for the rare species while the other one is more diverse for the dominants.

A program, DivOrd 1.50, was presented to calculate and display the diversity profiles of communities (Tóthmérész, 1993b). Eight methods

are included in the package. Mathematical background of the methods was also discussed. In this paper the new release of the program is discussed.

Rarefaction Diversity: Finite and Infinite Samples

Generally, a community may be characterized by an abundance vector

$$n=(n_1, n_2, \dots, n_i, \dots, n_s)$$

where n_i is the abundance of the i -th species of the community. Frequently enough to know the relative abundances of species; thus the community may be characterized by the

$$p=(p_1, p_2, \dots, p_i, \dots, p_s)$$

relative abundance vector, where p_i is the relative abundance of the species i .

The rarefaction diversity or species-individual curve for a spatially completely random, infinitely large community is defined by

$$S(m) = S - \sum_{i=1}^s (1 - p_i)^m$$

Smith and Grassle (1977) presented the minimum variance unbiased estimation of $S(m)$ as:

$$\hat{S}(m) = S - \sum_{i=1}^s \binom{N - n_i}{m} / \binom{N}{m}$$

where

$$\binom{N}{m} = \frac{N!}{(N - m)! m!}$$

This is, however, not simple to calculate because of the factorials. It is vital to use a good numerical approximation of the factorial function to ensure the correct result for very small and very large figures as well. The direct calculation is nonsense, especially when the data set is based on percentage covers of the vegetation, which is a continuous variable. I applied a fast and especially robust and reliable procedure which is based on the calculation of logarithm of the gamma function (Macleod, 1989).

Changes in the arrangement of the menu

The main menu has changed a little (Fig. 1). There is a new option called "Data Management" which includes the "Data Input" which was in the main menu in the 1.50 release. The "Other Samples to Compare" and "Result to Disk in HG Format" options also moved here from the main menu (Fig. 2).

1 - Data Management

Generalized Entropy Plots

2 - Rényi

3 - EXP(Rényi)

4 - Daróczy

5 - Patil & Taillie

Cumulative Relative Abundance Plots

6 - Logarithmic Dominance Plot

7 - Right-Tail-Sum Diversity Plot

Scale Parameter with Direct Interpretation

8 - Infinite Species-Individual Curve (Density Independent)

9 - Infinite Species-Area Curve (Density Dependent)

10 - Finite Species-Individual Curve (Density Independent)

11 - Finite Species-Area Curve (Density Dependent)

12 - Exit

Your choice :

Fig. 1. Main menu of the DivOrd 1.60.

I also changed the naming convention of the diversity orderings. The EXP(D(α)) version of the D(α) Rényi diversity index family is simply mentioned as EXP(Rényi). Sometimes this is more favourable than the Rényi index family itself, because it produces the number of species of the community when the value of the scale parameter is zero; and it is easier, or just more straightforward, to interpret the number of species than the logarithm of it. As a diversity profile this was proposed first by Patil and Taillie (1979); they

derived it in a unified framework alongside many other diversity index families. Hill (1973) also mentioned Rényi's original paper and used it after a proposal of Orlóci (Orlóci, 1991, p. 5, footnote 12), but he did not recognize at all that it may be useful for diversity ordering. Indeed at that time, even the idea of diversity ordering was not invented and published.

Data Management

1 - Data Input

2 - Other Samples to Compare

3 - Result to Disk in HG Format

4 - Main Menu

Your choice :

Fig. 2. Data management of the DivOrd 1.60.

And finally there are four new options in relation with the rarefaction diversity orderings. In the 1.60 release this group of methods of ordering is mentioned as "Scale Parameter with Direct Interpretation" indicating that in this case the scale parameter has a definite physical meaning which is related to the size of the sample in which the species were found. The new options are the following:

- 8 - Infinite Species-Individual Curve (Density Independent)
- 9 - Infinite Species-Area Curve (Density Dependent)
- 10 - Finite Species-Individual Curve (Density Independent)
- 11 - Finite Species-Area Curve (Density Dependent)

The density dependence and independence is represented in the same way as it was in the 1.50 release (Tóthmérész, 1993b) and the finite and infinite versions were discussed in the previous section.

The input of the samples' identity number also has changed a little (Fig. 3); it provides more information. Besides the total number of samples the file name and the label of the data set are also displayed on the screen.

File Name : demo-2.dat
 Label : Demo data for NuCoSA; DEMO-2.DAT
 There are 20 sample units.
 How many curves do you want to draw (less than or equal to 4)?
 3
 Please type the identity number of the sample sites:
 1.: 3
 2.: 12
 3.: 18

Fig. 3. The screen of identity number input of the compared sample sites.

Datafiles distributed with DivOrd

There are some changes in the demo files distributed with the program. All the previously distributed demo files can be found, just their name has changed and there are some new ones. This was motivated by a standardization; now, all the demo files are identical with the files of the NuCoSA package (Tóthmérész, 1993a).

There are 5 files distributed with the package. DEMO-1.DAT file contains a data set of 10 by 18 size. DEMO-2.DAT contains a data set of 20 by 56 size. DEMO-3.DAT is a data set of 10 by 20 size; this data set is a truncated version of the DEMO-4.DAT data set, which was registered at the "Rejtek Project" Research Area (Tóthmérész, 1989). It describes the changes of the vegetation along a transect and the vegetation is extremely low in diversity in the first half of the plot while it is more

diverse in the second half. DEMO-5.DAT file is one of the data sets presented in the paper of the 1.50 release (Tóthmérész, 1993b).

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