



SOFTWARE ABSTRACT

DIVERSI 2.1: New version of a program package for calculating diversity and related statistics

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Abstract: The recent version of the DIVERSI program package runs on IBM-PC compatible machines with DOS operating system or a business system which includes DOS client (such as WINDOWS NT, 2000, XP). All routines work with dbase data files. The program calculates diversity indices and their confidence intervals, the significance of diversity differences, index sensitivity and fit some abundance models to actual data. Quadratic entropy and members of the ESS and NESS similarity index family are also included. Hardware requirements, data file operations and examples are provided in a User's Guide. An example of calculating quadratic entropy is presented.

Introduction and some basic features

In his work on species and epidemiological diversity problems, as well as abundance distributions and similarity problems, the author has developed several computer programs, which are incorporated in this package. For a short review on the former version 1.1 see Izsák (1998). Many of the procedures programmed in this version, numbered 2.1, are new features.

The program, written in DBASE III PLUS runs in its recent form on IBM - PC compatible machines with DOS operating system or with a business system which includes DOS client (such as WINDOWS NT, 2000, XP). With business systems the DOS client can be launched by starting the program, then pressing ALT and ENTER simultaneously. The program was compiled and translated by CLIPPER. It can be started by the DIVERSI.EXE file. All routines work with dbase data files.

On old machines, the number of open files may exceed the limit. In that case, according to the error message, one has to reset some parameters in the AUTOEXE.BAT file which should include the command line SET CLIPPER = F050; R060. The number of buffers should be at least 8. In file CONFIG.SYS, in the command line FILES = A the parameter A should be at least 50. After setting the parameters and before launching the program, the computer should be restarted.

The package is freely available upon request from the author via e-mail. An attached User's Guide includes details of program installation and running, data file structure, creating a data file and data input/output.

The menu system

The routines and subroutines of the package are listed below. Further information is given in the comment sheet pertaining to each subroutine.

1. Calculation of diversity indices
 - 1.1. Brillouin index and relative Brillouin index
 - 1.2. Shannon – Wiener index and relative S – W index
 - 1.3. Hill indices
 - 1.4. Hurlbert indices
 - 1.5. Simpson indices
 - 1.5.a. Reciprocal Simpson index
 - 1.5.b. Gini – Simpson index
 - 1.6. Alpha parameter of the logarithmic series
 - 1.7. Quadratic entropy index
2. Jackknifed estimates of diversity indices with confidence interval at 0.95 probability level. Significance of diversity difference based on jackknifing
 - 2.1. Shannon – Wiener index
 - 2.2. Hill indices
 - 2.3. Hurlbert indices
 - 2.4. Simpson indices
 - 2.4a. Reciprocal Simpson index
 - 2.4b. Gini – Simpson index

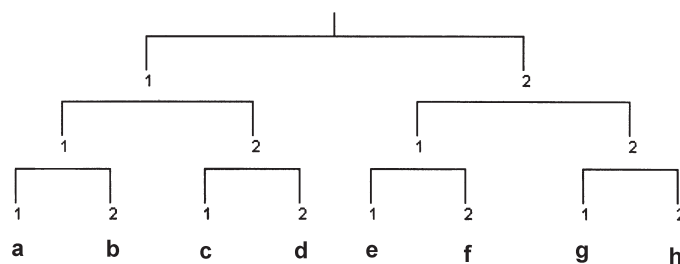


Figure 1. Taxonomic tree for hypothetical objects, used in the example.

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References....
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Datafile identifier: vals.dbf      Column   13
Calculation ? (Y/N)   Y           prompt
-----
  
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Figure 2. User screen of DIVERSI 2.1 when selecting the column to be used.

3. Fitting procedures for species abundance models

- 3.1. Logarithmic series distribution
- 3.2. Geometrical series distribution
- 3.3. Truncated lognormal distribution

4. Sensitivity investigations of diversity indices

- 4.1. Shannon – Wiener index
- 4.2. Hill indices
- 4.3. Hurlbert indices
- 4.4. Simpson indices
 - 4.4a. Reciprocal Simpson index
 - 4.4b. Gini – Simpson index

5. Further procedures

- 5.1. Smith's similarity and dissimilarity indices

6. Notes, References

- 6.1. Notes
- 6.2. References

Apart from minor rearrangements, this list does not differ essentially from that published in the software abstract on DIVERSI 1.1 (Izsák 1998). Also, notes on the routines apply to the recent version and are not repeated here.

An example of running DIVERSI 2.1

Calculate the quadratic entropy for the species abundances 2, 0, 3, 10, 5, 6, 7, 0, located in the first eight rows of the 13th column of the sample data file *VALS* supplied together with the program package. Notice that the sequence of the abundances is important in the present case.

Suppose that these abundances belong to the species a, b, c, d, e, f, g and h with taxonomic relationship expressed by the taxonomic tree shown in Fig. 1.

Each split in the tree is coded by 1 and 2, so that the taxonomic information can be summarized in tabular form as follows:

```

a111
b112
c121
d122
e211
f212
g221
h222
  
```

This matrix should be prepared and loaded into file *CICAI* before execution. First, the data file *VALS* is opened, then subroutine 1.7 is selected. The highlighted area in the comment screen will continue to display *Calculations Y(es)*, just press ENTER. The appearance of the screen after this step is shown in Fig. 2. Type number 13 to „Column”.

A new highlighted area will appear on the screen. Type in *CICAI* and press ENTER. The program generates the (taxonomic) distance matrix, according to the general principle published by Izsák and Papp (1995), see also the references to subroutine 6.2. The program will load the distance values in the data file *DISTMATR* and

carry out the calculations. The value of the quadratic index, that is 1.97612, will appear on the screen. To print the result, press F8. Further examples are given in the User's Guide.

Validation of the calculations

A feature of the program version 2.1 is the reference data file *VALS* containing 13 data columns (13 reference data sets), most of them taken from the literature on elementary diversity calculations. Where possible, we compare the numerical result calculated by DIVERSI 2.1 with that published in the widely known book of Magurran (1988) and comment possible differences in the result.

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