JUICE

program for management, analysis and classification of ecological data

2nd Edition of the Program Manual

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1st part

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1 Getting Started

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), the R program (R Development Core Team 2010) 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 7.0.45 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 Installation

This chapter explains how to install and initialise JUICE.

1.3.1 Content of the Installation Package

Information about actual installation version, sample data, literature, courses and other JUICE news is available at the web page:

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

The installation package can be downloaded directly from the internet address:

http://www.sci.muni.cz/botany/juice/jc06_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 path ‘Training data’ with a set of sample files and these files:

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 This file can be replaced directly without new installation by a newer version of the EXE file.

JCUPDATE.EXE – an automatic update procedute, which is activated from the JUICE program during actualisation.

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).

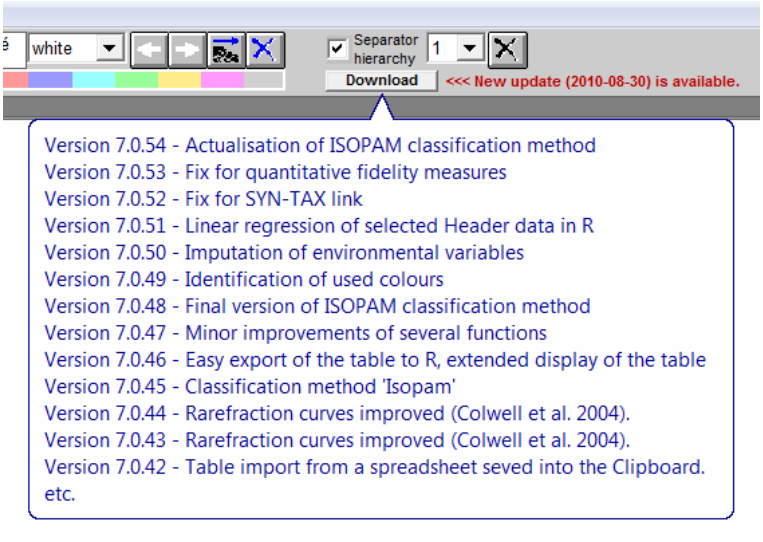
NEWFLORA.TXT – older species check list acceptable in the Czech Republic, Slovakia, Austria and Hungary based on unpublished nomenclature. Users from other countries should export the check list from TURBOVEG. (See Section 1.4.2.)

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 7.0’.

Note 1: *The program is able to indicate an existence of latest version, which is newer than currently installed on your computer. An actualisation can be done directly using the button ‘Download’ (Fig. 1), from the program menu Help, or the user can download a simple EXE file which must be copied directly into the existing JUICE directory (usually ‘C:\Program Files\JUICE 7.0’). If you install the program on a new computer, please use the full installation.*



<<< New update (2010-08-30) is available.

Version 7.0.54 - Actualisation of ISOPAM classification method
Version 7.0.53 - Fix for quantitative fidelity measures
Version 7.0.52 - Fix for SYN-TAX link
Version 7.0.51 - Linear regression of selected Header data in R
Version 7.0.50 - Imputation of environmental variables
Version 7.0.49 - Identification of used colours
Version 7.0.48 - Final version of ISOPAM classification method
Version 7.0.47 - Minor improvements of several functions
Version 7.0.46 - Easy export of the table to R, extended display of the table
Version 7.0.45 - Classification method 'Isopam'
Version 7.0.44 - Rarefraction curves improved (Colwell et al. 2004).
Version 7.0.43 - Rarefraction curves improved (Colwell et al. 2004).
Version 7.0.42 - Table import from a spreadsheet seved into the Clipboard.
etc.

Fig. 1: List of latest program versions and main improvements.
Such information is visible when the mouse cursor is placed over the button ‘Download’.

Note 2: *In a network (computer labs etc.), 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 predefined decimal delimiter must be a period '.'. The program will automatically try to convert a decimal comma to a decimal point when the program starts. A previous selection of the decimal point is restored after the program termination. 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.

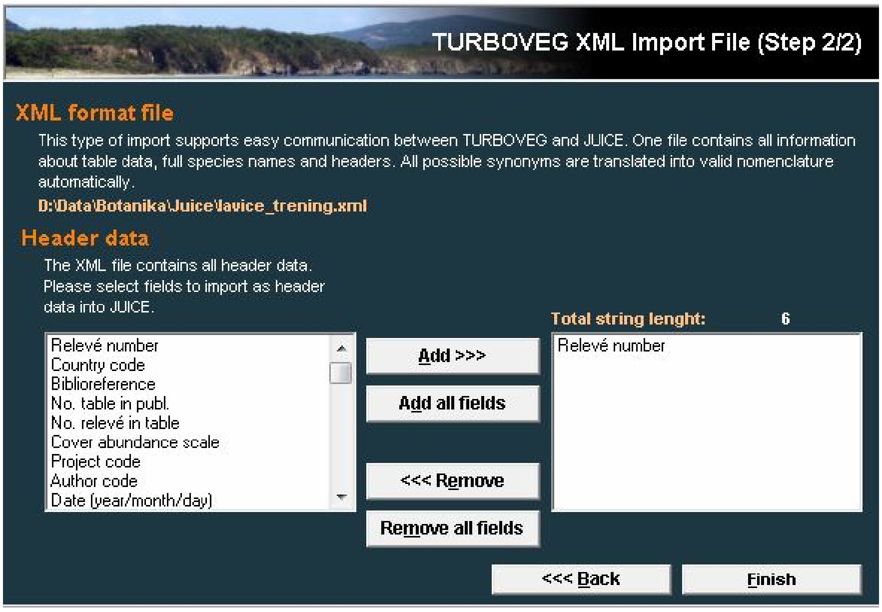
Note: *Each line of the INI file contains a parameter name and a parameter value separated by a double colon '::', thus it is possible to edit the file manually. However, almost all values can be managed directly from the program. Manually altering the INI file may cause problems. If you experience difficulty 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.



TURBOVEG XML Import File (Step 2/2)

XML format file

This type of import supports easy communication between TURBOVEG and JUICE. One file contains all information about table data, full species names and headers. All possible synonyms are translated into valid nomenclature automatically.

D:\Data\Botanika\Juice\lavice_trening.xml

Header data

The XML file contains all header data. Please select fields to import as header data into JUICE.

Total string lenght: 6

Relevé number
Country code
Biblioreference
No. table in publ.
No. relevé in table
Cover abundance scale
Project code
Author code
Date (year/month/day)

Relevé number

Fig. 2: 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 and mustn’t exceed 999 characters. This format is advantageous only in case if the TURBOVEG species check list is published and needn’t be modified before publication.

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.

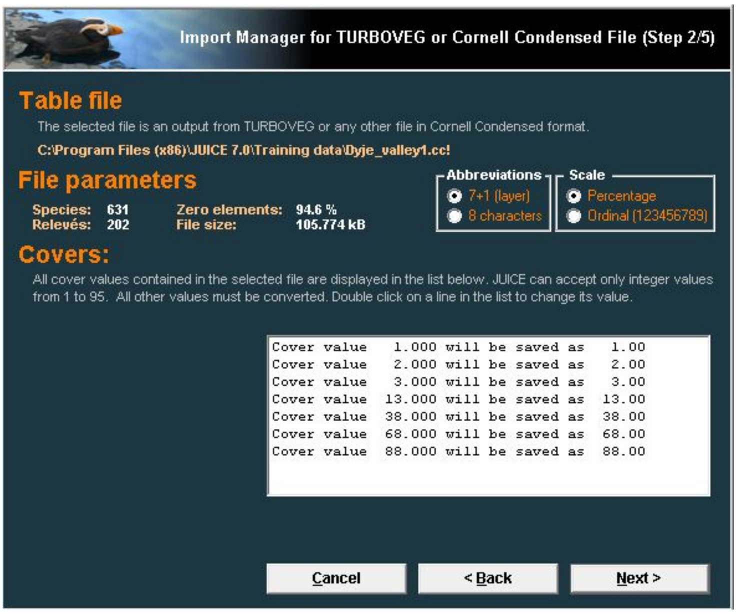
The third section of the file is reserved for relevé identification numbers. Each number has 8 characters, and there are 10 numbers per line. A sample CC! file can be downloaded from the JUICE web page and tested directly in the program.

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 1.4.8.)

The import process starts with selection of the CC! file. Then the following window appears:



Import Manager for TURBOVEG or Cornell Condensed File (Step 2/5)

Table file

The selected file is an output from TURBOVEG or any other file in Cornell Condensed format.

C:\Program Files (x86)\JUICE 7.0\Training data\Dyje_valley1.cc!

File parameters

Species: 631
Relevés: 202
Zero elements: 94.6 %
File size: 105.774 kB

Abbreviations: ● 7+1 (layer) ○ 8 characters

Scale: ● Percentage ○ Ordinal (123456789)

Covers:

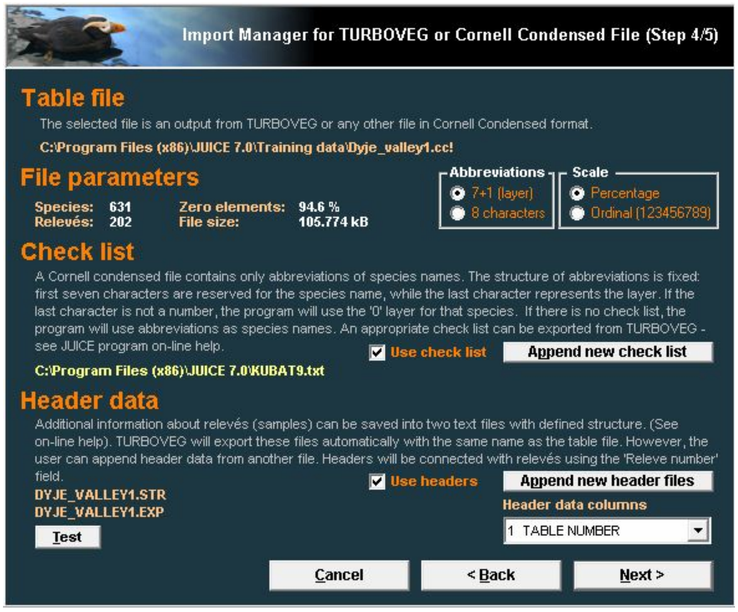
All cover values contained in the selected file are displayed in the list below. JUICE can accept only integer values from 1 to 95. All other values must be converted. Double click on a line in the list to change its value.

```
Cover value   1.000 will be saved as   1.00
Cover value   2.000 will be saved as   2.00
Cover value   3.000 will be saved as   3.00
Cover value  13.000 will be saved as  13.00
Cover value  38.000 will be saved as  38.00
Cover value  68.000 will be saved as  68.00
Cover value  88.000 will be saved as  88.00
```

Fig. 3: 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 0.01, 0.1, 0.2, 0.3, 0.5, or whole numbers from 1 to 100. 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.



Import Manager for TURBOVEG or Cornell Condensed File (Step 4/5)

Table file

The selected file is an output from TURBOVEG or any other file in Cornell Condensed format.

C:\Program Files (x86)\JUICE 7.0\Training data\Dyje_valley1.cc!

File parameters

Species: 631
Relevés: 202
Zero elements: 94.6 %
File size: 105.774 kB

Abbreviations: ● 7+1 (layer) ○ 8 characters
Scale: ● Percentage ○ Ordinal (123456789)

Check list

A Cornell condensed file contains only abbreviations of species names. The structure of abbreviations is fixed: first seven characters are reserved for the species name, while the last character represents the layer. If the last character is not a number, the program will use the '0' layer for that species. If there is no check list, the program will use abbreviations as species names. An appropriate check list can be exported from TURBOVEG - see JUICE program on-line help.

☑ Use check list

C:\Program Files (x86)\JUICE 7.0\KUBAT9.txt

Header data

Additional information about relevés (samples) can be saved into two text files with defined structure. (See on-line help). TURBOVEG will export these files automatically with the same name as the table file. However, the user can append header data from another file. Headers will be connected with relevés using the 'Releve number' field.

☑ Use headers

DYJE_VALLEY1.STR
DYJE_VALLEY1.EXP

Header data columns: 1 TABLE NUMBER

Fig. 4: 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 table 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:

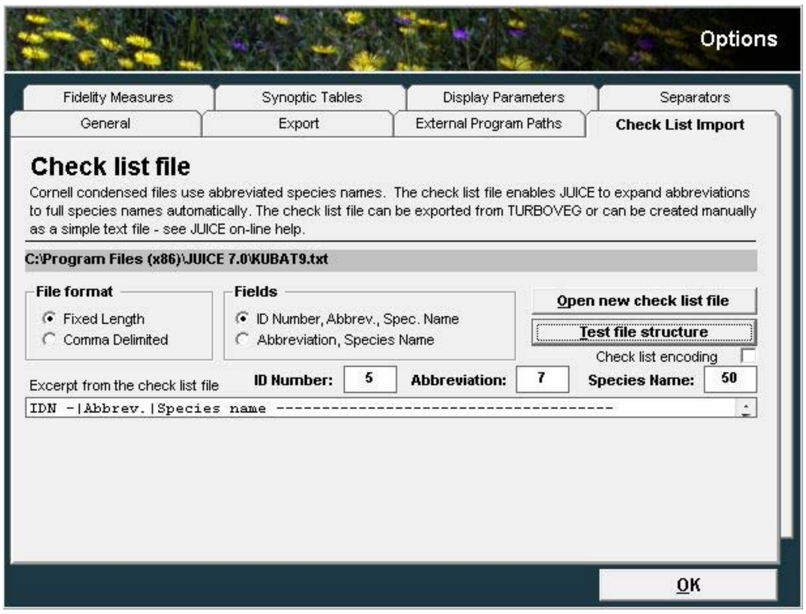
```
ABIEALB,Abies alba
ABIEGRA,Abies grandis
ABIE-SP,Abies species
ABITASA,Abietinella abietina var. abietina
ABITASH,Abietinella abietina var. hystricosa
ABITABI,Abietinella abietina
```

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/jc06_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 and the ‘Import’ menu). If no species list is defined, the program will open this window during the import of the CC! file:



Check list file

Cornell condensed files use abbreviated species names. The check list file enables JUICE to expand abbreviations to full species names automatically. The check list file can be exported from TURBOVEG or can be created manually as a simple text file - see JUICE on-line help.

C:\Program Files (x86)\JUICE 7.0\KUBAT9.txt

File format
● Fixed Length
○ Comma Delimited

Fields
● ID Number, Abbrev., Spec. Name
○ Abbreviation, Species Name

Check list encoding ☐

ID Number: 5
Abbreviation: 7
Species Name: 50

Excerpt from the check list file

```
IDN -|Abbrev.|Species name ------------------------------------
```

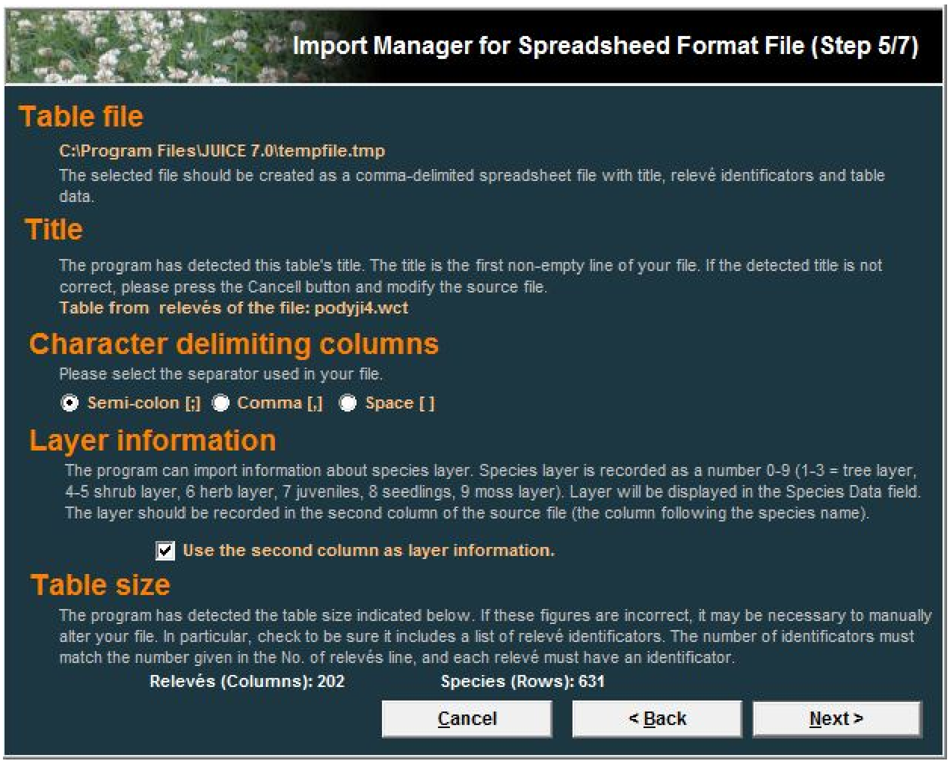
Fig. 5: Options (Check List Import).

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 (Microsoft® Excel® Table)

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.



Import Manager for Spreadsheed Format File (Step 5/7)

Table file

C:\Program Files\JUICE 7.0\tempfile.tmp

The selected file should be created as a comma-delimited spreadsheet file with title, relevé identificators and table data.

Title

The program has detected this table's title. The title is the first non-empty line of your file. If the detected title is not correct, please press the Cancell button and modify the source file.

Table from relevés of the file: podyji4.wct

Character delimiting columns

Please select the separator used in your file.

● Semi-colon [;] ○ Comma [,] ○ Space [ ]

Layer information

The program can import information about species layer. Species layer is recorded as a number 0-9 (1-3 = tree layer, 4-5 shrub layer, 6 herb layer, 7 juveniles, 8 seedlings, 9 moss layer). Layer will be displayed in the Species Data field. The layer should be recorded in the second column of the source file (the column following the species name).

☑ Use the second column as layer information.

Table size

The program has detected the table size indicated below. If these figures are incorrect, it may be necessary to manually alter your file. In particular, check to be sure it includes a list of relevé identificators. The number of identificators must match the number given in the No. of relevés line, and each relevé must have an identificator.

Relevés (Columns): 202 Species (Rows): 631

Fig. 6: Import Manager for Spreatsheet File

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 1.4.8.

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 ‘SIMPLE TEXT FILE’ format.). The user can change cover values by double click to the line on the list of found cover values during the import.

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
```

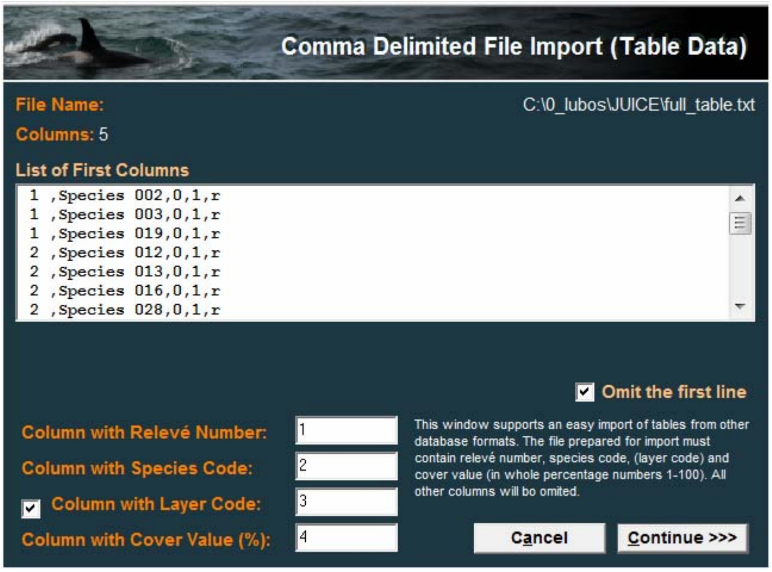
The **EXP** and **STR files** contain header data. (See Section 1.4.8.)

1.4.6 Comma Separated File (Databased Records)

This format uses coding of each non-empty cell of the table on separate line.

```
Relevé Number, Species Name, Layer Code, Percentage Cover
1, Fraxinus excelsior, 1, 3
1, Quercus petraea, 1, 63
1, Quercus petraea, 4, 13
1, Carpinus betulus, 1, 3
1, Cyclamen europaeus, 6, 3
2, Fagus sylvatica, 1, 88
…
```

The first line of the imborted file can contain field names. In case, it is not true, select 'Omit the first line'. Each line may contain any number of fields divided by comma or semi-colon. One of them must be an indicator of the plot (the number from 1 to 999,999), one of the species (character string of species name) and one of the species cover (percentage numbers 0.01, 0.1, 0.2, 0.3, 0.5 or integers from 1 to 100). Species layer is an optional field.



File Name: C:\0_lubos\JUICE\full_table.txt

Columns: 5

List of First Columns

```
 1 ,Species 002,0,1,r
 1 ,Species 003,0,1,r
 1 ,Species 019,0,1,r
 2 ,Species 012,0,1,r
 2 ,Species 013,0,1,r
 2 ,Species 016,0,1,r
 2 ,Species 028,0,1,r
```

☑ Omit the first line

Column with Relevé Number: 1

Column with Species Code: 2

☑ Column with Layer Code: 3

Column with Cover Value (%): 4

This window supports an easy import of tables from other database formats. The file prepared for import must contain relevé number, species code, (layer code) and cover value (in whole percentage numbers 1-100). All other columns will bo omited.

Fig. 7: Options (Check List Import).

1.4.7 Clipboard as Spreadsheet File

The spreadsheet can be imported to JUICE from the Clipboard. At first, the user must select the data (table) and copy them to the Clipboard. The data structure must be the same as for the ‘Import from spreadsheet file’. Other steps are the same as at the Section 1.4.4. This function is useful in situation when the user has a table opened in Microsoft® Excel® and wants to put this table or its part to the JUICE program for easier modification or manipulation with rows and columns.

1.4.8 Header Data

There are several 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. All header data exported from TURBOVEG in STR and EXP file can be also imported separately, i.e. independently from the table. Such function allows changing header information available for edited tables. 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.
3. Header data can be imported in comma or semi-colon delimited file.
4. If header data is in Microsoft Excel table format, it is possible to import them via Clipboard.

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 second column represents the name of the field.

```
 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)
```

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
```

Warning: *Each STR file or field headers in comma separated file / clipboard must contain the field ‘Relevé number’(or ‘Releve number’) specifying where to find the relevé’s unique identification number.*

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

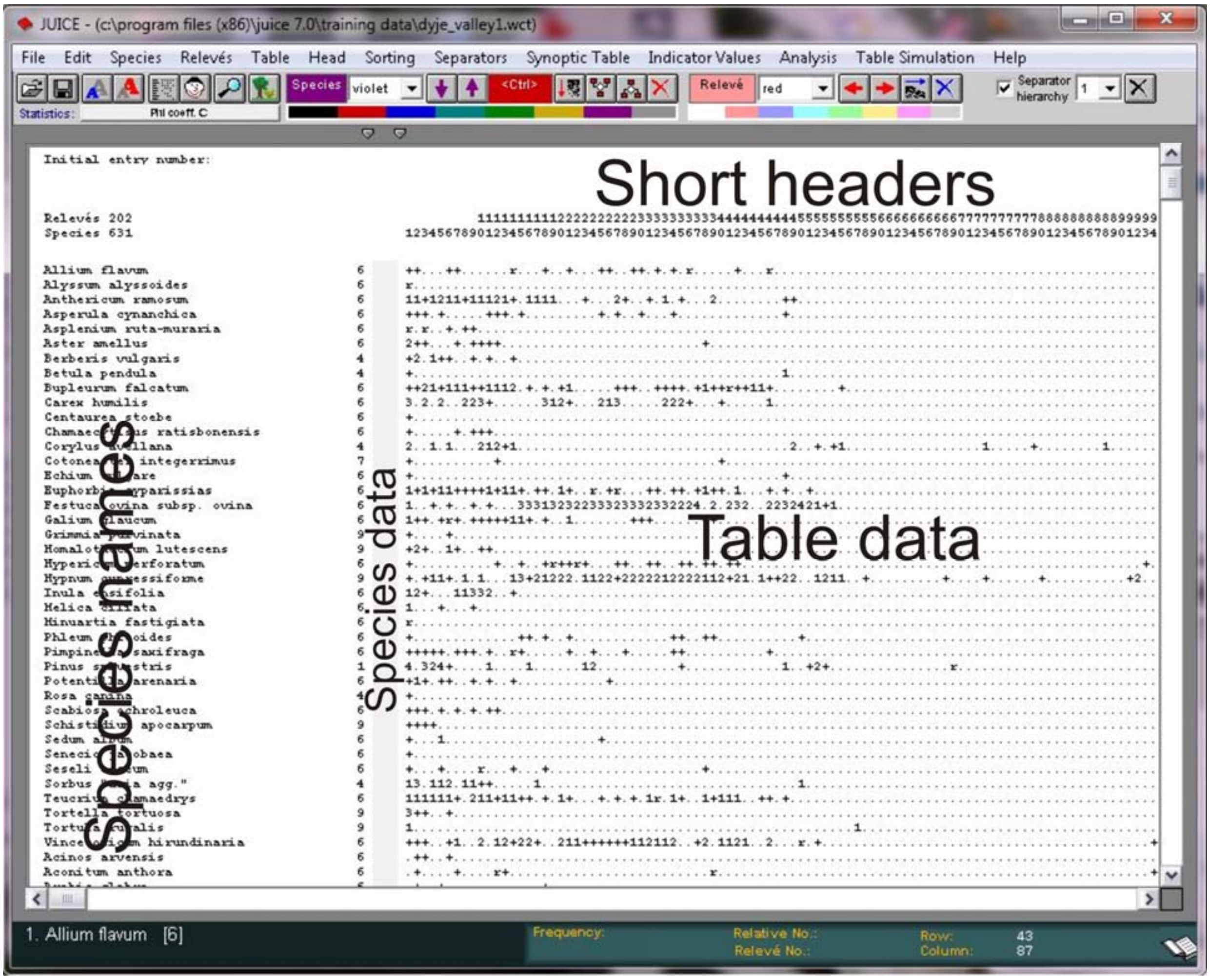


Fig. 8: Main window of the program.

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 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.

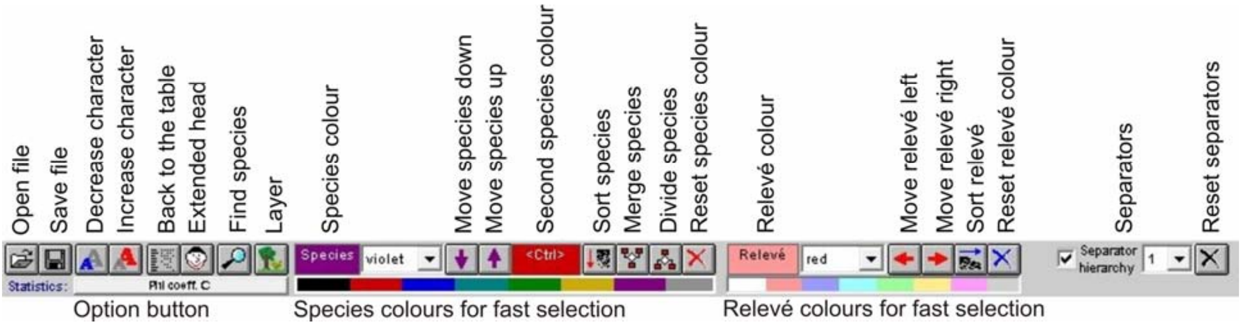


Fig. 9 The Icon Bar

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* ***Chyba! Nenalezen zdroj odkazů.****) 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 'Relative No.' (the relevé's relative number in the imported data set) and 'Relevé 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.

3. Anthericum ramosum [6]

Frequency: 37
Relative No.: 31
Relevé No.: 400074
Row: 41
Column:

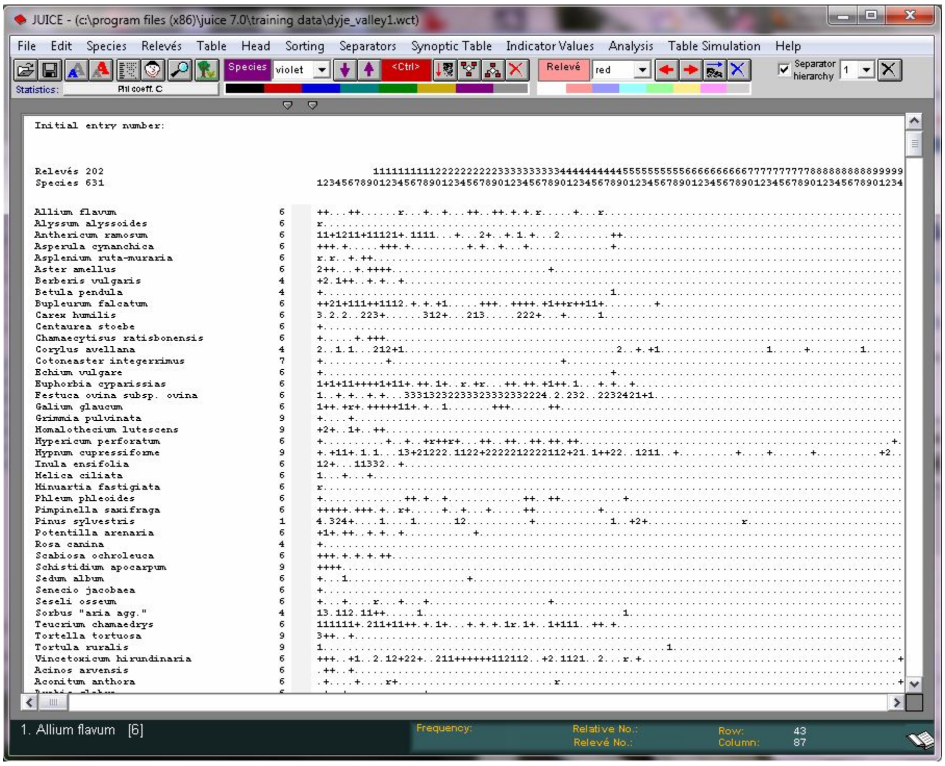
Fig. 10 The Status Bar

1.5.2 Mouse/Keyboard Functions

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

1.5.2.1 Functions sorted by displayed objects

In tables:



```
Initial entry number:


Relevés 202
Species 631

Allium flavum                    6
Alyssum alyssoides               6
Anthericum ramosum               6
Asperula cynanchica              6
Asplenium ruta-muraria           6
Aster amellus                    6
Berberis vulgaris                4
Betula pendula                   4
Bupleurum falcatum               6
Carex humilis                    6
Centaurea stoebe                 6
Chamaecytisus ratisbonensis      6
Corylus avellana                 4
Cotoneaster integerrimus         7
Echium vulgare                   6
Euphorbia cyparissias            6
Festuca ovina subsp. ovina       6
Galium glaucum                   6
Grimmia pulvinata                9
Homalothecium lutescens          9
Hypericum perforatum             6
Hypnum cupressiforme             9
Inula ensifolia                  6
Melica ciliata                   6
Minuartia fastigiata             6
Phleum phleoides                 6
Pimpinella saxifraga             6
Pinus sylvestris                 1
Potentilla arenaria              6
Rosa canina                      4
Scabiosa ochroleuca              6
Schistidium apocarpum            9
Sedum album                      6
Senecio jacobaea                 6
Seseli osseum                    6
Sorbus "aria agg."               4
Teucrium chamaedrys              6
Tortella tortuosa                9
Tortula ruralis                  9
Vincetoxicum hirundinaria        6
Acinos arvensis                  6
Aconitum anthora                 6
```

```
1. Allium flavum   [6]      Frequency:      Relative No.:      Row:     43
                                            Relevé No.:        Column:  87
```

Fig. 11: 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:

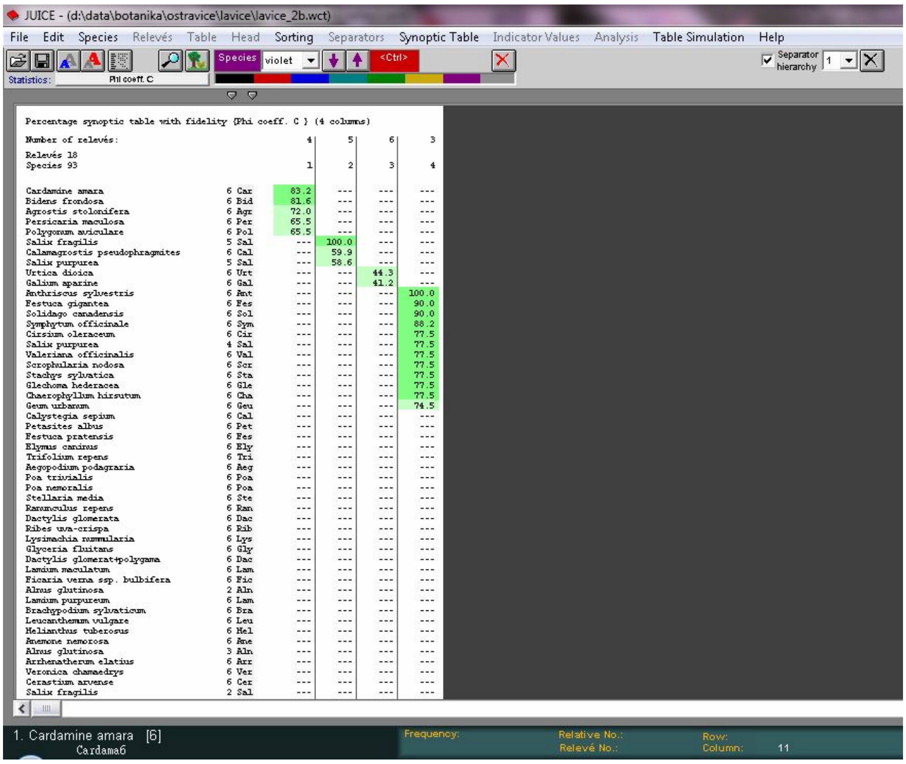
Left Button	Click	Highlight and select species.
Left Button	Double Click	Open dialog window for editing species name, layer and data.
Left Button	Click and Drag	Move currently selected species.
Shift + Left Button	Click	Make/remove separator line below currently selected species.
Right Button	Click	Repaint 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:



```
Percentage synoptic table with fidelity {Phi coeff. C } (4 columns)

Number of relevés:                                4|    5|    6|    3

Relevés 18
Species 93                                        1|    2|    3|    4

Cardamine amara                    6 Car       83.2|  ---|  ---|  ---
Bidens frondosa                    6 Bid       81.6|  ---|  ---|  ---
Agrostis stolonifera               6 Agr       72.0|  ---|  ---|  ---
Persicaria maculosa                6 Per       65.5|  ---|  ---|  ---
Polygonum aviculare                6 Pol       65.5|  ---|  ---|  ---
Salix fragilis                     5 Sal        ---|100.0|  ---|  ---
Calamagrostis pseudophragmites     6 Cal        ---| 59.9|  ---|  ---
Salix purpurea                     5 Sal        ---| 58.6|  ---|  ---
Urtica dioica                      6 Urt        ---|  ---| 44.3|  ---
Galium aparine                     6 Gal        ---|  ---| 41.2|  ---
Anthriscus sylvestris              6 Ant        ---|  ---|  ---|100.0
Festuca gigantea                   6 Fes        ---|  ---|  ---| 90.0
Solidago canadensis                6 Sol        ---|  ---|  ---| 90.0
Symphytum officinale               6 Sym        ---|  ---|  ---| 88.2
Cirsium oleraceum                  6 Cir        ---|  ---|  ---| 77.5
Salix purpurea                     4 Sal        ---|  ---|  ---| 77.5
Valeriana officinalis              6 Val        ---|  ---|  ---| 77.5
Scrophularia nodosa                6 Scr        ---|  ---|  ---| 77.5
Stachys sylvatica                  6 Sta        ---|  ---|  ---| 77.5
Glechoma hederacea                 6 Gle        ---|  ---|  ---| 77.5
Chaerophyllum hirsutum             6 Cha        ---|  ---|  ---| 77.5
Geum urbanum                       6 Geu        ---|  ---|  ---| 74.5
Calystegia sepium                  6 Cal        ---|  ---|  ---|  ---
Petasites albus                    6 Pet        ---|  ---|  ---|  ---
Festuca pratensis                  6 Fes        ---|  ---|  ---|  ---
Elymus caninus                     6 Ely        ---|  ---|  ---|  ---
Trifolium repens                   6 Tri        ---|  ---|  ---|  ---
Aegopodium podagraria              6 Aeg        ---|  ---|  ---|  ---
Poa trivialis                      6 Poa        ---|  ---|  ---|  ---
Poa nemoralis                      6 Poa        ---|  ---|  ---|  ---
Stellaria media                    6 Ste        ---|  ---|  ---|  ---
Ranunculus repens                  6 Ran        ---|  ---|  ---|  ---
Dactylis glomerata                 6 Dac        ---|  ---|  ---|  ---
Ribes uva-crispa                   6 Rib        ---|  ---|  ---|  ---
Lysimachia nummularia              6 Lys        ---|  ---|  ---|  ---
Glyceria fluitans                  6 Gly        ---|  ---|  ---|  ---
Dactylis glomerat+polygama         6 Dac        ---|  ---|  ---|  ---
Lamium maculatum                   6 Lam        ---|  ---|  ---|  ---
Ficaria verna ssp. bulbifera       6 Fic        ---|  ---|  ---|  ---
Alnus glutinosa                    2 Aln        ---|  ---|  ---|  ---
Lamium purpureum                   6 Lam        ---|  ---|  ---|  ---
Brachypodium sylvaticum            6 Bra        ---|  ---|  ---|  ---
Leucanthemum vulgare               6 Leu        ---|  ---|  ---|  ---
Helianthus tuberosus               6 Hel        ---|  ---|  ---|  ---
Anemone nemorosa                   6 Ane        ---|  ---|  ---|  ---
Alnus glutinosa                    3 Aln        ---|  ---|  ---|  ---
Arrhenatherum elatius              6 Arr        ---|  ---|  ---|  ---
Veronica chamaedrys                6 Ver        ---|  ---|  ---|  ---
Cerastium arvense                  6 Cer        ---|  ---|  ---|  ---
Salix fragilis                     2 Sal        ---|  ---|  ---|  ---
```

```
1. Cardamine amara   [6]
        Cardama6
```

Fig. 12: Synoptic table.

Functions are slightly different in synoptic tables:

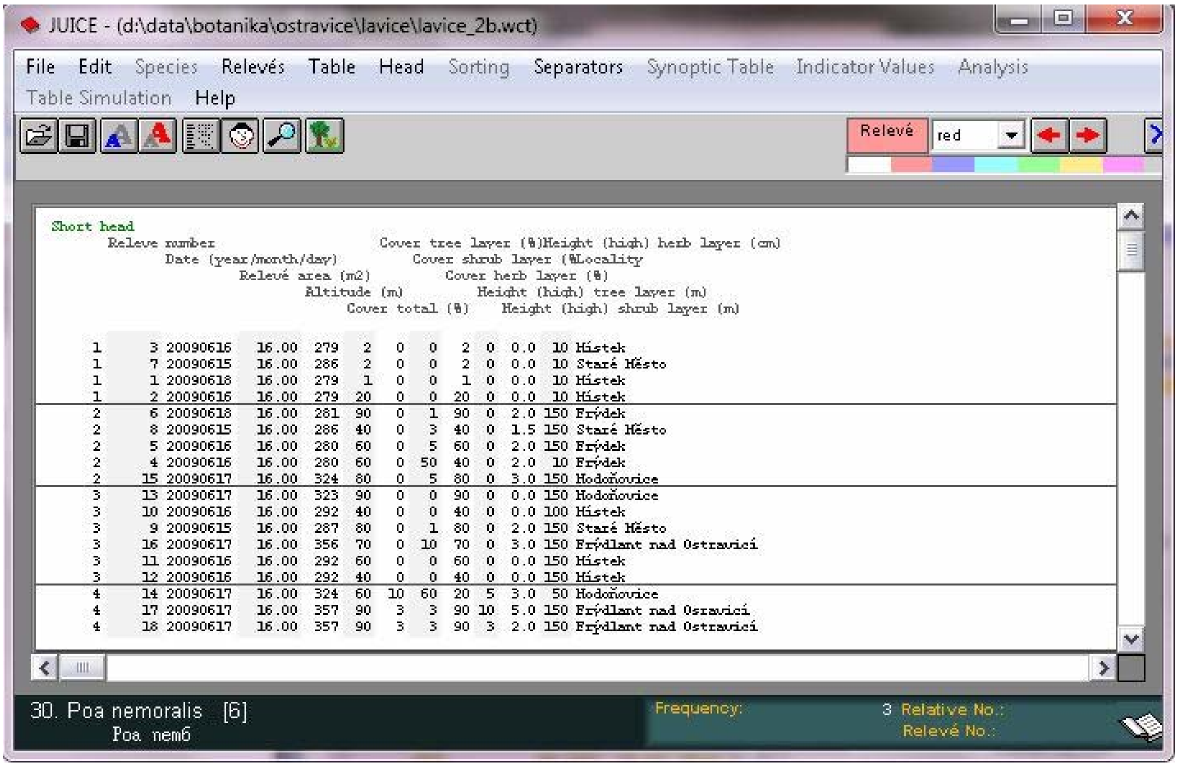
When the cursor is in the short headers:

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:



```
Short head
        Releve number                        Cover tree layer (%)Height (high) herb layer (cm)
                Date (year/month/day)             Cover shrub layer (%Locality
                           Relevé area (m2)             Cover herb layer (%)
                                    Altitude (m)             Height (high) tree layer (m)
                                          Cover total (%)     Height (high) shrub layer (m)

     1      3 20090616   16.00  279   2   0   0   2  0  0.0  10 Místek
     1      7 20090615   16.00  286   2   0   0   2  0  0.0  10 Staré Město
     1      1 20090618   16.00  279   1   0   0   1  0  0.0  10 Místek
     1      2 20090616   16.00  279  20   0   0  20  0  0.0  10 Místek
     2      6 20090618   16.00  281  90   0   1  90  0  2.0 150 Frýdek
     2      8 20090615   16.00  286  40   0   3  40  0  1.5 150 Staré Město
     2      5 20090616   16.00  280  60   0   5  60  0  2.0 150 Frýdek
     2      4 20090616   16.00  280  60   0  50  40  0  2.0  10 Frýdek
     2     15 20090617   16.00  324  80   0   5  80  0  3.0 150 Hodoňovice
     3     13 20090617   16.00  323  90   0   0  90  0  0.0 150 Hodoňovice
     3     10 20090616   16.00  292  40   0   0  40  0  0.0 100 Místek
     3      9 20090615   16.00  287  80   0   1  80  0  2.0 150 Staré Město
     3     16 20090617   16.00  356  70   0  10  70  0  3.0 150 Frýdlant nad Ostravicí
     3     11 20090616   16.00  292  60   0   0  60  0  0.0 150 Místek
     3     12 20090616   16.00  292  40   0   0  40  0  0.0 150 Místek
     4     14 20090617   16.00  324  60  10  60  20  5  3.0  50 Hodoňovice
     4     17 20090617   16.00  357  90   3   3  90 10  5.0 150 Frýdlant nad Osravicí
     4     18 20090617   16.00  357  90   3   3  90  3  2.0 150 Frýdlant nad Ostravicí

30. Poa nemoralis   [6]
      Poa nem6
```

Fig. 13: 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.)

1.5.2.2 Mouse Functions Sorted by Similar Functionality

Relevé/species selection:

Left Button	Click	Table	Select current relevé and species.
Left Button	Click	Synoptic Table	Select current species.
Left Button	Click	Header Table	Select current relevé.

Separators:

Shift + Left Button	Click	Table: Species or Short Headers	Add/remove species or relevé separator of selected hierarchy.
Shift + Left Button	Click	Synoptic Table: Species	Add/remove species separator of selected hierarchy.
Shift + Left Button	Click	Header Table	Add/remove relevé separator of selected hierarchy.

Colours:

Right Button	Click	Table and Synoptic Table: Species	Repaint indicated species with current species colour.
Right Button	Click	Table and Header Table: Relevé	Repaint indicated relevé with current relevé colour.
Ctrl + Right Button	Click	Table and Synoptic Table	Repaint indicated species with current secondary species colour.
Shift + Right Button	Click	Table and Synoptic Table	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.)
Shift + Right Button	Click	Table and Header Table	Repaint block of relevés with current relevé colour. (Click on the first relevé to be selected. Hold Shift and click on the last relevé. The entire relevé interval will be repainted.)

Manually moving species/relevé/relevé group:

Left Button	Click and Drag	Table: Species or Short Headers	Move currently selected species or relevé.
Left Button	Click and Drag	Synoptic Table: Short Headers	Move currently selected relevé group.

Editing species name or header data:

Left Button	Double Click	Table and Synoptic Table: Species	Open dialog window for editing species name, layer and data.
Left Button	Double Click	Table and Header Table: Header Data	Open window with function for editing header data.

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 1.8.4. Using colour-coding to gather relevés and species into blocks is explained in Section 1.5.5 below. Used colours are marked by black points in the bar with colours for fast selection.

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 other way is the menu 'Separators' for the automatically making or the removing separators in the table. There are four possibilities for making separators: make separators within short headers, within colours, within some special colour of relevés and the certain number of relevés ('each X relevés'). All separators can be removed from or to same relevé. User can remove only separators of certain hierarchy (for example only separators on the level 2). The separator appears on the right side of the indicated relevé or below the indicated species.

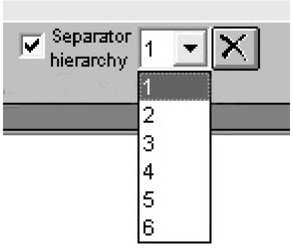


Fig. 14: Separator switches in the Menu bar.

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 or from the 'Settings' in the 'Separators' menu). The hierarchy of separators can be removed by the function 'Remove separators hierarchy' in the 'Separators' menu.

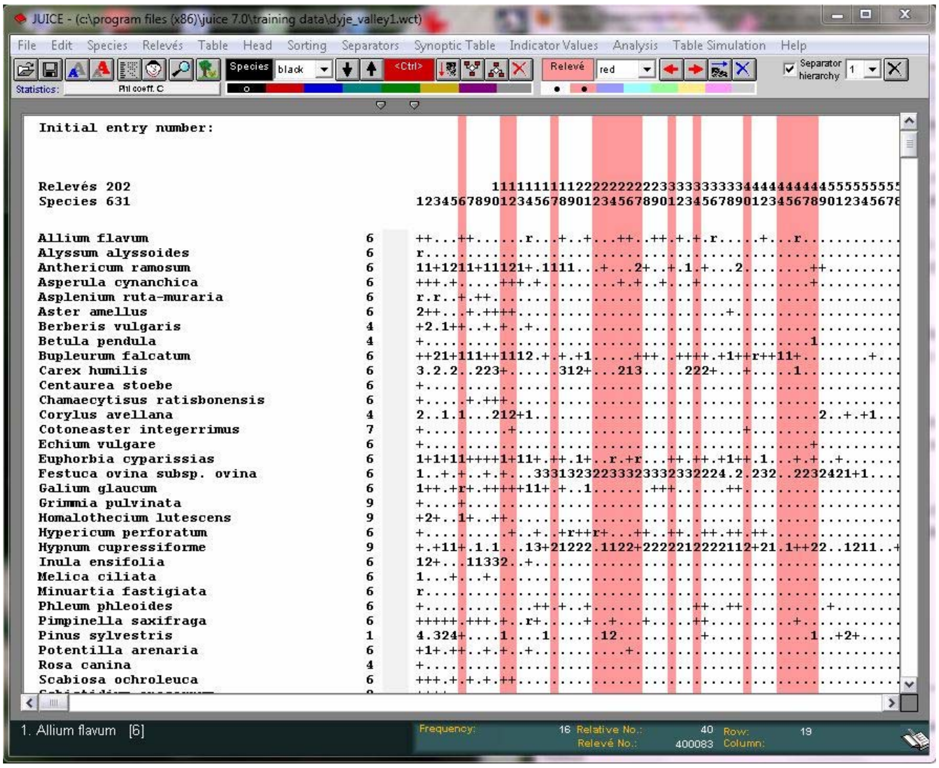
Some analysis demands the definition of groups as the dummy values. It enables the function 'Define Groups as a Dummy Variables in Header Data' in the 'Separators' menu. The function assigns the number 1 to the first group. Other groups have been assigned the number 0. This is included to the header data file as the last column. At the second step the function included in the number 1 to the second group and other groups have the number 0 etc.

***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.



Species: black

Relevé: red

☑ Separator hierarchy: 1

Statistics: Phi coeff. C

```
Initial entry number:



Relevés 202                                      1111111111222222222233333333334444444444555555555
Species 631                             1234567890123456789012345678901234567890123456789012345678

Allium flavum                       6   ++...++......r...+..+...++..++.+.+.r.....+...r............
Alyssum alyssoides                  6   r.........................................................
Anthericum ramosum                  6   11+1211+11121+.1111...+...2+..+.1.+...2........++.........
Asperula cynanchica                 6   +++.+.....+++.+.........+.+..+...+.............+..........
Asplenium ruta-muraria              6   r.r..+.++.................................................
Aster amellus                       6   2++...+.++++.........................+....................
Berberis vulgaris                   4   +2.1++..+.+..+............................................
Betula pendula                      4   +..............................................1..........
Bupleurum falcatum                  6   ++21+111++1112.+.+.+1.....+++..++++.+1++r++11+........+...
Carex humilis                       6   3.2.2..223+......312+...213.....222+...+.....1............
Centaurea stoebe                    6   +.........................................................
Chamaecytisus ratisbonensis         6   +.....+.+++...............................................
Corylus avellana                    4   2..1.1...212+1..................................2..+.+1...
Cotoneaster integerrimus            7   +..........+...........................+..................
Echium vulgare                      6   +..............................................+..........
Euphorbia cyparissias               6   1+1+11++++1+11+.++.1+..r.+r...++.++.+1++.1...+.+..+.......
Festuca ovina subsp. ovina          6   1..+.+..+.+...33313232233323332332224.2.232..2232421+1....
Galium glaucum                      6   1++.+r+.+++++11+.+..1.......+++......++...................
Grimmia pulvinata                   9   +....+....................................................
Homalothecium lutescens             9   +2+..1+..++...............................................
Hypericum perforatum                6   +..........+..+..+r++r+...++..++..++.++.++................
Hypnum cupressiforme                9   +.+11+.1.1...13+21222.1122+2222212222112+21.1++22..1211..+
Inula ensifolia                     6   12+...11332..+............................................
Melica ciliata                      6   1...+...+.................................................
Minuartia fastigiata                6   r.........................................................
Phleum phleoides                    6   +.............++.+..+............++..++..........+........
Pimpinella saxifraga                6   +++++.+++.+..r+.....+..+...+.....++..........+............
Pinus sylvestris                    1   4.324+....1....1......12..........+............1..+2+.....
Potentilla arenaria                 6   +1+.++..+.+..+...........+................................
Rosa canina                         4   +.........................................................
Scabiosa ochroleuca                 6   +++.+.+.+.++..............................................

1. Allium flavum   [6]          Frequency:      16  Relative No.:      40  Row:      19
                                                    Relevé No.:    400083  Column:
```

Fig. 15: 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.)

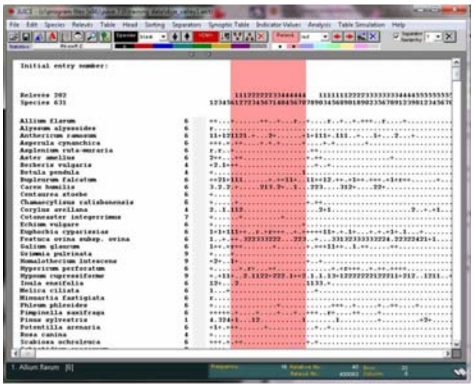


Fig. 16: The table after moving all selected relevés to the left.

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.

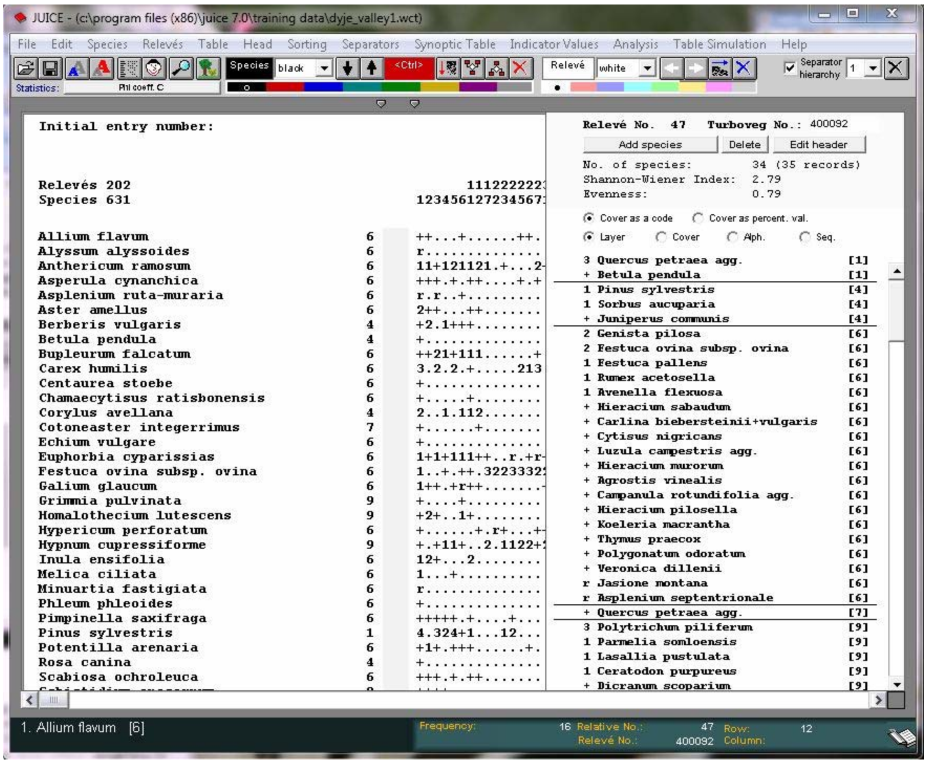
This will move all the relevés to the left. To move them to the right, move the rightmost relevé to the desired position and re-gather to the right.

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.



```
Initial entry number:



Relevés 202                                  111222222
Species 631                                  123456127234567

Allium flavum                         6      ++...+......++.
Alyssum alyssoides                    6      r..............
Anthericum ramosum                    6      11+121121.+...2
Asperula cynanchica                   6      +++.+.++....+.+
Asplenium ruta-muraria                6      r.r..+.........
Aster amellus                         6      2++...++.......
Berberis vulgaris                     4      +2.1+++........
Betula pendula                        4      +..............
Bupleurum falcatum                    6      ++21+111......+
Carex humilis                         6      3.2.2.+.....213
Centaurea stoebe                      6      +..............
Chamaecytisus ratisbonensis           6      +.....+........
Corylus avellana                      4      2..1.112.......
Cotoneaster integerrimus              7      +......+.......
Echium vulgare                        6      +..............
Euphorbia cyparissias                 6      1+1+111++..r.+r
Festuca ovina subsp. ovina            6      1..+.++.3223332
Galium glaucum                        6      1++.+r++.......
Grimmia pulvinata                     9      +....+.........
Homalothecium lutescens               9      +2+..1+........
Hypericum perforatum                  6      +......+.r+...+
Hypnum cupressiforme                  9      +.+11+..2.1122+
Inula ensifolia                       6      12+...2........
Melica ciliata                        6      1...+..........
Minuartia fastigiata                  6      r..............
Phleum phleoides                      6      +..............
Pimpinella saxifraga                  6      +++++.+....+...
Pinus sylvestris                      1      4.324+1...12...
Potentilla arenaria                   6      +1+.+++......+.
Rosa canina                           4      +..............
Scabiosa ochroleuca                   6      +++.+.++.......
```

```
Relevé No.  47   Turboveg No.: 400092

No. of species:           34 (35 records)
Shannon-Wiener Index:     2.79
Evenness:                 0.79

◉ Cover as a code    ○ Cover as percent. val.
◉ Layer    ○ Cover    ○ Alph.    ○ Seq.

3 Quercus petraea agg.                    [1]
+ Betula pendula                          [1]
-----------------------------------------------
1 Pinus sylvestris                        [4]
1 Sorbus aucuparia                        [4]
+ Juniperus communis                      [4]
-----------------------------------------------
2 Genista pilosa                          [6]
2 Festuca ovina subsp. ovina              [6]
1 Festuca pallens                         [6]
1 Rumex acetosella                        [6]
1 Avenella flexuosa                       [6]
+ Hieracium sabaudum                      [6]
+ Carlina biebersteinii+vulgaris          [6]
+ Cytisus nigricans                       [6]
+ Luzula campestris agg.                  [6]
+ Hieracium murorum                       [6]
+ Agrostis vinealis                       [6]
+ Campanula rotundifolia agg.             [6]
+ Hieracium pilosella                     [6]
+ Koeleria macrantha                      [6]
+ Thymus praecox                          [6]
+ Polygonatum odoratum                    [6]
+ Veronica dillenii                       [6]
r Jasione montana                         [6]
r Asplenium septentrionale                [6]
-----------------------------------------------
+ Quercus petraea agg.                    [7]
-----------------------------------------------
3 Polytrichum piliferum                   [9]
1 Parmelia somloensis                     [9]
1 Lasallia pustulata                      [9]
1 Ceratodon purpureus                     [9]
+ Dicranum scoparium                      [9]
```

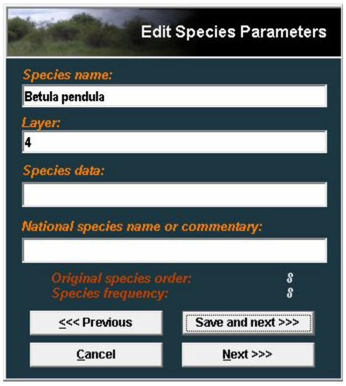
```
1. Allium flavum   [6]
Frequency:       16   Relative No.:      47   Row:      12
                      Relevé No.:    400092   Column:
```

Fig. 17: 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:



Species name: Betula pendula
Layer: 4
Species data:
National species name or commentary:
Original species order: 8
Species frequency: 8

Fig. 18: The window for editing species names, layers and species data.

a) Species names, layers, species data values and commentaries 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:

Field name: Locality
No. of characters: 100
Hnanice, Z svahy Lipiny nad levým břehem Dyje 3.3 km SZ obce
31

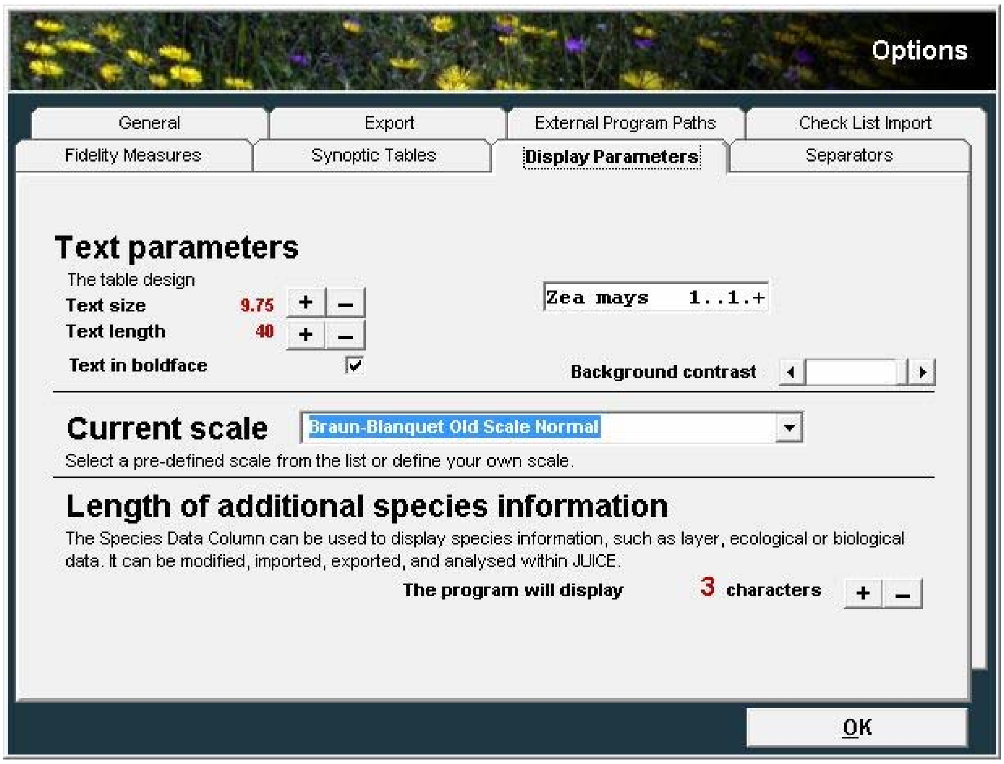
Fig. 19: Editing header data.

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.



Text parameters

The table design

Text size 9.75

Text length 40

Text in boldface ☑

Zea mays 1..1.+

Background contrast

Current scale Braun-Blanquet Old Scale Normal

Select a pre-defined scale from the list or define your own scale.

Length of additional species information

The Species Data Column can be used to display species information, such as layer, ecological or biological data. It can be modified, imported, exported, and analysed within JUICE.

The program will display 3 characters

Fig. 20: 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 the numbers 0.01, 0.1, 0.2, 0.3, 0.5 and all integer numbers from 1 to 100. 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 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:

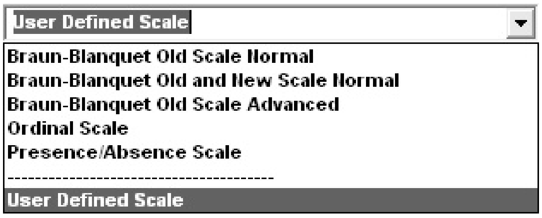
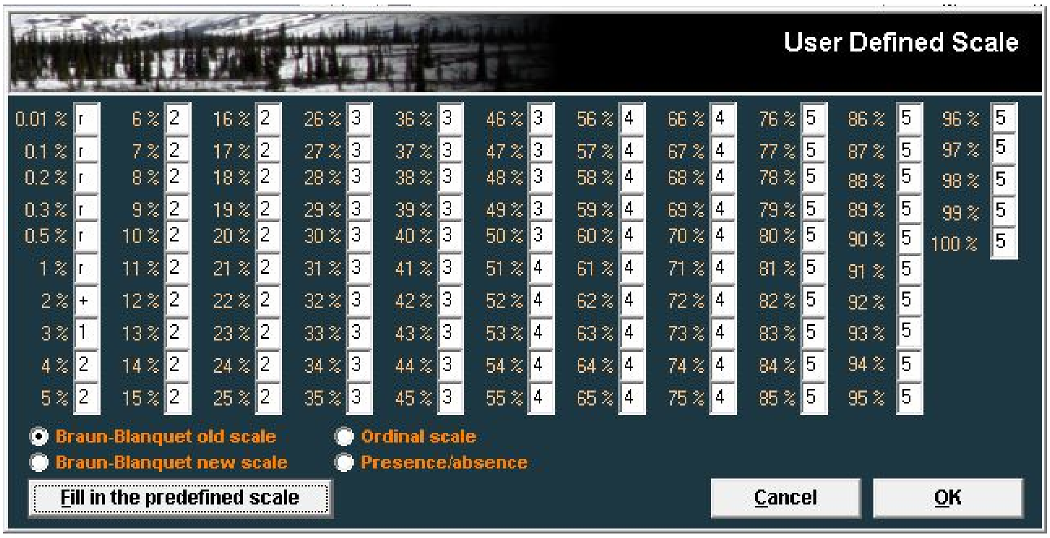


Fig. 21: Defined scales



0.01 %	r	6 %	2	16 %	2	26 %	3	36 %	3	46 %	3	56 %	4	66 %	4	76 %	5	86 %	5	96 %	5
0.1 %	r	7 %	2	17 %	2	27 %	3	37 %	3	47 %	3	57 %	4	67 %	4	77 %	5	87 %	5	97 %	5
0.2 %	r	8 %	2	18 %	2	28 %	3	38 %	3	48 %	3	58 %	4	68 %	4	78 %	5	88 %	5	98 %	5
0.3 %	r	9 %	2	19 %	2	29 %	3	39 %	3	49 %	3	59 %	4	69 %	4	79 %	5	89 %	5	99 %	5
0.5 %	r	10 %	2	20 %	2	30 %	3	40 %	3	50 %	3	60 %	4	70 %	4	80 %	5	90 %	5	100 %	5
1 %	r	11 %	2	21 %	2	31 %	3	41 %	3	51 %	4	61 %	4	71 %	4	81 %	5	91 %	5		
2 %	+	12 %	2	22 %	2	32 %	3	42 %	3	52 %	4	62 %	4	72 %	4	82 %	5	92 %	5		
3 %	1	13 %	2	23 %	2	33 %	3	43 %	3	53 %	4	63 %	4	73 %	4	83 %	5	93 %	5		
4 %	2	14 %	2	24 %	2	34 %	3	44 %	3	54 %	4	64 %	4	74 %	4	84 %	5	94 %	5		
5 %	2	15 %	2	25 %	2	35 %	3	45 %	3	55 %	4	65 %	4	75 %	4	85 %	5	95 %	5		

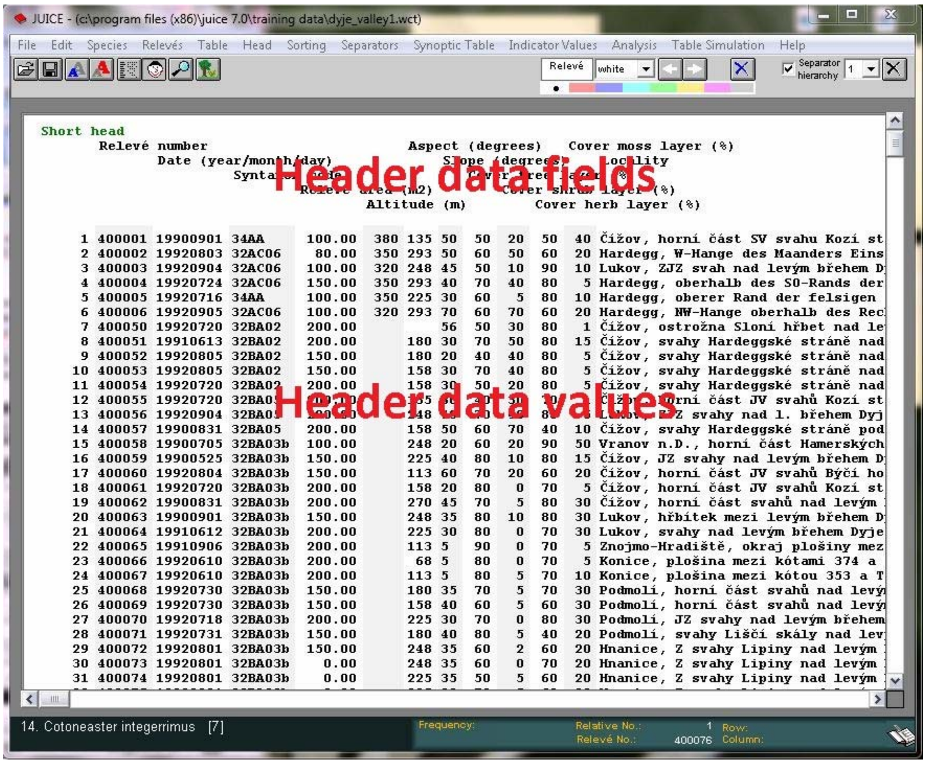
● Braun-Blanquet old scale
○ Braun-Blanquet new scale
○ Ordinal scale
○ Presence/absence

Fig. 22: Window for definition of user defined scale.

Every percentage number must be represented by one character code 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 1.4.8 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.



```
Short head
      Relevé number                        Aspect (degrees)   Cover moss layer (%)
              Date (year/month/day)           Slope (degrees)   Locality
                        Syntax. code            Cover tree layer (%)
                             Relevé area (m2)     Cover shrub layer (%)
                                     Altitude (m)      Cover herb layer (%)

  1 400001 19900901 34AA     100.00  380 135 50  50  20  50  40 Čížov, horní část SV svahu Kozí st
  2 400002 19920803 32AC06    80.00  350 293 50  60  50  60  20 Hardegg, W-Hange des Maanders Eins
  3 400003 19920904 32AC06   100.00  320 248 45  50  10  90  10 Lukov, ZJZ svah nad levým břehem D
  4 400004 19920724 32AC06   150.00  350 293 40  70  40  80   5 Hardegg, oberhalb des SO-Rands der
  5 400005 19920716 34AA     100.00  350 225 30  60   5  80  10 Hardegg, oberer Rand der felsigen
  6 400006 19920905 32AC06   100.00  320 293 70  60  70  60  20 Hardegg, NW-Hange oberhalb des Rec
  7 400050 19920720 32BA02   200.00          56  50  30  80   1 Čížov, ostrožna Sloní hřbet nad le
  8 400051 19910613 32BA02   200.00      180 30  70  50  80  15 Čížov, svahy Hardeggské stráně nad
  9 400052 19920805 32BA02   150.00      180 20  40  40  80   5 Čížov, svahy Hardeggské stráně nad
 10 400053 19920805 32BA02   150.00      158 30  70  40  80   5 Čížov, svahy Hardeggské stráně nad
 11 400054 19920720 32BA02   200.00      158 30  50  20  80   5 Čížov, svahy Hardeggské stráně nad
 12 400055 19920720 [illegible]                                   horní část JV svahů Kozí st
 13 400056 19920904 [illegible]                                   Z svahy nad l. břehem Dyj
 14 400057 19900831 32BA05   200.00      158 50  60  70  40  10 Čížov, svahy Hardeggské stráně pod
 15 400058 19900705 32BA03b  100.00      248 20  60  20  90  50 Vranov n.D., horní část Hamerských
 16 400059 19900525 32BA03b  150.00      225 40  80  10  80  15 Čížov, JZ svahy nad levým břehem D
 17 400060 19920804 32BA03b  150.00      113 60  70  20  60  20 Čížov, horní část JV svahů Býčí ho
 18 400061 19920720 32BA03b  200.00      158 20  80   0  70   5 Čížov, horní část JV svahů Kozí st
 19 400062 19900831 32BA03b  200.00      270 45  70   5  80  30 Čížov, horní část svahů nad levým
 20 400063 19900901 32BA03b  150.00      248 35  80  10  80  30 Lukov, hřbítek mezi levým břehem D
 21 400064 19910612 32BA03b  200.00      225 30  80   0  70  30 Lukov, svahy nad levým břehem Dyje
 22 400065 19910906 32BA03b  200.00      113 5   90   0  70   5 Znojmo-Hradiště, okraj plošiny mez
 23 400066 19920610 32BA03b  200.00       68 5   80   0  70   5 Konice, plošina mezi kótami 374 a
 24 400067 19920610 32BA03b  200.00      113 5   80   5  70  10 Konice, plošina mezi kótou 353 a T
 25 400068 19920730 32BA03b  150.00      180 35  70   5  70  30 Podmolí, horní část svahů nad levý
 26 400069 19920730 32BA03b  150.00      158 40  60   5  60  30 Podmolí, horní část svahů nad levý
 27 400070 19920718 32BA03b  200.00      225 30  70   0  80  30 Podmolí, JZ svahy nad levým břehem
 28 400071 19920731 32BA03b  150.00      180 40  80   5  40  20 Podmolí, svahy Liščí skály nad lev
 29 400072 19920801 32BA03b  150.00      248 35  60   2  60  20 Hnanice, Z svahy Lipiny nad levým
 30 400073 19920801 32BA03b    0.00      248 35  60   0  70  20 Hnanice, Z svahy Lipiny nad levým
 31 400074 19920801 32BA03b    0.00      225 35  50   5  60  20 Hnanice, Z svahy Lipiny nad levým
```

```
14. Cotoneaster integerrimus   [7]      Frequency:      Relative No.:       1  Row:
                                                        Relevé No.:    400076  Column:
```

Fig. 23: Header data display.

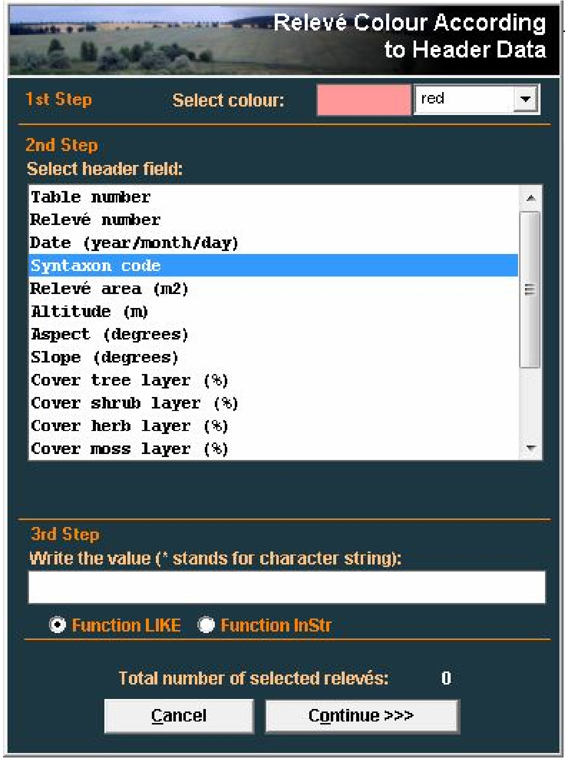
All screen parameters are defined similarly as in the Standard Display (See Section 1.5.8.). Mouse functions are described in Section 1.5.2. If it is necessary to change this data, the changes should be made in the source data set. However, it is possible to edit this information within JUICE. See Section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

Note: *It is possible to add a new header field to the header data from short headers. To add new information (number or code with maximum length of 6 characters) from short headers, you must open 'Head' menu and select 'Add Short Headers to Header Data' (See Section 1.8.6). Other possibility is to define the new field in TURBOVEG and re-export the header data. (See Section 1.4.8.)*

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:



Select colour: 🟥 red

Syntaxon code

● Function LIKE

Total number of selected relevés: 0

Fig. 24: 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.

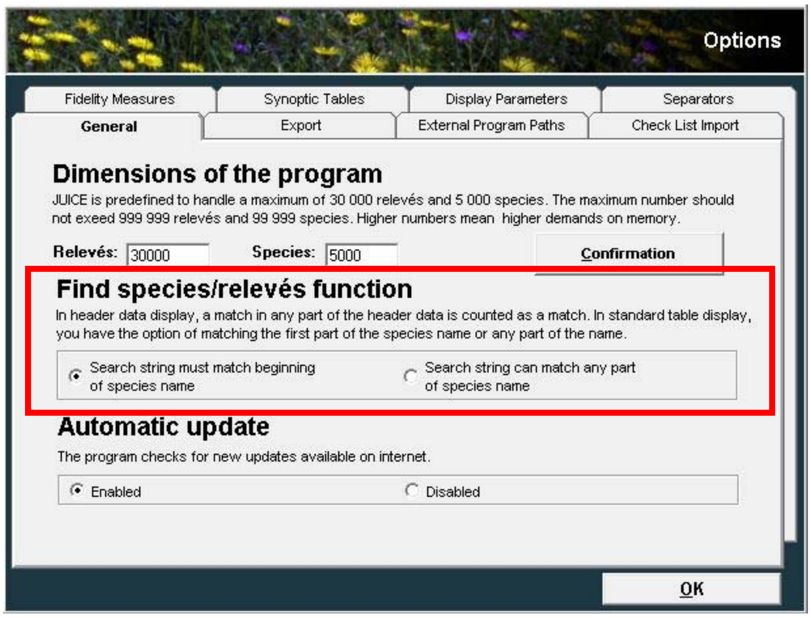
1.5.11 Searching

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 – 1, shrub – 4 and juvenile – 7). 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.*



Dimensions of the program

JUICE is predefined to handle a maximum of 30 000 relevés and 5 000 species. The maximum number should not exeed 999 999 relevés and 99 999 species. Higher numbers mean higher demands on memory.

Relevés: 30000 Species: 5000

Find species/relevés function

In header data display, a match in any part of the header data is counted as a match. In standard table display, you have the option of matching the first part of the species name or any part of the name.

● Search string must match beginning of species name ○ Search string can match any part of species name

Automatic update

The program checks for new updates available on internet.

● Enabled ○ Disabled

Fig. 25: 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.

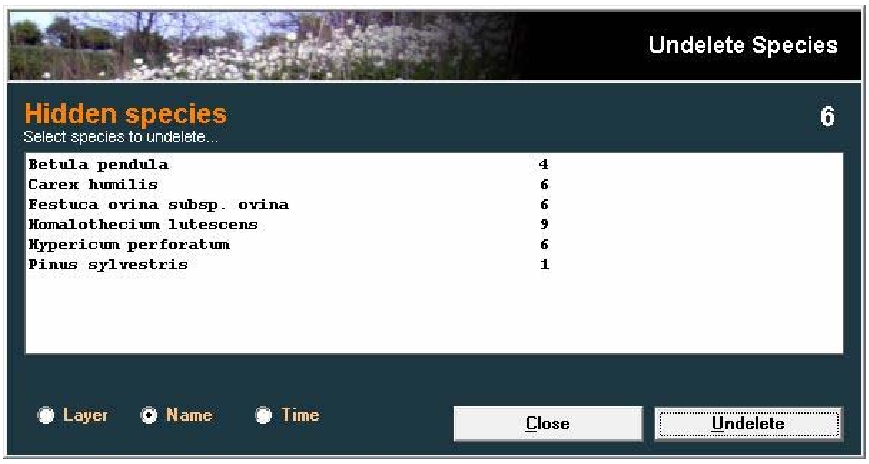
Note 1: *The default name and layer of the aggregation correspond to the first species in the list. If you wish to use a different species to provide the default name and layer, simply move that species to the top of the list. This information can also be entered manually.*

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.



Undelete Species

Hidden species

Select species to undelete...

6

Betula pendula	4
Carex humilis	6
Festuca ovina subsp. ovina	6
Homalothecium lutescens	9
Hypericum perforatum	6
Pinus sylvestris	1

○ Layer ● Name ○ Time

Fig. 26: 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.

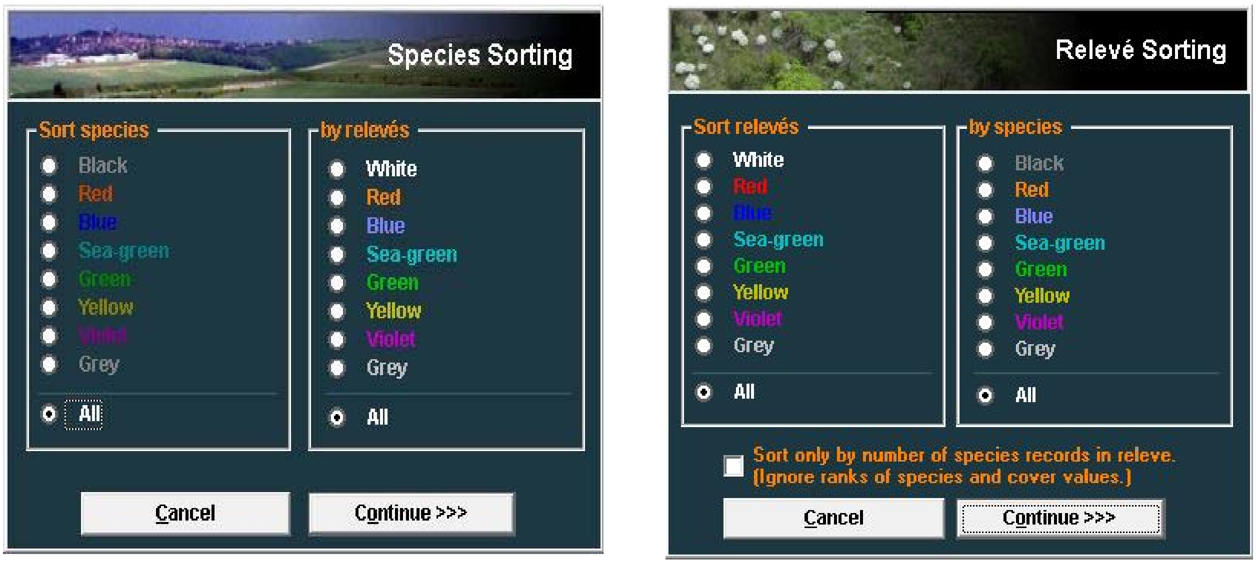


Fig. 27: Windows for sorting species and relevés.

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.

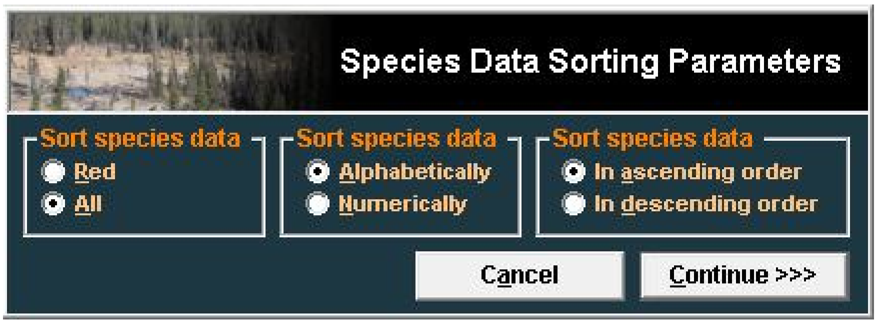
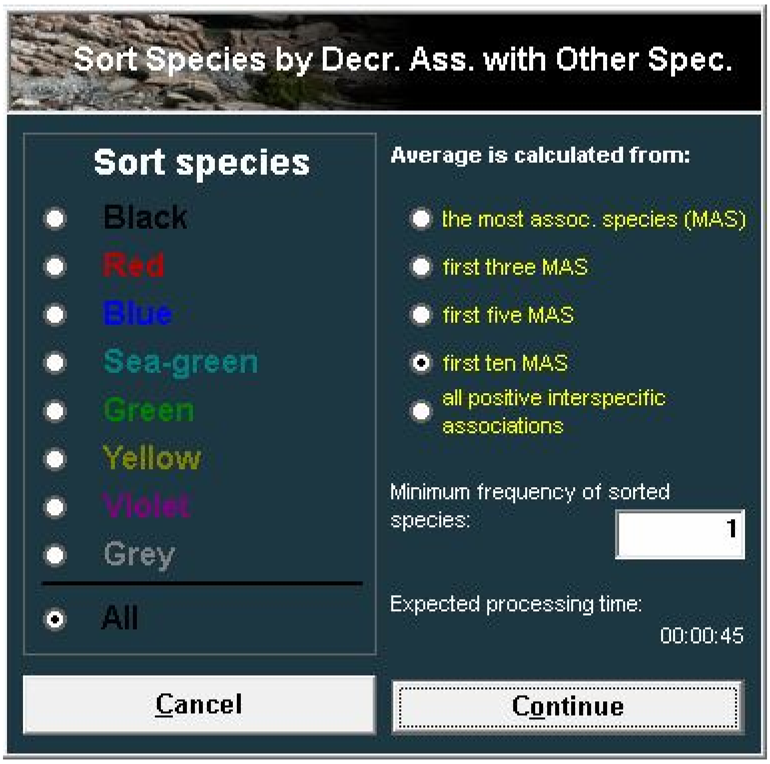


Fig. 28: Window with species sorting parameters.

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 the second part of this manual.

‘Sort species by Decreasing Association with Other Species’ 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.


Sort Species by Decr. Ass. with Other Spec.

Sort species
○ Black
○ Red
○ Blue
○ Sea-green
○ Green
○ Yellow
○ Violet
○ Grey
● All

Average is calculated from:
○ the most assoc. species (MAS)
○ first three MAS
○ first five MAS
● first ten MAS
○ all positive interspecific associations

Minimum frequency of sorted species: 1

Expected processing time: 00:00:45

Fig. 29: 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.*

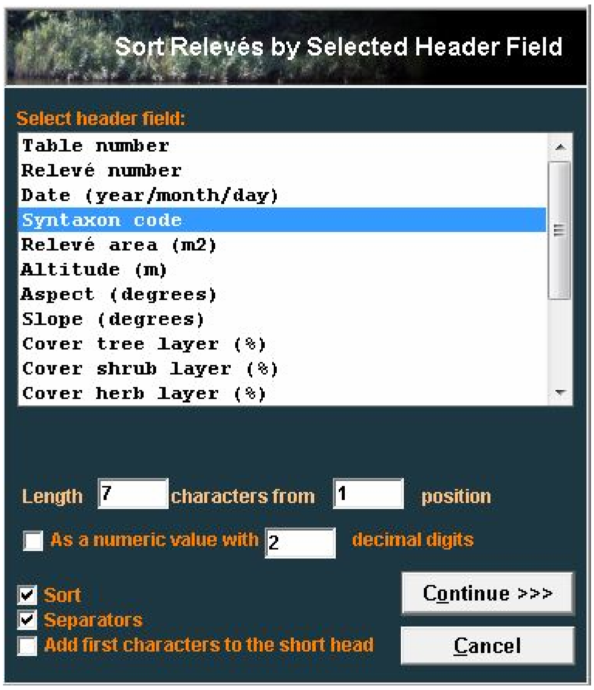
Warning 2: *The average fidelity value is written into the species data field. This enables the user to see the value, but it overwrites any existing species data. JUICE gives no warning before it does this.*

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.



Sort Relevés by Selected Header Field

Select header field:

Table number
Relevé number
Date (year/month/day)
Syntaxon code
Relevé area (m2)
Altitude (m)
Aspect (degrees)
Slope (degrees)
Cover tree layer (%)
Cover shrub layer (%)
Cover herb layer (%)

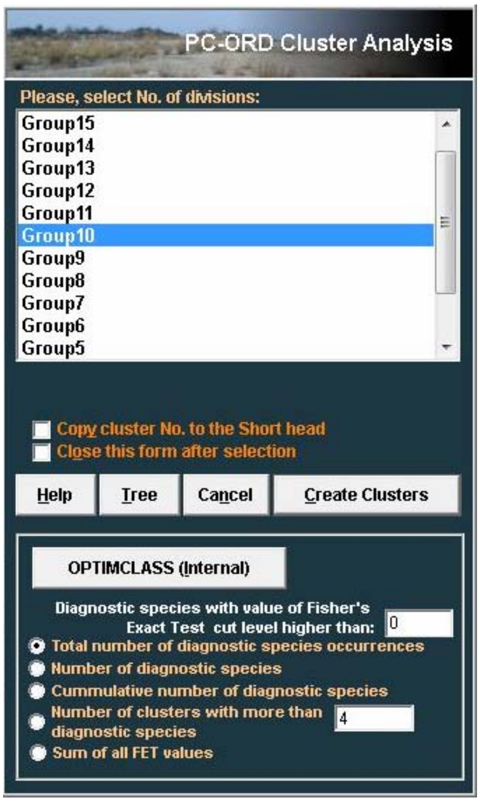
Length 7 characters from 1 position

☐ As a numeric value with 2 decimal digits

☑ Sort
☑ Separators
☐ Add first characters to the short head

Fig. 30: Sorting relevés by selected header data.

‘Sort Relevés by Classifications by Other Programs’ is used to display clusters computed by another program – either TWINSPAN, SYN TAX 2000, PC-ORD or MULVA. With PC-ORD, the cluster information must be saved in a comma-delimited file called ‘MATRIX2.CSV’. 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:



☐ Copy cluster No. to the Short head
☐ Close this form after selection

Diagnostic species with value of Fisher's Exact Test cut level higher than: 0

● Total number of diagnostic species occurrences
○ Number of diagnostic species
○ Cummulative number of diagnostic species
○ Number of clusters with more than 4 diagnostic species
○ Sum of all FET values

Fig. 31: 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:

18. Galium glaucum [6]
Galigla6
Frequency: 23
Relative No.: 104
Relevé No.: 401106
Row: 11
Column:

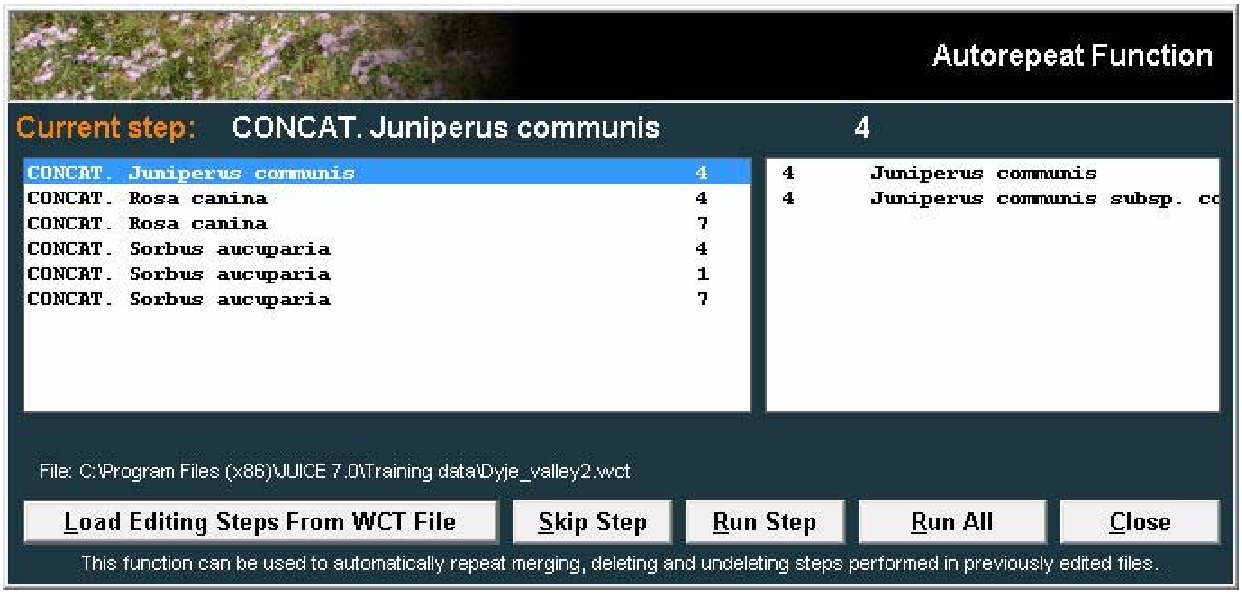
Fig. 32: Dendrogram of PC-ORD cluster analysis.

'OPTIMCLASS (Internal)' button is related to the function OPTIMCLASS, which will be described in the second part of this manual. It tests all selected partitions (use mouse pointer and click to the list of clusters using Shift or CTRL button) to the number of diagnostic species. The function can find a peak of diagnostic species over the different numner of clusters.

1.6.4 Autorepeat Function

When a new table is imported into JUICE, it is often necessary to merge species to aid analysis. (See Section1.6.1.) 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.



Current step: CONCAT. Juniperus communis 4

```
CONCAT. Juniperus communis          4
CONCAT. Rosa canina                 4
CONCAT. Rosa canina                 7
CONCAT. Sorbus aucuparia            4
CONCAT. Sorbus aucuparia            1
CONCAT. Sorbus aucuparia            7
```

```
4      Juniperus communis
4      Juniperus communis subsp. c
```

File: C:\Program Files (x86)\JUICE 7.0\Training data\Dyje_valley2.wct

This function can be used to automatically repeat merging, deleting and undeleting steps performed in previously edited files.

Fig. 33: 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 ('Skip Step').

Note: *This function is mostly 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's 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

The 'Species Data' submenu (from the 'Species' menu) has functions for writing 'Frequency'. 'Frequency' is the frequency of species occurrences in the data set. The species freuency can be calculated for (1) whole table, (2) relevés of selected colour and (3) relevés where the species riches a cover higher than the set threshold value. 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 Cover Values

Several cover values can be displayed in the species data column. 'Minimum Cover' is the species's minium cover in the data set. 'Maximum Cover' is the species's maximum cover value in the data set. 'Median Cover' and 'Avarage cover' are calculated from all nonzero cover values. It is also possible to display Standart deviation of nonzero covers.

1.7.4 Sequence and Species Colour

The 'Sequence' function writes consecutive numbers into the Species Data Column. The 'No. of Species Colour' function writes each species's current colour to the Species Data Column according to the following code: 0 – black, 1 – red, 2 – blue, 3 – sea-green, 4 – green, 5 – yellow, 6 – violet, 7 – grey.

1.7.5 Transformation of Species Data (Menu Calculator)

Numerical values (n) in the Species Data Column can be replaced by their squares (n^2), square roots ($\sqrt{n}$), multiplicative inverses ($1/n$), or their addition, multiplication or division by any constant value.

1.7.6 Statistics Summarizing Relevé Data

Short headers can contain data about the relevés such as means of Ellenberg indicator values, sums of species statistics, Shannon-Wiener indices, potential heat load etc. (See Section 1.8.) A statistic summarizing the short header data from the relevés in which the species occurs – such as minimum, maximum, mean median value and etc. – can be written to the Species Data Column. From the ‘Species’ menu select ‘Species Data’ and ‘Short Header Data’. This gives a menu of summarizing statistics to choose from.

1.7.7 Indicator Values

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 (See Section 1.9).

1.7.8 External Species Data

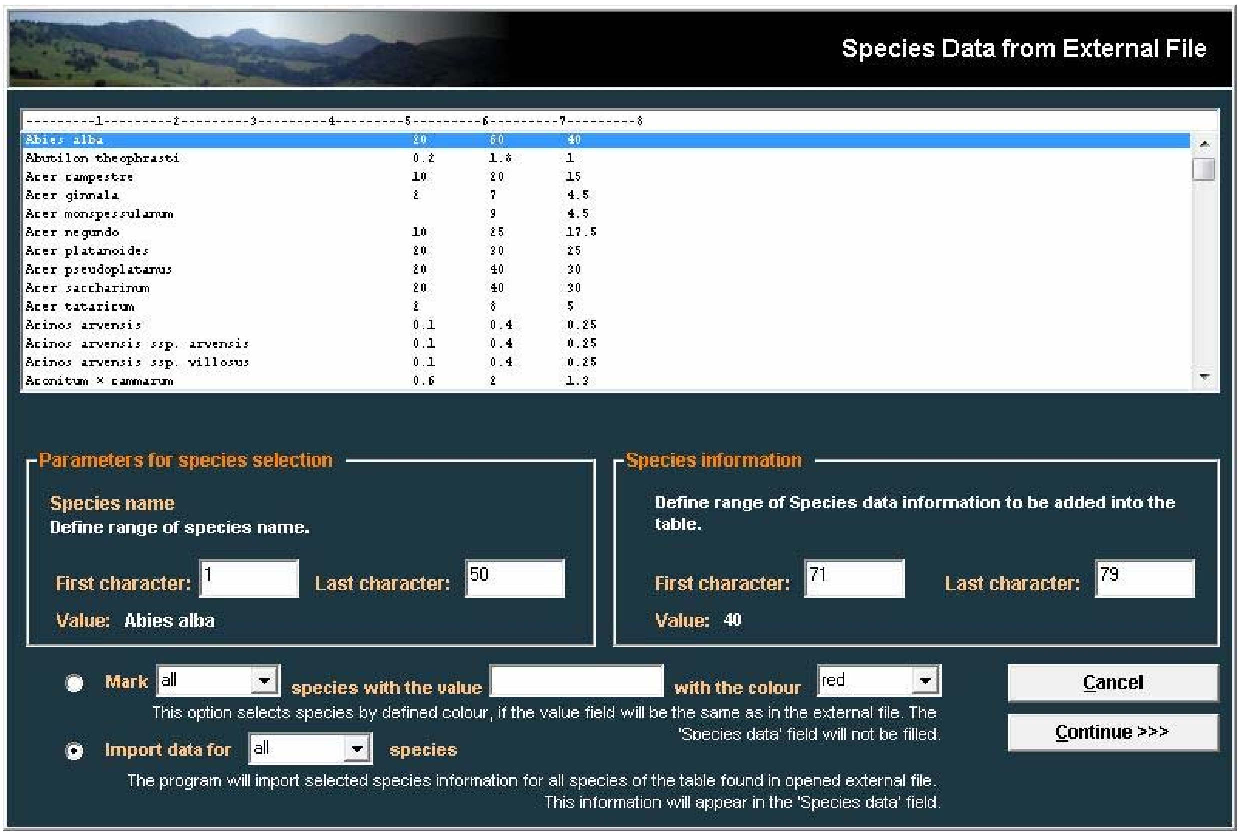
Other species data can be imported into JUICE if they are in a suitable format. An example of a simple text file (denoting ploidy level) accepted by JUICE is shown below:

```
...
Abies alba                         20        60       40
Abutilon theophrasti               0.2       1.8      1
Acer campestre                     10        20       15
Acer ginnala                       2         7        4.5
Acer monspessulanum                1         9        4.5
Acer negundo                       10        25       17.5
Acer platanoides                   20        30       25
Acer pseudoplatanus                20        40       30
Acer saccharinum                   20        40       30
Acer tataricum                     2         8        5
Acinos arvensis                    0.1       0.4      0.25
...
```

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

Note: *The menu ‘File’ contains submenu ‘Conversion’ (See Section* ***Chyba! Nenalezen zdroj odkazů.****.) where it is possible to convert coma or semi-colon delimited file to the file with fixed length of all fields.*

From the menu ‘Species’ select ‘Species Data’ and ‘External Species Data’. Enter the name of the file containing the external data. The following window will appear:



Species Data from External File

```
---------1---------2---------3---------4---------5---------6---------7---------8
Abies alba                                        20        60        40
Abutilon theophrasti                              0.2       1.8       1
Acer campestre                                    10        20        15
Acer ginnala                                      2         7         4.5
Acer monspessulanum                                         9         4.5
Acer negundo                                      10        25        17.5
Acer platanoides                                  20        30        25
Acer pseudoplatanus                               20        40        30
Acer saccharinum                                  20        40        30
Acer tataricum                                    2         8         5
Acinos arvensis                                   0.1       0.4       0.25
Acinos arvensis ssp. arvensis                     0.1       0.4       0.25
Acinos arvensis ssp. villosus                     0.1       0.4       0.25
Aconitum × cammarum                               0.6       2         1.3
```

Parameters for species selection

Species name
Define range of species name.

First character: 1 Last character: 50

Value: Abies alba

Species information

Define range of Species data information to be added into the table.

First character: 71 Last character: 79

Value: 40

○ Mark all species with the value with the colour red

This option selects species by defined colour, if the value field will be the same as in the external file. The 'Species data' field will not be filled.

● Import data for all species

The program will import selected species information for all species of the table found in opened external file. This information will appear in the 'Species data' field.

Fig. 34: 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 'Import data for [all] species' is chosen, the program will import selected species information for all species of the table found in opened external file. This information will appear in the ‘Species data’ field. If the same colour is chosen, the program will import species information only for the colour.

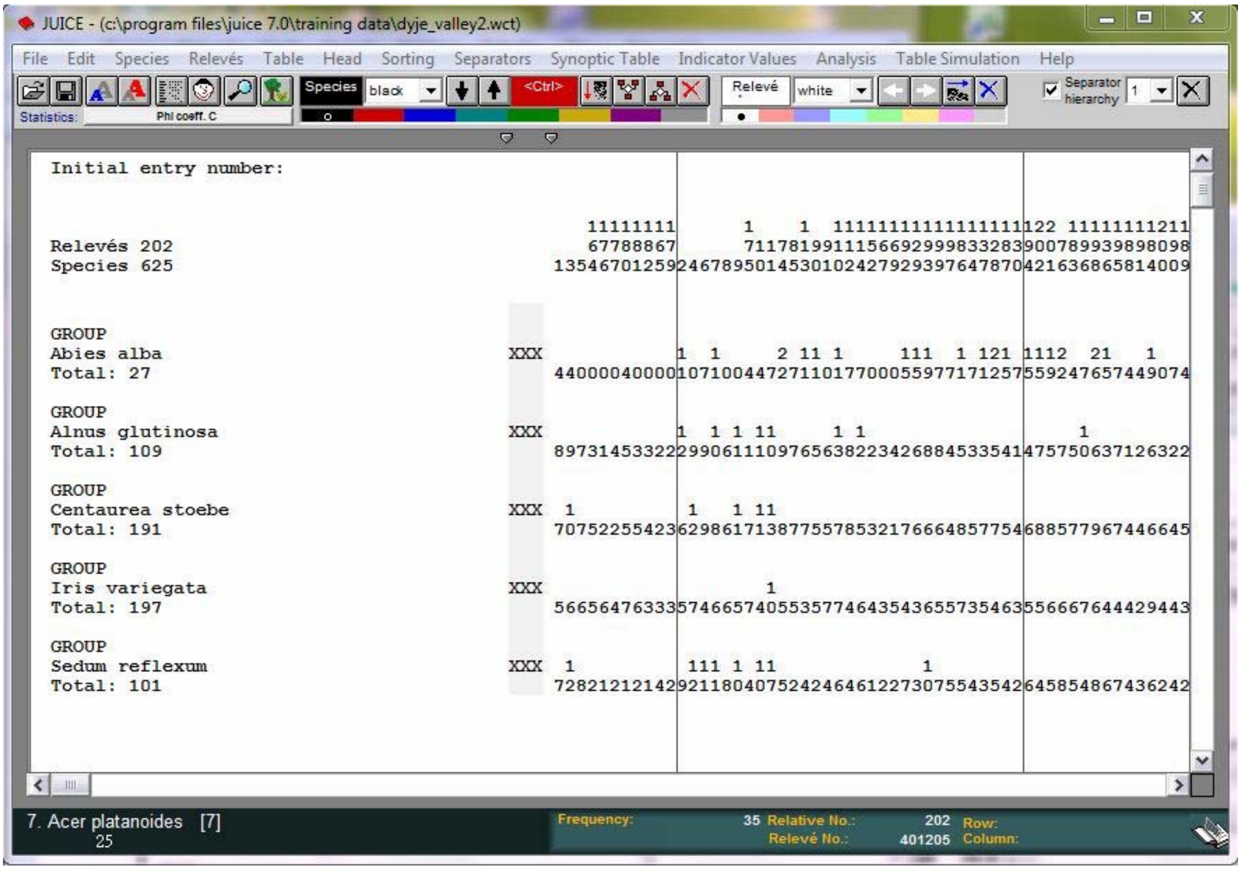
The option ‘Mark all species with the value with the colour’ selects species by defined colour, if the value field is the same as in the external file. The ‘Species data’ field will not be filled. For example the option ‘Mark [all] species with the value [0.25] with the colour [red]’ can be used to colour species with the value [0.25] without actually importing the data. It is also possible to only re-colour species of a certain colour.

1.7.9 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.



```
Initial entry number:


                                                11111111      1    1  11111111111111111122 11111111211
Relevés 202                                     67788867      7117819911156692999833283900789939898098
Species 625                                  135467012592467895014530102427929397647870421636865814009


GROUP
Abies alba                               XXX            1  1     2 11 1     111  1 121 1112  21   1
Total: 27                                    440000400001071004472711017700055977171257559247657449074

GROUP
Alnus glutinosa                          XXX            1  1 1 11     1 1                   1
Total: 109                                   897314533222990611109765638223426884533541475750637126322

GROUP
Centaurea stoebe                         XXX  1          1   1 11
Total: 191                                   707522554236298617138775578532176664857754688577967446645

GROUP
Iris variegata                           XXX                    1
Total: 197                                   566564763335746657405535774643543655735463556667644429443

GROUP
Sedum reflexum                           XXX  1          111 1 11             1
Total: 101                                   728212121429211804075242464612273075543542645854867436242
```

Fig. 35: Species group tables.

1.7.10 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. The minimum, the maximum and the standard deviation can be displayed. To view averages of species data, open the ‘Species’ menu, select ‘Species Data’ and ‘Species Data Averages’. The list of results appears in the clipboard.

1.7.11 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 1.7.8. From the ‘Species’ menu, select ‘Species Data’ and ‘Export Species Data’. For more information, see Section 1.10.9.

Species Data can be also stored to the clipboard in the form of spreadsheet table. Such function allows fast and easy data transfer between JUICE and other programs. In that case, use menu ‘Edit’ and ‘Copy Species Names, Layers and Species Data to the Clipboard’.

1.8 Short Headers and Header Data

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 **‘Initial Entry 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*

- A relevé’s **‘Original Number (Relevé 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.)
- When **‘Ordinal Number (in Curent Table)’** 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 field can contain up to six characters of information about the relevé arranged vertically in the topmost table part. They can be used to distinguish relevé groups in the data set and define them with separators or colours (as described in Section 1.8.4). 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 Number

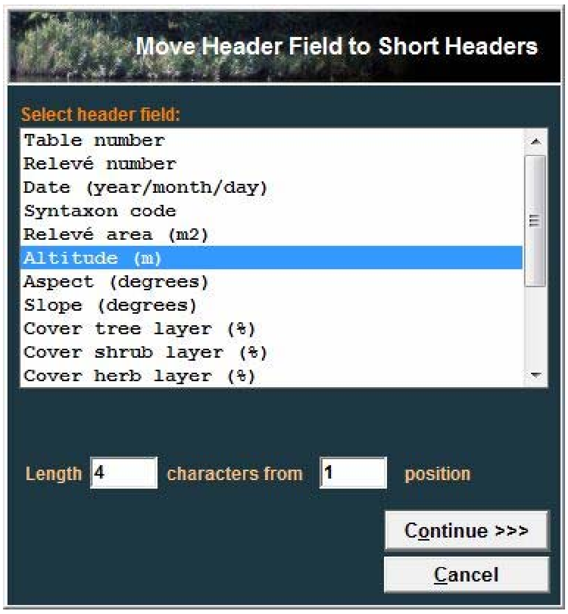
The function ‘Percentage Number of <colour> Species’ calculates percentage of all species of the selected colour from each relevé. Species with the same name originally recorded in several different layers are virtually merged and counted only once.

1.8.2.3 Percentage Cover

The function ‘Percentage Cover 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.

1.8.2.4 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.



Length 4 characters from 1 position

Fig. 36: Moving first part of selected header field into sort headers.

1.8.2.5 Diversity Indices

The function ‘Shannon-Wiener Index’ writes the index value to 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.

$$H' = -\sum_{i=1}^{S} p_i \ln p_i \quad , \qquad \text{(Eq. 1)}$$

where S is the number of species and p_i is the proportion of the individual species cover relative to the total cover. 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 function 'Simpson Index' is the second commonly used diversity index:

$$\lambda = \sum_{i=1}^{S} p_i^2 \qquad \text{(Eq. 2)}$$

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

1.8.2.6 Evenness

The program calculates two different measures of evenness:

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:

$$E_H = H'/H'_{\max} = H'/\ln S \, . \qquad \text{(Eq. 3)}$$

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 evenness available in JUICE is E_{var} which is equivalent to the arctan transformed Gaussian width (Smith & Wilson 1996):

$$E_{\mathrm{var}} = 1 - \frac{2}{\pi}\arctan\left(\frac{\sum_{i=1}^{S}\left(\ln(p_i) - \frac{\sum_{i=1}^{S}\ln(p_i)}{S}\right)^2}{S}\right) \qquad \text{(Eq. 4)}$$

1.8.2.7 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.

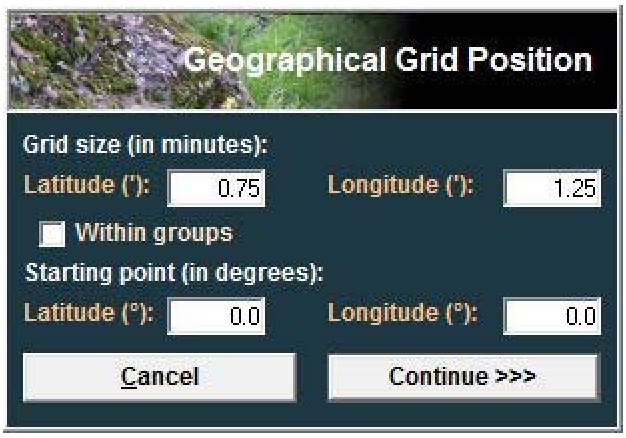
Such spatial stratification of table data is available if the header data contain information about geographical coordinates. There are two possibilities to archive coordinates: (1) fields LATITUDE and LONGITUDE (both 6, or both 7 characters), or (2) fields DEG_LAT and DEG_LON (13 characters), where latitude and longitude are archived in degrees. These fields must be included in the header data (files with suffix STR and EXP – see Section 1.4.8).

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

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

Example 3: DEG_LAT: 49.16357
DEG_LON: 16.47563

Selecting this function opens this window:



Grid size (in minutes):

Latitude ('): 0.75

Longitude ('): 1.25

☐ Within groups

Starting point (in degrees):

Latitude (°): 0.0

Longitude (°): 0.0

Fig. 37: 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 ‘Within groups’ 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.

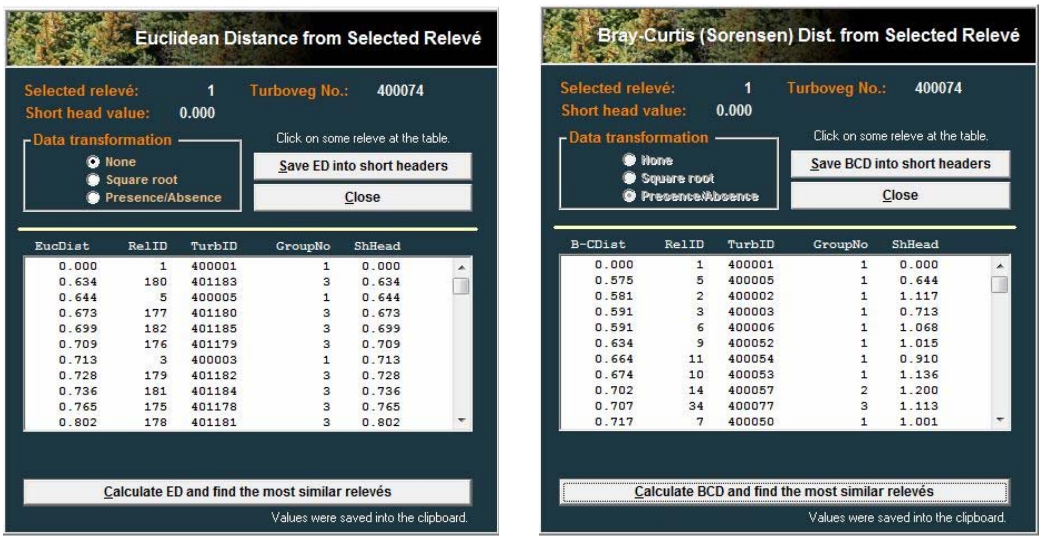
The ‘Starting point’ shifts the grid corner from [0, 0] coordinates.

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*

1.8.2.8 Distance from Selected Relevé

If the user wants to find the most similar relevés from the selected relevé, they can choose two measures of the distance.

The first one is the Euclidian Distance from the selected relevé. The program shows calculated Euclidian distance and finds the most similar relevés from the data set. Data can be transformed. The second one is the Bray-Curtis (Sorensen) distance from the selected Relevé. Both measures can be saved into the short headers or onto the clipboard.



Selected relevé: 1 Turboveg No.: 400074
Short head value: 0.000

Data transformation
● None
○ Square root
○ Presence/Absence

EucDist	RelID	TurbID	GroupNo	ShHead
0.000	1	400001	1	0.000
0.634	180	401183	3	0.634
0.644	5	400005	1	0.644
0.673	177	401180	3	0.673
0.699	182	401185	3	0.699
0.709	176	401179	3	0.709
0.713	3	400003	1	0.713
0.728	179	401182	3	0.728
0.736	181	401184	3	0.736
0.765	175	401178	3	0.765
0.802	178	401181	3	0.802

Values were saved into the clipboard.

Selected relevé: 1 Turboveg No.: 400074
Short head value: 0.000

Data transformation
○ None
○ Square root
● Presence/Absence

B-CDist	RelID	TurbID	GroupNo	ShHead
0.000	1	400001	1	0.000
0.575	5	400005	1	0.644
0.581	2	400002	1	1.117
0.591	3	400003	1	0.713
0.591	6	400006	1	1.068
0.634	9	400052	1	1.015
0.664	11	400054	1	0.910
0.674	10	400053	1	1.136
0.702	14	400057	2	1.200
0.707	34	400077	3	1.113
0.717	7	400050	1	1.001

Values were saved into the clipboard.

Fig. . 38: Window for calculation Euclidian and Bray-Curtis distance.

1.8.2.9 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).

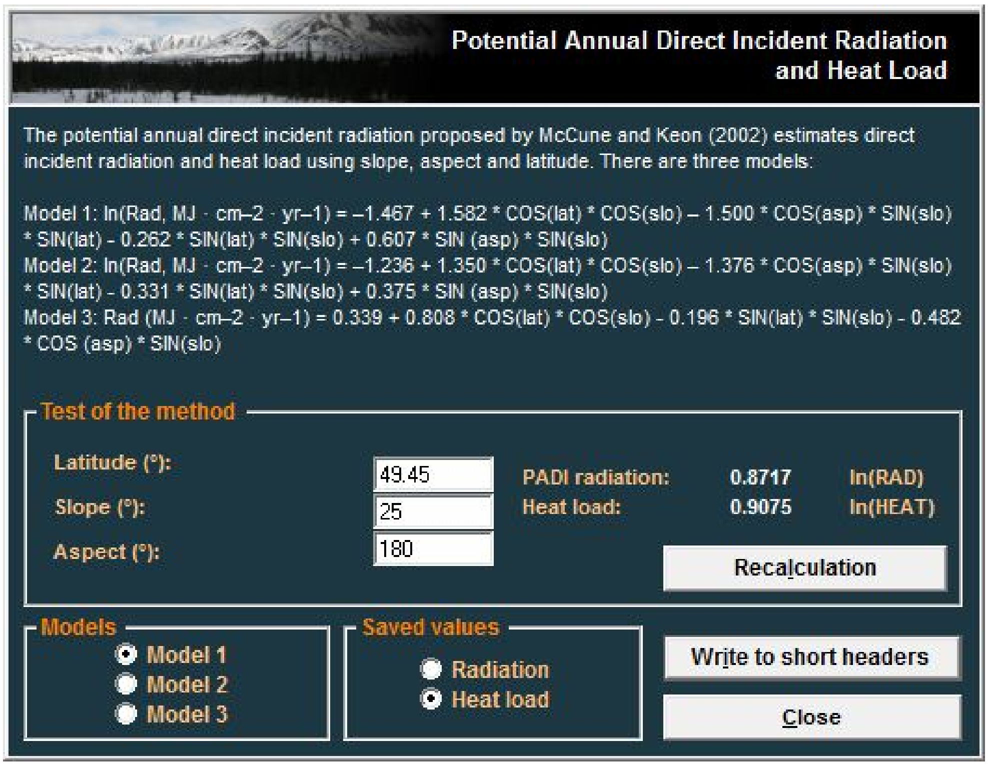
There are three available models:

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

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

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

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



Potential Annual Direct Incident Radiation and Heat Load

The potential annual direct incident radiation proposed by McCune and Keon (2002) estimates direct incident radiation and heat load using slope, aspect and latitude. There are three models:

Model 1: ln(Rad, MJ · cm–2 · yr–1) = –1.467 + 1.582 * COS(lat) * COS(slo) – 1.500 * COS(asp) * SIN(slo) * SIN(lat) - 0.262 * SIN(lat) * SIN(slo) + 0.607 * SIN (asp) * SIN(slo)
Model 2: ln(Rad, MJ · cm–2 · yr–1) = –1.236 + 1.350 * COS(lat) * COS(slo) – 1.376 * COS(asp) * SIN(slo) * SIN(lat) - 0.331 * SIN(lat) * SIN(slo) + 0.375 * SIN (asp) * SIN(slo)
Model 3: Rad (MJ · cm–2 · yr–1) = 0.339 + 0.808 * COS(lat) * COS(slo) - 0.196 * SIN(lat) * SIN(slo) - 0.482 * COS (asp) * SIN(slo)

Test of the method
Latitude (°): 49.45
Slope (°): 25
Aspect (°): 180
PADI radiation: 0.8717 ln(RAD)
Heat load: 0.9075 ln(HEAT)

Models
● Model 1
○ Model 2
○ Model 3

Saved values
○ Radiation
● Heat load

Fig. 39: Calculation of potential direct incident 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).*

1.8.2.10 Random functions

There are several functions for the randomization of the data set. The function ‘Random number’ adds a random number of each relevé to the Short headers. The function ‘Random Permutation of the Short Headers’ casually mixes short header values, while the function ‘Random Permutation of the Relevés’ mixes each relevé from the data set.

1.8.2.11 Sum, Mean, Standart deviation, Minimum and Maximum of Species Data

There are several functions for summarizing numerical Species data into short headers. ‘Mean of <colour> Species Data’ calculates the mean over all species of the indicated colour in the relevé. Sum, Median, Maximum and Minimum functions are similar.

1.8.2.12 Sum and Mean of Species Data Weighted by Cover

There are two functions which calculate mean and sum of the Species Data for coloured species weighted by their cover in the plot.

Note: These functions are only useful for analysing numerical species data.

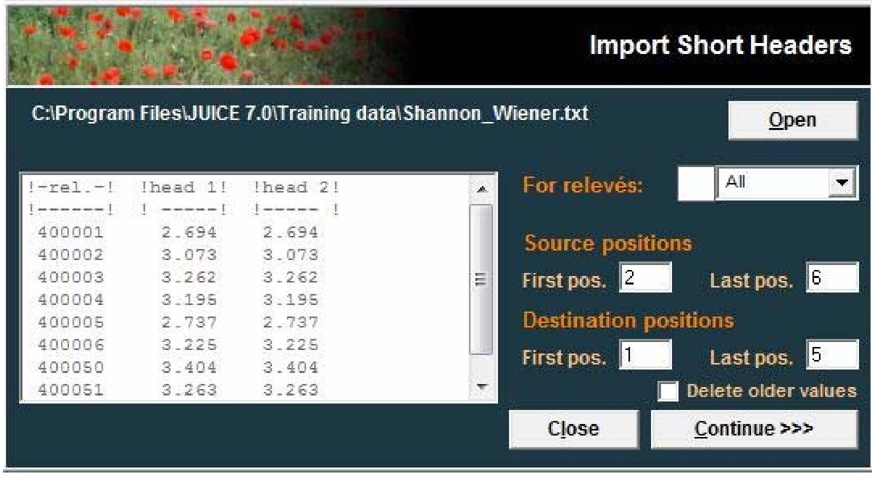
1.8.2.13 Ellenberg Indicator Values

Ellenberg indicator values can be written to the short headers by the button ‘Add Value to the head’ in the menu ‘Indicator Values’ and ‘Calculating for Relevés’. Before using this function, it is necessary that the indicator values are defined. See Section 1.9 for more information about Ellenberg Indicator Values.

1.8.3 Import and Export of External Short Header Data

External header data can be imported from a comma or semi-colon delimited 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 1.10.10).

The ‘Import Short Headers’ window is shown below:



C:\Program Files\JUICE 7.0\Training data\Shannon_Wiener.txt

```
!-rel.-!  !head 1!  !head 2!
!------!  ! -----!  !----- !
 400001      2.694     2.694
 400002      3.073     3.073
 400003      3.262     3.262
 400004      3.195     3.195
 400005      2.737     2.737
 400006      3.225     3.225
 400050      3.404     3.404
 400051      3.263     3.263
```

For relevés: All

Source positions
First pos. 2 Last pos. 6

Destination positions
First pos. 1 Last pos. 5

☐ Delete older values

Fig. 40: 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, five digits, from the second to the sixth characters after the relevé identification number, will be stored from the first to the fifth position of the short head.

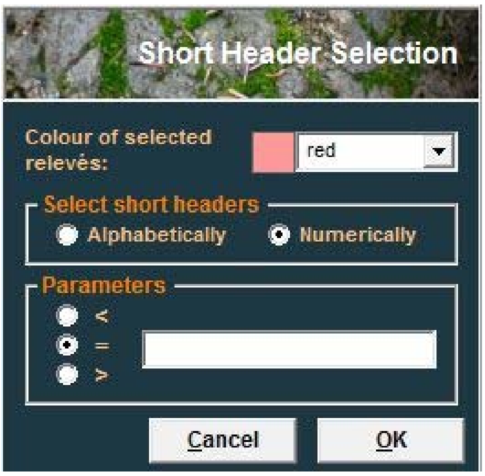
An exporting file of short headers is a simple text with columns divided by semi-colons. The export is located in the menu ‘File’ and ‘Export’ and ‘Export Short Headers’.

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.*

Note2: *Similarly, the short headers import and export can be realised indirectly using the clipboard from the menu ‘Edit’. These functions make an exchange of data between JUICE and any other program faster and more flexible.*

1.8.4 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.



Colour of selected relevés: red

Select short headers
○ Alphabetically ● Numerically

Parameters
○ <
● =
○ >

Fig. 41: Short header selection window.

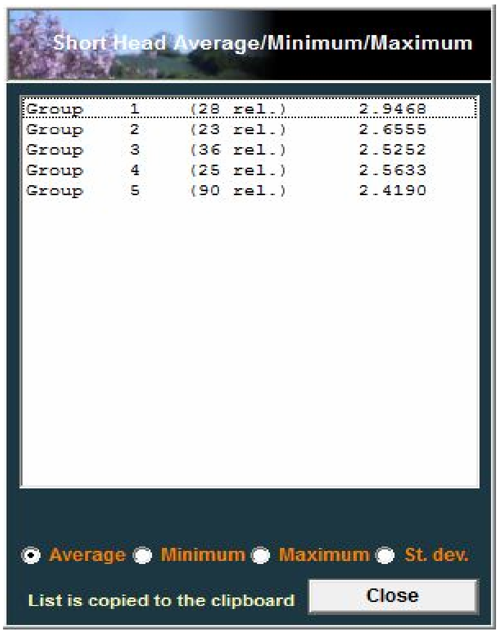
Note: *Alphabetical comparison should be used with text and numerical with numbers. The example below shows what happens when numbers are compared alphabetically:*

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.

1.8.5 Short Header Averages, Minima and Maxima

JUICE can measure the average, minimum, maximum or standard deviation 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, the maximum or the standard deviations. The list of values is also copied onto the clipboard and it can be pasted into a text editor with the command Ctrl+Insert or Ctrl+V.



```
Group     1     (28 rel.)      2.9468
Group     2     (23 rel.)      2.6555
Group     3     (36 rel.)      2.5252
Group     4     (25 rel.)      2.5633
Group     5     (90 rel.)      2.4190
```

● Average ○ Minimum ○ Maximum ○ St. dev.

List is copied to the clipboard

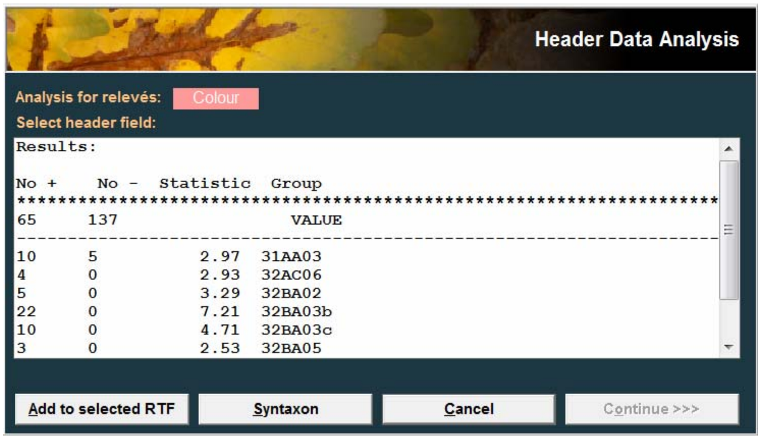
Fig. 42: Averages, minima, maxima or standart deviations from short headers calculated for each constancy column of the table.

1.8.6 Adding Short Headers to the Header Data

It is possible to add short headers to header data by function ‘Add Short headers to Header Data’ in the ‘Head’ menu. The user must write the name of the new column in the header data. Short headers will be then included to the Header data file as the last column.

1.8.7 Header data histogram

This function compares relevés of selected colour with the rest of the table and identifies the relation of some qualitative relevé characteristic (e.g. vegetation type) to relevés of selected colour. Field ‘Statistic’ represents currently selected type of fidelity measure.



Analysis for relevés: Colour

Select header field:

```
Results:

No +    No -  Statistic  Group
**********************************************************************
65      137                    VALUE
----------------------------------------------------------------------
10      5            2.97   31AA03
4       0            2.93   32AC06
5       0            3.29   32BA02
22      0            7.21   32BA03b
10      0            4.71   32BA03c
3       0            2.53   32BA05
```

Fig. 43: Header data histogram

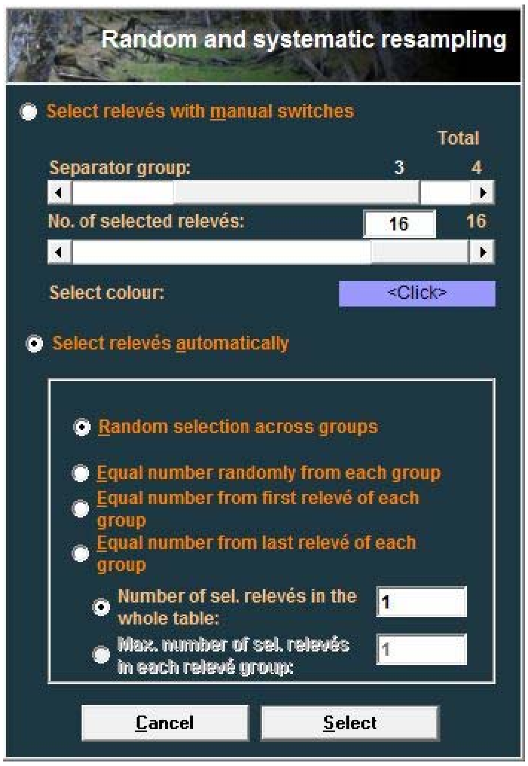
1.8.8 Relevé Colour According to the Head

From the ‘Head’ menu, select ‘Relevé Colour according to the Head’. Choose the colour, select the header data field and specify the value. This function is similar to searching relevés in chapter 1.5.10.

1.8.9 Resampling

1.8.9.1 Random and Systematic Resampling

The user can randomly select relevés both with manual switches and automatically. The first horizontal bar selects separator group, where group of relevés will be selected. The second bar specifies the number of selected relevés.



○ Select relevés with manual switches

Total

Separator group: 3 4

No. of selected relevés: 16 16

Select colour: <Click>

● Select relevés automatically

● Random selection across groups

○ Equal number randomly from each group

○ Equal number from first relevé of each group

○ Equal number from last relevé of each group

● Number of sel. relevés in the whole table: 1

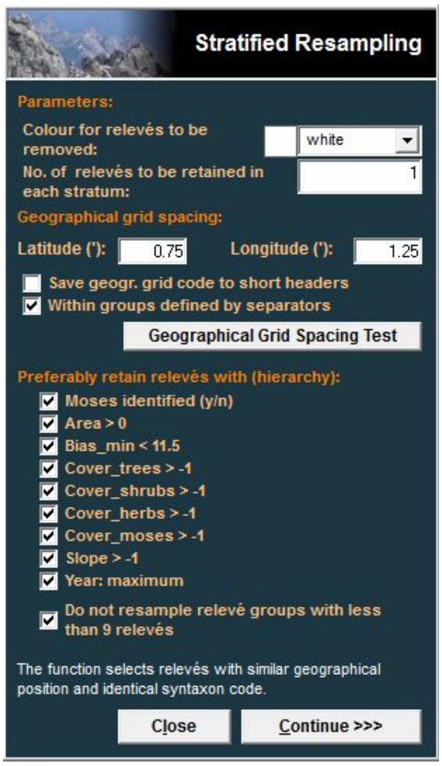
○ Max. number of sel. relevés in each relevé group: 1

Fig. 44: Random and systematic resampling

There are many possibilities for automatic selection of relevés. The user can define a number of selected relevés in the whole table, or the maximal number of selected relevés in each relevé group.

1.8.9.2 Geographical Resampling

This type of resampling creates a virtual geographical grid of defined size (in minutes of latitude and longitude) and the defined number of selected relevés will be selected from each cell of the grid with preference of relevés with higher quality of recorded data.



Stratified Resampling

Parameters:

Colour for relevés to be removed: white

No. of relevés to be retained in each stratum: 1

Geographical grid spacing:

Latitude ('): 0.75 Longitude ('): 1.25

☐ Save geogr. grid code to short headers
☑ Within groups defined by separators

Preferably retain relevés with (hierarchy):

☑ Moses identified (y/n)
☑ Area > 0
☑ Bias_min < 11.5
☑ Cover_trees > -1
☑ Cover_shrubs > -1
☑ Cover_herbs > -1
☑ Cover_moses > -1
☑ Slope > -1
☑ Year: maximum

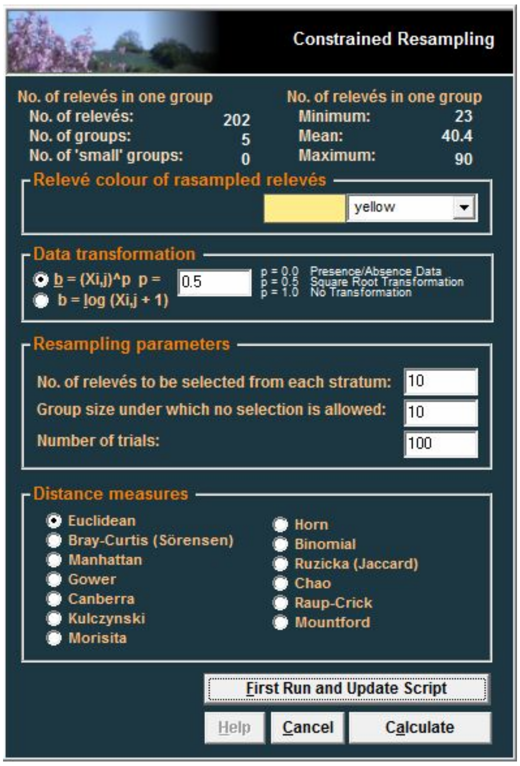
☑ Do not resample relevé groups with less than 9 relevés

The function selects relevés with similar geographical position and identical syntaxon code.

Fig. 45: Geographical stratification

1.8.9.3 Constrained Resampling

Many subsets of the source vegetation database selected randomly from the data set are sorted by decreasing mean dissimilarity between pairs of relevés, and then sorted again by increasing variance of these dissimilarities. Ranks from both sortings are summed for each subset, and the subset with the lowest summed rank is considered as the most representative (see Lengyel et al. 2010 for more details).



Constrained Resampling

No. of relevés in one group
No. of relevés: 202
No. of groups: 5
No. of 'small' groups: 0

No. of relevés in one group
Minimum: 23
Mean: 40.4
Maximum: 90

Relevé colour of rasampled relevés: yellow

Data transformation
● b = (Xi,j)^p p = 0.5
○ b = log (Xi,j + 1)

p = 0.0 Presence/Absence Data
p = 0.5 Square Root Transformation
p = 1.0 No Transformation

Resampling parameters
No. of relevés to be selected from each stratum: 10
Group size under which no selection is allowed: 10
Number of trials: 100

Distance measures
● Euclidean
○ Bray-Curtis (Sörensen)
○ Manhattan
○ Gower
○ Canberra
○ Kulczynski
○ Morisita
○ Horn
○ Binomial
○ Ruzicka (Jaccard)
○ Chao
○ Raup-Crick
○ Mountford

Fig. 46: Geographical (stratified) resampling and constrained resampling

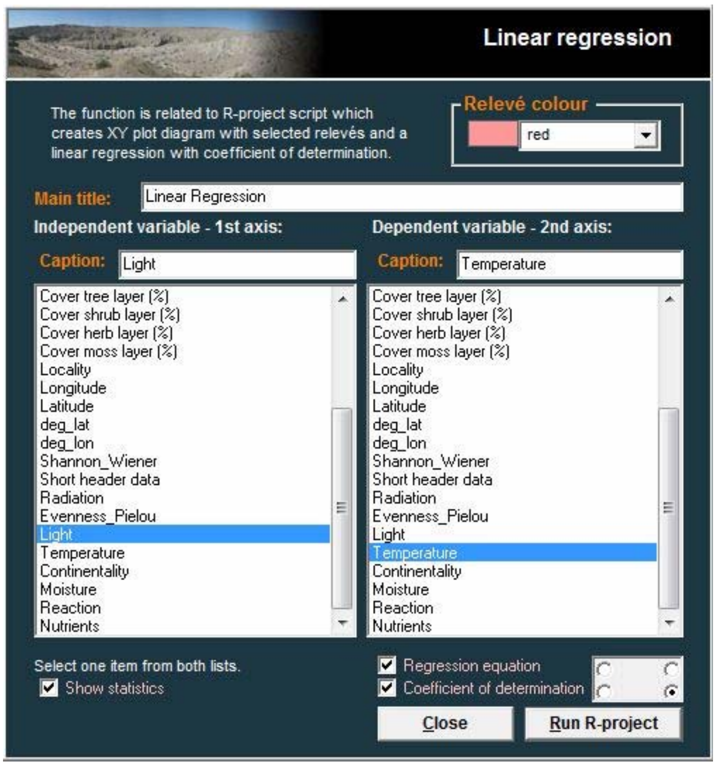
1.8.10 Imputation of Environmental Variable

Large databases contain many relevés, but few of them contain measured environmental data. The process of indirect estimation of environmental factor is based on similarity in species composition between relevés. The similarity is calculated as the Sørensen similarity index applied to presence/absence, square-root transformed or untransformed vegetation data. The environmental factor for the target relevé is then imputed as the mean of observed values from several of the most similar calibration plots. An average factor value is calculated from selected number of calibration plots which fit the condition of minimum and maximum Sorensen similarity value. Values are calculated from white relevés for relevés of selected colour. See the paper Tichý et al. (2010) for detailed information.

1.8.11 Linear Regression

The function ‘Linear regression’ in the ‘Head’ menu is related to R-project script, which creates X-Y plot diagram and the description of linear regression with coefficient of determination. If you will choose this function, the window shown below will appear. Independent variable can be selected from the left, while the dependent variable from the right list.

Note: *Don’t forget to install R-project on your computer and initiate the connection with the JUICE in the ‘Options’ window.*



Linear regression

The function is related to R-project script which creates XY plot diagram with selected relevés and a linear regression with coefficient of determination.

Relevé colour: red

Main title: Linear Regression

Independent variable - 1st axis:

Caption: Light

Dependent variable - 2nd axis:

Caption: Temperature

Select one item from both lists.

☑ Show statistics

☑ Regression equation

☑ Coefficient of determination

Fig. 47: Linear regression

The graph will appear after the selection of the button ‘Run R-project’. The graph can be copied into the clipboard (by CTRL+C), or saved in the ‘File’ menu of the ‘R Graphics’ window by function ‘Save as’ to several file formats.

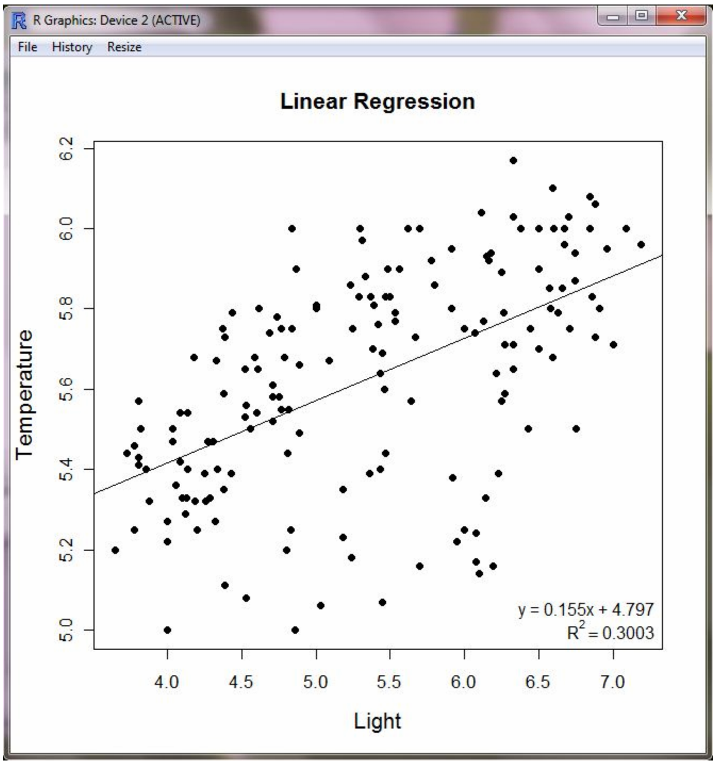
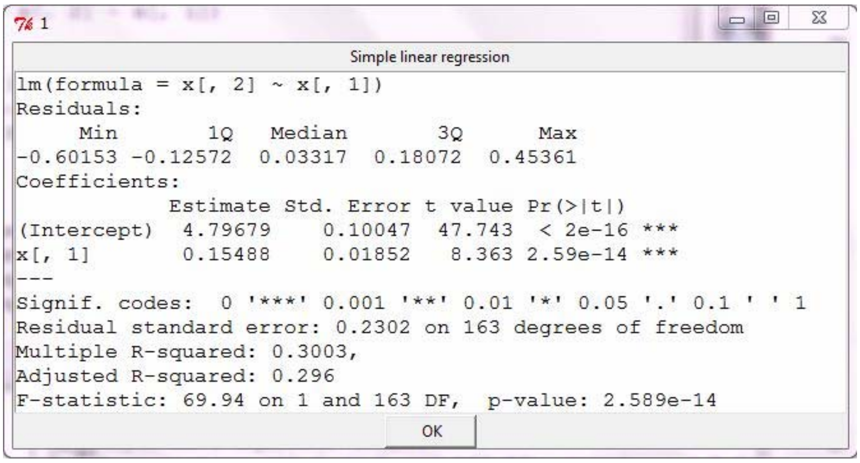


Fig. 48: Graph of the linear regression

‘Shown statistic’ check box means that the next window will be opened together with plot diagram:



```
lm(formula = x[, 2] ~ x[, 1])
Residuals:
     Min       1Q   Median       3Q      Max
-0.60153 -0.12572  0.03317  0.18072  0.45361
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  4.79679    0.10047  47.743  < 2e-16 ***
x[, 1]       0.15488    0.01852   8.363 2.59e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.2302 on 163 degrees of freedom
Multiple R-squared: 0.3003,
Adjusted R-squared: 0.296
F-statistic: 69.94 on 1 and 163 DF,  p-value: 2.589e-14
```

Fig. 49: List of the statistics of the linear regression

The function calculated the minimum, median and maximum of residuals, intercept. residual standard error, multiple and adjusted R-squared and F-statistic with the p-value. The signification of the result is expressed by stars.

1.8.12 Short Header Sorting

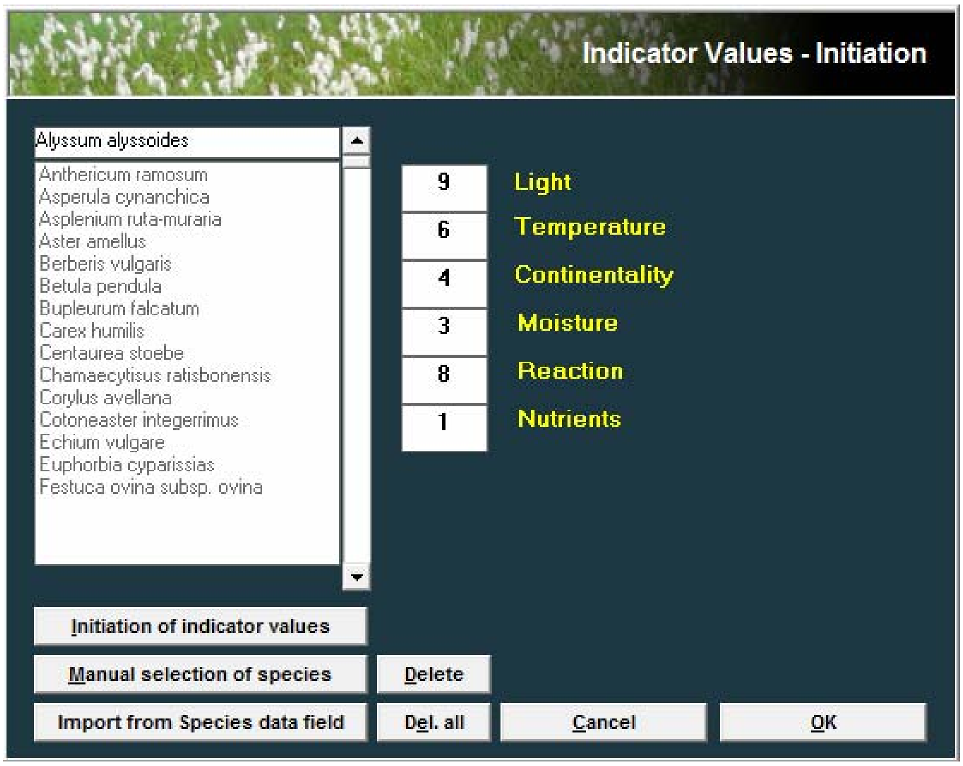
It is often desirable to sort relevés according to some criterion. First, the values under consideration should be written to the short headers as described in Section 1.8.2. Then, from the 'Sorting' menu, select 'Sort Short Headers'. For more information on sorting, see Section 1.6.3, especially Section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

1.9 Indicator Values

1.9.1 Initiation

In the first step Ellenberg indicator values (EIV) must be initiated in the 'Indicator Values' menu by the function Initiation of indicator values'. ELLENB.txt file in the installation package contains an information about original Ellenberg indicators values for the 'Light', 'Moisture', 'Continentality', 'Temperature', 'pH' or 'Nutrients'. Using this file, Ellenberg indicator values will be automatically initiated and shown in the table in the right side of the form. If you don't want to use the file from the package, you can create your own file with indicator values similar to ELLENB.txt file. Species both in that file and in the table must have the same name. The box on the left side displays species list and the upper text line highlights currently selected species. If EIV was not assigned, such species will be red coloured.

All EIVs for species may be matched manually from the text file. The box with species and EIVs from the file will open on the right side of the window. If you choose some record and press the button 'Replace', the program will import EIVs from the species in the right box to the chosen species in the left box. The next possibility is the import EIV from the species data field and last allows to enter values directly.



Alyssum alyssoides

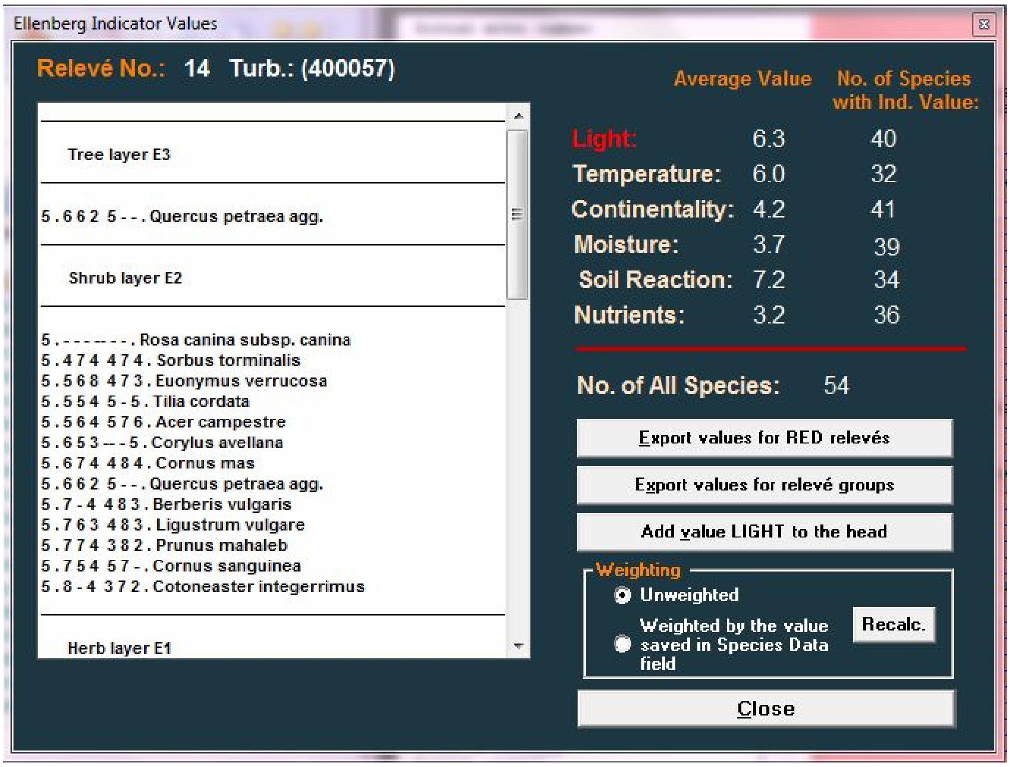
Anthericum ramosum
Asperula cynanchica
Asplenium ruta-muraria
Aster amellus
Berberis vulgaris
Betula pendula
Bupleurum falcatum
Carex humilis
Centaurea stoebe
Chamaecytisus ratisbonensis
Corylus avellana
Cotoneaster integerrimus
Echium vulgare
Euphorbia cyparissias
Festuca ovina subsp. ovina

9	Light
6	Temperature
4	Continentality
3	Moisture
8	Reaction
1	Nutrients

Fig. 50: Indicator Values - Initiation

1.9.2 Calculation of mean EIVs for selected relevés

The function ‘Calculation for relevé’ you will find in the ‘Indicators Values’ menu. The user has to choose by mouse one relevé from the table before the analysis. Then the window for the calculation of mean EIVs will appear. It considers a list of species from selected relevé and their EIV values in the right side and a list of mean EIV values (together with the number of species, from which the value is calculated) in the left side of the window. Calculated values can be exported for relevés of selected colour or for all data set (including the information about relevé groups) to the text file useful in other programs. If you want use the value in other analyses within JUICE program, you can add the calculated value for one EIV to short headers by the button ‘Add value EIV to the heads’. The choice of exported factor can be done by simple mouse clicking of its name. Mean EIV value can calculated from values related to species, which may be weighted by some value saved in the Species data field.



Relevé No.: 14 Turb.: (400057)

```
Tree layer E3

5 . 6 6 2  5 - - . Quercus petraea agg.

Shrub layer E2

5 . - - - -- - - . Rosa canina subsp. canina
5 . 4 7 4  4 7 4 . Sorbus torminalis
5 . 5 6 8  4 7 3 . Euonymus verrucosa
5 . 5 5 4  5 - 5 . Tilia cordata
5 . 5 6 4  5 7 6 . Acer campestre
5 . 6 5 3 -- - 5 . Corylus avellana
5 . 6 7 4  4 8 4 . Cornus mas
5 . 6 6 2  5 - - . Quercus petraea agg.
5 . 7 - 4  4 8 3 . Berberis vulgaris
5 . 7 6 3  4 8 3 . Ligustrum vulgare
5 . 7 7 4  3 8 2 . Prunus mahaleb
5 . 7 5 4  5 7 - . Cornus sanguinea
5 . 8 - 4  3 7 2 . Cotoneaster integerrimus

Herb layer E1
```

	Average Value	No. of Species with Ind. Value:
Light:	6.3	40
Temperature:	6.0	32
Continentality:	4.2	41
Moisture:	3.7	39
Soil Reaction:	7.2	34
Nutrients:	3.2	36

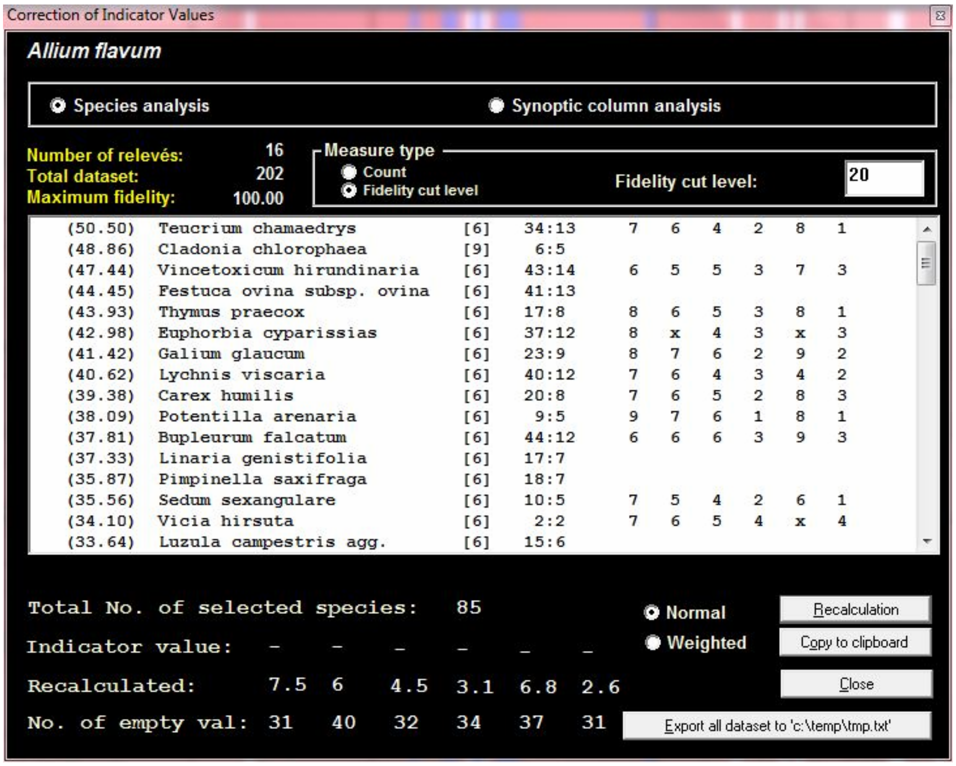
No. of All Species: 54

Weighting
● Unweighted
○ Weighted by the value saved in Species Data field

Fig. 51: Calculation EIV for relevés

1.9.3 Correction of Indicator Values

This function supports an estimation of EIVs for species, where such values were not defined. The program selects the most similar species to the target species, and from their EIV values, it will calculate a mean for species which fit a defined criteria.



```
Allium flavum

◉ Species analysis                    ○ Synoptic column analysis

Number of relevés:        16     Measure type
Total dataset:           202       ○ Count
Maximum fidelity:     100.00       ◉ Fidelity cut level      Fidelity cut level: 20

    (50.50)  Teucrium chamaedrys          [6]   34:13    7   6   4   2   8   1
    (48.86)  Cladonia chlorophaea         [9]    6:5
    (47.44)  Vincetoxicum hirundinaria    [6]   43:14    6   5   5   3   7   3
    (44.45)  Festuca ovina subsp. ovina   [6]   41:13
    (43.93)  Thymus praecox               [6]   17:8     8   6   5   3   8   1
    (42.98)  Euphorbia cyparissias        [6]   37:12    8   x   4   3   x   3
    (41.42)  Galium glaucum               [6]   23:9     8   7   6   2   9   2
    (40.62)  Lychnis viscaria             [6]   40:12    7   6   4   3   4   2
    (39.38)  Carex humilis                [6]   20:8     7   6   5   2   8   3
    (38.09)  Potentilla arenaria          [6]    9:5     9   7   6   1   8   1
    (37.81)  Bupleurum falcatum           [6]   44:12    6   6   6   3   9   3
    (37.33)  Linaria genistifolia         [6]   17:7
    (35.87)  Pimpinella saxifraga         [6]   18:7
    (35.56)  Sedum sexangulare            [6]   10:5     7   5   4   2   6   1
    (34.10)  Vicia hirsuta                [6]    2:2     7   6   5   4   x   4
    (33.64)  Luzula campestris agg.       [6]   15:6

Total No. of selected species:   85                 ◉ Normal
Indicator value:   -    -    -    -    -    -       ○ Weighted
Recalculated:      7.5  6    4.5  3.1  6.8  2.6
No. of empty val:  31   40   32   34   37   31
```

Fig. 52: Correction of Indicator Values

1.10 Exporting Data

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

1.10.1 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 1.4.8.

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.*

1.10.2 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.

1.10.3 Table Export

From the ‘File’ menu, select ‘Export’ and ‘Table’. This will open the ‘Table Export’ menu, which offers several different export formats.

The default, **‘to RTF File’**, appends table to 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).

The function **‘to Spreadsheet Format File’** will generate a stand-alone TXT file separated by semi-colons and accepted by spreadsheet programs sSee Section 1.4.4.). This table is divided into two parts: table and header.

The function **‘to Spreadsheet Format File (2nd version)’** will generate a stand-alone TXT file separated by semi-colons and accepted by spreadsheet programs. Nevertheless, the user can choose values for export of the table (percentage cover values, Braun-Blanquet cover codes and presence/absence data). Header data and cover values are in the same table, but this export has header information at the beginning. Furthermore, the former format presents header data by listing one relevé data per row, whereas this header format is transponed.

The function **‘to Database Files’** produces four 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), HEADER.TXT with all header data. (These are only the default names; the user can change them.) These three files have the fixed lenght. The fourth file is the FULL TABLE.TXT, which is separated by colon and replicates the data from TABLE.TXT, but in different format. These files can be imported into a database program and connected through Id. number of relevés.

The function **‘to Simple Text File’** saves the file as simple text (TXT) (see Section 1.4.5.).

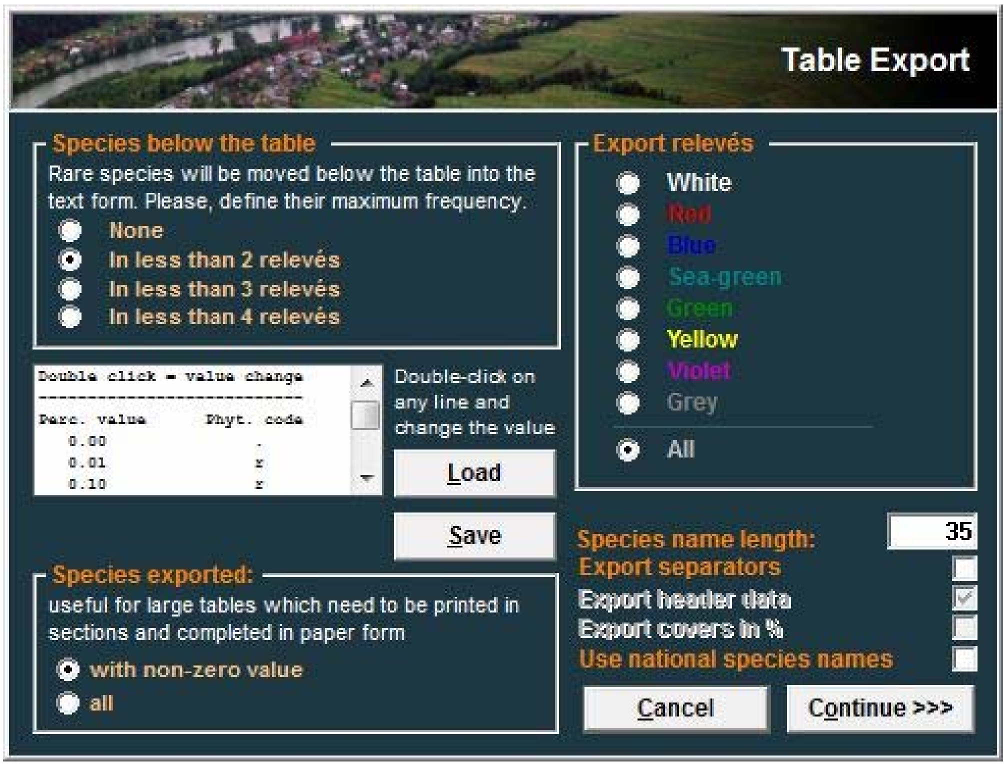


Table Export

Species below the table

Rare species will be moved below the table into the text form. Please, define their maximum frequency.

○ None
● In less than 2 relevés
○ In less than 3 relevés
○ In less than 4 relevés

```
Double click = value change
---------------------------
Perc. value      Phyt. code
   0.00                   .
   0.01                   r
   0.10                   r
```

Double-click on any line and change the value

Species exported:

useful for large tables which need to be printed in sections and completed in paper form

● with non-zero value
○ all

Export relevés

○ White
○ Red
○ Blue
○ Sea-green
○ Green
○ Yellow
○ Violet
○ Grey
● All

Species name length: 35
Export separators ☐
Export header data ☑
Export covers in % ☐
Use national species names ☐

Fig. 53: Table export

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 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 ‘Database Files’, 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.

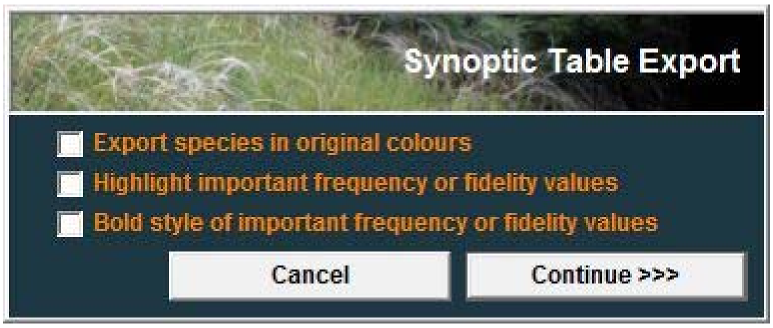
1.10.4 Synoptic Table Export

From the ‘File’ menu, select ‘Export’. If JUICE is in Synoptic Table Display mode (See the second part of this manual) the ‘Synoptic Table’ export function will be available. This provides four possibilities to:

1. Export the synoptic table into the current RTF export file for presentation or publication.
2. Export the synoptic table into CSV file separated by the semicolon for the using in spreadsheets programs.

3. Export the transposed synoptic table into CSV file separated by the semicolon.
4. 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:



☐ Export species in original colours
☐ Highlight important frequency or fidelity values
☐ Bold style of important frequency or fidelity values

Fig. 54: Window managing synoptic table export.

Synoptic tables may be saved in single or combined form (See the second part of this manual). All data will be saved similarly to the way they are displayed on the screen.

1.10.5 Other Exports into the RTF Export File

The current RTF export file is opened for running exports of interspecific associations created during COCKTAIL classification and Matching. More information about COCKTAIL classification is written in the second part of this manual.

1.10.6 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, R-project format TXT file a MULVA input file, SYN-TAX files or a MATLAB file. A text export of similarity indices of relevés to constancy columns is available from the menu ‘Analysis’ and ‘Matching’ (See the second part of this manual).

1.10.7 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.

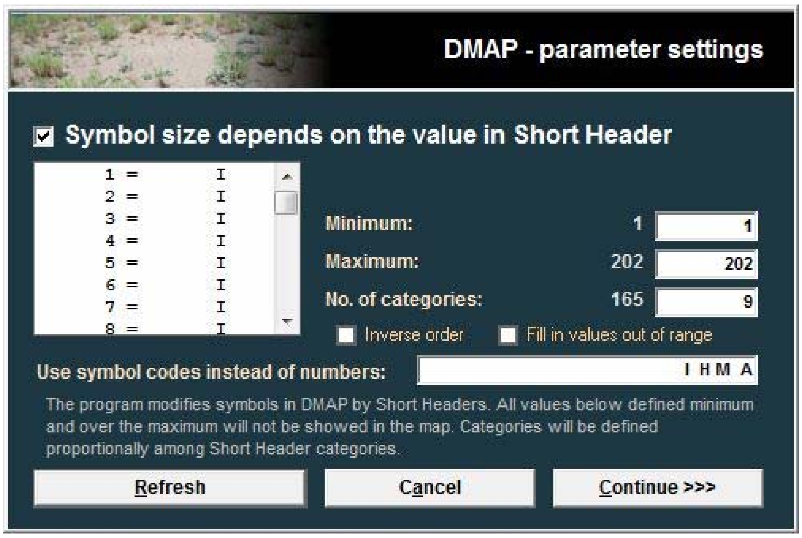
The header data must contain LATITUDE and LONGITUDE fields represented as six or seven characters corresponding to degrees, minutes and seconds (as explained in Section 0).

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.



DMAP - parameter settings

☑ Symbol size depends on the value in Short Header

1 = I
2 = I
3 = I
4 = I
5 = I
6 = I
7 = I
8 = I

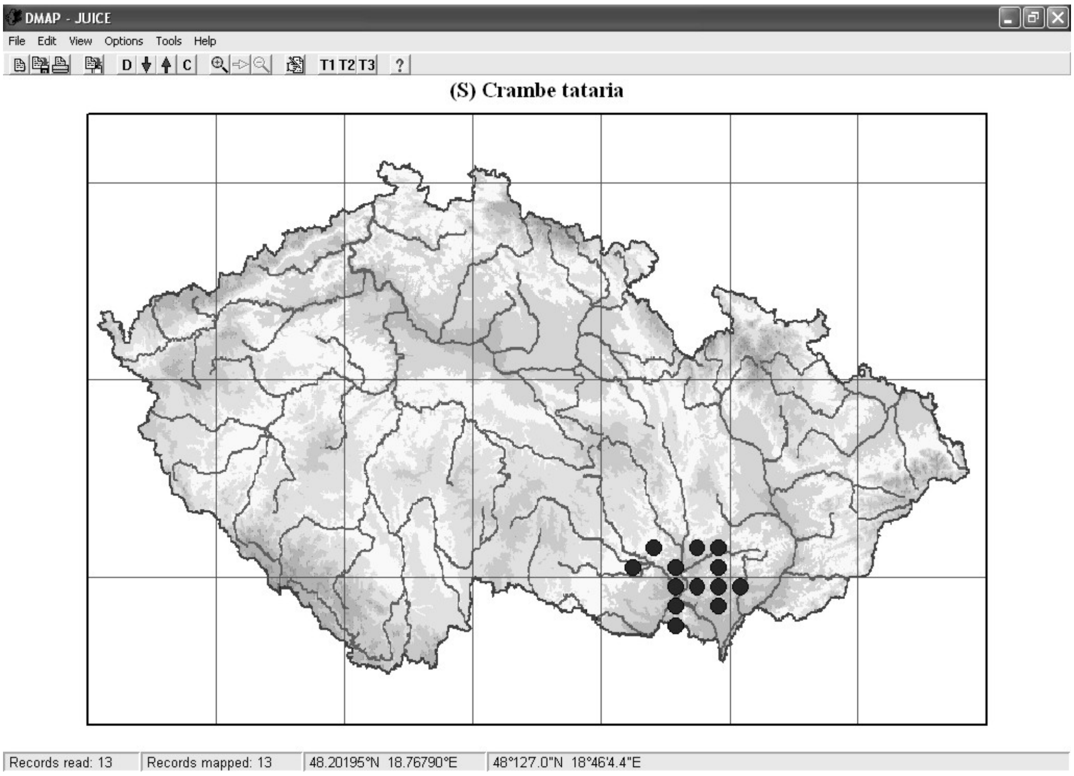
Minimum:	1	1
Maximum:	202	202
No. of categories:	165	9

☐ Inverse order ☐ Fill in values out of range

Use symbol codes instead of numbers: I H M A

The program modifies symbols in DMAP by Short Headers. All values below defined minimum and over the maximum will not be showed in the map. Categories will be defined proportionally among Short Header categories.

Fig. 55: Window managing synoptic table export.



(S) Crambe tataria

Records read: 13 | Records mapped: 13 | 48.20195°N 18.76790°E | 48°127.0"N 18°46'4.4"E

Fig. 56: Communication window and example of the distribution map created by D-MAP.

1.10.8 Relevé or species distribution in Google Earth

The program Google Earth is widely distributed freeware, which is useful for simple GIS mapping. JUICE supports mapping of relevé group, species or whole table distribution within

Google Earth in case if this software is installed (menu ‘File’ and ‘Export’ and ‘Mapping in GOOGLE EARTH’). All locations are highlighted by a special symbol with the relevé number and the label of relevé group.

1.10.9 Species Data Export

Species data (see Section 1.7) can be imported or created manually (see Section 1.5.7). Their simple format allows the saving them for the next future use. The information is related to species name, and then these data can be also imported into other similar tables, where the list of species occurring there is more or less the same. 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
```

1.10.10 Short Header Export

Short header data can be exported into a simple text file (see Section 1.8.3). The file contains Relevé number, Sort header value, Group number and a 1 or 0 representing presence or absence of a separator on the right side 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
```

1.10.11 Header Export

Header data can be exported into a simple text file by the function ‘Export Headers for <colour> Relevés’ in the ‘Export’ menu. This funtion calls following window, where the user can choose header fields for export to the text file. Information about headers is in the section 1.8.

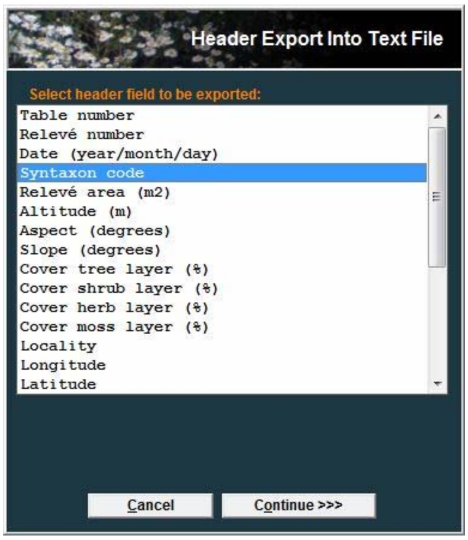


Fig. 57: Window for the export of headers to the text file

1.10.12 Export of the Interspecific Associations

The function ‘Export Interspecific Association’ (‘Export’ menu) creates pairwise associations between each pair of species, sorts them and selects one, three, five etc. the highest average values for selected type of fidelity. The information appears in currently initiated RTF export file. For more information about interspecific associations see in the second part of this manual.

1.11 Conversion

Different programs load the data in the different formats. The function ‘Conversion’ in the ‘File’ menu changes the semi-colon separated file or the comma separated files to the text file of the fixed length. At the first step, the user must choose the file for the conversion. And the second step is the saving of the new text file with the fixed length.