JUICE

program for management, analysis and classification of ecological data

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First part of the program manual

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1 JUICE

1.1 Introduction

JUICE is a Microsoft® WINDOWS® application for editing, classifying and analysing large phytosociological tables. It includes many functions for easy manipulation of table and header data. The program is optimised for use with TURBOVEG software (Hennekens & Schaminée 2001), which is currently the most widespread database program for storing phytosociological data in Europe; however, it is also possible to import data into JUICE from a spreadsheet data format file. In addition to basic functions useful for editing and publishing phytosociological tables, the program includes various analysis functions (such as Beals smoothing, Ellenberg indicator values, similarity indices, beta-diversity calculation, interspecific associations, and analysis of diagnostic, dominant and constant species of synoptic tables) and classification functions using COCKTAIL (Bruelheide 1996, 2001), TWINSPAN (Hill 1979) or cluster analysis included in the PC-ORD package (McCune & Mefford 1999). JUICE can create artificial data for testing. Tables, synoptic tables, headers and different types of analysis (including fidelities, species groups, indicator values and diagnostic species) can be exported in four data formats: (1) MS-DOS text, (2) Rich text format for word processors (e.g., Microsoft® WORD®), (3) spreadsheet format (e.g., Microsoft® EXCEL®) or (4) database format (Microsoft® ACCESS®). The program directly supports cooperation with the D-MAP mapping package (Morton 2005) and can create Cornell condensed files for other classification utilities such as CANOCO (ter Braak & Smilauer 2002). JUICE is continuously being developed (since 1998) by the Working Group for Vegetation Science at the Department of Botany, Masaryk University, Brno, Czech Republic. Free distribution of the program via internet has been available since 2001. This manual describes the possibilities of the program version 6.3.66. Newer versions may differ.

1.2 Copyright Information

JUICE is freeware which can be freely distributed as an original package. The program download on **www.sci.muni.cz/botany/juice.htm** is without registration. No official warranty or support is provided. Questions not covered by this manual or the FAQ can be sent to **tichy@sci.muni.cz**. In publications or reports containing outputs from the program, the paper with the basic information on the program (Tichý 2002) should be cited.

1.3 Getting Started

This chapter explains how to install and initialise JUICE.

1.3.1 Installation

The 4MB installation package can be downloaded from the internet address:

http://www.sci.muni.cz/botany/juice/jc05_ins.htm

There are two hyperlinks – a full installation download and a JUICE.EXE file download. New users must use the full installation for correct installation of all program components. The installation package contains these files:

JUICE.EXE – the program file. This file can be replaced directly without new installation by a newer version of the EXE file.

ELENB.TXT – Ellenberg indicator table (Ellenberg et al. 1992) formatted as simple text. The file covers six main environmental factors (light, temperature, continentality, humidity, pH/Ca and nitrogens/biomass productivity).

KUBAT.TXT – species check list useful for phytosociologists from the Czech Republic. The check list has a correct nomenclature published in Kubát et al. (2002).

NEWFLORA.TXT – older species check list acceptable in the Czech Republic, Slovakia, Austria and Hungary based on unpublished nomenclature. Users from other countries should export the check list from TURBOVEG. (See Section 1.4.2.)

TWINSPAN.EXE – a modified version of the famous freely distributed classification program. This version is integrated with JUICE. It can also be run as a stand-alone DOS program.

At the beginning of the installation, the user will have to specify if the program should check for older versions and reinstall them. This operation is strongly recommended, but in most cases it is possible to have several versions of JUICE installed on one computer.

When installation is complete, you may run the program from the icon group 'JUICE 6.3'.

Note 1: The latest version of the program can be also downloaded as a simple EXE file which must be copied directly into the existing JUICE directory (usually 'C:\Program Files\JUICE 6.3'). Update your program frequently. If you install the program on a new computer, please use the full installation.

Note 2: In a network, we recommend installing JUICE on each computer individually. Otherwise, there might be conflicts between multiple copies trying to access the same directory on the host computer. The starting path with .ini file and TWINSPAN must stay open for program outputs.

1.3.2   Computer Configuration

The program is written for the WINDOWS operating system in English/US format. The pre-defined decimal delimiter must be a period '.'. The program will automatically try to convert a decimal comma to a decimal point. Some known problems occur with Asian formats of the operating system. Therefore, if you encounter problems such as absence of communication with TWINSPAN or unreadable export files, try setting 'Regional Settings' to English/US.

The program has no special demands on computer hardware. However, listing through large tables may be slower on older computers.

1.3.3   Program Settings and INI File

JUICE saves the user's settings and restores them the next time the program is used. The settings are saved in the JUICE.INI file, which can be found in the same directory as the program. This file is automatically generated the first time the program is run and it is updated during table operations. If the file is deleted from the JUICE directory, the program will use predefined settings.

Note: Each line of the INI file contains a parameter name and a parameter value separated by a double colon '::', thus it is possible to edit the file manually. However, almost all values can be managed directly from the program. Manually altering the INI file may cause problems. If you experience difficulty with the INI file, simply delete it. JUICE will generate a new one in the correct format.

1.4 Data Import

The first step in working with JUICE is to open a table. JUICE does not support direct storage of phytosociological relevés. Therefore, all relevés must be entered using other software (such as TURBOVEG) and exported as a table that can be read by JUICE. JUICE accepts several different file formats:

1.4.1 XML Format

This format is useful for importing source data from the TURBOVEG database program (Hennekens & Schaminée 2001). The XML file contains full information about species names, synonyms, cover and header data, and it is not necessary to create any other file with additional information. The file structure is rather complicated, and manually entering data in this file format without TURBOVEG is not recommended.
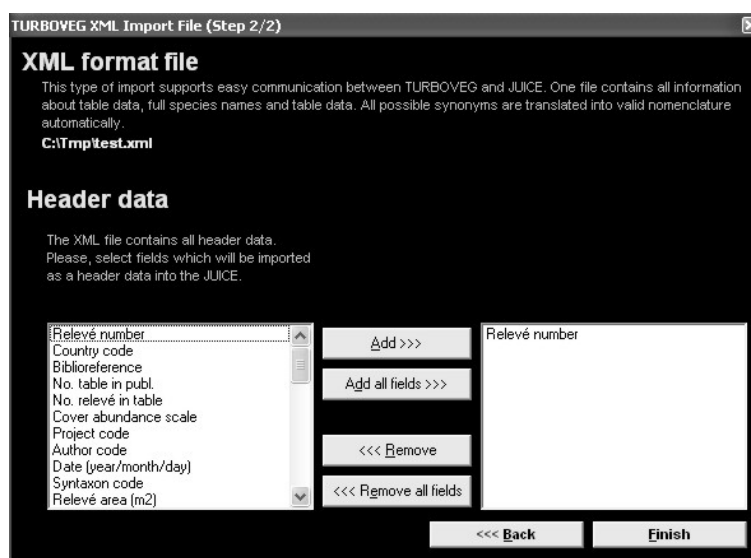
Fig. 1: XML file import.

The XML file contains all header data, but JUICE allows reduced header data information. The user must select the fields to be imported from the left list box using the 'Add' button. All selected fields appearing in the right list box will be imported.

1.4.2 Cornell Condensed (CC!) Format

The Cornell condensed format file consists of three parts: table data, species abbreviations and relevé numbers. Several types of CC! files exist – they differ especially in the table data format defined in the second line of the file. JUICE should accept any of these formats, as long as they conform to the following convention: the first number of the line gives the relative relevé number and the remainder of the line consists of pairs in which the first number refers to the species and the second number to the species' cover. Cover values may be expressed as percentages or as categories on an ordinal scale (1-9).

The species abbreviation section contains ten abbreviations per line. Each abbreviation consists of either 8 characters or 7 characters plus 1 character for the layer number.

The third section of the file is reserved for relevé identification numbers. Each number has 8 characters, and there are 10 numbers per line. A sample CC! file can be downloaded from the JUICE web page and tested directly in the program.

Example:

```
        Juice analysis                                                    T
        (I5,5(I5,F8.1))                                                   5
            1     1     2.0     2     2.0     3    13.0     4     1.0     5    38.0
            1     6     2.0     7     2.0     8     3.0     9     1.0    10     1.0
            1    11     3.0    12     3.0    13     3.0    14     3.0    15     1.0
            1    16     2.0    17     1.0    18     3.0    19    13.0    20     2.0
            1    21     2.0    22     1.0    23     1.0    24     2.0    25     2.0
            1    26     2.0    27     2.0    28     2.0    29     2.0    30    13.0
            2     1     1.0     5     2.0    10     2.0    16     3.0    21     2.0
            2    23     3.0    25     2.0    26    13.0    31     3.0    32     3.0
            2    33     2.0    34     2.0    35    13.0    36     1.0    37    13.0
            2    38     2.0    39     3.0    40     3.0    41    13.0    42     2.0
            2    43     2.0    44     1.0
            3     4     3.0     5     3.0     6     2.0    10     2.0    13     2.0
            3    16     3.0    18     2.0    21     2.0    23     2.0    25     3.0
            3    26     2.0    31     3.0    33     2.0    35    13.0    36     2.0
            3    38     3.0    39     3.0    40     2.0    41    38.0    45     2.0
            3    46     1.0    47     2.0    48     1.0    49     2.0    50     1.0
            3    51     2.0    52    13.0    53     2.0    54     2.0
            4     2     1.0     3     2.0     4     2.0     5    38.0     6     2.0
            4    10     3.0    13     3.0    20     1.0    23    13.0    25     3.0
            4    26     2.0    27     2.0    30    38.0    36     2.0    42     3.0
            4    55     2.0    56     2.0    57     3.0    58     2.0    59     2.0
            4    60     3.0    61     2.0    62     2.0    63     1.0    64     2.0
            4    65     1.0    66     2.0
        0000
        ACHI#MI6AGRIEUP6ARRHELA6ASTEAME6BRAYPIN6BUPLFAL6CENTSCA6CLINVUL6CORUSAN7CRATMON7
        DACYGLO6ELYMREP6FESTRUI6FRAGVES6GENITIN6HIERPIL6HIERSAB6KNAUKIT6MEDIFAL6ORIGVUL6
        PIMP#SA6PLAALAN6PRUUFRU6RANUPOA6SALVPRA6SANGMIN6STACREC6TARASEO6VERBC-A6VICITEN6
        ALYSALY6AREN#SE6ASPRCYN6CHAARAT6FESTVAL6FRAGVIR6GERASAN6INULENS6KOELMAC6MEDIMIN6
        POTEINC6ROSA#CN7TEUCCHA6THLSPER6ARENSER6COLTARB7MEDI*VA6PRUUSPI7ROSAPIM6RUBUCAE6
        SCABOCH6SESEOSS6STAC#RE6THYU#PA6ACERCAM7ASTAGLY6CAREMIC6CARIBET4CRATMON4CYTINIG6
        ERYNCAM6EUPHPOL6GALUVEU6HELINUM6PICRHIE6ROSARUB4
           400179   400180   400181   400182
```

Header data are imported automatically if header data files have the same name as the CC! file and have a correct format. (See Section 1.4.6.)

The import process starts with selection of the CC! file. Then the following window appears:
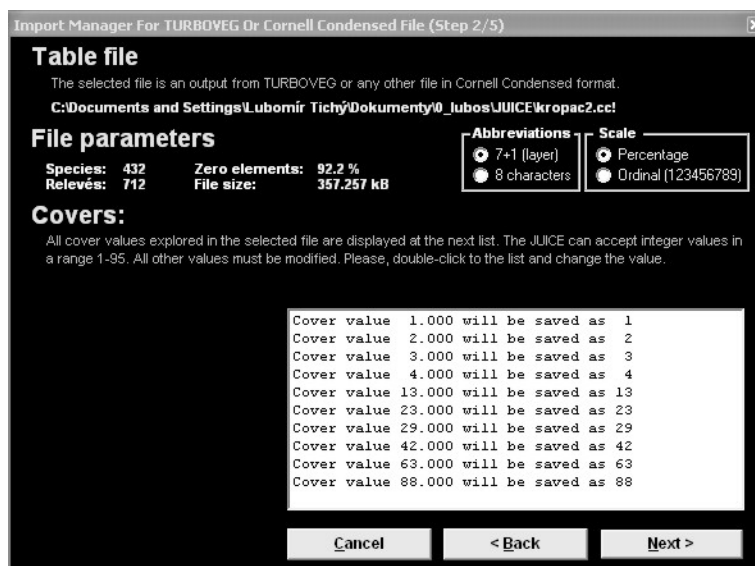
Fig. 2: Cornell condensed file import (1st and 2nd step).

The basic statistics of the selected file are presented under 'File parameters'. If they are incorrect, this indicates that the file is not suitable for this type of import. TURBOVEG files are defined with species abbreviations in the format '7+1' (7 characters encode the species name and the last character is reserved for the layer number); however, CC! files without layer identification can be imported by selecting the option '8 characters'. The scale is

detected automatically, but it can also be selected manually. (TURBOVEG exports only percentage values.)

The program checks all cover values and tries to convert them to whole numbers from 1 to 95. If a value cannot be imported automatically, it is necessary to supply the correct conversion. Double-clicking on a line in the 'Covers' list box opens a window for entering the corresponding value.

Fig. 3: Cornell condensed file import (3rd and 4th step).

The next step is to specify the species list. If the species list was loaded successfully and used for importing a previous table, the program will automatically use this pre-defined file as the source of full species names. However, it is possible to use a different species list or import species as abbreviations.

Header data will be loaded automatically from a pair of header data files with the same name as the CC! file with suffixes EXP and STR. It is also possible to import a tab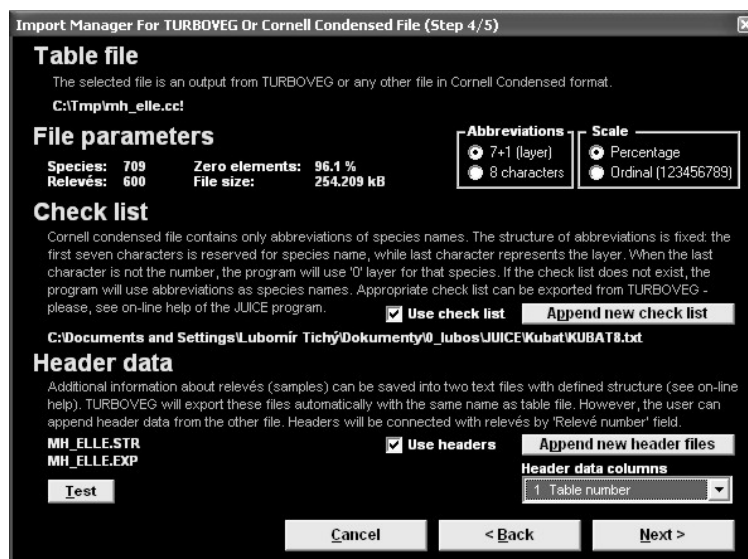le without header data or use a different header data file by clicking on the button 'Append new header files'. The program allows the use of headers from a different import package (e.g., headers with a differently defined list of fields). Such headers need not be complete. It is recommended that you test their compatibility with the 'Test' button. The test will identify the number of relevés with headers.

Note: Connecting table data with headers is only possible if the header data file contains the 'Relevé number' field with unique identification numbers.

1.4.3   Species Lists

Although the abbreviations used in Cornell condensed files should uniquely specify the species, the final presentation of the table usually requires full species names. The program uses a species list file in simple text format. Such a file can easily be exported from TURBOVEG. (From the 'Manage' menu in TURBOVEG, select 'Species Lists' and 'Edit'. Enter the name of the species list and select 'Export' and 'Limited List For JUICE'.) It can also be created manually as a comma-delimited file or a file with a fixed length for each line. Examples are shown below:

```
Format 1:
----I------I--------------------------------------------I
1    ABIEALBAbies alba
12251ABIEGRAAbies grandis
2    ABIE-SPAbies species
4    ABITASAAbietinella abietina var. abietina
5    ABITASHAbietinella abietina var. hystricosa
3    ABITABIAbietinella abietina
Each column has the same number of characters in each line. The first line defines three fields with 5, 7 and 50 characters.


Format 2:
1,ABIEALB,Abies alba
12251,ABIEGRA,Abies grandis
2,ABIE-SP,Abies species
4,ABITASA,Abietinella abietina var. abietina
5,ABITASH,Abietinella abietina var. hystricosa
3,ABITABI,Abietinella abietina
Data are in three comma-delimited columns.


Format 3:
ABIEALB,Abies alba
ABIEGRA,Abies grandis
ABIE-SP,Abies species
ABITASA,Abietinella abietina var. abietina
ABITASH,Abietinella abietina var. hystricosa
ABITABI,Abietinella abietina
Data are in two comma-delimited columns.
```

Note: The species list included in the JUICE installation package is useful only for central European users who are using TURBOVEG with the standard central European check list. Users from the Czech Republic can use the included KUBAT#.TXT check list with standard nomenclature (Kubát et al. 2002). A current version of this check list is available at:

http://www.sci.muni.cz/botany/juice/jc05_che.htm

A new species list file can be defined in the 'Check List Import' tab of the 'Options' window (available from the 'File' menu). If no species list is defined, the program will open this window during the import of the CC! file:

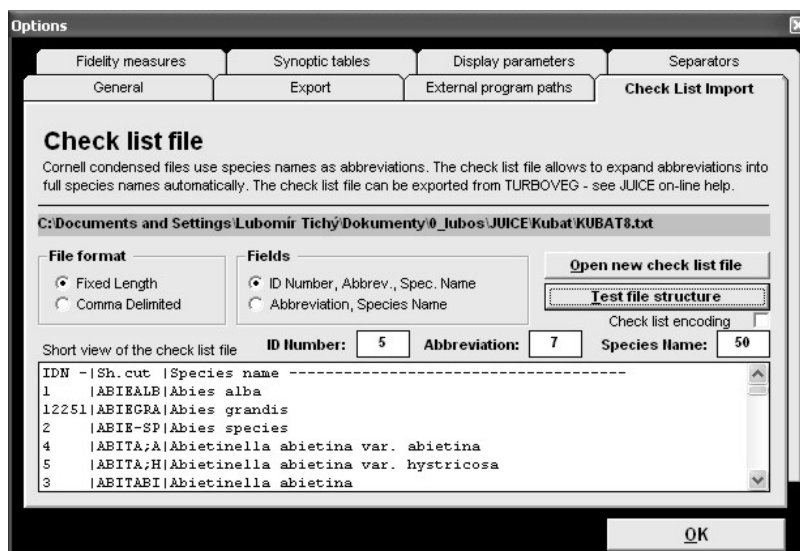Fig. 4: Options (Check List Import).

The button 'Open new check list file' allows the user to specify a new species list file. The 'ID Number', 'Abbreviation' and 'Species Name' boxes are used to define the number of characters reserved for each field. If the first line of the file defines the length of these fields, the values appear in the boxes automatically. The file format can be tested by clicking on the

'Test file structure' button. 'Check list encoding' must be switched on for the NEWFLORA.TXT file. Other files are not encoded.

1.4.4 Spreadsheet Format

A spreadsheet format file contains the title of the table (first line), the number of relevés, the relevé numbers, and the table itself (species name, layer and cover codes). Cover codes may be characters from the Braun-Blanquet scale (or any other) or percentage values.

The Import Manager begins by prompting you to select a file. When the file is selected, you are informed about the title of the table, the character used to delimit columns, layer information and table size (steps 2 through 5). If the file contains only species names without layer information, uncheck the box in step 4. In step 5, make sure that the indicated table size is correct. In step 6, make sure the table corresponds with real data.

The last step is to specify the cover values. If the scale is in Braun-Blanquet codes or percentage values, simply select the appropriate option. Otherwise, cover values must be specified manually. All codes which have been found in the table will be displayed in the list on the right side of the window. Double-click on a code to enter a percentage value for the cover represented by the code. The program can continue only if all codes are associated with a whole percentage value.

An example is given below. An example is also available on the JUICE web page.

```
Table from  relevés of the file: paseky.wct
Number of relevés: 5

;; 434111 ; 434112 ; 434113 ; 311728 ; 311725
Calamagrostis villosa;6;5;4;4;5;3
Avenella flexuosa;6;2;2;3;1;2
Vaccinium myrtillus;6;1;1;1;1;+
Rubus idaeus;4;2;2;2;1;.
Maianthemum bifolium;6;2;3;3;.;.
Veratrum album ssp. lobelianum;6;2;2;3;.;.
Oxalis acetosella;6;2;2;3;.;.
Senecio fuchsii;6;1;.;.;1;1
Equisetum sylvaticum;6;2;2;.;.;.
Phegopteris connectilis;6;2;2;.;.;.
Anemone nemorosa;6;2;2;.;.;.
Betula pendula;8;.;r;1;.;.
Picea pungens;4;.;.;.;2;2
Betula pendula;4;.;.;.;1;2
Galium saxatile;6;.;.;.;+;2
Trientalis europaea;6;.;.;.;+;+
Athyrium filix-femina;6;2;.;.;.;.
Deschampsia cespitosa;6;1;.;.;.;.
Luzula luzuloides;6;.;.;.;.;+
```

The second column represents layer; it is optional. All cover data can be converted into percentage numbers or some semi-quantitative scale. This format can use full species names or abbreviations.

The spreadsheet format must not contain header data. Header data can be imported separately as described in Section 1.4.6.

1.4.5 Text Format

For users without TURBOVEG, this is the easiest import format. The table consists of four files with the same name and different suffixes: TXT, TAB, EXP and STR. (Similar files can also be exported by JUICE. From the 'File' menu, select 'Export' and 'Table' and choose the 'TEXT FILE' format.)

The **TXT file** consists of three columns (species name, layer number and table data) separated by at least 5 spaces.

```
Anemone nemorosa               6    22....
Athyrium filix-femina          6    2....+
Atrichum undulatum             9    .....+
Avenella flexuosa              6    223123
Betula pendula                 4    ...12+
Betula pendula                 8    .r1...
Calamagrostis arundinacea      6    ....1.
Calamagrostis villosa          6    544533
Carex leporina                 6    ....++
Deschampsia cespitosa          6    1.....
Dryopteris dilatata            6    .....+
Epilobium angustifolium        6    ...+.+
Equisetum sylvaticum           6    22....
Fagus sylvatica                1    ....+.
Fagus sylvatica                4    ...1..
```

The **TAB file** is optional. Each line contains a unique relevé identification number (in a range from 1 to 999 999).

```
434111
434112
434113
311728
311725
311724
```

The **EXP** and **STR files** contain header data. (See Section 1.4.6.)

1.4.6   Header Data

There are three ways to import header data into JUICE:

1. Header data are included automatically in the XML file exported from TURBOVEG. You can select which fields to import during the import of this file into JUICE as described in Section 1.4.1.
2. When TURBOVEG exports a CC! file for JUICE, it automatically exports header data in an STR and an EXP file. The user must select header data fields to export during the export from TURBOVEG. Header data will import automatically with the CC! file if all the files have the same name.
3. All header data contained in an STR and EXP file can be imported separately. From the 'File' menu, select 'Import' and 'Header Data'. This is useful when (a) you wish to select different header data fields or (b) you need to add new header data to a spreadsheet format file or to any table without header data.

STR and EXP files are simple text files containing definitions and field values:

An **STR file** defines table data variable names and their starting character position in each line of the corresponding EXP file. The first column defines the first character of the field; the

```
 1   Table number
 6   Relevé number
12   Year
16   Month
18   Day
20   Author code
24   Altitude (m)
28   Aspect (degrees)
31   Slope (degrees)
33   Cover total (%)
36   Cover tree layer (%)
39   Cover shrub layer (%)
42   Cover herb layer (%)
45   Cover moss layer (%)
48   Mosses identified (y/n)
```

second column represents the name of the field.

Warning: *Each STR file must contain the field 'Relevé number' specifying where to find the relevé's unique identification number.*

An **EXP file** contains values of fields defined in a corresponding STR file (e.g., relevé information about the site and environmental factors). All fields must be consistent with the format specified in the STR file.

```
 1400753199606050001 260    5 100  0  0100 20Y
 2400754199606050001 280   20 90   0  0 90  3Y
 3400756199606050001 250   15 80   0  0 80  1Y
 4400813199606190001 200   10100  0  0100  0Y
 5402212199706280001 240   20  0   0  0 70 10Y
 6403158       0139   27025  0  0  0 80  0Y
 7403159       0139   27025  0  0  0 70  0Y
 8403161       0139   15810  0  0  0 95  0Y
 9403162       0139   15825  0  0  0 95  0Y
10403166       0139   2485   0  0  0 90  0Y
11403167       0139   22510  0  0  0 95  0Y
12403168       0139   22510  0  0  0 95  0Y
13403169       0139   22510  0  0  0 95  0Y
14403171       0139   22515  0  0  0 95  0Y
15403174       0139    9030  0  0  0 95  0Y
```

1.5 The Basics of Working with Tables

This section describes the most basic functions for organising phytosociological data imported into JUICE. The entire process is graphically oriented and more or less intuitive, but the following text will explain some of the hidden features of the program.
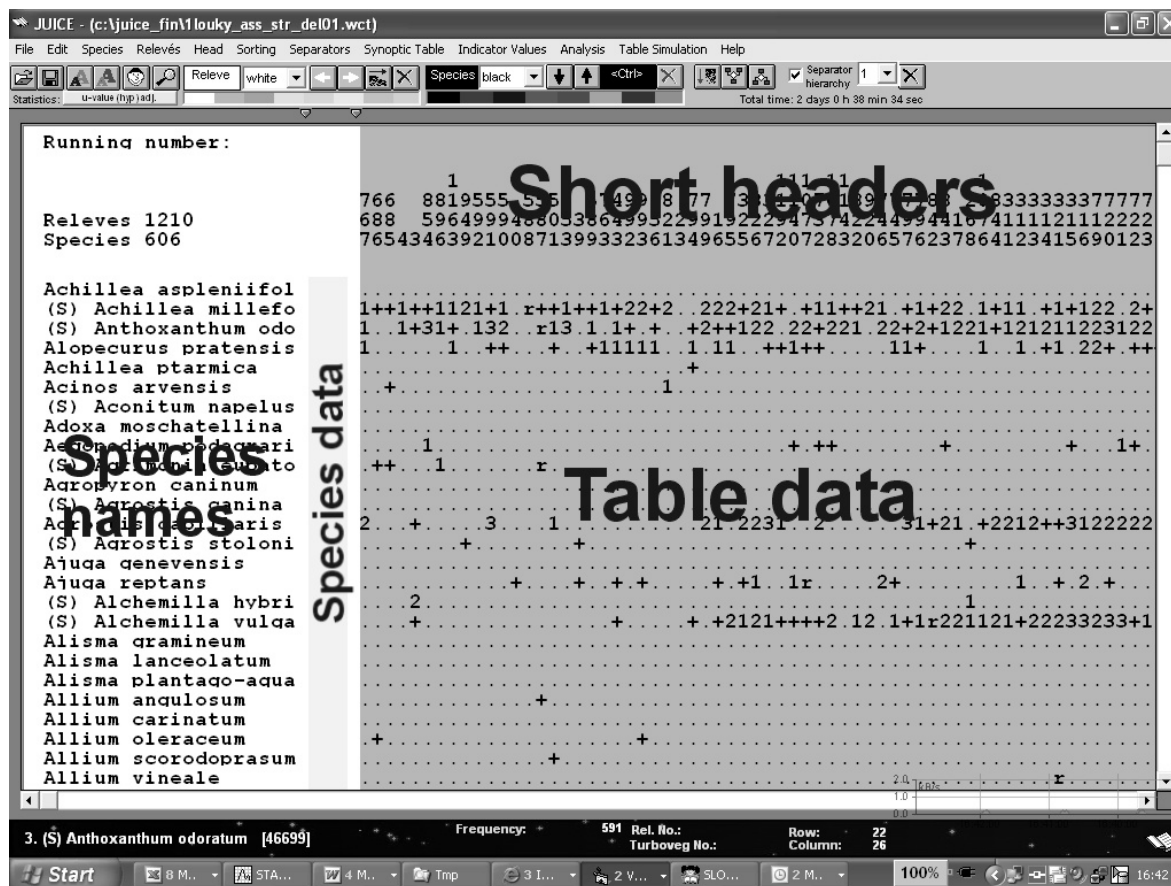
1.5.1 Table Window Components

Fig. 5: Main window of the program.

The table window is divided into three parts: short headers, species names and table data. The Species Data Column can hold additional information about a species such as layer, biological information or Ellenberg indicator value (Ellenberg et al. 1992).

The Menu Bar, with twelve items, is at the top of the window. The Icon Bar is below the Menu Bar. Some menu functions are directly accessible as icons. See the figure below.
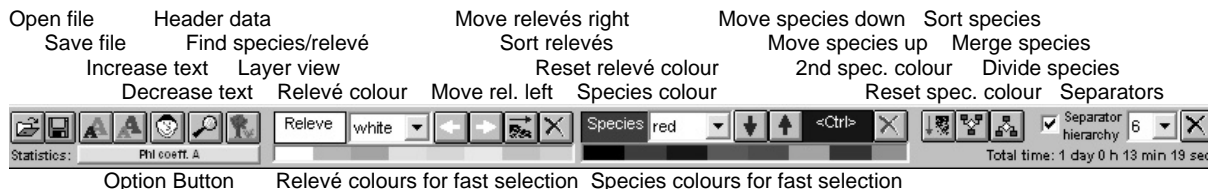

Note 1: The buttons 'Reset relevé colour' and 'Reset species colour' have two functions: One click of the left mouse button will reset the currently selected colour, while double-clicking will reset all colours. (See Sections 1.5.2 and 1.5.3 for more information on colours.)

Note 2: The Option Button opens the 'Options' window (also available from the 'File' menu). Its purpose is to provide quick access to the 'Fidelity' tab (see Section 1.10.3) but other

option tabs are available (such as the 'Display parameters' tab described in Section 1.5.8 below).

The Status Bar at the bottom of the window contains information about the last species selected: its order in the list, its full species name (to a maximum of 50 characters), its layer number and its total frequency in the data set. The values 'Rel. No.' (the relevé's relative number in the imported data set) and 'Turboveg No.' (a unique TURBOVEG number in the range 1-999 999) refer to the most recently selected relevé. The 'Row' and 'Column' values give the current position of the cursor in the table.
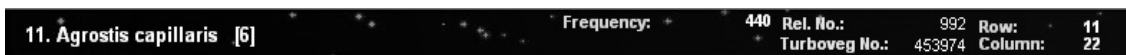
1.5.2   Mouse/Keyboard Functions

Working with table data requires the use of the mouse in combination with the keyboard.
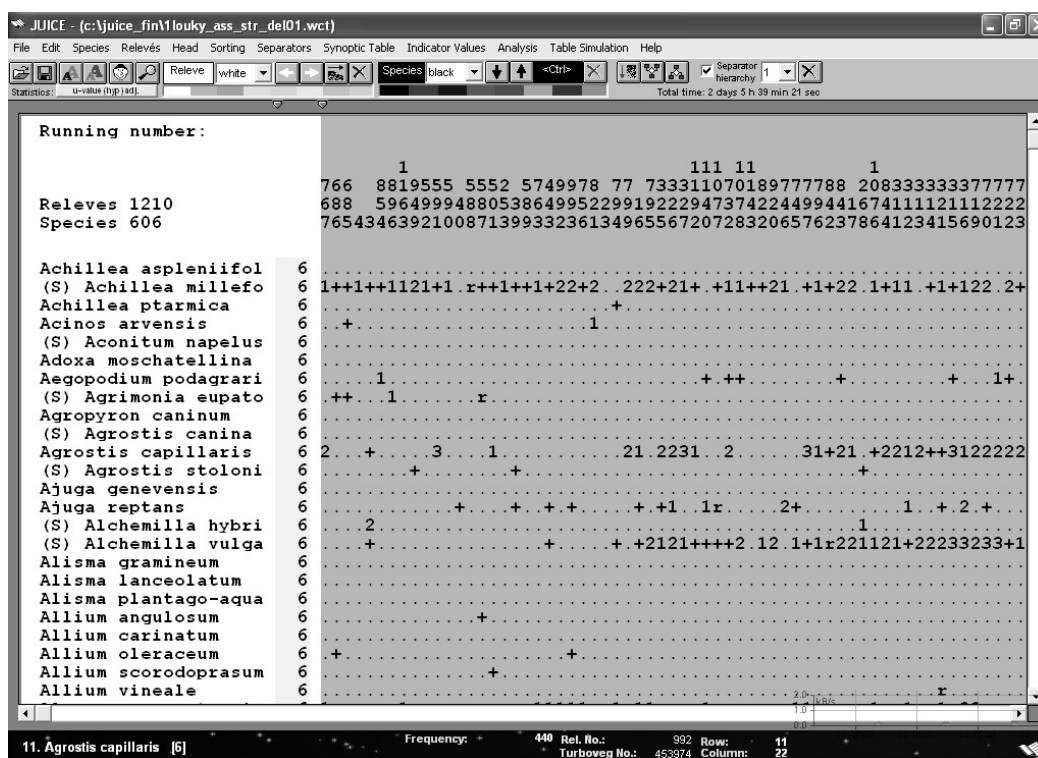
In tables:

Fig. 6: Table.

The three parts of the table (see Section 1.5.1 above) are sensitive to different operations:

When the cursor is in the short headers:

Left button	Click	Highlight and select relevé.
Left button	Double click	Display list of species in selected relevé and save selected relevé in text form to clipboard.
Left button	Click and drag	Move currently selected relevé
Shift+left button	Click	Make/remove separator line to the right of currently selected relevé.
Right button	Click	Repaint currently selected relevé with current relevé colour.
Shift+right button	Click	Repaint block of relevés with current relevé colour. (Click on the leftmost relevé to be selected. Hold Shift and click on the rightmost relevé. The entire relevé interval will be repainted.)

When the cursor is in the species names:

Left button	Click	Highlight and select species.
Left button	Double click	Open dialog window for editing species name, layer and data.
Left button	Click and drag	Move currently selected species.
Shift+left button	Click	Make/remove separator line below currently selected species.
Right button	Click	Repaint currently selected species with current species colour.
Ctrl+right button	Click	Repaint currently selected species with current secondary species colour.
Shift+right button	Click	Repaint block of species with current species colour. (Click on the first species to be selected. Hold Shift and click on the last species. The entire species interval will be repainted.)

When the cursor is in the table data:

Left button	Click	Highlight and select species and relevé.
Left button	Double click	Display list of species in selected relevé and save selected relevé in text form to clipboard.
Right button	Click	Repaint currently selected species with current species colour.
Ctrl+right button	Click	Repaint currently selected species with current secondary species colour.
Shift+right button	Click	Repaint block of species with current species colour. (Click on the first species to be selected. Hold Shift and click on the last species. The entire species interval will be repainted.)

In synoptic tables:

Fig. 7: Synoptic table.

Functions are slightly different in synoptic tables:

When the cursor is in the short headers:

Left button	Click and drag	Move currently selected relevé group (column).

When the cursor is in the species names:

Left button	Click	Highlight and select species.
Left button	Double click	Open dialog window for editing species name, layer and data.
Left button	Click and drag	Move currently selected species.
Shift+left button	Click	Make/remove separator line below currently selected species.
Right button	Click	Repaint currently selected species with current species colour.
Ctrl+right button	Click	Repaint currently selected species with current secondary species colour.
Shift+right button	Click	Repaint block of species with current species colour. (Click on the first species to be selected. Hold Shift and click on the last species. The entire species interval will be repainted.)

In header data:

Fig. 8: Header data.

These functions are defined for Header Data Display:

When the cursor is in the header data:

Left button	Double click	Display list of species in selected relevé and save selected relevé in text form to clipboard.
Shift+left button	Click	Make/remove separator line below currently selected relevé.
Right button	Click	Repaint currently selected relevé with current relevé colour.
Shift+right button	Click	Repaint block of relevés with current relevé colour. (Click on the top relevé to be selected. Hold Shift and click on the bottom relevé. The entire relevé interval will be repainted.)

1.5.3 Colours

As indicated in the previous section, relevés and species can be assigned colours. These colour codes can then be used for data processing, analysis and classification. Relevés and species each have eight colours available, which can be selected from the Icon Bar. The basic colour for relevés is white, while for species it is black. Colours enable organisation or analysis of data in a selected part of the data set. Colour coding makes selection and manipulation of groups of relevés or species easier and quicker, and sorted data may have a clearer structure. The mouse commands for colouring relevés and species are described in Section 1.5.2 above. Colours can also be assigned according to information in the short headers, as described in Section 1.8.3. Using colour-coding to gather relevés and species into blocks is explained in Section 1.5.5 below.

1.5.4 Separators

Separators divide a table into sections. This is necessary for defining synoptic tables or species group tables. Such tables are used to analyse constancy, fidelity and similar measures of a relevé group's relation to species or a species group's relation to relevés.

Separators are placed or removed by holding down the Shift key and clicking on the relevé or species with the left mouse button. (See Section 1.5.2.) The separator appears on the right side of the indicated relevé or below the indicated species.
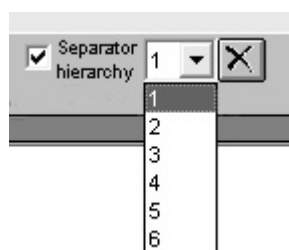
Fig. 9: Separator switches in the Menu bar.

The program includes the option to work with six hierarchical layers of separators. Level 1 can be used for major groupings, level 2 can be used for subgroupings, and so on. When the hierarchy is turned on, the user can choose how many levels will be displayed. The top level, level 1, is always on, while the bottom level, level 6, is only on if the user chooses to display all 6 levels. These switches can be found on the Icon Bar or under the 'Separators' tab of the 'Options' window (which can be opened from the 'File' menu).

Note: *Moving synoptic columns (see Section 1.5.2) will destroy relevé separator hierarchy. All separators in different levels will be changed into separators of the top level.*

1.5.5   Gathering Species or Relevés into Blocks

Before separators can be used to define species or relevé groups, it is necessary to gather similar items to the same part of the table. While it is possible to manually drag each individual row or column to the appropriate place, it is quicker and easier to use colour-coding. This is a two-step process. The example below illustrates gathering relevés into a block. The process for species is analogous.

Give the relevés to be gathered a single colour, distinct from the other relevés in the table.
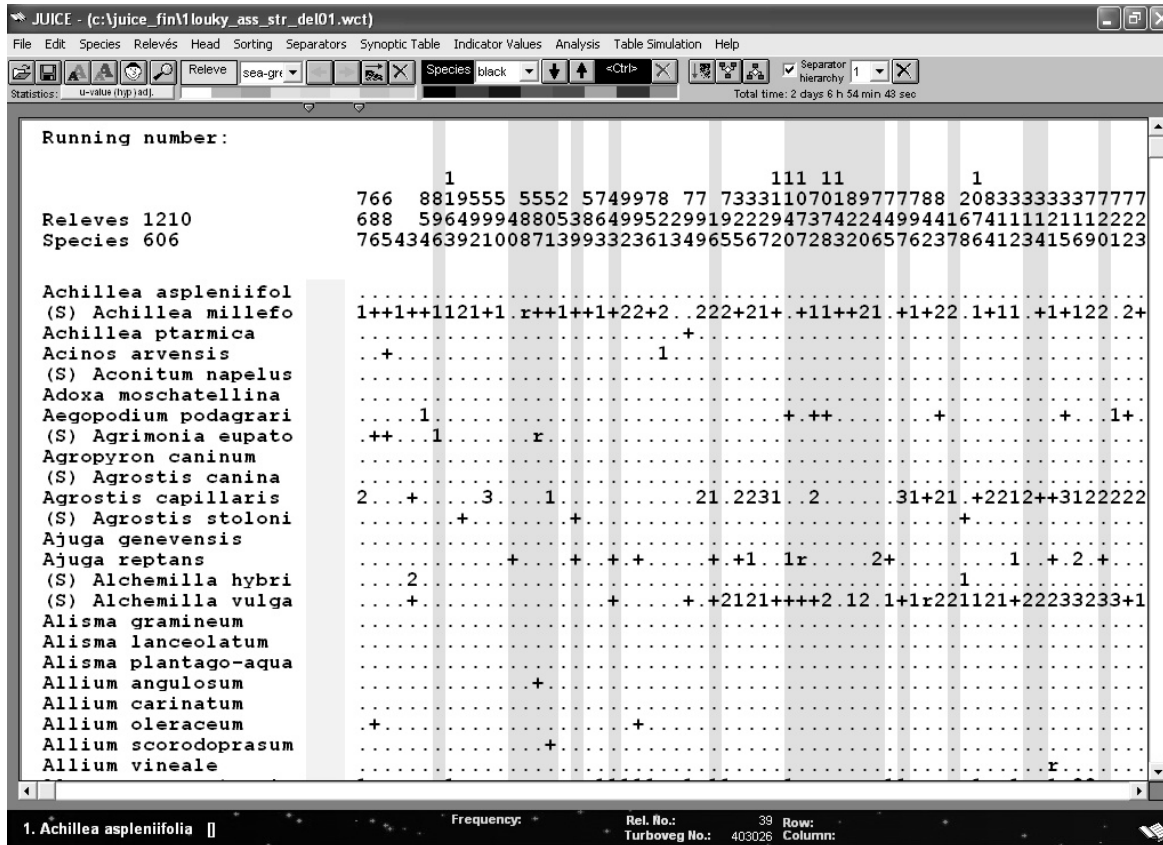
Fig. 10: The table with selected relevés.

Gather the relevés using the arrow buttons on the Icon Bar or the 'Move Relevés' function in the 'Sorting' menu. Specify whether the relevés are to be gathered to the left or to the right. (The illustration below shows relevés that have been gathered to the left.)
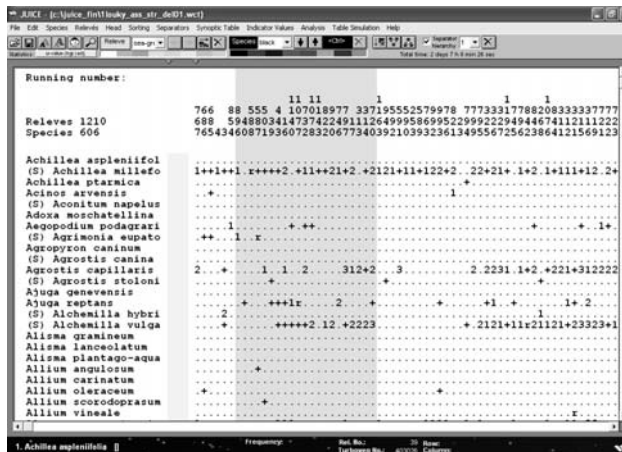
Fig. 11: The table after moving all selected relevés to the left.

Note that JUICE does not gather all the relevés to the leftmost edge of the table. They are simply gathered to the leftmost (or rightmost) relevé of the selected colour. To move the block of relevés to the left, use this trick:

1. Drag the leftmost relevé in the block to the place the block should be.
2. Gather the relevés to the left again.

This will move all the relevés to the left. To move them to the right, move the rightmost relevé to the desired position and re-gather to the right.

If the program seems to not respond to an attempt to gather relevés or species, make sure the correct colour is selected in the Icon Bar. JUICE only gathers relevés or species of the selected colour.

JUICE can also group species and relevés automatically without using colours. The 'Sorting' menu contains several other options for sorting species and relevés. See Section 1.6.3.

1.5.6 Relevé Overview Display

Each relevé in the table can be displayed in condensed form by double-clicking on it. (See Section 1.5.2.) Species in the relevé can be sorted by layer, cover, alphabetical order or current position in the table. When the relevé display is opened or its sorting method is changed, the relevé is copied into the clipboard memory – the user can paste this information into a text editor or other program.

Fig. 12: Selected relevé displayed at the right site of the window.

1.5.7   Editing Species and Header Data

JUICE is not database-oriented software for data archiving. All changes are saved only in the current table without impacting a database source. Therefore, we strongly recommend archiving phytosociological or ecological data in a database program (e.g., TURBOVEG) and making all changes in the original data set.

However, it is possible to modify some data in an existing JUICE file:

Fig. 13: The window for editing species names, layers and species data.

a) Species names, layers and species data values can be edited by double-clicking on the species name.

b) Cover values displayed in the table can be edited from the 'Table Simulation' menu. Selecting 'Add/Remove Species Cover' opens a window for specifying the value to be written into the table.

Warning: In cover-value editing mode, the program changes mouse functions. The left mouse button writes the specified cover value to the indicated position in the table, while the right mouse button deletes the value in the indicated position (i.e., overwrites it with cover value 0). It is best to save a backup file before editing cover data because JUICE does not keep track of the original values, so these cover modifications are irreversible. After data modification, select the 'Table Simulation' menu and 'Add/Remove Species Cover' once more, and mouse functions will return to normal.

c) Header data can be accessed from the Relevé Overview Window. (See Section 1.5.6.) Clicking on the 'Edit header' button opens the following window:

Fig. 14: Editing header data.

The two arrow buttons enable selection of the field to be edited. Click the right arrow button until the desired field name appears. Type the new value into the text box. Then press the 'Save' button. If the 'Save' button is not pressed, the value will not change. The left arrow button initially does nothing, but after the right arrow button has been pressed, the left arrow button can be used to go back to a previous field.

1.5.8   Screen Options

Display parameters are defined in the 'Options' window under the 'Display parameters' tab. It is possible to modify:

1. Displayed length of species names
2. Width of species data field
3. Size and style of text
4. Background contrast.
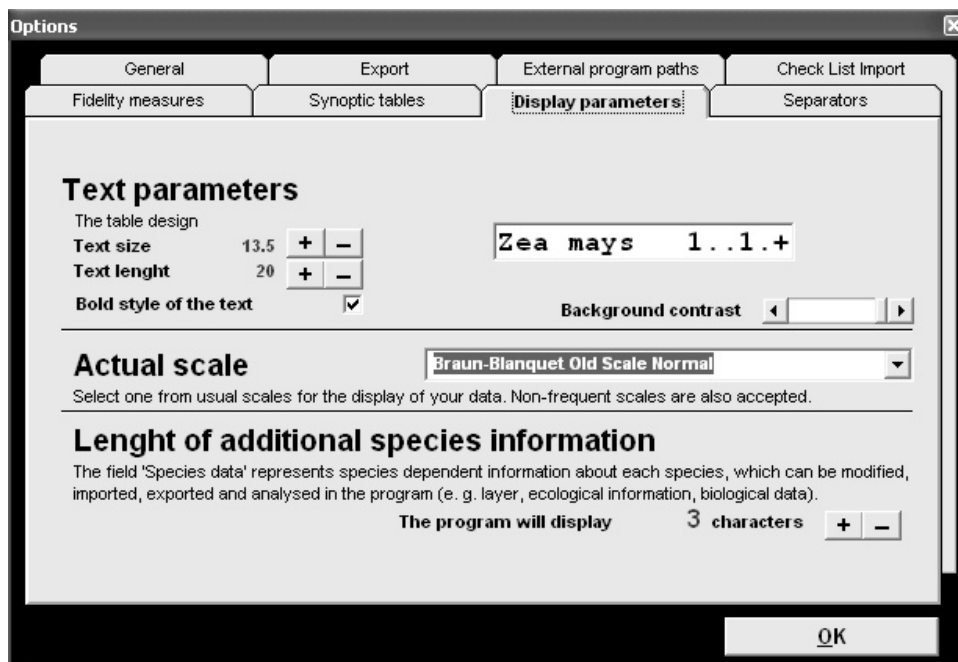
Fig. 15: Options window (Display Parameters)

Note: The width of the Species and Species Data Columns can also be modified using the markers at the top of the table. Text size can also be modified using the two text size icons on the Icon Bar.

1.5.9   Defining Scales

All cover data are saved in the form of percentage numbers. The program accepts integer numbers from 0 to 100. Each number from 1 to 94 can be assigned a character, while numbers from 95 to 100 are assigned the same character. The program has four predefined scales: 'Braun-Blanquet Old', 'Braun-Blanquet Old and New', 'Ordinal' and 'Presence/Absence'. All other scales must be defined by the user. The scale is selected in a

Fig. 16: Defined scales

combo box in the 'Display parameters' tab of the 'Options' window. Selecting 'User Defined Scale' turns on the 'Modify' button. Clicking on this button opens the following window:

Fig. 17: Window for definition of user defined scale.

Every percentage number must be represented by one character which will be displayed in the table. This scale is saved in the JUICE.INI file and is loaded each time JUICE is started.

1.5.10 Header Data

Full header data are displayed separately. JUICE must be switched from Standard Display to Header Data Display by selecting 'Extended Head' from the 'Head' menu or by clicking on the Head Icon on the Icon Bar. In Header Data Display mode, each relevé has its own row. The header data fields are in the same order as in the EXP and STR files. (See Section 1.4.6 for more information on these files.) All names of fields defined in the STR file are written at the top of the table. All table data must contain the field 'Relevé number', which is a unique identification number connecting headers with table data.

Fig. 18: Header data display.

All screen parameters are defined similarly as in the Standard Display. (See Section 1.5.8.) Mouse functions are described in Section 1.5.2. If it is necessary to change this data, the changes should be made in the source data set. However, it is possible to edit this information within JUICE. See Section 1.5.7.

Note: It is not possible to add a new header field to the header data. To add new information, define the new field in TURBOVEG and re-export the header data. (See Section 1.4.6.)

1.5.10.1   Selecting Relevés by Header Data

Section 1.5.5 explains how to organise colour-coded relevés into blocks. JUICE includes functions for colour-coding relevés according to their header data:

1. Select a relevé colour on the Icon Bar.
2. Open the 'Head' menu and select 'Relevé Colour According To The Head'. This will open the following window:

Fig. 19: Window for colouring relevés by header data.

3. From the list, select the relevant field.
4. In the text box, type the text to be matched.
5. Hit the 'Continue' button.

Relevés matching the text are given the indicated colour. The number in the 'Selected relevés' field indicates how many relevés match the text.

JUICE provides two text-matching functions. 'Function LIKE' requires exact matching of the text in the box, but it supports wildcard characters. A # symbol represents any character and a * symbol represents any string of characters. For example, '1##' can be used to select all relevés at an altitude of 100-199 m because it matches text like '132' and '149' but not '711' (the first character is not '1') nor '1324' (the text is more than 3 characters long). The text '1*' would match all numbers beginning with '1' including '1', '13', '149', and '1324'.

'Function InStr' looks for matches in any part of the selected field. It does not support wildcard characters. For example, to colour all relevés that mention Germany in their locality, use 'Function InStr' with 'Germany' in the text box. (Note that this is equivalent to using 'Function LIKE' with '*Germany*' in the text box.) But to select only relevés with localities that *begin* with the word 'Germany', use 'Function LIKE' with 'Germany*' in the text box.

1.5.11 Searching

Finding a certain species or relevé can be difficult in larger tables. The 'Find Species' and 'Find Relevé' functions (available in the 'Species' or 'Relevé' menu or from the Icon Bar) will display a text box in the Status Bar below the table. Type in part of the species name and press the 'Find Species/Head' button. The program will find the next species name that begins with that text and highlight the selected row. Pressing the button again will find and highlight the next matching species.

Example: *The table sorted by layers contains the species 'Alnus glutinosa' in three layers (tree, shrub and juvenile). After the first selection of the 'Find' button, the program will display the part with the selected species in the tree layer, the second selection will move the table to the species in the shrub layer, the third selection will find 'Alnus glutinosa' in the juvenile layer, and the fourth selection will move the display back to the position with the selected species in the tree layer.*

When JUICE is in Header Data Display (see Section 1.5.10), the text box can be used to search for relevés that match the text. In this case, a match occurs if the text appears anywhere in the relevé's header data. The list will scroll so that the next relevé that matches the indicated text is highlighted at the top of the list window.

Note: *It is also possible to match the text with any part of a species name. The mode of searching can be changed in the 'Find Species/Relevés function' section of the 'General' tab in the 'Options' window.*
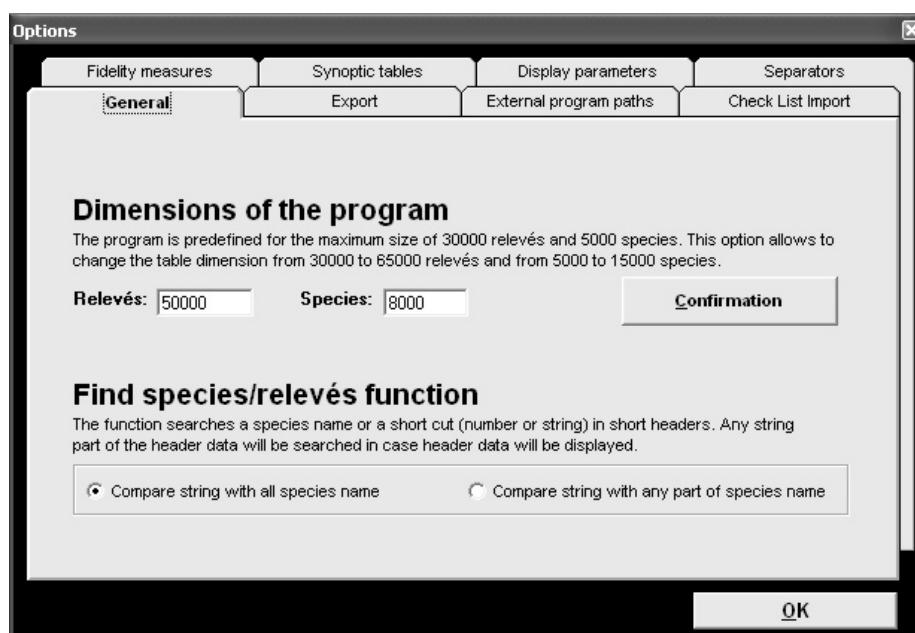
Fig. 20: Options (General).

1.5.12 The 'Undo' Function

Some operations (colours, relevé/species positions, separators etc.) are reversible. Often, an incorrect step can be repaired with the 'Undo' function (in the 'Edit' menu).

Notes: *'Undo' is only supported for one operation. It is not possible to 'Undo' multiple mistakes. In addition, the 'Undo' function does not support changes in data structure (species names, cover codes, deleting relevés and species etc.). We recommend that you create backup WCT files as frequently as possible.*

1.6 Editing Tables

Analysis, classification or publication of phytosociological tables requires a clear data set without residuals or incorrectly identified species and with correct nomenclatorial background. If the source data set consists of relevés in different scales and taxonomical concepts sampled by different authors, it is necessary to unify the data. This section describes how to accomplish these operations.

1.6.1   Merging Species

Species should be merged immediately after importing the table. To merge nominally different taxa into one taxon, follow these steps:

1. Sort the species list into alphabetical order. (From the 'Sorting' menu, select 'Sort species alphabetically' and 'ALL'.)
2. Choose a secondary species colour. Species of this colour will be merged. To select the colour, hold down the Ctrl key and click on the colour on the Icon Bar. The box labelled '<Ctrl>' will display the selected colour.
3. Mark species to be aggregated with this secondary colour. Hold down the Ctrl key while *right* clicking on the species name. Make sure no other species are marked with this colour.
4. From the 'Species' menu, select 'Merge <selected> Species' or press Ctrl+L.
5. Confirm name and layer of the new aggregated species. All the species contained in the resulting aggregated species are automatically deleted from the data set.

The cover of the aggregation is calculated under the assumption that covers can overlap and that they do so independently of each other:

Example: Species 1 – cover 50 %, Species 2 – cover 30 %, Species 3 – cover 20 %. JUICE starts with 50%, the cover of the first species. Under the independence assumption, the second species covers 30% of the area covered by Species 1 and 30% of the area not covered by Species 1. This gives an additional 15% cover (0.5 × 0.3 = 0.15). These two species occupy together 0.50 + 0.15 = 0.65 = 65 % of the sample plot. Species 3 covers 20% of this covered area and 20% of the remaining 35%. The area covered only by Species 3 is 7% (0.20 × 0.35 = 0.07). The total area covered by at least one of the three species will be:

$$0.50 + (1.00 - 0.50) \times 0.30 + (1.00 - 0.65) \times 0.20 = 0.72 = 72\ \%.$$

Note that this is equivalent to calculating the area not covered by any species. Under the independence assumption this area is:

$$(1 - 0.50) \times (1 - 0.30) \times (1 - 0.20) = 0.28 = 28\%.$$

This means 72% is covered by at least one of the three species.

This independence assumption is most appropriate when merging different layers for the same species. When merging distinct species of one layer into an aggregate, it may be more reasonable to assume the covers are mutually exclusive. In this case the average cover values computed by JUICE may underestimate the resulting cover; however, other aggregate statistics, such as presence/absence, remain valid.

Note 1: The default name and layer of the aggregation correspond to the first species in the list. If you wish to use a different species to provide the default name and layer, simply move that species to the top of the list. This information can also be entered manually.

Note 2: Merged species are removed from the table. However, each merged species can be returned to the table with the function 'Undelete Species' from the 'Species' menu. See Section 1.6.2.

1.6.2   Deleting and Undeleting Species and Relevés

To delete species from the table, give them a colour and select 'Delete <colour> Species' from the 'Species' menu.

Species which have been deleted from the table or merged into an aggregation can be retrieved using the 'Undelete Species' function from the 'Species' menu. This opens a list of deleted species, which can be sorted by layer, name or time of deletion. Select the species to be restored and press the 'Undelete' button. Multiple species can be selected with Ctrl+click. A block of species can be selected by clicking on the first species and Shift+clicking on the last species.
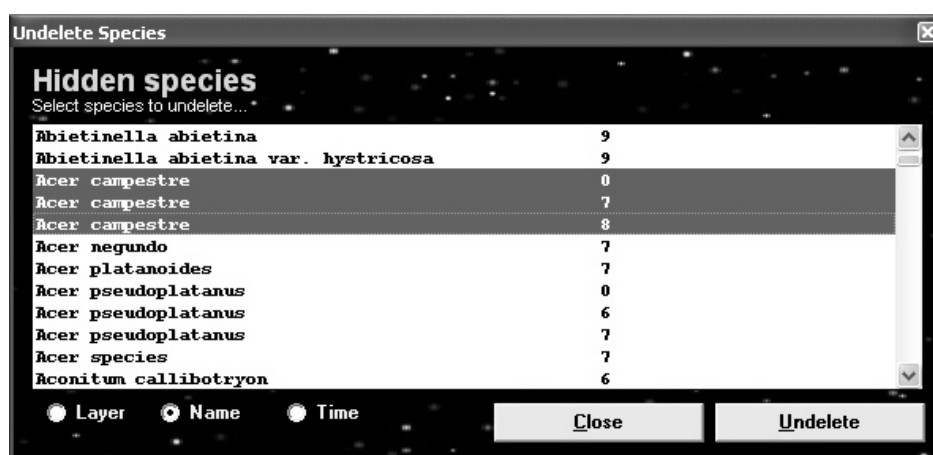
Fig. 21: Window for undeleting species.

Relevés can also be deleted. From the 'Relevé' menu select 'Delete <colour> Relevés'. However, there is no way to restore a deleted relevé.

1.6.3   Sorting Species, Species Data and Relevés

Several types of sorting are available from the 'Sorting' menu. In addition to basic species and relevé sorts, JUICE can also sort according to headers, average Ellenberg indicator values, clusters calculated in PC-ORD etc.

1.6.3.1   Sorting Species and Relevés

From the 'Sorting' menu, choose either 'Sort Species' (Ctrl+D) or 'Sort Relevés' (Ctrl+U). These functions sort species by relevés or relevés by species. The sorting hierarchy is according to (1) frequency, (2) order of relevés (species) and (3) cover. This means that a species which occurs in more relevés is ranked higher. If two species occur in the same number of relevés, the one that occurs in the relevé listed first in the table is ranked higher. Two species that have the same frequency and the same first relevé are ranked according to cover. An analogous system applies to relevés.

Colours can be used to limit the list of species and relevés to be sorted.
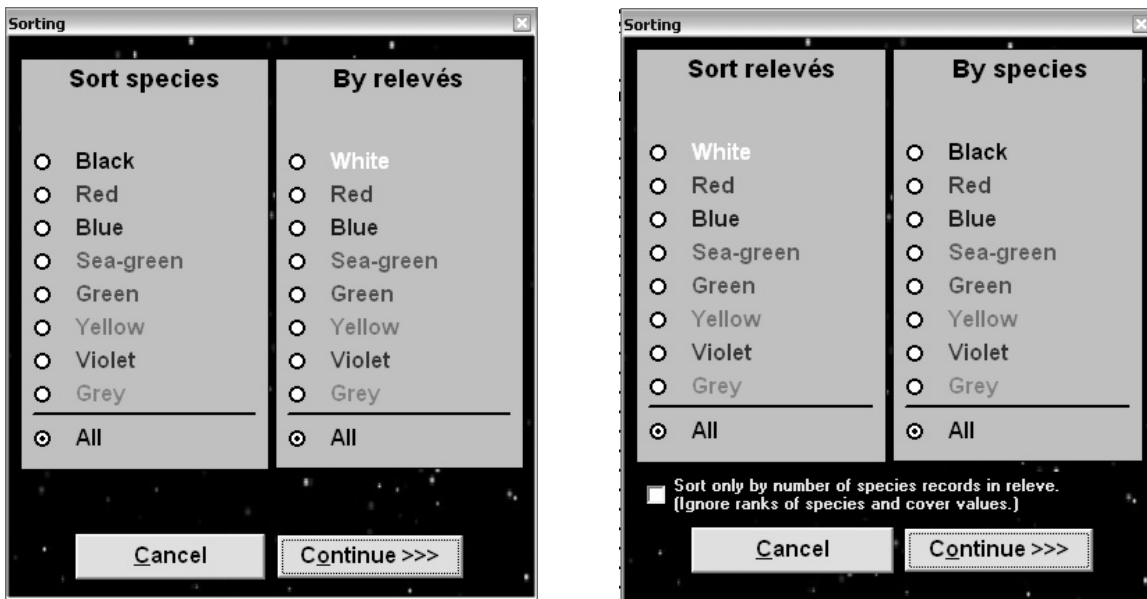
Fig. 22: Windows for sorting species and relevés.

Note: The relevé 'Sorting' window has a check box for altering the sorting method. When the box is checked, only frequency matters and the order of relevés with the same number of species records will not be changed.

1.6.3.2 Other Species Sorting Functions

'Sort Species Alphabetically' can sort all species into alphabetical order or it can be restricted to only sort the species of the selected colour.

'Sort Species By Species Data' sorts according to the information stored in the Species Data Column. (See Section 1.7 for information on how to write data to this column.) This column can contain many types of information such as layer, Ellenberg indicator value, frequency or any other biological information about the species. The 'Species Sorting Parameters' window has several options. The sort can be restricted to species of the selected colour or expanded to include all species. Data can be sorted in alphabetical or numerical order and the order can be ascending or descending.
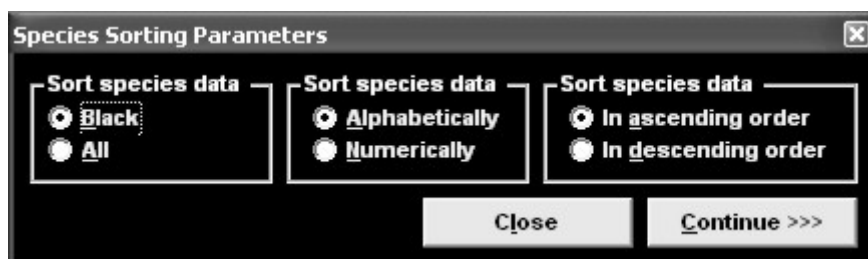
Fig. 23: Window with species sorting parameters.

Note: Numbers should be sorted in numerical order (1, 2, 3, 11, 12, 13, 21, 22, 23) while text strings must be sorted in alphabetical order. If the above numbers are sorted in alphabetical order, the result is: (1, 11, 12, 13, 2, 21, 22, 23, 3).

'Sort Species in Synoptic Table' is available only in Synoptic Table Display mode. The 'Sorting' window has several options. Species can be sorted by various criteria such as constancy, fidelity or average cover. Colour selection can be used to restrict the species included in the sort. This function is described in more detail in Section 1.11.11.

'Sort Species by Median Cover' sorts species by the median of all non-zero cover values in the table. In relatively large and diverse data sets this can be used for deducing the theoretical abundance of each species under optimal conditions. The median cover value is not displayed after sorting. To view the median cover value and other species information, select 'Species Statistics' from the 'Species' menu. (To return to Standard Display mode, select 'Species Statistics' again.)

'Sort Species by Average Vegetation Richness' is similar to the previous function. Average vegetation richness (AVR) is calculated by averaging the number of species in all relevés in which the species occurs. AVR is not displayed after sorting. To view AVR and other species information, select 'Species Statistics' from the 'Species' menu. (To return to Standard Display mode, select 'Species Statistics' again.)

'Dependence Sorting' uses interspecific associations as the main sorting criterion. Interspecific associations between all possible pairs of species are calculated according to the selected fidelity index. For each species, the average value of the selected fidelity measure of the most similar species is calculated, and the data set is subsequently sorted by these average values. The number of similar species considered can be 1, 3, 5, 10 or the calculation can include all the species that occur in any relevé with the species in question.
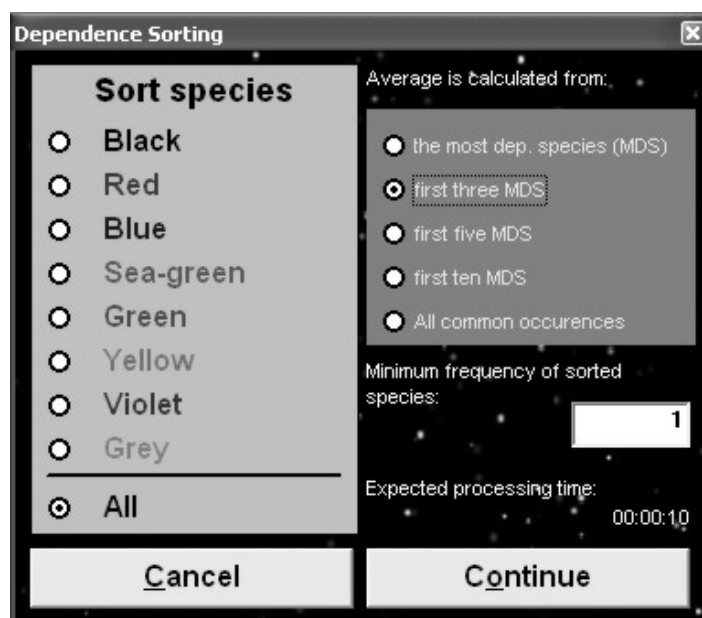
Fig. 24: Sorting species by maximum fidelity values.

Warning 1: Check the estimated time of calculation. After pressing the 'Continue' button it is not possible to cancel the process.

Warning 2: The average fidelity value is written into the species data field. This enables the user to see the value, but it overwrites any existing species data. JUICE gives no warning before it does this.

1.6.3.3   Other Relevé Sorting Functions

'Sort Short Headers' is useful when important relevé data are stored in the short headers. Short headers can contain ecological information about the relevé, relevé number, number of selected species or other information. To write information to the short headers, select 'Store Values To Short Headers' from the 'Head' menu. (This information is described in detail in Section 1.8.2.)

Note: Short headers are limited to 6 characters. Numbers should be sorted in numerical order (1, 2, 3, 11, 12, 13, 21, 22, 23) while text strings should be sorted in alphabetical order. If the example sequence above is sorted in alphabetical order, the result is: (1, 11, 12, 13, 2, 21, 22, 23, 3).

'Sort Relevés by Header Data' allows sorting according to any field in the header data. This function includes the option to write the initial characters of the selected header data field to the short headers (so the user can see the values according to which the relevés have been sorted) and the option to add separators after each group of relevés with identical values.

Fig. 25: Sorting relevés by selected header data.

'Sort Relevés by Clusters' is used to display clusters computed by another program – either PC-ORD or MULVA. With PC-ORD, the cluster information must be saved in a comma-delimited file called 'MATRIX2.CSV'. This file can be imported with the function 'Sort Relevés By Clusters (PC-ORD)'. With MULVA, the table should be exported as a MULVA input file (from the 'File' menu, choose 'Export' and 'Mulva Input File'). Once analysed in MULVA, the resulting file, PRINDA (without suffix), can be loaded with the function 'Sort Relevés By Clusters (MULVA)'. The sorting window using PC-ORD outputs is shown here:
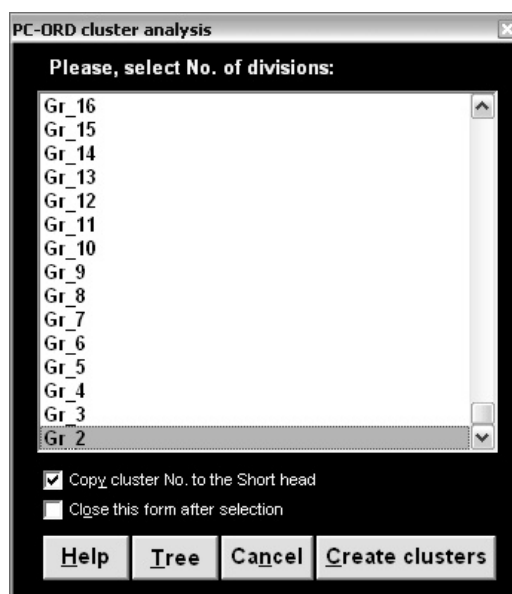
Fig. 26: Sorting species by PC-ORD clusters.

Double-clicking on the desired level of classification will sort the data set accordingly. The
'Tree' button can be used to display a simple clustering hierarchy. The Y-axis is not scaled in
this chart:
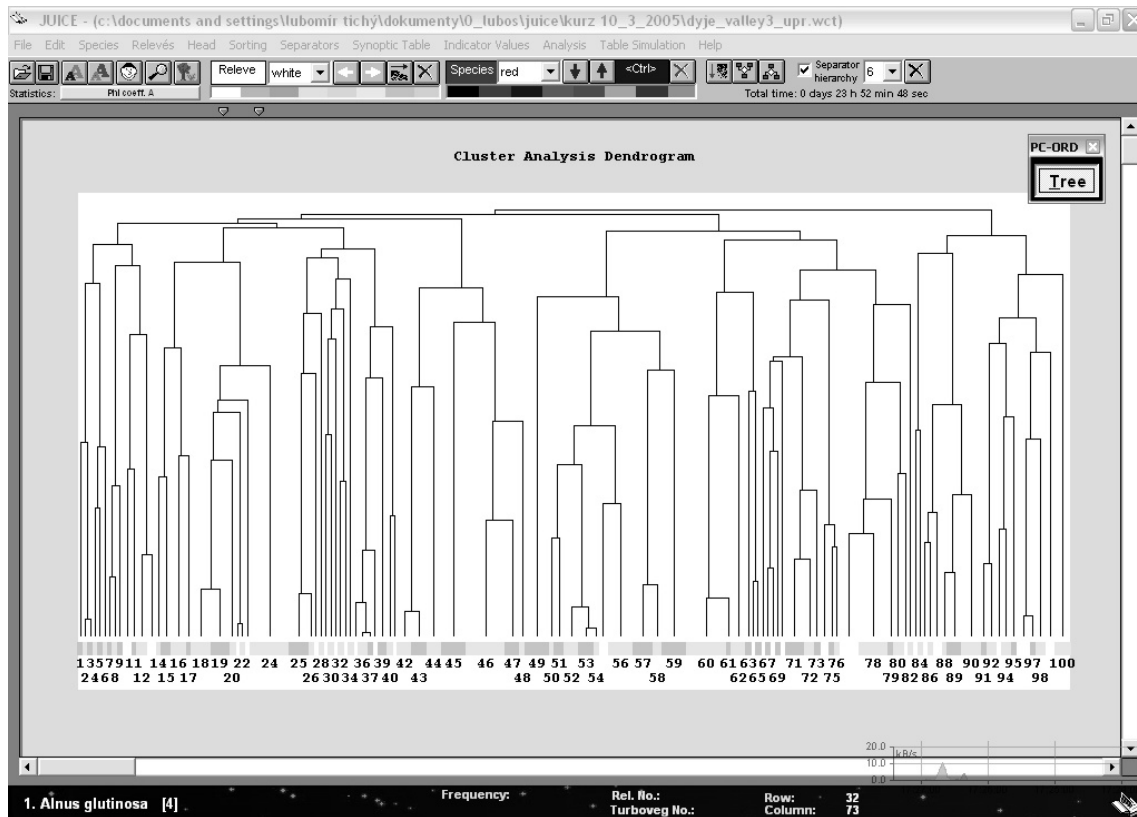
Fig. 27: Dendrogram of PC-ORD cluster analysis.

1.6.4   Autorepeat Function

When a new table is imported into JUICE, it is often necessary to merge species to aid
analysis. (See Section 1.6.1.) The user may also wish to delete species that are not of interest
to the current project. (See Section 1.6.2.) When new relevés are added to the original data set
(e.g., in TURBOVEG) it will be necessary to perform the same mergings and deletions in the
newly exported file. The 'Autorepeat' function, available from the 'Species' menu, can be
used to avoid the tedium of repeating the same editing operations in multiple files.

When the 'Autorepeat Function' window opens, press the 'Add functions from WCT file'
button. This will allow you to select a previously edited file as a model for how the current
file should be edited.
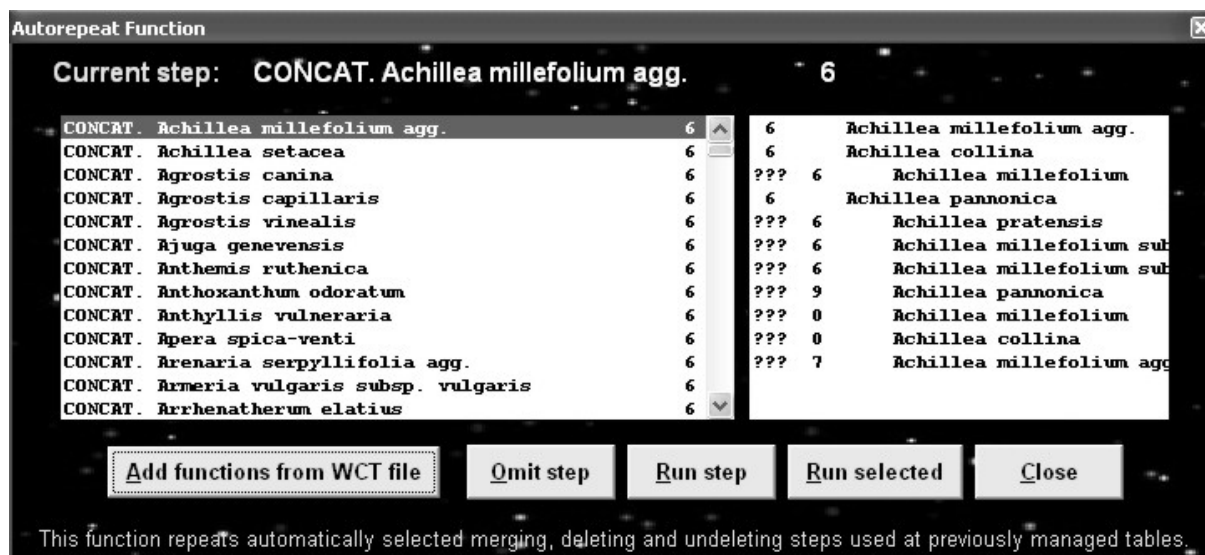
Fig. 28: Autorepeat function.

The 'Autorepeat Function' window will then contain two lists. On the left is a list of the steps that were performed to edit the selected file. On the right is a list of the species that were affected by the highlighted step. Species prefaced by '???' were present in the model file but are not present in the current file.

Pressing the 'Run Selected' button will cause all the editing steps from the model file to be performed on the current file. Alternatively, the user can choose, step-by-step, to either perform the highlighted step ('Run Step') or skip it ('Omit Step').

Note: This function is most useful when the current table has exactly the same species as the previously edited table. When the current table has additional species, the results will often be unexpected. Suppose, for example, that the model file had Quercus robur in two layers that were subsequently merged, but the current file has Quercus robur in three layers. After performing the merge step from the model file, only two of the instances of Quercus robur will be merged. The third must be merged manually. The optimal application of this function is to perform the same merging, deleting, or undeleting criteria in different sub-sets of one large data set or in the same data set after slight modifications of the source database.

1.7 Species Data

The second column with the light-grey background can hold additional species data (such as layers, ecological characteristics or biological information) which can be used in sorting and analysis. (Section 1.6.3.2 explains how to sort species by species data.) Species data can have up to 50 characters; however not all the characters are displayed. By default, the Species Data Column has a width of three characters. It can be enlarged in the 'Display Parameters' tab of the 'Options' window, as described in Section 1.5.8.

JUICE can write some information to the Species Data Column automatically. From the 'Species' menu, select 'Species Data'. The functions available are explained below.

1.7.1   Layers

A species' layer is expressed as a number from 0 to 9. It is recommended that you use the same convention as the TURBOVEG database program:

0 – not defined; 1 – tree layer (high) ; 2 – tree layer (middle) ; 3 – tree layer (low) ; 4 – shrub layer (high) ; 5 – shrub layer (low) ; 6 – herb layer (high) ; 7 – juveniles; 8 – seedlings; 9 – moss layer.

Layer is the most important information about the species. It is displayed automatically at the bottom Status Bar near the selected species's name. Layer can be displayed in the Species Data Column: from the 'Species' menu, select 'Species Data' and 'Layer View' or select the Layer Icon on the Icon Bar. (See Section 1.5.1.) Layer can be displayed as a number, as text or both.

1.7.2   Frequency and Cover Values

The 'Species Data' submenu (from the 'Species' menu) has functions for writing 'Frequency', 'Maximum Cover' or 'Median Cover' to the Species Data Column. 'Frequency' is the frequency of species occurrences in the data set. 'Maximum Cover' is the species's maximum cover value in the data set. 'Median Cover' is calculated from all non-zero cover values. These statistics can also be viewed by selecting 'Species Statistics' from the 'Species' menu. (To return to Standard Display, it is necessary to select 'Species Statistics' again.)

1.7.3   Ellenberg Indicator Values

Ellenberg indicator values can be written to the Species Data Column: from the 'Species' menu select 'Species Data' and 'Indicator Value'. This opens a menu for selecting whether to display indicator values for 'Light', 'Moisture', 'Continentality', 'Temperature', 'pH', or 'Nutrients'. Before using this function, it is necessary that the indicator values be defined. More information on Ellenberg indicator values will be included in later editions of this manual.

1.7.4   External Species Data

Other species data can be imported into JUICE if they are in a suitable format. An example of a simple text file (denoting ploidy level) accepted by JUICE is show below:

```
...
Aira caryophyllea                          2, 4
Aira praecox                               2
Aira species                               -
Ajuga chamaepitys                          4
Ajuga genevensis                           4
Ajuga pyramidalis                          4
Ajuga reptans                              4
Ajuga species                              -
Alcea biennis                              -
Alcea rosea                                2
Alcea species                              -
Alchemilla alpina                          8
...
```

Each line has the same number of characters. Species name and other information occupy the same position.

From the 'Species' menu select 'Species Data' and 'External Species Data'. Enter the name of the file containing the external data. The following window will appear:
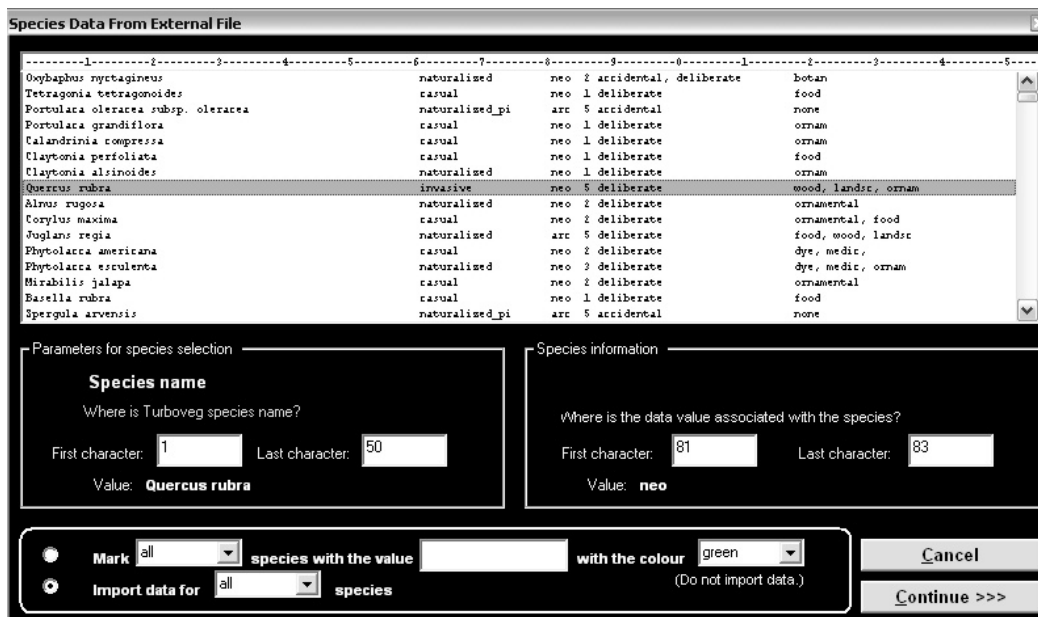
Fig. 29: Window for import of species data from external file.

Species names in the external data file and the current table must have the same nomenclature. The 'Parameters for species selection' and 'Species information' bounds must be entered manually. The first number tells JUICE where to find the first character of the field and the second number tells JUICE where to find the last character. The scale displayed above the file excerpt can be used as a guide. For example, the column below the first '1' corresponds to character number 10 and the column below the first '2' corresponds to character number 20.

Warning 1: Make sure that the range entered under 'Parameters for species selection' is large enough to include the longer species names. Ideally, the 'Last character' of the species name should be the character immediately preceding the first column of data. If JUICE seems not to be loading in data for species with longer names, this indicates the entered range may be too small. Of course, specifying too large a range will also cause problems.

Warning 2: To ensure that the external data file will be readable, separate columns with spaces and not with tabs. (Your text editor should be able to display the file in a fixed-width font, such as Courier.) Even though a TAB may appear the same as several spaces, JUICE will interpret it as a single character. This could result in nonsense in the Species Data Column or it could make it impossible to tell JUICE where species names begin and end, resulting in a blank Species Data Column.

Note: The example window shown above illustrates that the external data file can contain several columns of data. You can choose which column to import simply by specifying the range. Note that if the column contains only one character, the 'First character' and 'Last character' values will be the same.

If the option 'Connect selected data with [all] species' is chosen, the designated data will be imported into JUICE. It is also possible to choose to import data only for species of a certain colour.

For example, the option 'Mark [all] species with the value [arc (an abbreviation for archeophytes)] with the colour [green]' can be used to colour species according to external data without actually importing the data. It is also possible to only re-colour species of a certain colour. The example above will colour all species that have the abbreviation 'arc' in the indicated column in the external data file.

1.7.5 Species Group Tables

In addition to the functions for writing data to the Species Data Column described above, the 'Species Data' submenu has four functions for displaying species group tables. Species group tables are similar to synoptic tables, but constancy is defined not for groups of relevés, but for groups of species. Each constancy row is identified by the name of the first species in the group. The species data is displayed if it is the same for all species in the group; otherwise, the field is filled with repetitions of the letter X.

Each constancy row has 6 characters. Digits are displayed vertically.

The species group table can display frequency (percentage values 0-100 %), categories (I-V), total cover (aggregate cover values from 0 to 100 % are calculated as described in Section 1.6.1) or absolute species numbers. To return to Standard Display, select 'Species Group Table' again.

Fig. 30: Species group tables.

1.7.6 Species Data Averages

Groups of species defined by separators can have different species data values. If these data are numerical, it is possible to calculate averages, which can reveal differences between species groups. To view averages of species data, open the 'Species' menu, select 'Species Data' and 'Species Data Averages'.

1.7.7 Species Data Exports

Species data displayed in the Species Data Column can be saved into a simple text file, which can then be imported into other tables as described in Section 1.7.4. From the 'Species' menu, select 'Species Data' and 'Export Species Data'. For more information, see Section 1.9.8.

1.8 Short Headers

Short headers can contain up to six characters displayed vertically above the table data. Not limited to identification numbers, this field can contain any brief information about a relevé that could be useful for relevé identification, classification or sorting. Various functions for specifying what is displayed in the short headers are found in the 'Head' menu. Relevés can be sorted according their short headers as explained in Section 1.6.3.3.

1.8.1   Identification Numbers

The 'Head' menu has functions for displaying any of four different relevé identification numbers:

- The **'Running Number'** of a relevé tells what order it was in when the table was first imported. This number is displayed by default.

  Note: This number is not constant. When relevés are deleted from the table, the running numbers of the remaining relevés are updated, but the relative order of the running numbers remains unchanged. For example, if three relevés of lower running number are deleted, relevés 44 and 45 will be re-numbered 41 and 42. The name 'running number' refers to the fact that this is the internal order in which JUICE processes or 'runs through' the relevés.

- A relevé's **'Turboveg Number'** is a constant, unique relevé identification number important for TURBOVEG users or other users who have their relevés identified by special numbers.
- When **'Group Number'** is selected, every relevé in the first group is given the number 1, every relevé in the second group is given number 2, and so on. (Groups are defined by separators placed by the user. See Section 1.5.4.) If a relevé is moved to a different group, its group number will not change until this function is selected again.
- When **'Sequence Number'** is selected, all relevés are re-numbered in the order they currently appear. If a relevé is moved, its sequence number will not be updated until this function is selected again.

1.8.2   Other Short Header Values

Short headers can contain up to six characters of information about the relevé. They can be used to distinguish relevé groups in the data set and define them with separators or colours (as described in Section 1.8.3). The functions described below are found in the 'Head' menu under 'Store Values To Short Headers'.

1.8.2.1   Number of Species

The function 'Count <colour> Species' counts all species of the selected colour (which could correspond to all mosses or trees, for example). Species with the same name originally recorded in several different layers are virtually merged and counted only once.

1.8.2.2   Percentage Cover

The function 'Percentage Abundance Of <colour> Species' calculates total percentage cover of the selected species. This can be used to distinguish relevés in which the selected group of species is dominant from those relevés in which the group plays a marginal role. The total

cover is calculated on the assumption that species covers can overlap and that they do so independently. See Section 1.6.1 for an example.

1.8.2.3 Short Headers with Header Data

The 'Header Data' function allows the user to write header data to the short headers. Any header data can be stored in the short headers; however, because the short headers can not display more than six characters, some header data fields (such as locality, geology or remarks) are not appropriate for conversion.
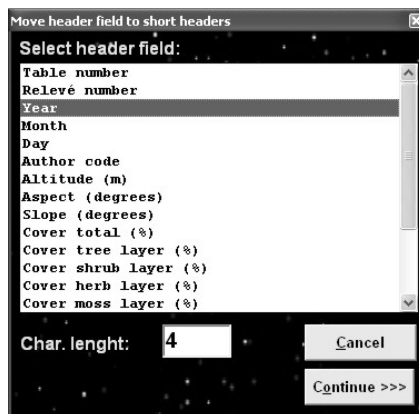
Fig. 31: Moving first part of selected header field into sort headers.

1.8.2.4 Shannon-Wiener Index and Evenness

The functions 'Shannon-Wiener Index' and 'Equitability' write these values to the short headers. The Shannon-Wiener index is one of several measurements of biodiversity (Hill 1973). It takes into account the number of species and the evenness of the species. The index is increased either by having more unique species, or by having a greater evenness.

$$H' = -\sum_{i=1}^{S} p_i \ln p_i \quad , \tag{Eq. 1}$$

where S is the number of species and p_i is the proportion of the individual species cover relative to the total cover.

The program calculates two different measures of evennes:

Shannon's equitability (E_H) proposed by Pielou (1975) is calculated by dividing H' by H'_{max}. (Here $H'_{max} = \ln S$.) Equitability has a value between 0 and 1, with 1 representing complete evenness:

$$E_H = H'/H'_{max} = H'/\ln S. \tag{Eq. 2}$$

This value is also displayed in the Relevé Overview Window (see Section 1.5.6) which can be opened by double-clicking on the short header.

The second measure of evennes available in JUICE is E_{var} which is equivalent to the arctan transformed Gaussian width (Smith & Wilson 1996):

$$E_{var} = 1 - \frac{2}{\pi} \arctan\left(\frac{\sum_{i=1}^{S} \left(\ln(p_i) - \frac{\sum_{i=1}^{S} \ln(p_i)}{S}\right)^2}{S}\right) \tag{Eq. 3}$$

1.8.2.5   Geographical Position Index

The 'Geographical Position Index' calculates a virtual grid, assigns the same number to relevés in the same square and writes this number to the short headers.

Such spatial stratification of table data is available if the header data contain information about geographical coordinates. The fields LATITUDE and LONGITUDE (both 6, or both 7 characters) must be included in the header data (files with suffix STR and EXP – see Section 1.4.6).

Example 1:   LATITUDE: 491357   = 49°13'57"
                 LONGITUDE: 163420   = 16°34'20"

Example 2:   LATITUDE: 0491357   = 49°13'57"
                 LONGITUDE: 0163420   = 16°34'20"

Selecting this function opens this window:
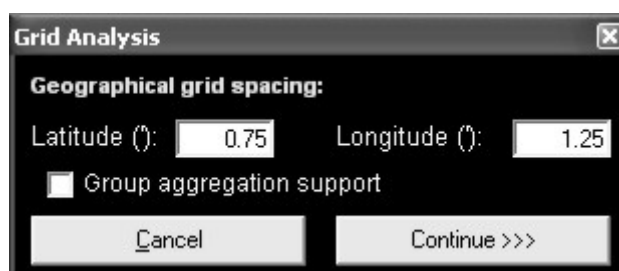
Fig. 32: Window for calculation of grid cell relative numbers.

The window is used to define the size of the grid spacing. The default values can be altered according to your project requirements. When you press 'Continue', the program will calculate an index for each grid cell and the indices will be written to the short headers.

The 'Group aggregation support' checkbox is useful when the data are divided by separators. When the box is checked, each relevé group is analysed as a stand-alone data set.

Note: The grid indices do not indicate relative position. The square containing the first relevé is assigned the index 1. The square containing the first relevé that is not in square 1 is assigned the index 2, and so on. Thus relevés with consecutive indices are not necessarily in adjacent grid boxes on the virtual map.

1.8.2.6   Potential Annual Direct Irradiation (PADI) And Heat Load

The function 'Potential Annual Direct Irradiation And Heat Load' can be used to calculate PADI or heat load for relevés based on slope, aspect and latitude as proposed by McCune and Keon (2002).

There are three available models:

Model 1: $\ln(\text{Rad, MJ} \cdot \text{cm}^{-2} \cdot \text{yr}^{-1}) = -1.467 + 1.582 * \cos(\text{lat}) * \cos(\text{slo}) - 1.500 * \cos(\text{asp}) * \sin(\text{slo}) * \sin(\text{lat}) - 0.262 * \sin(\text{lat}) * \sin(\text{slo}) + 0.607 * \sin(\text{asp}) * \sin(\text{slo})$

Model 2: $\ln(\text{Rad, MJ} \cdot \text{cm}^{-2} \cdot \text{yr}^{-1}) = -1.236 + 1.350 * \cos(\text{lat}) * \cos(\text{slo}) - 1.376 * \cos(\text{asp}) * \sin(\text{slo}) * \sin(\text{lat}) - 0.331 * \sin(\text{lat}) * \sin(\text{slo}) + 0.375 * \sin(\text{asp}) * \sin(\text{slo})$

Model 3: $\text{Rad (MJ} \cdot \text{cm}^{-2} \cdot \text{yr}^{-1}) = 0.339 + 0.808 * \cos(\text{lat}) * \cos(\text{slo}) - 0.196 * \sin(\text{lat}) * \sin(\text{slo}) - 0.482 * \cos(\text{asp}) * \sin(\text{slo}),$

where 'asp' is aspect, 'slo' is slope and 'lat' is latitude.

Fig. 33: Calculation of potential direct incient radiation and heat load.

The window allows the user to select a model and test it on sample data. The user may then choose whether to write radiation or heat load to the short headers. For relevés which lack information about latitude, slope and aspect, a null value is written.

Note: For more information, read the original paper of McCune and Keon (2002). Latitude should be included into header data (See the Section 0).

1.8.2.7   Sum, Average, Minimum, Maximum and Multiplication of Species Data

There are several functions for summarizing numerical species data in the short headers. 'Average of <colour> Species Data' calculates the average over all species of the indicated colour in the relevé. Sum, Maximum and Minimum functions are similar.

 'Multiplication Of Species Data Values' is an average calculated as follows:

$$\frac{SD_1 \cdot SD_2 ... \cdot SD_n}{(\text{mean } SD)^n},$$

(Eq. 4)

where n is the number of species in the relevé, SD_i is the species data value for species *i* and mean *SD* is the average of species data values taken over all species in the table.

These functions apply to the species data currently in the Species Data Column. See Section 1.7 for more information about species data, including how to write values to the Species Data Column. These functions are only useful for analysing numerical species data.

1.8.2.8   Ellenberg Indicator Values

Ellenberg indicator values can be written to the short headers. More information on Ellenberg indicator values will be included in later versions of this manual.

1.8.2.9 Importing External Short Header Data

External header data can be imported from a text file. From the 'File' menu, select 'Import' and 'Short Headers'. The data file must have a column of relevé numbers (6 characters) paired with a column of short header values (6 characters). Short header files in this format can be exported from JUICE: from the 'File' menu, select 'Export' and 'Short Headers'. (See also Section 1.9.9.)

The 'Import Short Headers' window is shown below:
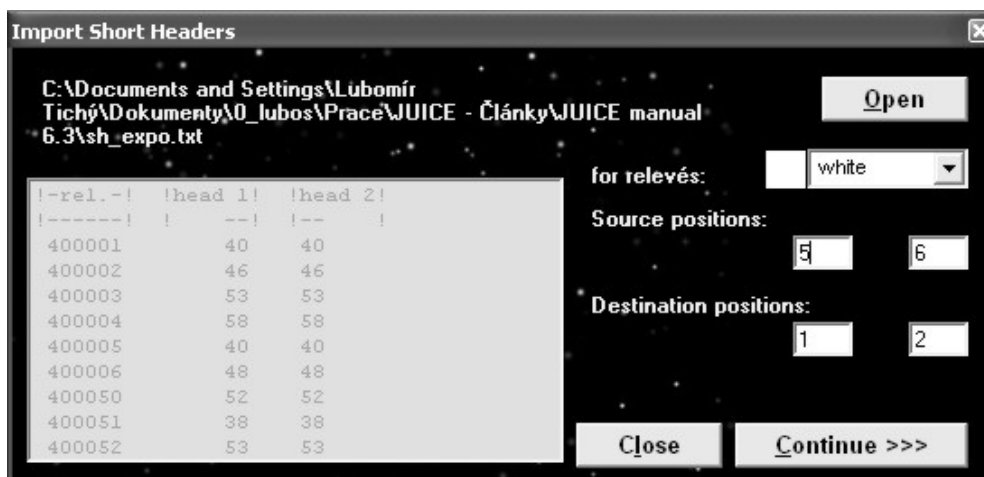
Fig. 34: Window for import of short headers.

The 'Open' button opens a browse window for finding the file with appropriate header data. The colour in the 'for relevés' field restricts which short headers will be updated. The 'Source positions' fields are used to specify the beginning and end of the header data in the source file, while the 'Destination positions' specify the position in the short header. In the example above, 2 digits, the fifth and sixth characters after the relevé identification number, will be stored at the first and second position of the short head. The third through sixth characters of the short head will not be overwritten.

Note: If you respect the convention of reserving 6 characters for header data, you can combine several header data values for one relevé. For example, it is possible to use one file to import class number (2 digits) into the first two characters and another file to import year (4 digits) into the last four characters of the short header field. This will enable you to sort the table with classes as the main criterion and year as the secondary criterion.

1.8.3 Colouring Relevés According to Short Header

Relevés do not have to be coloured manually. It is possible to colour them according to the data in the short headers. From the 'Head' menu, select 'Short Header Selection'. This opens the window shown below. Choose a colour, enter a value and specify whether to mark headers greater than, less than or equal to the entered value.
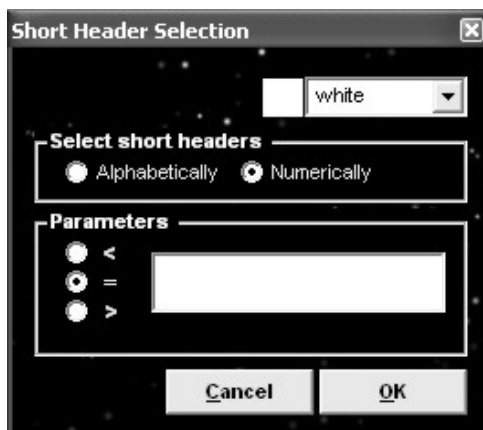
Fig. 35: Short header selection window.

Note: Alphabetical comparison should be used with text and numerical with numbers. The example below shows what happens when numbers are compared alphabetically:

Numerical comparison: 12.345 > 9.8765
Alphabetical comparison: "12.345" < "9.8765"

With numerical comparison, text is interpreted as a number. If the text contains no digits, it has a value of zero.

1.8.4 Short Header Averages, Minima and Maxima

JUICE can measure the average, minimum or maximum value of the short headers within each group of relevés. (Groups are defined by separators. See Section 1.5.4.) From the 'Head' menu, select 'Short Header Averages'. The window shown below will appear. By default, the average value of the short header across each group is displayed. There are option buttons for displaying the average, the minimum, or the maximum. The list of values is also copied onto the clipboard. It can be pasted into a text editor with the command Ctrl+Insert or Ctrl+V.

Fig. 36: Averages, minima and maxima from short headers calculated for each constancy column of the table.

1.8.5   Short Header Sorting

It is often desirable to sort relevés according to some criterion. First, the values under consideration should be written to the short headers as described in Section 1.8.2. Then, from the 'Sorting' menu, select 'Sort Short Headers'. For more information on sorting, see Section 1.6.3, especially Section 1.6.3.3.

1.9 Exporting Data

JUICE can produce several types of data – phytosociological tables, synoptic tables, ecological information about relevés or species, etc. To make this information available for use by other programs, JUICE supports many types of exports.

1.9.1   Saving Files in JUICE

Once the source table data are imported into JUICE, they can be saved in JUICE's format, which may include extra parameters. From the 'File' menu, select 'Save' and enter a name for the file. Actually, three files are generated when a table is saved: a WCT, an STR and an EXP file. The WCT file has a special binary structure not suitable for manual editing, but the other two are simple text files containing header data in the same form as they were imported. See Section 1.4.6.

Note: Although the 'File' menu does not explicitly have a 'Save As' option, 'Save' actually works the way 'Save As' does in many other programs. A dialog box will open and you will have the opportunity to either confirm that you want to save the file under its current name or to enter a new name. Thus it is possible to save an altered file under a different name without overwriting an older version of the file. Furthermore, before JUICE overwrites an existing file, it asks for confirmation.

1.9.2   The Current Export File

JUICE's standard export is a rich text format (RTF) file to which subsequent exports are appended without overwriting previous exports. This is useful for exporting running results from interspecific associations or COCKTAIL analysis, for example. The file into which JUICE will export appears at the top of the 'Export' menu (available from the 'File' menu). Clicking on this 'Current File:' function opens a window where the current export file name can be changed. If the name is not changed but the 'Save' button is pressed, JUICE interprets this as a command to wipe the export file clean and start over. (JUICE asks for confirmation before erasing the contents.) Another way to access this window is through the 'Export' tab of the 'Options' window: clicking on the 'Change File' button will open the export file name window.

1.9.3   Table Export

From the 'File' menu, select 'Export' and 'Table'. This will open the 'Table Export' window, which has several options, as can be seen in the picture below.

The 'File format' box offers several different export formats. The default, **'MS WORD (SDF)'**, appends the table to the RTF file described in the previous section. All other formats prompt the user for a file name and export the data to this new file (overwriting any previous file of the same name).

An **'MS EXCEL (CD)'** export will generate a stand-alone CSV file accepted by spreadsheet programs. (See Section 1.4.4.) This table is divided into two parts: table and header.

An **'MS ACCESS'** export produces three files: SPECIES.TXT, which contains species names, layers and Ellenberg indicator values (if they have been imported), TABLE.TXT with table data (species number, relevé number and percentage cover) and HEADER.TXT with all header data. (These are only the default names; the user can change them.) These files can be imported into a database program and connected as three tables.

A **'TEXT FILE'** export saves the file as simple text (TXT). (See Section 1.4.5.)

A **'CSV HEAD+TABLE'** creates a spreadsheet table. Whereas the 'MS EXCEL (CD)' export has header information at the end, this export has header information at the beginning. Furthermore, the former format presents header data by listing one relevé's data per row, whereas this format lists one field per row with each row containing each relevé's data value for that field.
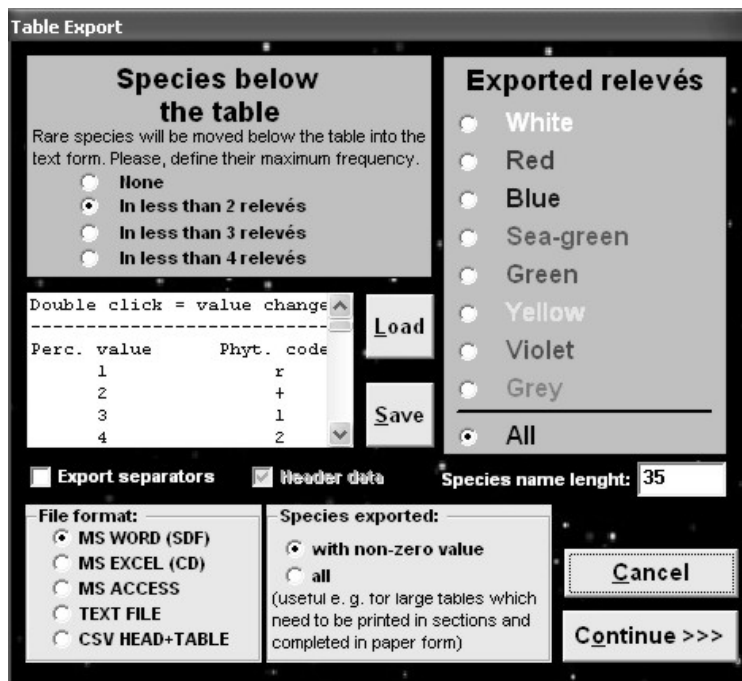
Fig. 37: Window for table exports.

It is possible to restrict export to relevés of a certain colour. The 'Species Exported' box gives the option of exporting all species in the table or only those species which appear in the selected relevés.

Note: Exporting all species can be useful. To export a large table for printing, select a screen-full of relevés at a time and export all species. When the resulting files are printed out, the species lists will be complete and the printouts can be physically spliced together.

The standard RTF export ('MS WORD (SDF)') file can contain separators. There is also the option (again, only for RTF export) to include only species which appear in at least 2, 3 or 4 relevés, listing the rarer species below the table in condensed form. The length of the species name can be limited, with a maximum length from 4 to 50 characters.

JUICE remembers original percentage cover values as whole numbers (1-95), but they are replaced by single characters during export (except for the 'MS ACCESS' format, where percentage numbers are exported). The list in the 'Table Export' window contains a list of percentages ('Perc. value') on the left paired with the character to be exported ('Phyt. code'). To change an export character, double-click on the corresponding percentage value. Newly defined scales can be saved for future use by pressing the 'Save' button. Later, they can be loaded with the 'Load' button.

1.9.4   Synoptic Table Export

From the 'File' menu, select 'Export'. If JUICE is in Synoptic Table Display mode (see Section 1.11) the 'Synoptic Table' export function will be available. This provides two possibilities to:

1. Export the synoptic table into the current RTF export file for presentation or publication.
2. Export the synoptic table into a Cornell condensed (CC!) file for analysis by another program such as CANOCO (ter Braak & Smilauer 2002) or PC-ORD (McCune & Mefford 1999). This option is available only when a 'Percentage Constancy' synoptic table is displayed.

Option 1 opens the following window, where the parameters of exporting the table may be modified:
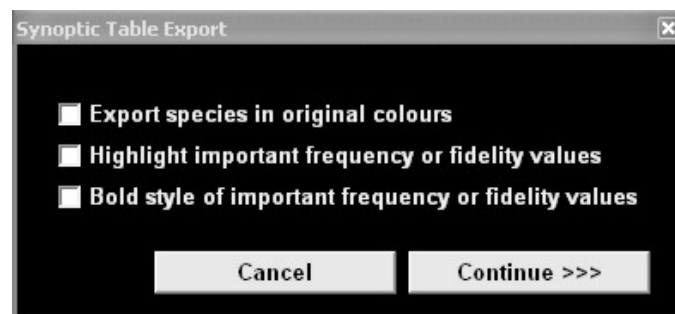
Fig. 38: Window managing synoptic table export.

Synoptic tables may be saved in single or combined form. (See Section 1.11.9.) All data will be saved similarly to the way they are displayed on the screen.

1.9.5   Other Exports into the RTF Export File

The current RTF export file is opened for running exports of interspecific associations created during COCKTAIL classification. More information about COCKTAIL classification will be included in later versions of this manual.

1.9.6   Special Export Formats

The 'Export' submenu of the 'File' menu includes the option to export the table in a variety of other special formats, enabling the data processed by JUICE to be analysed more precisely. The program supports table export as a Cornell condensed file, a MULVA input file, SYN-TAX files or a MATLAB file.

1.9.7   Export for D-MAP File

D-MAP (Morton 2005) is simple GIS software which is very useful for presentation of spatial data on a national or regional scale. In comparison with sophisticated GIS software, it gives faster and generally better results because small, clear maps with reduced details for publication are usually required for publication. JUICE supports easy communication with D-MAP.

The header data must contain LATITUDE and LONGITUDE fields represented as six or seven characters corresponding to degrees, minutes and seconds (as explained in Section 0).

The D-MAP software must be installed on the computer. The file group setup of D-MAP will help to create group 'JUICE <title>' with manually defined boundaries and parameters. Distribution data will be stored in the JUICE.DIS file.

Parameters such as frame, grid spacing and symbol size must be stored in the PAR file in D-MAP.

From JUICE's 'Options' window, select the 'External Program Paths' tab and define the D-MAP path. This will allow you to run D-MAP automatically after export selection.

JUICE can export spatial data for three different parameters for: selected species (to see the distribution of selected species), a group of selected relevés (to see the spatial distribution of a vegetation type) or all species in the table.
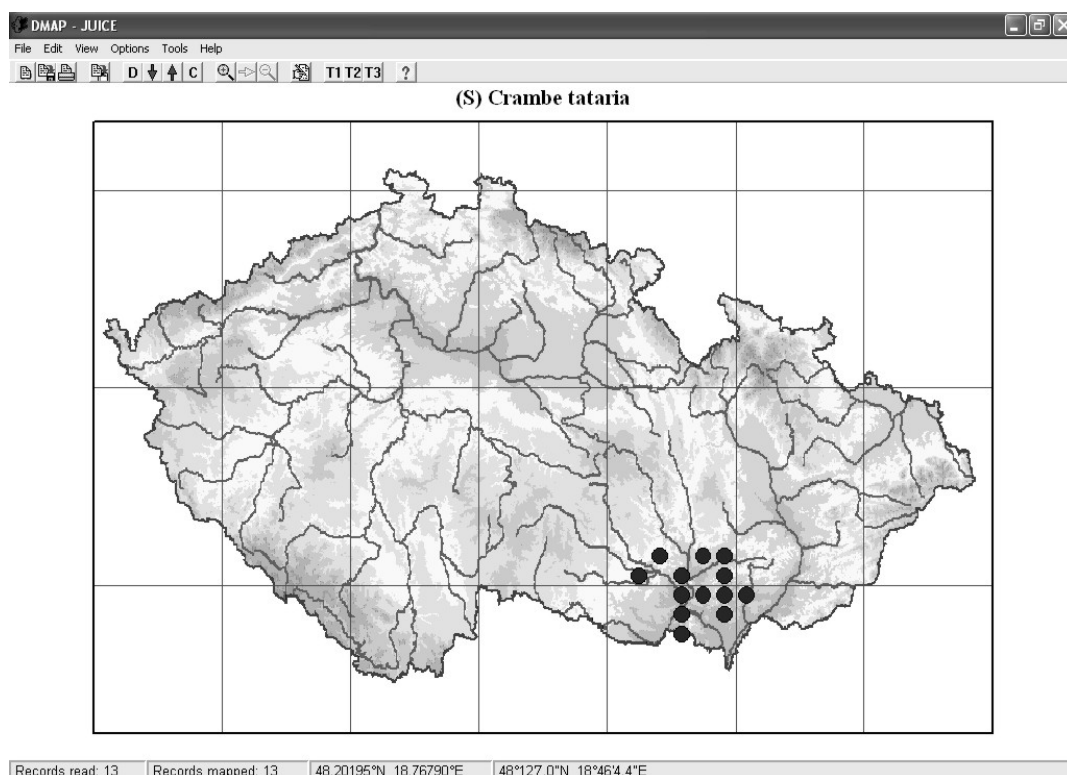
Fig. 39: Example of the distribution map created by D-MAP.

1.9.8   Species Data Export

Species data (see Section 1.7) imported or created manually (see Section 1.5.7) can be saved as a text file for future use. These data can then be imported into similar tables. The export file has the following structure (species name, layer and species data value):

```
Fallopia convolvulus                      6    arc
Lapsana communis                          6    arc
Silene latifolia subsp. alba              6    arc
Viburnum opulus                           4    nat
Sorbus aucuparia subsp. aucuparia         4    nat
Ranunculus sceleratus                     6    nat
Populus x canadensis                      1    neo
Epilobium ciliatum                        6    neo
Pinus nigra                               1    neo
```

1.9.9 Short Header Export

Header data can be exported into a simple text file for later retrieval. See Section 1.8.2.9. The file contains the relevé number, short header value, group number and a 1 or 0 representing presence or absence of a separator to the right of the relevé:

```
400001;    40; 1 ; 0
400002;    46; 1 ; 0
400003;    53; 1 ; 1
400004;    58; 2 ; 0
400005;    40; 2 ; 0
400006;    48; 2 ; 1
400050;    52; 3 ; 0
400051;    38; 3 ; 0
400052;    53; 3 ; 1
400053;    52; 4 ; 0
400054;    73; 4 ; 0
400055;    56; 4 ; 0
```

1.10 The Fidelity Concept

Chytry, M., Tichy, L. & Holt, J.

Statistical fidelity measurements are useful for measuring species concentration in vegetation units and comparing diagnostic values among species in a particular vegetation unit or among vegetation units for a particular species. A completely statistical approach to determination of diagnostic species by measuring fidelity, proposed by Chytrý et al. (2002), is included in JUICE. The program has 13 different fidelity measures available from the 'Fidelity measures' tab of the 'Options' window. (See Section 1.10.3.) They are for use in synoptic tables as described in Section 1.11.

1.10.1   Fidelity Measures

The fidelity measures available in JUICE can consider either binary presence/absence data or quantitative cover data. For simplicity, only four fidelity measures, using presence/absence data, will be discussed in this section. Measures that take cover into account will be discussed in Section 1.10.6. For details on other fidelity measures, refer to Chytrý et al. (2002).

Here the same notation is used as in Bruelheide (1995, 2000) and Chytrý et al. (2002):

> N … number of relevés in the data set,
> N_p … number of relevés in the target vegetation unit,
> n … number of occurrences of the species in the data set,
> n_p … number of occurrences of the species in the target vegetation unit.

(To see how these quantities are defined when quantitative cover data are taken into account, see Section 1.10.6.)

a) The **u value for a hypergeometric distribution** (Chytrý et al. 2002), further referred to as **u_{hyp}**, compares the observed number of occurrences of the species in the vegetation unit (n_p) with the expected number of occurrences ($\mu = n \cdot N_p / N$). The fidelity values calculated using this coefficient are not influenced by species cover or abundance (unless n and n_p are defined as in Section 1.10.6). The u value is defined as the deviation of the observed frequency of the species occurrence in the vegetation unit from the expected frequency, compared with the standard deviation:

$$u_{hyp} = (n_p - \mu) / \sigma_{hyp} \; . \tag{Eq. 5}$$

The measure counts the number of standard deviations between the observed data and the result expected under the null hypothesis that species occurrences are independent of the target vegetation unit. Thus u_{hyp} provides a measure of the statistical significance of the observed relationship. It can take on positive or negative values with the range depending on the number of relevés in the dataset. The maximum u value, $\sqrt{N-1}$, is achieved when $N_p = n = n_p$. Fidelity rankings according to u_{hyp} will be identical to rankings according to chi squared or the phi coefficient.

b) The **phi coefficient of association** between species and vegetation units (Sokal & Rohlf 1995, Chytrý et al. 2002) is a statistical measure of association between two categories, which can be used as measure of fidelity. It can be defined as:

$$\Phi = \frac{u_{hyp}}{\sqrt{N-1}} = \frac{N \cdot n_p - n \cdot N_p}{\sqrt{n \cdot N_p \cdot (N-n) \cdot (N-N_p)}} \; . \tag{Eq. 6}$$

Traditionally, the phi coefficient considers only presence/absence, so fidelity values calculated using this coefficient are not influenced by species cover or abundance. The values of the phi coefficient range from −1 to 1, but for convenience, they are multiplied by 100 in the program. The highest phi value of 1 is achieved if the species occurs in all relevés of the vegetation unit and is absent elsewhere. A positive value lower than 1 means that the species is absent from some relevés of the vegetation unit or present in some relevés outside the vegetation unit. A value of 0 is obtained when the relative frequency of the species in the vegetation unit equals the relative frequency in the rest of the dataset, thus indicating no relation between the target species and the target vegetation unit.

An advantage of the phi coefficient over some other statistical fidelity measures is its independence of data set size. On the other hand, the phi coefficient contains no information about statistical significance.

The phi coefficient (along with u value and χ^2) is more or less dependent on the relative size of vegetation units. If the target vegetation unit represents 10% of the total data set (Fig. 40a), Φ is relatively high for species that are not very common within the target unit, provided the species are very rare outside the target unit. However, for species that are common outside the unit, even the species with high frequency within the target vegetation unit are given low phi values. On the other hand, if the target unit makes up 50% of the total data set (Fig. 40b), species must generally have higher frequencies within the target unit in order to have high phi values; if a species has a high frequency within the target unit, a relatively high phi value can be attained even with a smaller difference in frequency between the target and other units.
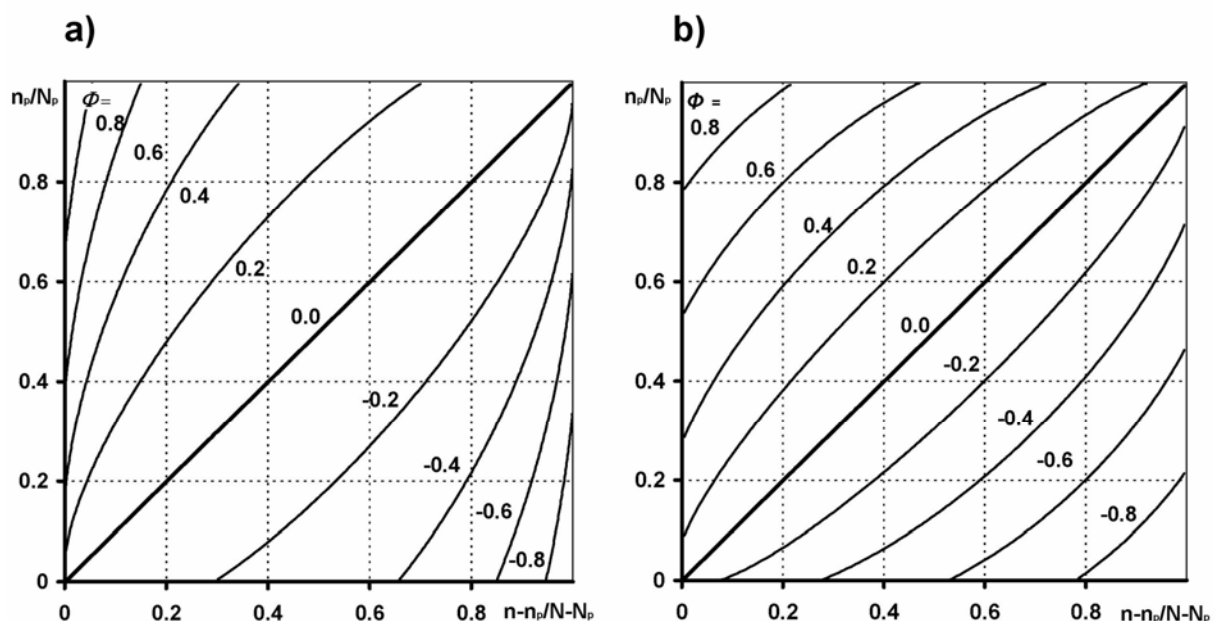
Fig. 40: Dependence of the phi coefficient on the relative frequency of species occurrences within (vertical axis) and outside (horizontal axis) the target vegetation unit, shown for vegetation units equal to (a) 10% and (b) 50% of the size of the total data set.

c) The **Dufrêne-Legendre Indicator Value** (Dufrêne & Legendre 1997) is defined as the product of relative species abundance and relative species frequency within the target vegetation unit. Relative species abundance is the mean abundance of the species in the target vegetation unit compared to all vegetation units in the data set; the sum of mean abundances in each vegetation unit is used instead of the sum of actual abundances over all relevés in order to remove the effect of unequal vegetation unit size. JUICE only computes the Dufrêne-Legendre Indicator Value for presence/absence data, which means that the relative abundance

is replaced by the relative frequency in the target vegetation unit divided by the sum of relative frequencies in all vegetation units of the data set. For a comparison between a target vegetation unit and the rest of the data set, the Dufrêne-Legendre Indicator Value can be expressed as:

$$IndVal = \frac{n_p/N_p}{n_p/N_p + (n-n_p)/(N-N_p)} \cdot \frac{n_p}{N_p}. \qquad \text{(Eq. 7)}$$

This formula can be easily extended to a comparison of vegetation units within the classified data sets by replacing the species frequency outside the target vegetation unit, $(n-n_p)/(N-N_p)$, in the denominator, by the sum of relative frequencies in all the other vegetation units of the given typology.

The Dufrêne-Legendre Indicator Value is independent of the relative size of the target vegetation unit. It implicitly standardizes the size of all vegetation units in the data set, including the target vegetation unit. All vegetation units are weighted equally, and changing N_p does not influence the resulting numerical value.

The categorical form of the Dufrêne-Legendre Indicator Value probably deviates from most researchers' intuitive expectations of the properties of a suitable fidelity measure. The next figure shows that the Dufrêne-Legendre Indicator Value gives a rather high weight to common species. It could be said, however, that the Dufrêne-Legendre Indicator Value is a fidelity measure which emphasizes the group's fidelity to the species, i.e., the value is a good indicator of how frequent the species is within the vegetation unit but it is less affected by occurrences of the species outside the vegetation unit.
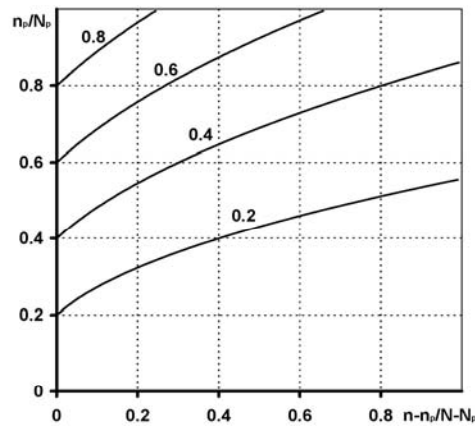
Fig. 41: Dependence of the Dufrêne-Legendre Indicator Value on the relative frequency of species occurrences within (vertical axis) and outside (horizontal axis) the target vegetation unit.

Note: *The Dufrêne-Legendre Indicator Value's relationship to independence can be seen by comparing Fig. 40 (a or b) with Fig. 41. In each figure, the diagonal from the lower left to the upper right is the case of independence – the species is as frequent inside the vegetation unit as it is outside the vegetation unit. Note that this diagonal corresponds to the Φ = 0 isoline in Fig. 40 but it is crossed by the isolines in Fig. 41. IndVal assigns this diagonal a value of p/2 (where p = n/N) as can be seen from where the 0.2 and 0.4 isolines cross it.*

d) **Fisher's exact test** calculates $P(f(o) \geq n_p)$, the true probability of obtaining the observed number of occurrences of the species in the vegetation unit under the null hypothesis of independence. It may yield very small probability values, including those smaller than 10^{-100}, which are difficult to cope with in practical work. For this reason, $- \log_{10} P(f(o) \geq n_p)$ is a more practical quantity to use for a measure. Fisher's exact test is used either as a stand-alone fidelity measure or as a correction for calculation of missing information on statistical significance if the fidelity synoptic table with phi coefficient is displayed.

Note: Negative values of fidelity represent information which is not important in the context of most studies. Negative values are displayed only in the 'Interspecific Associations' window. (More on interspecific associations will be included in later versions of this manual.) They are hidden in synoptic tables.

1.10.2 Fidelity Measurements for Vegetation Units of Unequal Size

All the fidelity measures included in JUICE, except the Dufrêne-Legendre Indicator Value, are affected by the relative size of vegetation units. Unfortunately, nearly every classification of relevés yields vegetation units of different sizes. To remove the dependence of the fidelity measures on the vegetation unit size, it is better to make a virtual standardization of the target vegetation unit (N_p) to a new value, hereafter called N_p', which is constant for all vegetation units within the data set, without changing species frequencies within and outside each target vegetation unit, i.e., the quantities n_p / N_p and $(n - n_p) / (N - N_p)$, respectively. For example, in a data set with two vegetation units, we can set $N_p' = N/2$, i.e., equal to half of the total size of the data set, which enables us to compare the two vegetation units as if they were of the same size. Thus the resulting fidelity values are less dependent on the sampling effort and data set structure. Similarly, in a data set with four vegetation units, we can set $N_p' = N/4$. However, it is not necessary that the sum of N_p' values for all vegetation units within the data set equal N, the total size of the data set. For example, in a data set of four vegetation units, we can set $N_p' = N/2$, and compute a fidelity measure for the first vegetation unit as if this group were 50% of the total data set size and the other three groups together were also 50%. We can then compute a fidelity measure for the second vegetation unit as though it were 50% of the total data set size and so on. Such standardizations make sense in combination with the phi coefficient, but not so much with u_{hyp} or other statistical fidelity measures because data standardization violates their relationships to statistical significance.

A scheme of different standardizations of the size of vegetation units is presented in the next figure. Each line represents a data set, segments are vegetation units labelled A, B, C and D and segment length corresponds to the number of relevés in each group. The thick part of each segment represents relevés with occurrence of the given species; the thin part represents relevés where the species is absent. In figures (b) to (d), the four lines represent the four standardizations used for calculation of species fidelity to the target vegetation units A, B, C and D.
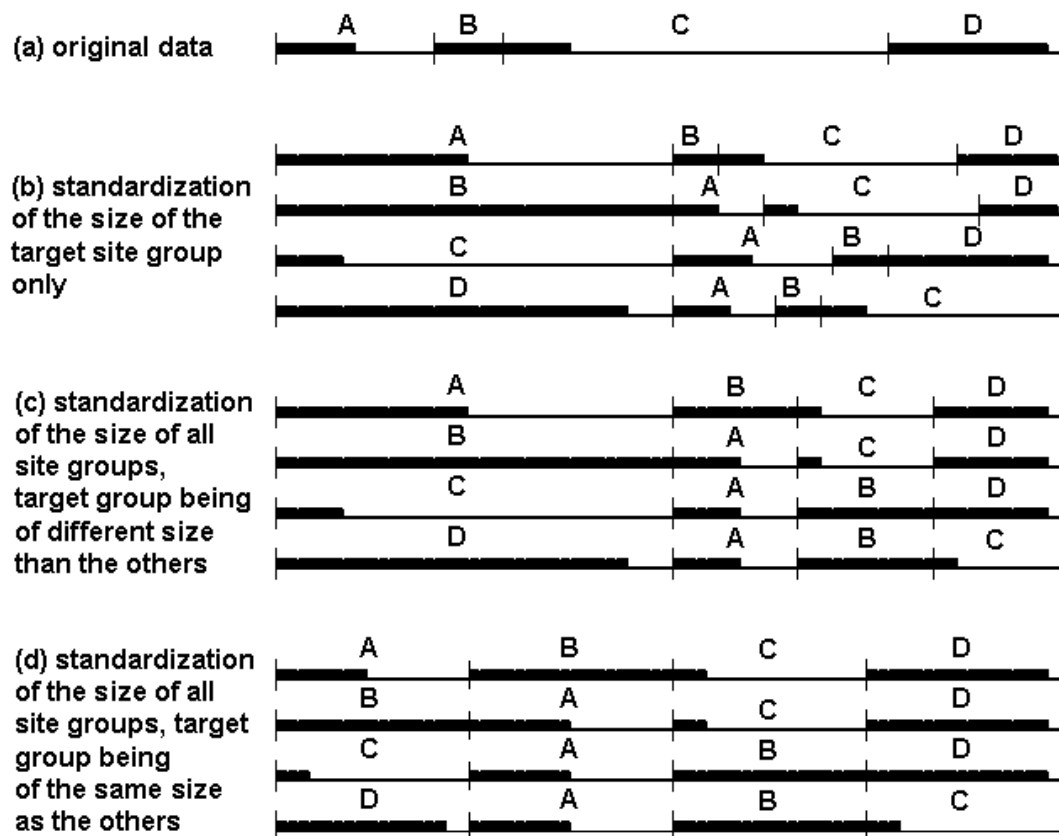
Fig. 42: A scheme of different standardizations of the size of relevé groups. Each line represents a data set, segments are groups labelled A, B, C and D and segment length corresponds to the number of relevés in each group. The thick part of each segment represents relevés that contain the given species, the thin part represents relevés where the species is absent. In figures (b) to (d), the four lines represent the four standardizations used for calculation of species fidelity to the target groups A, B, C and D.

Part (a) of the figure shows a simple artificial data set with vegetation units of unequal size. The phi coefficient depends on the size of the vegetation units. Standardizing the data set removes this dependence. After the standardizations in Fig. 42c or Fig. 42d, the fidelity measure depends only on the relative frequencies within each relevé group. The standardized size of the target vegetation unit can differ from the size of the other vegetation units (Fig. 42c) or be the same as the other vegetation units (Fig. 42d). The phi values after such standardization are entirely independent of the size of the vegetation units and can be directly compared across different vegetation units.

In some cases, however, it may not be desirable to standardize the size of all vegetation units in the data set. If diagnostic species for a few similar community types are determined using a large database, it may be useful to perform fidelity calculations with a data set that also includes relevés from other, unrelated community types (Chytrý et al. 2002). This approach finds diagnostic species that are of more general validity because they are tested against the background of other community types in the same geographical area. The additional relevés are usually treated (theoretically) as a single vegetation unit. Standardization to the size of other vegetation units would greatly and undesirably reduce its effect. However, its size can be held constant while the size of the other groups is standardized.

The phi coefficient applied to a data set with vegetation units standardized to equal size is independent of the actual differences in size of individual vegetation units. However, it depends on the standardized size of the target vegetation unit (N_p'), which may be either

equal to the size of the other vegetation units or set to any arbitrary value between 1 and $N-1$. Setting the standardized size of the target vegetation unit ($N_p{}'$) to a higher value gives a higher weight to common species and their frequency in the target vegetation unit. By contrast, setting $N_p{}'$ to a lower value gives a higher weight to rare species and to the differences in species frequency within and outside the target vegetation unit. Changing the $N_p{}'$ value can thus be used as a tool for modifying the properties of the phi coefficient with respect to weighting common or rare species.

The dependence of the phi coefficient on the relative size of the target vegetation unit can be tested in JUICE. See Section 1.10.3 below and Section 1.11 on synoptic tables.

1.10.3 Selecting Fidelity Measures and Standardization in JUICE

The current fidelity measure is displayed on the Option Button on the left side of the Icon Bar. (See Section 1.5.1.) Pressing this button opens the 'Fidelity measures' tab of the 'Options' window.
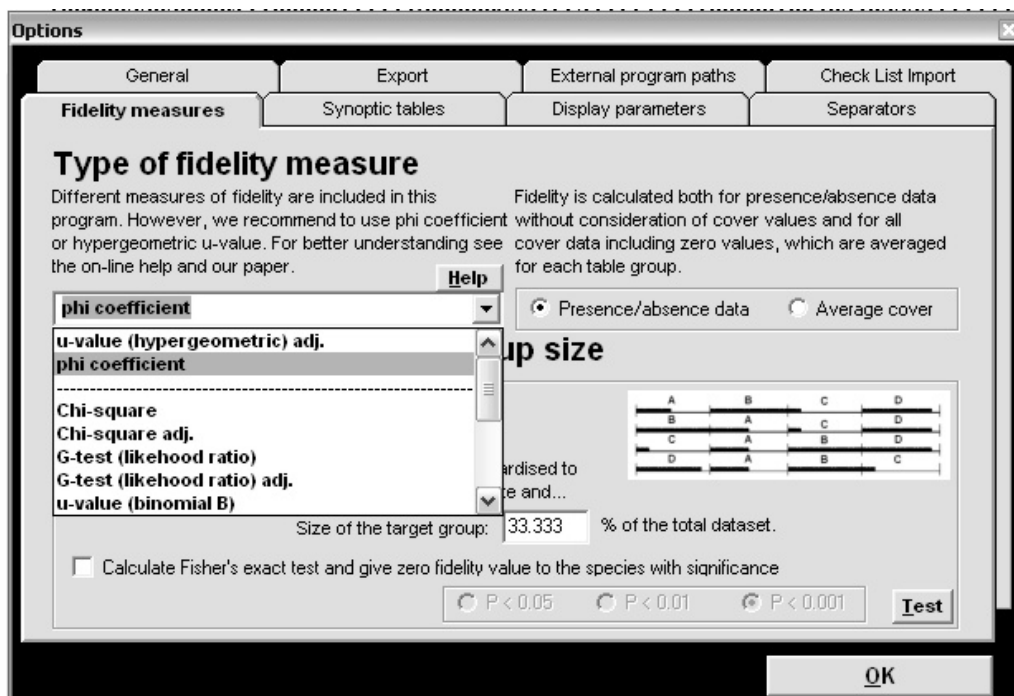

Fig. 43: Selecting a fidelity measure from the 'Fidelity measures' tab of the 'Options' window.

The user can select one of thirteen different fidelity measures, which are used to analyse presence/absence or quantitative data in association with various program functions (such as fidelity synoptic tables, interspecific associations or the COCKTAIL method).

JUICE versions 6.3.57 and higher have relevé group size standardization as discussed in Section 1.10.2 above. The parameters of standardization can be adjusted in the 'Fidelity measures' tab of the 'Options' window.
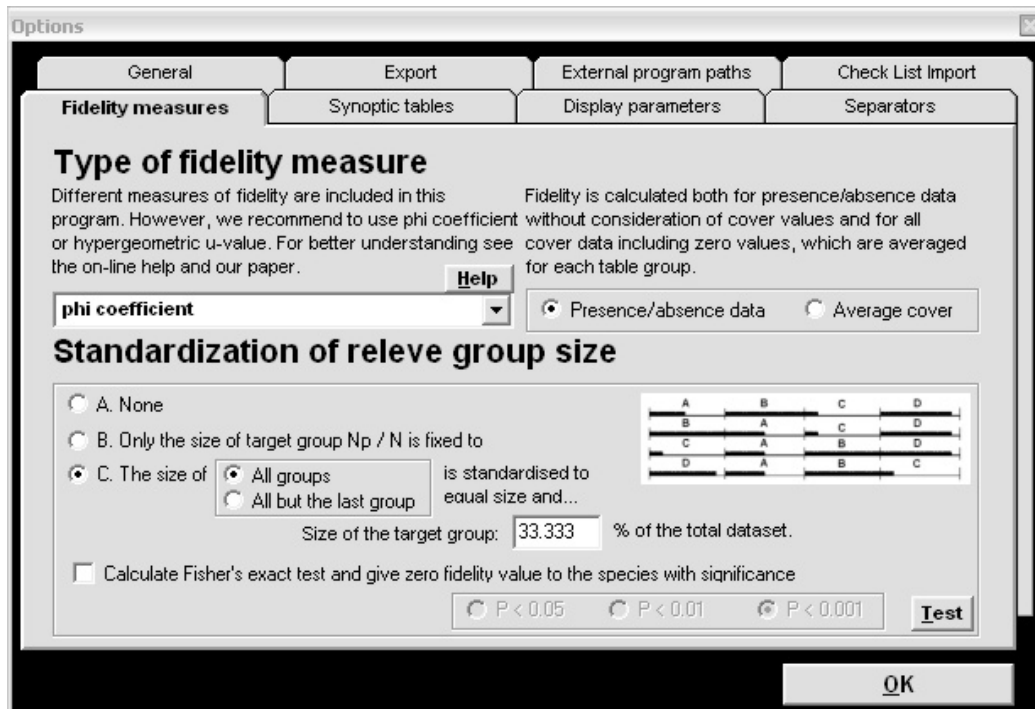
Fig. 44: Selecting a standardization method and 'Presence/absence' versus 'Average cover' from the 'Fidelity measures' tab of the 'Options' window.

Option A is to use the given data without standardization. Option B standardizes the size of the vegetation unit relative to the rest of the dataset. Option C has two steps: (1) it sets the target group to the indicated size and then (2) sets all the other groups (or all but the last) to be the same size as each other. The picture on the right side of the frame graphically represents the chosen standardization applied to a dataset divided into four vegetation units.

Warning: Because the Dufrêne-Legendre Indicator Value implicitly standardizes the data set, it is only available with option C. A side-effect is that when the user scrolls through the list of measures, JUICE automatically switches to option C when 'Dufrene and Legendre' is highlighted. If a different standardization is desired (for a different measure) it must be re-selected manually. Similarly, highlighting 'Dufrene and Legendre' will cause JUICE to switch from 'Average cover' to 'Presence/Absence data'.

Note 1: The data standardizations are available only for synoptic tables and related functions; thus they are only applicable to classified or partly classified datasets. All other functions using fidelity as a statistical measure (such as COCKTAIL classification and Interspecific associations) use the original data.

Note 2: You can test the standardization with real data. From a synoptic table with fidelities (see Section 1.11) open the 'Fidelity measures' tab of the 'Options' window. Changing the parameters will change the fidelity values in the synoptic table, and you will have a clear overview of what happens to your data after standardization.

Checking the Fisher's exact test check box excludes phi coefficient fidelity values which are not statistically significant: they are assigned a fidelity of 0. The level of significance can be chosen.

1.10.4 Fidelity Tests

This function is included for users who would like to test fidelity measures with theoretical values. From the 'Help' menu select 'Fidelity Measure Test'. This opens the following window:

Fig. 45: Window for testing fidelity measures.

The fidelity measures in JUICE depend on four parameters:

N … number of relevés in the data set,
N_p … number of relevés in the target vegetation unit,
n … number of occurrences of the species in the data set,
n_p … number of occurrences of the species in the target vegetation unit.

The program uses the fidelity measure that has been selected from the 'Fidelity measures' tab of the 'Options' window. (See Section 1.10.3.) The current measure is displayed in the 'Test Fidelity Measure Yourself' window and on the Option Button on the Icon Bar.

Note 1: *Standardization methods for the phi coefficient, available from the 'Fidelity measures' tab, do not affect this calculation.*

Note 2: *The fidelity value is copied onto the clipboard and it can be pasted into other programs.*

1.10.5 Tests of Data Structure Using Different Types of Standardization

JUICE also has a function for visualising the effect of data standardization on the phi coefficient. From the 'Help' menu, select 'Advanced Fidelity Measure Test'.
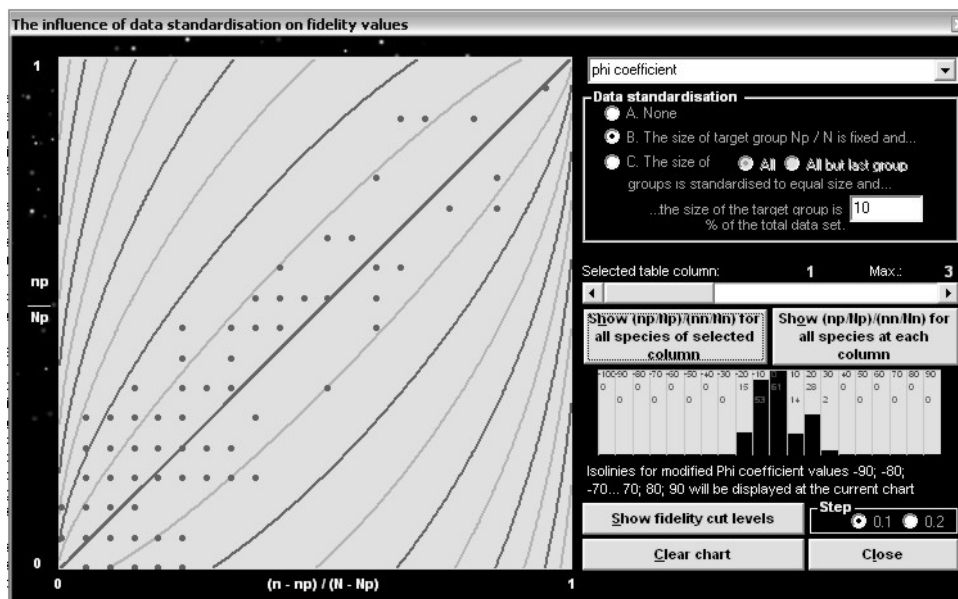

Fig. 46: Window for visualising 'The influence of data standardisation on fidelity values'.

The window contains a contour diagram depicting the dependence of the fidelity measure (phi coefficient) on the relative frequency of species occurrences within (vertical axis) and outside (horizontal axis) the target vegetation unit. This diagram depends on the relative size of the vegetation unit, a parameter which begins at 10% and can be adjusted by the user. The curves are phi value isolines of -0.9, -0.8 ... 0.9. Each dot is a species frequency inside and outside the selected first vegetation unit. The user can select parameters and graphically test each vegetation unit.

1.10.6 Quantitative Fidelity Measures

JUICE (versions 6.3.66 and higher) can calculate fidelities not only from presence/absence data but also from quantitative cover values. For quantitative calculation, variables are defined as:

> n … sum of all covers of the species in the data set,
> n_p … sum of all covers of the species in the target vegetation unit.

Covers range in the interval [0,1].

The fidelity measure calculations are analogous to those described above in Section 1.10.1.

The choice between presence/absence or quantitative fidelity measurement is available from the 'Options' window. (See Fig. 44.)

Note: *Quantitative fidelity measures are only available for synoptic tables. Functions 'COCKTAIL Groups' and 'Interspecific Associations' are calculated using presence/absence data.*

1.11 Synoptic Tables

Synoptic tables summarise the results of any classification of relevés. Therefore, they are one of the basic results of all phytosociological analyses and studies. They give an overview of classified vegetation units in the data set and help the researcher understand sophisticated relations among species in context with environment. Synoptic tables can contain several types of information which can be used for additional sorting of species and analysis of diagnostic, constant and dominant species. JUICE supports many different types of synoptic tables, which can be used separately or in combination.

The columns of the synoptic tables are defined by the separators in the standard table. Separators are placed or removed by holding down the Shift key and clicking on a relevé with the left mouse button. (See Section 1.5.4 for more details.) To display a synoptic table, select the type of table from the 'Synoptic Table' menu. To return to Standard Table Display, select that type of table again.

1.11.1 Synoptic Table Display

The Synoptic Table Display has the same three parts as the Standard Table Display (species, short headers and synoptic table data – see Section 1.5.1). Mouse functions in the synoptic table are described in Section 1.5.2. Several menu items are not available in Synoptic Table Display mode.

Note: Columns in the synoptic table can be moved by clicking and dragging just as you do with relevés in Standard Table Display mode. This gives a way to move a block of relevés without using colours. Simply delimit the block with separators, switch to a synoptic table, move the column, and switch back.

Values that exceed a certain threshold are highlighted. These thresholds can be set in the 'Synoptic tables' tab of the 'Options' window. It is also possible to select the highlighting colours as well as to turn the highlighting feature on or off.
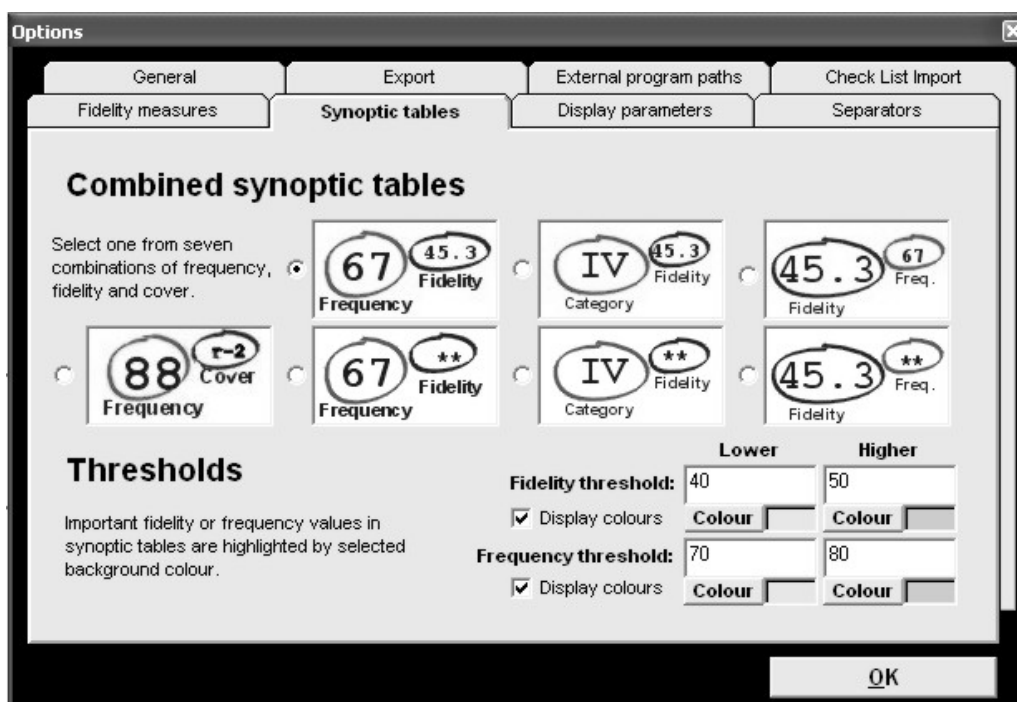

Fig. 47: The 'Synoptic tables' tab of the 'Options' window.

For more sophisticated synoptic table graphic display, two thresholds with different colours can be defined. Values greater than the 'Lower' threshold will be given one colour and values which exceed the 'Higher' threshold will be given the other colour. For single-colour highlighting, the 'Lower' threshold can be set to a value equal to or greater than the 'Higher' threshold. Colours can be completely switched off with the 'Display colours' check box.

Note: If a value is entered that causes the 'Lower' threshold to be greater than the 'Higher' threshold, the 'Higher' threshold is changed automatically. This means that it may be impossible to lower the 'Higher' threshold without first lowering the 'Lower' threshold.

1.11.2   Percentage Constancy Synoptic Table

This type of synoptic table shows percentage constancy of species for each relevé group. This function considers only presence/absence of the species without discrimination of cover values. The value of percentage constancy is rounded to the nearest natural number in the interval from 0 to 100, except that all non-zero values less than 1 are converted to the number 1.

Fig. 48: Synoptic table with percentage constancy.

1.11.3   Categorical Synoptic Table

Constancy can also be displayed in a categorical form. There are five constancy categories widely used in phytosociological literature: I (0 %-20 %); II (20 %-40 %); III (40 %-60 %); IV (60 %-80 %); V (80 %-100 %). Such synoptic tables are clearer and all columns are easily comparable. However, differences between categories are hard to judge. The differences between two consecutive categories could be anywhere from 1% to 39%. Moreover, species in the same category could have percentages differing by as much as 19%, so a given species may have constancy more similar to species in a different category compared to species in its own category.

```
Categorial synoptic table

Number of releves:        3 | 11 | 14 |  6 | 42 | 42 | 66 | 18

releves 202
Species 631               1 |  2 |  3 |  4 |  5 |  6 |  7 |  8


Poa trivialis             .| IV | II | .  | .  | .  | .  | .
Deschampsia cespitos     II| IV | .  | II | I  | I  | .  | .
Equisetum arvense         .| IV | II | II | .  | .  | .  | .
Aegopodium podagrari      .| II | V  | II | I  | I  | .  | .
Urtica dioica             .|III | V  | IV | II | I  | I  | .
Geum urbanum              .|III | V  | II | I  | II | I  | .
Stellaria nemorum         .| .  | IV | .  | .  | .  | .  | .
Galium aparine            .| II | IV | II | I  | I  | I  | .
Pulmonaria obscura+o      .| II | IV |III |III | IV | I  | .
Sambucus nigra            .| II | IV | .  | I  | .  | .  | .
Galeobdolon montanum      .| I  | IV | II |III | I  | .  | .
Phalaris arundinacea      .| II | IV | .  | .  | .  | .  | .
Oxalis acetosella         .| II |III | V  |III | I  | .  | .
Carex sylvatica           .| I  | I  | V  | .  | I  | .  | .
Glechoma hederacea+h      .| .  | IV | V  | I  | I  | .  | .
Carex remota             II| I  | I  | V  | .  | .  | .  | .
Dryopteris filix-mas      .| I  | I  | II | V  | I  | I  | .
Carpinus betulus          .| .  | II |III |III | V  | II |III
Hepatica nobilis          .| .  | I  | I  |III | V  | .  | I
Dactylis polygama         .| I  | I  | II | II | IV | I  | .
Quercus petraea agg.      .| .  | .  | .  | I  |III | V  |III
```

Fig. 49: Synoptic table with categorical constancy.

1.11.4   Synoptic Table with Absolute Frequency ('Absolute Constancy')

In this synoptic table, the total number of relevés in the relevé group is displayed at the top of each column. The entries in the table are the number of species occurrences in the relevé groups. The highlighting scheme is the same as for percentage synoptic tables – it corresponds to relative frequency.

```
Absolute frequency synoptic table

Number of releves:        3 | 11 | 14 |  6 | 42 | 42 | 66 | 18

releves 202
Species 631               1 |  2 |  3 |  4 |  5 |  6 |  7 |  8


Poa trivialis             .|  8 |  3 | .  | .  | .  | .  | .
Deschampsia cespitos      1|  8 | .  | 2  | 1  | 2  | .  | .
Equisetum arvense         .|  8 |  3 | 2  | .  | .  | .  | .
Aegopodium podagrari      .|  3 | 14 | 2  | 3  | 3  | .  | .
Urtica dioica             .|  6 | 14 | 4  | 12 | 1  | 2  | .
Geum urbanum              .|  5 | 12 | 2  | 4  | 9  | 2  | .
Stellaria nemorum         .|  .  | 11 | .  | .  | .  | .  | .
Galium aparine            .|  3 | 11 | 2  | 8  | 5  | 7  | .
Pulmonaria obscura+o      .|  3 | 11 | 3  | 19 | 26 | 1  | .
Sambucus nigra            .|  3 | 11 | .  | 4  | .  | .  | .
Galeobdolon montanum      .|  1 | 11 | 2  | 25 | 7  | .  | .
Phalaris arundinacea      .|  3 | 10 | .  | .  | .  | .  | .
Oxalis acetosella         .|  3 |  6 | 5  | 18 | 5  | .  | .
Carex sylvatica           .|  1 |  2 | 5  | .  | 1  | .  | .
Glechoma hederacea+h      .|  .  |  9 | 5  | 3  | 3  | .  | .
Carex remota              1|  1 |  1 | 5  | .  | .  | .  | .
Dryopteris filix-mas      .|  1 |  2 | 2  | 34 | 3  | 1  | .
Carpinus betulus          .|  .  |  5 | 3  | 22 | 34 | 15 | 8
Hepatica nobilis          .|  .  |  1 | 1  | 22 | 34 | .  | 2
Dactylis polygama         .|  2 |  1 | 2  | 14 | 31 | 1  | .
Quercus petraea agg.      .|  .  | .  | .  | 6  | 23 | 59 | 10
```

Fig. 50: Synoptic table with absolute constancy.

1.11.5   Fidelity Synoptic Table

This table uses the fidelity concept as described in Section 1.10. The fidelity between the species and the relevé group is displayed. Highlighting thresholds are set in the 'Fidelity threshold' section of the 'Synoptic tables' tab of the 'Options' menu. (See Section 1.11.1.) Fidelity can be calculated either from presence/absence or from quantitative cover data. (See Section 1.10.6.)

Fig 51: Synoptic table with fidelity values.

Note: Negative fidelities are usually less useful for table explanation. Therefore, the program displays all values of zero or less as dashes.

1.11.6   Synoptic Tables and Cover (Maximum, Average, Median, Modus)

A synoptic table can also be used for presenting cover values. These are selected from the 'Abundance Value' submenu of the 'Synoptic Table' menu. As an example, suppose a species has the following cover values in a group of 11 relevés (percentage number with cover code):

1(r)   1(r)   1(r)   2(+)   3(1)   4(2m) 8(2a) 8(2a) 18(2b) 38(3) 63(4).

The maximum cover for this species will be 63, the average will be 13 (rounded), the median will be 4 and the modus (the most frequent value) will be 1.

These statistics only consider relevés in which the species is present. To find the average cover over all relevés in the group, use Barkman's Total Cover (Barkman 1989) as described in Section 1.11.8 below.

Note: Cover values in a synoptic table are always displayed as percentage numbers.

1.11.7   Zlatnik's Combined Scale

Another type of table available from the 'Abundance Value' submenu is 'Zlatnik's Combined Value' (Plíva & Průša 1969). Czech foresters use a special synoptic table in which values are defined according to this table:

Fig 52: Information window with Zlatnik's scale.

These values combine species relative frequencies with maximum cover. To see this table in JUICE, open the 'Synoptic Table' menu, select 'Sort Species In Synoptic Tables' and press the '?' button next to 'Zlatnik's value'.

1.11.8   Average Cover (Barkman's Total Cover Value)

The average cover (AC) within a relevé group as defined by Barkman (1989) is:

AC = SUM(% Cover) / number of relevés.

Note: *The 'number of relevés' includes those with a cover value of zero (i.e., where the species is absent).*

Fig. 53: Synoptic table with average covers.

1.11.9   Combined Synoptic Tables

Standard synoptic tables contain only one important aspect of the data set while others are not presented. Information such as frequency, fidelity and cover can be presented in multiple

tables, but this takes up space and it can be difficult to see relationships between the tables. JUICE can display two values in a combined synoptic table, thus overcoming these disadvantages. Selecting 'Combined Synoptic Table' from the 'Synoptic Table' menu displays a combined synoptic table and opens the 'Synoptic tables' tab of the 'Options' window:
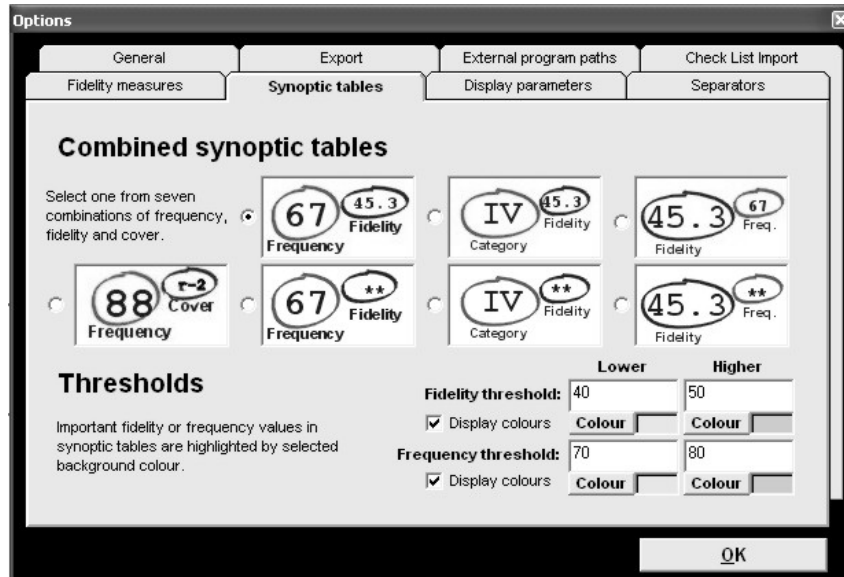
Fig. 54: Selecting a combined synoptic table from the 'Synoptic tables' tab of the 'Options' window.

From this tab, one of seven combinations of frequency, fidelity and cover can be displayed.

The highlighting thresholds for frequency and fidelity (see Section 1.11.1) are applied to their own columns in the table. For example, if the frequency and fidelity combination is selected, the combined table will look like this:

Fig. 55: Combined synoptic table with frequency and fidelity.

These tables can be exported into the current RTF export file as described in Section 1.9.

Note: *In a combined synoptic table, columns of relevés cannot be moved. Other mouse functions are the same as in regular synoptic tables.*

1.11.10 Synoptic Table Export

From the 'File' menu select 'Export' and 'Synoptic Table'. For more information, see Section 1.9.4.

1.11.11 Sorting Species in Synoptic Tables

The 'Sort Species In Synoptic Table' function is available from the 'Sorting' menu or the 'Synoptic Table' menu. It is only active during Synoptic Table Display mode. Selecting this function opens the following window:
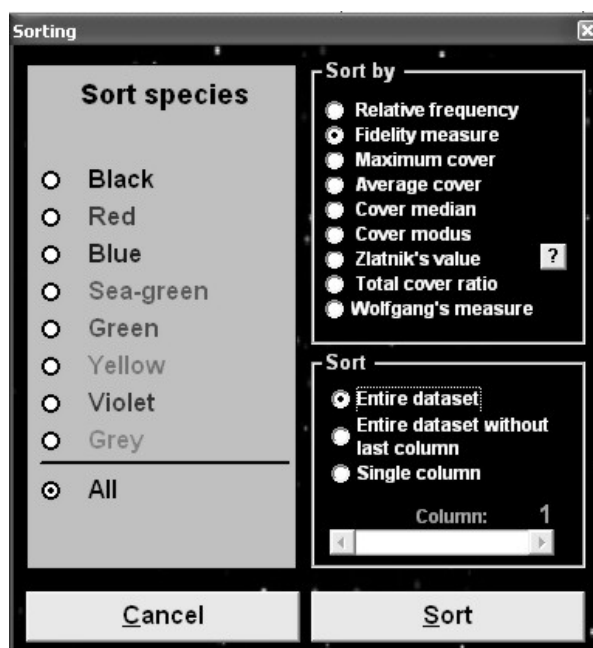
Fig. 56: The synoptic table 'Sorting' window.

Species can be sorted according to several different measures. The user has the option to sort the 'Entire dataset', the 'Entire dataset without last column' or a 'Single column'. The window contains a slide bar for selecting which column will be sorted by the 'Single Column' sort. The function can be restricted to sort only species of a certain colour.

The 'Entire dataset' sort is a cumulative sorting function:

1. When this function is called, the user is prompted to define a sorting cut-off level. The default cut-off level for relative frequency and fidelity will be the same as the 'Lower' threshold defined in the 'Synoptic tables' tab of the 'Options' window. (See Section 1.11.1.) Furthermore, changing this cut-off level for sorting changes the 'Lower' threshold for highlighting.
2. Once the cut-off level is defined, the first column is sorted.
3. Species with values higher than the cut-off level are held fixed at the top of the table. The remaining species are sorted in the second column.
4. The process repeats for each column until the entire table is sorted.

The sorting function 'Entire dataset without last column' sorts the table similarly except that the last column is not sorted.

Note: The actual sorting algorithm is more complicated than that described above. Species that have values above the cut-off level in two columns are moved below the species that exceed the cut-off level in only one column. These are followed by species that have values above the cut-off level in three columns, four columns and so on. The result will be a table with uniquely diagnostic (or constant or dominant) species in blocks at the top, followed by blocks of species which are diagnostic for multiple groups.

1.11.12 Analysis of Synoptic Columns Combining with Exporting the Results

The program can extract diagnostic, constant and dominant species from each synoptic column. This function is widely used for analysis of classification results and interpretation of vegetation clusters.

Fig. 57: Window for detailed analysis of synoptic tables.

From the 'Synoptic Table' menu, select 'Analysis Of Synopt. Columns'. Initially, the three lists will appear blank. Select the column to analyse (using the slide bar at the bottom) and then press the 'Refresh' button. Three species lists will appear:

> **'Diagnostic species'** are those with fidelity higher than the 'Lower' fidelity threshold (defined in the 'Synoptic tables' tab of the 'Options' menu – see Section 1.11.1).
> **'Constant species'** are those with relative frequency higher than the 'Lower' frequency threshold (also defined in the 'Synoptic tables' tab). However, only constant species that are not diagnostic will be included in the list unless the 'Include diagnostic species' check box is checked.
> **'Dominant species'** are defined as all species that have cover values higher than the cover threshold. A species appears in this list if its cover exceeds the threshold value in any relevé of the selected vegetation unit. The list of dominant species can be

limited to species that exceed a certain minimum relative frequency as specified in the 'Minimum freq.' box.

Species are displayed with layer number and fidelity or frequency value. If the 'Show references' check box is checked, species that appear in more than one list will be cross-indexed to the other list or lists ('Dg' for diagnostic, 'C' for constant and 'Dm' for dominant).

Note 1: The display is not updated when a display mode check box or a threshold value is changed. To enact the desired display changes, press the 'Refresh' button.

Note 2: Changing the 'Fidelity threshold' or the 'Frequency threshold' changes the threshold throughout the program, just as though it were changed in the 'Synoptic tables' tab of the 'Options' window.

Species in the lists can be selected with the mouse or keyboard and assigned a selected colour in the table by pressing the 'Mark in the table' button.

Note: Shift+click can be used to select a block of species. In particular, to select an entire list, click on the top species and then Shift+click on the bottom species. Ctrl+click can be used to select multiple species which are not in a block or to deselect a currently selected species.

All information can be saved into the current rich text format export file. (See Section 1.9.2.) Pressing the 'Export' button opens the following window:
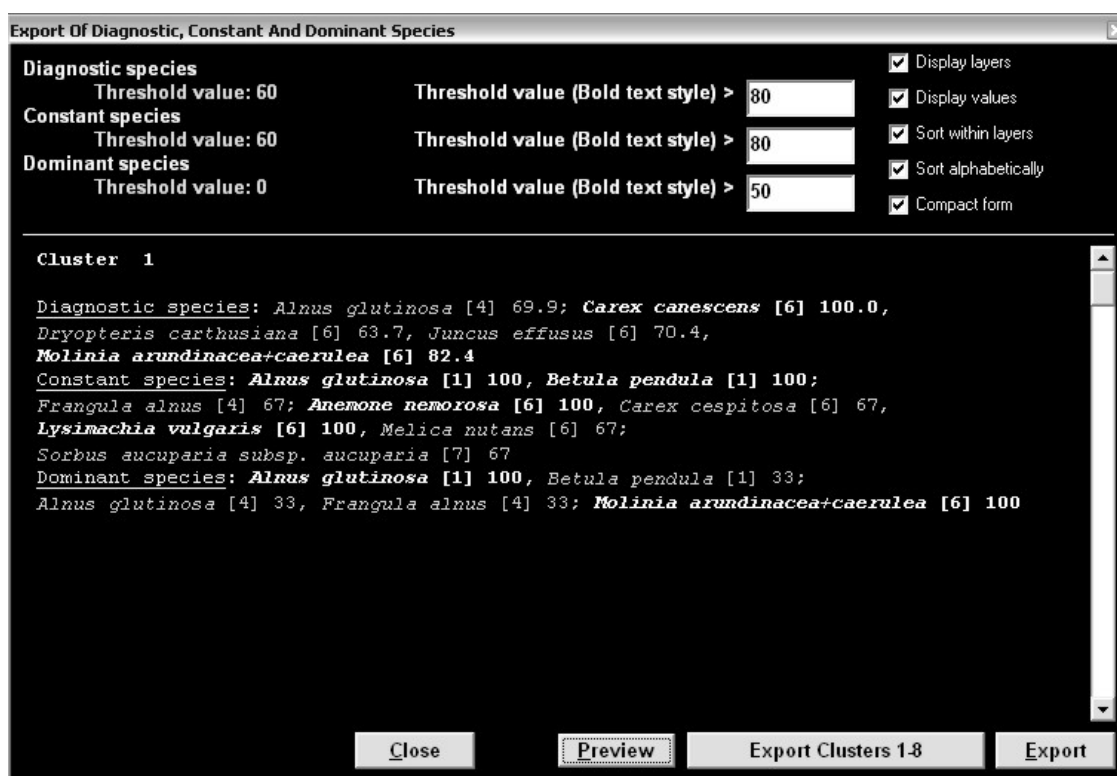
Fig. 58: Window for 'Export Of Diagnostic, Constant And Dominant Species'.

The list can be formatted as unsorted, sorted alphabetically or within layers, with or without frequencies or fidelities, with or without layers and in compact or extended form. The 'Lower' threshold values are fixed – they have been defined in the previous window. The 'Higher' threshold values ('Bold text style') correspond to the values set in the 'Synoptic tables' tab. They may be reset to any value equal to or higher than the lower threshold. (Changing the 'Bold text style' value for diagnostic or constant species in this window has the same effect as changing the 'Higher' fidelity or frequency threshold value in the 'Synoptic tables' tab.) Species exceeding these values will be displayed in bold style. The sample

species list in the lower part of the window will not change until the user presses the 'Preview' button.

The user can export information for a single cluster (column) with the 'Export' button. The information for the entire data set can be exported by pressing the 'Export Clusters' button. All data are saved into the current RTF export file. (See Section 1.9.2.)

1.11.13 Uniqueness of Vegetation Unit

Uniqueness was used in the paper of Chytry & Tichy (2003) to identify unique vegetation units in the data set. It expresses whether there are similar vegetation units of the same rank (e.g., class or alliance). A vegetation unit is unique if none of its diagnostic species has simultaneously diagnostic status in other vegetation units, while its uniqueness decreases if it shares its diagnostic species with other vegetation units.

1.11.13.1 Theoretical Background

Uniqueness is calculated in two steps. First, an Asymmetric Similarity Index between every pair of vegetation units j and k is calculated as

$$T_{jk} = \frac{\sum_i \Phi_{ij} \cdot \Phi_{ik}}{\sum_i \Phi_{ij}^2},$$
(Eq. 8)

where Φ_{ij} is the fidelity of species i to vegetation unit j, Φ_{ik} is the fidelity of species i to vegetation unit k and the sums only include species with $\Phi_{ij} > 0.05$ and $\Phi_{ik} > 0.05$. This index ranges in the interval $[0, \infty)$ and yields the highest values for those pairs of vegetation units in which a large proportion of diagnostic species of vegetation unit j are also diagnostic species of vegetation unit k. It is an asymmetric similarity measure because in cases of low numbers of diagnostic species in vegetation unit j and high numbers in k, where most of the diagnostic species of j are shared with k, the similarity of j to k is high while the similarity of k to j is moderate. The Similarity Index is calculated separately for all pairs of classes and all pairs of alliances (suballiances). For every pair j and k, two indices are calculated, one for the similarity of j to k and the other for the similarity of k to j.

Second, the Uniqueness Index for each vegetation unit is calculated using this formula:

$$U_j = \frac{1}{\sum_k T_{jk}}.$$
(Eq. 9)

This Uniqueness Index is low for those vegetation units whose diagnostic species are mostly shared with other vegetation units.

1.11.13.2 Uniqueness in JUICE

The 'Uniqueness' function is available for synoptic tables with fidelities. After selecting 'Uniqueness' from the 'Synoptic Tables' menu, the following window will appear:
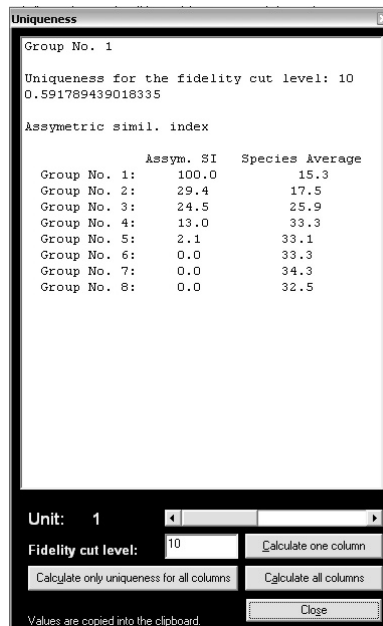
Fig. 59: Uniqueness and Asymmetric Similarity Indices calculation.

The list of species compared is limited to those with fidelities higher than the defined threshold value. This value depends on the selected fidelity measure and method of data standardization. The vegetation unit can be selected with the scroll bar. After pressing the 'Calculate one column' button, the calculated Uniqueness Index and a list of Asymmetric Similarity Indices are displayed. This information is also saved onto the clipboard.

Note: *The 'Calculate only uniqueness for all columns' and 'Calculate all columns' buttons are for copying the indicated information to the clipboard (from which it can be pasted into another program). The information actually displayed in the window will be the full information for the highest-numbered relevé group.*

1.11.14 Average Values of Constancy Columns

The 'Average Values Of Constancy Columns' function of the 'Synoptic Tables' menu calculates the average for each synoptic table column. The displayed values (relative frequency, fidelity, average cover etc.) are averaged and these averages are displayed in a separate window:

Fig. 60: Average values of constancy columns.

The results can be saved onto the clipboard for further use.

1.11.15 Crispness of Classification

Classification methods usually produce results with hierarchically distributed clusters. Sometimes it is difficult to determine an optimal number of clusters providing the highest 'separation power' for species. JUICE includes a function, proposed in the paper of Botta-Dukát et al. (2005), for identifying the optimal number of clusters.

1.11.15.1 *Theoretical Background*

The calculation is based on G statistics, which can be easily calculated for contingency tables of any size (Sokal & Rohlf 1995). Calculated for a $2 \times c$ contingency table (where c is the number of clusters), the G statistic does not measure the fidelity of a species to individual clusters, but the species's capacity to distinguish the clusters within a given partition (the 'separation power' of the species). The average of separation powers is called the 'crispness of the classification'. The higher the average separation power, the better the clusters can be distinguished by the diagnostic species, i.e., the better the classification.

The problem is that the expected separation power and consequently the crispness of classification increase with increasing number of clusters, even if relevés are assigned randomly to clusters. This effect has to be eliminated before comparing partitions with different numbers of clusters. In a random classification, separation powers have approximately a chi-squared distribution with $c-1$ degrees of freedom (Sokal & Rohlf 1995). According to the central limit theorem (e.g., Zar 1999: 76–77), if the number of species is high, which is the case in most data sets, the crispness of classification has approximately a normal distribution with expected value $c-1$ and standard deviation $\sqrt{2(c-1)/S}$, where S is the number of species.

The effect of the number of clusters is removed by subtracting this expected value and dividing the difference between the observed and expected value by the standard deviation. In this way the crispness values are standardized and can be compared among partitions with different numbers of clusters. Local maxima of crispness may indicate optimal numbers of clusters.

1.11.15.2 *Optimal Use of This Function in JUICE*

This function is used to its full power in conjunction with the function 'Sort Relevés By Clusters' (see Section 1.6.3.3):

1. Call the function 'Sort Relevés By Clusters'. Open the resulting file produced by PC-ORD (or MULVA) or classify the data set using the 'Cluster Analysis (PC-ORD)' function from the 'Analysis' menu. The sorting window will appear automatically after the analysis. This window is always displayed on top, but the table remains active.
2. From the 'Synoptic Table' menu, select a table with frequency or fidelity values. Repeated selection of different numbers of clusters will automatically change the displayed synoptic table.
3. Choose a species colour and use it to select a list of species as a source for calculation of crispness of classification.
4. Call the 'Crispness Of Classification' function from the 'Synoptic Table' menu. This window, which is also always on top of the main window, will appear:
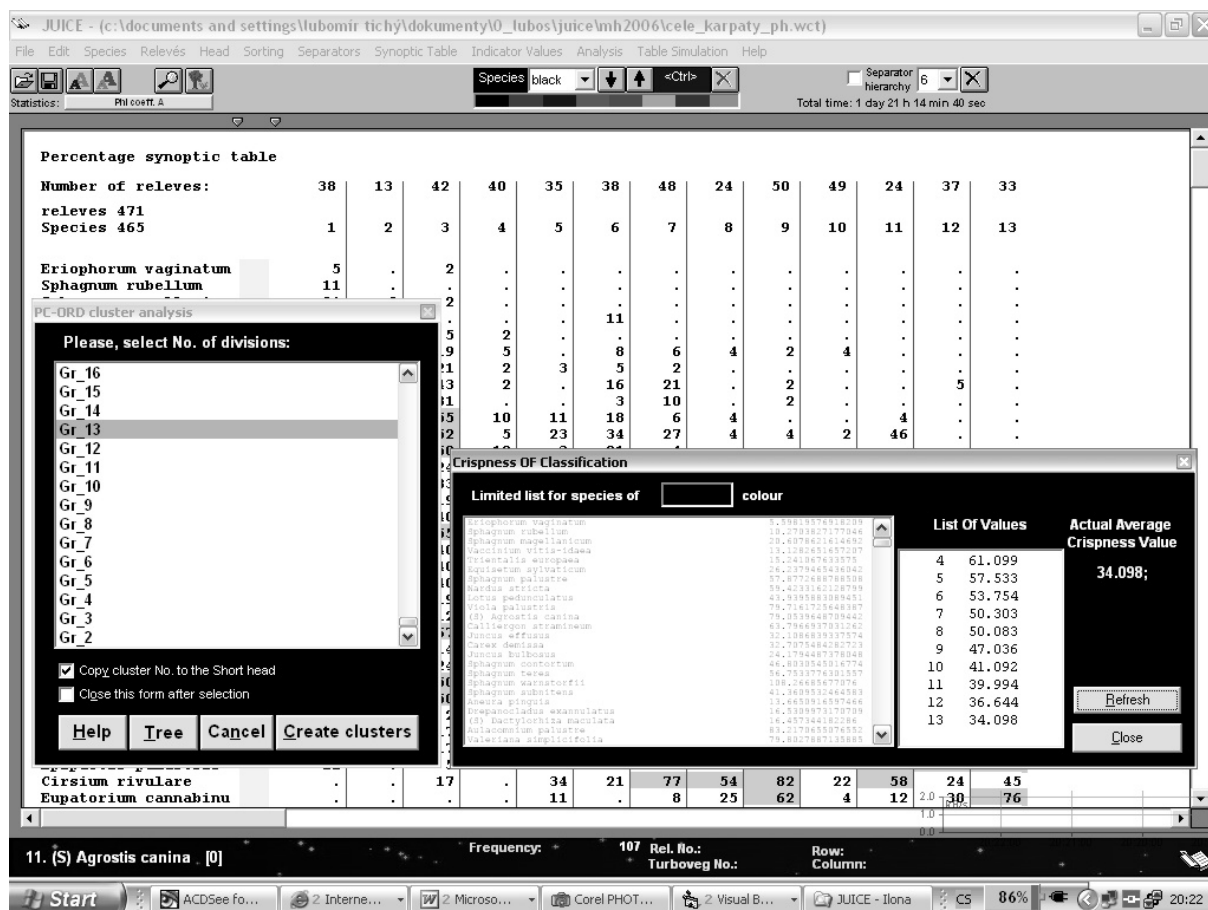
Fig. 61: The sorting function and the 'Crispness Of Classification' window overlaid on top of a synoptic table.

5. Press the 'Refresh' button. The program will calculate the appropriate value for the selected number of clusters.
6. In the 'cluster analysis' window, select a new number of clusters. The synoptic table will change. Press the 'Refresh' button in the 'Crispness Of Classification' window to calculate a new crispness value. (All values are saved onto the clipboard.)
7. Iterate these steps with increasing numbers of clusters.

Note 1: The program can calculate crispness of classification with a limited list of species. It is recommended, e.g., to exclude rare species (such as those occurring in fewer than 10 relevés) from this analysis.

Note 2: It is also possible to search for maximum crispness using hierarchical separators. (See Section 1.5.4.) Varying separator level will change the number of columns in the synoptic table. (This can be useful, e.g., with results from TWINSPAN classification.)

1.11.16 Comparison of Two Synoptic Tables

If the synoptic table is displayed in the form of percentage frequency or fidelity, it is possible to compare two synoptic tables and find their total similarity. This function was used in the paper Knollová et al. (2005) for comparison of several different classifications. The program calculates a crossing table of euclidean distances between all pairs of synoptic columns in two synoptic tables.

Note: Calculation of fidelities can be modified by data standardization, Fisher's exact test and selection of presence/absence versus quantitative data as described in Section 1.10.3.

1.11.16.1   Theoretical Background

The distance $d(\text{TAB1}_i; \text{TAB2})$ between the *i*-th column of one table, TAB1, and all columns of a second table, TAB2, is calculated according to the formula:

$$d(\text{TAB1}_i; \text{TAB2}) = \frac{\min_j(ED_{ij}) \cdot (n_{\text{TAB2}} - 1)}{(\sum_j ED_{ij}) - \min_j(ED_{ij})},$$ (Eq. 10)

where *i* and *j* denote columns of classified resampled data sets TAB1 and TAB2, respectively; ED_{ij} is the euclidean distance between phi coefficients in columns TAB1_i and TAB2_j; $\min_j(ED_{ij})$ is the shortest distance between the column TAB1_i and any of the columns TAB2_j; and n_{TAB2} is the number of columns in the table TAB2. In this way we obtain the distance between the selected column of table TAB1 and the most similar column of table TAB2, divided by the average distance between the selected column and all other columns of TAB2. The distance between the tables TAB1 and TAB2 is computed by averaging the distance values for individual columns table of TAB1:

$$d(\text{TAB1}; \text{TAB2}) = \frac{\sum_i d(\text{TAB1}_i; \text{TAB2})}{n_{\text{TAB1}}}.$$ (Eq. 11)

This 'distance' is actually an asymmetric measure, i.e., the distances $d(\text{TAB1}; \text{TAB2})$ and $d(\text{TAB2}; \text{TAB1})$ differ. Therefore the same procedure is applied in the opposite direction:

$$d(\text{TAB2}_j; \text{TAB1}) = \frac{\min_i(ED_{ij}) \cdot (n_{\text{TAB1}} - 1)}{(\sum_i ED_{ij}) - \min_i(ED_{ij})},$$ (Eq. 12)

$$d(\text{TAB2}; \text{TAB1}) = \frac{\sum_j d(\text{TAB2}_j; \text{TAB1})}{n_{\text{TAB2}}}.$$ (Eq. 13)

Finally the symmetric distance $D(\text{TAB2}; \text{TAB1})$ between tables TAB2 and TAB1 is calculated as an average of $d(\text{TAB1}; \text{TAB2})$ and $d(\text{TAB2}; \text{TAB1})$:

$$D(\text{TAB2}; \text{TAB1}) = \frac{d(\text{TAB1}; \text{TAB2}) + d(\text{TAB2}; \text{TAB1})}{2}.$$ (Eq. 14)

This method can be used for calculating the symmetric distances between any two tables.

1.11.16.2   Comparing Two Synoptic Tables within JUICE

To use JUICE to compare two synoptic tables:

1. Load the first table. All records must be unique, without duplicity of either species name or layer. (Such species must be merged. See Section 1.6.1.)
2. Classify the table and display it in the form of a synoptic table (using either frequency or fidelity).
3. From the 'Synoptic Table' menu, select 'Compare Two Synoptic Tables' and 'Save Image Of Synoptic Table' to save the table.
4. Load the second table and display it in the same form as the first one.
5. From the 'Synoptic Table' menu, select 'Compare Two Synoptic Tables' and 'Load Image And Compare'.

The program will display the resulting distance. A crossing table of all euclidean distances is saved onto the clipboard.

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