

SDRSimplex

User's Manual

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Introduction

The WINDOWS application **SDRSimplex** has been written to calculate the Similarity-Richness difference-Species replacement simplex as proposed by Podani and Schmera (2011). Full description of the procedure is given in this Oikos paper, and is not reproduced here.

Input files – a sample run

In general, any data matrix containing presence-absence or abundance data can be analyzed. The program accepts species as rows or as columns (i.e., sites as columns or rows, respectively); the program prompts the user to specify which arrangement is actually given.

In the example, we analyze the random data set as given in Figure 3 (top left) of Podani and Schmera (2011). The file format is as follows:

```
random
15 6
1 1 1 1 1 1
1 1 1 1 1 0
0 1 1 1 1 0
1 1 1 1 0 0
0 0 1 1 1 0
1 1 0 1 0 0
1 1 0 0 0 1
1 1 1 0 0 0
0 0 0 1 1 1
1 0 1 0 0 0
0 0 0 0 1 1
1 0 1 0 0 0
1 0 0 1 0 0
0 1 1 0 0 0
0 1 0 0 0 0
```

The data file follows the SYNTAX 2000 raw data format. The first line in each file is a title, the second line contains the number of rows (n) and the number of columns (m) of the matrix. Then follow n lines, each corresponding to a species (or site). If necessary, each row in the matrix can be broken into several lines. It

is important, however, that every new row in the matrix begins in a new line in the file. At the end, please enter a linefeed character. In the example above, we have 15 species and 6 sites, but the program accepts the same matrix in transposed form as well. The input file must be present in the same directory as the program. Abundances are automatically converted into presence/absences.

Sample run and output

The routine is a stand-alone application. After double-clicking the **SDRSimplex** icon, a dialog window appears on the monitor. Suppose that the input file is `TEST.TXT`. First, this filename has to be specified by the user and then we specify whether sites are in columns (0) or rows (1). Then, the program prints the percentage value of matrix fill, and then outputs the simplex results in percentages, first for the 2D simplex (S, D and R) and then for the three 1D simplices (R+D, S+R and S+D). The latter, the nestedness simplex is calculated in two different ways, as described in the paper (i.e., removing only the anti-nestedness fraction or the anti-nestedness AND the richness identity fractions from S+D). Finally, the program lists three default filenames for the detailed output.

```

ENTER INPUT FILENAME
test.txt
0=analysis between cols, 1=analysis between rows
0

MATRIX FILL =      50.0000  %

                                PERCENTAGES

S   SIMILARITY                  34.3239
R   SPECIES REPLACEMENT         44.0949
D   RICHNESS DIFFERENCE         21.5813

R+D BETA DIVERSITY              65.6761
S+R RICHNESS AGREEMENT          78.4187
ANTI-NESTEDNESS FRACTION        .000000
S+D-ANTI NESTEDNESS             55.9051
RICHNESS IDENTITY FRACTION      10.0000
S+D-ANTI-RIDENT NESTEDNESS      45.9051


FULL SET OF SIMPLEX SCORES SAVED IN FILE resu.ord FOR NONHIER
FULL SET OF COORDINATES SAVED IN FILE simplex.dat
    15 PAIRS TAKE    10 POSITIONS
REDUCED SET OF SIMPLEX SCORES SAVED IN REDUC.ORD FOR NONHIER
STOP

```

In the output file `resu.ord`, we find the 2D simplex scores which can be directly displayed as a ternary plot using the **Ternary plot** graphics option in the

NonHier module of the SYN-TAX 2000 package (Podani 2001). In this file true simplex scores are given for each pair of sites (starting with pair 1-2, then 1-3, 2-3, 1-4, 2-4, 3-4, etc.), rather than percentages. The output sequence by columns is R, D and S

```

random
15  3
    .500      .000      .500
    .500      .000      .500
    .500      .083      .417
    .615      .231      .154
    .364      .455      .182
    .500      .000      .500
    .500      .083      .417
    .500      .250      .250
    .364      .455      .182
    .500      .083      .417
    .364      .273      .364
    .500      .417      .083
    .222      .222      .556
    .400      .400      .200
    .286      .286      .429
50.000    34.324    44.095    21.581    65.676    78.419
55.905      .000

```

The file `simplex.dat` contains the coordinates of points for reproducing the point scatter using any graphics program that displays 2D scatter diagrams. The last three points specify the corners of the triangle.

```

random
18  2
    1.061      .613
    1.061      .613
    .943      .613
    .653      .754
    .514      .445
    1.061      .613
    .943      .613
    .707      .613
    .514      .445
    .943      .613
    .771      .445
    .471      .613
    .943      .272
    .566      .490
    .808      .350
    .707      1.225
    0.000      .000
    1.414      .000

```

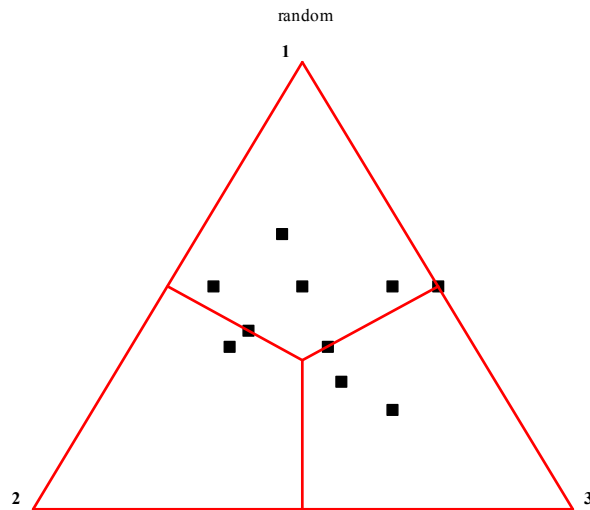
File `reduc.ord` contains simplex scores only for those points that do not overlap. This file may be useful to display the ternary plot, with reduced

memory use, when there are too many overlapping points. In the present example, the number of points reduces from 15 to 10. The output sequence by columns is R, D and S

```
random
10 3
.500000 .000000 .500000
.500000 8.333334E-02 .416667
.615385 .230769 .153846
.363636 .454545 .181818
.500000 .250000 .250000
.363636 .272727 .363636
.500000 .416667 8.333334E-02
.222222 .222222 .555556
.400000 .400000 .200000
.285714 .285714 .428571
```

The Ternary plot

Using **NonHier** (Podani 2001), we get the following graphics result, when displaying the data from either `resu.ord` or `reduc.ord`



In this diagram, “3” corresponds to the S corner, “2” corresponds to the D corner and “1” corresponds to the R corner. Each pair of sites is represented by a square symbol.

References

Podani, J. 2001. SYN-TAX 2000. Computer programs for data analysis in ecology and systematics. User’s Manual. – Scientia.

Podani J. and D. Schmera. 2011. A new conceptual and methodological framework for exploring and explaining pattern in presence-absence data. – *Oikos*, **120**, 1625–1638.