Turboveg for Windows

Version 2
24-8-2012

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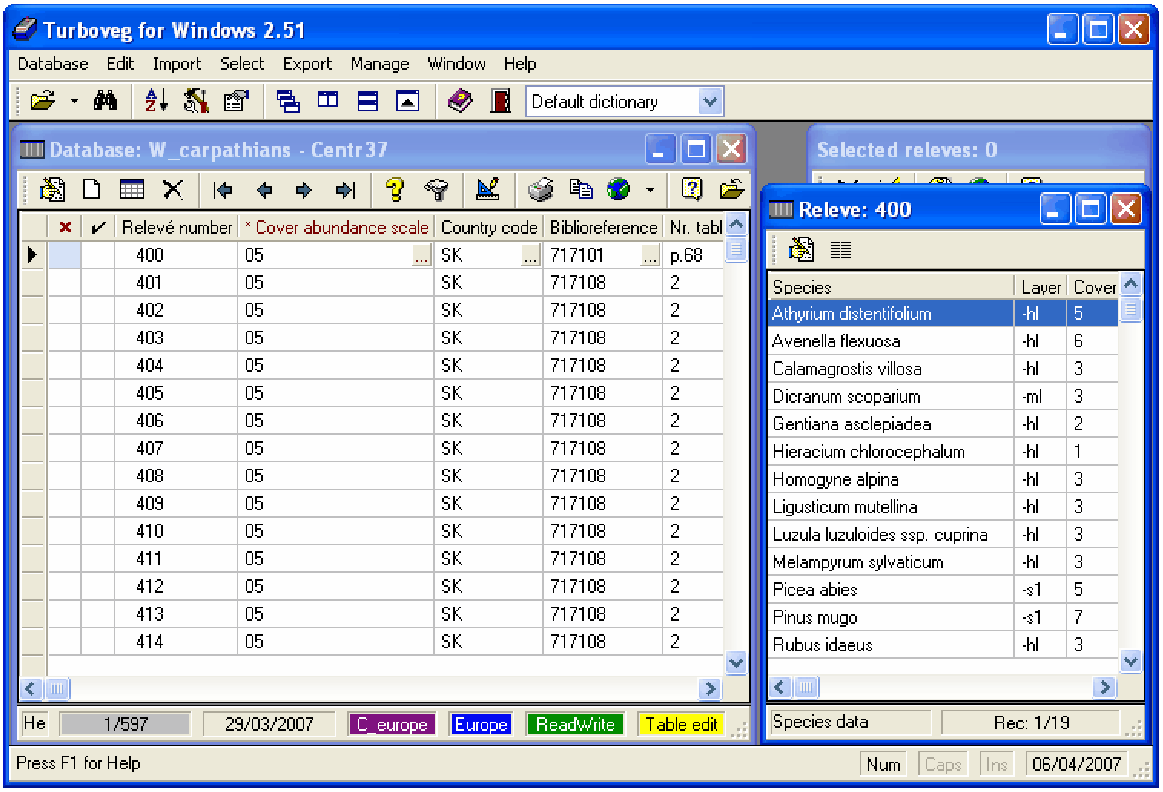
1 Introduction

Turboveg for Windows is a program designed for the storage, selection, and export of vegetation data (relevés).
Data can be imported manually (separate relevés or tables) and automatically (import of data files).
You can select relevés by choosing one or several of the header data or by choosing a species or a combination of species.
Several filters are available to export the selected relevés to enable further analysis with various programs (e.g. *MS Access,Twinspan*, *Canoco*, *PC-ORD*, *Mulva*, *Syntax-5*, *Excel*, *Juice, ArcView, ArcGIS, GoogleEarth*).

The standard structure of the table is fixed, but you can easily extend this standard structure by defining extra fields to fit your own needs. You can extend both the header data (e.g. a field for soil type) and the species data (e.g. add a field for the phenology of the species). Each database can have its own extension.

If you have never worked with Turboveg before than it is recommended to read the **Getting started** 10 section of this Help first.



✗	✓	Relevé number	* Cover abundance scale	Country code	Biblioreference	Nr. tabl
		400	05	SK	717101	p.68
		401	05	SK	717108	2
		402	05	SK	717108	2
		403	05	SK	717108	2
		404	05	SK	717108	2
		405	05	SK	717108	2
		406	05	SK	717108	2
		407	05	SK	717108	2
		408	05	SK	717108	2
		409	05	SK	717108	2
		410	05	SK	717108	2
		411	05	SK	717108	2
		412	05	SK	717108	2
		413	05	SK	717108	2
		414	05	SK	717108	2

Species	Layer	Cover
Athyrium distentifolium	-hl	5
Avenella flexuosa	-hl	6
Calamagrostis villosa	-hl	3
Dicranum scoparium	-ml	3
Gentiana asclepiadea	-hl	2
Hieracium chlorocephalum	-hl	1
Homogyne alpina	-hl	3
Ligusticum mutellina	-hl	3
Luzula luzuloides ssp. cuprina	-hl	3
Melampyrum sylvaticum	-hl	3
Picea abies	-s1	5
Pinus mugo	-s1	7
Rubus idaeus	-hl	3

Part

II

2 General

2.1 Getting started

I you have never worked with *TURBOVEG* before, probably one of first things you want to do, is to enter relevés into a database. The following steps can be taken in order to enter data, select the data stored in the database, and to export the relevés to a relevant format for further analysis (e.g. a classification using the software program *JUICE*).

Every dialog window has a **Help** button. **Use it** if you do not know what to do.

1. Create a database if no database is available or if you want to start with an empty one. From the menu select **Database | New.** The only two entries to be filled in are **Database name** and **Range for system numbers.** An empty database will be created. Two new empty windows are opened; the window on the left site will contain the so-called header data, the window on the right site is reserved for species data (species name, vegetation layer and cover abundance).

2. Start entering (single) relevés by selecting **Edit | Add a relevé** from the menu. In two steps a relevé can be entered. The first step will serve to put in so-called header data, species data are entered with the second step.
   If there is relevant information (e.g. measured pH values for each relevé) which can not be stored in one of the available fields, the possibility exists to extend the database. See **Modify the database structure** 23 for details.

   There are more methods in *Turboveg* to enter relevés into a database:

   Manually:
   Edit | Add a table 34
   To avoid entering the species for each relevé in the (printed) table a matrix of relevés and species can be generated that can be filled. In this case the species data are first entered into the database, in the second step the header data can be completed.

   By means of computerized tables:
   Import | Cornell condensed species file 45
   Import | Free format species data file 48
   Import | Free format header data file 52

3. Once we have stored relevés in a database, selections can be made in various ways. The simplest method is to open the database, and to press the *Spacebar* on each relevé we want to select. Make sure that the window with the header data is active. Selected relevés will get a flag and the lines become yellow. De-selecting a relevé may also be achieved by pressing the *Spacebar*.
   If all relevés from the database need to be selected a one-click action can be performed by selecting **Select | Select all releves of current database** 62 from the menu. The same can be done for de-selecting all relevés by selecting **Select | Deselect all releves of current database** 62.
   For sophisticated selections choose **Select | Build query** 63. Selection criteria can be

defined on the basis of combinations of header data items and/or combinations of species. Also the species cover abundance can be taken into account.
The selected relevés are listed in a separate window. This is the window that is first opened (and remains opened) when a Turboveg session is started.

A selection is not restricted to one database. You may open several databases and perform a selection in one run. The only restriction is that the relevés in the selected databases have a unique system number. To open more database select **Database | Open** 20 and mark (mouse click or press the *Spacebar*) the desired database names.

4. For further analyses of the data *TURBOVEG* offers quite a few export formats. One of most commonly used formats is the Cornell condensed format. A Cornell condensed formatted file can serve as an input file for e.g. *TWINSPAN* and *CANOCO*. To create a Cornell condensed file select **Export | Cornell condensedspecies file** 70 from the menu. In the export file only those relevés will be included that are listed in the window with selected relevés. This can even be achieved when all databases are closed.
   For further analyses with JUICE it is recommended to export the selection to a 'Standard XML file' (**Export | Standard XML file** 68), instead of using the obsolete export function to 'JUICE input files'. JUICE is an excellent software program for classification; it can handle more than 30.000 relevés in spread sheet.

To be continued...

2.2 Network installation

Use the installation program (TVSETUPxxxx.EXE) to install *Turboveg for Windows* on the server. Then make a shortcut to *Turboveg* on each working station where the program will be used. The program TVWIN32.EXE is by default present in the directory <network drive>:\TURBOWIN\BIN\.
Activate the property window of the Turboveg shortcut and make sure that the working directory is not the same as the program package-containing directory. You can set the working directory under "Properties"->"Shortcut"->"Start in"
TVWIN32.EXE can be executed with a parameter, e.g. 'C:\TURBOWIN'. In this case Turboveg will be forced to store its initialisation file – TVWIN.INI – in the directory C:\TURBOWIN. If Turboveg is executed without a parameter the Windows directory will be used to store the initialisation file.

After the installation the following directory structure **can** be build on the server (the set-up program copies all the files on to one drive, and one directory).

	all	manager	remarks
F:\TURBOWIN\BIN	RO	RO	
\HELP	RO	RO	
\IDENTIFY	RO	RO	
\MAPS	RO	RO	
G:\TURBOWIN\USERS	RW	RW	(incidentally used to administrate a new

```
user)

H:\TURBOWIN\POPUP     RO       RW

I:\TURBOWIN\SPECIES   RO       RW (incidentally used to change the
properties
                                   of the ecological database)
J:\TURBOWIN\DATA      RW       RW (this directory holds the common
databases)


RO=ReadOnly  RW=ReadWrite (including Create rights)
```

The subdirectories HELP, IDENTIFY, and MAPS are linked to the subdirectory \BIN (containing executables) and can therefore NOT be located on another disk or subdirectory.

If desired, all other subdirectories that are not directly linked to the subdirectory \BIN can be moved to other disks.

In addition, on every working station the following directory structure can be build:

```
C:\TURBOWIN\DATA         (the directory that holds the private databases)
           \OLD_SELS
```

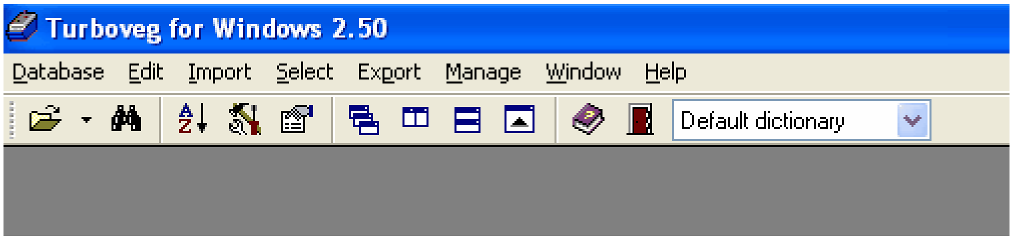
Start *Turboveg* on the desired working station. The first time Turboveg is executed directories have to be defined. In most cases the default directories can be accepted.

2.3 Usage of keyboard, mouse and toolbars

Menus and buttons on the dialogue windows can, in most cases, be activated by both the mouse and the keys.
You can activate the main menu by pressing *Alt*+ one of the underlined characters (e.g. *Alt+ D* activates the menu **Database**). Within a menu you can choose an option by pressing the underlined character (e.g. clicking R selects the sub-menu **Rename**).

In a dialogue window you can activate the desired button by pressing *Alt* + the underlined character present in the text on this button.

Often used functions can also be activated by using the buttons on the toolbars. The toolbars to the more common functions is presented below.



2.4 User management

User management only concerns the **network version.**
The following table shows an overview of the functions in *Turboveg for Windows* and the privileges of the **manager** and **users** (4 types).

	Manager	Users			
		I	II	III	IV
Edit a common database	X	X	X*		
Edit a private database	X	X	X	X	X
Search and replace in a common database	X	X	X*		
Search and replace in a private database	X	X	X	X	X
Import data in a common database	X	X	X*		
Import data in a private database	X	X	X	X	X
Add indicator values to a common database	X	X	X*		
Add indicator values to a private database	X	X	X	X	X
Edit popup lists	X				
Configure the ecological database	X				
Select relevés	X	X	X	X	X
Export relevés from a common database	X	X	X	X	
Export relevés from a private database	X	X	X	X	X
Change privileges users	X				
Create a common database	X				
Create a private database	X	X	X	X	X
Rename a common database	X				
Rename a private database	X	X	X	X	X
Delete a common database	X				
Delete a private database	X	X	X	X	X
Modify structure of a common database	X				

Modify structure of a private database	X	X	X	X	X
Renumber a common database	X				
Renumber a private database	X	X	X	X	X
Organise header data	X	X	X	X	X
Re-index a common database	X				
Re-index a private database	X	X	X	X	X
Change attributes of a common database	X				
Change attributes of a private database	X	X	X	X	X
Backup a common database	X	X	X		
Backup a private database	X	X	X	X	X
Restore a common database	X				
Restore a private database	X	X	X	X	X
Edit a protected species list	Partly				
Edit a non-protected species list	X				

Privileges of users of common databases:
I: Edit and export permission for all databases
II: Edit permission for some databases, export permission for all databases
III: No edit permission, export permission for all databases
IV: Neither edit nor export permission for all databases

* Edit permission for only some, manager-defined databases

2.5 Database structure

A database is build up by three tables and three index files.

Tables	**Index files**	
TVHABITA.DBF	TVHABITA.CDX	(table with header data)
TVABUND.DBF	TVABUND.CDX	(table with species data)
REMARKS.DBF	REMARKS.CDX	(table with remarks)

The default structure of the tables is as follows.

- **TVHABITA.DBF**

```
Field name
¦          Type
¦            ¦    Width
```

```
¦            ¦    ¦  Decimals
¦            ¦    ¦  ¦    Description

RELEVE_NR    N    6  0    Relevé number (= system number)
COUNTRY      C    2  0    Country code
REFERENCE    C    6  0    Publication reference number
TABLE_NR     C    6  0    Number of table in publication
NR_IN_TAB    C    3  0    Relevé number in table
COVERSCALE   C    2  0    Cover scale
PROJECT      C    3  0    Project code
AUTHOR       C    4  0    Author code
DATE         C    8  0    Date (year/month/day)
SYNTAXON     C    7  0    Syntaxon code
SURF_AREA    N    7  2    Surface area (m²)
UTM          C   15  0    UTM grid reference
ALTITUDE     C    4  0    Altitude (m)
EXPOSITION   C    3  0    Aspect (`NWZO')
INCLINATIO   C    2  0    Inclination (degrees)
COV_TOTAL    N    3  0    Total cover (%)
COV_TREES    N    3  0    Cover trees (%)
COV_SHRUBS   N    3  0    Cover shrubs (%)
COV_HERBS    N    3  0    Cover herb layer (%)
COV_MOSSES   N    3  0    Cover mosses (%)
COV_LICHEN   N    3  0    Cover lichens (%)
COV_ALGAE    N    3  0    Cover algae (%)
COV_LITTER   N    3  0    Cover litter (%)
COV_WATER    N    3  0    Cover open water (%)
COV_ROCK     N    3  0    Cover bare rock (%)
TREE_HIGH    N    2  0    Height (high) tree layer (m)
TREE_LOW     N    2  0    Height low tree layer (m)
SHRUB_HIGH   N    4  1    Height (high) shrub layer (m)
SHRUB_LOW    N    4  1    Height low shrub layer (m)
HERB_HIGH    N    3  0    Mean height high herb layer (cm)
HERB_LOW     N    3  0    Mean height low herb layer (cm)
HERB_MAX     N    3  0    Maximum height herb layer (cm)
CRYPT_HIGH   N    3  0    Mean height cryptogame layer (mm)
MOSS_IDENT   C    1  0    Mosses identified (Yes/No)
LICH_IDENT   C    1  0    Lichens identified (Yes/No)
REMARKS      C   56* 0    Remarks
```

*The total length of the remarks field covers a maximum of 1000 bytes. However, the first 56 bytes is stored in the table TVHABITA.DBF, and the remaining bytes are stored in the table REMARKS.DBF.

- **TVABUND.DBF**

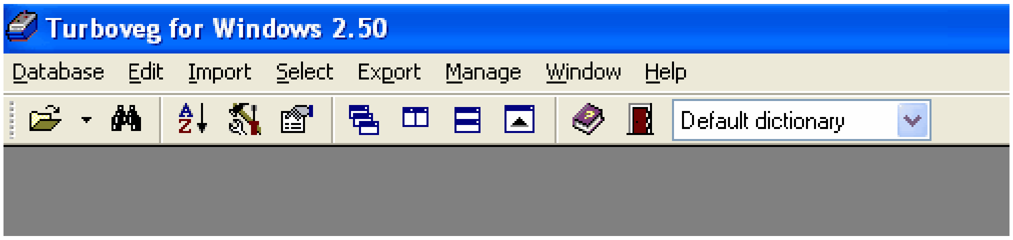
```
RELEVE_NR    N    6  0    Relevé number (= system number)
SPECIES_NR   N    5  0    Species number
COVER_CODE   C    2  0    Cover abundance code
LAYER        N    1  0    Vegetation layer
```

- **REMARKS.DBF**

```
RELEVE_NR     N    6  0    Relevé number (= system number)
REMARKS       C    25 0    Remarks
```

2.6 Popup lists

The *Turboveg* databases are linked to so-called popup lists (lookup tables) with a.o. authors, literature references, cover scales, syntaxa (plant communities), and species. In the databases an author, for example, is stored by its code; the translation to its full name is stored in the lookup table containing authors names.
The table structure of the popup lists (as a matter a fact this counts for all the tables used by Turboveg) is defined in a **database dictionary**. Therefore it is possible to (re)build all the tables from the dictionary.
A Turboveg system can handle multiple dictionaries, each dictionary has its own set of lookup tables.
A dictionary is indicated with a name; the standard dictionary is called 'Default dictionary'. Dictionaries can be preselected by selecting a dictionary name from the drop down menu which is located on the toolbar of the main window.



Also see: **Modify popup lists** 84

2.7 Linking an ecological database

You can link an ecological database to each and every species list. There are a few preconditions concerning format, content, and directory of the database to be stored.

- The format of the database has to be DbaseIII+.
- The name of the database table has to be ECODBASE.DBF, and it must be stored in the same directory that contains the species list. For example for South Africa the species list is by default stored in the directory C:\TURBOWIN\SPECIES\SOUTHAFR.
- It has to contain a field that holds the species numbers, since the species numbers form the link with the species list that is present in Turboveg. If the species numbers are stored in the first column of the database, and the field specifications are:
  - Field name = ”SPECIES_NR”
  - Field type = “N”
  - Field length = 5

- Field decimals = 0
then the management of the list can be done within Turboveg. Otherwise an external management tool that can handle dBaseIII+ formatted files is required

- Do not make fields larger than necessary, and define field type as “C” (character). Compared with a numerical field (field type = “N”) a clear distinction can be made between missing values and ‘0’ in a character field.

An ecological database can also be created and management within Turboveg. Therefore select **Manage | Species lists | Edit | <species list concerned>.** On the dialog window to maintain the species list click the **Create** or **Modify** button.

See also: **Configuring an ecological database** 89

In the ecological database all kind of plant traits can be stored. These can be indicator values (e.g. Ellenbergs indicator values) or morphological, chorological, phytosociological, phenological, and other characteristics.
If you want to make calculations based on the values of a certain item make sure that only numerical values are stored in the database for that particular item.
For example, if you want to know the mean altitude of all species in the relevés than do not store the following values in the database: “0-1000”, “200-2000”, etc. Create two fields instead, one field holding the minimal altitude, and one holding the maximal altitude. As a result two mean values can be calculated, one for minimal altitude, and one for maximum altitude.
Items with which we never can calculate are for example are life-form, phytosociological status, flowering periode, etc.

Using the data from the ecological database, the mean value of an indicator value of each relevé can be calculated (see **Add ecological indicator values** 33). In addition, if exporting a selection to a table you can add for each species one or more parameters from the ecological database (see **Export to a spread sheet table** 72).

2.8 Trouble shooting

- **The relevés do no longer contain species**.
Probably the index file of the species database has been damaged. Solution: Choose **Database**, **Re-index** to remake all indexes belonging to the damaged database.

- **When the indicator values are added it appears that for some relevés no calculations have been made.**
Possible solution: Choose **Database**, **Re-index** to remake all indexes belonging to the damaged database. Then recalculate the indicator values.

- **It is not possible to calculate ecological indicator values per relevé.**
Possibly the ecological database is present but not yet configured. See **Configuring an ecological database** 89

- **The wrong species list is linked to the database.**
  Choose **Database**, **Modify attributes** and select the required database from the list. Select the proper species list and click on **Save attributes** to store the new definition.

Part

III

3 Database

3.1 Open

Menu: **Database | Open**

In the left panel the species list(s) (blue books) and folders (if present) are presented in a tree view.
Select the species list (and folder if present) that holds the database(s) you want to open.

Databases: You can select one or more databases by pressing SPACE or by clicking the mouse. But, if you have selected several databases you can only select relevés. Modifying relevés is only possible when you have selected only one database (see **Selecting relevés** 63).

Open: This is to open the selected databases.

Select all: Select all names that are present in the list **Databases**.

Deselect all: Deselect all names that are present in the list of Databases.

Rescan: Re-scan the hard disk for present databases.

3.2 Close

Menu: **Database | Close**

It is recommended to close a database when you have finished working with it, especially in the case of the network version. If, for instance, user A wants to renumber database Z, he can only do so in case he is the only user of that database (database Z is exclusively opened by him). If user B is using the same database, user A will get a message that the database cannot be exclusively opened for him and that he thus cannot renumber this database.

3.3 New

Menu: **Database | New**

Database name: Enter the name of the new database.

Folder: If desired you can enter or select the name of a folder. Folders are especially useful if you have many databases that must be ordered in a meaningful way.

Species list: Choose a species list to be linked to the database.

Distribution map: Choose a distribution map to be linked to the database. The usage of an internal map is considered obsolete. For mapping it is recommended to use a GIS package.

Range for relevé numbers: Specify the range for the relevé numbers. In a system in which several databases form a combined relevé system it is recommended to give each database a unique range of relevé numbers.
When entering relevés this defined range serves as a check. Numbers located outside the range of the database are not allowed.

Area: Specify whether the database is common or private. Note that only the manager can create common databases.

Structure header database: In case an extension of the structure of the database for header data has been defined in the database dictionary, you can create a so-called extended database for header data.

Structure species database: If an extension of the structure of the species database has been defined in the database dictionary, you can create a so-called extended species database.

See also: **Modify database attributes** 25

3.4 Rename

Menu: **Database | Rename**

Choose the desired database and click on **Rename**. Enter the new name, and if you are working in a network, the desired **Area** to store it.

3.5 Delete

Menu: **Database | Delete**

Choose the desired database and click on **Delete**.

3.6 Renumber

Menu: **Database | Renumber**

Renumbering a database is for example useful when relevés from other sources have to be incorporated into an already existing database system. All relevés, either within a database or among databases, need to have a unique number.

Starting with number: Enter the number of the first relevé in the database.

Save old number in database field: Mark if you want to save the old number. Choose a field in the database for header data in which the old number has to be stored.

Click **OK** to renumber.

3.7 Re-index

Menu: **Database | Re-index**

To re-index a database is only necessary in the case that index files have been corrupted. This can occur when the program is interrupted unwillingly (e.g. due to a disconnection between the working station and server, or a power failure).

3.8 Combine databases

You can combine databases in three different ways.

1. Remove the previous selection (if present) and select (**Select**) the relevés in the source database (you do not have to select all relevés). Export the selected relevés to a *Turboveg* database (**Export | Turboveg database**) and specify the name of the target database.
   Data in fields unique for the source database will **not** be copied to the target database. If these data have to be copied you need to use method 2.
2. Remove the previous selection (if present) and select (**Select**) the relevés that have to be combined; relevés can be selected from several databases. Export the selection to a new *Turboveg* database (**Export | Turboveg database**). When data present in all fields (regardless whether they are unique for a specific database or not) have to be copied you have to choose **Extended** under **Structure header database**.
3. The most convenient option is (**Database | Append another database** 23), which will append another database to an active (open) database.

Please note that the above mentioned options only will work if all the databases that need to be combined are linked to the same species list.
If the databases are linked to different species lists, then a different procedure needs to be followed:
1. Each database needs to be exported to a 'Standard XML file'. See **Export | Export to standard XML** 68 file for details concerning this option.
2. Create a new, and thus empty, database. You may connect this database to any species

list.
3. Import each XML file successively in the database. With the first XML to be imported you must choose which species list will serve a the right taxon base. Instead of choosing an existing list you may also enter a non existing taxon list name. Turboveg will then build up a complete new species list. For more information concerning the import of XML file please see **Import | Import standard Turboveg XML file** 42

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3.9 Append another database

Menu: **Database | Append another database**

This option serves as an easy to use method to extend an opened database with **all** relevés of another database. The additional relevés are automatically renumbered. Fields of the selected database that are not present in the active database (target database) can be copied.

Choose the database you want to append and click on **Append**.

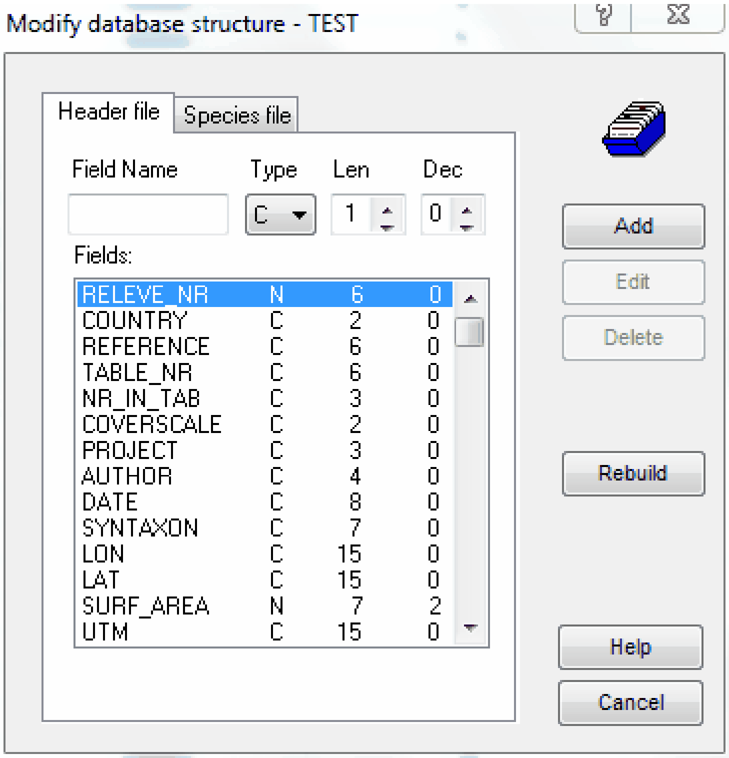
Multi user-version: Only the *manager* has permission to append a database to a common database.

Also see **Combining databases** 22

3.10 Modify database structure

Menu: **Database | Modify structure**

You can add fields to the database to store additional header data (select **Header file**) and additional species data (select **Species file**).



Modify database structure - TEST

Field Name:
Type: C
Len: 1
Dec: 0

Fields:

Field Name	Type	Len	Dec
RELEVE_NR	N	6	0
COUNTRY	C	2	0
REFERENCE	C	6	0
TABLE_NR	C	6	0
NR_IN_TAB	C	3	0
COVERSCALE	C	2	0
PROJECT	C	3	0
AUTHOR	C	4	0
DATE	C	8	0
SYNTAXON	C	7	0
LON	C	15	0
LAT	C	15	0
SURF_AREA	N	7	2
UTM	C	15	0

It can be useful to add fields in case you have systematically collected (environmental) data which do not fit in the standard fields (e.g. soil type, pH, management, and sociability and phenology). By doing so you can also export these extra fields to various formats. An example is the export of the extended header data to Cornell condensed format. When the species data are also exported to Cornell condensed format, you can perform a Canonical Correspondence Analysis using the program CANOCO.

You can delete or change existing fields, on the condition that these do not belong to the standard structure. The standard structure of the database for header data contains all fields up to and including the “remarks“ field; and that for the species data up to and including the “layer“ field.
For the species data table there is a restriction of maximum 15 additional fields, whereas for the header data table there is no such restrictions.

Add a field: Enter the name of the field to be added at **Field Name**. Enter the field type (**Type**), field length (**Len**) and the number of decimals (**Dec**). Add this new information to the existing list by clicking **Add**.
Field type can be “N“ (Numerical) or “C“ (Character).

If the number of decimals is greater than zero, then you have to enlarge the field length by one, viz. the position of the decimal point.

To change a field: Select the field to be changed (**Fields**). Change one or more attributes (field name, field type, field length, and number of decimals) and store the changes with **Replace.**

To delete a field: Select the field to be deleted and click **Delete**.

You store the modifications in the database structure by clicking **Rebuild**.

3.11 Organise header data

Menu: **Database | Organize form header data**

This option enables the definition of both the table and the form containing header data of the database currently open. You can control the number and the order of the items.

Available: List of available items.

Selected: List of selected items.

Add: Add items marked in the list **Available** to the list **Selected**.

Add all: Add all items marked in the list **Available** to the list **Selected**.

Remove: Remover items marked from the list **Selected**.

Remove all: Remove all items marked from the list **Selected**.

3.12 Modify database attributes

Menu: **Database | Modify attributes**

Choose the database in which one or more attributes have to be changed. Only change the **Species list** when the database is empty (no relevés).
Specify the lowest and highest relevé number in **Range of relevés.** Be sure there is no overlap in numbering with other databases. In a stand-alone database you can, for example, set a range from 1 to 999999.
To be able to enter relevés, the minimum and maximum should be higher than 0.

View: A list of all databases and their minimum and maximum relevé number is shown. The databases are sorted according to relevé number.

See: **Create a new database** 20

3.13 Statistics

Menu: **Database | Statistics**

3.14 Hunt duplicates

Menu: **Database | Hunt duplicates**

Duplicates may occur when relevés from various sources (field books, literature, and computerised databases) are imported into *Turboveg* databases. Duplicates can be detected by calculating the floristic similarity between two relevés using the formula: $i = c/(A + B - c)$ (= Jacquard-index), where c is the number of species shared, A the number of species unique to one relevé and B the total number of species of the other relevé. If $i = 0$ there is no floristic similarity between the relevés, if $i = 1$ the relevés are identical.
This formula can be extended in such a way that the cover abundance of the species is also taken into account: $Sr_{ij} = \sum_k y_{ki} y_{kj} / (\sum_k y_{ki} 2 + \sum_k y_{kj} 2 - \sum_k y_{ki} y_{kj})$ (Similarity ratio of Ball).

Compare with…: Select the database to compare with the already opened database. You can also hunt duplicates in the same database.

Restrict comparison: You can speed up the comparison by specifying **Year** and/or **Locality** . Then, only relevés with similar dates and/or locality will be compared.

Calculation: Calculation of the similarity-index can be based on the presence or absence of species (**Qualitative)** or on the cover abundance of the relevés (**Quantitative**).

A matrix is presented where for each relevé compared the four most alike relevés are shown. Double-click on one of the grid cells to see a comparison between two relevés.

Save: The matrix can be written to a file.

3.15 Identification

Menu: **Database | Identification**

The program *ASSOCIA* enables a syntaxonomical identification of relevés using a reference system. Please refer to the manual of *ASSOCIA* for a theoretical background of the calculations.

Synsystematic system: Choose a reference system.

Store results in database: Mark if the results of the analysis (syntaxon codes) have to be stored in a *Turboveg data*base. The information will be stored in separate columns, which will be automatically added to the database.

Save analysis ASSOCIA: Mark if the export files of *Associa* have to be saved.

Configure ASSOCIA: Please refer to the manual of *Associa* for an explanation of the settings. In most cases the default settings will do.

At **Max. number of alternatives (2-10)** you can specify the number of alternatives the program has to present. *Turboveg* will make as many extra columns as specified.

3.16 Backup/Restore

Menu: **Database | Backup/Restore**

This option serves to copy relevé databases, species lists, and popup lists from the hard disk to a diskette and reverse. Choose **Backup** to copy from the hard disk to a diskette or directory and **Restore** to copy from a diskette or directory to the hard disk.
It is possible to backup more than one database or list to a diskette.

- Tab-sheet **Backup**

Backup a…: Select the group from which an item must be selected (relevé database, species list, or popup list)

Backup to: Specify to which device/directory you want to back up the database.

Format: Choose **TvDos** if the database has to be opened with the DOS version of *Turboveg*. If not, choose **TvWin**.

Backup: Execute the backup of the database to a diskette.

- Tab-sheet **Restore**

Restore from: Specify from which device/directory a database has to be restored.

Copy to area: Specify whether the database has to be restored to a private or common area. The manager is the only person authorised to restore databases to the common area.

Scan disk: The names of the *Turboveg* databases present on the device selected will be listed on the screen. You can choose a database from this list.

3.17 Copy from/to

Menu: **Database | Copy from/to**

Part

IV

4 Edit

4.1 Switch edit mode

Menu: **Edit | Switch edit mode**

Switch edit mode allows to switch between editing of header data in forms (Form edit) or by editing directly in the header data table (Table edit).
To switch mode you may also click the yellow region on the status bar at the bottom of header data table.

4.2 Modify header data

Menu: **Edit | Modify header data**

The header data are shown on one or more pages of a form. You can select pages with the mouse or by pressing *Alt* + <*number of the page*> (e.g. *Alt+1*).
Fields, which are marked with a question mark, are supported by a popup list. The popup can be consulted by double-clicking on the question mark **?**.

The cover abundance scale is the only field you are obliged to fill in.

The number of subjects (fields) and their order can be changed and modified in each database.
See: **Modify form header data** 25

Confirm: When you have edited the header data and you want to close this option and/or continue browsing (back or forwards) the program will ask whether the changes must be saved. If you want to continue browsing you can delete the mark to ensure this question will not longer pop-up. The data will then be automatically saved.

Next: Show the header data of the next relevé.

Previous: Show the header data of the previous relevé.

Save: Finish changing the header data and save the changing.

Close: Finish changing the header data but do not save the changing.

4.3 Modify species data

Menu: **Edit | Modify species data**

Choose a species (taxon) from the **Species list** by typing the search code. Then select a **Layer** and enter the cover value and - if applicable - other species attributes. Press **Add** to add the taxon to the list of selected species.

It is strongly recommended to only use the keyboard when entering the species names and the associated attributes. Always press *Enter* to skip from one entry to another.

Modify: You can change a species present in the list **Selected species**. The data of this species will be put again on the form. Pressing **Replace** after a change replaces the old species with the new species in the list of selected species. **Undo** undoes the change. You can also change species in the list **Selected species** by double clicking (or pressing *Enter*) on the desired species.

4.4 Replace species

Menu: **Edit | Replace species**

This options allows to replace to replace one taxon into another. The action is irreversible!

Range of relevés: Enter the range of relevé numbers to be changed.

Species: Specify the value to be replaced at **Old** and the new value at **New**. Species numbers and layer designation can be entered directly, but clicking **>>** will popup the species list.

4.5 Replace all synonyms with accepted names

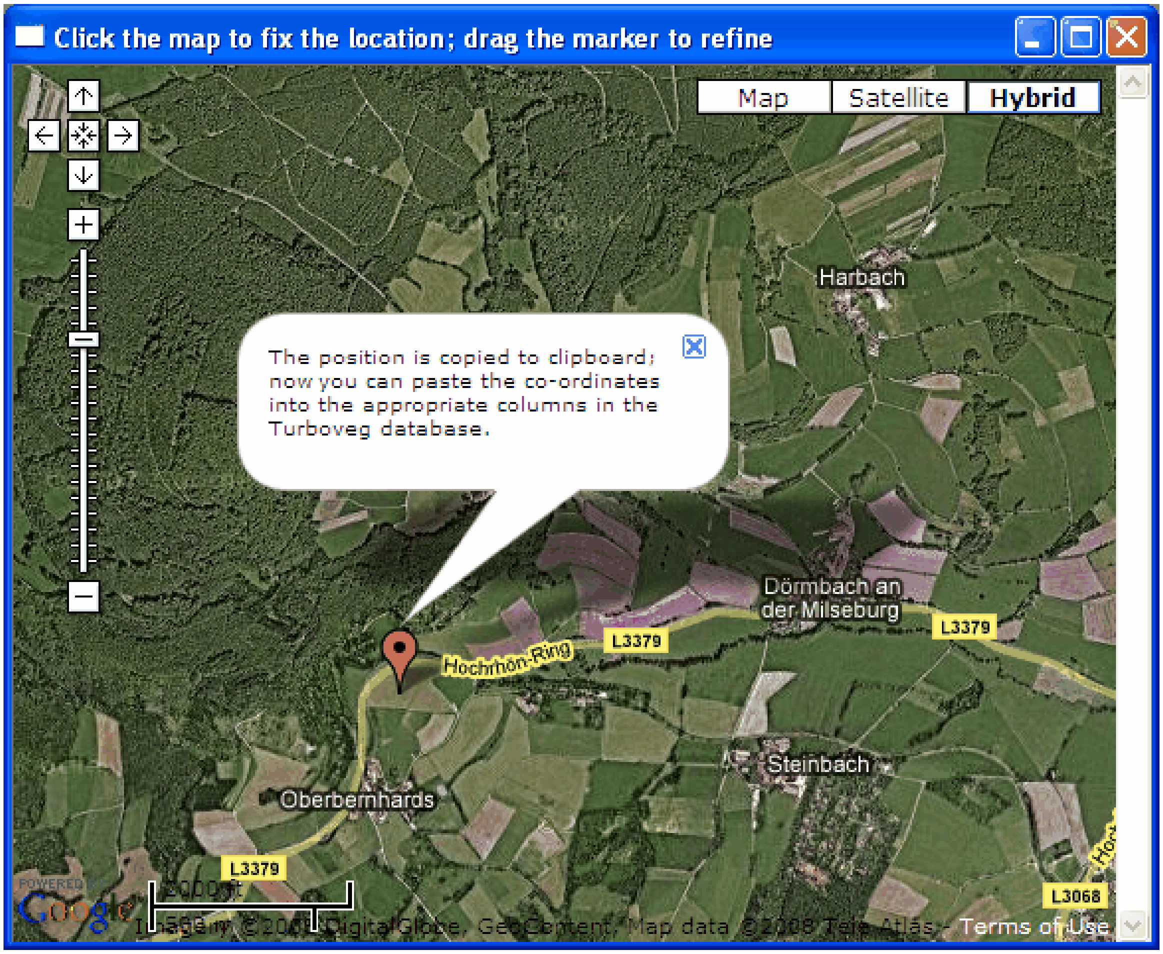
Menu: **Edit | Replace all synonyms with accepted names**

This options allows to convert all taxon synonyms into accepted taxon names. The action is irreversible!

4.6 Geo-referencing using Google Maps

Menu: **Edit | Geo-referencing using Google Maps**

Geo-referencing relevés with a longitude and latitude value is easy with the build-in web browser addressing Google Maps. Use the zoom tool on the left site of the map to zoom in , zoom out and move the map to all sites. You may also use the the mouse wheel to zoom in and out and by holding the left mouse button down the map can be dragged around.

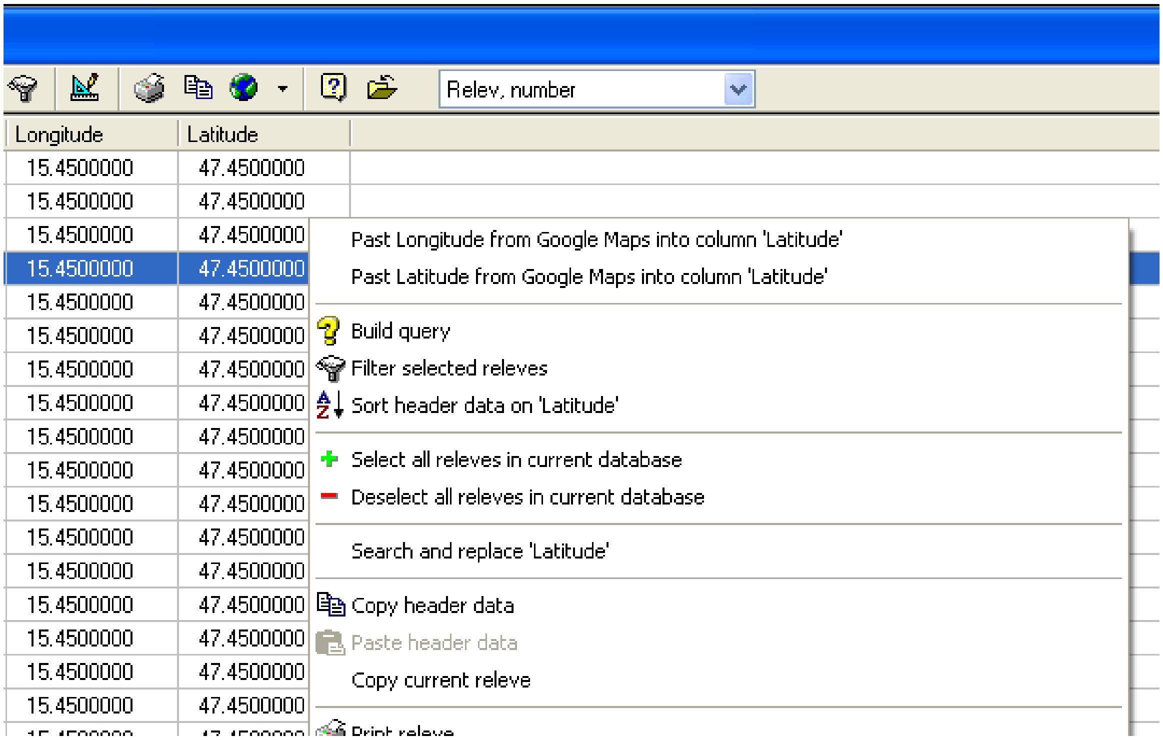


Click the map to fix the location; drag the marker to refine

The position is copied to clipboard; now you can paste the co-ordinates into the appropriate columns in the Turboveg database.

To fix a position just double click with the mouse on the site where the relevé has been recorded. A message box appears telling which further steps have to be taken. The longitude/ latitude-position is copied to clipboard and can then be pasted into the table with header data (it doesn't work on the form presentation). To retrieve the values from the clipboard right click on the header data table and choose the the appropriate option in the context menu.

Make sure that columns for longitude and latitude are available in the header data table. If this is not the case then use the Modify structure 25 option in Turboveg to add these fields. Because Turboveg wants to store the longitude/latitude values as decimal degrees, it is recommended to define both both fields as Numerical, with a width of 12 tokens and 7 decimals



Longitude	Latitude
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000
15.4500000	47.4500000

4.7 Add ecological indicator values

Menu: **Edit | Add indicator values**

This option serves to calculate the mean, standard deviation, median, and number of observations of ecological indicator values (e.g. Ellenberg values for nitrogen, pH, etc.) of each relevé and stores these data in separate columns in the database. If the columns are not yet present, they will be added automatically to the database.

Range of relevés: Specify the range of relevé numbers on which you want to perform the calculations.

Scaling cover values: Specify whether the cover values do (**Ordinal** or **Percentage**) or do not (**Boolean**; only presence or absence of species) has to be taken into account.

Ecological items: Choose one or several items for which the calculations should be done.

Add columns for…: Specify which statistics have to be calculated.

Add: Execute the calculation. The extra columns will be added at the end of the table with header data. The name of the columns consist of three parts, separated by an *under score*: <alias name subject>_<scale>_<calculation> (e.g. ***ph_mea_b*** is: *ph*, *mean* and *boolean*).

See **Configure the ecological database** 89 to define the alias names of the items.

4.8 Add diversity index values

Menu: **Edit | Add diversity index values**

This option servers to calculate diversity index values (Richness, Shannon diversity, Evenness, Simpson's index of diversity) of each relevé and stores these data in separate columns in the database. If the columns are not yet present, they will be added automatically to the database.

Range of relevés: Specify the range of relevé numbers on which you want to perform the calculations.

Add columns for…: Specify which index values have to be calculated.

Add: Execute the calculation. The extra columns will be added at the end of the table with header data.

Calculations

n_i: the abundance of species i
S: the number of species in a relevé (= **Richness-index**)
p_i: the relative abundance of each species (as percentage cover), calculated as the proportion of the total number of species (S)

Shannon-index = $- \mathrm{Sum}(p_i * \mathrm{Ln}(p_i))$
Eveness-index = Shannon-index / Ln(S)
Simpson-index = $- \mathrm{Sum}(p_i^2)$

4.9 Add a relevé

Menu: **Edit | Add a relevé**

When entering single relevés in a database already containing data, you will be asked whether you want to accept the header data of the currently selected relevé.
You will first need to enter the header data, followed by the species data.

4.10 Add a table

Menu: **Edit | Add a table**

Number of relevés in table: Specify the number of relevés you want to add.
If you have a large table (more than 20 to 30 relevés) to process it is recommended to split the table in two or more parts. 20 to 30 relevés will fit on the screen. This does not mean that you have to add the species for each part of the table separately. Add the species in the first table part and mark the option **Restore species list from previous table** when processing the other parts The species list will automatically be copied to the other table parts.

Cover scale: Choose cover abundance scale. The scale chosen will be used for all relevés in the table. It is not possible to use different cover abundance scales in a table.

Restore species list from previous table: Mark this option to use the species list of the previous table. It is possible to delete species from this list.

Sort table according to species names: Mark this option if the species in the table must be sorted alphabetically.

4.11 Delete relevés

Menu: **Edit | Delete relevés**

You must first mark relevés before they can be removed from the database physically. You can mark in three ways:

In the table with header data:
- By double clicking on the first column in the table with header data.

In the dialog Edit | Delete relevés:
- By defining a range of relevé numbers (Define range)
- By defining a list of relevé numbers (Define list)

Press *Enter* or click on **Delete** to remove the relevés physically from the database.

4.12 Replace header data

Menu: **Edit | Replace header data**

Item: Choose the subject (field) in which you want to search and replace.

Range of relevés: Enter the range of relevé numbers to be changed.

Automatic conversion: Check this option if an automatic conversion needs to be taken place (Dutch version only).

Replace with data from other item: Check this option if data data needs to be replaced with data from another column in the database.

Value: Specify the value to be replaced at **Old** and the new value at **New**.

Several exceptions occur at the ‘remarks’ field:
- If **Old** is empty, the contents of **New** will be added to the remarks.
- If **Old** is not empty, the characters written in **Old** will be replaced by the characters written in **New**.
- If “<enter>“ is present in **Old** all hard and soft page breaks in the remarks will be replaced by spaces.
- If “$fieldname“ (e.g. “$pqnr“) is present in **New** the contents of that field will be added to the remarks.

Match: select how the new value matches the old value.
- whole field: replacement takes place if Old value matches value in field
- part of field: replacement takes place if Old value matches value in field, even if Old value is only part of value in field
- exact position in field: replacement takes place if Old value matches value in field from position as indicated in **Old**

For all fields:
- If “*“ is present in **Old** then all values of the selected field will be removed.

4.13 Combine relevés

Menu: **Edit | Combine relevés**

Using this option you can combine different relevés into a new one. Species that occur in more than one relevé are summed up using the following formula:

$$C = A + (100 - A) * B / 100$$

where C = summed cover in percentages, A = cover in percentages of a species in relevé A and B = the cover in percentages of the same species in relevé B. We assume that the species have a random distribution in the plot.
The cover of each species is multiplied with the quotient of the size of the plot in which the species exists divided by total size of all plots.

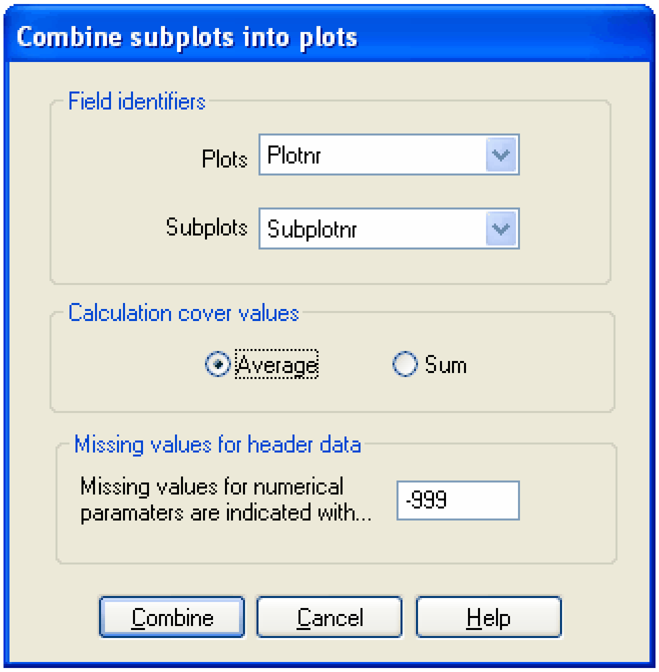
Preserve layer differentiation: indicate whether species that occur in different vegetation layers (strata) should be combined.

For a slightly more sophisticated way of summing up relevés consider using the option **Combine subplots into plots** 37.

4.14 Combine subplots into plots

Menu: **Edit | Combine subplots into plots**

Use this option to combine subplots (or nested plots) in a single plot (relevé). Concerning the species cover two methods can be applied. One is a simply summarization of values (only used when the subplots have been recorded with the so-called Sigg-scale). The other one is the calculation of a mean cover value for each species. It is assumed that each subplot has the same surface area, thus the mean value is simply the summarization of the cover values of a species in the subplots in which it occurs divided by the total number of subplots belonging to a certain plot.
You must indicate which fields holds the identifiers for the plot number and subplot number.
Turboveg will only combine those subplots which have non-empty values for plot no. and subplot no (in case of a numerical field the value must be greater zero).
The cover of the species in the resulting plot will always be in percentages, regardless the cover scale method used in subplots.



Plots: Plotnr

Subplots: Subplotnr

● Average ○ Sum

Missing values for numerical paramaters are indicated with... -999

Concerning the header data Turboveg will only calculate mean values for fields that are defined as numerical (e.g. 'Total cover'). In case a certain value is equal to the defined missing value the value is ignored. For fields that are defined as character (e.g. 'Author') the value of the first subplot is copied into to combined plot.

4.15 Combine vegetation layers

Menu: **Edit | Combine vegetation layers**

With this option for each species vegetation layers can be combined into one layer with the following formula:

$$C = A + (100 - A) * B / 100$$

where C = summed cover in percentages, A = percentages cover in of a species in layer A and B = the percentage cover of the same species in layer B. It is assumed that the species is randomly distributed in the plot.

By careful! As with many other functions in Turboveg this option converts the data irreversible. It is therefore recommended to create a backup first!

4.16 Copy current relevé

Menu: **Edit | Copy current relevé**

With this option you can copy both header data and species data of the current selected relevé into a new relevé.The copy becomes the last relevé in the database.

4.17 Filter selected relevés

Menu: **Edit | Filter selected relevés**

Selected relevés in a database (marked in column two of the table with header data) can be filtered. This can be useful when species or header data of the selected relevés need to be changed or edited. When the filter is active 'search and replace' actions will only take place within the selected relevés (see **Replace header data** 35 and **Replace species** 31)

4.18 Copy relevé to clipboard

Menu: **Edit | Copy relevé to clipboard**

All data from a relevé can be copied to the clipboard.
Using a word processor you can insert the text in a document.
In case an ecological database is linked to the relevé, the ecological indicator values, the means, standard deviation, median, and the number of observations will be added for each species.

Here below you see an example of a relevé that has been copied to the clipboard.

```
=> Relevé number: 7001

Country code                  : 45
Biblioreference               : 000023
Nr. table in publ.            :      2
Nr. relevé in table           :
Cover abundance scale         : Percentage (%)
Author code                   : 0002
Date (year/month/day)         : 1986/08/11
Relevé area (m2)              : 0.00
UTM grid system code          :   - -  -     -
Altitude (m)                  :
Aspect (degrees)              :
Slope (degrees)               :
Cover total (%)               : 0
Cover tree layer (%)          : 0
Cover shrub layer (%)         : 0
Cover herb layer (%)          : 0
Cover moss layer (%)          : 0
Cover lichen layer (%)        : 0
Cover algae layer (%)         : 0
Cover litter layer (%)        : 0
Cover open water (%)          : 0
Cover bare rock (%)           : 0
Height (highest) trees (m)    : 0
Height lowest trees (m)       : 0
Height (highest) shrubs (m)   : 0.0
Height lowest shrubs (m)      : 0.0
Aver. height (high) herbs (cm): 0
Aver. height lowest herbs (cm): 0
Maximum height herbs (cm)     : 0
Maximum height cryptogams (mm): 0
Mosses identified (y/n)       :
Lichens identified (y/n)      :
Litter                        : 0.0

                                                 L     T     K     F     R     N
  S
----------------------------------------------------------------------------------
-----
Alopecurus pratensis                     40      6     x     5     6     6     7
  0
Caltha palustris ssp. palustris          80      7     x     x     9=    x     6
  0
Carex species                            20

Cerastium fontanum ssp. fontanum         20

Glyceria maxima                          99      9     5     x     10    8     9
  0
Mentha aquatica                          20      7     5     3     9=    7     5
  0
Persicaria amphibia                      20      8     6     x     x     x     6
  0
Phalaris arundinacea                     40      7     5     x     8~    7     7
  0
Poa pratensis ssp. pratensis             80
```

```
Taraxacum species                        20

Urtica dioica                            20      x     x     x     6     7     9
  0
Zostera marina                           80      x     6     2     12    7     6
  8
                                             -------------------------------------
-----
Mean indicator value                            7.3   5.4   3.3   8.6   7.0   6.9
 1.0
Standard deviation                              1.0   0.5   1.5   2.1   0.6   1.5
 2.8
Median value                                    7.0   5.0   3.0   9.0   7.0   6.5
 0.0
# of observation (n)                            6.0   5.0   3.0   7.0   6.0   8.0
 8.0
```

4.19 Search a relevé

Menu: **Edit | Search a relevé**

Searching a relevé in a complex database system with several databases and thousands of relevés is no problem when you use the relevé number (= system number), provided that each relevé in the system has a unique number.
When you enter the relevé number (= system number) *Turboveg* will search the number in all available databases. If the number is present, the relevant database will be opened and the selected relevé shown on the screen.

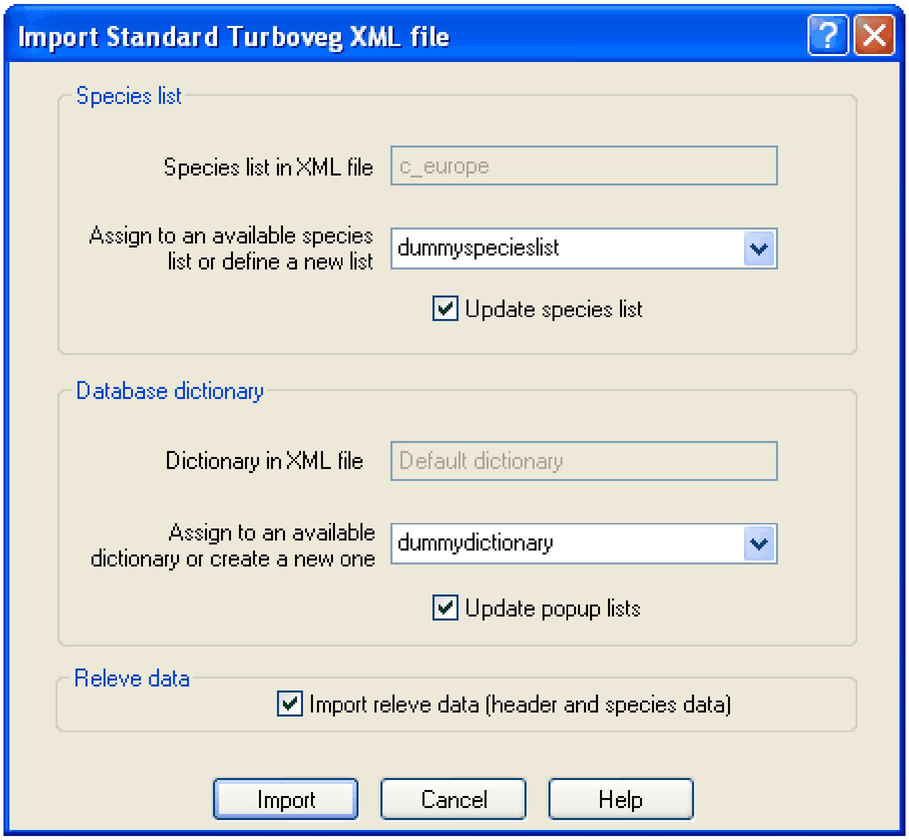
Part V

5 Import

5.1 Import Turboveg XML file

Menu: **Import | Turboveg standard XML file**

The Turboveg standard XML file is an excellent format to exchange data between different Turboveg systems. Importing data in this format enables synchronization of all popup lists (lookup tables), as far as data from the popup lists concerned are included. If for example the file contains taxa from species list A and the receiving database is connected to species list B, then species list B can be extended with taxa from species list A that are new for species list B. The same counts for all other popup lists. It is clear that the synchronization should be handled with care, otherwise the popup lists may end up in a mess.
If you are not familiar with this import function it is recommended to first experiment a little bit and to import a standard XML file using dummy names for the species list and the dictionary. It is also recommended to always import the standard XML file into an empty database.
In the screen shot below the taxa are derived from the species list 'C_Europe' but redirected to a species list called 'dummyspecieslist'. If this list does not exist than it will created and filled with the species present in the XML file. The same counts for the popup lists as defined in the database dictionary. In those cases do not forget to check the options **Update species list** and **Update popup lists**.



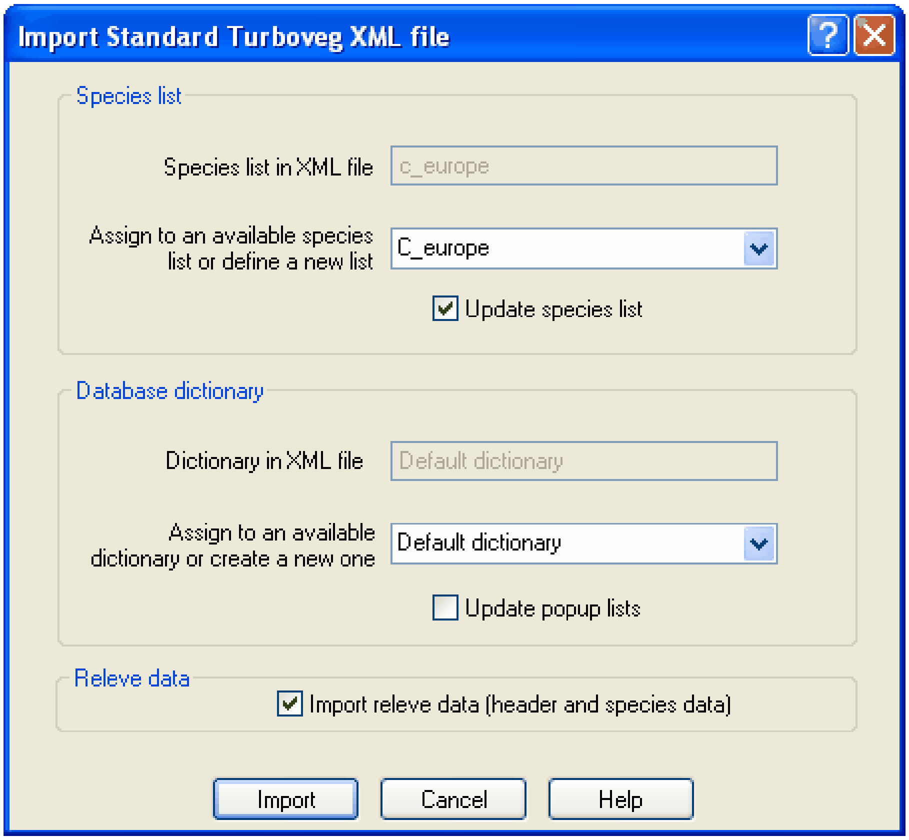
Species list in XML file: c_europe
Assign to an available species list or define a new list: dummyspecieslist
☑ Update species list

Dictionary in XML file: Default dictionary
Assign to an available dictionary or create a new one: dummydictionary
☑ Update popup lists

☑ Import releve data (header and species data)

Dummy species lists and dictionaries can easily be removed. See **Delete a species list** 88 and **Delete a dictionary** 84.

If you have become more familiar with this import function than you can start importing species into existing species lists.



Import Standard Turboveg XML file

Species list

Species list in XML file: c_europe

Assign to an available species list or define a new list: C_europe

☑ Update species list

Database dictionary

Dictionary in XML file: Default dictionary

Assign to an available dictionary or create a new one: Default dictionary

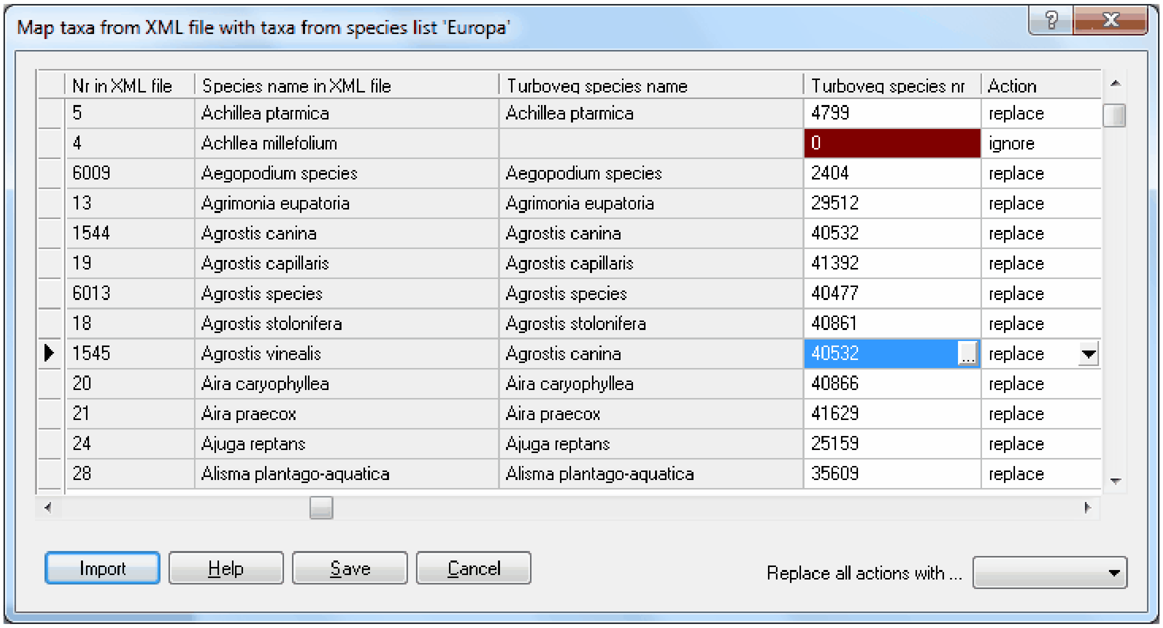
☐ Update popup lists

Releve data

☑ Import releve data (header and species data)

Even when the **Update species list** option is checked there is no danger that the species list can get messed up, because there is an extra step in the import procedure to be taken. An additional dialog window will open up showing all taxa - mapped or not mapped - occurring in the XML file.
Three actions can be undertaken:

1. A taxon from the XML file can be **replaced** with a taxon from the Turboveg species list. Therefore click the ... icon to popup the species lookup table.
2. A taxon from the XML file can be **ignored**
3. A taxon from the XML file can be marked as **new**. In that case Turboveg will add this name as a new taxon to the list if you have explicitly allowed Turboveg to add new species in the first dialog window.



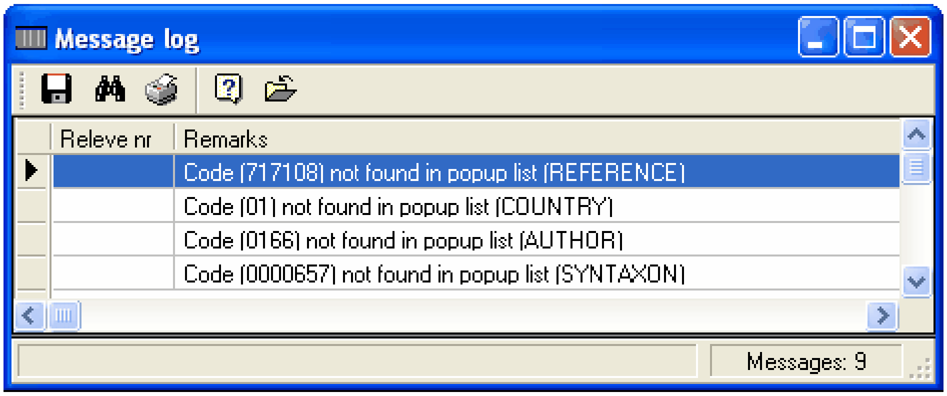
Map taxa from XML file with taxa from species list 'Europa'

Nr in XML file	Species name in XML file	Turboveg species name	Turboveg species nr	Action
5	Achillea ptarmica	Achillea ptarmica	4799	replace
4	Achllea millefolium		0	ignore
6009	Aegopodium species	Aegopodium species	2404	replace
13	Agrimonia eupatoria	Agrimonia eupatoria	29512	replace
1544	Agrostis canina	Agrostis canina	40532	replace
19	Agrostis capillaris	Agrostis capillaris	41392	replace
6013	Agrostis species	Agrostis species	40477	replace
18	Agrostis stolonifera	Agrostis stolonifera	40861	replace
1545	Agrostis vinealis	Agrostis canina	40532	replace
20	Aira caryophyllea	Aira caryophyllea	40866	replace
21	Aira praecox	Aira praecox	41629	replace
24	Ajuga reptans	Ajuga reptans	25159	replace
28	Alisma plantago-aquatica	Alisma plantago-aquatica	35609	replace

Replace all actions with ...

Import: Continue importing the data. All species that are not mapped to a Turboveg species number will be ignored.
Save: Save the mapping to an Excel file.
Cancel: Cancel the whole import procedure

Unfortunately a mapping facility as described here is not (yet) available for all other lookup tables (authors, projects, syntaxa, etc.). Therefore you should handle the option **Update popup lists** with care. In any case Turboveg will list all the non-mappable values in the **Message log** window. Using this list you can modify the popup lists yourself, and deciding whether or not to add certain values to the popup lists.



Message log

Releve nr	Remarks
	Code [717108] not found in popup list [REFERENCE]
	Code [01] not found in popup list [COUNTRY]
	Code [0166] not found in popup list [AUTHOR]
	Code [0000657] not found in popup list [SYNTAXON]

Messages: 9

Also see: [Export to Standard XML file](68) 68

5.2 Import TurbovegCE XML file

Menu: **Import | TurbovegCE XML file**

5.3 Import Cornell condensed species file

Menu: **Import | Cornell condensed species file**

You can import computerised vegetation tables in Cornell condensed format (input format for e.g. TWINSPAN, CANOCO) to a database. When doing so, **only** the species, cover values, and original relevé numbers will be read in. All other header data, with the exception of the cover scale, need to be entered manually (see example below).

After the Cornell condensed file has been read the following must be checked en choices must be made.

- Check the species code translation.
- Choose the cover scale (how to store the numerical cover values as cover codes in the database) and check the transformation.
- Choose a database field in which the relevé identifiers (e.g. relevé numbers) must be stored.

The species codes that are translated ‘by hand’ will be stored in a so-called shadow list. With each session this list will be used to translate species codes that are not in the *Turboveg* species list. The shadow list is called **ccshadow.dbf** and by default stored in the directory **..\TURBOWIN\DATA**.

Species: In the first column of the table de species codes are stored which are extracted from the Cornell file. The second, third, and fourth column holds respectively the species name, the species code, and the vegetation layer. Codes that are could not be translated by *Turboveg* are presented in blue colour. Double click or press *Enter* to popup the species list for selecting the desired species.

Assign all species with layer code ‘0’ to…: All species without an indication for a vegetation layer can be assigned automatically here.

Species list: Click this button to popup the species list.

Export: Click to export list of translated species to a file.

Merge: Shadow lists from different sources can be combined. Useful if you are working in a team, and want to profit from other ones labour (importing Cornell files).

Cover values: The first column holds the numerical values found in the Cornell file. The second column is the corresponding code according to the chosen scale. Double click or press *Enter* to modify the code.

Store cover values in field…: Cover values are by default stored in the field “Cover abundance”. There are however more possibilities to save the species attributes if the species table is extended with extra fields (see **Modify database structure** 23).

Translate values using cover scale…: Choose the scale according to which the values must be translated.

Store original relevés identifiers in…: You can store the original relevé identifiers (in most cases these are numebers) in a field in the table with header data. This is by default the **remarks** field.
However, it is recommended to store the relevé numbers in a separate field. When such a field is not yet present, you have to add it first. See **Modify database structure** 23

Click **Import** to load the data into the database.

An example:

```
Selection: 15 releves                                                  T
(I5,5(I5,F8.1))                                                       5
    1    1     3.0    2     8.0    3     8.0
    2    2     2.0    4     8.0    5    18.0    6     8.0    7     2.0
    2    8     2.0    9     2.0   10    38.0   11     8.0   12    38.0
    2   13     3.0   14     2.0
    3    1     2.0    2     2.0    5     8.0    6     8.0    7    18.0
    3    8     4.0    9     8.0   10    18.0   11     8.0   12    38.0
    3   15    68.0   16     3.0   17     3.0   18     3.0   19     2.0
    3   20     8.0
    4    2     8.0    3    18.0   21     4.0
    5    1     2.0    2     8.0    9     1.0   16     2.0
    6    1     3.0    9     2.0   10     8.0   11     8.0   16     3.0
    6   20    38.0
    7    1     3.0    2     2.0    7     3.0    9     2.0   10    38.0
    7   11     4.0   15     2.0   16     8.0   19     2.0   20     8.0
    7   21     8.0   22     2.0   23     2.0   24     2.0   25     2.0
    8   26    38.0
    9    8     1.0   26    18.0   27    18.0   28     2.0
   10    7     8.0   10     2.0   14     3.0   16     2.0   24     3.0
   10   26     4.0   27     1.0   28     2.0   29     2.0   30     4.0
   10   31     8.0   32     2.0   33     2.0
   11    1     8.0    5     2.0   11    18.0   13     2.0   14     4.0
   11   28     2.0   32     8.0
   12   24    68.0   29     2.0   34     3.0
   13   27    38.0
   14   35     3.0   36    68.0   37     8.0
   15   35     2.0   36    18.0   37    68.0
0000
GAZAR;U6LIMISCA6PLAAC;C6ACACCYC7ANTSLIT6CARBDEL6CHRSM-R7CYNANAT6PASSRIG7PHYILIT6
PSORREP6RHOCDIG6SILEPRI6ZALUMAR6EUGECAP7FICILAT6HELHTER6METAMUI7PENCHEP6SYNCSOR6
DELOECK6ASPRRAC6SENELIT6SPORVIR6STEASEC6EHRHV;M6ARCOPOP6DASISUF6GLADGUE6HELHPRA6
MARI/SP6SENEELE6STOEPLU7THINDIS6DISHCRA6SAROPER6SAROPIL6
   50097   50098   50099   50100   50101   50102   50103   50104   50105   50106
```

```
    50107    50108    50109    50110    50111
```

5.4 Import Excel table

For importing an Excel table with species **and** header data the following steps should be taken in Excel:

1. Copy or cut the header data
2. Create or select an empty sheet
3. In the Edit menu select **Past special**
4. Select **Transpose** and click Ok
5. In Turboveg select the option 'Import free format species data' and select the sheet the holds the species data. For next steps click here 48.
6. For importing the header data select the option 'Import free format header data table' and select the sheet with header data.For next steps click here 52.

Excel table with header and species data

Table number		1	2	3	4	5	6	7	8	9	10
Releve number		101787	101788	101789	101790	101791	101792	101793	101794	101795	101796
Country code		CZ	CZ	CZ	CZ	CZ	CZ	CZ	CZ	CZ	CZ
Biblioreference		401824	401824	401824	401824	401824	401824	401824	401824	401824	401824
Year		1998	1998	1998	1998	1998	1998	1998	1998	1998	1998
Author code		0122	0122	0122	0122	0122	0122	0122	0122	0122	0122
Syntaxon code		35AC	35AC	35AC	35AC	35AC	35AC	35AC	35AC	35AC	35AC
RelevΘ area (m2)		104.00	173.00	334.00	259.00	98.00	158.00	143.00	69.00	196.00	79.00
Altitude (m)		1350	1350	1350	1350	1350	1350	1350	1350	1350	1350
Aspect (degrees)		135	135	135	135	135	135	135	135	135	135
Slope (degrees)		5	10	10	10	10	10	10	10	10	10
Cover total (%)		97	97	97	97	98	98	98	98	98	98
Cover tree layer (%)		0	0	20	0	0	0	0	0	0	0
Cover shrub layer (%)		95	93	90	89	90	90	90	97	95	90
Cover herb layer (%)		97	80	80	78	40	75	80	70	80	75
Anthoxanthum odoratum	hl	1	.	.	.	.	.	+	.	+	+
Avenella flexuosa	hl	3	2	2	2	2	2	3	2	3	3
Galium saxatile	hl	1	.	+	+	.	+	+	.	.	+
Homogyne alpina	hl	1	+	1	+	+	2	2	1	1	1
Molinia caerulea	hl	+	.	.	.	.	+	+	.	+	+
Pinus mugo	s1	5	5	5	5	5	5	5	5	5	5
Trientalis europaea	hl	1	+	1	+	+	1	+	+	1	+
Calamagrostis villosa	hl	.	1	2	+	1	.	.	.	.	.
Silene dioica	hl	.	+	.	.	.	.	1	.	.	.
Vaccinium myrtillus	hl	.	1	2	1	1	1	2	1	2	3
Picea abies	t1	.	.	+	.	.	.	.	.	.	.
Sorbus aucuparia ssp. glabrata	s1	.	.	.	.	.	+	+	.	.	.
Vaccinium vitis-idaea	hl	.	.	.	.	.	+	.	.	.	.

Athyrium distentifolium	hl	.	.	.	.	.	.	+	.	+	+

Header data separated (copy or cut) from the species data, transposed and pasted into another sheet

Table number	Releve number	Country code	Biblioreference	Year	Author code	Syntaxon code	Releve area (m2)	Altitude (m)	Aspect (degrees)	Slope (degrees)	Cover total (%)	Cover tree layer (%)	Cover shrub layer (%)	Cover herb layer (%)
1	101787	CZ	401824	1998	0122	35AC	104.00	1350	135	5	97	0	95	97
2	101788	CZ	401824	1998	0122	35AC	173.00	1350	135	10	97	0	93	80
3	101789	CZ	401824	1998	0122	35AC	334.00	1350	135	10	97	20	90	80
4	101790	CZ	401824	1998	0122	35AC	259.00	1350	135	10	97	0	89	78
5	101791	CZ	401824	1998	0122	35AC	98.00	1350	135	10	98	0	90	40
6	101792	CZ	401824	1998	0122	35AC	158.00	1350	135	10	98	0	90	75
7	101793	CZ	401824	1998	0122	35AC	143.00	1350	135	10	98	0	90	80
8	101794	CZ	401824	1998	0122	35AC	69.00	1350	135	10	98	0	97	70
9	101795	CZ	401824	1998	0122	35AC	196.00	1350	135	10	98	0	95	80
10	101796	CZ	401824	1998	0122	35AC	79.00	1350	135	10	98	0	90	75

5.5 Import free format species data table

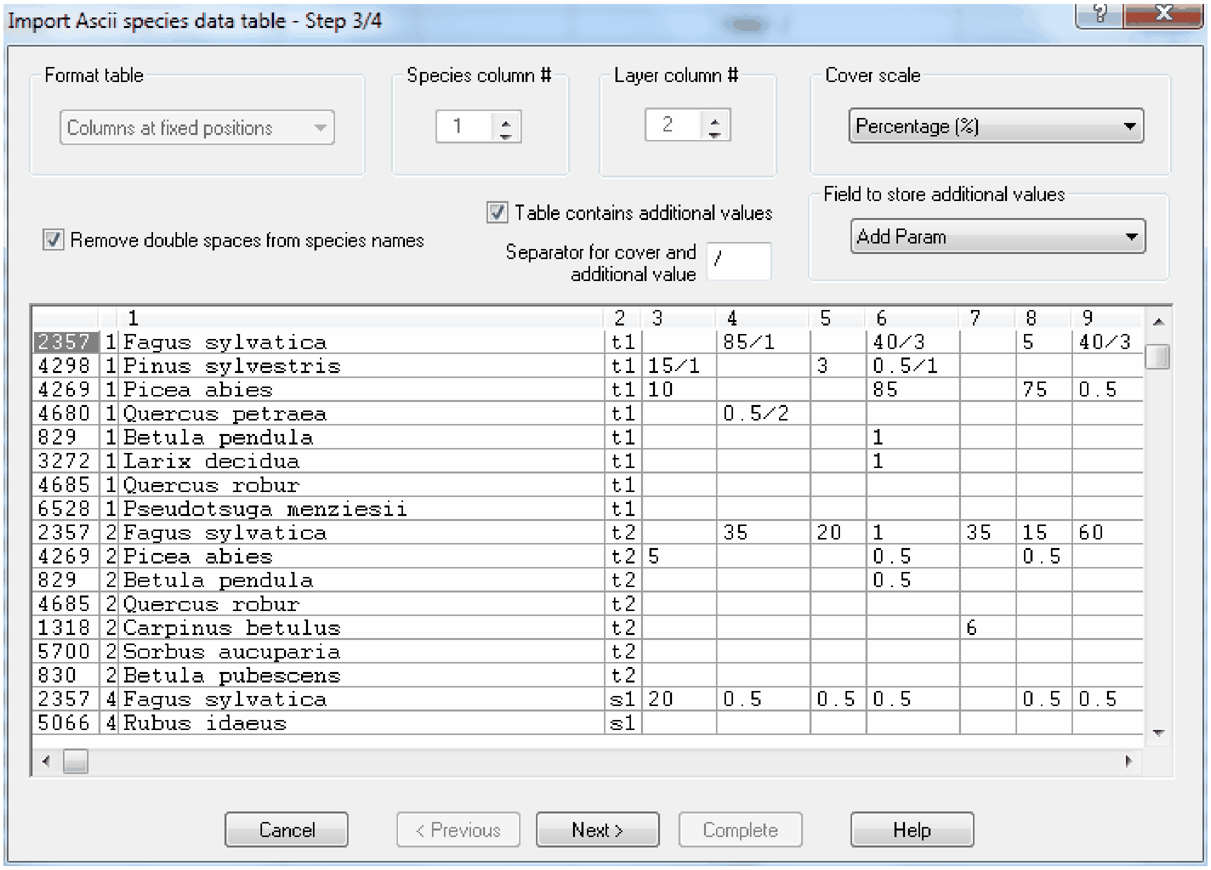
Menu: **Import | Free format species data table**

By using a *wizard* you can import a table containing species data into a database in four steps.
Input formats permitted are: SDF (fixed column width), comma delimited, tab delimited, semicolon delimited, space delimited, dBaseIII+, and MS Excel (up to version 2007).
See the two examples below. Please note that delimited formatted tables, dBaseIII+ files, and especially Excel sheets are much easier to import than SDF formatted tables. Also note that all the data of one relevé are organized in one column.

If you planning to import a corresponding file with header data than you must import the species data table first **followed** by the import of the header data table.

It's recommended to import the species data table into an empty database. Please note that relevés numbers are **not** taken from the table but are created **automatically**.

If you want to import a table (e.g. Excel) with header and species data, then you should separate the header from the species part and perform two imports, one on the header data and one on the species data. An example how to do this is explained here 47.



Import Ascii species data table - Step 3/4

Format table: Columns at fixed positions

Species column #: 1

Layer column #: 2

Cover scale: Percentage (%)

Field to store additional values: Add Param

☑ Table contains additional values

☑ Remove double spaces from species names

Separator for cover and additional value: /

		1	2	3	4	5	6	7	8	9
2357	1	Fagus sylvatica	t1		85/1		40/3		5	40/3
4298	1	Pinus sylvestris	t1	15/1		3	0.5/1			
4269	1	Picea abies	t1	10			85		75	0.5
4680	1	Quercus petraea	t1		0.5/2					
829	1	Betula pendula	t1				1			
3272	1	Larix decidua	t1				1			
4685	1	Quercus robur	t1							
6528	1	Pseudotsuga menziesii	t1							
2357	2	Fagus sylvatica	t2		35	20	1	35	15	60
4269	2	Picea abies	t2	5			0.5		0.5	
829	2	Betula pendula	t2				0.5			
4685	2	Quercus robur	t2							
1318	2	Carpinus betulus	t2					6		
5700	2	Sorbus aucuparia	t2							
830	2	Betula pubescens	t2							
2357	4	Fagus sylvatica	s1	20	0.5	0.5	0.5		0.5	0.5
5066	4	Rubus idaeus	s1							

Before taking step 1 confirm whether each cell in the table does or does not only contains species cover values, but also additional values. If that is the case then check the option **Table contains additional values.** If additional value are taken into account then also indicate which seperator (the dot ('.') is taken als default) has been used to distinguish between cover value and additional value. Also select a database field in which the additional value need to b stored. If such a field is not available then first go to **Modify database structure** 23 and add an extra species parameter.
A typical example is a combination of cover value and sociability value, both separated by a dot. However, in the example shown above species are represented by percentage values in which the dot is used to indicate decimals and the slash ('/') to separate cover percentage values from additional values.

Step 1: If the columns in the table are separated with a delimiter, e.g. a comma, a tab, or a semicolon, you first have to choose the right format with **Format table**. After having selected the right delimiter the table will be reformatted automatically.
If the format of the table is “Columns at fixed positions“ then you have to mark each new column. You can do this by clicking the grey cell on top of the table, or by placing the blue box on the desired column with the arrow keys and subsequently pressing the *Space bar*. Click the **Next** button when all columns have been marked. The table will then be reformatted

automatically.

Step 2: Species column # indicates in which column the species are listed. The numbers are present at the top of the columns. Select the correct number and click the **Next** button. *Turboveg for Windows* will try to translate the species names found in the indicated column into species numbers.
If the table also contains values for sociability then the option **Table contains sociability values should be switch on**. If these values need to be stored in the database then the appropriate field in the database should be selected from the drop down menu (**Field to store sociability values**). Make sure that such a field is available at the time that the import is in process. Turboveg currently only distinguishes sociability values if they are separated from cover values with a dot (e.g. 2a.3).

Step 3: Species *Turboveg* could not translate are presented in blue color. Select these species one by one, and double-click or press *Enter* to search the species number. A dialogue box with the *Turboveg* species list appears. Choose the desired species and if required also the layer and confirm with *Enter*.
The species numbers are listed in the first column of the table, the vegetation layer in the second column.

Mark the columns which holds the relevés and need to be imported in the same way as is mentioned in step 1.

Next specify the cover abundance scale (**Cover scale**). The scale selected may differ from the one used for the original data, giving the opportunity to switch from one scale to another (which can result in loosing information on the cover abundance of the species).

Press **Next.** *Turboveg for Windows* checks if the cover values are in congruence with the cover abundance scale. For each cover value found in the input file Turboveg gives the possibility to select a cover value from a list. Select the desired value and click the **Replace all** button. Empty (missing) values in the input file are represented by a dot ('.') and are also presented by Turboveg as a cover value candidate. In this case click the **Ignore all** button.

Step 4: Press **Complete** to read the species table into the database.

An example of a table in SDF format:

```
Table number                       1 2 3 4 5 6 7 89 101112131415

Gazania rigens v. uniflora-hl      1 . + . + 1 1 .. . 2a. . . .
Plantago crassifolia v. crassifoli 2a. . 2b. . . . .. . . . . . .
Acacia cyclops-jl                  . 2a. . . . . .. . . . . . .
Anthospermum littoreum-hl          . 2b2a. . . . .. . + . . . .
Carpobrotus deliciosus-hl          . 2a2a. . . . .. . . . . . .
Chrysanthemoides monilifera s. rot . + 2b. . . 1 .. 2a. . . . .
Cynanchum natalitium-hl            . + 2m. . . . .r . . . . . .
Passerina rigida-jl                . + 2a. r + + .. . . . . . .
Phylica litoralis-hl               . 3 2b. . 2a3 .. + . . . . .
Psoralea repens-hl                 . 2a2a. . 2a2m.. . 2b. . . .
Rhoicissus digitata-hl             . 3 3 . . . . .. . . . . . .
```

```
Silene primuliflora v. primuliflor . 1 . . . . . .. . + . . . .
Zaluzianskya maritima-hl           . + . . . . . .. 1 2m. . . .
Eugenia capensis-jl                . . 4 . . . + .. . . . . . .
Ficinia lateralis-hl               . . 1 . + 1 2a.. + . . . . .
Helichrysum teretifolium-hl        . . 1 . . . . .. . . . . . .
Metalasia muricata-jl              . . 1 . . . . .. . . . . . .
Pentaschistis heptamera-hl         . . + . . . + .. . . . . . .
Syncarpha sordescens-hl            . . 2a. . 3 2a.. . . . . . .
Asparagus racemosus-hl             . . . . . . + .. . . . . . .
Senecio litorosus-hl               . . . . . . + .. . . . . . .
Sporobolus virginicus-hl           . . . . . . + .. 1 . 4 . . .
Stenotaphrum secundatum-hl         . . . . . . + .. . . . . . .
Ehrharta villosa v. maxima-hl      . . . . . . . 32b2m. . . . .
Arctotheca populifolia-hl          . . . . . . . .2br . . 3 . .
Dasispermum suffruticosum-hl       . . . . . . . .+ + + . . . .
Gladiolus gueinzii-hl              . . . . . . . .. + . + . . .
Helichrysum praecinctum-hl         . . . . . . . .. 2m. . . . .
Senecio elegans-hl                 . . . . . . . .. + 2a. . . .
Stoebe plumosa-jl                  . . . . . . . .. + . . . . .
Thinopyrum distichum-hl            . . . . . . . .. . . 1 . . .
Disphyma crassifolium-hl           . . . . . . . .. . . . . 1 +
```

An example of a table in comma delimited format:

```
Table number,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,
,,,,,,,,,,,,,,,,,
Gazania rigens v. uniflora-hl ,1,.,+,.,+,1,1,.,.,.,2a,.,.,.,.,
Plantago crassifolia v. crassifolia-hl ,2a,.,.,2b,.,.,.,.,.,.,.,.,.,.,.,
Acacia cyclops-jl ,.,2a,.,.,.,.,.,.,.,.,.,.,.,.,.,
Anthospermum littoreum-hl ,.,2b,2a,.,.,.,.,.,.,.,+,.,.,.,.,
Carpobrotus deliciosus-hl ,.,2a,2a,.,.,.,.,.,.,.,.,.,.,.,.,
Chrysanthemoides monilifera s. rotundata,.,+,2b,.,.,.,1,.,.,2a,.,.,.,.,.,
Cynanchum natalitium-hl ,.,+,2m,.,.,.,.,.,r,.,.,.,.,.,.,
Passerina rigida-jl ,.,+,2a,.,r,+,+,.,.,.,.,.,.,.,.,
Phylica litoralis-hl ,.,3,2b,.,.,2a,3,.,.,+,.,.,.,.,.,
Psoralea repens-hl ,.,2a,2a,.,.,2a,2m,.,.,.,2b,.,.,.,.,
Rhoicissus digitata-hl ,.,3,3,.,.,.,.,.,.,.,.,.,.,.,.,
Silene primuliflora v. primuliflora-hl ,.,1,.,.,.,.,.,.,.,.,+,.,.,.,.,
Zaluzianskya maritima-hl ,.,+,.,.,.,.,.,.,.,1,2m,.,.,.,.,
Eugenia capensis-jl ,.,.,4,.,.,.,+,.,.,.,.,.,.,.,.,
Ficinia lateralis-hl ,.,.,1,.,+,1,2a,.,.,+,.,.,.,.,.,
Helichrysum teretifolium-hl ,.,.,1,.,.,.,.,.,.,.,.,.,.,.,.,
Metalasia muricata-jl ,.,.,1,.,.,.,.,.,.,.,.,.,.,.,.,
Pentaschistis heptamera-hl ,.,.,+,.,.,.,+,.,.,.,.,.,.,.,.,
Syncarpha sordescens-hl ,.,.,2a,.,.,3,2a,.,.,.,.,.,.,.,.,
Asparagus racemosus-hl ,.,.,.,.,.,.,+,.,.,.,.,.,.,.,.,
Senecio litorosus-hl ,.,.,.,.,.,.,+,.,.,.,.,.,.,.,.,
Sporobolus virginicus-hl ,.,.,.,.,.,.,+,.,.,1,.,4,.,.,.,
Stenotaphrum secundatum-hl ,.,.,.,.,.,.,+,.,.,.,.,.,.,.,.,
Ehrharta villosa v. maxima-hl ,.,.,.,.,.,.,.,3,2b,2m,.,.,.,.,.,
Arctotheca populifolia-hl ,.,.,.,.,.,.,.,.,2b,r,.,.,3,.,.,
Dasispermum suffruticosum-hl ,.,.,.,.,.,.,.,.,+,+,+,.,.,.,.,
Gladiolus gueinzii-hl ,.,.,.,.,.,.,.,.,.,+,.,+,.,.,.,
Helichrysum praecinctum-hl ,.,.,.,.,.,.,.,.,.,2m,.,.,.,.,.,
Senecio elegans-hl ,.,.,.,.,.,.,.,.,.,+,2a,.,.,.,.,
```

```
Stoebe plumosa-jl ,.,.,.,.,.,.,.,.,.,+,.,.,.,.,.,
Thinopyrum distichum-hl ,.,.,.,.,.,.,.,.,.,.,.,.,1,.,.,.,
Disphyma crassifolium-hl ,.,.,.,.,.,.,.,.,.,.,.,.,.,.,.,1,+,
```

5.6 Import free format header data table

Menu: **Import | Free format header data table**

Using a *wizard* you can import a table containing header data into a database in two steps. Input formats permitted are: SDF (fixed column width), comma delimited, tab delimited, semicolon delimited, space delimited, dBase III+, and MS Excel (up to version 2007). See the two examples below. Please note that delimited formatted tables, dBase III+ files, and especially MS Excel sheets are much easier to import than SDF formatted tables. Also note that all the data of one relevé should be organized in one row.

If you planning to import a corresponding file with species data than you first need to the species data table **followed** by the header data table.

If you want to import a(n Excel) table with header and species data, then you should separate the header from the species part and perform two imports, one on the header data and one on the species data. An example how to do this explained here 47.

Step 1: If the columns in the table are delimited with a comma, a tab, a semicolon, or a blank, then you first have to choose the right format from **Format table**. After having changed the delimiter the table will be reformatted automatically.
If the columns in the table are not delimited (“Columns at fixed positions“) then you will need to specify where each new column in the table starts. You can do this by marking (click the grey cell on top of the table) the first cell of each new column. Press **Next** when all columns are marked. The table will then be reformatted automatically.

Field names in row indicate in which line the field descriptions are stored. Zero means that there are no descriptions included in the file.

Step 2: Specify in which fields the data of specified columns have to be incorporated. Select a column and press the *Space bar* or click the column header (grey cells).
A dialogue box appears in which you have to specify in which existing or new database field the data have to be loaded.
One of the columns has to be marked as a **Key field.** The key field is the link between the source (the file to be imported) and the target (the database table with header data). It is important that the values in the source field and target field are unique.
With **Multiply with…** you can define a numerical factor with which the values from the input file must be multiplied before they are written to the database.

It is not necessary to mark all fields. This enables you to skip information that can be ignored.

Press **Complete** to read the table into the database.

An example in SDF format:

```
    1 50097199612   4 15        3
    2 50098199612  13100       12
    3 50099199612  16100       16
    4 50100199612   4 20        3
    5 50101199612   4  5        4
    6 50102199612  15 50        6
    7 50103199612   5 50       15
    8 50104199612   4 30        1
    9 50105199612   2 40        4
   10 50106199612   2 20       13
   11 50107199612   5 40        7
   12 50108199612   7 60        3
   13 50109199612   5 35        1
   14 50110199612   0 70        3
   15 50111199612   0 90        3
```

Column definition:

Kolomno.	Description
1	Table number
6	Relevé number
12	Year
16	Month
18	Altitude (m)
22	Cover total (%)
25	Landtype
29	Soil_type
31	Number of species

An example in comma delimited format:

```
table_nr,releve_nr,year,month,altitude,total_cover,landtype,soiltype,nr_of_spec
1,50097,1996,12,4,15,,,3
2,50098,1996,12,13,100,,,12
3,50099,1996,12,16,100,,,16
4,50100,1996,12,4,20,,,3
5,50101,1996,12,4,5,,,4
6,50102,1996,12,15,50,,,6
7,50103,1996,12,5,50,,,15
8,50104,1996,12,4,30,,,1
9,50105,1996,12,2,40,,,4
10,50106,1996,12,2,20,,,13
11,50107,1996,12,5,40,,,7
12,50108,1996,12,7,60,,,3
13,50109,1996,12,5,35,,,1
14,50110,1996,12,0,70,,,3
15,50111,1996,12,0,90,,,3
```

5.7 Import SORT file ('Tabulator Tabelle')

Menu: **Import | SORT export table ('Tabulator Tabelle')**

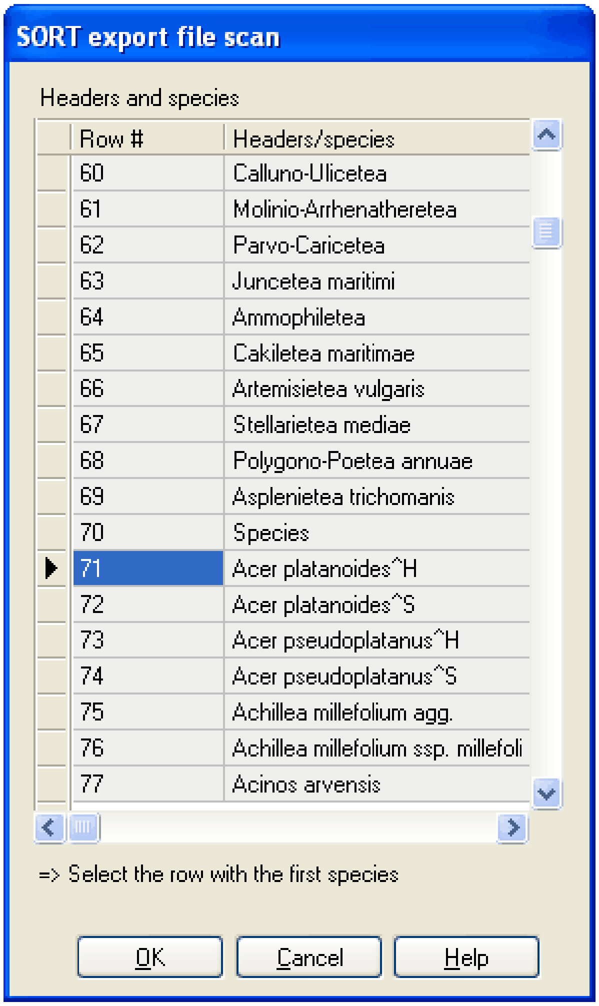
This option allows the import of a special export file from SORT, called 'Tabulator Tabelle'. The first four lines of this file may look as follows:

D:\TODO\HENNEKENS\SORT\DATA\K_06-8.STF 01.11.07 12:52

SORT 4.0 - TABELLE: Steilkuestenvegetation bei Heiligenhafen
--

Crucial is the presence of the word 'SORT' on the third line, and the fours line the presence of the character string '--------'.

Upon loading the SORT file Turboveg tries to locate a line that starts with the word 'Artname'. If this line does not occur a window will appear in which you can indicate which line holds the first species. Continue by selecting the **OK** button.

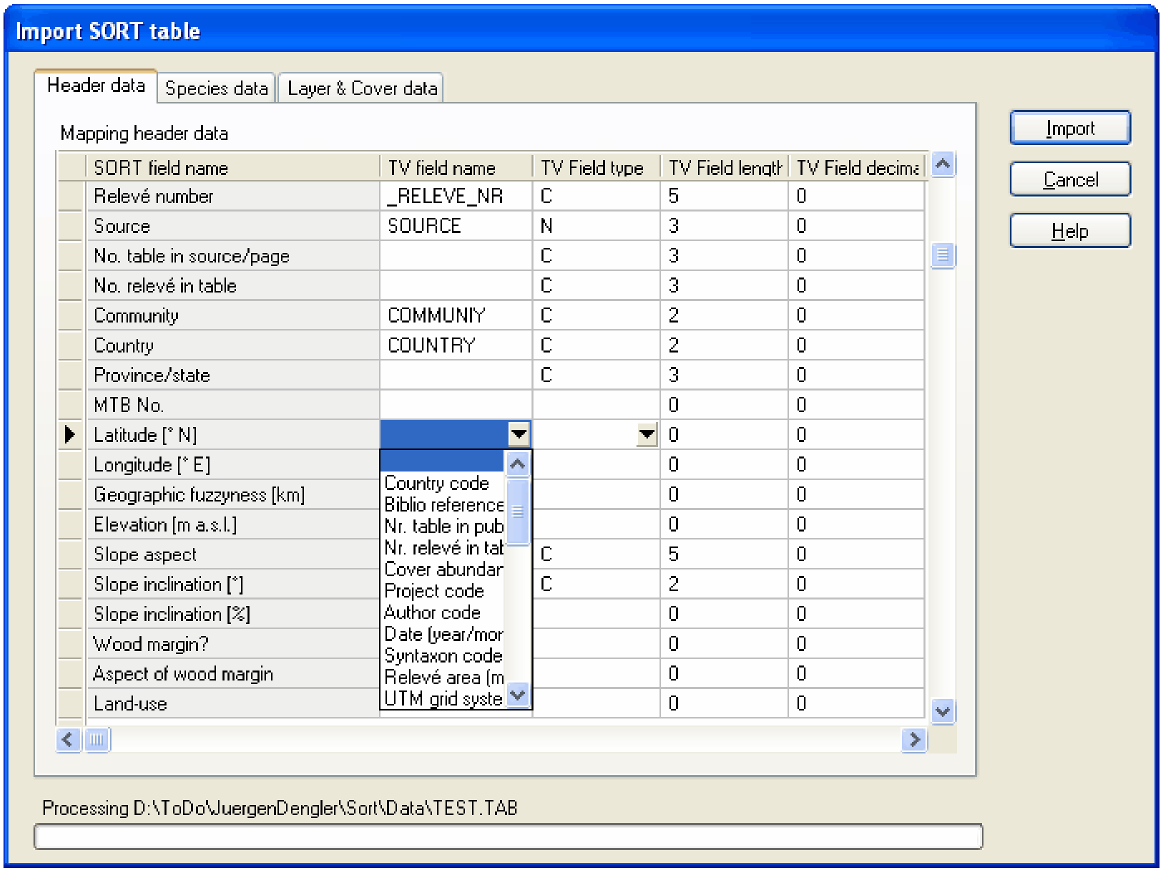


	Row #	Headers/species
	60	Calluno-Ulicetea
	61	Molinio-Arrhenatheretea
	62	Parvo-Caricetea
	63	Juncetea maritimi
	64	Ammophiletea
	65	Cakiletea maritimae
	66	Artemisietea vulgaris
	67	Stellarietea mediae
	68	Polygono-Poetea annuae
	69	Asplenietea trichomanis
	70	Species
▶	71	Acer platanoides^H
	72	Acer platanoides^S
	73	Acer pseudoplatanus^H
	74	Acer pseudoplatanus^S
	75	Achillea millefolium agg.
	76	Achillea millefolium ssp. millefoli
	77	Acinos arvensis

=> Select the row with the first species

After having examined the SORT file Turboveg displays a window with three tab sheets. The first sheet lists all the header data columns (fields) found in the SORT file. In the seconds column you can map the SORT fields to Turboveg fields. By clicking a cell in the second column a drop down list appears from which a field name can be selected. If an appropriate field name is not available you can write down a name yourself. Always confirm changes by pressing the ENTER key.

Values for field type, field length, and fields decimals are defined by Turboveg automatically. These values can be changed, but should never be set to lower values.

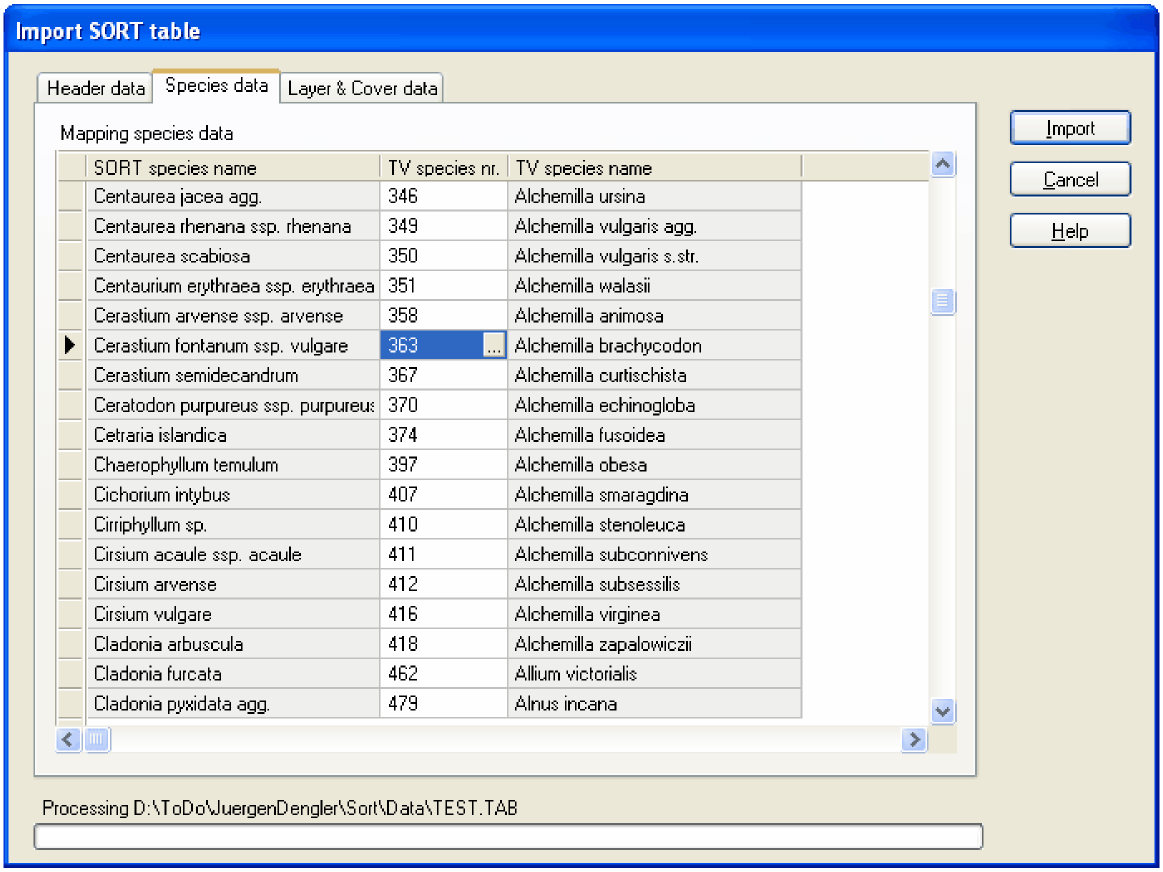


Mapping header data

SORT field name	TV field name	TV Field type	TV Field lengtł	TV Field decima
Relevé number	_RELEVE_NR	C	5	0
Source	SOURCE	N	3	0
No. table in source/page		C	3	0
No. relevé in table		C	3	0
Community	COMMUNIY	C	2	0
Country	COUNTRY	C	2	0
Province/state		C	3	0
MTB No.			0	0
Latitude [° N]			0	0
Longitude [° E]			0	0
Geographic fuzzyness [km]			0	0
Elevation [m a.s.l.]			0	0
Slope aspect		C	5	0
Slope inclination [°]		C	2	0
Slope inclination [%]			0	0
Wood margin?			0	0
Aspect of wood margin			0	0
Land-use			0	0

Processing D:\ToDo\JuergenDengler\Sort\Data\TEST.TAB

The second tab sheet lists all the species names found in the SORT file. Upon loading the file Turboveg will try to match these names with the names from the species list which is connected to active database. If there is no match than the number in the second column is set to zero. Click the ... icon to popup the species lookup table if you want to match a species name manually.



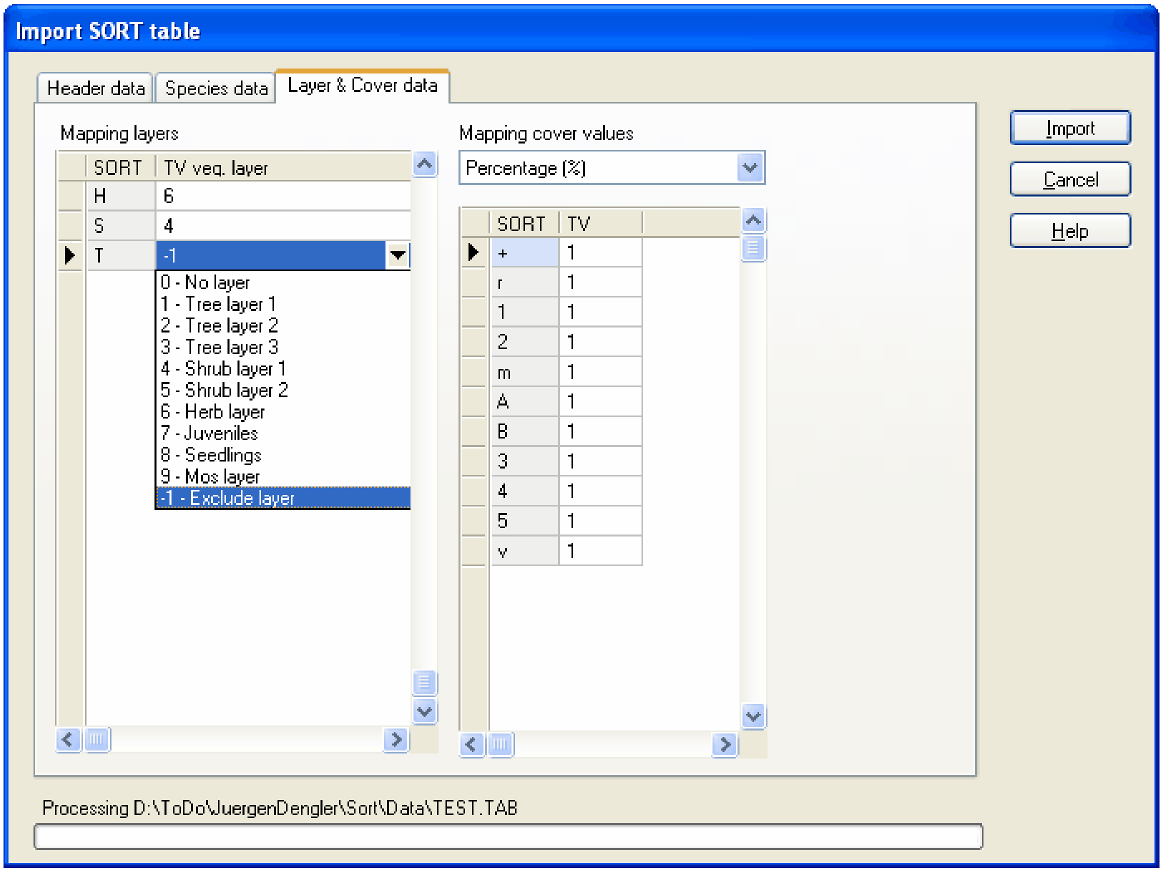
Mapping species data

SORT species name	TV species nr.	TV species name
Centaurea jacea agg.	346	Alchemilla ursina
Centaurea rhenana ssp. rhenana	349	Alchemilla vulgaris agg.
Centaurea scabiosa	350	Alchemilla vulgaris s.str.
Centaurium erythraea ssp. erythraea	351	Alchemilla walasii
Cerastium arvense ssp. arvense	358	Alchemilla anımosa
Cerastium fontanum ssp. vulgare	363	Alchemilla brachycodon
Cerastium semidecandrum	367	Alchemilla curtischista
Ceratodon purpureus ssp. purpureus	370	Alchemilla echinogloba
Cetraria islandica	374	Alchemilla fusoidea
Chaerophyllum temulum	397	Alchemilla obesa
Cichorium intybus	407	Alchemilla smaragdina
Cirriphyllum sp.	410	Alchemilla stenoleuca
Cirsium acaule ssp. acaule	411	Alchemilla subconnivens
Cirsium arvense	412	Alchemilla subsessilis
Cirsium vulgare	416	Alchemilla virginea
Cladonia arbuscula	418	Alchemilla zapalowiczii
Cladonia furcata	462	Allium victorialis
Cladonia pyxidata agg.	479	Alnus incana

Processing D:\ToDo\JuergenDengler\Sort\Data\TEST.TAB

The third column consists of two parts.
The first parts holds a table with the SORT indicators for vegetation layers in the first column. In the second column the SORT layer can be mapped to a predefined Turboveg layer. Setting the value in the second column to -1 all the species connected to that SORT layer will not be imported.

The second part holds all the cover values found in the SORT table. You first need to select the cover scale method from the drop down list on top, then map each of the SORT values with a Turboveg cover value.



Mapping layers

SORT	TV veg. layer
H	6
S	4
T	-1

Mapping cover values: Percentage (%)

SORT	TV
+	1
r	1
1	1
2	1
m	1
A	1
B	1
3	1
4	1
5	1
v	1

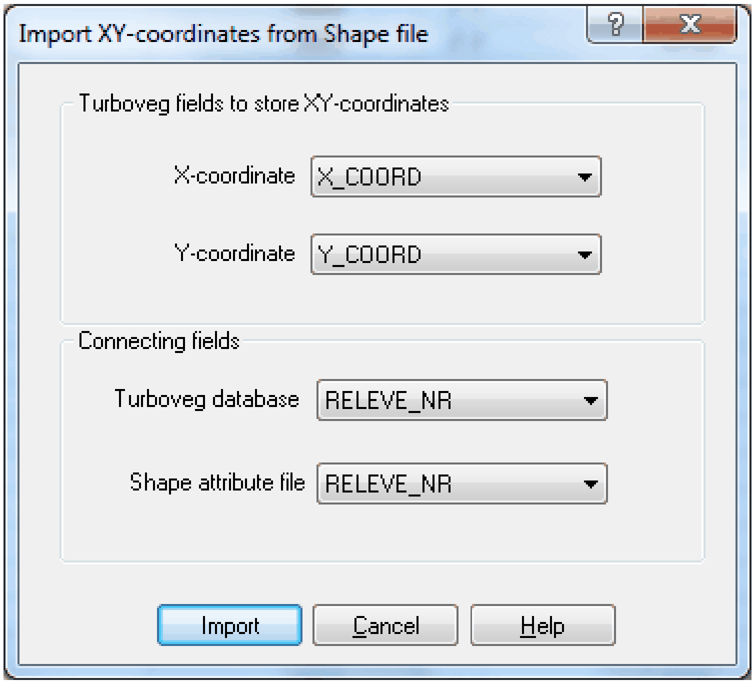
Processing D:\ToDo\JuergenDengler\Sort\Data\TEST.TAB

Click the **Import** button if all values in all three sheets are set according to your wishes

5.8 Import XY-coordinates from Shapefile

Menu: **Import | XY-coordinates from Shapefile**

XY-coordinates can be imported from a shapefile if the records in the shapefile can be linked to the releves in the target database. Typically that would be the releve number, but in fact any identifier can be taken, as long as each value is unique in the database. Before you start the import procedure make sure that appropriate fields are available in the Turboveg database to store the XY-values. Concerning the shapefile **only point data** is accepted.



Import XY-coordinates from Shape file

Turboveg fields to store XY-coordinates

X-coordinate: X_COORD

Y-coordinate: Y_COORD

Connecting fields

Turboveg database: RELEVE_NR

Shape attribute file: RELEVE_NR

Part

VI

6 Select

6.1 Select current relevé

Menu: **Select | (De)select current relevé**

You can manually select or deselect a relevé in several ways:

- Use the menu **Select, (De)select current relevé**.
- Press *Spacebar*.
- Double-click in the table with header data the second column.

6.2 Select all relevés in current database

Menu: **Select | Select all relevés in current database**

All relevés from the active database can be added to a selection in one go (see window with selected relevés).

6.3 Deselect all relevés in current database

Menu: **Select | Deselect all relevés in current database**

All relevés from the active database can be deleted from a selection in one go (see window with selected relevés).

6.4 Flip the selection in current database

Menu: **Select | Flip selection in current database**

This option enables to deselect marked relevés and conversely to select (mark) not yet selected relevés (see window with selected relevés) from the active database.

6.5 Select relevés random

Menu: **Select | Random select**

You have to specify the number of relevés to be selected randomly.

You can execute this selection on only one database at the time; when doing so, the already existing selection will be automatically removed.

6.6 Build a query

Menu: **Select | Build query**

You can select relevés from one or in more databases by defining selection criteria. Selection criteria can be one or several items from the **Header data** and/or **Species data**.

Tab sheet **Header data**

First choose (**Select item**) the header data you want to select. Then press **Define range** to define a range (e.g. 1930-1950) or **Define list** to enter a list of data (e.g. 1931, 1935, 1956, …).
You perform the selection by pressing **Execute**. It is also possible to combine several criteria with **Combine criteria with**. First choose how to combine the new criterion with the already selected criterion. There are three possibilities.

- *and*: restrict the selection;
- *or*: enlarge the selection;
- *and not*: restrict the selection.

Then select an item (**Select item**) and enter the data at **Define range** or **Define list**.
When combining criteria you can also add a selection on species. However, the selection on species always restricts the selection based on the header data.

Tabsheet **Species data**

The selection on species is executed in the same way as the selection on header data (see above). The items to be chosen (e.g. sociability, fertility, phenology), however, are not present by default. These species attributes can only be entered when they are present in the database. See: **Modify database structure** 23.

Most common is a selection on species. Two ways of making species lists can be chosen: **And/Or** and **And Not**. Choosing **And/Or** you make a list of which some or all species have to be present in the relevés. You have to define which species always have to be present and the number of the other chosen species that have to be present (**Select .. out of ..**). Choose **And not to** make a list of species that should be absent in the relevés. In both lists you can also specify the cover value of the chosen species.
This method to define species enables a selection of clearly delimited vegetation types in your databases.

General tasks.

Execute: Perform the selection.

Undo: Delete the latest defined criterion. It depends on the tabblad selected whether the latest criterion of the header data or of the species will be deleted.

Save: Save the selection criteria to a file.

Retrieve: Retrieve an earlier selection from a file.

Embargo filter: Mark this option to exclude relevés, which are embargoed. Both authors and/or projects can be placed under an embargo. See **Modify popup lists** 84 to change the embargo flag of authors and/or projects.

Current selection: Specify what to do with the previous selection. Their relevé numbers are listed in the window at the right part of the screen.
There are three possibilities which resemble **Combine criteria with**:

- *Delete*: delete the previous selection (default).
- *Restrict*: restrict the previous selection.
- *Extend*: extend the selection.

6.7 Clear a selection

Menu: **Select | Clear**

This option deletes all selected relevés. You can also clear the window with selected relevés by double clicking the icon on the toolbar.

6.8 Save a selection

Menu: **Select | Save**

When saving a selection only the relevé numbers of the selected relevés will be stored. By default this file will be stored in the directory <Turboveg installation folder>\Old_sels.

6.9 Retrieve a selection

Menu: **Select | Retrieve**

When you retrieve a selection only the relevé numbers will be replaced in the window with selected relevés. You can then export the data of the selected relevés by various options.

Part VII

7 Export

7.1 Export to Turboveg database

Menu: **Export | TURBOVEG database**

Export to a *Turboveg* database is for example useful when you want to copy the selected relevés to another computer system, where *Turboveg* is also implemented.
It can also be used to copy all relevant relevés to be used in a specific project into one database

Database name: Specify the name of the database. This can be an existing or a new.

Empty target database: Mark this option to empty the target database.

Area: Only the manager can create a **Common** database or add relevés to a common database. It is only possible to create or change databases in the private area.
This option is only relevant for the network version.

Turboveg version: Choose TvDos (9.x) when the target database will be used in the DOS version of *Turboveg*.

Structure header database: When one or more of the selected databases have an extended structure of the header data, you have the option to copy (choose **extended**) or not to copy (choose **standard**) the extended structure.

Structure species database: When one or more of the selected databases have an extended structure of the species data, you have the option to copy (choose **extended**) or not to copy (choose **standard**) the extended structure.

Please note that relevés first need to be selected before they can be exported.

Also see: **Export to XML file (standard)** 68

7.2 Export to MS ACCESS database

Menu: **Export | MS ACCESS database**

Please note that relevés first need to be selected before they can be exported.

7.3 Export to standard XML file

Menu: **Export | Standard XML file**

Unlike the **Export to Turboveg database** 68 the Export to standard XML file not only exports all the header and species data of a selected data set, but also the interpretation of all the codes present in the data (e.g. author codes, project codes, species numbers). Even the database dictionary used is included in the export file. The receiver of an the XML file can thus build up a complete new Turboveg system from scratch. Therefore this export is the best format to exchange data between Turboveg users and not the export to a Turboveg database.

The Standard XML file is also an excellent input file for JUICE.

Target directory: Specify the directory to store the output file. Click to select a directory from a list.

Output file: Specify the name of the output file.

Encoding: Select encoding schema if your data needs to be parsed by other software than Turboveg

Exclude relevés that have no species: Exclude empty relevés from export.

Description: Optionally describe the selected data set

Send file as e-mail attachment: If you check this option the export file will autonomically be compressed (zip format) and attached to an e-mail.

Submit data to EURODAT: Check this option if you want to upload the selected data to the European Vegetation Data Bank (EURODAT). The option is temporarily disabled.

Please note that relevés first need to be selected before they can be exported.

7.4 Export to XML project file for TurbovegCE

Menu: **Export | XML project file for TurbovegCE**

7.5 Export to ESVeg compatible XML file

Menu: **Export | ESVeg compatible XML file**

ESVeg compatible XML files are suitable to be imported in VegetWeb.

Please note that relevés first need to be selected before they can be exported.

7.6 Export to a Cornell condensed species file

Menu: **Export | Cornell condensed species file**

Export to a Cornell condensed file enables analysis with various programs, for example CEDIT, SHAKE, TWINSPAN, CANOCO, PC-ORD, VEGRO, VEGRON, CLUTAB, DENDRO, and ELLEN.

Target directory: Specify the directory to store the output file. Click to select a directory from a list.

Output file: Specify the name of the output file.

Combine/Exclude layers: Specify whether you want to combine species that are divided over more than one vegetation layer or that you want to exclude species that are present in one or more layers.

Exclude species: Exclude species based on their characteristics as defined in the ecological database. See **Exclude species**

Format: Choose **Classic** if you want to apply an old version of TWINSPAN, **Canoco** format is valid for most programs that need Cornell condensed file as input. Choose **Vespan** when you want to analyse your data using the software package VESPAN. For VEGRO and VEGRON **Canoco** format should be selected.

Transformation cover values: By default cover values are exported in percentage. Using a transformation you can down weight cover values. Choose **User defined** to define your own classes for transformation.

Standardization to site total means that each cover value of a species will be divided by the sum of all cover values of the species in the relevé. In some cases this standardizationenables a more reliable comparison among relevés (e.g. relevés of fishes in open water).

Code relevés using…: In the Cornell condensed file the relevés are identified with a code, which is by default the relevé (= system) number. However, you can also choose another identification code from the list. This code, preferably, has to be unique.

Exclude empty relevés: Exclude empty relevés (no species) in case the program that will have the output file as import file can not handle empty relevés. An example of such a program is TWINSPAN. In case you want to perform a numerical classification using TWINSPAN in JUICE you also have to exclude empty relevés.

Add a dummy species in the case of an empty relevé: Add one dummy species (code DUMMYSPE) with cover value 0.1% to an empty relevé.

Title: You can optionally specify a title.

Please note that relevés first need to be selected before they can be exported.

7.7 Export to a user defined header data file

Menu: **Export | User defined header data file**

Target directory: Specify the directory to store the output files. Click to select a directory from a list.

Output file 1: Specify the name of output file 1. This file contains the data.

Output file 2: Specify the name of output file 2. This file contains information on the structure of output file 1.
Output file 2 is only required if you choose SDF or delimited format.

Exclude relevés that have no species: Optionally exclude relevés that have no species.

Format: Choose an export format. There are four possibilities.

- SDF: Columns have a fixed width.
- Delimited: Columns do not have a fixed width, but are separated by a delimiter. You have to specify which delimiter has to be used to separate the columns and in what way numerical values with decimals need to be formatted.
  You can load the delimited format in e.g. MS Excel (up to version 2007).
- DbaseIII+:
- Cornell condensed*:* This format is required if you want to perform a Canonical Correspondence Analysis with CANOCO. For each chosen subject you also have to indicate whether the variables must be treated as numerical or nominal values.

Select items: Select the subjects to be present in the output file by double clicking or pressing *Ins*.

Save: Save the selected subjects as pre-set.

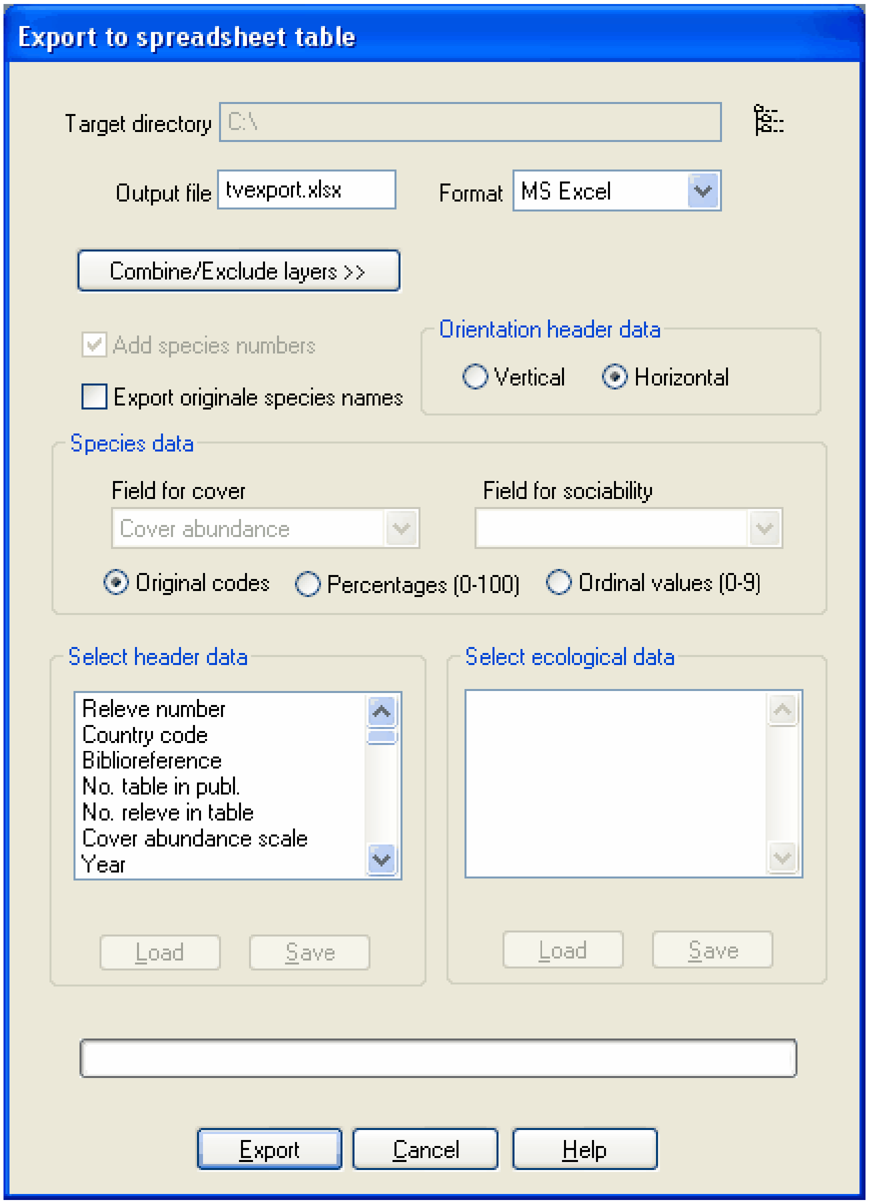
Load: Load the pre-set selection of subjects.

Please note that relevés first need to be selected before they can be exported.

7.8 Export to a spreadsheet table

Menu: **Export | Spreadsheet table**

Selected relevés can be exported to a non-ordered table. The format of the table can either plane Ascii (with tab or semi colon separated columns) or MS EXCEL.
You have the choice to extend the table with header data and with data from the ecological database.



Export to spreadsheet table

Target directory: C:\

Output file: tvexport.xlsx

Format: MS Excel

☑ Add species numbers

☐ Export originale species names

Orientation header data: ○ Vertical ● Horizontal

Species data

Field for cover: Cover abundance

Field for sociability:

● Original codes ○ Percentages (0-100) ○ Ordinal values (0-9)

Select header data:

- Releve number
- Country code
- Biblioreference
- No. table in publ.
- No. releve in table
- Cover abundance scale
- Year

Target directory: Specify the directory to store the export file. Click to select a directory from a list.

Output file: Enter the name of the export file.

Combine/Exclude layers: Specify whether you want to combine species that are divided over more than one vegetation layer and/or that you want to exclude species that are present in one or more layers.

Add species numbers: Do you want to add an extra column with species numbers?

Species data: By default cover abundance codes are exported. If available however, you may also select another species parameter. If cover abundance is selected then you may also decide to export cover values as percentage values or ordinal values (1 up to 9). If sociability values are also stored in the database then you can export these values as well. Cover abundance values will be the be combined with sociability values, separated with a dot (e.eg 2a.3) .

Orientation header data: Choose **Vertical** if each relevé may contain only one character per column. The values will be written over several rows (thus vertically).
Choose **Horizontal** if the column width may be more than one character.

Cover: Choose the way the cover values must be presented, either by the original codes, in ordinals (1-9) or in percentage (0-100).

Select header data: Select one or more header data that have to be present at the top of the table.
Using **Load** and **Save** you can retrieve previous and save current selected header items.

Select ecological data: If available you can select one or more ecological parameters which will be added to the table as extra columns. See **Linking an ecological database** 16.
Using **Load** and **Save** you can retrieve current and save previous selected items.

Please note that relevés first need to be selected before they can be exported.

7.9 Export to a SDF formatted database

Menu: **Export | SDF formatted database**

7.10 Export to JUICE input files

Menu: **Export | JUICE input files**

JUICE (Tichý 2001) is an excellent program designed for editing and classifying large phytosociological tables. The maximum capacity is 30.000 relevés in one table, and many functions are included for easy manipulation of phytosociological tables, including header data. Various options include calculation of average Ellenberg values for relevés, export of table data into other programs, mapping of species occurrence from actual data sets, etc. JUICE includes TWINSPAN for classification, which is implemented as an external service. It is recommended for smaller datasets.
The most important feature of JUICE however, is the classification of relevés using the Cocktail classification method (Bruelheide 1995, 2000). This method tests the statistical coincidence of species occurrence in order to find reasonable groups of diagnostic species, as they are traditionally used in phytosociology. Vegetation classification is subsequently created by combination of different species groups.

Export to JUICE input files is a combination of a Cornell condensed species file and a user defined header data file. The latter is optional.

Target directory: Specify the directory to store the export file. Click to select a directory from a list.

Name for all export files (.cc!, .exp, .str): Enter the name for all the possible export files. The extensions are added automatically. In order to apply header data in JUICE, the prefix for all file names must be the same.

Combine/Exclude layers: Specify whether you want to combine species that are divided over more than one vegetation layer and/or that you want to exclude species that are present in one or more layers.

Include header data: Mark this options if you want header data to be included in the JUICE table.

Select header data: Select at least one header item to be exported.
Using **Load** and **Save** you can retrieve previously and save currently selected header items.

For a more convenient input file for JUICE see: **Export to XML file (standard)** 68

Please note that relevés first need to be selected before they can be exported.

7.11 Export to ESPRESSO/TAB input file

Menu: **Export | ESPRESSO/TAB input file**

Please note that relevés first need to be selected before they can be exported.

7.12 Export to MULVA input file

Menu: **Export | MULVA input file**

Please note that relevés first need to be selected before they can be exported.

7.13 Export to SYNTAX-5 input files

Menu: **Export | SYNTAX-5 input files**

Please note that relevés first need to be selected before they can be exported.

7.14 Export to SYNTAXON input file

Menu: **Export | SYNTAXON input file**

Please note that relevés first need to be selected before they can be exported.

7.15 Export to TAXAL input file

Menu: **Export | TAXAL input file**

Please note that relevés first need to be selected before they can be exported.

7.16 Export to FUZPHY input files

Menu: **Export | FUZPHY input files**

Please note that relevés first need to be selected before they can be exported.

7.17 Export to species check list

Menu: **Export | Species check list**

Please note that relevés first need to be selected before they can be exported.

7.18 Export to herbarium etiquettes

Menu: **Export | Herbarium etiquettes**

Please note that relevés first need to be selected before they can be exported.

7.19 Export to herbarium etiquettes from template

Menu: **Export | Herbarium etiquettes from template**

When a selection is based on one or a number of species Turboveg can create herbarium etiquettes for the selected species (and only those species). The export to etiquettes can only be done directly after the selection has been made.

A sample template as MS Excel document is located in the folder '<installation folder>\Herbarium'. This sample can modified to fit your own needs.

Important is that each etiquette consumes a fixed number of rows (x) and columns (y). Also the number of etiquettes on a row (z) is fixed.
The very first line of the Excel sheet contains three parameters indicating the above mentioned dimensions:

1. **RowBlockCount**=x (located in row1, column 1)
2. **ColBlockCount**=y (located in row 1, column 2)
3. **BlockCount**=z (located in row 1, column 3)

The number of etiquettes that can be created is only limited by the number of rows that Excel can handle in a sheet.

In each etiquettes the character string placed between square brackets (e.g. '[RELEVE_NR]') refers to a field name in the Turboveg database (so called placeholders) . When creating the etiquettes Turboveg will replace the placeholders with values derived from the selected relevés.
An exception is the placeholder [SPECIES_NAME]. There is no equivalent field name in a Turboveg database, but Turboveg will replace this placeholder with a species name.

Please note that relevés first need to be selected before they can be exported.

7.20 Export to Shapefile

Menu: **Export | Shapefile**

If meant for ESRI ArcGIS then it is recommended to after importing the Shapefile in a project to export it and rename it. This procedure will avoid corruption of the attribute table when removing or adding columns.

Please note that relevés first need to be selected before they can be exported.

7.21 Export to mapping file

Menu: **Export | Mapping file**

Please note that relevés first need to be selected before they can be exported.

7.22 Export to distribution map

Menu: **Export | Distribution map**

The distribution of the selected relevés will be shown and printed.

Print: Send the distribution map to the printer or to a graphics file.

Please note that relevés first need to be selected before they can be exported.

7.23 Export to Google Earth

Menu: **Export | Google Earth**

Please note that relevés first need to be selected before they can be exported.

7.24 Export to Darwin Core Archive

Menu: **Export | Darwin Core Archive**

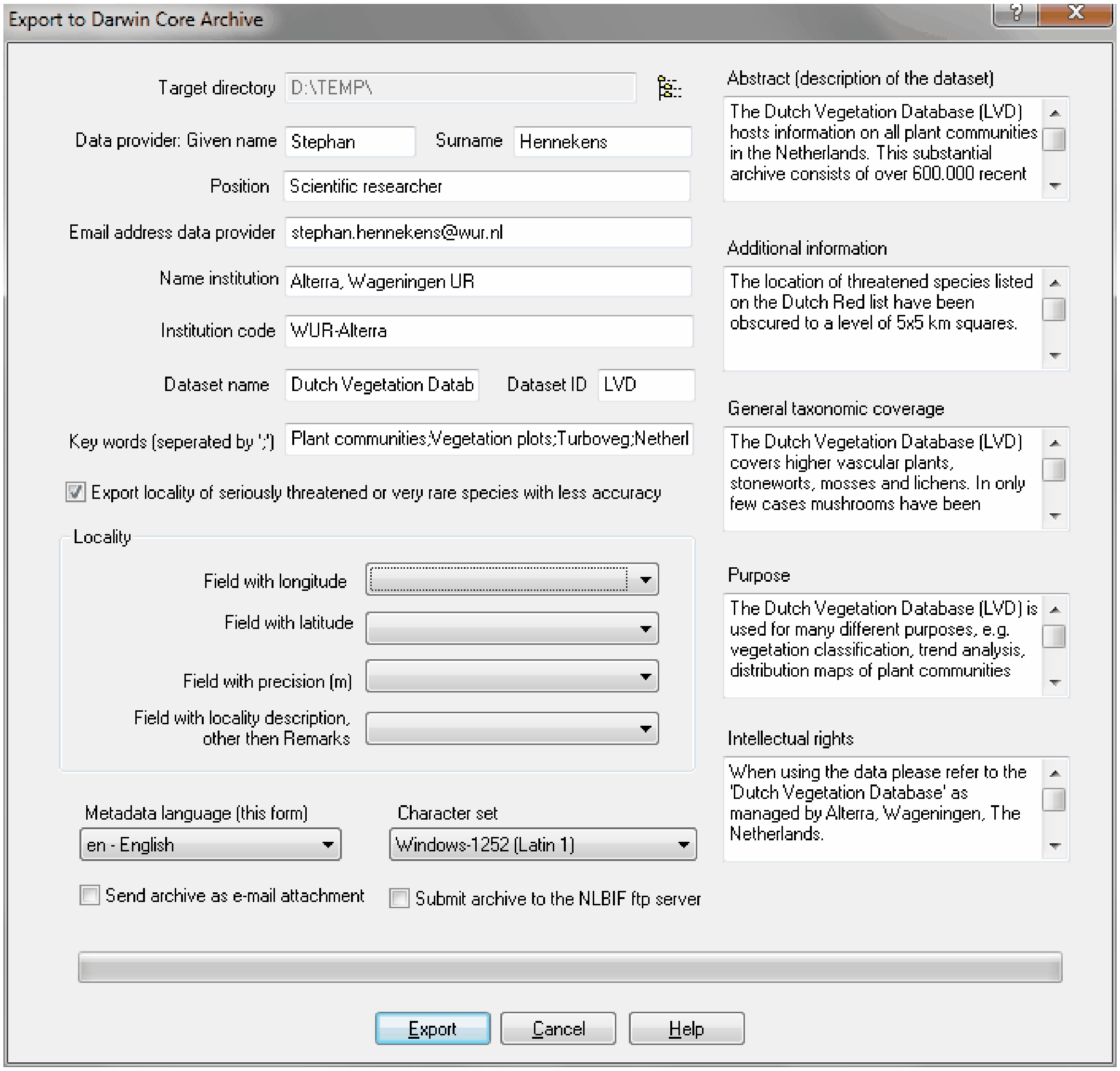
This option is currently in beta stage!

The export to Darwin Core Archive in Turboveg is developed to facilitate the publication of species information derived from vegetation relevés to GBIF (Global Biodiversity Information Facility). Read more about Darwin Core Archive here.
A Darwin Core Archive consists of an eml file and a zip file. The eml file (also included in the zip file) contains meta information of the database, the zip file contains the actual data and the xml file describing the columns in the data file. The data file is a simple straight forward TAB delimited text file. Both eml and zip file should be sent to - most likely - the contact person of the national GBIF node.

To explain how to fill in the extensive export form in Turboveg, an example is presented below of how it is done for data from the Dutch National Vegetation Database. Please note that the institution name and code should somehow be standardized, at least at national level. Therefore it is recommended to consult the national GBIF node before creating and uploading Darwin Core Archives.

After the export has been created the selection of relevés is automatically saved to a file, which name is composed by 'DWCA', the name of institute and the date. By retrieving a selection of a previously made export, a data set can be uploaded once more. This is useful if in course of time the data has been improved. A previously made selection can be easily be retrieved by choosing 'Select', 'Retrieve' in the Turboveg menu.

Please note that GBIF also has developed the IPT (Integrated Publishing Tool), a software platform to facilitate the efficient publishing of biodiversity data on the Internet, using the GBIF network. Read more about the IPT here.



Target directory: D:\TEMP\

Data provider: Given name: Stephan Surname: Hennekens

Position: Scientific researcher

Email address data provider: stephan.hennekens@wur.nl

Name institution: Alterra, Wageningen UR

Institution code: WUR-Alterra

Dataset name: Dutch Vegetation Datab Dataset ID: LVD

Key words (seperated by ';'): Plant communities;Vegetation plots;Turboveg;Netherl

☑ Export locality of seriously threatened or very rare species with less accuracy

Field with longitude:

Field with latitude:

Field with precision (m):

Field with locality description, other then Remarks:

Metadata language (this form): en - English

Character set: Windows-1252 (Latin 1)

☐ Send archive as e-mail attachment ☐ Submit archive to the NLBIF ftp server

Abstract (description of the dataset): The Dutch Vegetation Database (LVD) hosts information on all plant communities in the Netherlands. This substantial archive consists of over 600.000 recent

Additional information: The location of threatened species listed on the Dutch Red list have been obscured to a level of 5x5 km squares.

General taxonomic coverage: The Dutch Vegetation Database (LVD) covers higher vascular plants, stoneworts, mosses and lichens. In only few cases mushrooms have been

Purpose: The Dutch Vegetation Database (LVD) is used for many different purposes, e.g. vegetation classification, trend analysis, distribution maps of plant communities

Intellectual rights: When using the data please refer to the 'Dutch Vegetation Database' as managed by Alterra, Wageningen, The Netherlands.

Please note that relevés first need to be selected before they can be exported.

7.25 Relevé data sheets

Menu: **Export | Relevé data sheets**

The header data and species data of the selected relevés can be copied to a file. An example of a relevé is showed below.

Header data: Header data can, optionally, be written to a file.

Remarks: Remarks can, optionally, be written to a file.

Ecological data: Ecological data (e.g. mean Ellenberg nitrogen indication values per relevé), can optionally, be written to a file, provided that the database with ecological data is linked (see **Linking an ecological database** 16).

Empty entries: Empty header data can, optionally, be inserted in the list.

An example:

```
=> Relevé number: 7002

Country code                  : 45
Biblioreference               : 000023
Nr. table in publ.            :      3
Nr. relevé in table           :
Cover abundance scale         : Percentage (%)
Project code                  :
Author code                   : 0002
Date (year/month/day)         : 1986/08/08
Syntaxon code                 :
Relevé area (m2)              : 0.00
UTM grid system code          :   - -  -     -
Altitude (m)                  :
Aspect (degrees)              :
Slope (degrees)               :
Cover total (%)               : 0
Cover tree layer (%)          : 0
Cover shrub layer (%)         : 0
Cover herb layer (%)          : 0
Cover moss layer (%)          : 0
Cover lichen layer (%)        : 0
Cover algae layer (%)         : 0
Cover litter layer (%)        : 0
Cover open water (%)          : 0
Cover bare rock (%)           : 0
Height (highest) trees (m)    : 0
Height lowest trees (m)       : 0
Height (highest) shrubs (m)   : 0.0
Height lowest shrubs (m)      : 0.0
Aver. height (high) herbs (cm): 0
Aver. height lowest herbs (cm): 0
Maximum height herbs (cm)     : 0
Maximum height cryptogams (mm): 0
Mosses identified (y/n)       :
Lichens identified (y/n)      :
Litter                        : 0.0
Peatlayer                     : 0.0
Ph                            : 0.00
Conductiv                     : 0.00
Grazing                       :
Haymaking                     :
Sand                          :
Sandwclay                     :
Claywsand                     :
Clay                          :
```

```
Silt                          :
Peat                          :
Soildescr                     :

Community                     :


Stevns +

                                  L     T     K     F     R     N     S
-------------------------------------------------------------------------
Agrostis stolonifera      70      8     x     5     7~    x     5     0
Alopecurus geniculatus    45      9     6     3     8=    7     7     2
Alopecurus pratensis      80      6     x     5     6     6     7     0
Anthriscus sylvestris     5       7     x     5     5     x     8     0
Caltha palust s. palus    50      7     x     x     9=    x     6     0
Cardam praten s. prate    75      4     x     x     6     x     x     0
Cerast fontan s. fonta    45
Deschampsia cespitosa     20      6     x     x     7~    x     3     0
Elymus repens             10      7     6     7     x~    x     7     0
Festuca pratensis         65      8     x     3     6     x     6     0
Festuca rubra             15
Filipendula ulmaria       30      7     5     x     8     x     5     0
Glyceria fluitans         20      7     x     3     9=    x     7     0
Holcus lanatus            60      7     6     3     6     x     5     1
Juncus compressus         5       8     5     3     8=    7     5     1
Juncus effusus            10      8     5     3     7     3     4     0
Lolium perenne            20      8     6     3     5     7     7     0
Myosotis scorpioides      1       7     x     5     8~    x     5     0
Persicaria amphibia       25      8     6     x     x     x     6     0
Phalaris arundinacea      35      7     5     x     8~    7     7     0
Poa praten s. praten      99
Ranunculus repens         99      6     x     x     7~    x     7     1
Rumex acetosa             30      8     x     x     x     x     6     0b
Taraxacum species         45
Trifolium repens          40      8     x     x     5     6     6     1
Triglochin palustre       5       8     x     x     9=    x     1     3
Urtica dioica             10      x     x     x     6     7     9     0
                              ------------------------------------------
Mean indicator value             7.2   5.6   4.0   7.0   6.3   5.9   0.4
Standard deviation               1.1   0.5   1.3   1.3   1.4   1.7   0.8
Median value                     7.0   6.0   3.0   7.0   7.0   6.0   0.0
# of observation (n)            22.0   9.0  12.0  20.0   8.0  22.0  23.0
```

Please note that relevés first need to be selected before they can be exported.

7.26 Analyze header data

Menu: **Export | Analyze header data**

This option enables to visualize the relation between two header data items (including species number and excluding remarks) in a graph. The graph is presented by a Visual Basic Component which gives you the possibility to manipulate the graph. The screen shot below is meant to clarify this option. However, this help does not contain a full explanation of this option.

X-axis: Select an item to represent the X-axis (double-click or press on *Ins*). Basically you can choose each desired item.

Y-axis: Select an item to represent Y-axis (double-click or press on *Ins*). If you select the same item as was selected for the X-axis, the frequency of the chosen item will be calculated (e.g. the number of times each syntaxon is present in the selection). In all other cases you have to choose a numerical item (e.g. number of species per relevé), since the data have to be reduced to means per unit of the X-axis.

Interval: State the difference between two values on the X-axis (e.g. year: 1930-1995, 1935-1940, etc.). You can only choose intervals higher than 0 if the subject is numerical (e.g. year, and thus not syntaxon).
The following is applied at the calculations: >= lower limit and < upper limit.

Sort labels: Mark this option if the labels on the X-axis have to be sorted.

Exclude empty entries: Mark this option if missing values have to be omitted from the calculations.

If you have finished the settings, click **Draw** to visualize the graph.

A screen shot showing a graphic is given below. Click on the icons of the toolbar for elucidating their function.

Please note that relevés first need to be selected before they can be exported.

7.27 Analyze ecological data

Menu: **Export | Analyze ecological data**

Please note that relevés first need to be selected before they can be exported.

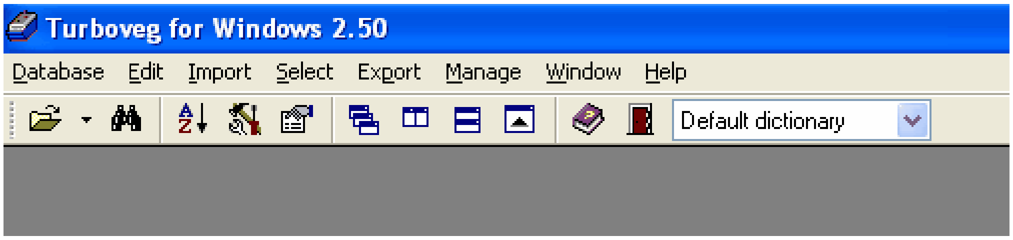
Part VIII

8 Manage

8.1 Modify popup lists

Menu: **Manage | Popup lists | Edit | <select a list to edit>**

Before you start modifying a popup lust make sure that you have selected the right dictionary (see also **Popup lists** 16). A dictionary van be selected from the drop down menu located on the toolbar of the main window.



Only the manager is authorized to change the popup lists.

In a popup list you can modify, delete or add a record. Hereto you have to activate a cell by pressing *Enter* or by double clicking.

The lookup table for Authors and Projects contain an “Embargo“ field, which you can set on “T“ (True) or “F“ (False). Setting the value on True, means that the relevés concerned can only be selected and/or exported under strict conditions.

Add: Add a record.

Delete: Delete a record.

Export: Save the list to a file.

8.2 Delete a dictionary

Menu: **Manage | Popup lists | Delete**

You can delete a dictionary by selecting a name from the list.
This option deletes all the popup lists belonging to the selected dictionary.

Also see **Popup lists** 16

8.3 Modify a species list

Menu: **Manage | Species lists | Edit | <choose the list you want to modify>**

Species lists can be changed or extended with new species or synonyms. There are protected and unprotected species lists. The Dutch version of *Turboveg for Windows* is by default linked to the Dutch species list (higher plants and cryptogams), which is a protected list. This means that the user is not allowed to and cannot make changes in species numbers lower than 90.000. You can only add species by using a species number higher than 90.000.

Edit: Change the species selected (see **Modify or add species**)

Add new: Add a species.

Add synonym: Add a synonym of the selected species.

Delete: Remove the selected species.

Export: Save the species list to a file.

Modify (eco database): If present, this option can be used to modify the ecological database. See **Linking an ecological database** 16 and **Modifying an ecological database** 89

Configure (eco database): If present, this option can be used to configure the ecological database. See **Linking an ecological database** 16 and **Configure the ecological database** 89

8.4 Create a new species list

Menu: **Manage | Species lists | New | Create empty species list**

You can create a new species list by entering a unique name in the **Name** field, followed by pressing **Enter**. See **Modify species list** 85
to learn more on how to add species to the list.

8.5 Import a species list

Menu: **Manage | Species lists| New | Import from file**

Use this option if you have a computerised species list ready. In order to import this file the format be dBaseIII. If your list is not in a dbaseIII format then use for example MS-Excel to

save the list as a dBaseIII file**.** Make sure that on the very first line of the Excel table the column names are defined. The column names will be used the define the field names in the dBase file. If you do not define the column names, and the first line holds the first species in the list, than that species will get lost.
See below for some examples of species lists that will be accepted.

After selecting the input file, Turboveg will come up with a dialog window. In this window a snapshot is given of a few records of the input file. The snapshot shows what field holds what kind of information.

- Target

Name species list: Enter the name of the species list you want to create. This name might not conflict with others names species list. (Turboveg can handle multiple species list; however, a relevé database is connected to only one species list).

- Source

Synonyms included: Confirm if the input file has a separate field with information on the status of the species (synonym or valid). You can select the field on the right side of the checkbox.
In general an empty field indicates a valid species, whereas a non-empty field indicates a synonym. If the field type is logical (or boolean) than FALSE indicates a valid species, and TRUE a synonym. Is the field type numerical than 0 indicates a valid species, and any other number > 0 a synonym. In case of a character field, a blank (empty, or space) indicates a valid species, and any other character a synonym.
If synonyms are included then there are two options of how the synonyms are related to there valid counter parts.

1. **A synonym follows directly after its valid counter part.**
2. **The row position of the synonym in the list is trivial, but then a species number must be included to set the relation to the valid counter part.**

Species numbers included: Confirm if the input file has a separate field with species numbers. You can select the field on the right side of the checkbox.
If you do not confirm this option than Turboveg will generate numbers for you, from 1 up to as many valid species there are in the list.
If you confirm, Turboveg will check whether the numbers are unique, as far as it concerns valid species. If it turns out that the numbers are not unique that redo the import and do not confirm this option.

7 character abbreviation included: Confirm if the input file has a separate field with species codes. You can select the field on the right side of the checkbox.
If you do not confirm this option than Turboveg will generate species codes for you. In general Turboveg will generate codes where the first 4 characters are derived from the genus name, and other 3 characters are derived from the epitheton.
If you confirm, Turboveg will check whether the codes are unique, as far as it concerns valid species. If it turns out that the codes are not unique that redo the import and do not confirm this option.

Common names included: Confirm if the input file has a separate field with information on common names. Common names are also known as non-scientific, or trivial names. You can select the field on the right side of the checkbox.

Genus names included: Confirm if in the input file genera are included as separate taxa. For example *Abies species*, or *Zostara species*. If you do not confirm, Turboveg will automatically add a record for each genus present in the list.

Author citation included: Confirm if the species names are made up with author citation.

Create protected list: Create a protected species list if you want to share the list with other users, and want to avoid that changes can be made (in order to keep species data from different users compatible). The exception applies for species with numbers 90.000 or higher.

Species names: Select the name of the field (column) in the input file that holds the species names.

- Examples of species lists

- A very basic list (indication for subspecies or variant left out):

```
Cladonia glauca
Cladonia gracilis
Cladonia gracilis gracilis
Cladonia gracilis elongata
Cladonia gracilis turbinata
Cladonia grayi
Cladonia humilis
Cladonia incrassata
Cladonia macilenta
```

- A basic list:

```
Cladonia glauca
Cladonia gracilis
Cladonia gracilis ssp. gracilis
Cladonia gracilis ssp. elongata
Cladonia gracilis ssp. turbinata
Cladonia grayi
Cladonia humilis
Cladonia incrassata
Cladonia macilenta
```

- A more sophisticated list (author citation included):

```
Cladonia glauca Floerke
Cladonia gracilis (L.) Willd.
Cladonia gracilis (L.) Willd. ssp. gracilis
Cladonia gracilis (L.) Willd. ssp. elongata (Ach.) Ahti
```

```
Cladonia gracilis (L.) Willd. ssp. turbinata (Ach.) Ahti
Cladonia grayi G. Merr. ex Sandst.
Cladonia humilis (With.) J.R. Laundon
Cladonia incrassata Floerke
Cladonia macilenta Hoffm.
```

- List with valid species and synonyms (indicated with ’S’)

```
    Cladonia glauca Floerke
    Cladonia gracilis (L.) Willd.
    Cladonia gracilis (L.) Willd. ssp. gracilis
    Cladonia gracilis (L.) Willd. ssp. elongata (Ach.) Ahti
S   Cladonia elongata (Wulfen.) Hoffm.
S   Cladonia nigripes (Nyl.) Trass
S   Cladonia gracilis (L.) Willd. var. nigripes (Nyl.) Ahti
    Cladonia gracilis (L.) Willd. ssp. turbinata (Ach.) Ahti
S   Cladonia gracilis (L.) Willd. var. dilatata auct.
    Cladonia grayi G. Merr. ex Sandst.
    Cladonia humilis (With.) J.R. Laundon
    Cladonia incrassata Floerke
    Cladonia macilenta Hoffm.
```

- list with valid species, synonyms, species numbers, and species codes

```
    176 CLAOGLA Cladonia glauca Floerke
    177 CLAOGRC Cladonia gracilis (L.) Willd.
    178 CLAOG-G Cladonia gracilis (L.) Willd. ssp. gracilis
    179 CLAOG-E Cladonia gracilis (L.) Willd. ssp. elongata (Ach.) Ahti
S   179 CLAOG-E Cladonia elongata (Wulfen.) Hoffm.
S   179 CLAOG-E Cladonia nigripes (Nyl.) Trass
S   179 CLAOG-E Cladonia gracilis (L.) Willd. var. nigripes (Nyl.) Ahti
    180 CLAOG-T Cladonia gracilis (L.) Willd. ssp. turbinata (Ach.) Ahti
S   180 CLAOG-T Cladonia gracilis (L.) Willd. var. dilatata auct.
    181 CLAOGRA Cladonia grayi G. Merr. ex Sandst.
    182 CLAOHUM Cladonia humilis (With.) J.R. Laundon
    183 CLAOINC Cladonia incrassata Floerke
    184 CLAOMAI Cladonia macilenta Hoffm.
```

8.6 Delete a species list

Menu: **Manage | Species lists | Delete**

You can delete a species list by selecting a name from the list.

8.7 Modify an ecological database

Menu: **Manage | Species list | Edit | <choose the list you want to modify> | <click Modify>**

Add column: Add a new column to store species information.

Delete column: Remove a column (the current one) from the database.

Search: Search a species. You can also pop-up the search-dialog by pressing the *Spacebar*.

Synchronize: Extend the database with species that are present in the species list, but are not present in the ecological database. This means that you never have to add species by hand.

To edit data press *Enter* or double-click on a cell

8.8 Configuring an ecological database

Menu: **Manage | Species lists | Edit | <choose a species list> | <click on Configure >**

All fields present in the ecological database are shown in a table.

- Specify for each item an alias name in the column **Long alias**.
- Choose an item that serves as the key field when linking to the species list (species number). Click or press *Enter* on the column **Key field** to set the value to .T. (True).
- Specify with which items the calculations have to be made. These have to be items that are represented by numerical values, such as the Ellenberg indicator values. Click or press *Enter* on the column **Calculate field** to set the value to .T. (True). Specify a four-character abbreviation in the column **Short alias**.

To save the settings after completing, press **Save**.

8.9 Format longitude/latitude

Menu: **Manage | Format longitude/latitude**

Make a choice here how you have stored (if any) longitude/latitude values; as 'Decimal values', or as 'Degrees, Minutes, Seconds'. In the latter case the format should be defined.

8.10 Modify user privileges

Menu: **Manage | Users**

This option only concerns the network version.

Edit: Change the rights of a user.

New: Add a new user.

Delete: Remove a user from the list.

8.11 TurbovegCE settings

Menu: **Manage | TurbovegCE settings**

This options enables the definition of settings for TurbovegCE (Turboveg Compact Edition) on a PocketPC (PDA) using a management tool. This tool will not appear if a proper communication between desktopPC and PDA is not established. For communication between the two devices ActiveSync needs to be installed.

User: enter the name of the person who is going to work with the PDA concerned. The user name will be included in names of export files.

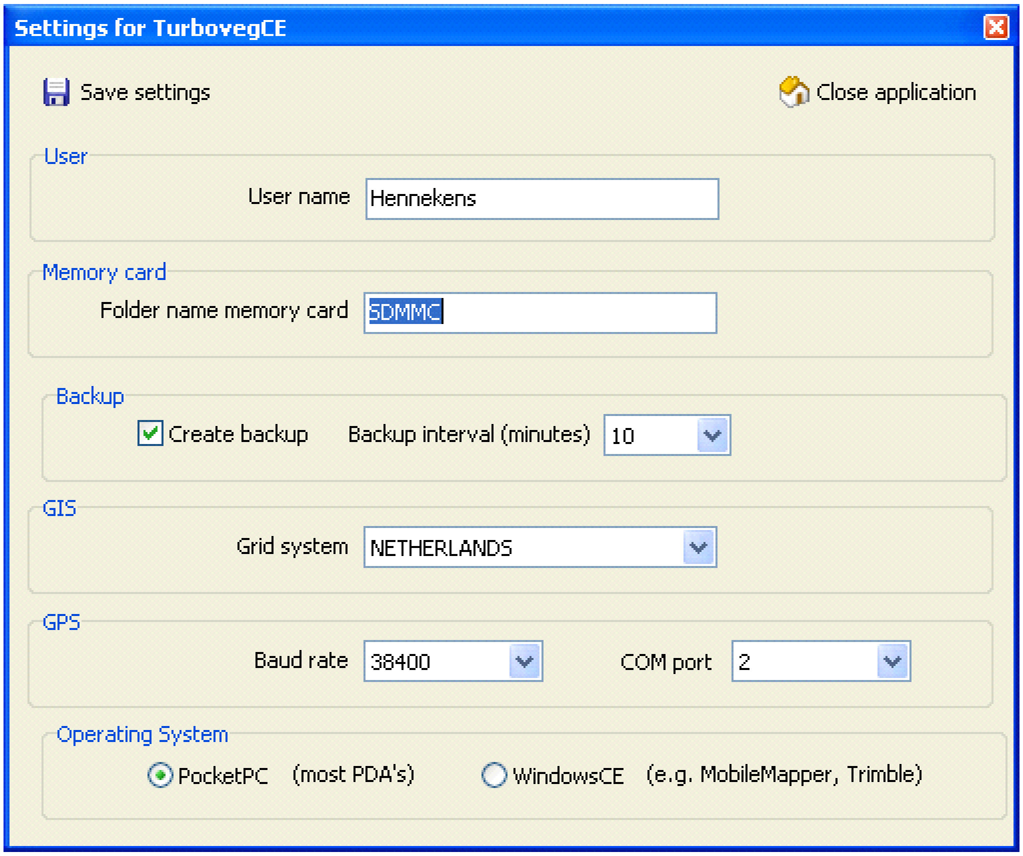
Memory card: It is very important to indicate the proper name for the memory card (if present). To find out what the exact name of the card on PDA is use the Windows Explorer to browse the directory structure. If properly indicated TurbovegCE will store most information on this card (backups, export and import files, maps, etc), not only saving main memory space, but also ensuring the safest storage of data.

Backup and Backup interval: It is recommended to switch on the automatic creation of backups.

Grid system: To be able to work with GIS maps (only Shapefiles are currently supported by TurbovegCE) a grid system should be selected. However, if your study area is outside the Netherlands, Germany or Ireland than 'NO GRID' should be selected.

Baud rate and COM port: Information on Baud rate and COM port concern the GPS receiver and should be obtained from its documentation.

Operating System: Select the Operating System running on the PDA concerned.



User

User name: Hennekens

Memory card

Folder name memory card: SDMMC

Backup

☑ Create backup

Backup interval (minutes): 10

GIS

Grid system: NETHERLANDS

GPS

Baud rate: 38400

COM port: 2

Operating System

● PocketPC (most PDA's)

○ WindowsCE (e.g. MobileMapper, Trimble)

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