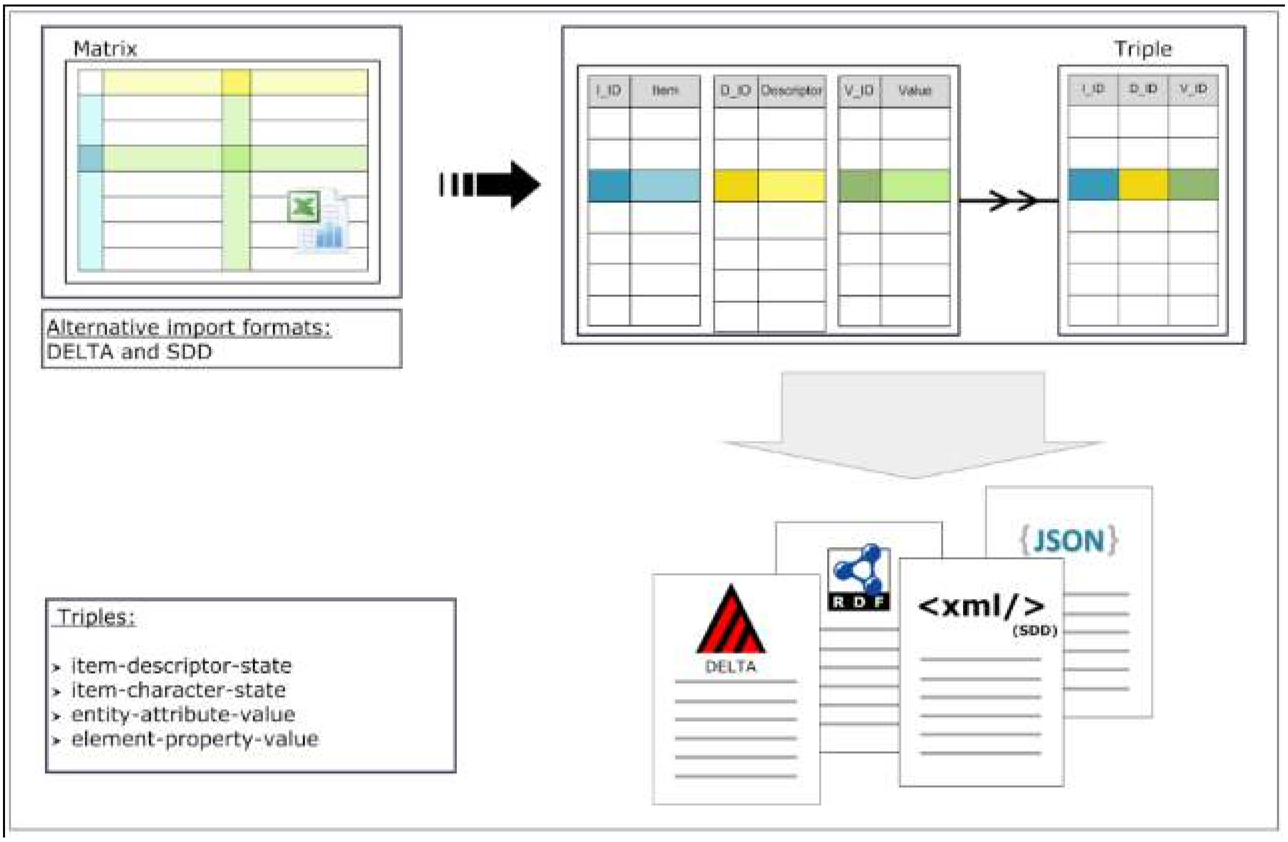
DiversityDescriptions

DiversityDescriptions (version 4) is part of the database framework Diversity Workbench. Each DWB module is devoted to a specific data domain. The domain of DiversityDescriptions covers the knowledge about descriptions of organisms and **descriptions of any** other **item**/ element/ entity which are object of diversity research. It can be used to describe individual organisms, research items/ objects (e.g. specimens, observation and measurement events, plots) as well as taxa, syntaxonomic entities (e.g. species, plant-sociological entities, ecosystems).

- The **descriptions** are characterized by a **triple structure**, namely 'item-descriptor-state' or 'item-descriptor-value' or 'item-character-character state' or 'entity-attribute-value' or 'element-property-value'.
- The **states or values**, which build the item/description, can be generalized to one of the presently supported data types (categorical states, quantitative values and statistical measures, molecular sequence data and free-form text as a fall-back option).
- The **descriptors** (= characters, attributes, properties) are not limited to morphological characters and functional traits, but could address physiological, ecological, behavioral and even interview parameter, some molecular descriptors and descriptors of data content schemes.



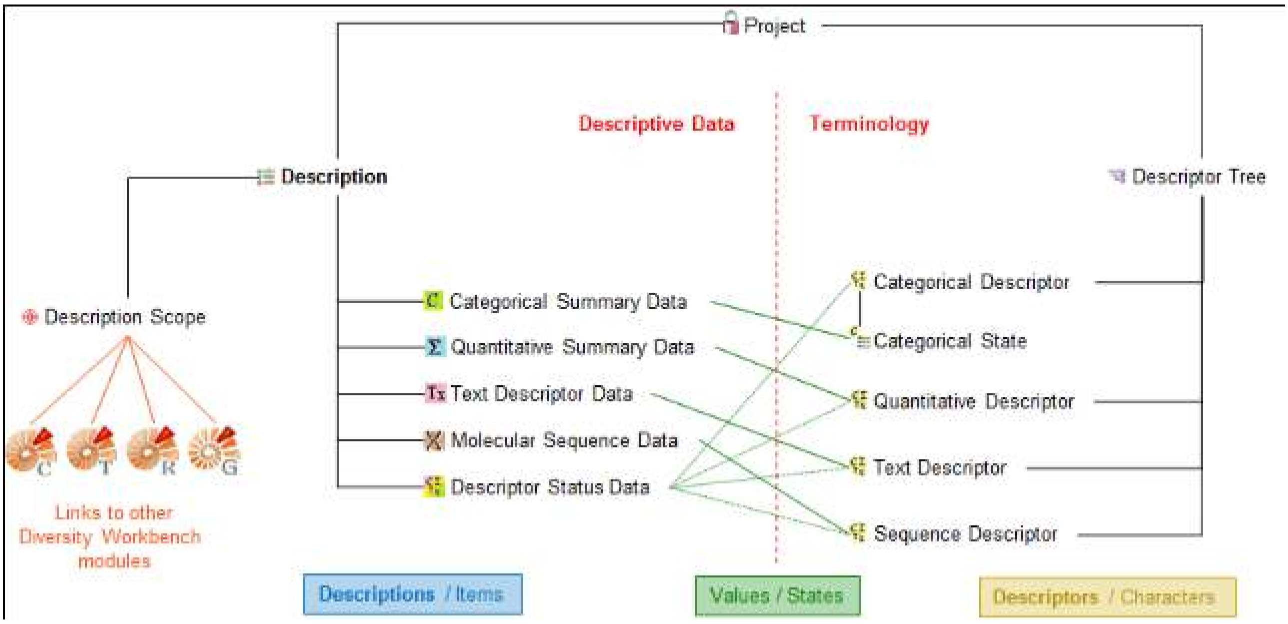
The image below gives a rough overview how the triple structure is represented in the data tables of DiversityDescriptions. A detailled database diagram including all tables and their data columns can be found here. At the right side you can see the descriptors and categorical states that build the **"descriptive terminology"**. Currently four descriptor types are supported:

1. **Categorical descriptor**

may be used for representing discrete enumerable categorical states, e.g. color: red - green - blue

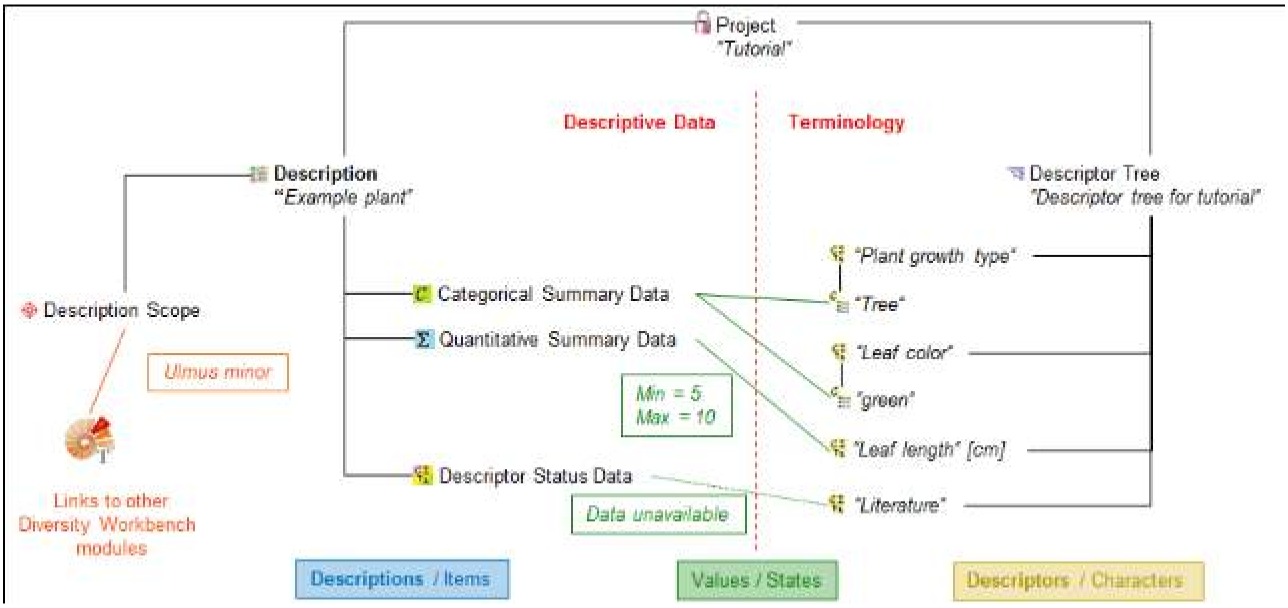
2. **Quantitative descriptor**
   may be used for storing numeric values, e.g. minimum, maximum, mean
3. **Text descriptor**
   free-form text, applicable if no other descriptor type is suitable
4. **Molecular sequence descriptor**
   may be used for storing nucleotide or protein sequences

While the first three descriptor types are most commonly known in the context of descriptive data, the molecular sequence descriptor is designed according the SDD standard of TDWG. (An alternate entry point to SDD can be found here.) In most cases molecular sequence data may be mapped to text descriptor data, e.g. for export to a DELTA file.



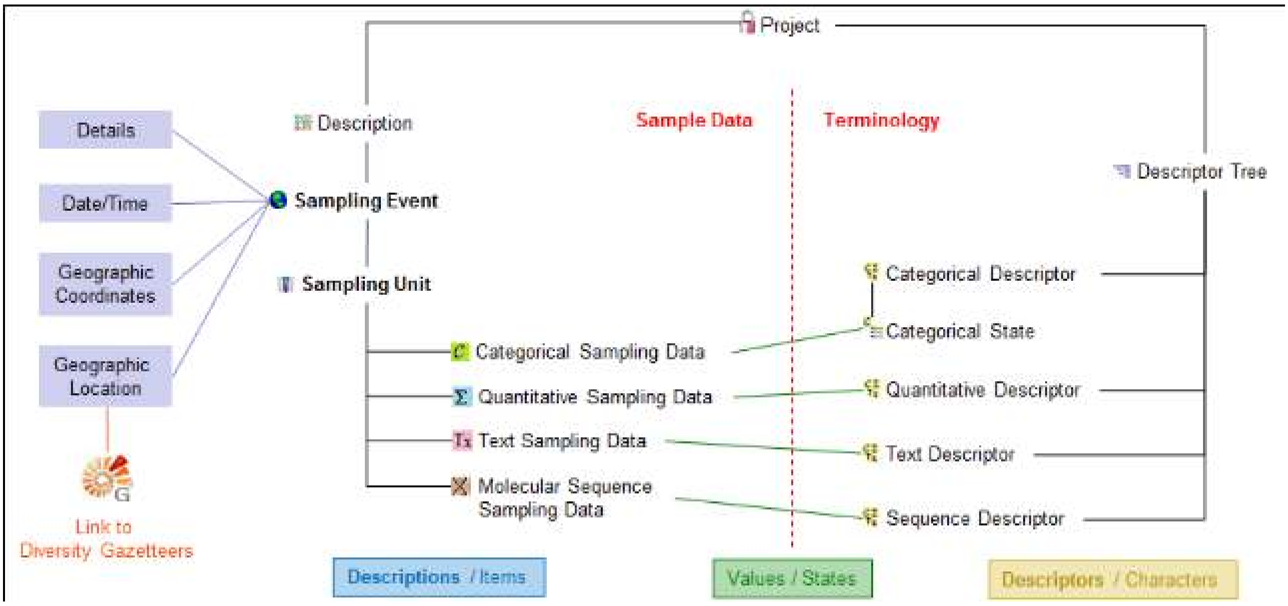
At the left side of the image above there are the **"descriptive data"**, which consist of the single description or item and the associated summary data. In analogy to the four descriptor types there are categorical and quantitative summary data, text descriptor data and molecular sequence data that reference the corresponding descriptor and store the actual values for the item (green lines). For an item description scopes can be specified, e.g. taxon names or specimens, which may optionally be linked to the corresponding module of the Diversity Workbench (orange lines at the very left). Additionally for each descriptor a data status may be specified, e.g. to indicate that a certain descriptor/character should be specified but actually no data are available (Descriptor Status Data).

To make this very abstact overview a little bit more tangible, find in the image below a tiny example taken from the tutorial. The "Example plant" is a "Tree" and has the "Leaf color" "green" (Categorical Summary Data). Its "Leaf length" is between 5 and 10 cm (Quantitative Summary Data) and for "Literature" (currently) no data are available. Additionaly the taxon name "Ulmus campetris" has been associated to the "Example plant" (Description Scope).



DiversityDescriptions keeps only descriptive data. Data of other realms like e.g. taxonomy are handled in separate modules. For an overview of the available modules see Diversity Workbench. DiversityDescriptions might also be used as a stand-alone application.

Besides the descriptive data that represent the summarized data e.g. for a certain species, Diversity Descriptions provides the feature of appending Sample Data to each description.



To each description or item several **"sampling events"** may be appended, which build the anchor for the **"sampling units"**. The sampling event holds additional data like the date and time or a time span when the data were collected, the geographic location and coordinates. The sampling unit represents a tuple of values that belong to an individual probe, e.g. an evaluated organism (see image above). The sample data may be exported together with the descriptive data to the SDD format, which provides full sample data support. Optionally sample data may be exported to the DELTA format, where each sampling unit is mapped to a separate item.

DiversityDescriptions 4 is based on Microsoft SQL-Server (version 2008 R2 or newer recommended) and the .Net Framework, Version 4.8.

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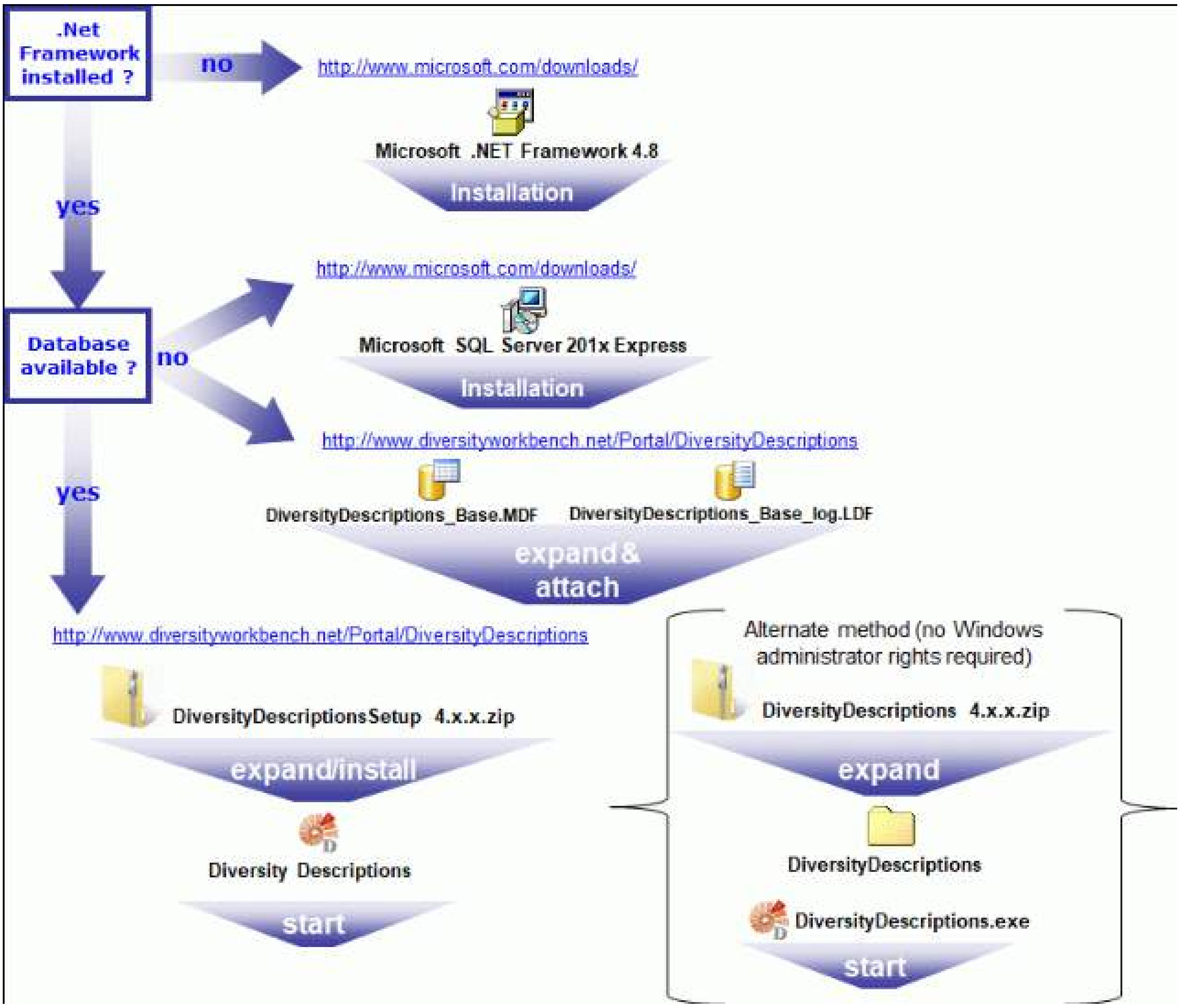
Even if you are already familiar with other Diversity Workbench modules, it is strongly recommended to take a look into the Tutorial to get an overview of the main features of DiversityDescriptions.

Installation

To run DiversityDescriptions, you need the database and the client. All parts are free and can be downloaded from http://www.microsoft.com/downloads/ and http://www.diversityworkbench.net/Portal/.

The image below gives an overview of the installations and files needed. Starting with Diversity Descriptions 4.x.x an installer tool will be provided, which copies the needed files into the program files directory of the system. For installation Windows admin rights are required. As an alternate way the well-known method of providing a .zip file with the program directory might be provided, too. In any way the user files will be kept separated from the program files (see Resources directory).



Client

The client is based on the .Net framework **version 4.8** from Microsoft. If not already present, you have to install the framework first. Download and install the Microsoft .NET Framework (see http://www.microsoft.com/downloads/ for the latest versions).

Download the files for DiversityDescriptions from http://www.diversityworkbench.net/Portal/ provided as a zip archive. In case of a setup file (.msi) execute the installer and follow the instructions. In case of a compressed program folder, copy all files (DiversityDescriptions.exe

, DiversityDescriptions.chm , DiversityWorkbench.dll ...) into your working directory.

Please observe the general download notes of the DiversityWorkbench page!

Database

For the installation of a local database see the section Installation of the database.

Menu

Overview of the menu in DiversityDescriptions:

Connection

Database ...	Choose one of the databases available on the ser will be listed to which the user has access permis
Reconnect to database	Reconnect to the actual database and reload bas
Auto connect	Automatically connect to database (only with wir
Module connections ...	Edit the connections to the other modules within
Timeout for database ...	Set the timeout for database queries.
Timeout for web requests ...	Set the timeout for web requests.
Transfer previous settings ...	Transfer the settings for IP-Address and port of t database, login etc. of a previous version of the version.
Current server activity ...	View current activities on the database server.
Quit	Quit the application and stop all processes starte

Edit

Descriptions	Select edit mode for descriptions.
Descriptors	Select edit mode for descriptors.
Projects	Select edit mode for projects.
Tranlsations ...	Edit or view translations.
Summarize descriptions ...	Summarize description data.
Summarize sampling data ...	Summarize sampling data.

Grid

Description grid ...	Edit or view descriptions in a grid.
Sample data grid ...	Edit or view sample data in a grid.
Table editor	
Projects ...	Edit the projects in the query result list.
Sampling events ...	Edit the sampling events for the descriptions in th
Descriptions ...	Edit the descriptions in the query result list.
Description scopes ...	Edit the scopes of the descriptions in the query r
Description resources ...	Edit the resources for descriptions in the query re
Descriptors ...	Edit the descriptors in the query result list.
Descriptor resources ...	Edit the resources for descriptors in the query re
Categorical states ...	Edit the categorical states of the descriptors in t
Categorical state resources ...	Edit the resources for the categorical states of th result list.
Descriptor tree node resources ...	Edit the resources for the descriptor tree nodes result list.
Resource variants ...	Edit the resources for entities in the query result
Translations ...	Edit the translations for entities in the query resu

Query

Show query	Show the query window.
Preferred project ...	Set or view the preferred project for query windo
Extended query ...	Extended query for description data.

Data

Save dataset	Save the actual dataset in the database.
Restore from log ...	Restore deleted datasets from the log tables in th administrator).
Generate document ...	Generate a document with descriptions, descripto query list.
Import	
Import wizard	Import wizard.
Matrix wizard ...	Import descriptor, description and sample data fr text file.
Sample data ...	Import sample data for descriptions from a tabula
Descriptions ...	Import descriptions from a tabulator separated te
Descriptors ...	Import descriptors from a tabulator separated tex
Import resources	Import resources.
Description resources ...	Import description resources from a tabulator sep
Descriptor resources ...	Import descriptor resources from a tabulator sepa
Categorical state resources ...	Import categorical state resources from a tabulat
Descriptor tree node resources ...	Import descriptor tree node resources from a tab
Resource variants ...	Import resource variants from a tabulator separat to append resource variants.
Organize sessions ...	Organize import sessions.
Import SDD ...	Import SDD files.
Import DELTA ...	Import DELTA files.
Import questionnaire data ...	Import revised data received from HTML forms.
Export	
Matrix wizard ...	Export descriptor and description data as tabulat generate an import schema for the Matrix Import
Export data ...	Export data in a structured data file format (SDD
Export questionnaires ...	Export description data of a project or from a que
Export lists	Export tabulator separated lists.
Sample data list ...	Export sample data list.
Descriptions list ...	Export descriptions list.
Descriptors list ...	Export descriptors list.
Resource data list ...	Export resource data list document for review an modified data.
Export CSV ...	Export database tables in CSV format.
Cache database ...	Export data of selected projects into a cache dat
Backup database ...	Create a backup of the database.
File operations	File operations (no database connection needed)
Convert SDD file ...	Convert a SDD file to DELTA or EML without data
Convert DELTA file ...	Convert an DELTA file to SDD or EML without dat

Check SDD file ...	Check if an SDD file is compliant to the XML sche
Check EML file ...	Check if an EML file is compliant to the XML sche

Administration

Change password ...	Changing the password of a user.
Database	
Database tools ...	Tools for the administration of the objects in the
Documentation ...	Generate documentation of the information mode
Logins ...	Administration of the logins of the server their pe
Maintenance ...	Maintenance of database entries, especially, if c
Rename database ...	Rename the current database.
Set published address ...	Setting the address published for links by other n
Linked server ...	Administration of the linked servers.
Projects ...	Administration of the projects.
Resources directory ...	Changing the the resources directory.

Help

Manual	Opens the user manual.
Feedback ...	Opens a window for sending feedback.
Feedback history ...	Opens a window for browsing former feedback.
Edit feedback ...	Opens a window for feedback editing - only for sp
Statistics ...	Overview of statistical data for the database cor
Info ...	Show the version of the program and correspondi
Websites	Websites related to Diversity Descriptions.
Download application ...	Download Diversity Descriptions from the website project.
Information model ...	Inspect the information model on the website of t project.
SDD homepage ...	Visit the TDWG homepage for the SDD standard.
EML homepage ...	Visit the KNB homepage for the EML standard.
DELTA homepage ...	Visit the DELTA homepage for the DELTA standar
Example files ...	Visit the repository of Diversity Descriptions exan
Error log	View the actual error log file.
Keep error log	Change the error log settings to "Keep error log".
Clear error log at program start	Change the error log settings to "Clear error log a
Clear error log	Clear the actual error log file.

Update

Update database ...	Update the database to the current version.
Update client ...	Download the current version of the client.

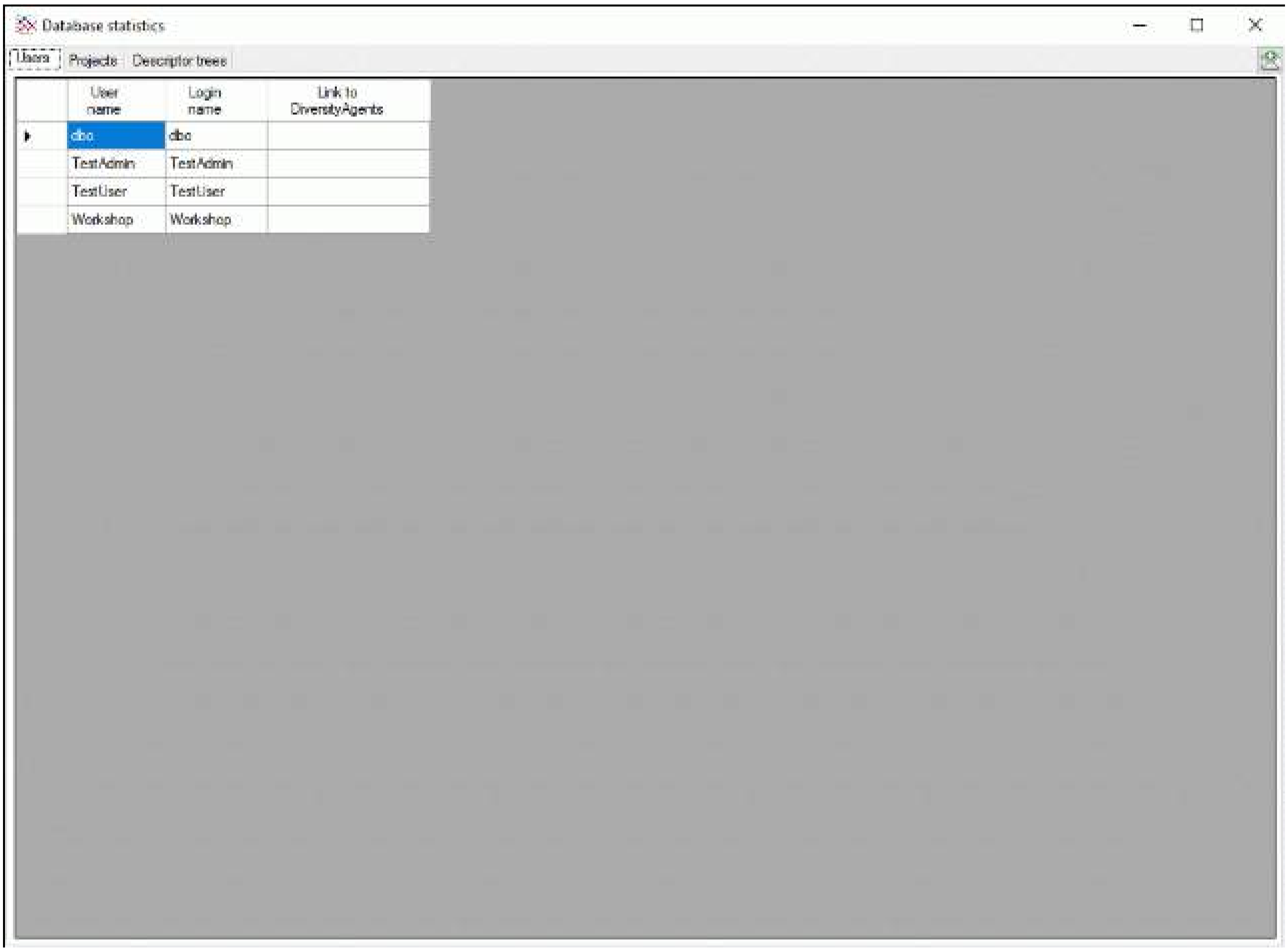
Manual

The online manual DiversityDescriptions.chm must be placed in your application folder, together with the application DiversityDescriptions.exe and the library DiversityWorkbench.dll. To get information to any topic in the application DiversityDescriptions and open this manual, just click on the field you need information about and press F1. To open the manual from the menu, choose **Help -> Manual ...**.

Statistics

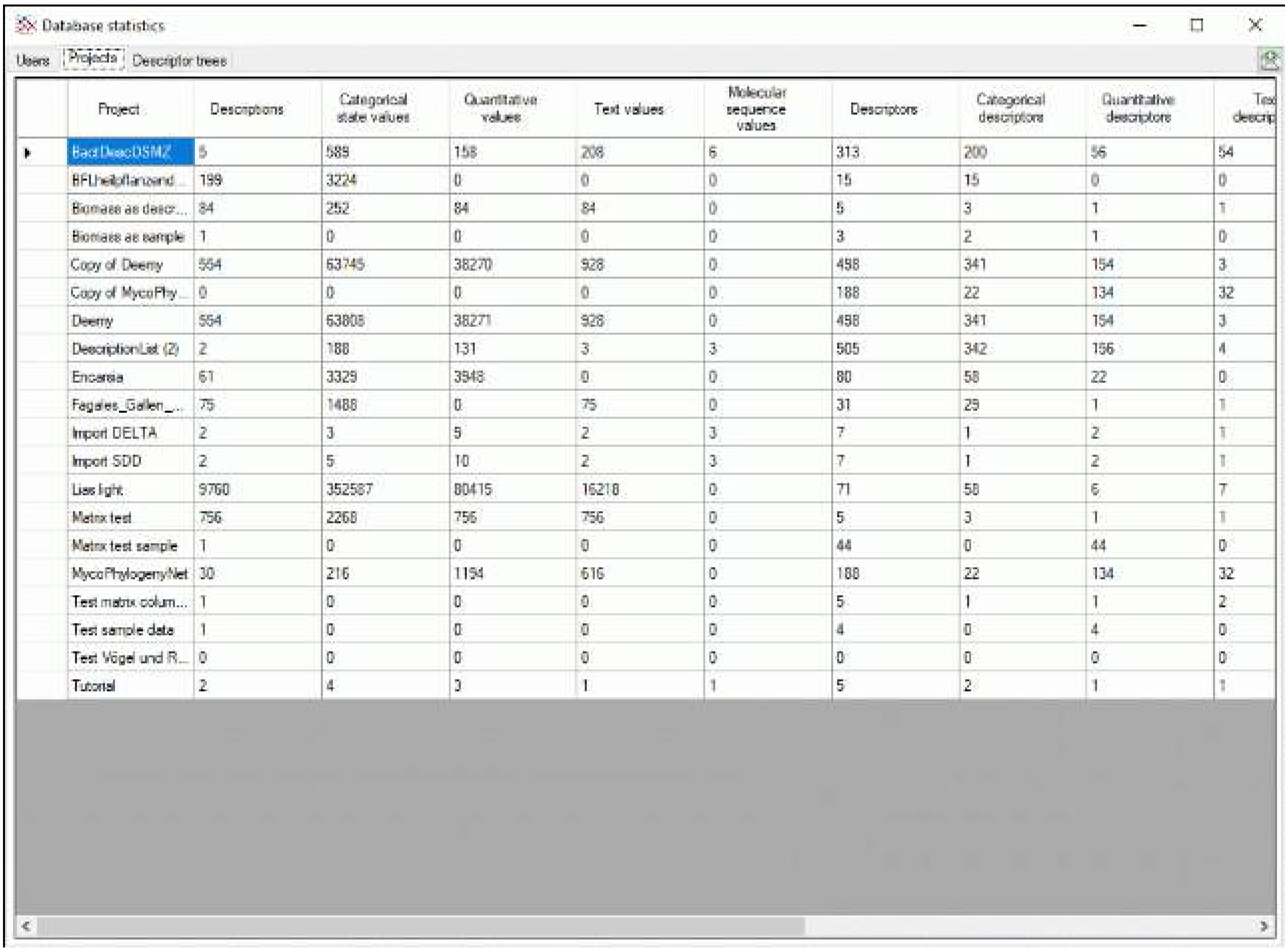
For statistical information about the database contents choose **Help -> Statistics ....**

The **Users** tab shows information about the users with access to the database. This output may be restrictied to your own data if you do not have sufficient acces rights (see image below).



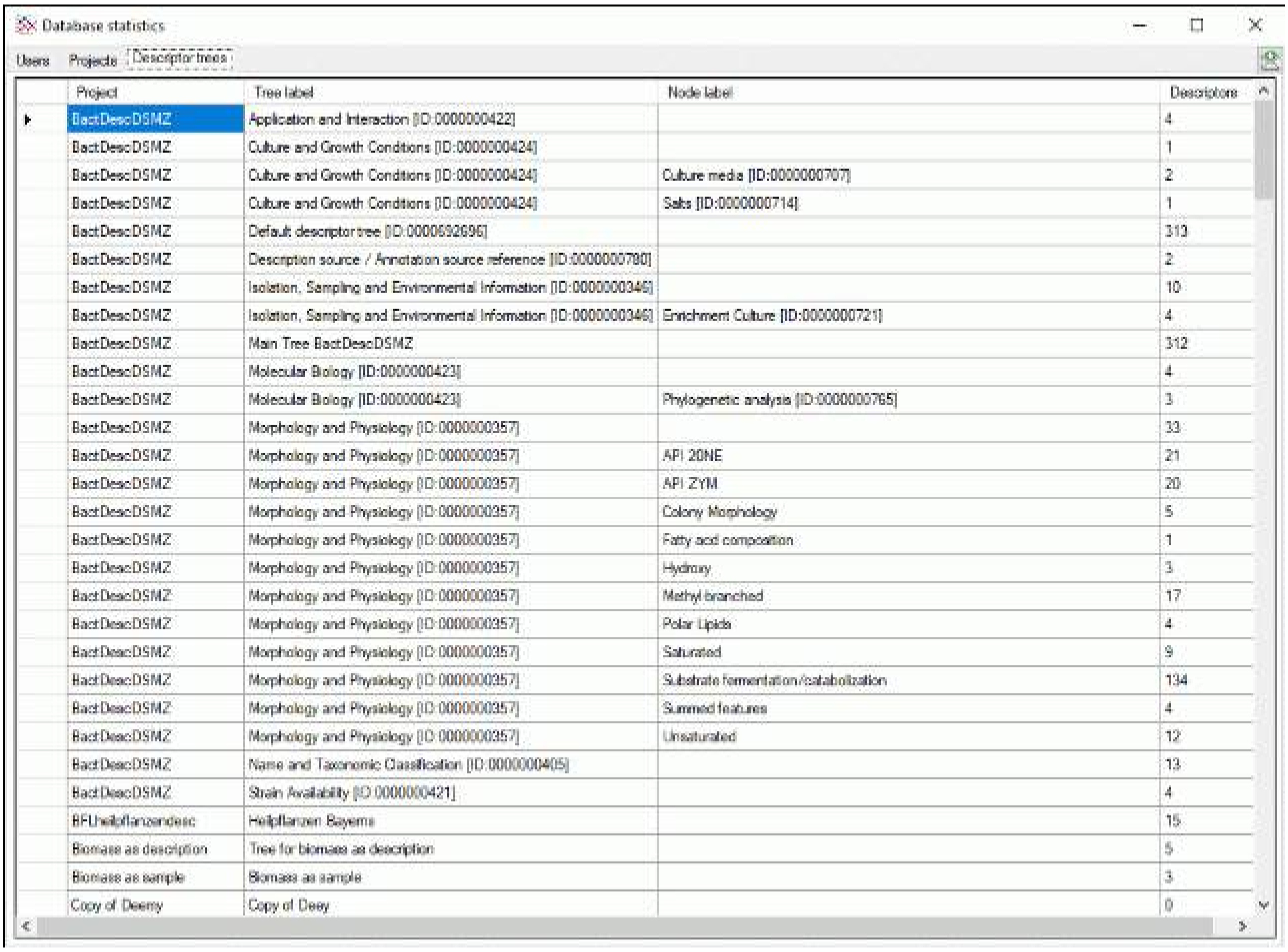
User name	Login name	Link to DiversityAgents
dbo	dbo	
TestAdmin	TestAdmin	
TestUser	TestUser	
Workshop	Workshop	

The **Projects** tab shows information about the local projects in the database and the entered data (see image below).



Project	Descriptions	Categorical state values	Quantitative values	Text values	Molecular sequence values	Descriptors	Categorical descriptors	Quantitative descriptors	Tex descrip
BactDescDSMZ	5	589	158	208	6	313	200	56	54
BFLheilpflanzend...	199	3224	0	0	0	15	15	0	0
Biomass as descr...	84	252	84	84	0	5	3	1	1
Biomass as sample	1	0	0	0	0	3	2	1	0
Copy of Deemy	554	63745	38270	928	0	498	341	154	3
Copy of MycoPhy...	0	0	0	0	0	188	22	134	32
Deemy	554	63808	38271	928	0	498	341	154	3
DescriptionList (2)	2	188	131	3	3	505	342	156	4
Encarsia	61	3329	3948	0	0	80	58	22	0
Fagales_Gallen_...	75	1488	0	75	0	31	29	1	1
Import DELTA	2	3	5	2	3	7	1	2	1
Import SDD	2	5	10	2	3	7	1	2	1
Lias light	9760	352587	80415	16218	0	71	58	6	7
Matrix test	756	2268	756	756	0	5	3	1	1
Matrix test sample	1	0	0	0	0	44	0	44	0
MycoPhylogenyNet	30	216	1194	616	0	188	22	134	32
Test matrix colum...	1	0	0	0	0	5	1	1	2
Test sample data	1	0	0	0	0	4	0	4	0
Test Vögel und R...	0	0	0	0	0	0	0	0	0
Tutorial	2	4	3	1	1	5	2	1	1

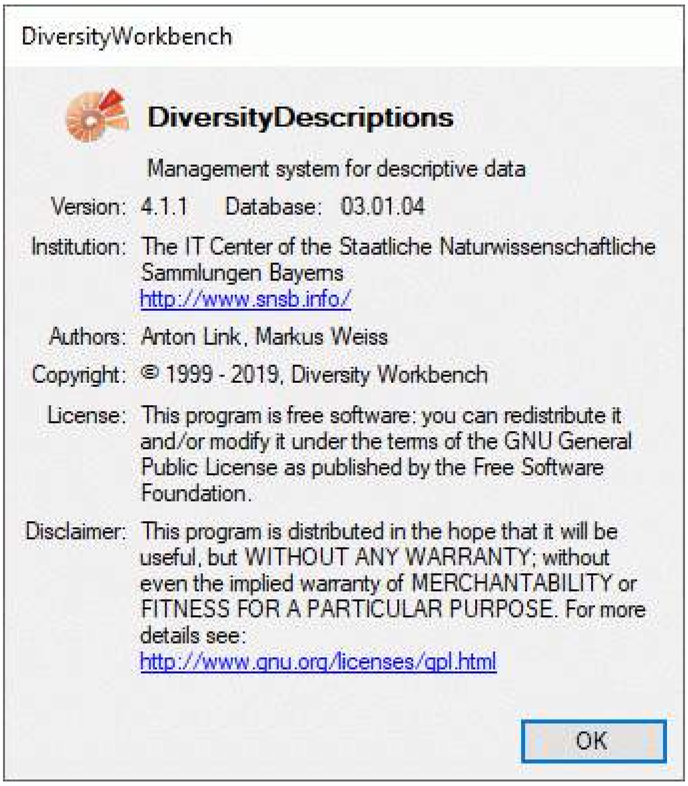
The **Descriptor trees** tab shows information about the local projects in the database, their descriptor trees and nodes and the number of assigned descriptors (see image below).



Project	Tree label	Node label	Descriptors
BactDescDSMZ	Application and Interaction [ID:0000000422]		4
BactDescDSMZ	Culture and Growth Conditions [ID:0000000424]		1
BactDescDSMZ	Culture and Growth Conditions [ID:0000000424]	Culture media [ID:0000000707]	2
BactDescDSMZ	Culture and Growth Conditions [ID:0000000424]	Salts [ID:0000000714]	1
BactDescDSMZ	Default descriptor tree [ID:0000692696]		313
BactDescDSMZ	Description source / Annotation source reference [ID:0000000780]		2
BactDescDSMZ	Isolation, Sampling and Environmental Information [ID:0000000346]		10
BactDescDSMZ	Isolation, Sampling and Environmental Information [ID:0000000346]	Enrichment Culture [ID:0000000721]	4
BactDescDSMZ	Main Tree BactDescDSMZ		312
BactDescDSMZ	Molecular Biology [ID:0000000423]		4
BactDescDSMZ	Molecular Biology [ID:0000000423]	Phylogenetic analysis [ID:0000000765]	3
BactDescDSMZ	Morphology and Physiology [ID:0000000357]		33
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	API 20NE	21
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	API ZYM	20
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Colony Morphology	5
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Fatty acid composition	1
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Hydroxy	3
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Methyl branched	17
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Polar Lipids	4
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Saturated	9
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Substrate fermentation/catabolization	134
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Summed features	4
BactDescDSMZ	Morphology and Physiology [ID:0000000357]	Unsaturated	12
BactDescDSMZ	Name and Taxonomic Classification [ID:0000000405]		13
BactDescDSMZ	Strain Availability [ID:0000000421]		4
BFUheilpflanzendesc	Heilpflanzen Bayerns		15
Biomass as description	Tree for biomass as description		5
Biomass as sample	Biomass as sample		3
Copy of Deemy	Copy of Deey		0

Version

For information about the version of the client application and the database choose **Help-> Info ...**



Management system for descriptive data

Version: 4.1.1 Database: 03.01.04

Institution: The IT Center of the Staatliche Naturwissenschaftliche Sammlungen Bayerns http://www.snsb.info/

Authors: Anton Link, Markus Weiss

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The current version in the example above is 4.1.1. The required database version is 3.1.4.

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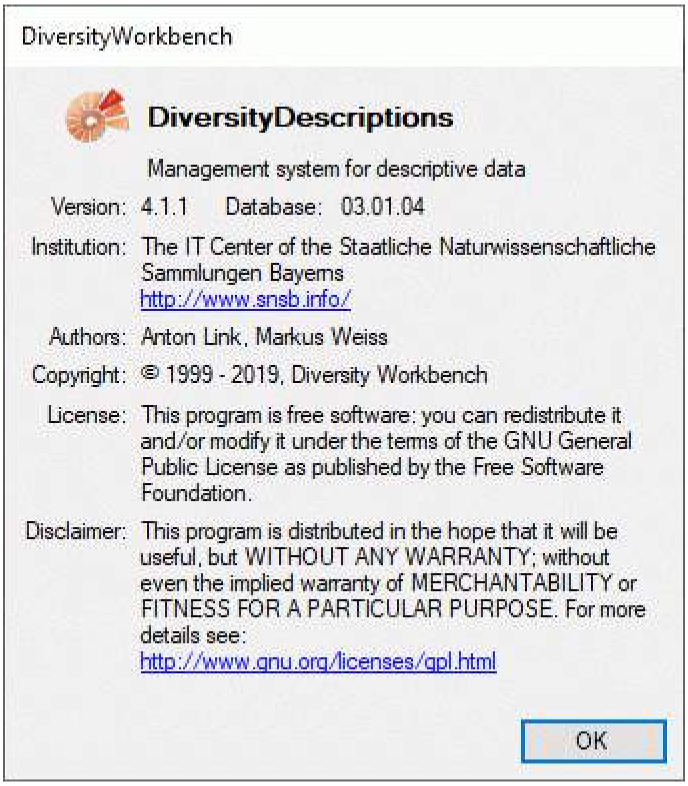
For information about the license of the client software choose **Help -> ℹInfo ...**



DiversityDescriptions

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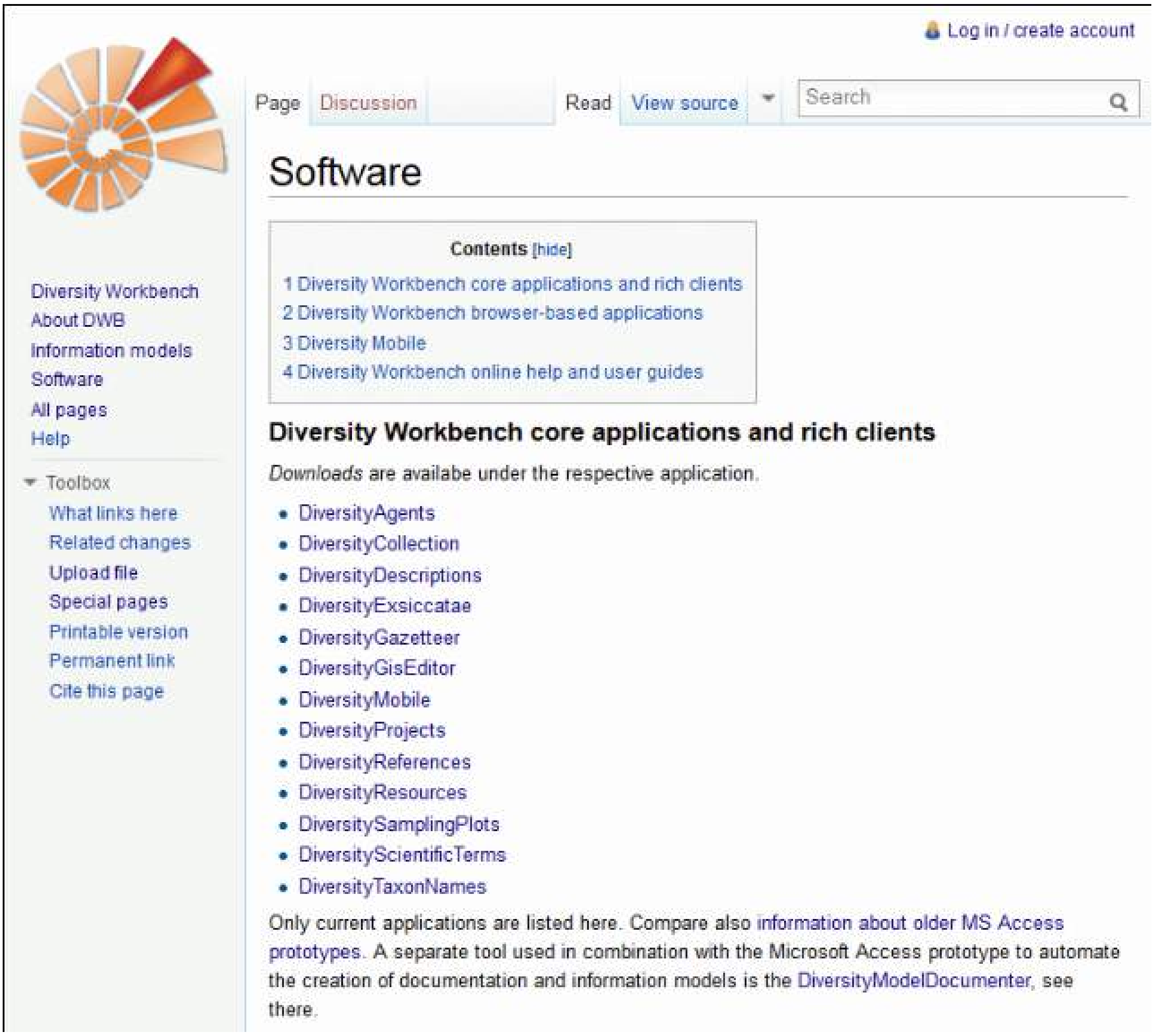
Update of database and client

DiversityDescriptions is still in development. Therefore regular updates for the database and the client will be provided. When you start the program and connect to a database, the program will check if it is compatible with the database or if the database needs an update. In any of these cases write access to the database will be locked to prevent possible data corruption. If a new client version is required, an **Update** entry in the menu bar will appear. This menu will contain an **Update client ...** entry. Click on it to open the webpage where you can download the cient as shown below.



Software

Contents [hide]

1 Diversity Workbench core applications and rich clients
2 Diversity Workbench browser-based applications
3 Diversity Mobile
4 Diversity Workbench online help and user guides

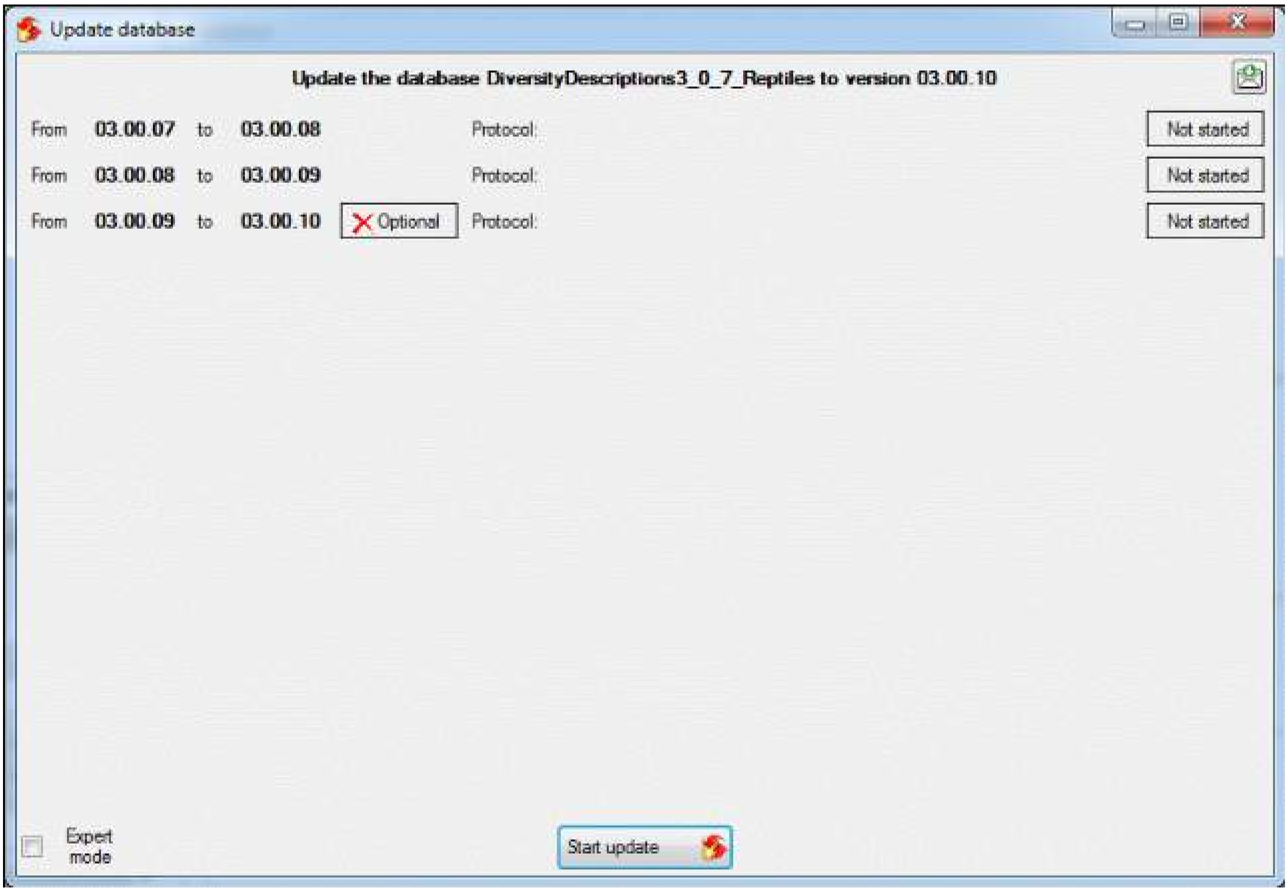
Diversity Workbench core applications and rich clients

Downloads are availabe under the respective application.

- DiversityAgents
- DiversityCollection
- DiversityDescriptions
- DiversityExsiccatae
- DiversityGazetteer
- DiversityGisEditor
- DiversityMobile
- DiversityProjects
- DiversityReferences
- DiversityResources
- DiversitySamplingPlots
- DiversityScientificTerms
- DiversityTaxonNames

Only current applications are listed here. Compare also information about older MS Access prototypes. A separate tool used in combination with the Microsoft Access prototype to automate the creation of documentation and information models is the DiversityModelDocumenter, see there.

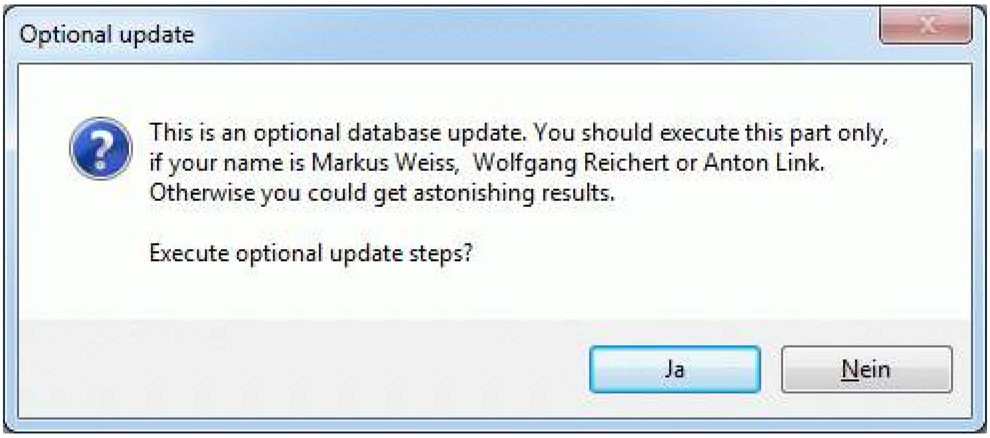
If you are database owner (role = "db_owner" or user = "dbo") and the database needs to be updated, the **Update** entry will appear in themenu bar and contain an **Update database ...** entry. Select this entry to open a window as shown below to run the provided update scripts, delivered with the client software. These scripts needs to run consecutively, so e.g. to update from version 3.0.7 to 3.0.10 you have to run the scripts DiversityDescriptionsUpdate_030007_to_030008, DiversityDescriptionsUpdate_03008_to_030009 and DiversityDescriptionsUpdate_030009_to_030010. The program will guide you through these steps and check for the scripts. All you have to do is click the **Start update** button.



Update the database DiversityDescriptions3_0_7_Reptiles to version 03.00.10

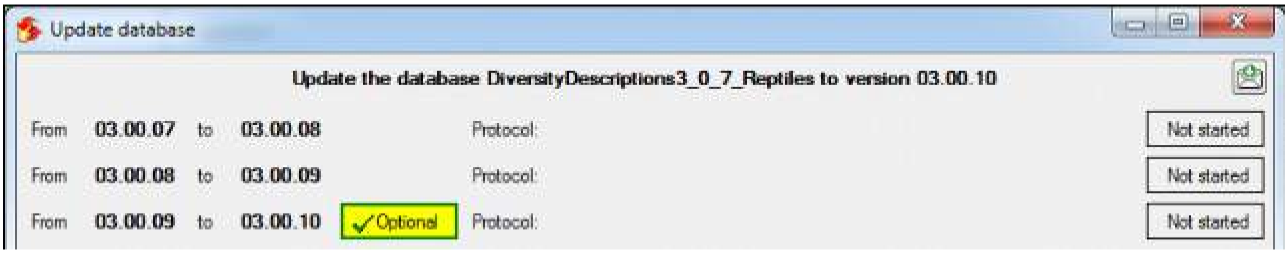
From 03.00.07 to 03.00.08 Protocol: Not started
From 03.00.08 to 03.00.09 Protocol: Not started
From 03.00.09 to 03.00.10 ✗ Optional Protocol: Not started

In some cases updates may be optional, e.g. if a special adjustment for dedicated projects shall be introduced. By default these optional updates will be skipped (see picture above, last update script). By clicking on ✗ **Optional** you get a description of the optional update and will be offered to activate it (see pictures below).



This is an optional database update. You should execute this part only, if your name is Markus Weiss, Wolfgang Reichert or Anton Link. Otherwise you could get astonishing results.

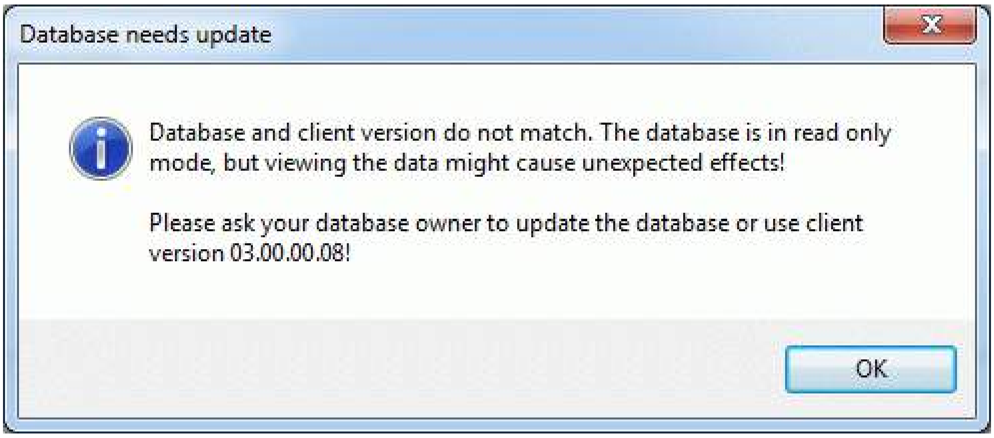
Execute optional update steps?



Update the database DiversityDescriptions3_0_7_Reptiles to version 03.00.10

From 03.00.07 to 03.00.08 Protocol: Not started
From 03.00.08 to 03.00.09 Protocol: Not started
From 03.00.09 to 03.00.10 ✓ Optional Protocol: Not started

If you do not have sufficient rights to update the database, a message window will appear that informs you about a compatible client version. You may contact the database owner to perform the database update or download the appropriate client software by selecting **Help -> Websites -> Download application ...** from the menu.

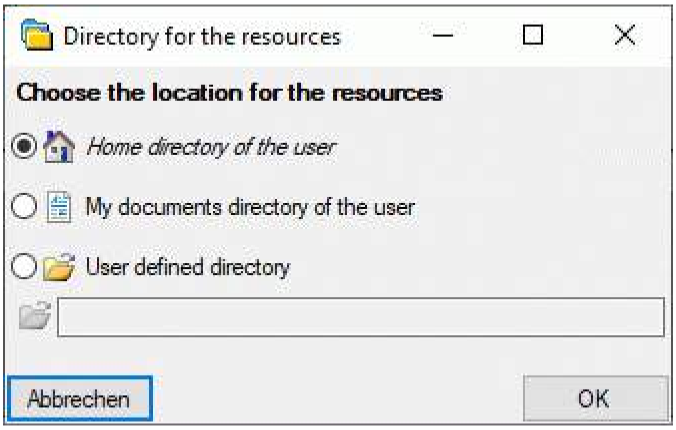


Database and client version do not match. The database is in read only mode, but viewing the data might cause unexpected effects!

Please ask your database owner to update the database or use client version 03.00.00.08!

Resources directory

In the resources directory all files are stored that have been generated by Diversity Descriptions, e.g. due to export. Furthermore you may store files here that shall be used for data import into the Diversity Descriptions database and the error log file. The resources directory may be set via the menu **Administration->** **Resources directory ...** (see image below).



There are 3 possibilities for the resources directory:

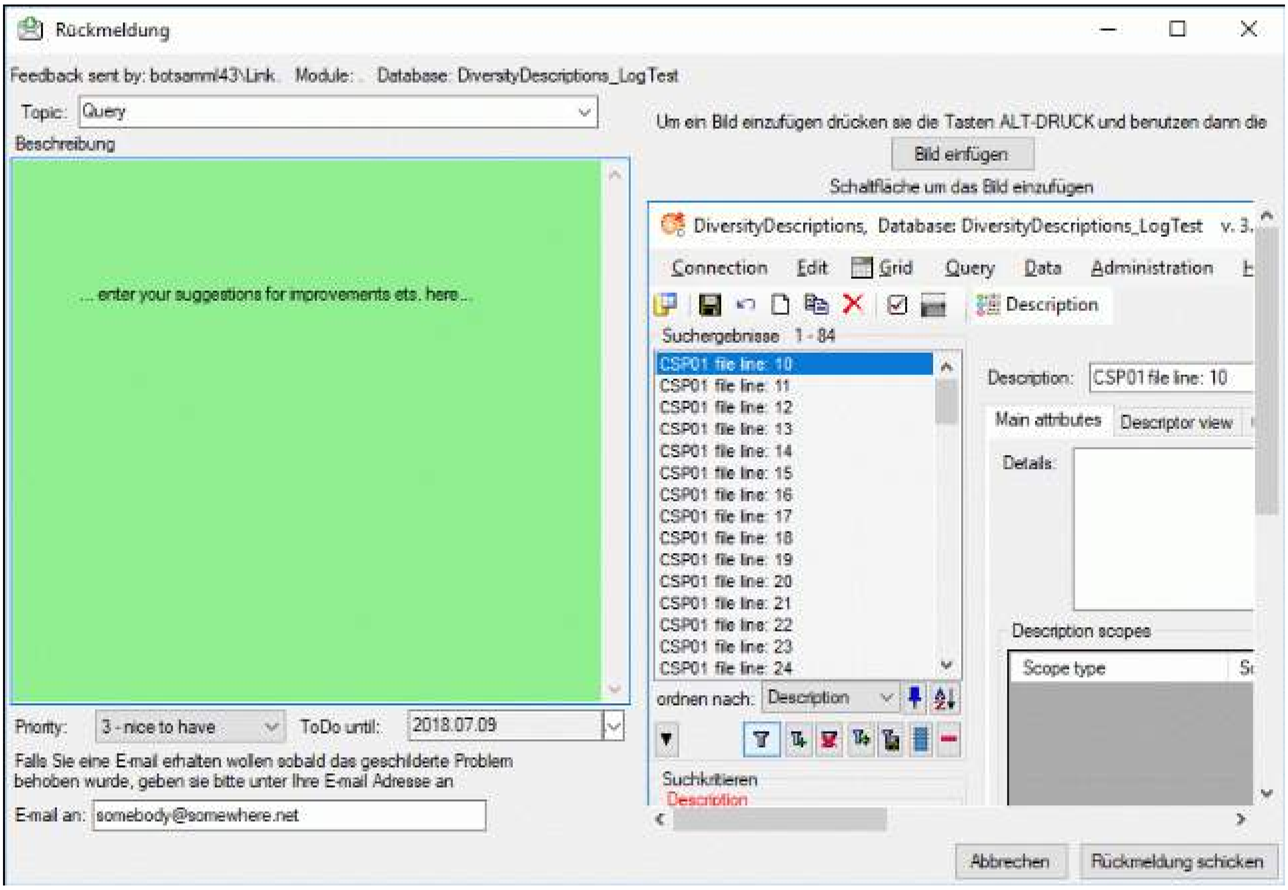
- Select the "Home directory" of the user (may be definded via %HOMEDRIVE%%HOMEPATH%)
- Select the "My Documents" directory of the user
- Select any directory you have read/write access (User defined)

The default is set to Home. Below this node the directories "DiversityWorkbench" will be created and below that "DiversityDescriptions", which will contain all files that a Diversity Descripiton user needs user need access to. If you install additional Diversity Workbench applikations and use resources directory option "Home directory", they will all get dedicated directories under "..<user>\DiversityWorkbench\".

Certain directories are hidden (Query, Settings, Spreadsheet) and are handled by the software i.e. the content should not be changed by the user. The other folders (Export, Import and so on) are a copy of folders placed in the program directory (see below).

Feedback

If you have suggestions for improvement, need any changes in the program or encounter an error you can give a feedback to the administrator. Click on the [**ALT**] and [**PRINT**] buttons to get a screen shot of your current form. After creating the screen shot choose **Help ->** **Feedback** from the menu to open the feedback window as shown below.



Feedback sent by: botsamml43\Link. Module: . Database: DiversityDescriptions_LogTest

Topic: Query

Beschreibung

... enter your suggestions for improvements ets. here...

Priority: 3 - nice to have

ToDo until: 2018.07.09

Falls Sie eine E-mail erhalten wollen sobald das geschilderte Problem behoben wurde, geben sie bitte unter Ihre E-mail Adresse an

E-mail an: somebody@somewhere.net

Um ein Bild einzufügen drücken sie die Tasten ALT-DRUCK und benutzen dann die Bild einfügen Schaltfläche um das Bild einzufügen

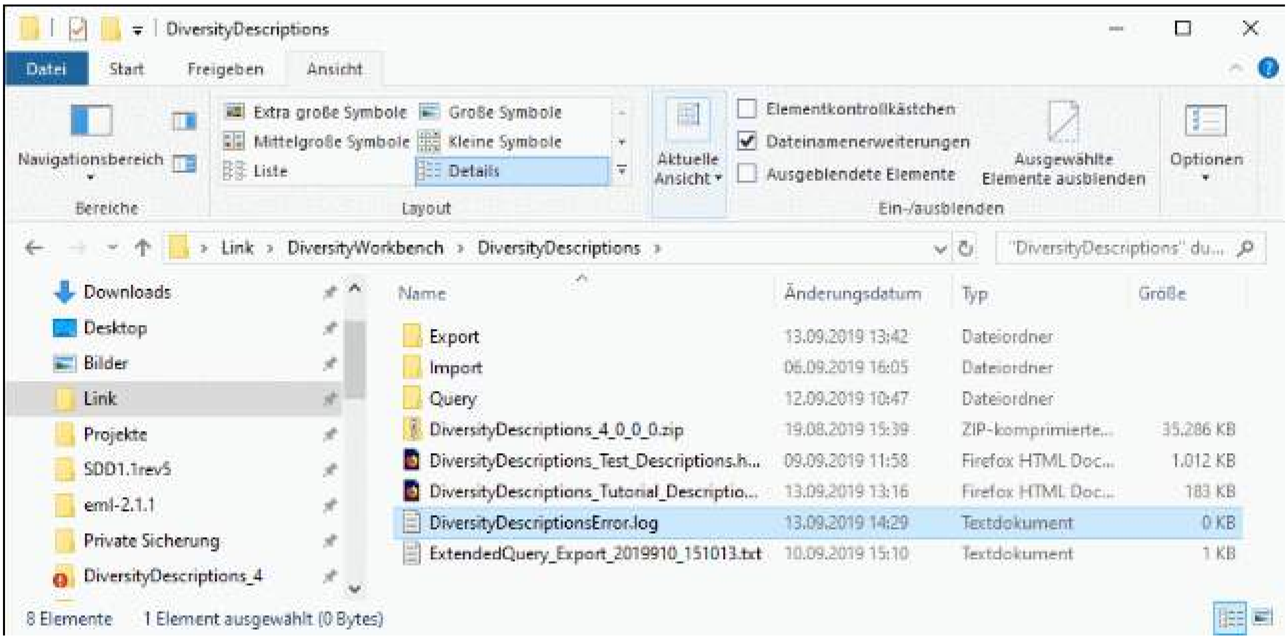
Click on the Insert image button to insert the screen shot and give a comment about your problem. Then click on the Send feedback button to send your feedback to the administrator. If you want to receive a message, when the problem you described is solved, please enter you e-mail address in the field under the descrption.

To inspect you former feedbacks, choose **Feedback history...** from the **Help** menu. A window will open, where you can browse your old feedback together with the state of progress.

In case you do not have access to the central database for the feedbacks, the program will open your mail client to send an e-mail. In case of bugs in the program it would help if you attach the file **DiversityDescriptionsError.log** located in your application directory (see below).

Error logging

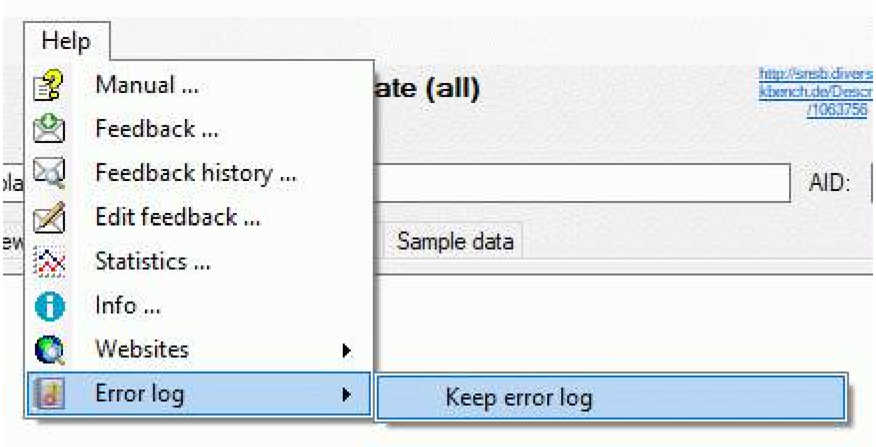
If any error messages show up through working with the application you can find further details concerning the part of the application where the error occured and the parameters involved in the file **DiversityDescriptionsError.log** located in your application's resources directory (see image below).



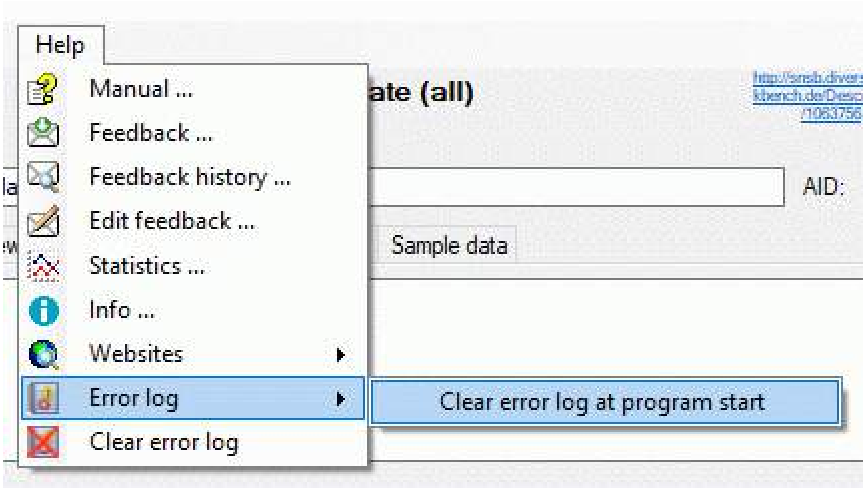
☐ Elementkontrollkästchen
☑ Dateinamenerweiterungen
☐ Ausgeblendete Elemente

Name	Änderungsdatum	Typ	Größe
Export	13.09.2019 13:42	Dateiordner	
Import	06.09.2019 16:05	Dateiordner	
Query	12.09.2019 10:47	Dateiordner	
DiversityDescriptions_4_0_0_0.zip	19.08.2019 15:39	ZIP-komprimierte...	35.286 KB
DiversityDescriptions_Test_Descriptions.h...	09.09.2019 11:58	Firefox HTML Doc...	1.012 KB
DiversityDescriptions_Tutorial_Descriptio...	13.09.2019 13:16	Firefox HTML Doc...	183 KB
DiversityDescriptionsError.log	13.09.2019 14:29	Textdokument	0 KB
ExtendedQuery_Export_2019910_151013.txt	10.09.2019 15:10	Textdokument	1 KB

You may open the error log file by clicking **Help -> Error log**. By default the error log file will be cleared each time when the application ist started. With option **Help-> Error log -> Keep error log** you may change this setting to keep the error log (see image below).

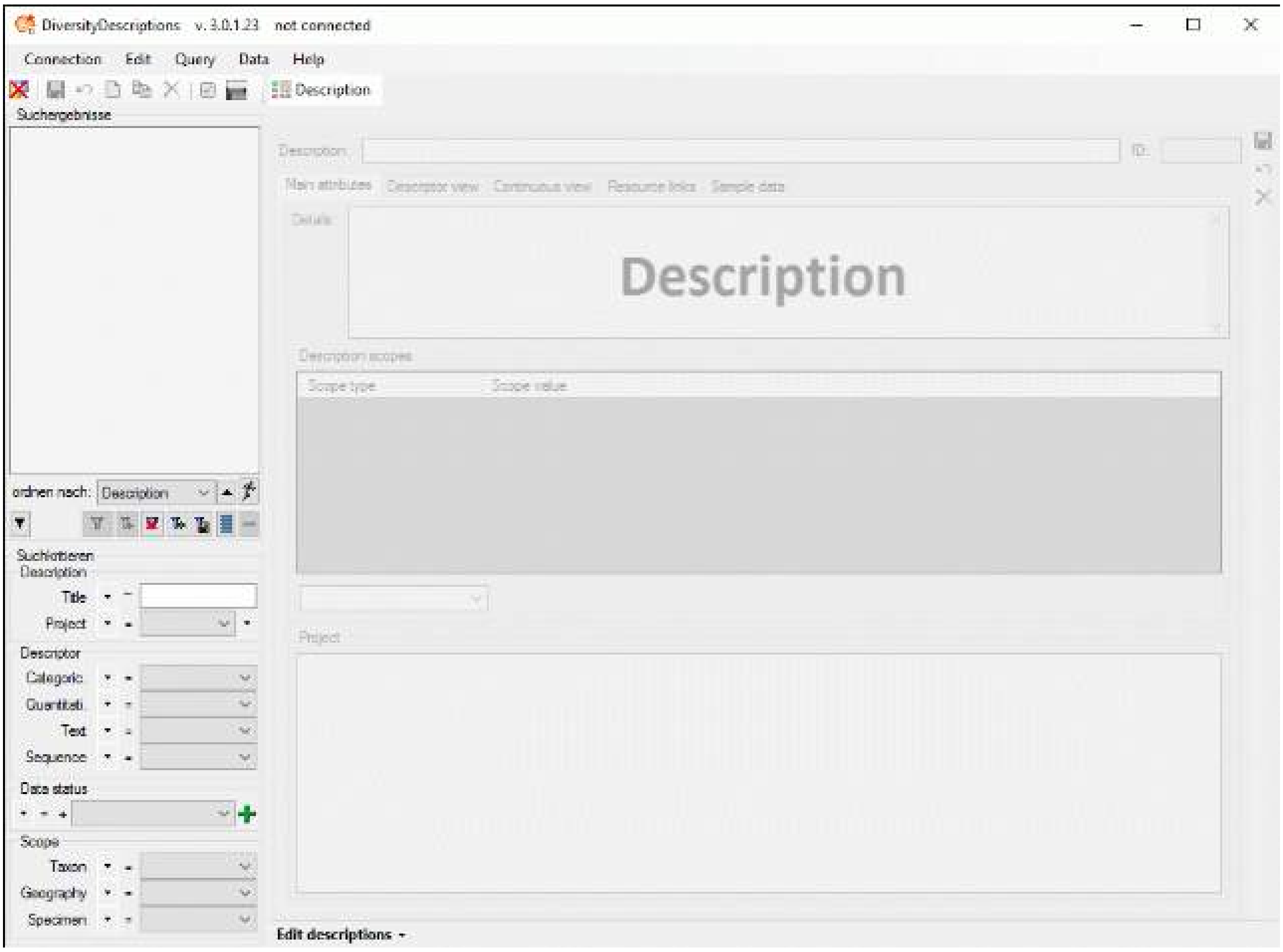


With option **Help-> Error log -> Clear error log at program start** you change this setting to the original default. If you decide to keep the error log file, you have the option to clear its contents with option **Help-> Clear Error log** (see image below).

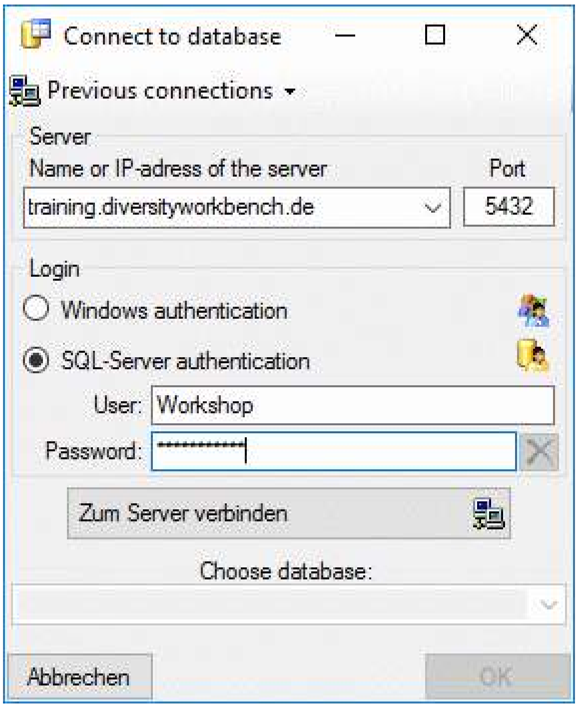

Help
Manual ...
Feedback ...
Feedback history ...
Edit feedback ...
Statistics ...
Info ...
Websites
Error log
Clear error log
Clear error log at program start
Sample data
AID:

Tutorial - first steps

This tutorial will guide you through the first basic steps in DiversityDescriptions. After the installation, make sure you have access to the database. To start the programm double click on the DiversityDescriptions.exe in the directory where you copied the files of DiversityDescriptions. The main window will open.

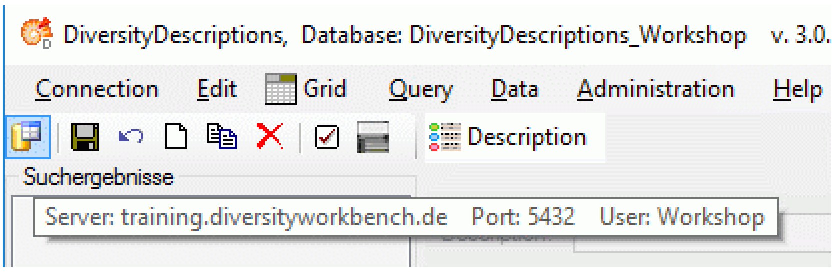


In this tutorial it is assumed that you installed a local database server and are running DiversityDescriptions with the DiversityDescriptions_Base database available at the DiversityWorkbench portal. If you open this window for the first time, you need to connect to the database. Click on the button or choose **Connection -> Database...** from the menu. A window will open where you may enter your account information and choose the database (see image below, for further information see database access).



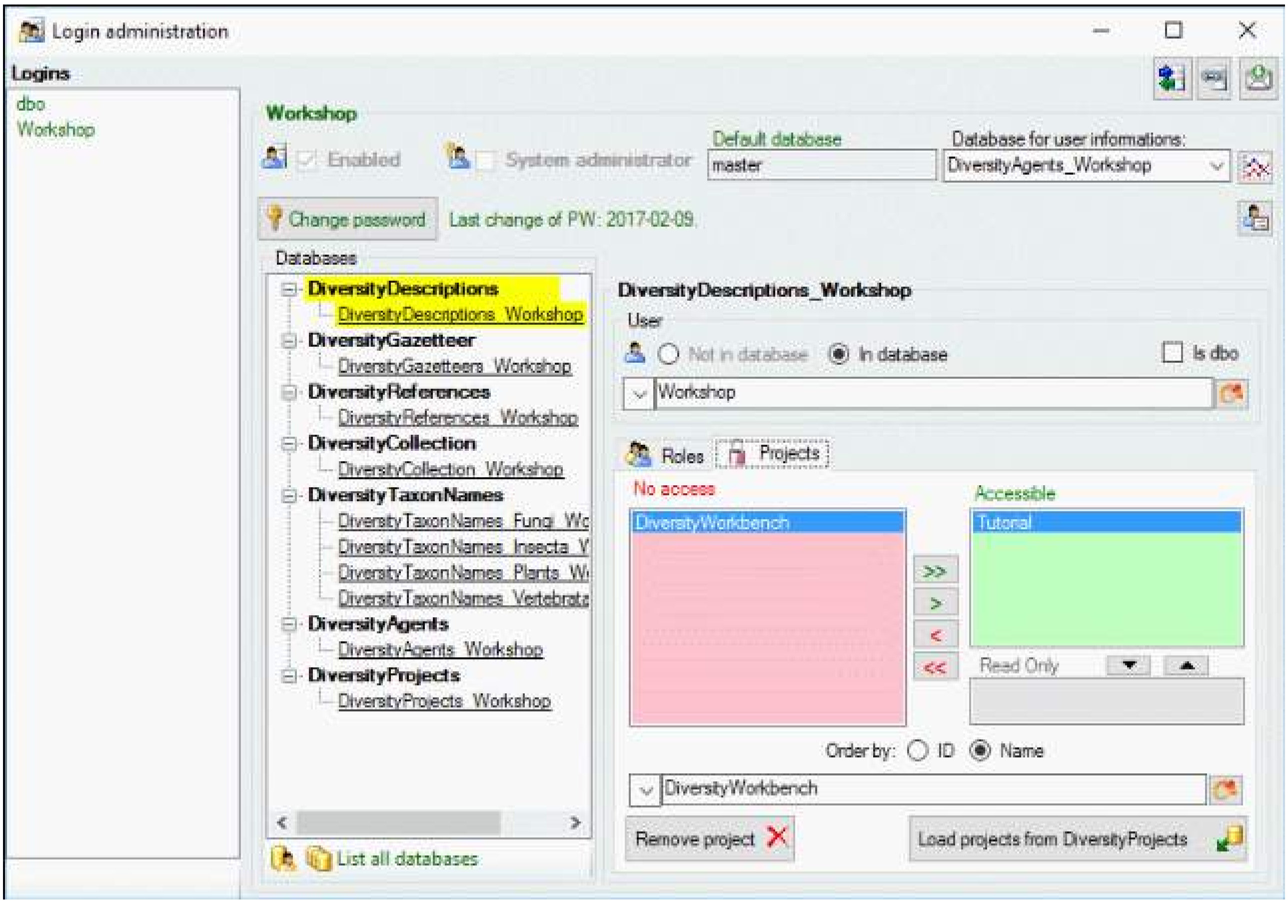
Name or IP-adress of the server: training.diversityworkbench.de
Port: 5432
○ Windows authentication
● SQL-Server authentication
User: Workshop
Password: ************

After connecting to the server and choosing a database click on the **OK** button to return to the main form. As indicated by the symbol in the right upper corner, you are now connected to the database. The tooltip of the button will show your current login information (see below). To enable an automatic connection for the next start of DiversityDescriptions select menu item **Connection->Auto connect**.



Server: training.diversityworkbench.de Port: 5432 User: Workshop

To get access to at least one workbench project open the login administration from menu **Administration->Database ...->Logins ...**. Assumed you are working with the same Windows accout the has been used for installation of the Microsof SQL-Server, you are the "database owner" (dbo), which has the highest database access rights. In this case select entry "dbo" from "Logins", then click on the database "DiversityDescriptions_Base" and open the "Projects" tab in the login administration (see below). There is only one entry in, the default workbench project "DiversityWorkbench", in the "No access" area. Select this entry and click the **>** button to make it accessible. Usually "DiversityWorkbench" is not used but a project is loaded from DiversityProjects instead. However in this tutorial we want to demonstrate use of DiversityDescriptions as a stand-alone application. Finally close the login administration window.



Logins: dbo, Workshop

Workshop

☑ Enabled ☐ System administrator

Default database: master

Database for user informations: DiversityAgents_Workshop

Last change of PW: 2017-02-09

Databases
- DiversityDescriptions
  - DiversityDescriptions_Workshop
- DiversityGazetteer
  - DiversityGazetteers_Workshop
- DiversityReferences
  - DiversityReferences_Workshop
- DiversityCollection
  - DiversityCollection_Workshop
- DiversityTaxonNames
  - DiversityTaxonNames_Fungi_W
  - DiversityTaxonNames_Insecta_V
  - DiversityTaxonNames_Plants_W
  - DiversityTaxonNames_Vertebrata
- DiversityAgents
  - DiversityAgents_Workshop
- DiversityProjects
  - DiversityProjects_Workshop

DiversityDescriptions_Workshop

User: ○ Not in database ● In database ☐ Is dbo

Workshop

No access: DiversityWorkbench

Accessible: Tutorial

Order by: ○ ID ● Name

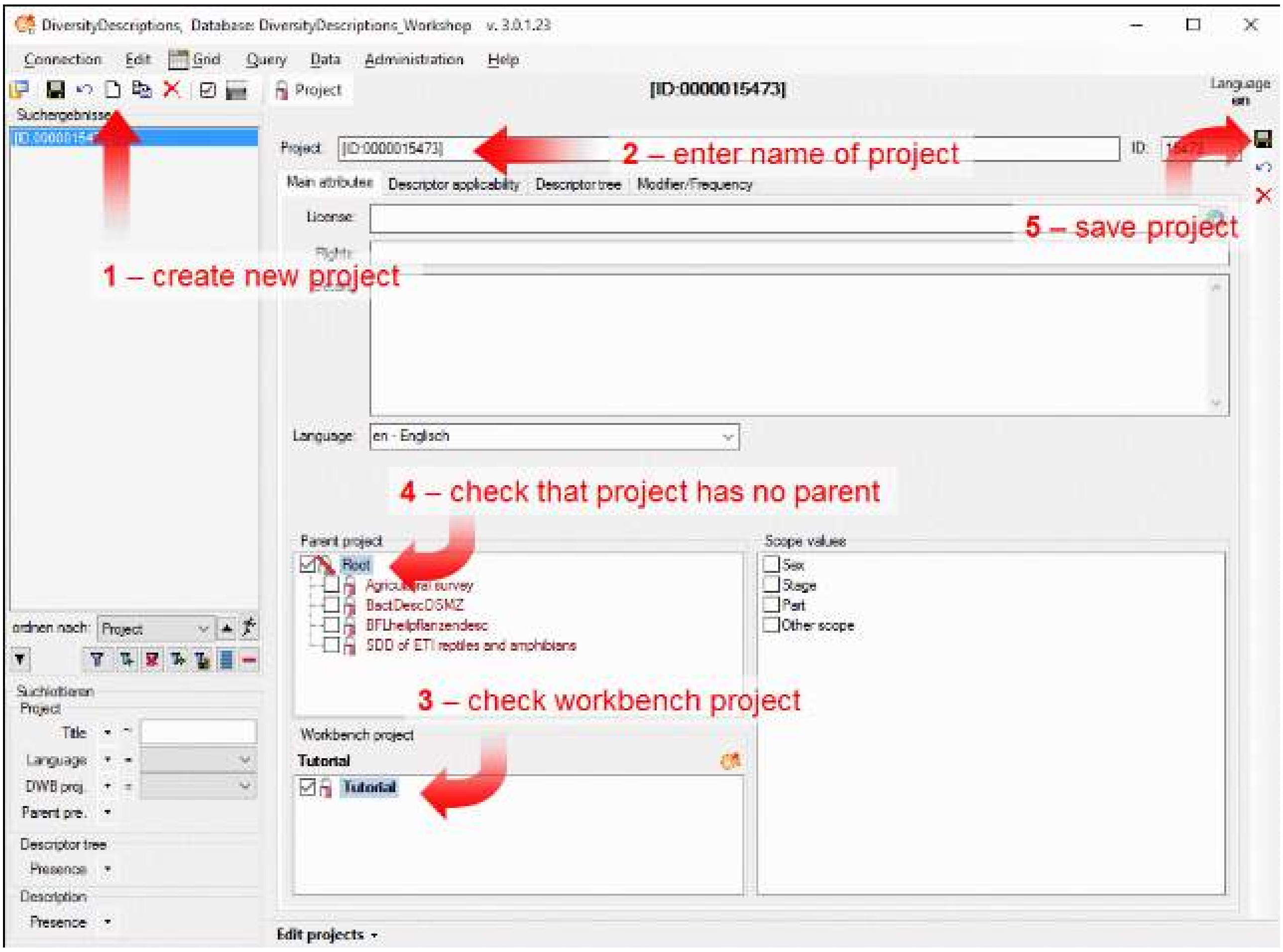
DiversityWorkbench

This tutorial is continued in the sections listed below.

- section Create a new local project
- section Enter a text descriptor
- section Enter a quantitative descriptor
- section Enter categorical descriptors
- section Enter description data
- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Create a new local project

To create a new local project, select edit mode projects from menu **Edit->Projects**. Now click on the button in the upper left panel (see point **1** in image below). In case of more than one workbench project being available in the database, the software will ask you to select the workbench project assigned to the new local project (see Projects for further information).



1 – create new project

2 – enter name of project

3 – check workbench project

4 – check that project has no parent

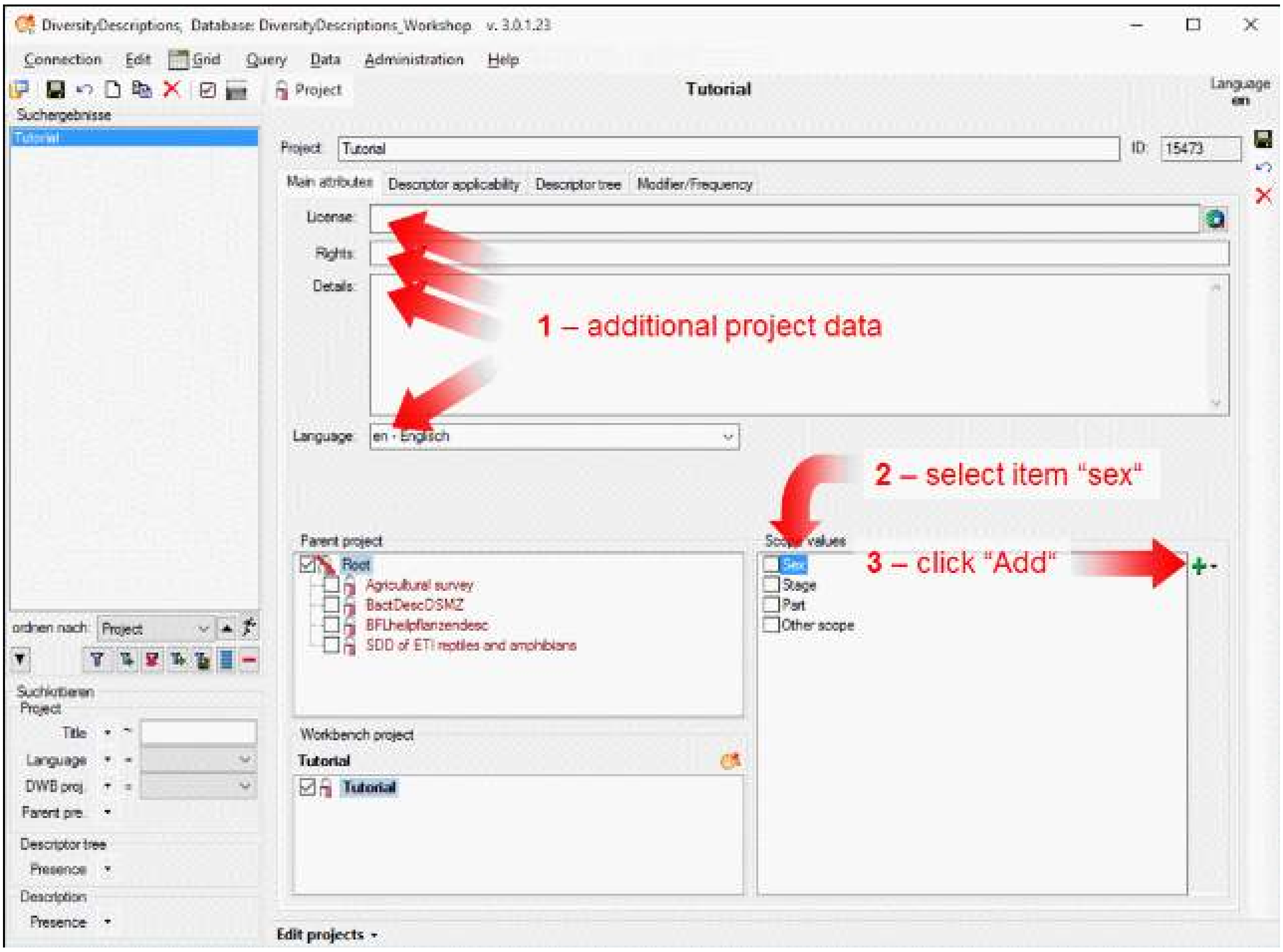
5 – save project

Project: [ID:0000015473]

Language: en - Englisch

The new local project is created with a numeric name. Change it to "Tutorial" (see point **2** in image above). Then check the workbench project (should be "DiversityWorkbench") and that no other local project is selected as a parent of the new one (see points **3** and **4** in image above). Finally save the project (see point **5** in image above) and the project name will be updated in the header and the query panel at the left side of the window (see image below).

If you like, you may now enter additional project data like a detailled project descripition ("Details"), a copyright text ("Rights"), the address of a license text in the internet ("License" - button opens a browser window to navigate to the license page) and you may select the project's lanuage (see point **1** in image below).



Project: Tutorial

ID: 15473

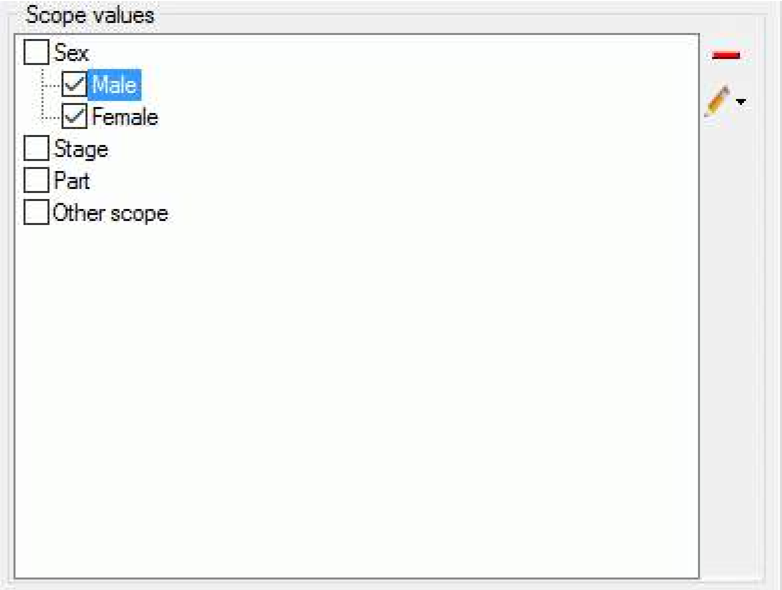
Language: en - Englisch

1 – additional project data

2 – select item “sex”

3 – click “Add”

If you want to use scope values for sex in your descriptive data, select the scope category "sex" (see point **2** in image above). Now the "Add" button ✚ is enabled. When you click on the button (see point 3 in the image above) a drop-down menu offers predefined sex values. Select "Male", then again click on the "Add" button ✚ and select value "Female". The two values are now appended to item "sex". To make them available for the tutorial project click on the boxes before the values to set them checked (see image below).



For the other scope categories no predefined values exit. When you click the "✚ Add" button, values with a numeric name will be appended that can be renamed by clicking on button "Edit" and selecting menu item " Edit scope name".

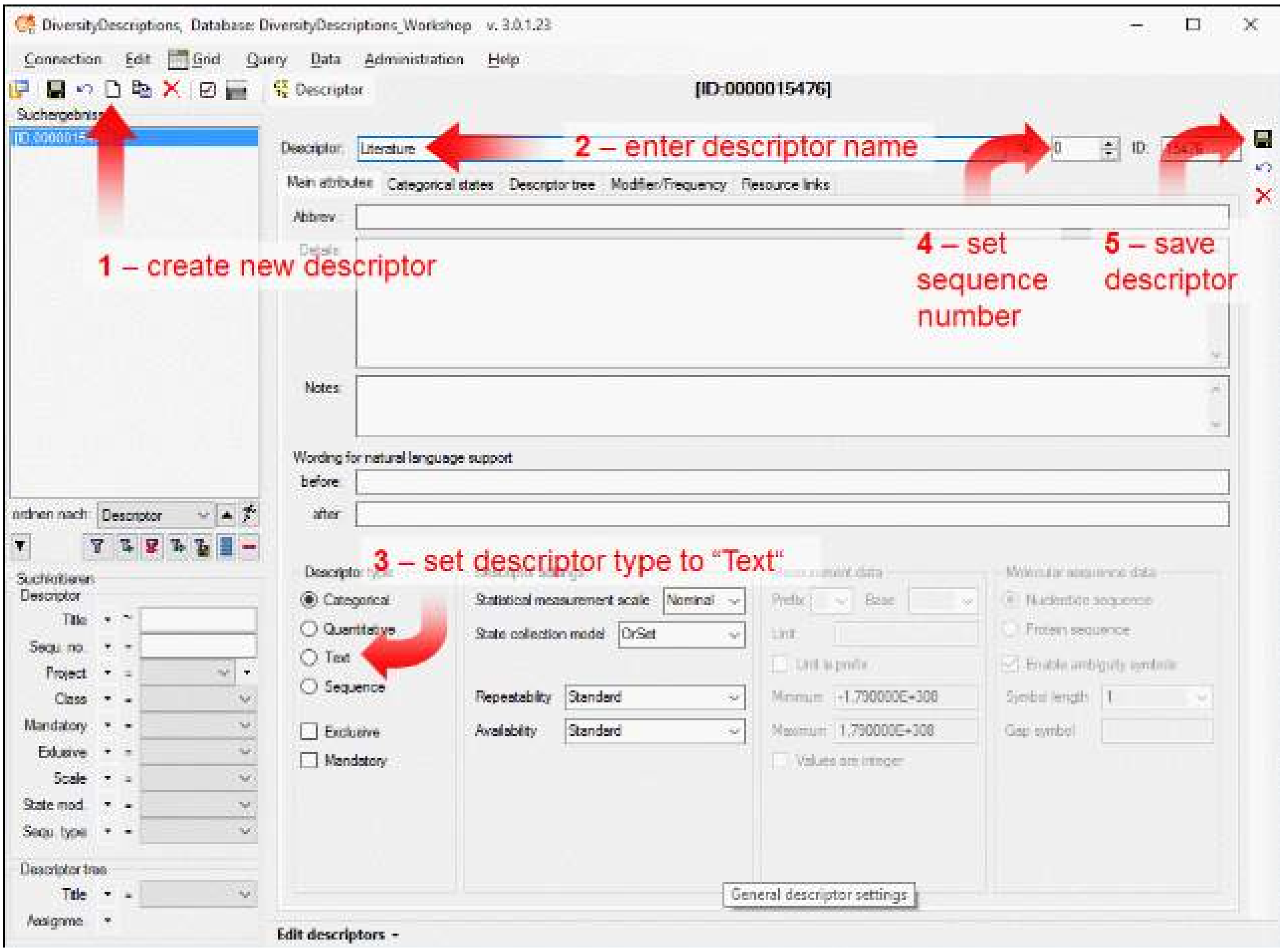
A more detailled description of all editing options can be found in the Edit projects section of this manual.

This tutorial is continued in the sections listed below.

- section Enter a text descriptor
- section Enter a quantitative descriptor
- section Enter categorical descriptors
- section Enter description data
- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Enter a text descriptor

To create a new text descriptor, select edit mode descriptors from menu **Edit->Descriptors**. Now click on the button in the upper left panel (see point **1** in image below).



DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.1.23

[ID:0000015476]

Descriptor: Literature

Sequence: 0

ID: 15476

Descriptor type: ● Categorical ○ Quantitative ○ Text ○ Sequence

☐ Exclusive

☐ Mandatory

Statistical measurement scale: Nominal

State collection model: OrSet

Repeatability: Standard

Availability: Standard

Minimum: -1,790000E+308

Maximum: 1,790000E+308

1 – create new descriptor

2 – enter descriptor name

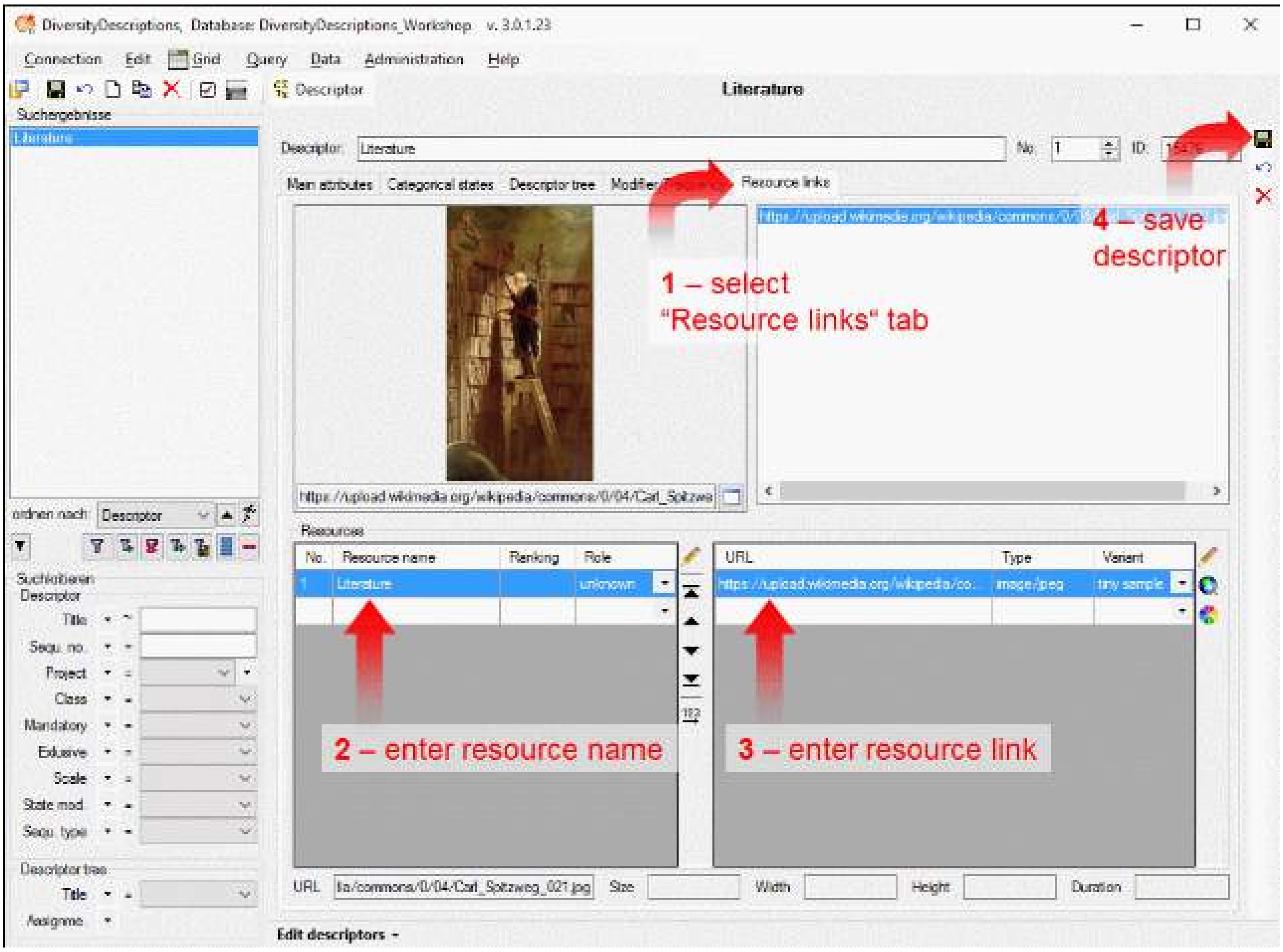
3 – set descriptor type to “Text“

4 – set sequence number

5 – save descriptor

The new descriptor is created with a numeric name. Change it to "Literature" (see point **2** in image above), because this descriptor shall allow insert of literature references or citations as free form text into the description data. Then set the descriptor type to "Text" (see points **3** in image above) and set the sequence number to "1" (see points **4** in image above). Finally save the descriptor (see point **5** in image above) and the descriptor name will be updated in the header and the query panel at the left side of the window.

If you like, you may now enter additional descriptor data like a detailled project description ("Details") or "Notes". But we want to attach a resource link to our new text descriptor, that symbolizes the descriptor's duty. Therefore select the "Resource links" tab (see point **1** in image below) and enter the resource name "Literature" (see point **2** in image below). Now you can enter the URL of a picture that is reachable in the internet (see point **3** in image below, a link to Wikipedia was used). Alternatively you may double-click on the "URL" field to open a browser window, where you can navigate to the picture location. Finally, don't forget to save your changes (see point **4** in image below).



Descriptor: Literature No: 1

1 Literature unknown

https://upload.wikimedia.org/wikipedia/co... image/jpeg tiny sample

URL: ...ia/commons/0/04/Carl_Spitzweg_021.jpg

1 – select "Resource links" tab

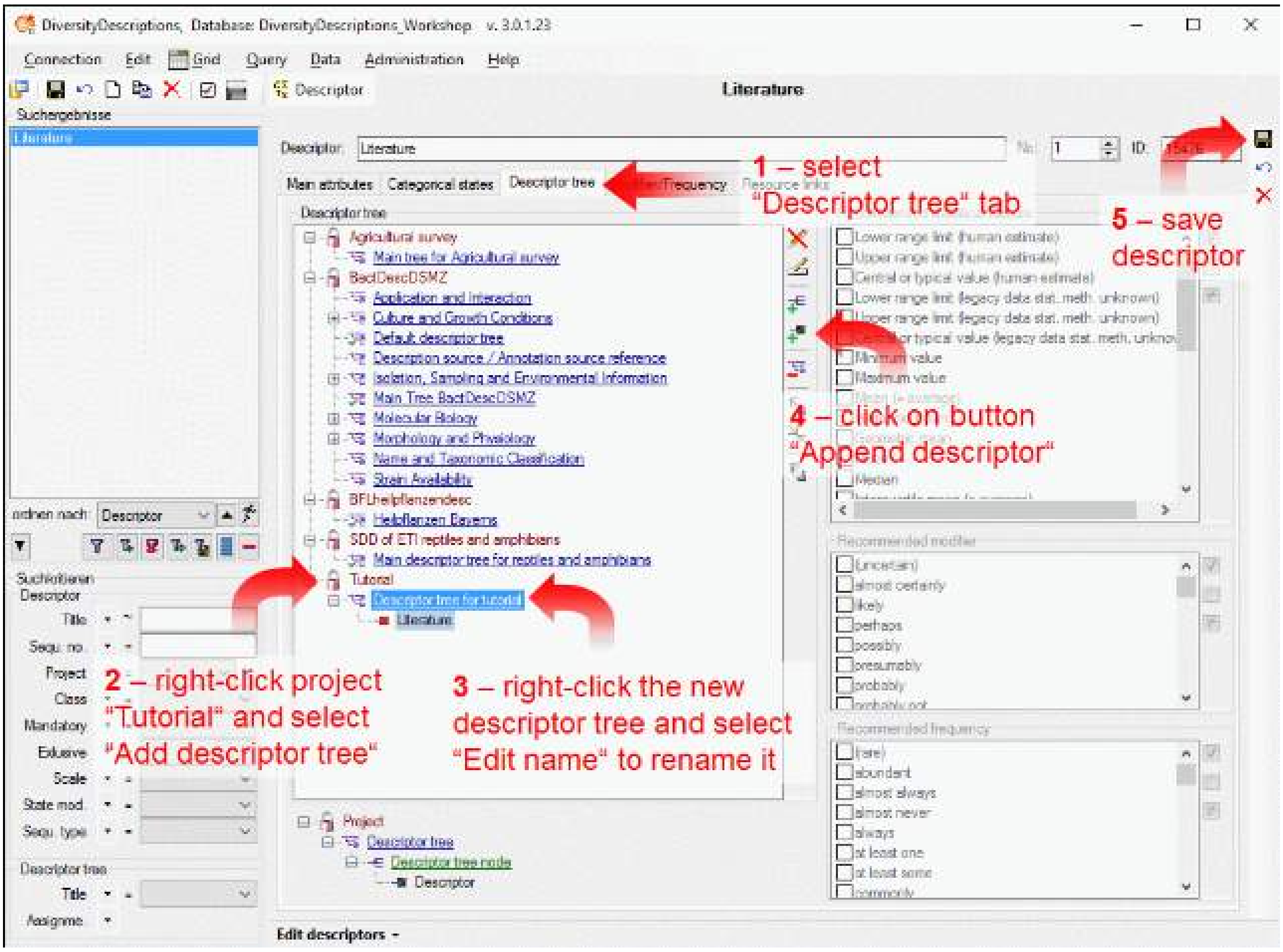
2 – enter resource name

3 – enter resource link

4 – save descriptor

Until now the descriptor is not assigned to any project, i.e. it cannot be used for entering descriptive data. Assignment of descriptors to projects is done by using "descriptor trees". This allows on the one hand a thematical grouping of the descriptors, on the other hand the descriptors may be appended to several trees simultaniously. I.e. descriptors my be used in several distinct projects.

Since no descriptor tree has been created yet, select the "Descriptor tree" tab (see point **1** in image below), right-click the project "Tutorial" and select context menu entry "Add descriptor tree" (see point **2** in image below). A new descriptor tree is appended to the project "Tutorial" with a numeric name. Right-click the descriptor tree and select "Edit name" from the context menu to change the name to "Descriptor tree for tutorial" (see point **3** in image below). To append the actual descriptor to the tree, click button + at the right tool bar (see point **4** in image below). In the "Descriptor tree" tab most functions are alternatively accessible by the tool bar at the right or by the context menu that opens when you right-click a tree node. Finally, don't forget to save your changes (see point **5** in image below).



1 – select "Descriptor tree" tab

2 – right-click project "Tutorial" and select "Add descriptor tree"

3 – right-click the new descriptor tree and select "Edit name" to rename it

4 – click on button "Append descriptor"

5 – save descriptor

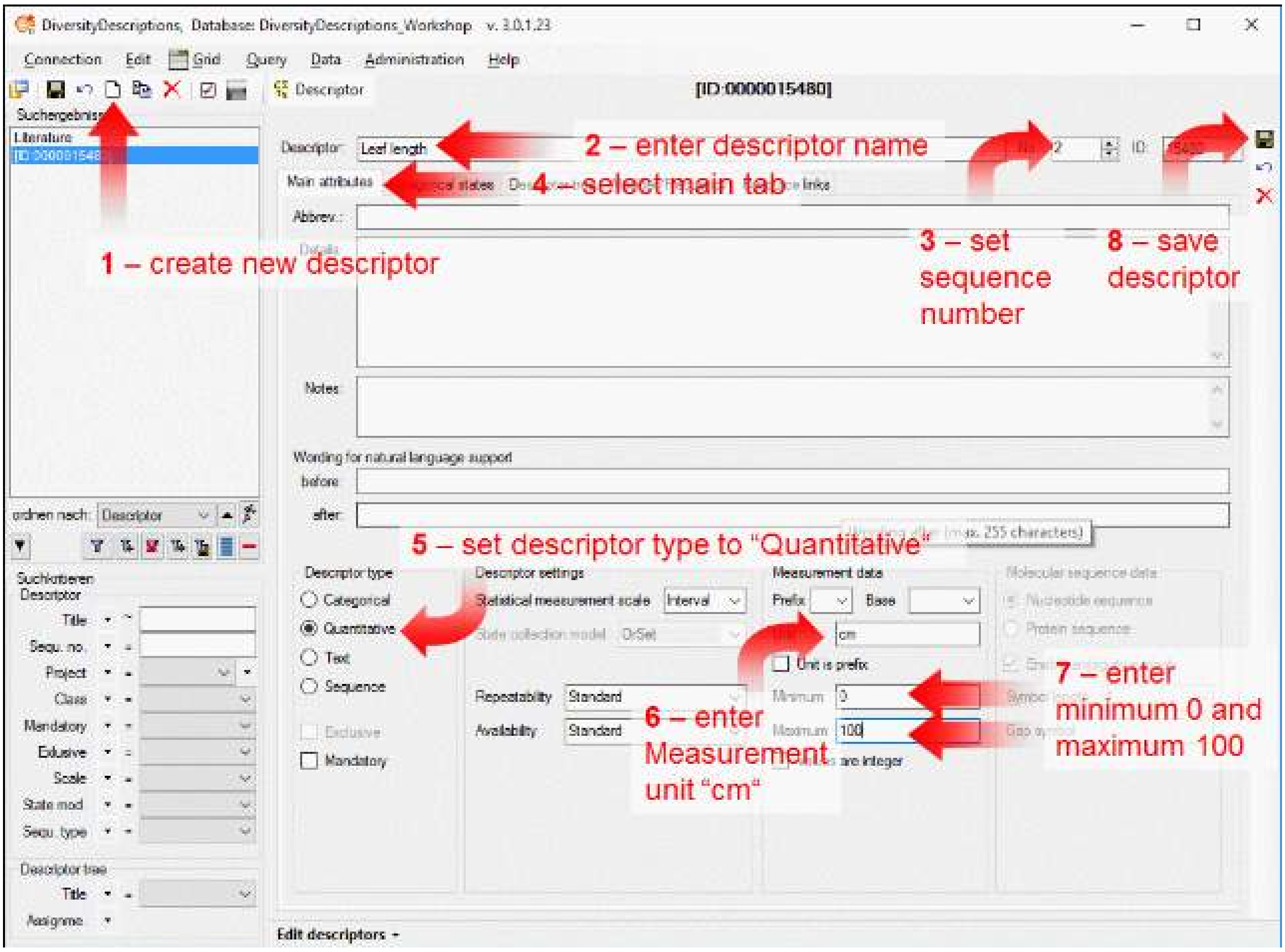
A more detailled description of all editing options can be found in the Edit descriptors section of this manual.

This tutorial is continued in the sections listed below.

- section Enter a quantitative descriptor
- section Enter categorical descriptors
- section Enter description data
- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Enter a quantitative descriptor Σ

To create a new quantitative descriptor, select edit mode descriptors from menu **Edit->Descriptors**. Now click on the 🗋button in the upper left panel (see point **1** in image below).



DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.1.23

[ID:000015480]

Descriptor: Leaf length

Nr.: 2

1 – create new descriptor

2 – enter descriptor name

3 – set sequence number

4 – select main tab

5 – set descriptor type to “Quantitative”

6 – enter Measurement unit “cm“

7 – enter minimum 0 and maximum 100

8 – save descriptor

Descriptor type: ○ Categorical ● Quantitative ○ Text ○ Sequence

Statistical measurement scale: Interval

Repeatability: Standard

Availability: Standard

Measurement unit: cm

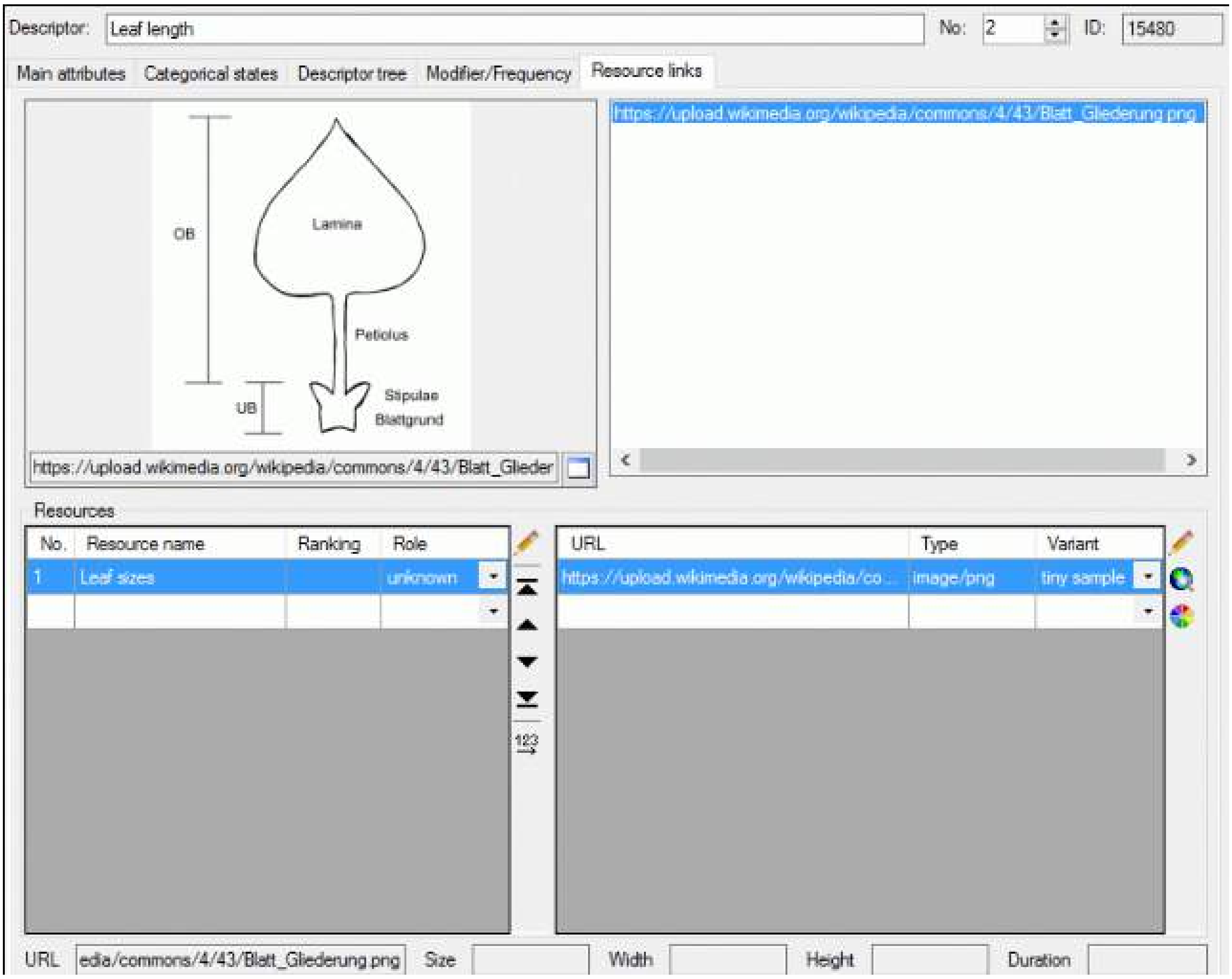
☐ Unit is prefix

Minimum: 0

Maximum: 100

The new descriptor is created with a numeric name. Change it to "Leaf length" (see point **2** in image above) and set the sequence number to "2" (see points **3** in image above). Now switch to the main tab and set the descriptor type to "Quantitative" (see points **4** and **5** in image above). For the quantitative descriptor we enter the measurement unit "cm", a minimum and a maximum value (see points **6** and **7** in image above). Finally save the descriptor (see point **8** in image above) and the descriptor name will be updated in the header and the query panel at the left side of the window.

As for the text descriptor we want to attach a resource link to our new quantitative descriptor, that symbolizes the descriptor's duty (see image below, a link to Wikipedia was used).



Descriptor: Leaf length No: 2 ID: 15480

https://upload.wikimedia.org/wikipedia/commons/4/43/Blatt_Gliederung.png

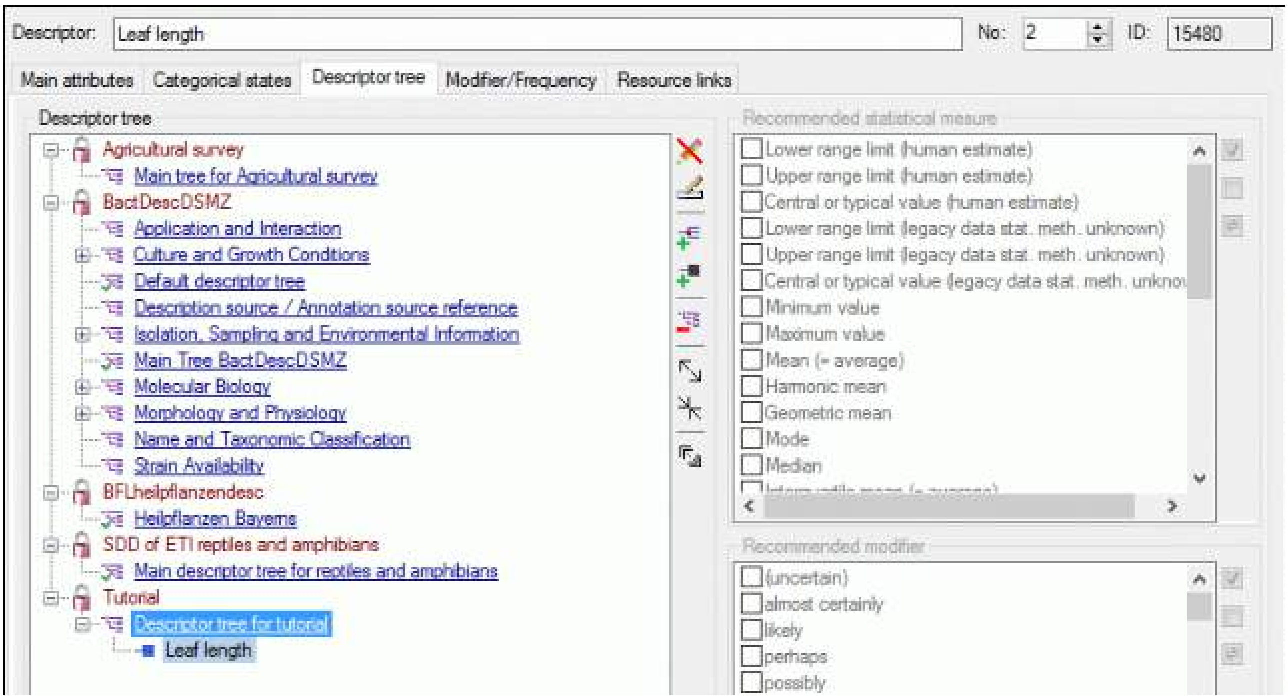
https://upload.wikimedia.org/wikipedia/commons/4/43/Blatt_Glieder

No.	Resource name	Ranking	Role
1	Leaf sizes		unknown

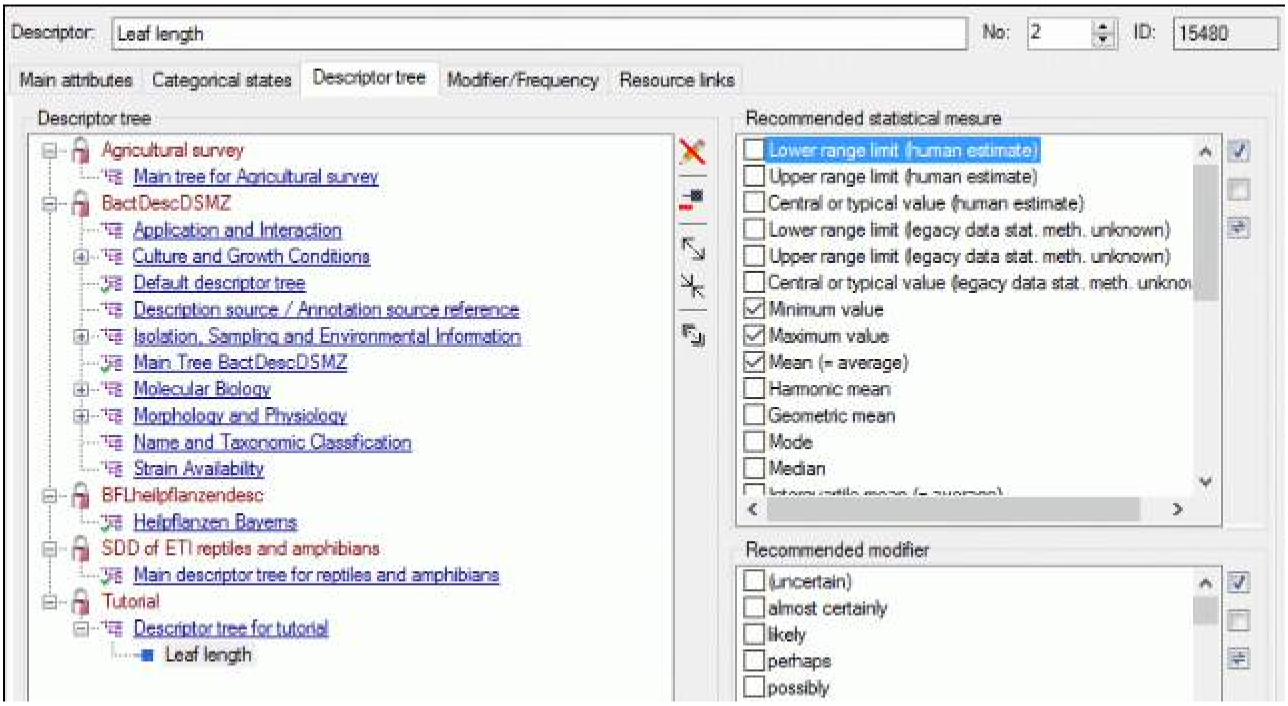
URL	Type	Variant
https://upload.wikimedia.org/wikipedia/co...	image/png	tiny sample

URL edia/commons/4/43/Blatt_Gliederung.png Size Width Height Duration

Certainly the quantitative descriptor shall be attached to the "Descriptor tree for tutorial" that was created in the last step. In the descriptor tree tab select "Descriptor tree for tutorial" and click button tab select "Descriptor tree for tutorial" and click button + at the right tool bar (see image below).


Descriptor: Leaf length
No: 2
ID: 15480

For quantitative descriptors a number of statistical measures are defined, for which values can be entered in the descriptive data. In the descriptor tree fo each descriptor of descriptor tree node may be specified, which values shall be used in the descriptive data. A click on button ✎ opens the recommended statistical measures on the right side of the window (see image below). Select the quantitative descriptor in the descriptor tree and then check the statistical measures "Minimum value", "Maximum value" and "Mean" (see image below).


Descriptor: Leaf length
No: 2
ID: 15480

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unkno
☑ Minimum value
☑ Maximum value
☑ Mean (= average)
☐ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

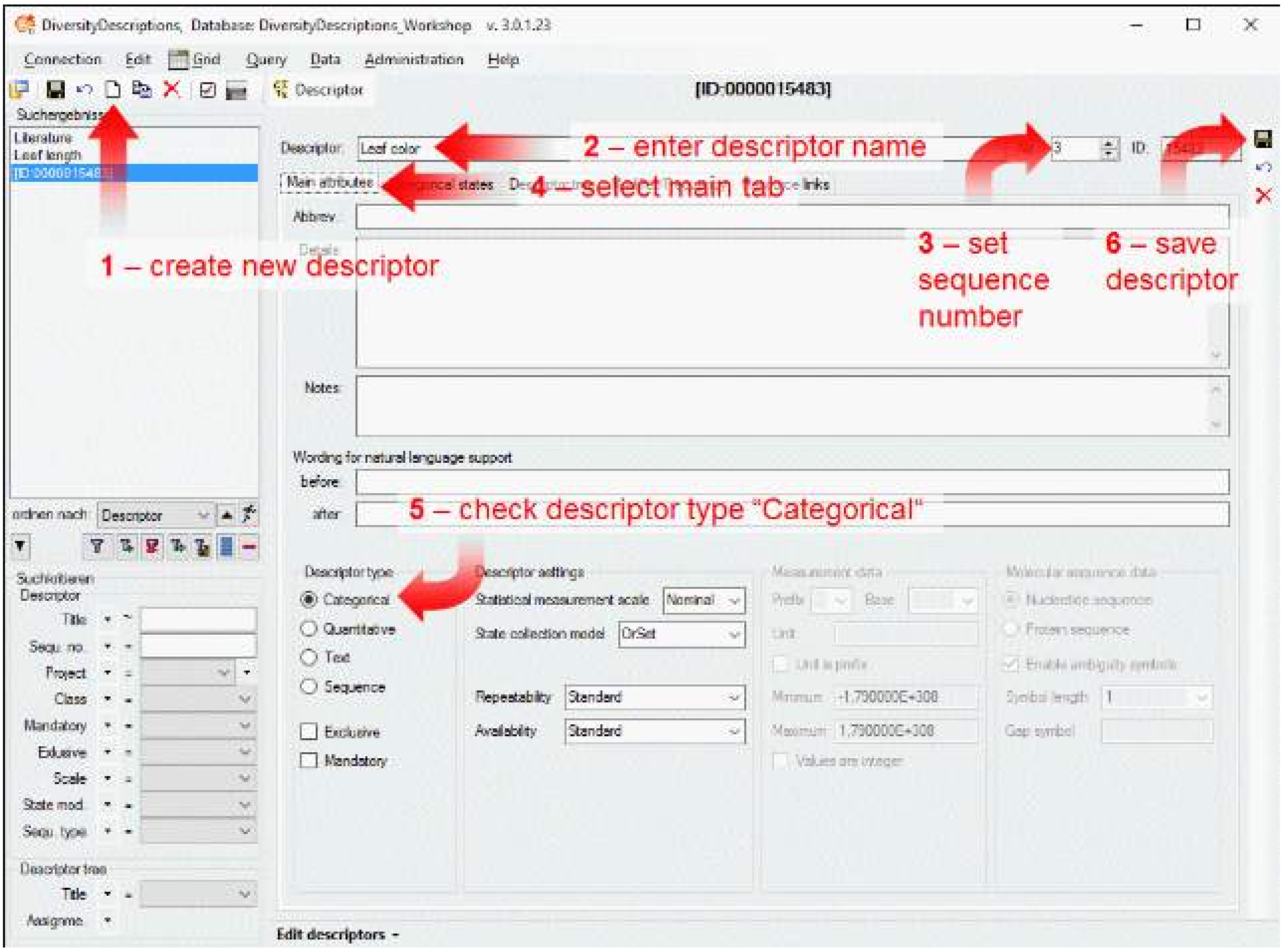
A more detailled description of all editing options can be found in the Edit descriptors section of this manual.

This tutorial is continued in the sections listed below.

- section Enter categorical descriptors
- section Enter description data
- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Enter categorical descriptors

To create a new categorical descriptor, select edit mode descriptors from menu **Edit->Descriptors**. Now click on the 🗋button in the upper left panel (see point **1** in image below).



Descriptor: Leaf color

ID: 15483

Descriptor type
- ● Categorical
- ○ Quantitative
- ○ Text
- ○ Sequence
- ☐ Exclusive
- ☐ Mandatory

Descriptor settings
- Statistical measurement scale: Nominal
- State collection model: OrSet
- Repeatability: Standard
- Availability: Standard

Measurement data
- Minimum: -1,790000E+308
- Maximum: 1,790000E+308
- ☐ Values are integer

Molecular sequence data
- Symbol length: 1

1 – create new descriptor

2 – enter descriptor name

3 – set sequence number

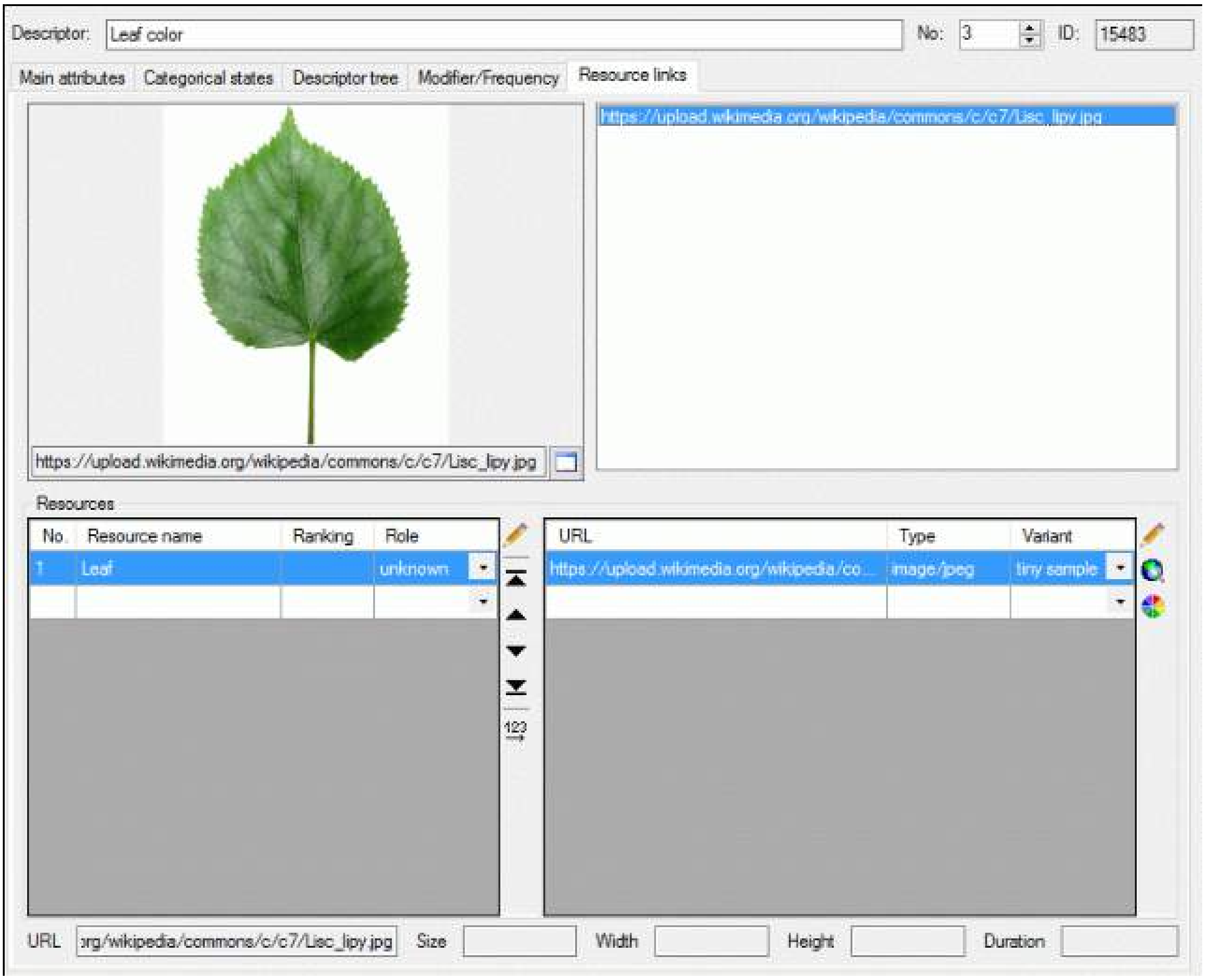
4 – select main tab

5 – check descriptor type "Categorical"

6 – save descriptor

The new descriptor is created with a numeric name. Change it to "Leaf length" (see point **2** in image above) and set the sequence number to "3" (see points **3** in image above). Now switch to the main tab and check that the descriptor type is "Categorical" (see points **4** and **5** in image above). Finally save the descriptor (see point **6** in image above) and the descriptor name will be updated in the header and the query panel at the left side of the window.

As for the other descriptors we want to attach a resource link to our new categorical descriptor, that symbolizes the descriptor's duty (see image below, a link to Wikipedia was used).



Descriptor: Leaf color
No: 3
ID: 15483

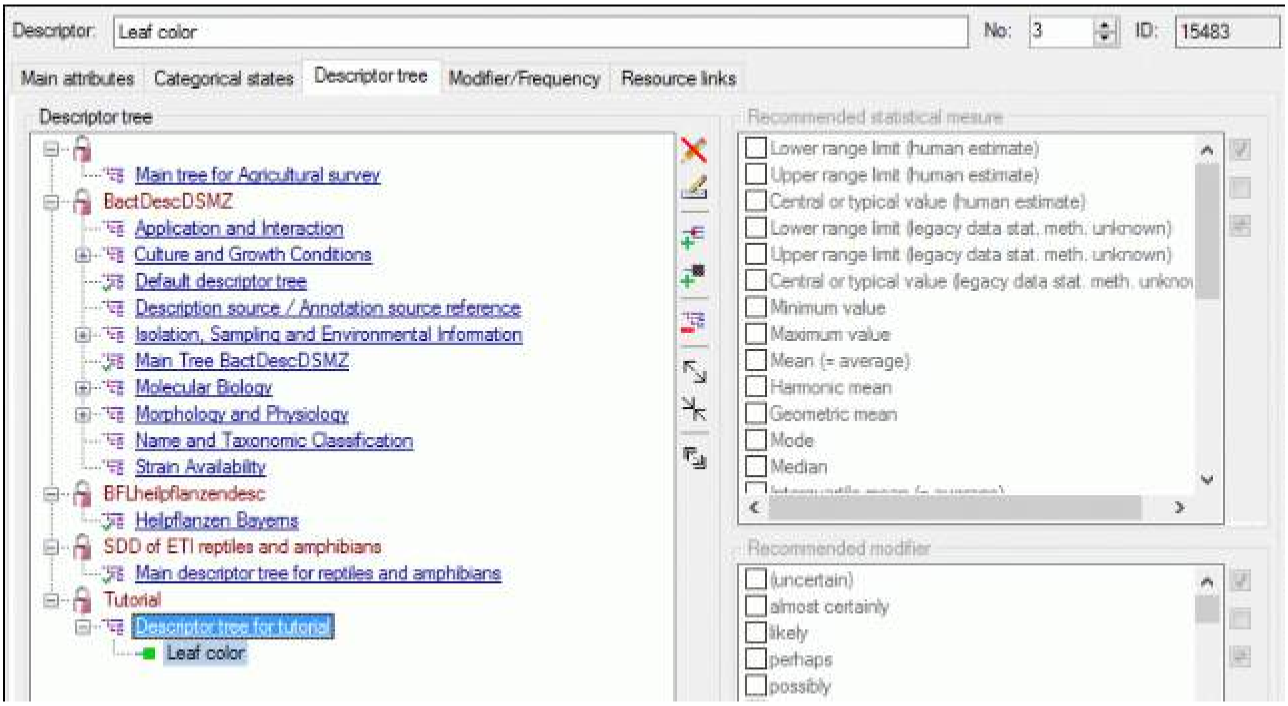
https://upload.wikimedia.org/wikipedia/commons/c/c7/Lisc_lipy.jpg

No.	Resource name	Ranking	Role
1	Leaf		unknown

URL	Type	Variant
https://upload.wikimedia.org/wikipedia/co...	image/jpeg	tiny sample

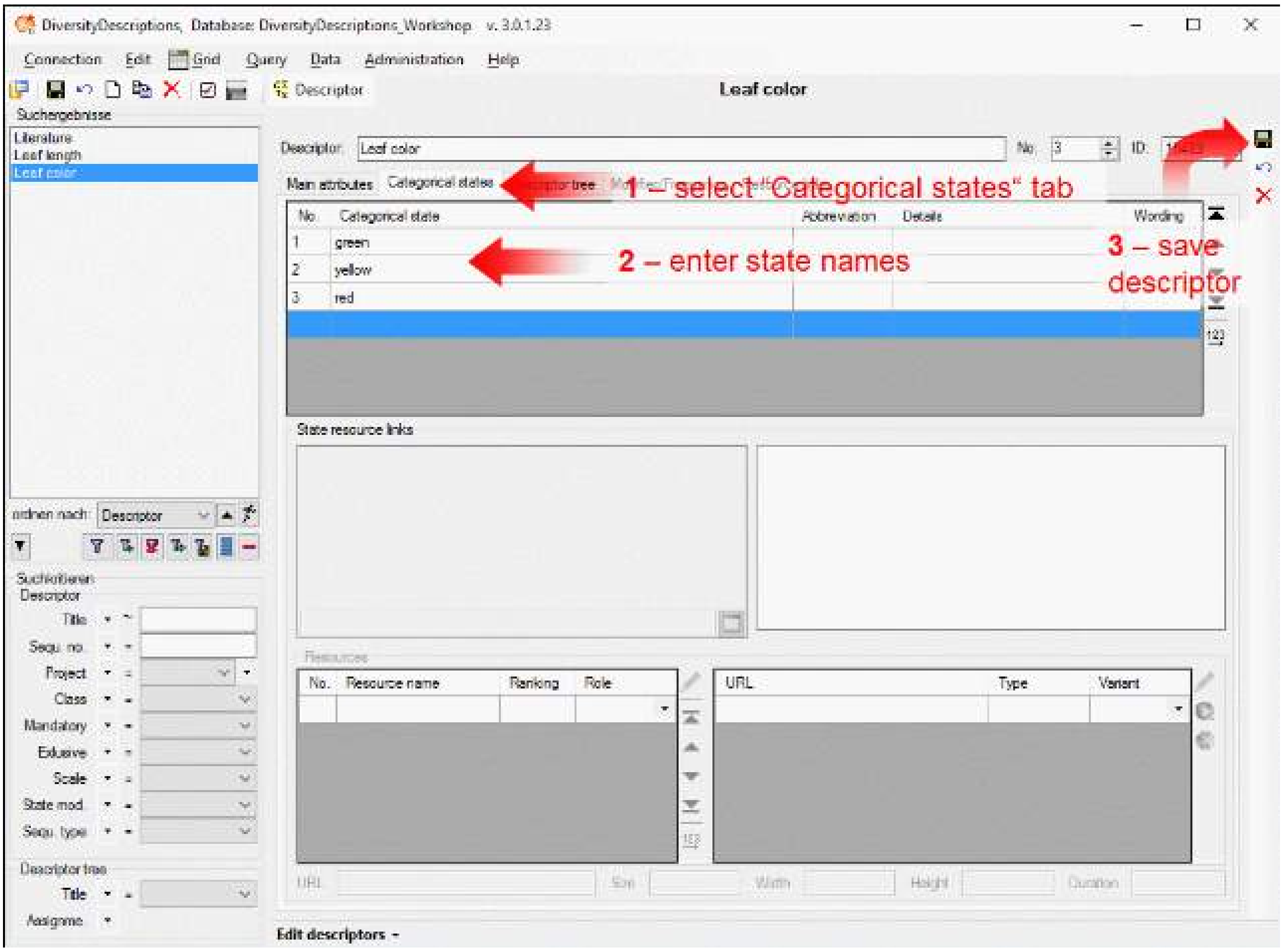
URL: rg/wikipedia/commons/c/c7/Lisc_lipy.jpg
Size:
Width:
Height:
Duration:

Certainly the categorical descriptor shall be attached to the "Descriptor tree for tutorial" that was created in the last step. In the descriptor tree tab select "Descriptor tree for tutorial" and click button + at the right tool bar (see image below).



Descriptor: Leaf color No: 3 ID: 15483

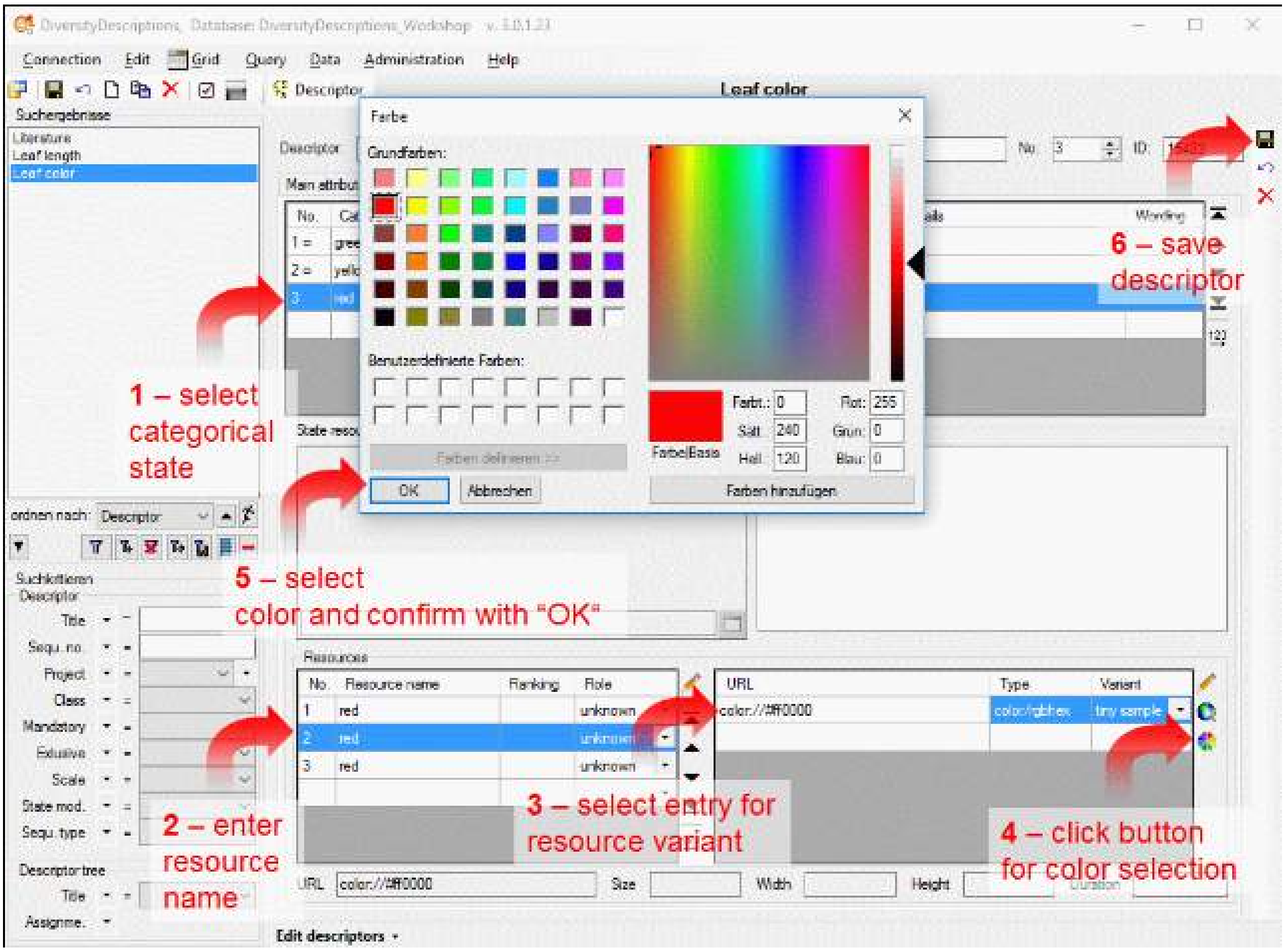
For categorical descriptors we have to define categorical states, which define the possible character values. Select the "Categorical states" tab (see point **1** in image below) and enter the three categorical state names "green", "yellow" and "red" in the table (see points **2** in image below). Finally save the descriptor (see point **3** in image below).



Descriptor: Leaf color No: 3

No.	Categorical state	Abbreviation	Details	Wording
1	green			
2	yellow			
3	red			

For each categorical state resources may be assigned. Therefore select the categorical state where you want to enter the resources (see point **1** in image below) and enter a resource name (see points **2** in image below). In this case we do not assign an URL to a picture but attach color values. Therefore click the color button in the task bar and select a color value (see points **3** to **5** in image below). Finally save the descriptor (see point **6** in image below).



1 – select categorical state

2 – enter resource name

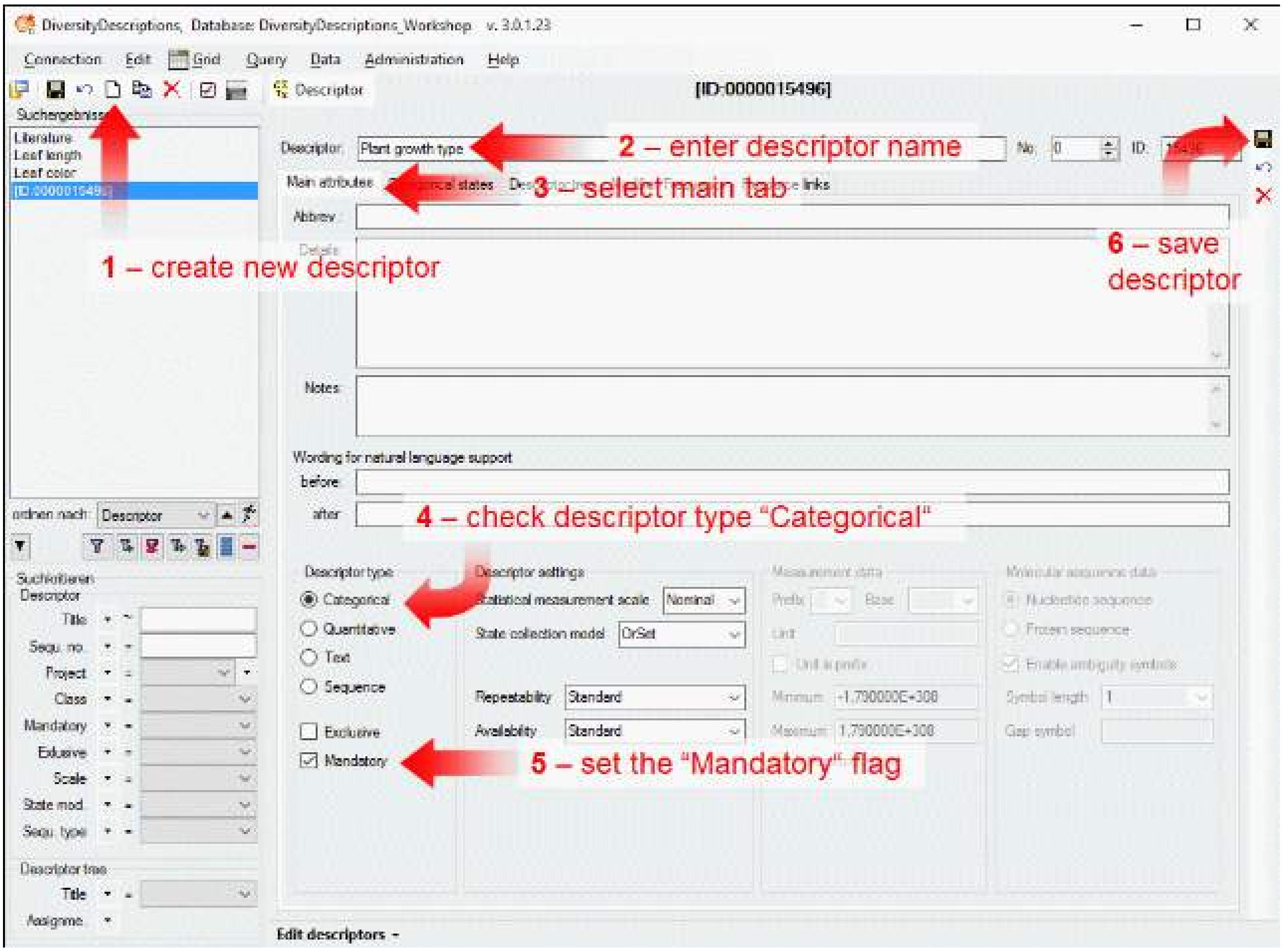
3 – select entry for resource variant

4 – click button for color selection

5 – select color and confirm with "OK"

6 – save descriptor

For our tutorial we need a second each categorical descriptor. Create the categorical descriptor "Plant growth type" (see points **1** to **4** in image below). This descriptor shall always be used in the descriptions, therefor mark it as mandatory (see point **5** in image below). Finally save the descriptor (see point **6** in image below).


DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.1.23

[ID:000015496]

Descriptor: Plant growth type

No: 0

ID: 15496

Descriptor type:
● Categorical
○ Quantitative
○ Text
○ Sequence

☐ Exclusive
☑ Mandatory

Statistical measurement scale: Nominal

State collection model: OrSet

Repeatability: Standard

Availability: Standard

1 – create new descriptor

2 – enter descriptor name

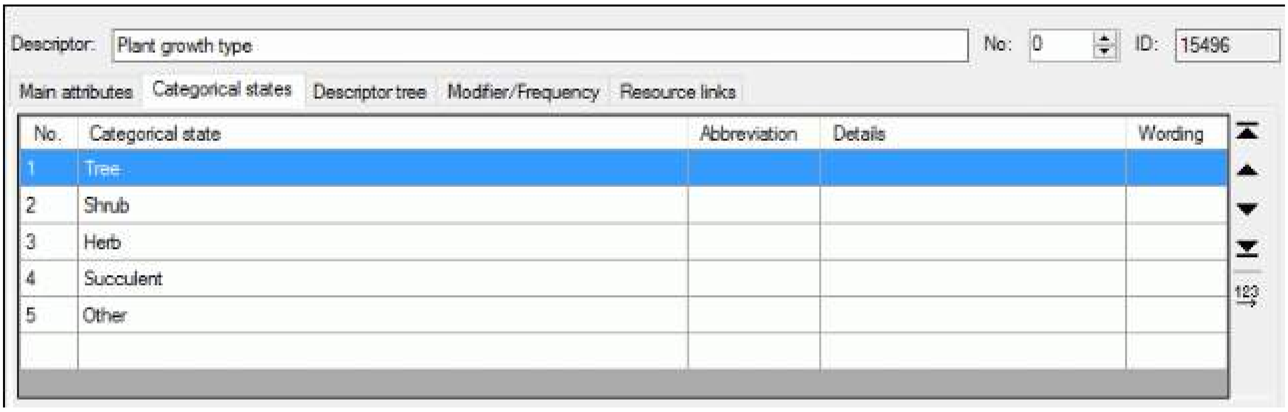
3 – select main tab

4 – check descriptor type “Categorical“

5 – set the “Mandatory“ flag

6 – save descriptor

For descriptor "Plant growth type" enter the categorical states "Tree", "Shrub", "Herb", "Succulent" and "Other" (see image below).

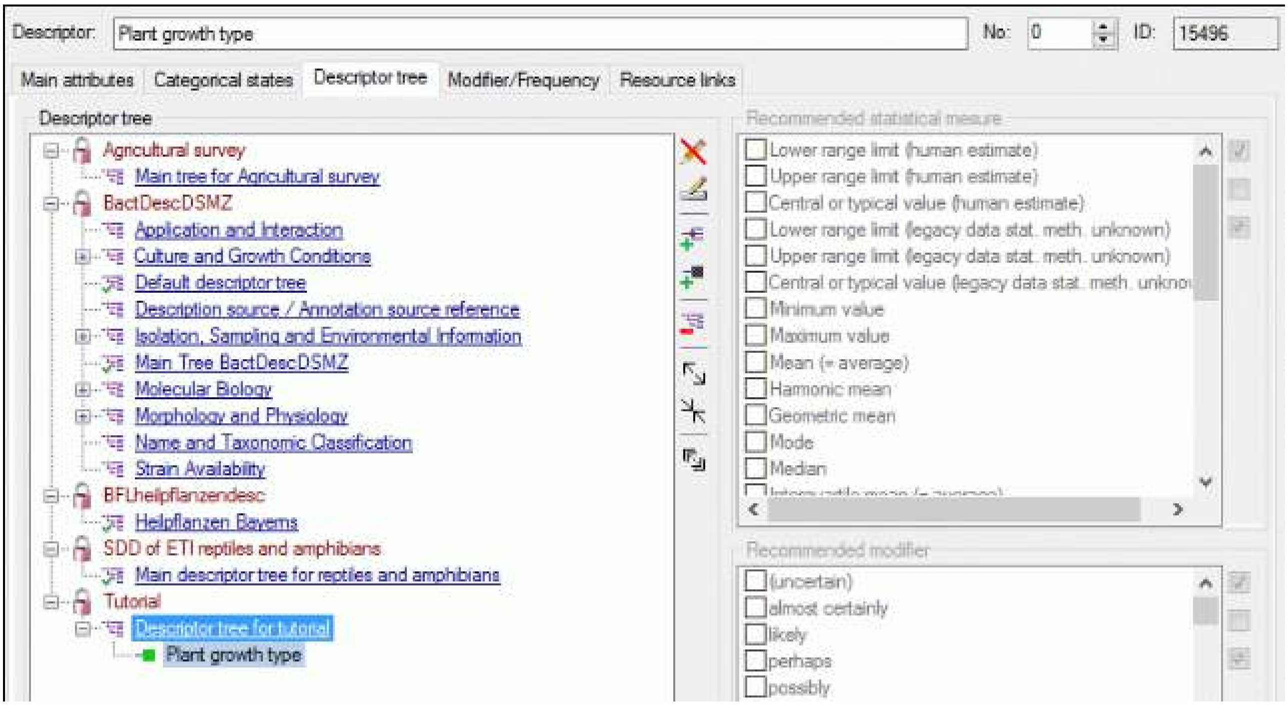

Descriptor: Plant growth type

No: 0

ID: 15496

No.	Categorical state	Abbreviation	Details	Wording
1	Tree			
2	Shrub			
3	Herb			
4	Succulent			
5	Other			

Finally append descriptor "Plant growth type" to the descriptor tree for tutorial (see image below).



Descriptor: Plant growth type

No: 0

ID: 15496

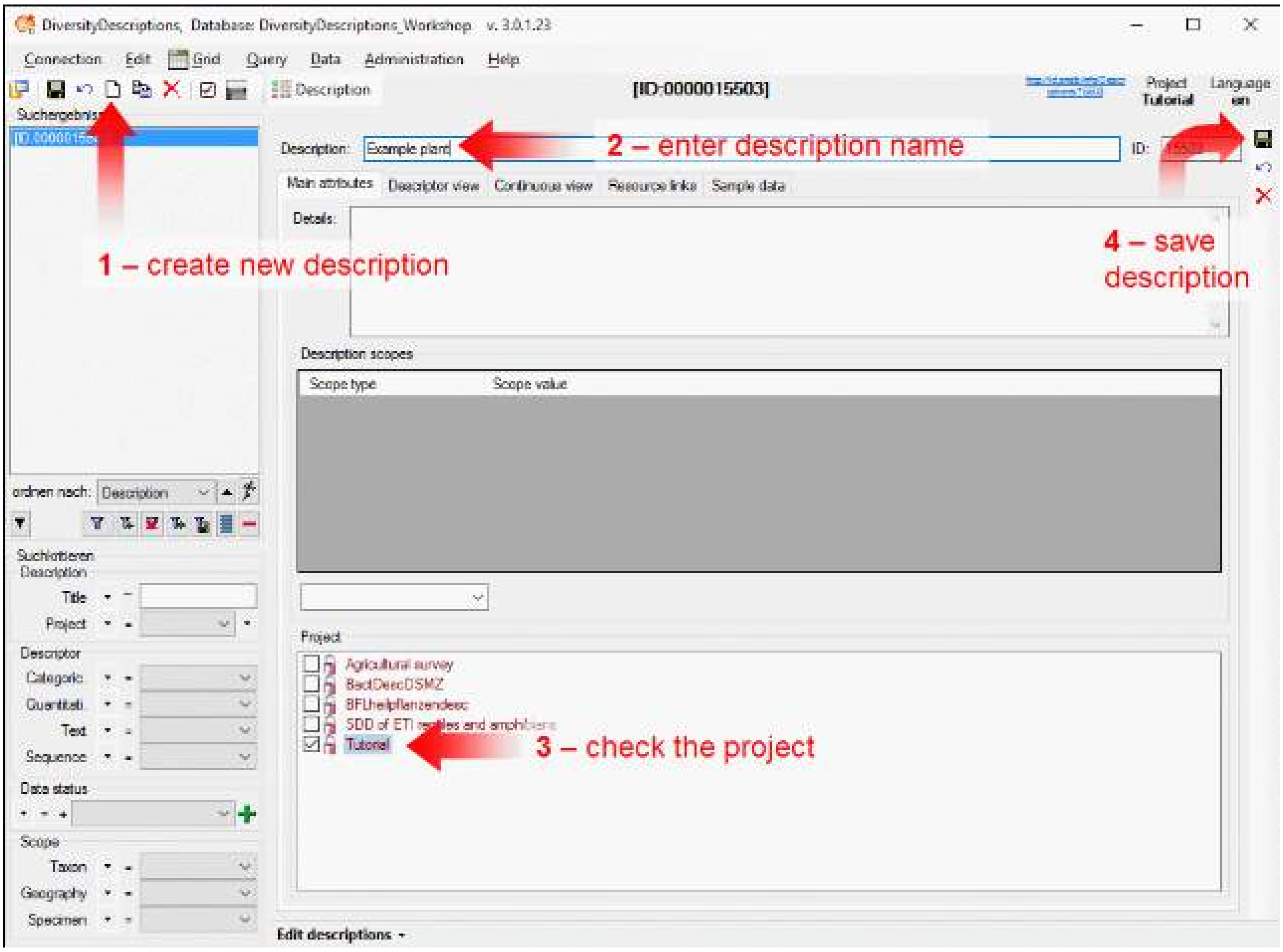
A more detailled description of all editing options can be found in the Edit descriptors section of this manual.

This tutorial is continued in the sections listed below.

- section Enter description data
- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Enter description data

Now that we have entered several descriptors and categorical states we have defined a "terminology" to enter descriptive data. To create a new description, select edit mode descriptions from menu **Edit->Descriptions**. Now click on the 🗋button in the upper left panel (see point **1** in image below). If you are asked for the project, select "Tutorial".



DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.1.23

[ID:0000015503]

Description: Example plant

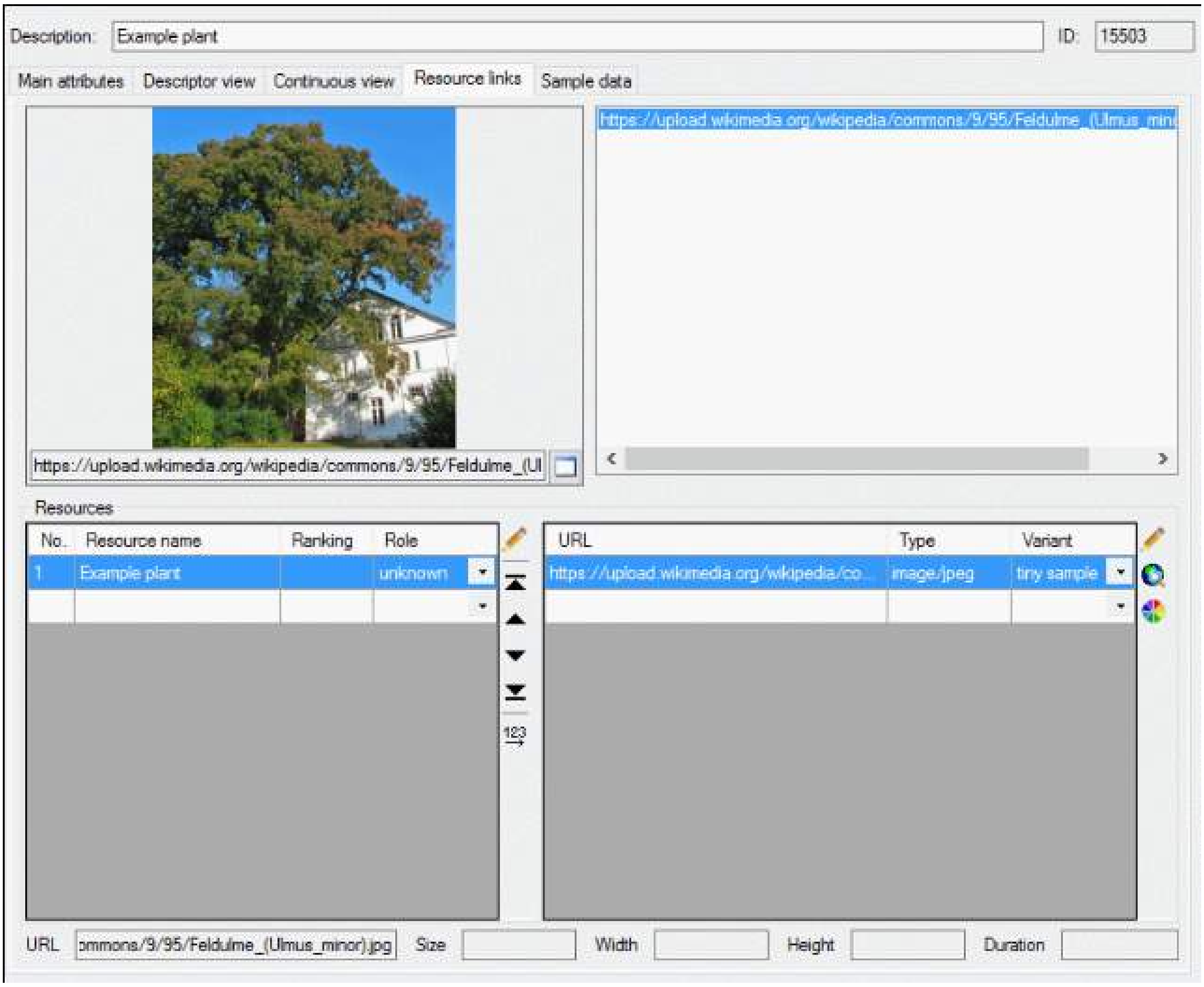
Project: Tutorial

Language: en

The new description is created with a numeric name. Change it to "Example plant" (see point **2** in image above) and check that project "Tutorial" is assigned to the new description (see points **3** in image above). Finally save the description (see point **4** in image above) and the description name will be updated in the header and the query panel at the left side of the window.

Enter resources for the description

As described for the descriptors, for each description resources may be assigned. Therefore click on the "Resource links" tab, which looks exactly the same as described in chapter "Enter a text descriptor" (see image below, a link to Wikipedia was used).



Description: Example plant   ID: 15503

https://upload.wikimedia.org/wikipedia/commons/9/95/Feldulme_(Ulmus_min

https://upload.wikimedia.org/wikipedia/commons/9/95/Feldulme_(Ul

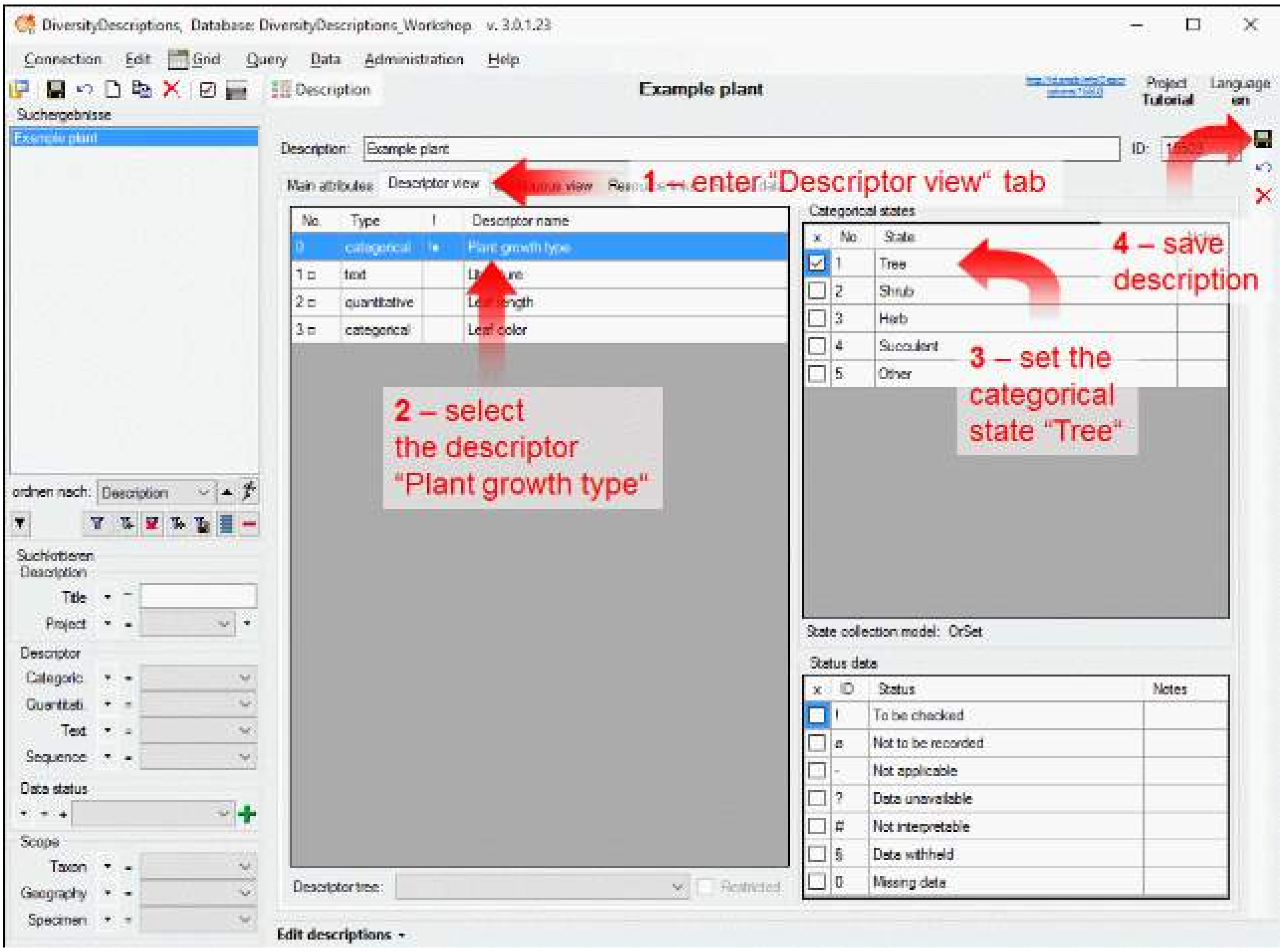
No.	Resource name	Ranking	Role
1	Example plant		unknown

URL	Type	Variant
https://upload.wikimedia.org/wikipedia/co...	image/jpeg	tiny sample

URL: ommons/9/95/Feldulme_(Ulmus_minor).jpg   Size: Width: Height: Duration:

Enter descriptive data

Now let's start entering the descriptive data. Open the "Descriptor view" tab (see point **1** in image below). In the left part of the window there is a list of the desriptors. Select descriptor "Plant growth type" (see point **2** in image below) and on the right side the associated categorical states are diplayed. Click on the square in columne "x" besides the state "Tree" to set the check mark (see point **3** in image below). Finally save the description (see point **4** in image above).



Description: Example plant

State collection model: OrSet

No.	Type	!	Descriptor name
0	categorical	•	Plant growth type
1 ▫	text		Li re
2 ▫	quantitative		Le ength
3 ▫	categorical		Leaf color

x	No	State
☑	1	Tree
☐	2	Shrub
☐	3	Herb
☐	4	Succulent
☐	5	Other

x	ID	Status	Notes
☐	!	To be checked	
☐	≡	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

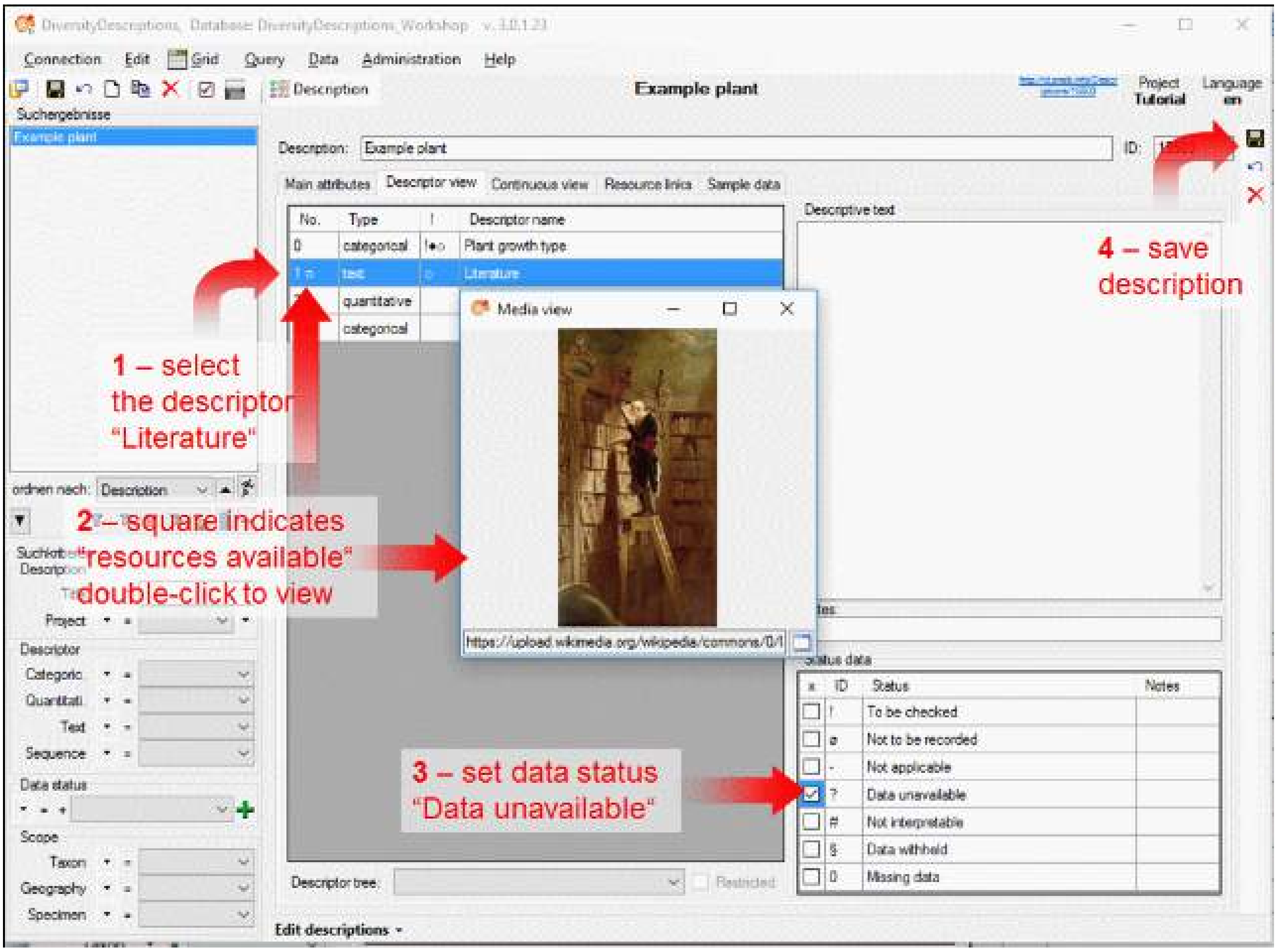
1 – enter "Descriptor view" tab

2 – select the descriptor "Plant growth type"

3 – set the categorical state "Tree"

4 – save description

Next select the descriptor "Literature" tab (see point **1** in image below). In principle you could enter a text in the right area "Descriptive text", but for this example two other things shall be demonstrated. In the first column of the descriptor list the sequence number ("Nr.") is displayed. A small square behind the number indicates that resources have been attached to the descriptor (see point **2** - upper arrow - in image below). You can view the attached resources by a double-click on the sequence number (see point **2** - right arrow - in image below). In some cases you do not have data available for a certain descriptor but you want to express that data should be entered. Therefore you can sen one or more "Status data" values in the right lower part of the window (see point **3** in image below). Finally save the descriptor (see point **4** in image below).



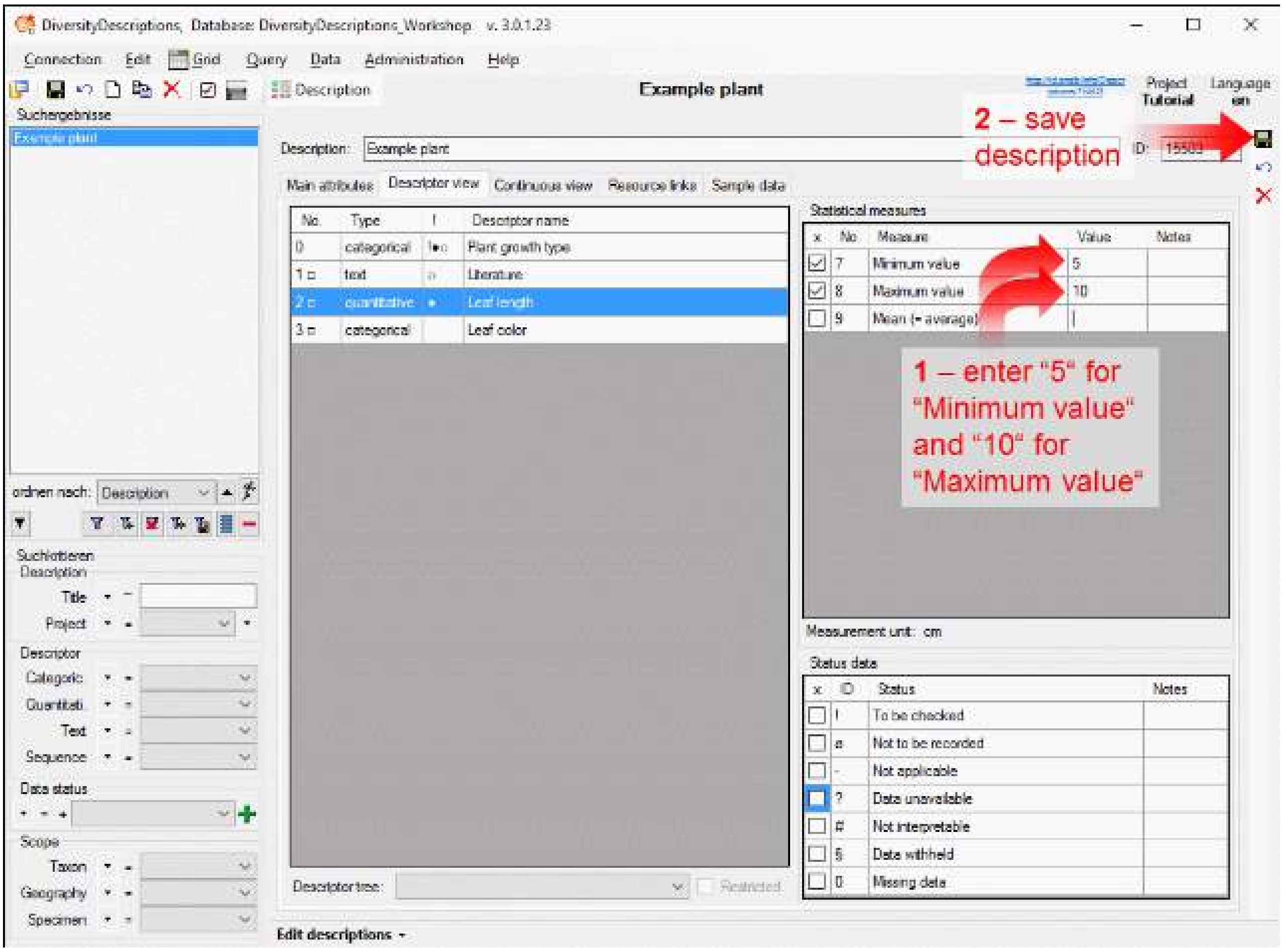
1 – select the descriptor "Literature"

2 – square indicates "resources available" double-click to view

3 – set data status "Data unavailable"

4 – save description

For each categorical state resources may be assigned. Therefore select the categorical state where you want to enter the resources (see point **1** in image below) and enter a resource name (see points **2** in image below). In this case we do not assign an URL to a picture but attach color values. Therefore click the button in the "..." column and select a color value (see points **3** and **4** in image below). Finally save the descriptor (see point **5** in image below).



2 – save description

1 – enter "5" for "Minimum value" and "10" for "Maximum value"

Description: Example plant

ID: 15503

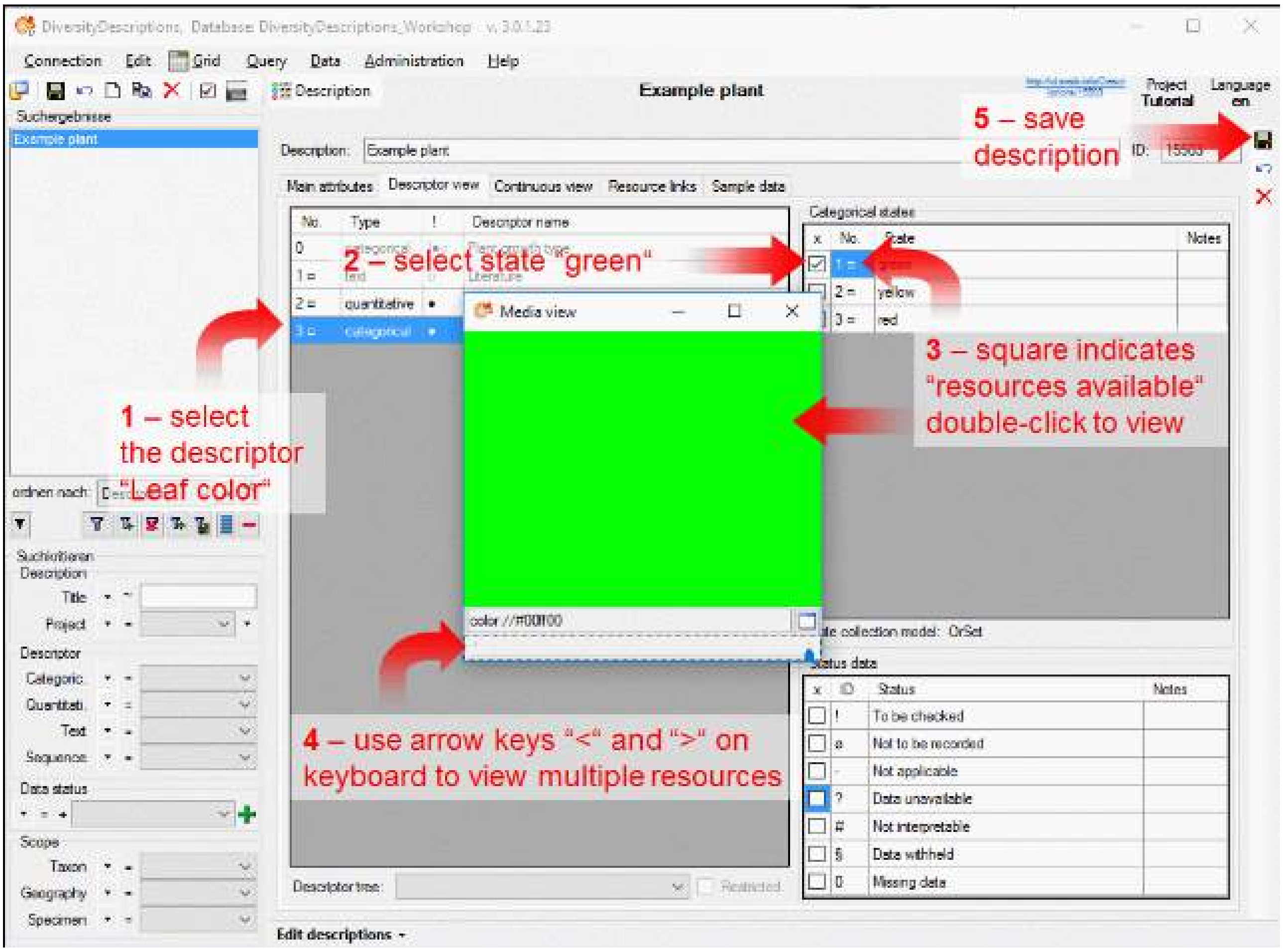
No.	Type	!	Descriptor name
0	categorical	!●○	Plant growth type
1 □	text	○	Literature
2 □	quantitative	●	Leaf length
3 □	categorical		Leaf color

x	No	Measure	Value	Notes
☑	7	Minimum value	5	
☑	8	Maximum value	10	
☐	9	Mean (= average)		

Measurement unit: cm

x	ID	Status	Notes
☐	!	To be checked	
☐	a	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

The last descriptor not yet used is "Leaf color". Select it from the descriptor list an chek the categorical state "gree" (see points **1** and **2** in image below). The square in column "Nr." of the "Categorical states" indicates that resources are attached. Double-click it to view the resources (see point **3** in image below). Since we attached three different colors for that categorical state, you may scroll through the different resources by using the "right" and "left" arrow key on the keyboard (see point **4** in image below). Finally save the descriptor (see point **5** in image below).



1 – select the descriptor "Leaf color"

2 – select state "green"

3 – square indicates "resources available" double-click to view

4 – use arrow keys "<" and ">" on keyboard to view multiple resources

5 – save description

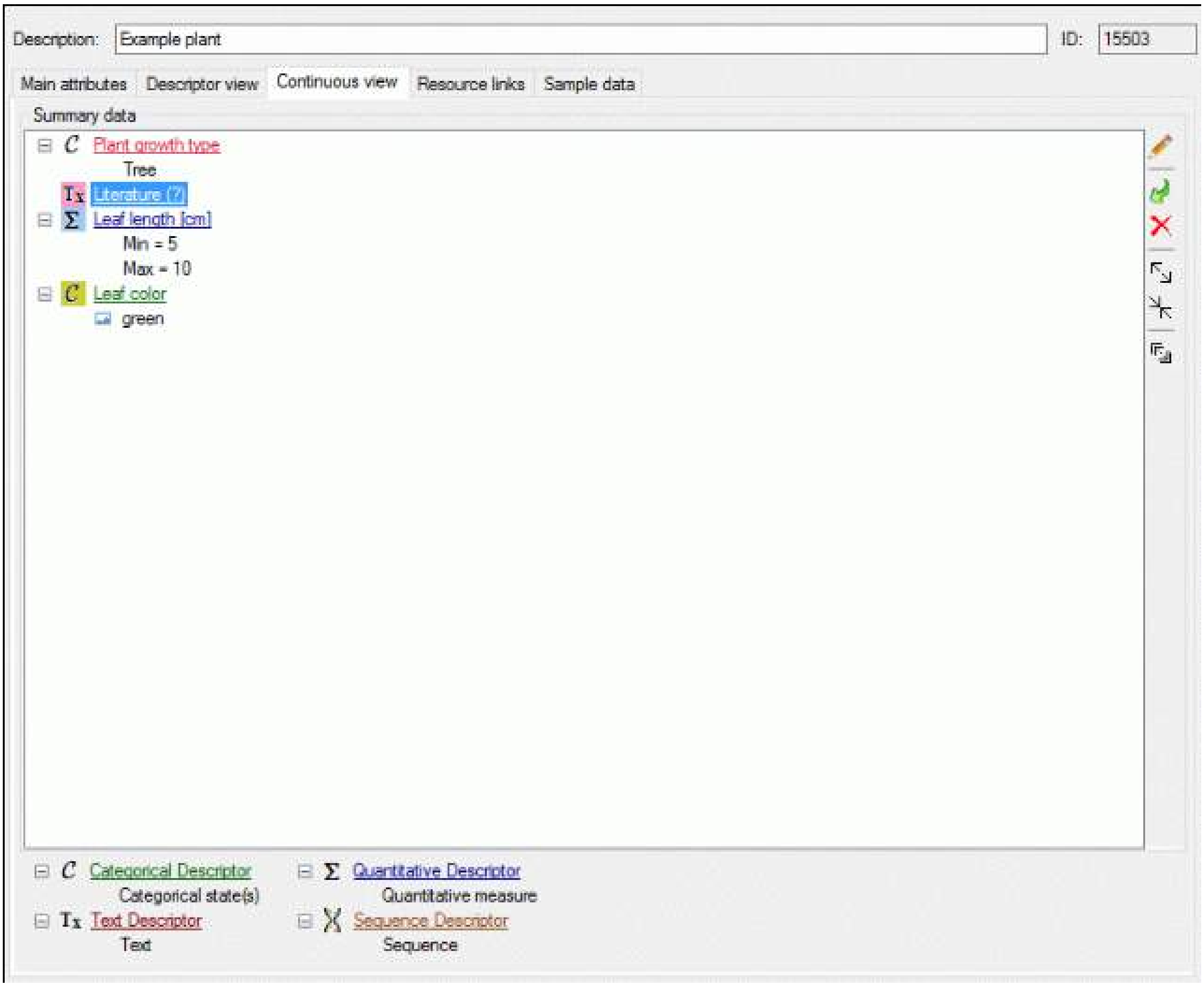
Description: Example plant

color://#00ff00

State collection model: OrSet

An alternate description data view

If you have defined many descriptors and one specific description references only a small amount of the descriptors, the "Descriptor view" might be quite confusing. In this case an alternate representation, the "Continuous view" might be helpful (see image below). Here only the descriptors that have been referenced in the description data are shown and the values (categorical states, statistical measures or plain text data) are attached at the descriptors. Additionally some extra information is color coded, e.g. "Plant type" is displayed in light red text because it is a mandatory descriptor. For details check the Edit descriptions section of this manual.


Description: Example plant

ID: 15503

Plant growth type
Tree

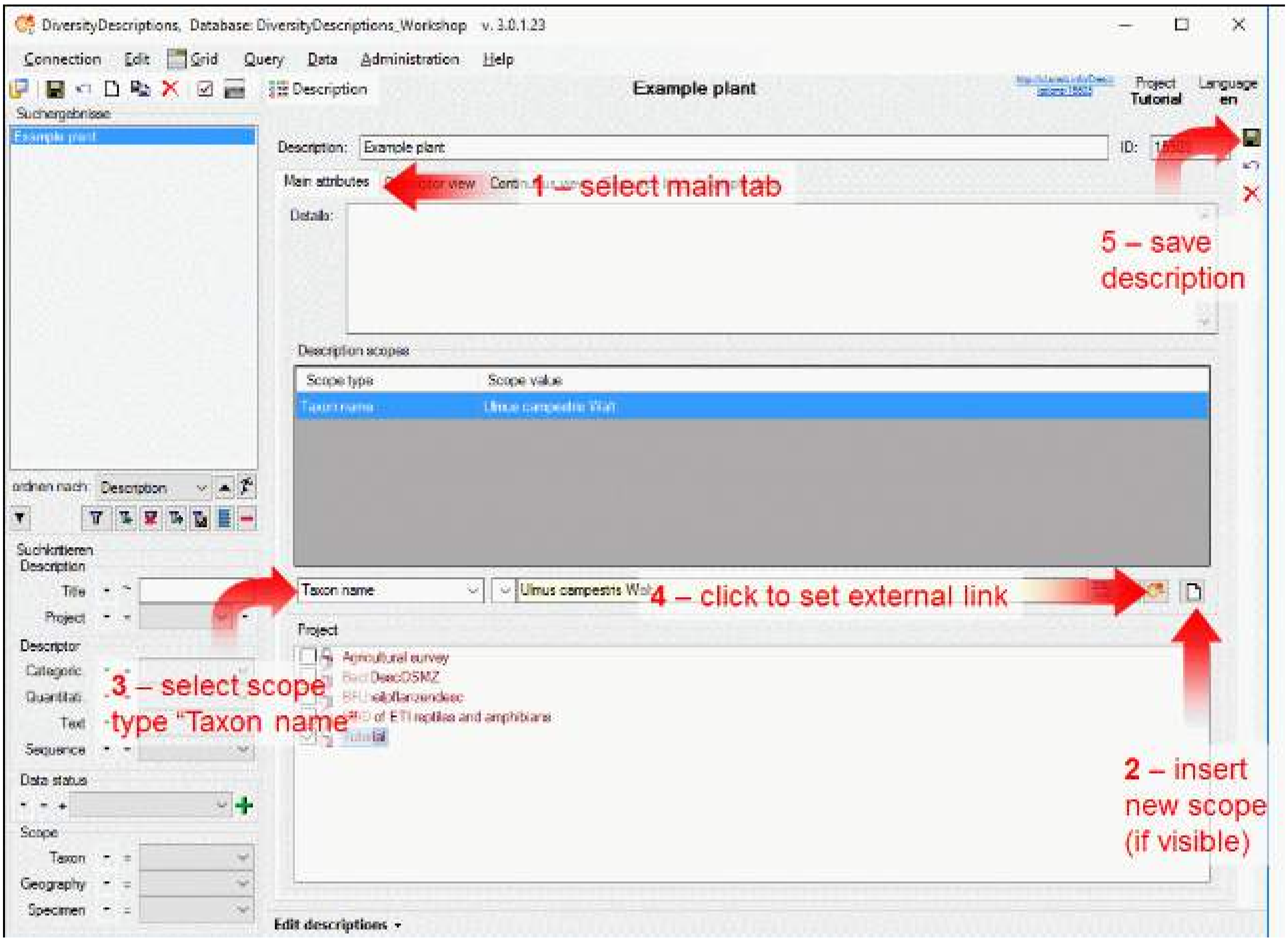
Literature (?)

Leaf length [cm]
Min = 5
Max = 10

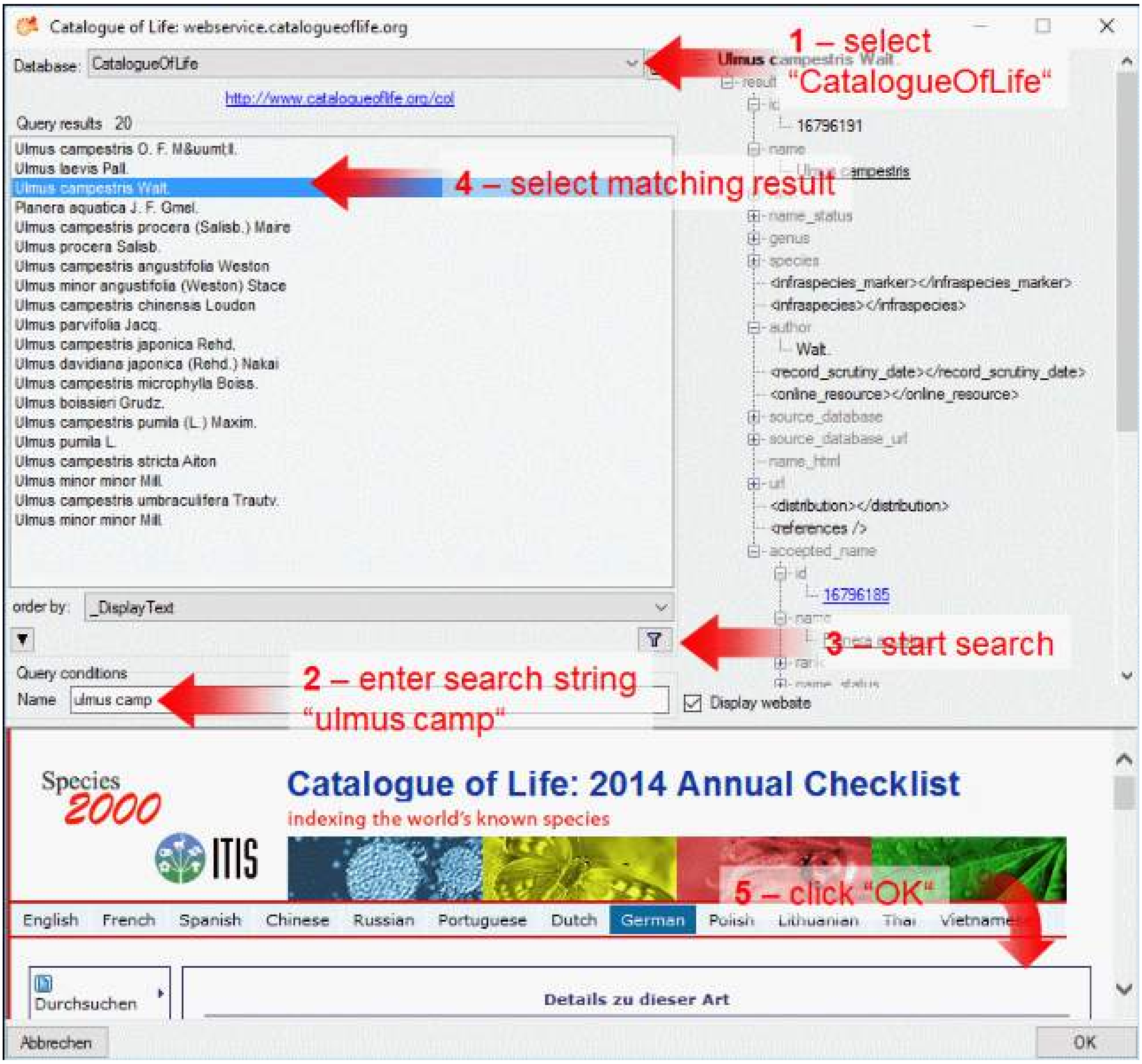
Leaf color
green

Enter description scope

As last step in this section the insert of "Description scopes" shall be demonstrated. In our example we want to enter a taxon name and link it to a taxon name service in the internet.



First select the "Main attributes" tab and click button 🗋if visible (see points **1** and **2** in image above). When you now select the scope type "Taxon name" (see point **3** in image above) you could enter a taxon name, e.g. "Ulmus campestris", in the text box that appears right from the scope type. But we want to create a link to the internet service "Catalogue Of Life", therefore press button . Now a separate window opens (see image below). Select "CatalogueOfLife" as database (see point **1** in image below). Enter the search string "ulmus camp" in the query field and start a search (see points **2** and **3** in image below). When you select a search reult (see point **4** in image below), you can watch the stored data in the lower part of the window. Finally click "OK" to store the link (see point **5** in image below).


Catalogue of Life: webservice.catalogueoflife.org

Database: CatalogueOfLife

1 – select "CatalogueOfLife"

http://www.catalogueoflife.org/col

Query results 20

Ulmus campestris O. F. Müll.
Ulmus laevis Pall.
Ulmus campestris Walt.
Planera aquatica J. F. Gmel.
Ulmus campestris procera (Salisb.) Maire
Ulmus procera Salisb.
Ulmus campestris angustifolia Weston
Ulmus minor angustifolia (Weston) Stace
Ulmus campestris chinensis Loudon
Ulmus parvifolia Jacq.
Ulmus campestris japonica Rehd.
Ulmus davidiana japonica (Rehd.) Nakai
Ulmus campestris microphylla Boiss.
Ulmus boissieri Grudz.
Ulmus campestris pumila (L.) Maxim.
Ulmus pumila L.
Ulmus campestris stricta Aiton
Ulmus minor minor Mill.
Ulmus campestris umbraculifera Trautv.
Ulmus minor minor Mill.

4 – select matching result

order by: _DisplayText

3 – start search

Query conditions

Name: ulmus camp

2 – enter search string "ulmus camp"

☑ Display website

Ulmus campestris Walt.
result
id
16796191
name
Ulmus campestris
name_status
genus
species
<infraspecies_marker></infraspecies_marker>
<infraspecies></infraspecies>
author
Walt.
<record_scrutiny_date></record_scrutiny_date>
<online_resource></online_resource>
source_database
source_database_url
name_html
url
<distribution></distribution>
<references />
accepted_name
id
16796185
name
rank
name_status

5 – click "OK"

For scope type "Taxon name" links to three different internet services may be set. If you use the DiversityWorkbench module DiversityTaxonNames, you can build an own taxon database and link entries to descriptions. Other scoe types that allow linking to DiversityWorkbench modules are "Geographic area" (DiversityGazzeteers), "Reference" (DiversityReferences), "Specimen" (DiversityCollection) and "Observation" (DiversityCollection also). Additionally there are the scope types "Sex", "Stage", "Part" and "Other scope", which have certain values defined in the Edit projects section. Remember that in step Create a new project we inserted the sex values "Male" and "Female" and assigned them for the tutorial project. Try to insert the scope value "Female" for the example description!

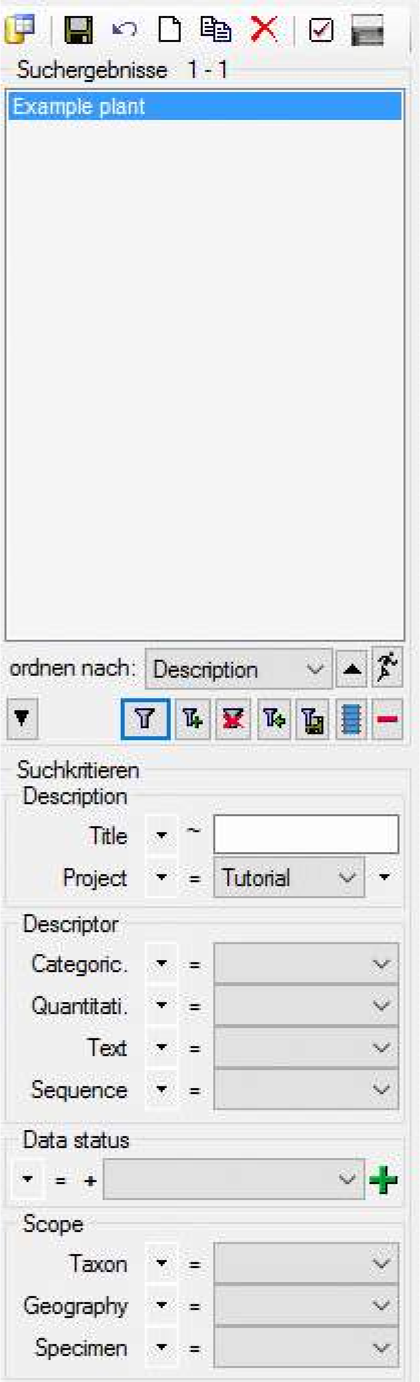
A more detailled description of all editing options can be found in the Edit descriptions section of this manual.

This tutorial is continued in the sections listed below.

- section Searching the database
- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Searching the database

To search for data in the database use the query sector in the left part of the window. Depending on the actually chosen edit mode - **Descriptions**, **Descriptors** or **Projects** - the query searches for descriptions, descriptors or (local) drojects. The query conditions are changed depending on the edit mode, too (see images below).



Suchergebnisse 1 - 1

Example plant

ordnen nach: Description

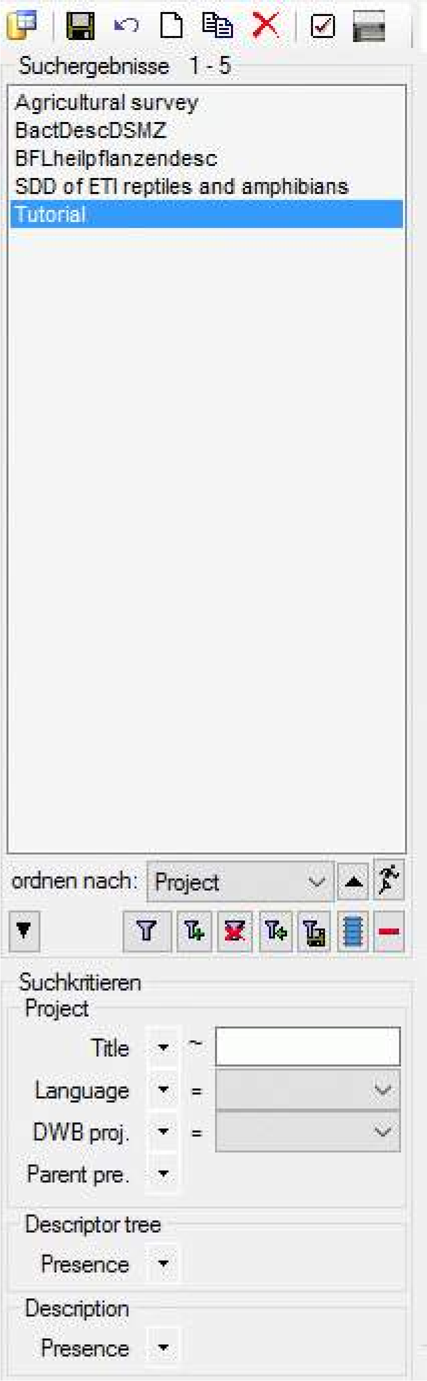
Project = Tutorial

Suchergebnisse 1 - 4

Leaf color
Leaf length
Literature
Plant growth type

ordnen nach: Descriptor

Project = Tutorial

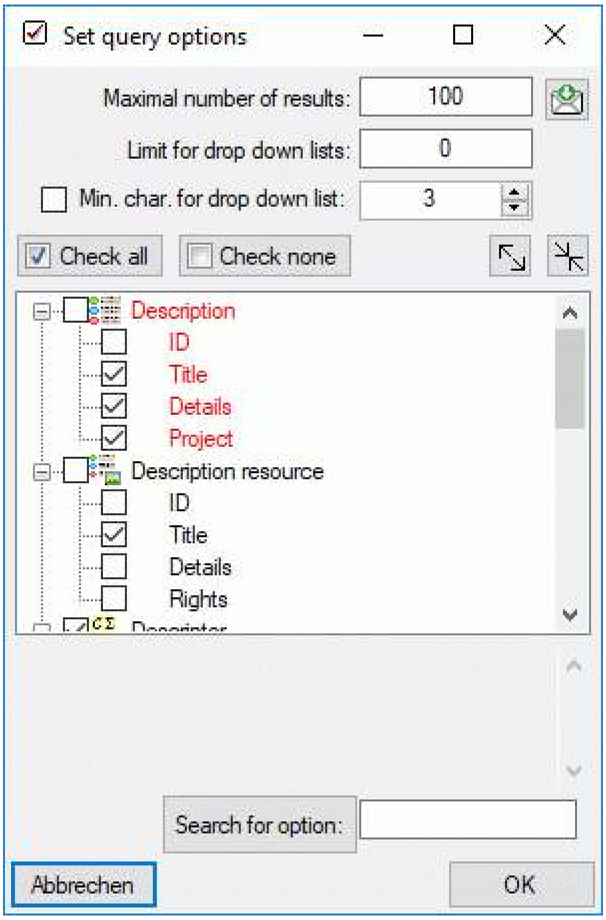


Suchergebnisse 1 - 5

Agricultural survey
BactDescDSMZ
BFLheilpflanzendesc
SDD of ETI reptiles and amphibians
Tutorial

ordnen nach: Project

To select the query conditions click on the ☑button in the top panel. A window will open as shown below.



Maximal number of results: 100

Limit for drop down lists: 0

☐ Min. char. for drop down list: 3

☐ Description
- ☐ ID
- ☑ Title
- ☑ Details
- ☑ Project

☐ Description resource
- ☐ ID
- ☑ Title
- ☐ Details
- ☐ Rights

☑ Descriptor

With the **Maximum number of results** you may limit the package size which should be retrieved from the server. For a slow connection to the database server choose a low value (e.g. 100 as set by default).

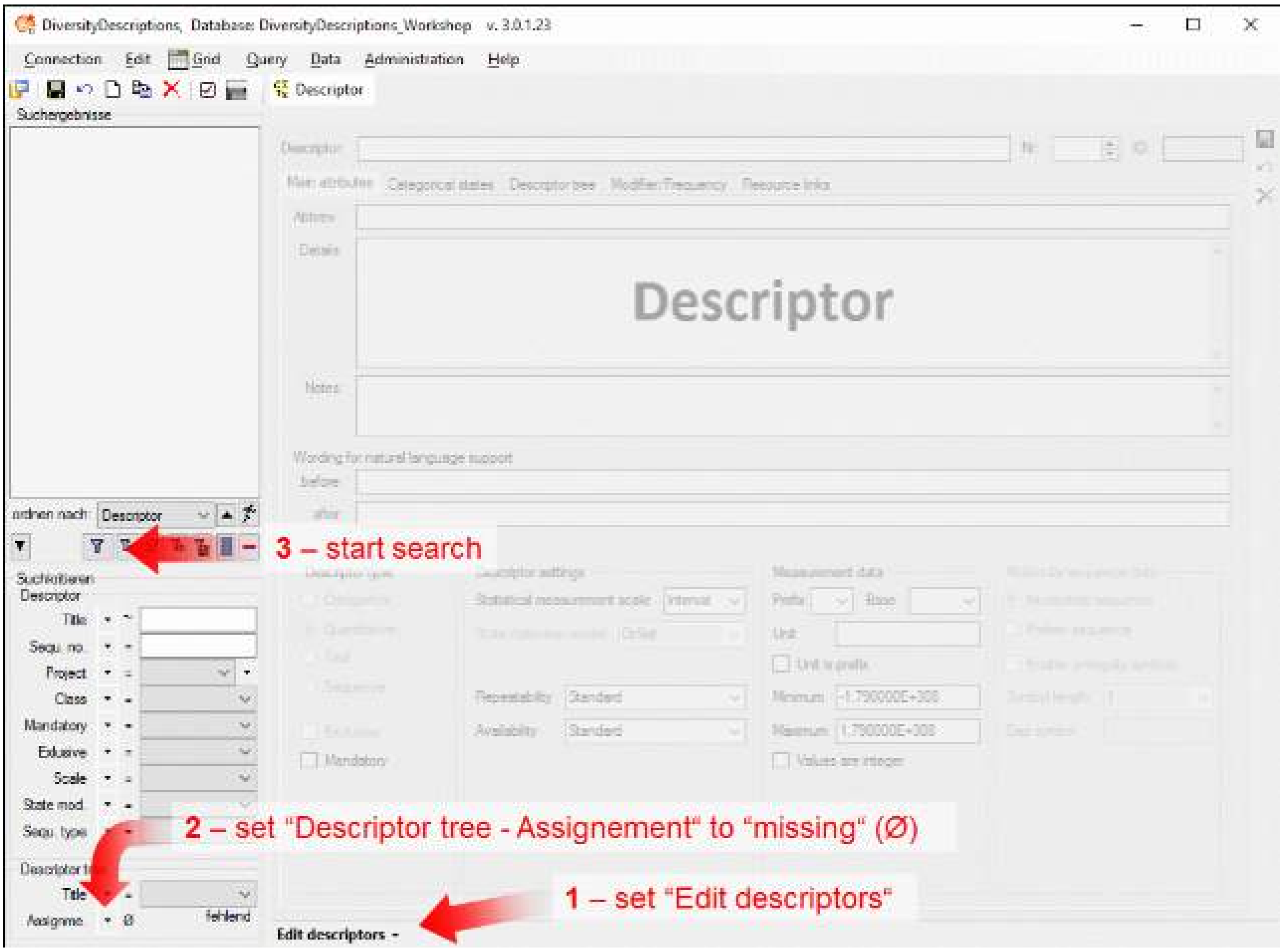
The **Limit for drop-down lists** restricts the maximum number of drop-down lists which should be created. For a slow connection to the database server choose a low value. The default is set to 0 which means no drop-down lists will be created.

Click on the **Check none** button to clear the previous selection or click **Check all** to select all conditions. Alternatively you may display or hide each single query condition by checking or unchecking the entry in the list.

After all query conditions are set, click on the ▽button to start the query. In the result list you should find the description, descriptors or project created in this tutorial. To save your current query click on the 💾button on the right of the ▽button. A window will open as shown below. For more details see the section Save query.

When you enter new descripors to the databas it may happen that you forgot to assign it to descriptor tree. That means, those desriptor cannot be used for entering description data. Another action that may generate such orphaned descriptors is to delete a project. With that action implicitely the associated descriptions and descriptor trees will be removed from the database, but the descriptors will not be deleted, because they might be assigned to a different descriptor tree (and project).

To find and delete orphaned descriptors, set mode "Edit descriptors" (see point **1** in image below). Then set query condition "Descriptor tree - Assignment" to "missing" (see point **2** in image below) and start the search (see point **3** in image below). If you want to deleted the found descriptors, you can select them in the resulg list (multiple selection is possible) and click button ✕to delete them.



3 – start search

2 – set "Descriptor tree - Assignement" to "missing" (Ø)

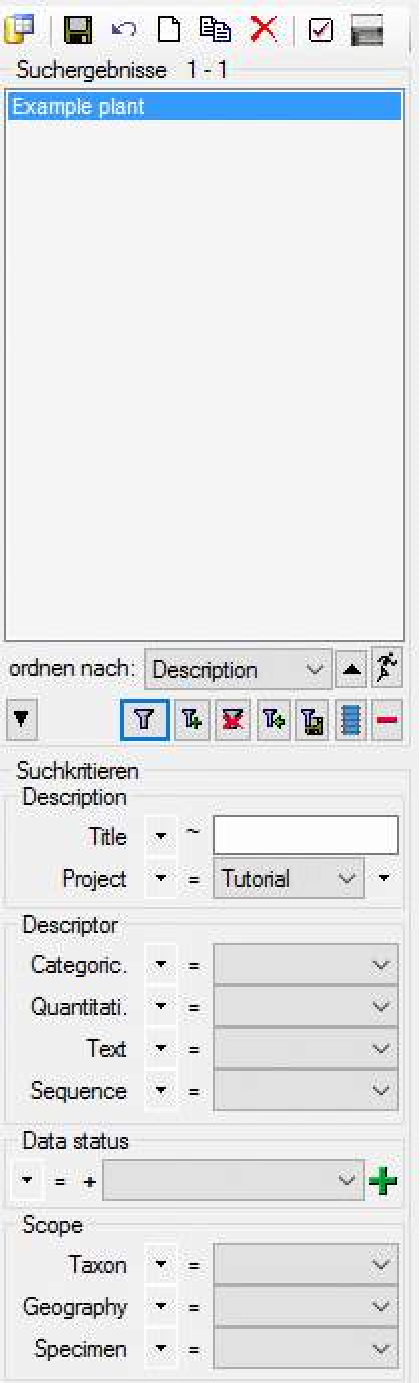
1 – set "Edit descriptors"

This tutorial is continued in the sections listed below.

- section Generate an HTML document
- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Generate an HTML document

Now that we have entered our first description data and learned how to find them in the database, we want to share that data. Search for the description of the example plant as described in the previous tutorial step (see image below).



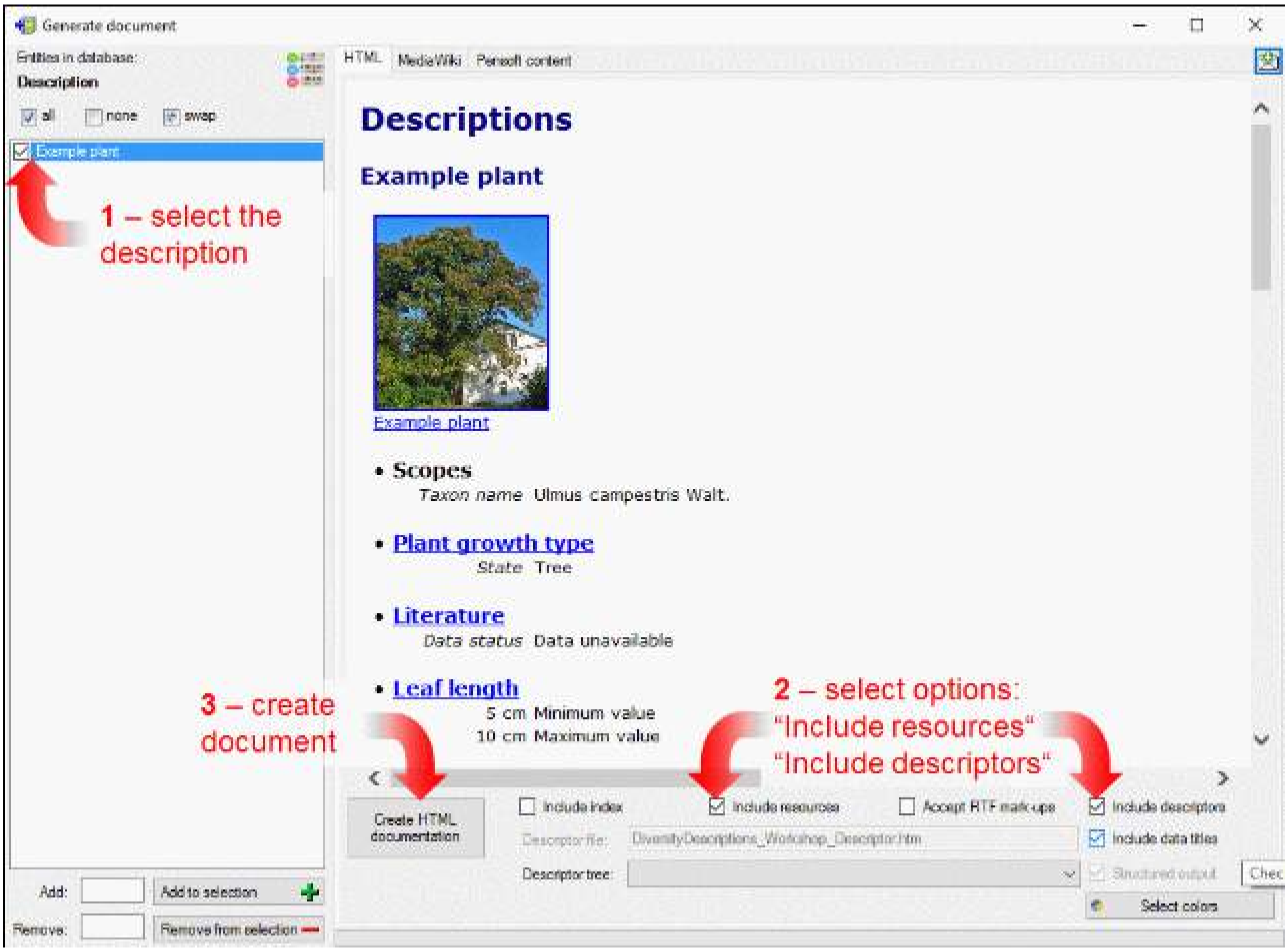
Suchergebnisse 1 - 1

Example plant

ordnen nach: Description

Project = Tutorial

From the menu choose **Data ->** **Generate document ...** and a window will open as shown below. Select the "Example plant" (see point **1** in image below). Then set the options **Include resources** to show the images we have assigned and **Include descriptors** to generate the descriptor definitions in the same document (see point **2** in image below). Finally click on button **Create HTML documentation** and the data will be shown in the HTML window (see point **3** in image below). If you scroll down or click on a descriptor name in the description data you will find the descriptor data. In the working directory of Diversity Descriptions a HTML file has been generated that might be used to publish your data.



☑ Example plant

1 – select the description

Descriptions

Example plant

Example plant

- **Scopes**
  Taxon name Ulmus campestris Walt.
- **Plant growth type**
  State Tree
- **Literature**
  Data status Data unavailable
- **Leaf length**
  5 cm Minimum value
  10 cm Maximum value

2 – select options:
“Include resources“
“Include descriptors“

3 – create document

☐ Include index ☑ Include resources ☐ Accept RTF mark-ups ☑ Include descriptors

Descriptor file: DiversityDescriptions_Workshop_Descriptor.htm ☑ Include data titles

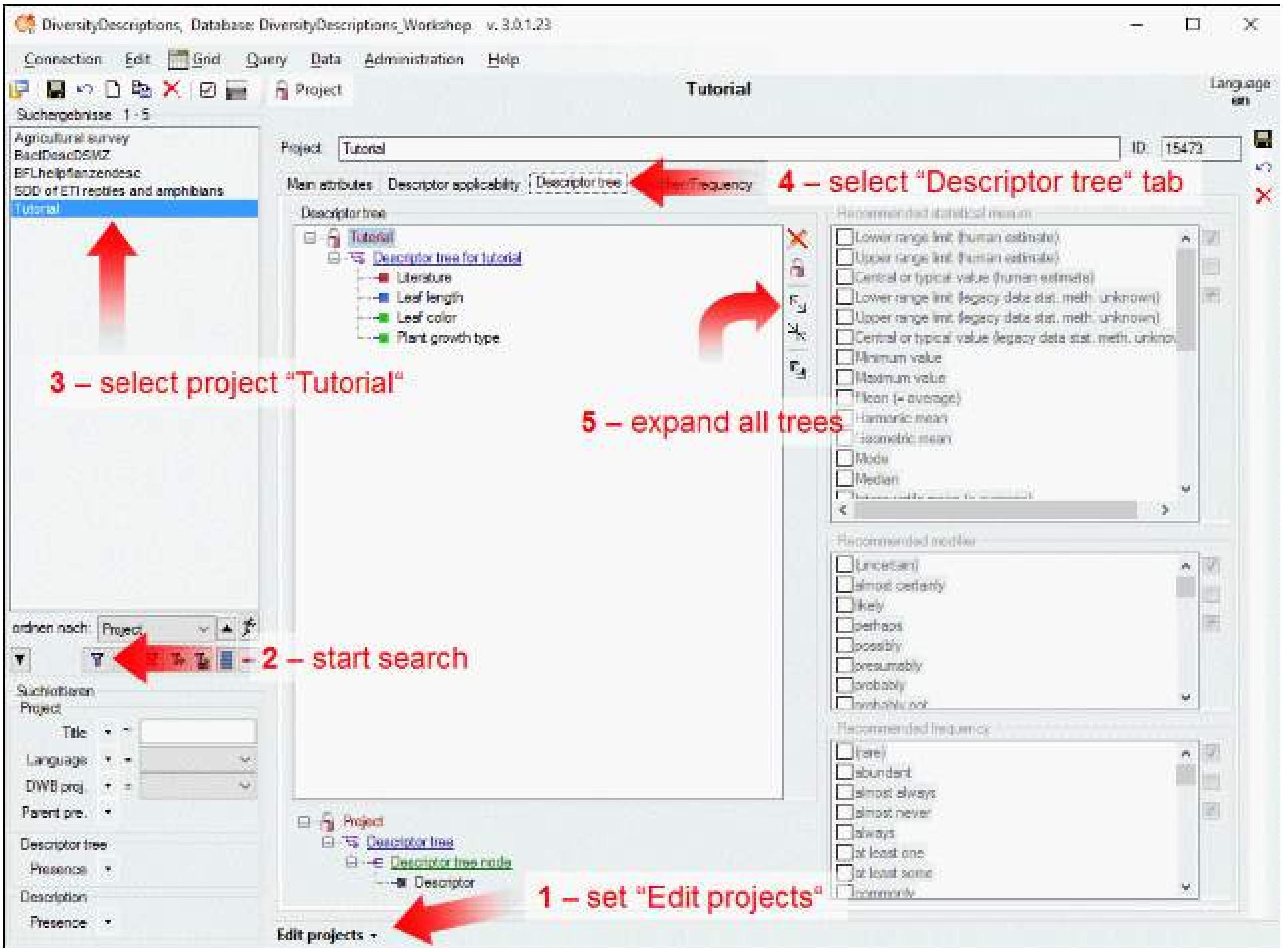
Descriptor tree: ☑ Structured output

This tutorial is continued in the sections listed below.

- section Sort the descriptors
- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Sort the descriptors

In the tutorial steps when we created a new descriptor, we usually set the field "Nr." (sequence number), which determines the sequence the descriptors are displayed in several lists, e.g. when you enter description data. If you like to change that display sequence, it is quite uncomfortable, to go through all descriptors and change the sequence numbers manually, but there is a much more comfortable way. Select edit mode projects from menu **Edit->Projects** or from the bottom control (see point **1** in image below). Now click on the ▼ button to find the project "Tutorial" (see points **2** and **3** in image below). Open the "Descriptor tree" tab and expand the trees (see points **4** and **5** in image below).



Project: Tutorial ID: 15473

4 – select “Descriptor tree“ tab

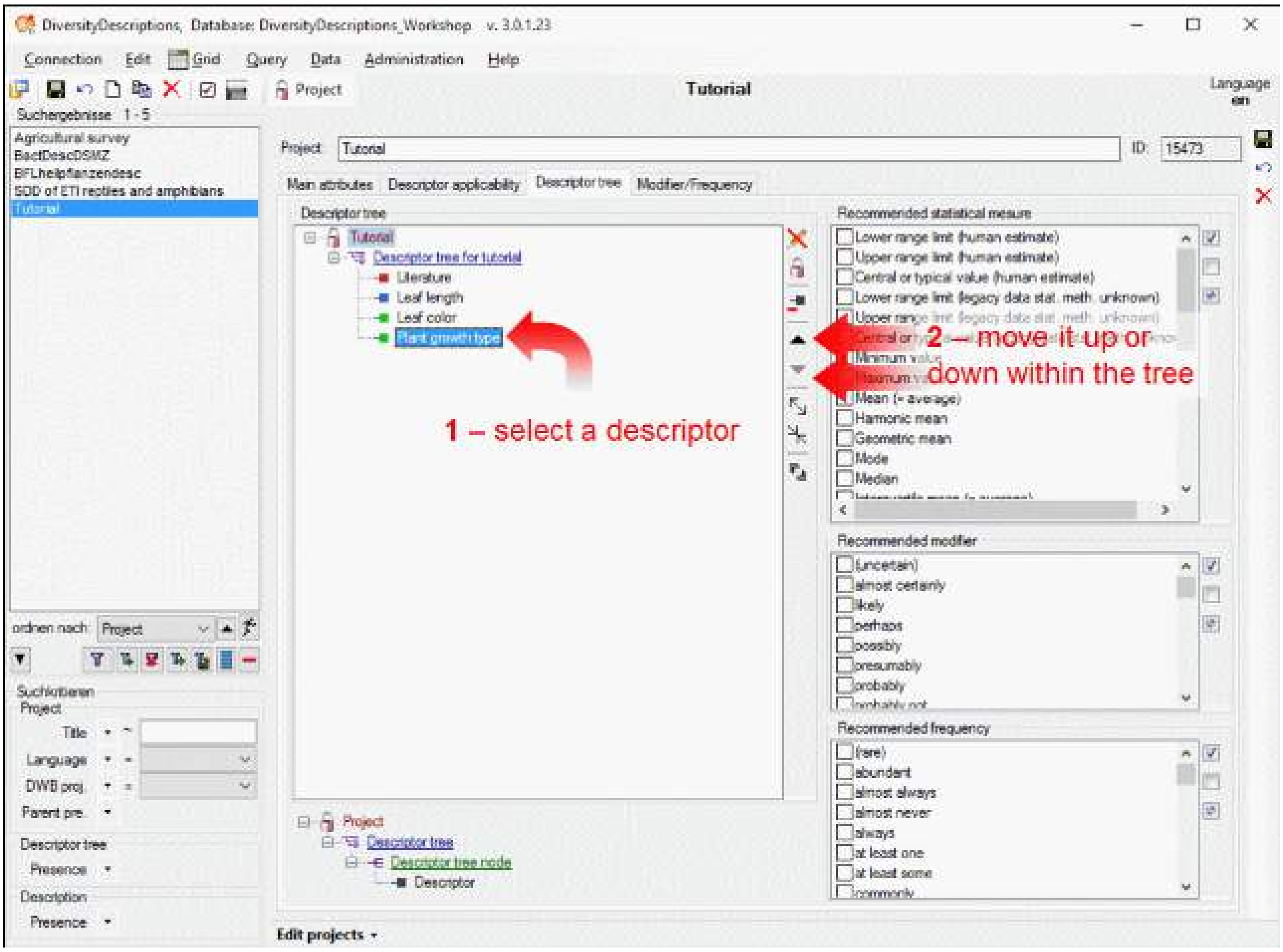
3 – select project “Tutorial“

5 – expand all trees

2 – start search

1 – set “Edit projects“

The "Descriptor tree" tab in the "Edit projects" mode looks almost like that one in the "Edit descriptors" mode. But there are some important differences. If you are in the "Edit descriptor" mode, only the actually selected descriptor will be displayed in the tree. In the "Edit projects" mode all descriptors are diplayed! Therefore the descriptors may now be shifted up and down to change the order (see points **1** and **2** in image below).

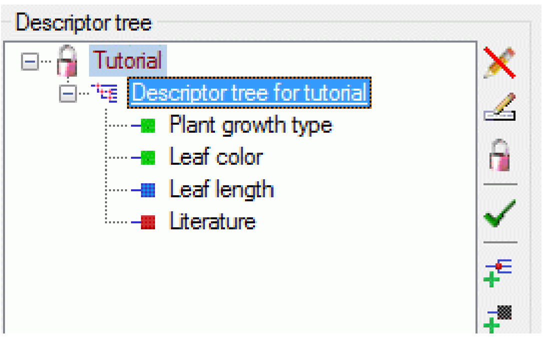


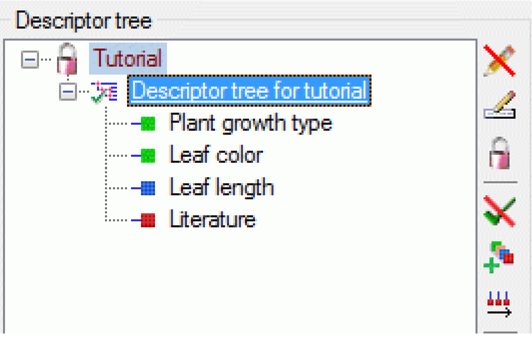
Project: Tutorial ID: 15473

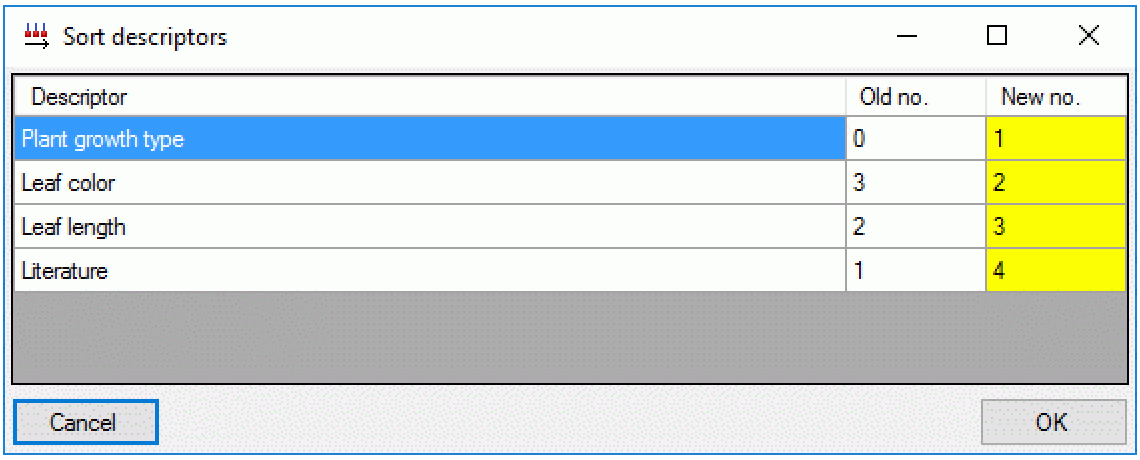
1 – select a descriptor

2 – move it up or down within the tree

Now select the "Descriptor tree for tutorial" and click button ✓(see image below left). With this action you indicate that this descriptor tree should be complete, i.e. it contains all descriptors for the project. Now the additional button ⇉ is displayed that allows to take over of the descriptor tree order to the descriptor's sequence numbers (see image below right).

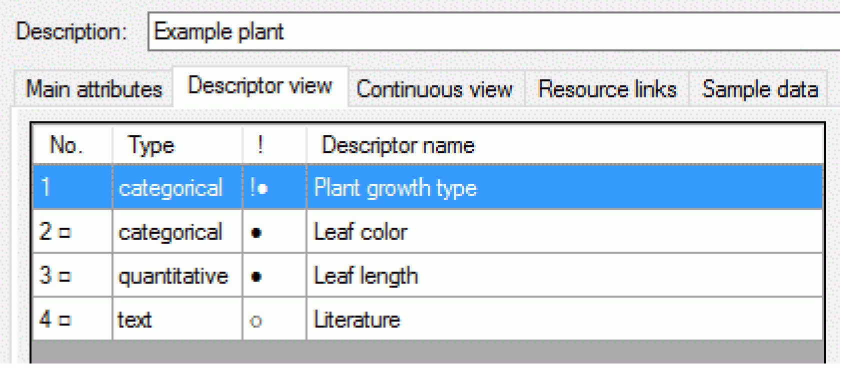






Descriptor	Old no.	New no.
Plant growth type	0	1
Leaf color	3	2
Leaf length	2	3
Literature	1	4

When you click on button a window opens that displays the changed sequence numbers of the descriptors (see imabe above). After confirming the changes with "OK" the new order will be effective in the descriptor list of the "Edit descriptions" (see image below).



Description: Example plant

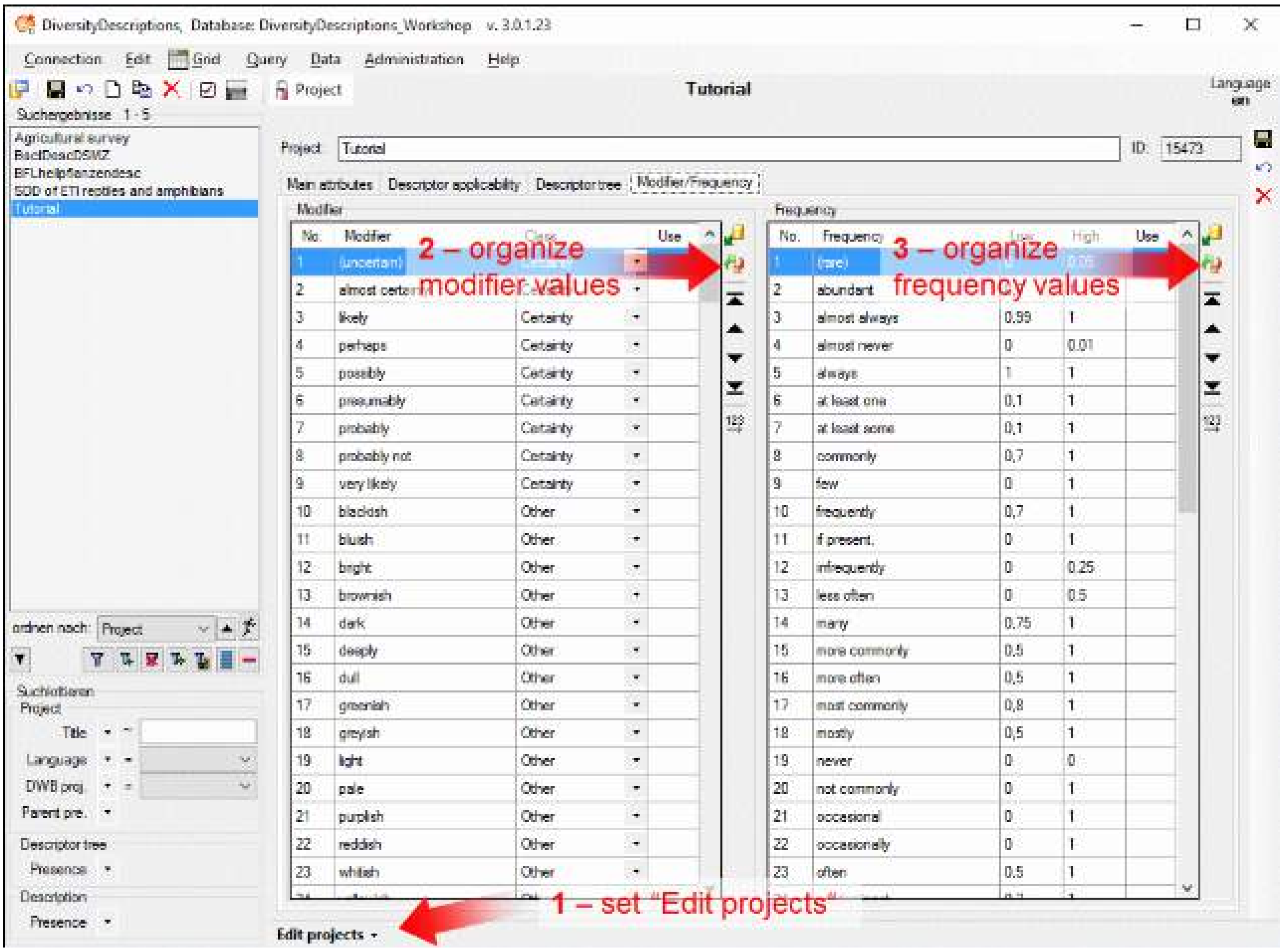
No.	Type	!	Descriptor name
1	categorical	!●	Plant growth type
2 ▫	categorical	●	Leaf color
3 ▫	quantitative	●	Leaf length
4 ▫	text	○	Literature

This tutorial is continued in the sections listed below.

- section Assign modifiers
- section Enter descriptor dependencies

Tutorial - Assign modifiers

Modifiers may be used in the description data for an additional characterization of categorical or quantitative descriptor data. There are five different modifier categories: **Certainty**, **Seasonal**, **Diurnal**, **Misinterpretation** and **Other**. An additional modifier class, **Frequency** is only applicable for categorical descriptors. Although you are allowed to define own modifier values, there is a large number of commonly used predefined modifier and frequency values, which should be preferred. We now want to insert those predefined values into the database.



Project: Tutorial

ID: 15473

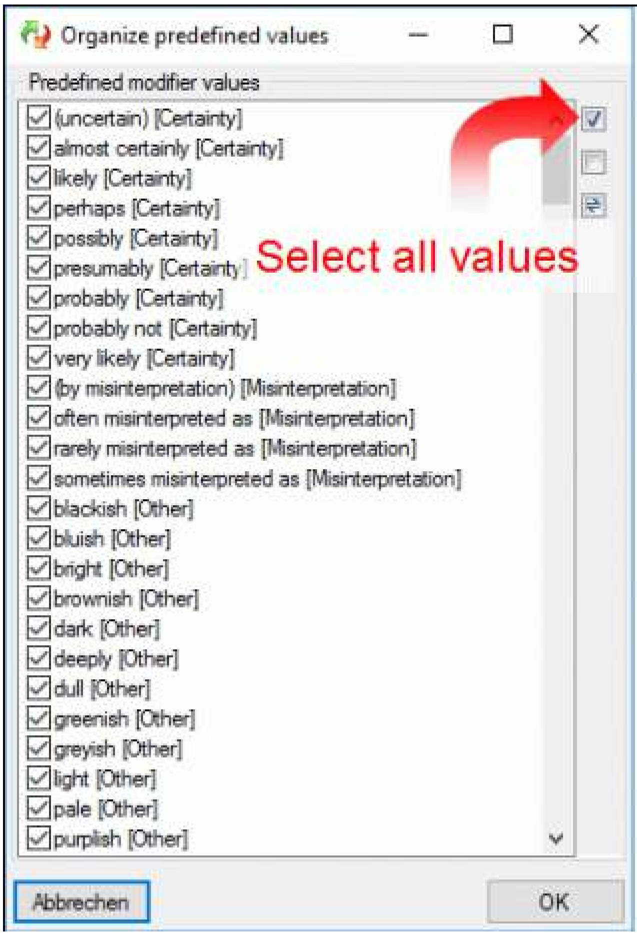
Modifier

No.	Modifier	Class	Use
1	(uncertain)		
2	almost certa		
3	likely	Certainty	
4	perhaps	Certainty	
5	possibly	Certainty	
6	presumably	Certainty	
7	probably	Certainty	
8	probably not	Certainty	
9	very likely	Certainty	
10	blackish	Other	
11	bluish	Other	
12	bright	Other	
13	brownish	Other	
14	dark	Other	
15	deeply	Other	
16	dull	Other	
17	greenish	Other	
18	greyish	Other	
19	light	Other	
20	pale	Other	
21	purplish	Other	
22	reddish	Other	
23	whitish	Other	

Frequency

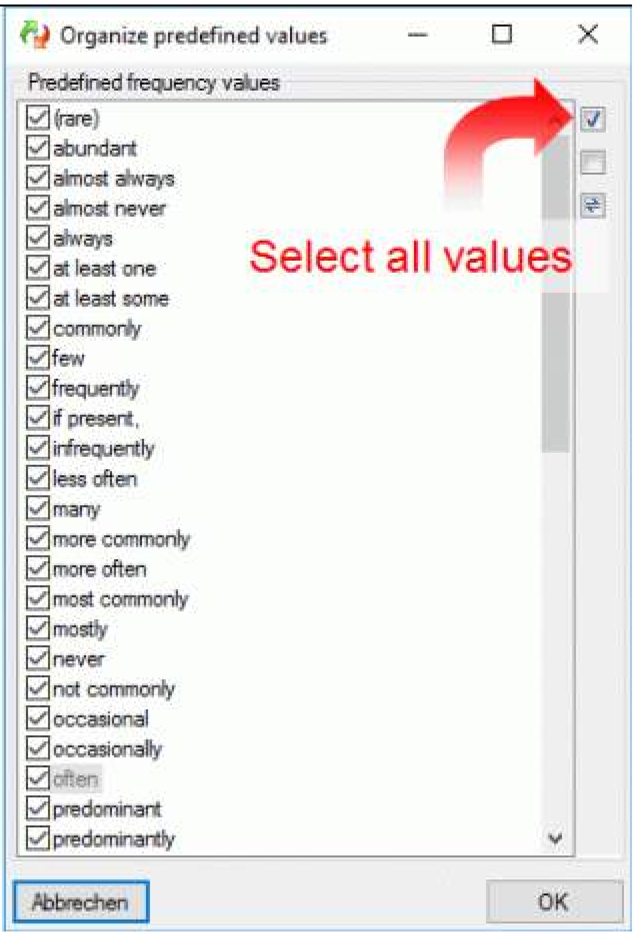
No.	Frequency	Low	High	Use
1	(rare)		0.05	
2	abundant			
3	almost always	0.99	1	
4	almost never	0	0.01	
5	always	1	1	
6	at least one	0,1	1	
7	at least some	0,1	1	
8	commonly	0,7	1	
9	few	0	1	
10	frequently	0,7	1	
11	if present.	0	1	
12	infrequently	0	0.25	
13	less often	0	0.5	
14	many	0.75	1	
15	more commonly	0,5	1	
16	more often	0,5	1	
17	most commonly	0,8	1	
18	mostly	0,5	1	
19	never	0	0	
20	not commonly	0	1	
21	occasional	0	1	
22	occasionally	0	1	
23	often	0.5	1	

Select edit mode projects from menu **Edit->Projects** and open the "Modifier/Frequency" tab (see point **1** in image above). The modifier and frequency tables should both be empty. A click on button in the modifier section (see point **2** in image above) opens a window with the predefined values (see impage below left). Click on button ☑ selects all values from the list. Click "OK" and all modifier values are now inserted in the modifier table. Proceed in the same way with the frequency values (see point **3** in image above and image below right). The values are now available for all projects in the database.



Predefined modifier values

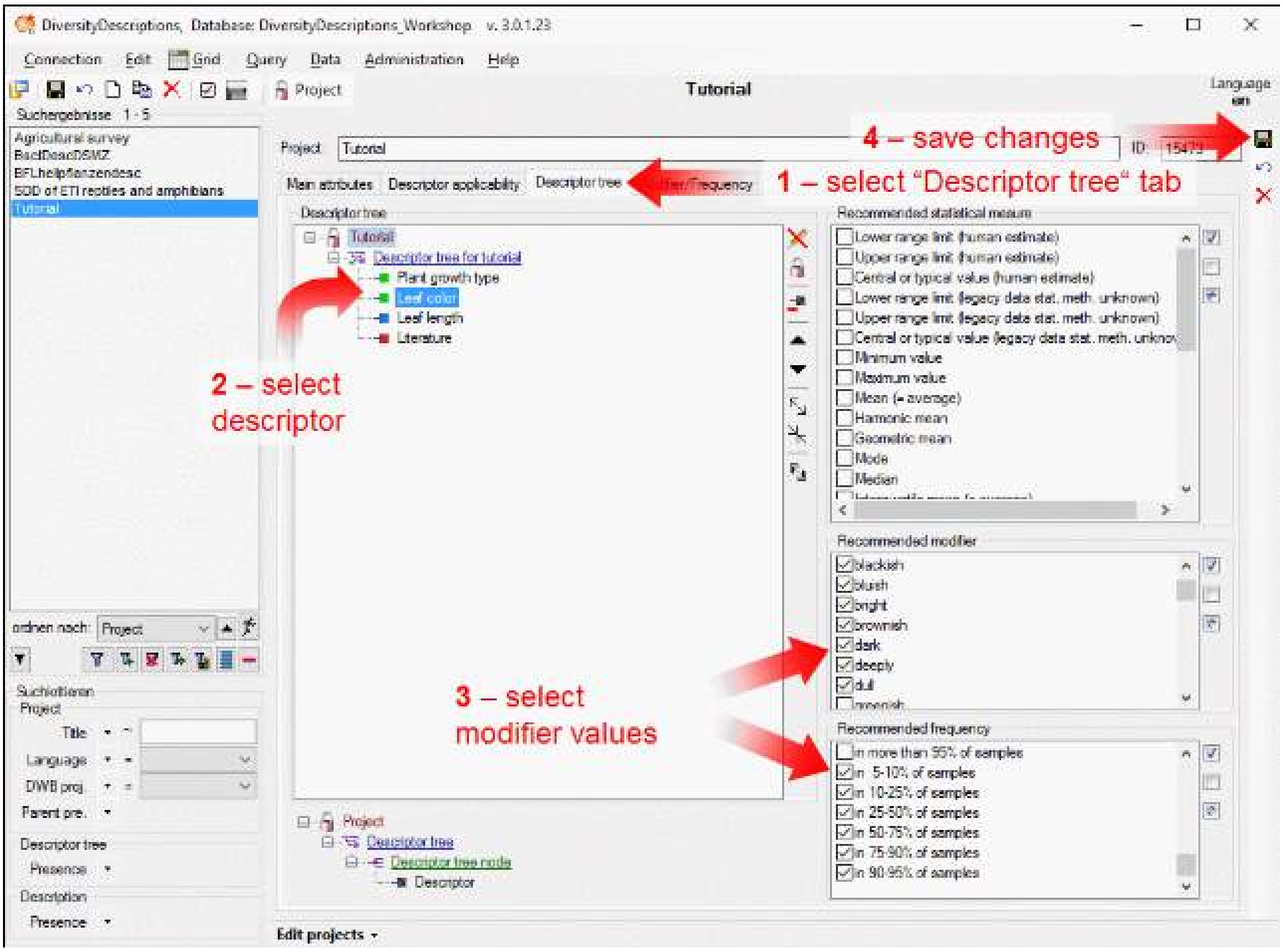
- ☑ (uncertain) [Certainty]
- ☑ almost certainly [Certainty]
- ☑ likely [Certainty]
- ☑ perhaps [Certainty]
- ☑ possibly [Certainty]
- ☑ presumably [Certainty]
- ☑ probably [Certainty]
- ☑ probably not [Certainty]
- ☑ very likely [Certainty]
- ☑ (by misinterpretation) [Misinterpretation]
- ☑ often misinterpreted as [Misinterpretation]
- ☑ rarely misinterpreted as [Misinterpretation]
- ☑ sometimes misinterpreted as [Misinterpretation]
- ☑ blackish [Other]
- ☑ bluish [Other]
- ☑ bright [Other]
- ☑ brownish [Other]
- ☑ dark [Other]
- ☑ deeply [Other]
- ☑ dull [Other]
- ☑ greenish [Other]
- ☑ greyish [Other]
- ☑ light [Other]
- ☑ pale [Other]
- ☑ purplish [Other]



Predefined frequency values

- ☑ (rare)
- ☑ abundant
- ☑ almost always
- ☑ almost never
- ☑ always
- ☑ at least one
- ☑ at least some
- ☑ commonly
- ☑ few
- ☑ frequently
- ☑ if present,
- ☑ infrequently
- ☑ less often
- ☑ many
- ☑ more commonly
- ☑ more often
- ☑ most commonly
- ☑ mostly
- ☑ never
- ☑ not commonly
- ☑ occasional
- ☑ occasionally
- ☑ often
- ☑ predominant
- ☑ predominantly

To use certain modifiers in the descriptive data, the allowed values must be assigned to certain descriptors. This is done int the descriptor tree in almost the same way as the assignment of statistical measures to quantitative descriptors. Select the "Descriptor tree" tab (see point **1** in image below) and click button ✏ to dispay the recommended values. Then select descriptor "Leaf color" and select some modifier and frequency values (see point **3** in image below). Finally save all changes (see point **4** in image below).



4 – save changes

1 – select “Descriptor tree“ tab

2 – select descriptor

3 – select modifier values

Recommended statistical measure

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unknow
☐ Minimum value
☐ Maximum value
☐ Mean (= average)
☐ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

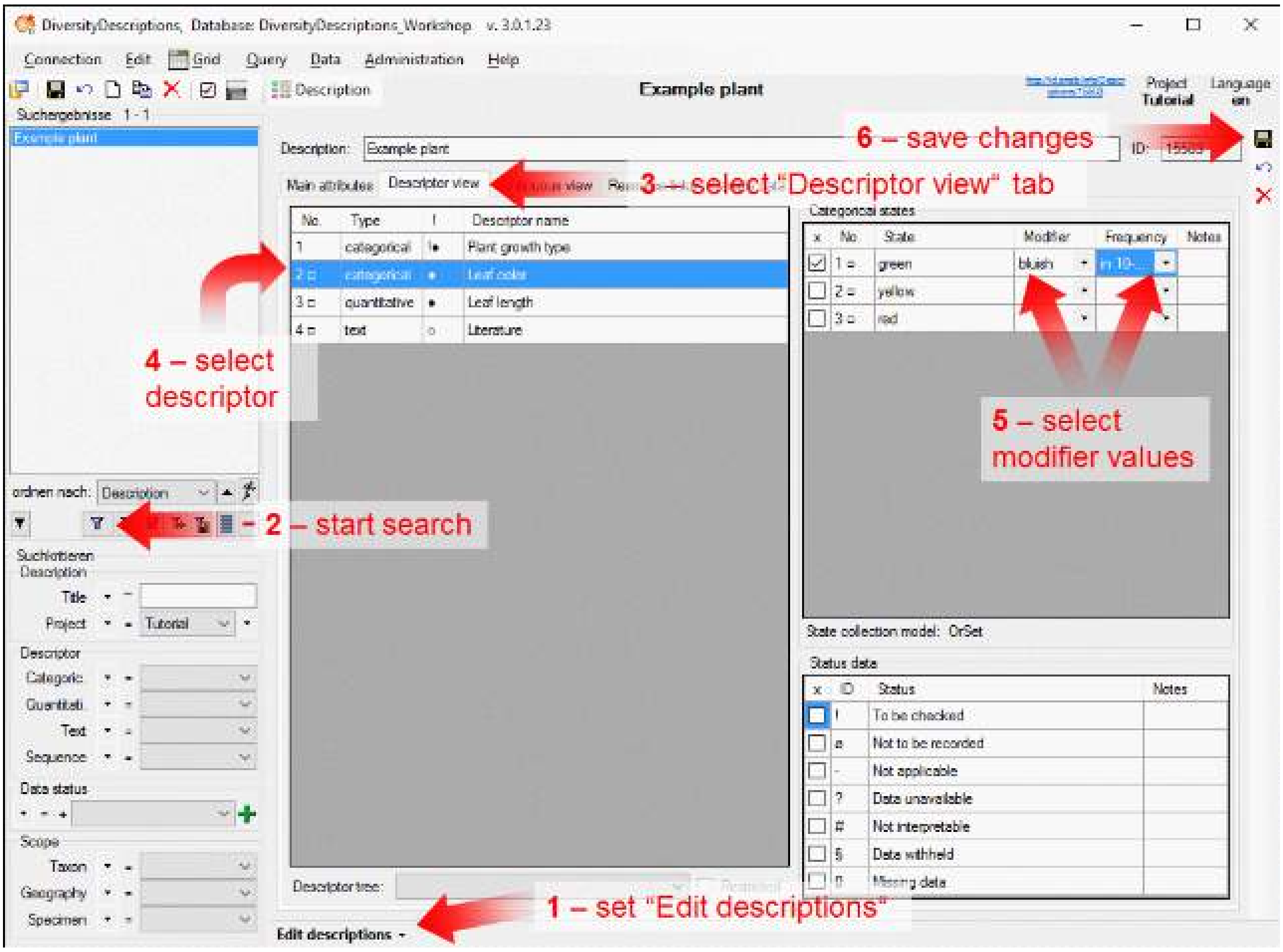
Recommended modifier

☑ blackish
☑ bluish
☑ bright
☑ brownish
☑ dark
☑ deeply
☑ dull
☐ greenish

Recommended frequency

☐ in more than 95% of samples
☑ in 5-10% of samples
☑ in 10-25% of samples
☑ in 25-50% of samples
☑ in 50-75% of samples
☑ in 75-90% of samples
☑ in 90-95% of samples

Now let's try out the modifiers in our example description. Select edit mode descriptions and search for the example plant (see points **1** and **2** in image below). Open the "Descriptor view" tab and select descriptor "Leaf color" (see points **3** and **4** in image below). In the "Categorial states" section you can now find two additional columns "Modifier" and "Frequence" where you may select from the values you assigned in the previeous step (see point **5** in image below). Finally save all changes (see point **6** in image below).



No.	Type	!	Descriptor name
1	categorical	!●	Plant growth type
2	categorical	●	Leaf color
3	quantitative	●	Leaf length
4	text	○	Literature

x	No	State	Modifier	Frequency	Notes
☑	1	green	bluish	in 10-...	
☐	2	yellow			
☐	3	red			

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	¤	Missing data	

1 – set "Edit descriptions"

2 – start search

3 – select "Descriptor view" tab

4 – select descriptor

5 – select modifier values

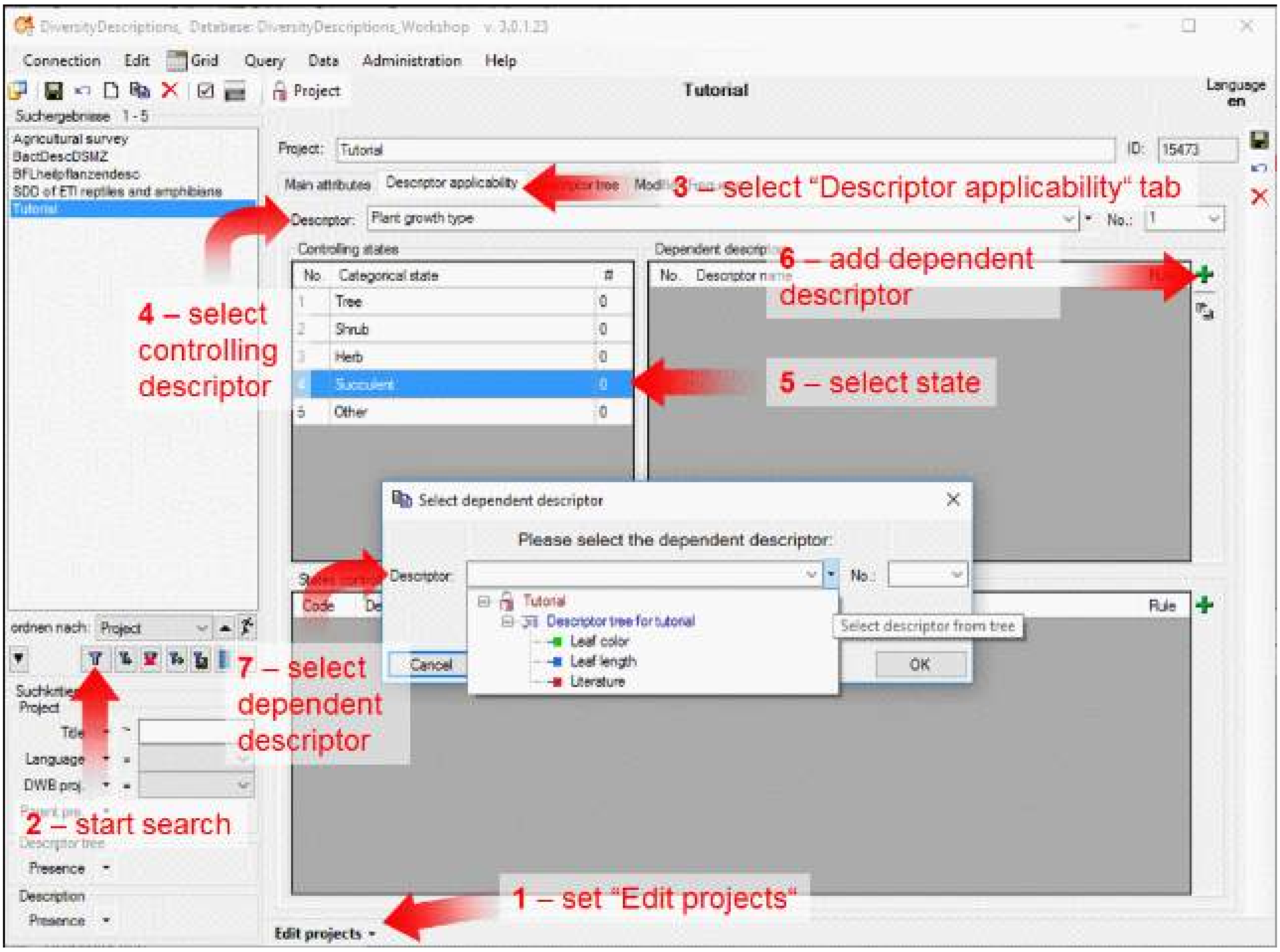
6 – save changes

This tutorial is continued in the section listed below. ow.

- section Enter descriptor dependencies

Tutorial - Enter descriptor dependencies

In our final tutorial step we take a short look on the descriptor applicability rules. In out example we have two descriptors dealing with leaf properties, "Leaf color" and "Leaf length". If you have chosen the categorical state "Cactus" for the descriptor "Plant growth type", it usually does not make sense specifying leaf properties. You can enter such kind of descriptor dependencies in a formal way.



Agricultural survey
BactDescDSMZ
BFLheilpflanzendesc
SDD of ETI reptiles and amphibians
Tutorial

Project: Tutorial
ID: 15473
Descriptor: Plant growth type
No.: 1

No.	Categorical state	#
1	Tree	0
2	Shrub	0
3	Herb	0
4	Succulent	0
5	Other	0

Select dependent descriptor

Please select the dependent descriptor:

Descriptor:
No.:

Tutorial
Descriptor tree for tutorial
Leaf color
Leaf length
Literature

Select descriptor from tree

3 – select “Descriptor applicability“ tab

6 – add dependent descriptor

4 – select controlling descriptor

5 – select state

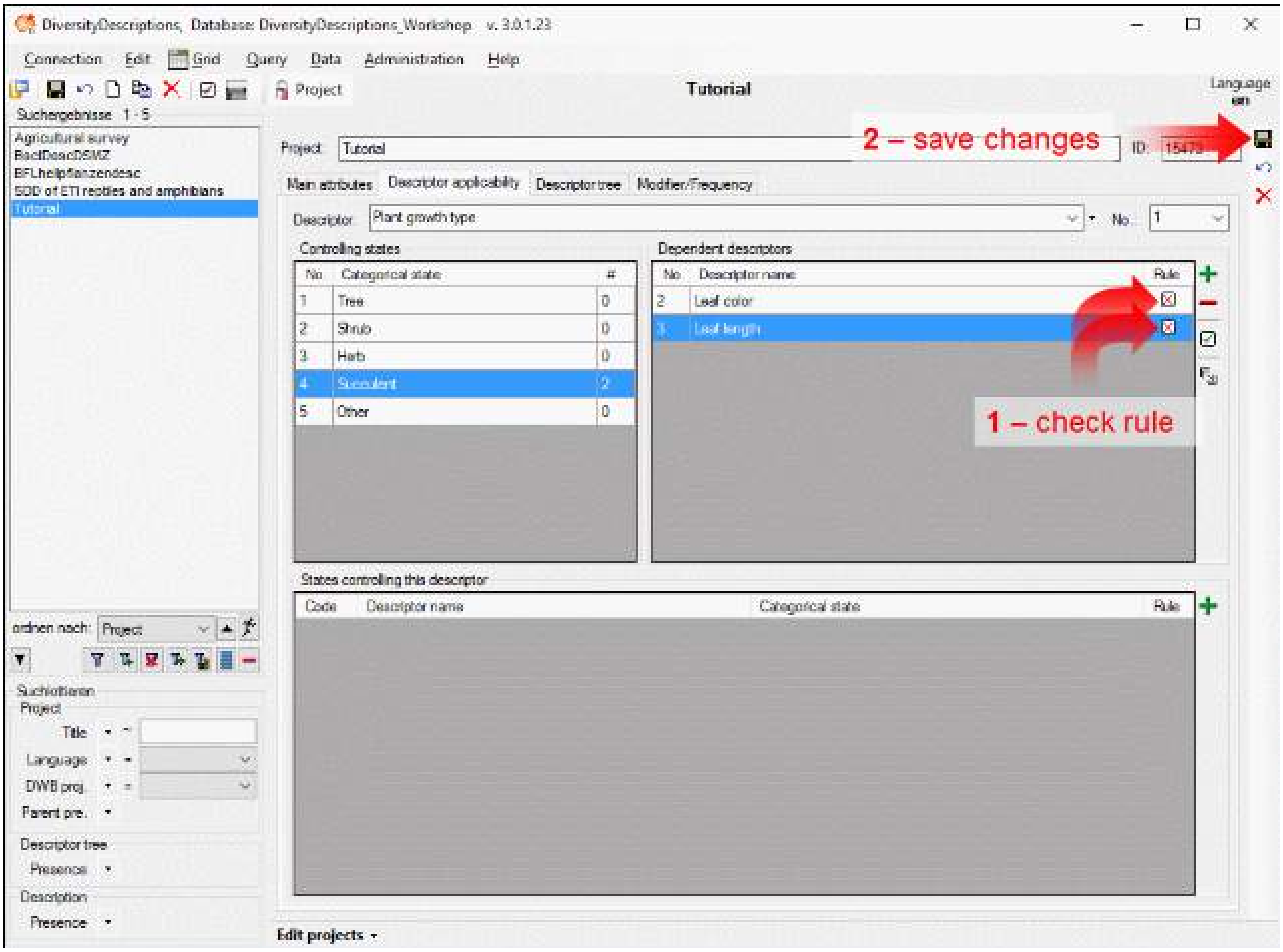
7 – select dependent descriptor

2 – start search

1 – set “Edit projects“

Select edit mode projects from menu **Edit->Projects** , search for project "Tutorial" and open the "Descriptor applicabilities" tab (see points **1** to **3** in image above). Select the controlling descriptor "Plant type" (see point **4** in image above) and in the section "Controlling states" a list of the descriptor's categorical states is displayed. Select the controlling state "Succulent" (see point **5** in image above) and then click on button ✚to enter the first controlled descriptor (see point **6** in image above). This opens a selection window where you select descriptor "Leaf color" (see point **7** in image above). Repeat the last step to insert descriptor "Leaf length" as second controlled descriptor.

After that check that for the two dependent descriptors the applicability rule "inapplicable" is set (see point **1** in image below). Finally save all changes (see point **2** in image below).



Agricultural survey
BactDescDSMZ
BFLhelpflanzendesc
SDD of ETI reptiles and amphibians
Tutorial

Project: Tutorial ID: 15479

Descriptor: Plant growth type No.: 1

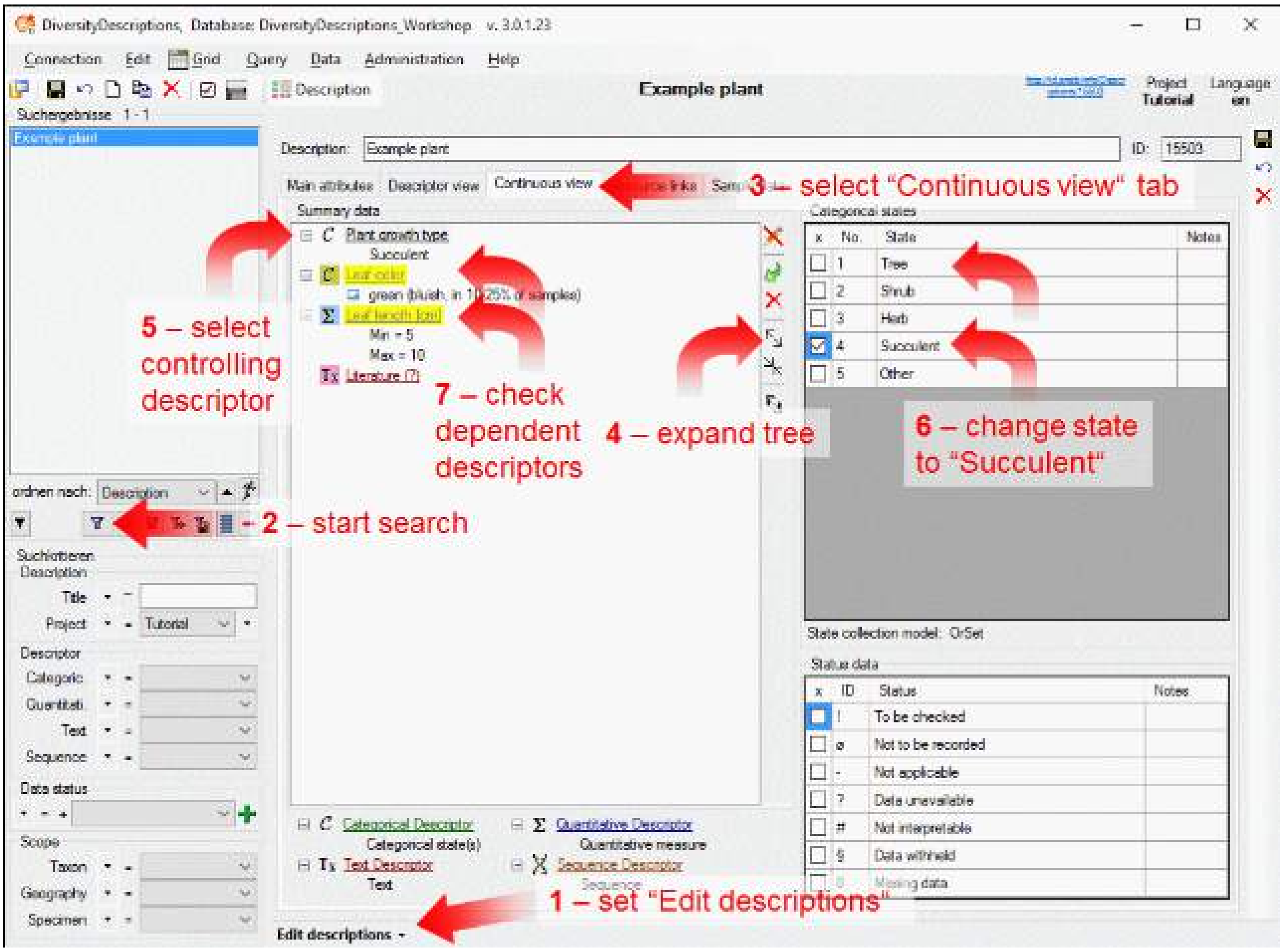
ordnen nach: Project

No	Categorical state	#
1	Tree	0
2	Shrub	0
3	Herb	0
4	Succulent	2
5	Other	0

No	Descriptor name	Rule
2	Leaf color	☒
3	Leaf length	☒

Code	Descriptor name	Categorical state	Rule

To try out the applicability rules, select edit mode descriptions and search for the example plant (see points **1** and **2** in image below). Open the "Descriptor view" tab, expand the tree and select descriptor "Plant growth type" (see points **3** to **5** in image below). Click on button ✏ to show the "Categorial states". Deselect state "Tree" and select state "Succulent" instead (see point **6** in image below). In the "Summary data" section the text color of the descriptors "Leaf color" and "Leaf length" changes to **grey** to indicate that the descriptor is not applicable. Since for that descriptors values have been specified, the backround color is changed to **yellow** to indicate that the applicability rules are broken (see point **7** in image below).



Description: Example plant ID: 15503

x	No.	State	Notes
☐	1	Tree	
☐	2	Shrub	
☐	3	Herb	
☑	4	Succulent	
☐	5	Other	

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	[illegible]	Missing data	

1 – set "Edit descriptions"

2 – start search

3 – select "Continuous view" tab

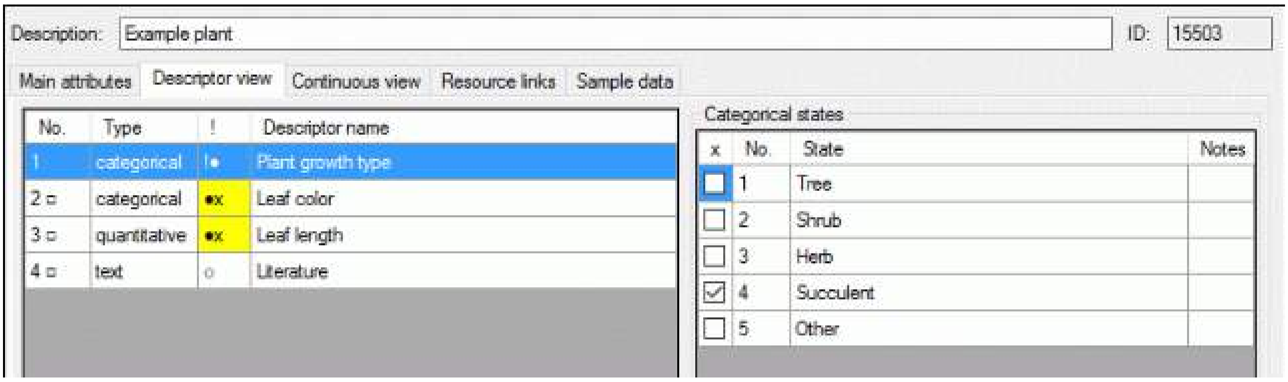
4 – expand tree

5 – select controlling descriptor

6 – change state to "Succulent"

7 – check dependent descriptors

In the "Descriptor view" tab the "descriptor inapplicable" property is indicated by an "x" in column "!" of the descriptor list (see image below).



Description: Example plant ID: 15503

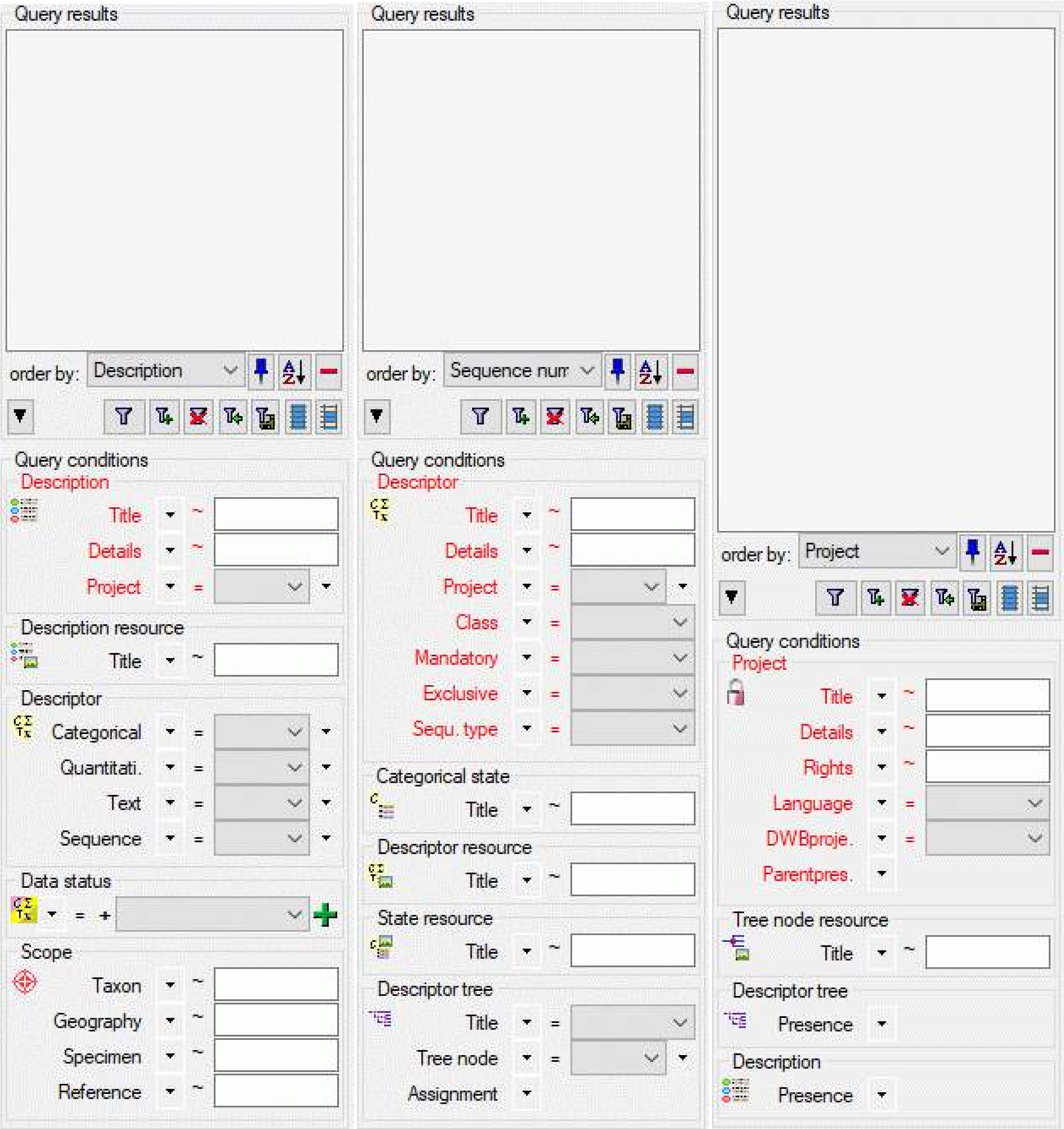
No.	Type	!	Descriptor name
1	categorical	!●	Plant growth type
2 ◻	categorical	●x	Leaf color
3 ◻	quantitative	●x	Leaf length
4 ◻	text	○	Literature

x	No.	State	Notes
☐	1	Tree	
☐	2	Shrub	
☐	3	Herb	
☑	4	Succulent	
☐	5	Other	

Queries - overview

With the user defined queries, you can define any query condition - this is the default query mode.

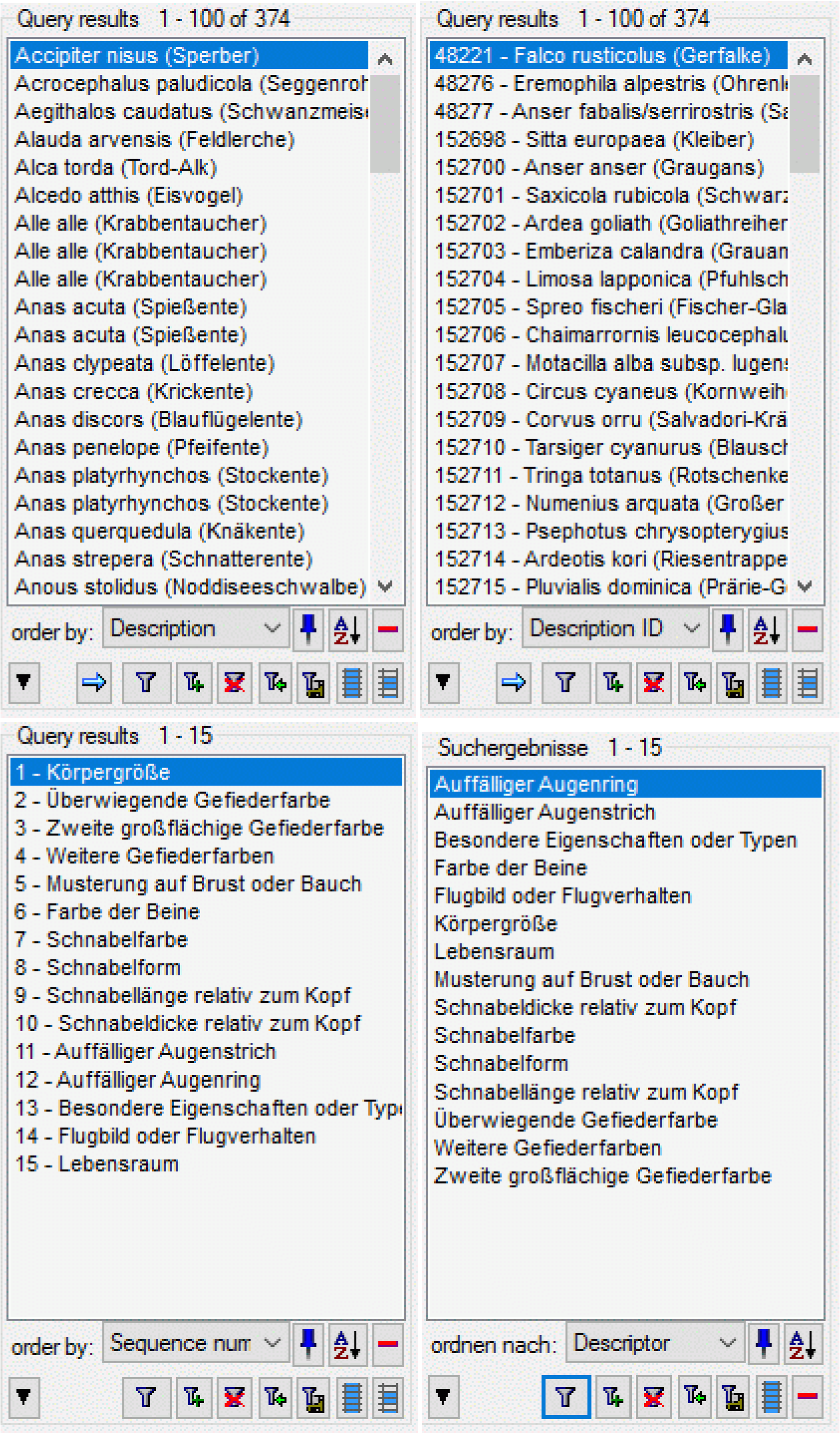
Depending on the active edit mode you get one of three different query option panels as shown in the pictures below.



The extended query provides a detailled seach for descriptions with specific descriptor data. It is accessible from the menu **Query** -> **Extended query ...** if the edit mode **Edit descriptions** is selected.

Result list

The result list displays the descriptions, descriptors or projects found in a query.



Query results 1 - 100 of 374

Accipiter nisus (Sperber)
Acrocephalus paludicola (Seggenroh
Aegithalos caudatus (Schwanzmeis
Alauda arvensis (Feldlerche)
Alca torda (Tord-Alk)
Alcedo atthis (Eisvogel)
Alle alle (Krabbentaucher)
Alle alle (Krabbentaucher)
Alle alle (Krabbentaucher)
Anas acuta (Spießente)
Anas acuta (Spießente)
Anas clypeata (Löffelente)
Anas crecca (Krickente)
Anas discors (Blauflügelente)
Anas penelope (Pfeifente)
Anas platyrhynchos (Stockente)
Anas platyrhynchos (Stockente)
Anas querquedula (Knäkente)
Anas strepera (Schnatterente)
Anous stolidus (Noddiseeschwalbe)

order by: Description

Query results 1 - 100 of 374

48221 - Falco rusticolus (Gerfalke)
48276 - Eremophila alpestris (Ohrenl
48277 - Anser fabalis/serrirostris (Sa
152698 - Sitta europaea (Kleiber)
152700 - Anser anser (Graugans)
152701 - Saxicola rubicola (Schwarz
152702 - Ardea goliath (Goliathreiher
152703 - Emberiza calandra (Grauan
152704 - Limosa lapponica (Pfuhlsch
152705 - Spreo fischeri (Fischer-Gla
152706 - Chaimarrornis leucocephalu
152707 - Motacilla alba subsp. lugens
152708 - Circus cyaneus (Kornweih
152709 - Corvus orru (Salvadori-Krä
152710 - Tarsiger cyanurus (Blausch
152711 - Tringa totanus (Rotschenke
152712 - Numenius arquata (Großer
152713 - Psephotus chrysopterygius
152714 - Ardeotis kori (Riesentrappe
152715 - Pluvialis dominica (Prärie-G

order by: Description ID

Query results 1 - 15

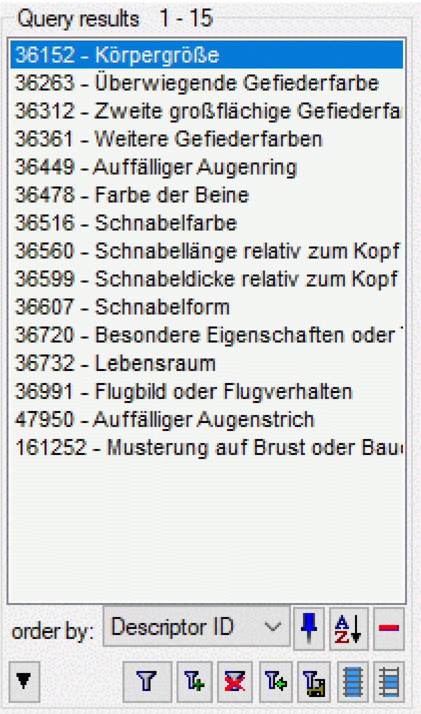
1 - Körpergröße
2 - Überwiegende Gefiederfarbe
3 - Zweite großflächige Gefiederfarbe
4 - Weitere Gefiederfarben
5 - Musterung auf Brust oder Bauch
6 - Farbe der Beine
7 - Schnabelfarbe
8 - Schnabelform
9 - Schnabellänge relativ zum Kopf
10 - Schnabeldicke relativ zum Kopf
11 - Auffälliger Augenstrich
12 - Auffälliger Augenring
13 - Besondere Eigenschaften oder Typ
14 - Flugbild oder Flugverhalten
15 - Lebensraum

order by: Sequence num

Suchergebnisse 1 - 15

Auffälliger Augenring
Auffälliger Augenstrich
Besondere Eigenschaften oder Typen
Farbe der Beine
Flugbild oder Flugverhalten
Körpergröße
Lebensraum
Musterung auf Brust oder Bauch
Schnabeldicke relativ zum Kopf
Schnabelfarbe
Schnabelform
Schnabellänge relativ zum Kopf
Überwiegende Gefiederfarbe
Weitere Gefiederfarben
Zweite großflächige Gefiederfarbe

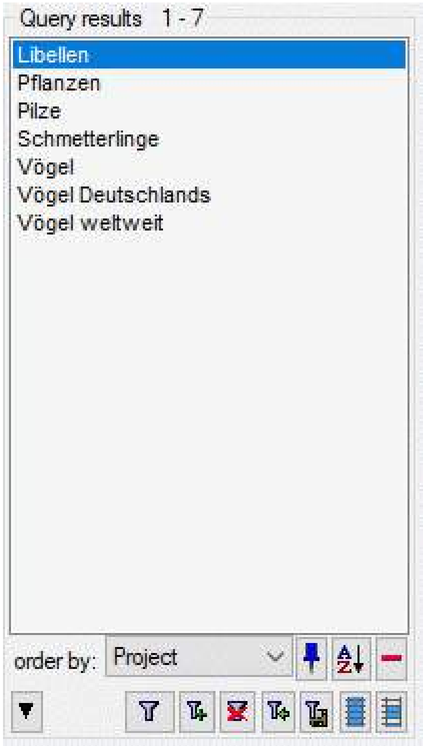
ordnen nach: Descriptor



Query results 1 - 15

36152 - Körpergröße
36263 - Überwiegende Gefiederfarbe
36312 - Zweite großflächige Gefiederfa
36361 - Weitere Gefiederfarben
36449 - Auffälliger Augenring
36478 - Farbe der Beine
36516 - Schnabelfarbe
36560 - Schnabellänge relativ zum Kopf
36599 - Schnabeldicke relativ zum Kopf
36607 - Schnabelform
36720 - Besondere Eigenschaften oder
36732 - Lebensraum
36991 - Flugbild oder Flugverhalten
47950 - Auffälliger Augenstrich
161252 - Musterung auf Brust oder Bau

order by: Descriptor ID



Query results 1 - 7

Libellen
Pflanzen
Pilze
Schmetterlinge
Vögel
Vögel Deutschlands
Vögel weltweit

order by: Project

Query results 1 - 7

48278 - Libellen
48280 - Pilze
48282 - Pflanzen
161084 - Vögel
161107 - Vögel Deutschlands
161494 - Schmetterlinge
161495 - Vögel weltweit

order by: Project ID

For example the descriptors may be displayed with their name or their sequence number as shown in the images above.

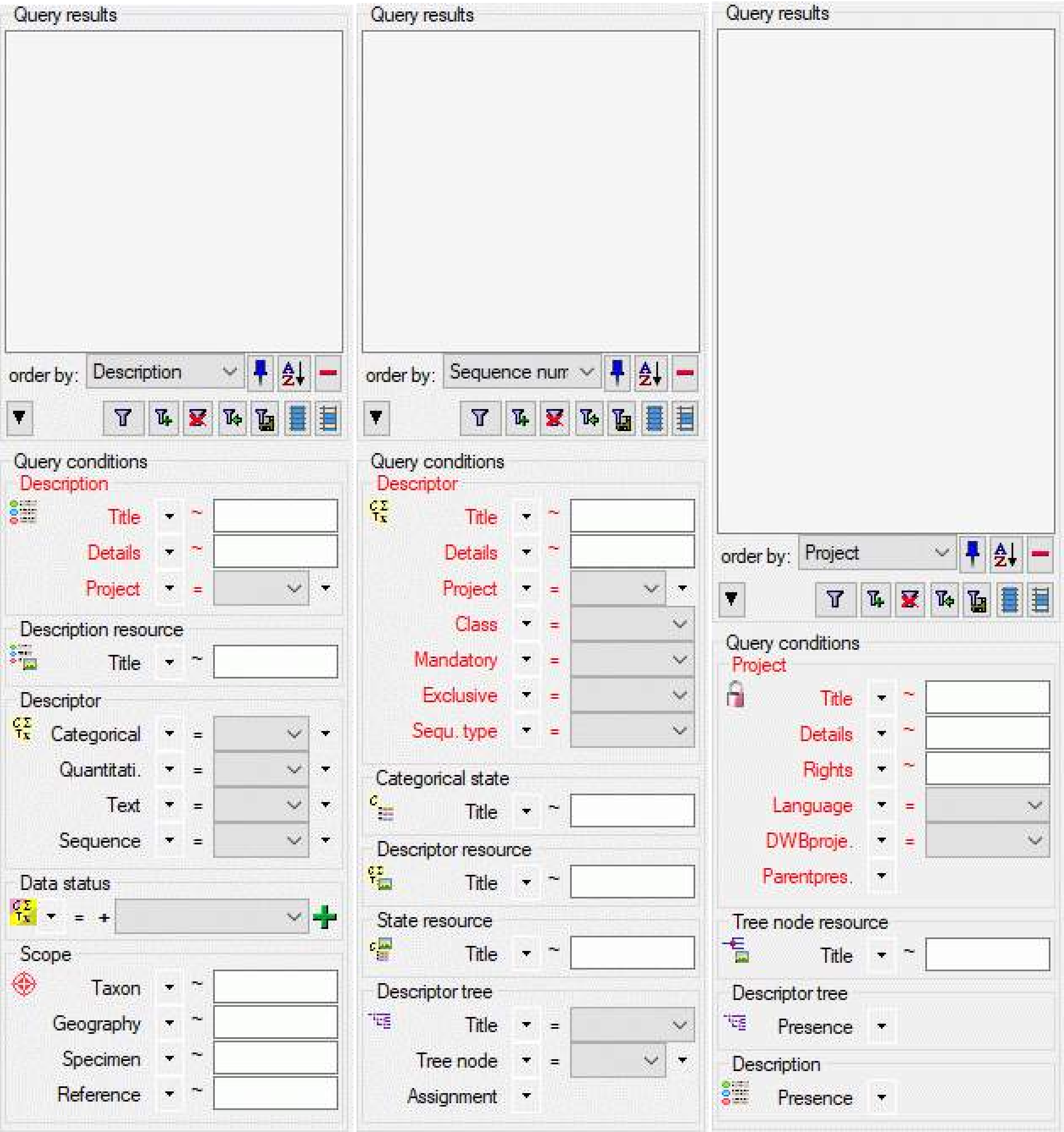
You can restrict the maximal number of results together with the query options (click on the ☑ button), for example if you have a slow connection to the database. As a default the maximal number is set to 100. If the number of datasets according to your query is higher than the maximal value set in the query options this will be indicated in the header of the list.

To search for items, enter the restrictions in the fields for the search conditions and click on the ▽ button. The items found in the database will be shown in the result list. To add items that match differing search conditions click on the button. If the list of items is longer than your maximal number of returned items you can browse the next items with the ⇨ button. If you want to remove entries from the selected list, choose them in the list and click on the − button. If you want to keep the selected entries in the list and remove the rest, click on the button. This will not delete the data from the database, but remove them from your query result.

Query

Depending on the activated edit mode you get one of the three query options pannel below. The options for a fast search are displayed in the main window beneath the list of the items.

You can change this arrangement using the / button to place the query options on the left side of the item list.



order by: Description

order by: Sequence num

order by: Project

To search for an item enter the restrictions in the fields for the search conditions and click on the button. The entities found in the database will be shown in the result list. To add items with differing search conditions click on the button. To clear all entries in the query fields use the button. If the list of items is longer than your maximal number of returned items you can browse the next items with the button. To move back to the previous block of items click on the button.

If you want to remove entries from the selected list, choose them and click on the − button. If you want to keep the selected entries in the list and remove the rest, click on the ☰ button. This will not delete the data from the database, but remove them from your query result. With the AZ↓ resp. ZA↓ buttons you can change the order of the results between ascending and descending.

To hide the area containing the search fields click on the ▼ button. If the search area is hidden and you want to start a new search, just click on the ▲ button.

With the button 📌 you may control auto-remember of the last submitted query parameter. If you re-start the application and connect to the same database, the last used query will automatically be submitted. If you prefer to switch off auto-remember, click the button 📌 and it will change to 📌. In the main menu **Query -> Preferred project ...** you may select a project that will be used as a pre-selection for Description and Descriptor query, if no other query parameter have been restored.

Within the query options you have several possibilities to specify your search restriction. Use the drop down button to change between the operator. The available operators are shown in the table below.

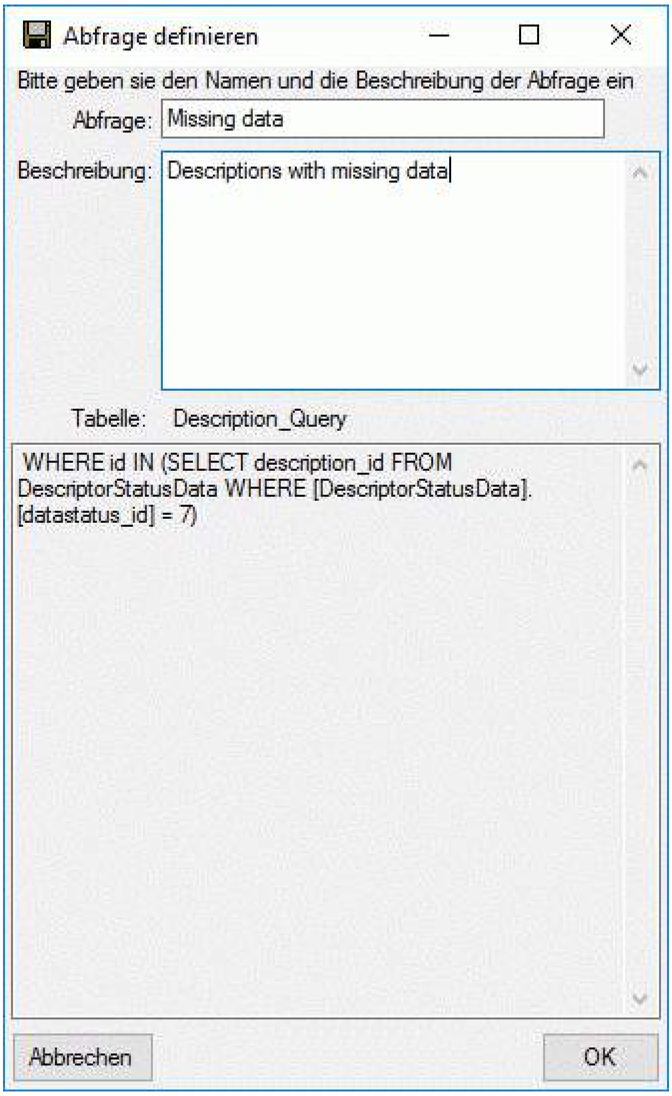
Operator	**Meaning**	**Example**
Text		
~	search for an entry like ...	Pinus s[iy]lvestris % (you can use wildcards)
=	search for an entry exactly equal to ...	Pinus silvestris L.
≠	search for an entry not like ...	Pinus s[iy]lvestris % (you can use wildcards)
Ø	search for an entry where a value is missing ...	
•	search for an entry where a value is present ...	
-	search for an entry between ... and ...	2000 - 2005
|	search within a list of entries, separated by "|"	2000 | 2003 | 2005
Numeric		
=	search for an entry exactly equal to ...	2006
<	search for an entry lower than ...	2006
>	search for an entry bigger than ...	2006
-	search for an entry between ... and ...	2000 - 2005
|	search within a list of entries, separated by "|"	2000 | 2003 | 2005

∅	search for an entry where a value is missing ...	
•	search for an entry where a value is present ...	
Date		
=	search for an entry exactly equal to ...	20.3.2006
<	search for an entry lower than ...	20.3.2006
>	search for an entry bigger than ...	20.3.2006
∅	search for an entry where the date is missing ...	
•	search for an entry where the date is present and complete ...	
Hierachy		
=	search for an entry exactly equal to ...	M-Fungi
≠	search for an entry that is not equal to ...	M-Fungi
∅	search for missing entry ...	
•	search for present entry ...	
Δ	search including childs in a hierarchy ...	M-Fungi
XML		
/	Search for entries containing a given XML node	settings
¬	Search for entries not containing a given XML node	settings
∅	search for missing entry ...	
•	search for present entry ...	

For yes/no fields you will get an checkbox with 3 options: ☑= yes, ☐= no, 🟩= undefined

Save query

If you want to save a current query, click on the button. A window as shown below will open where you can specify the title and description of you query.



Bitte geben sie den Namen und die Beschreibung der Abfrage ein

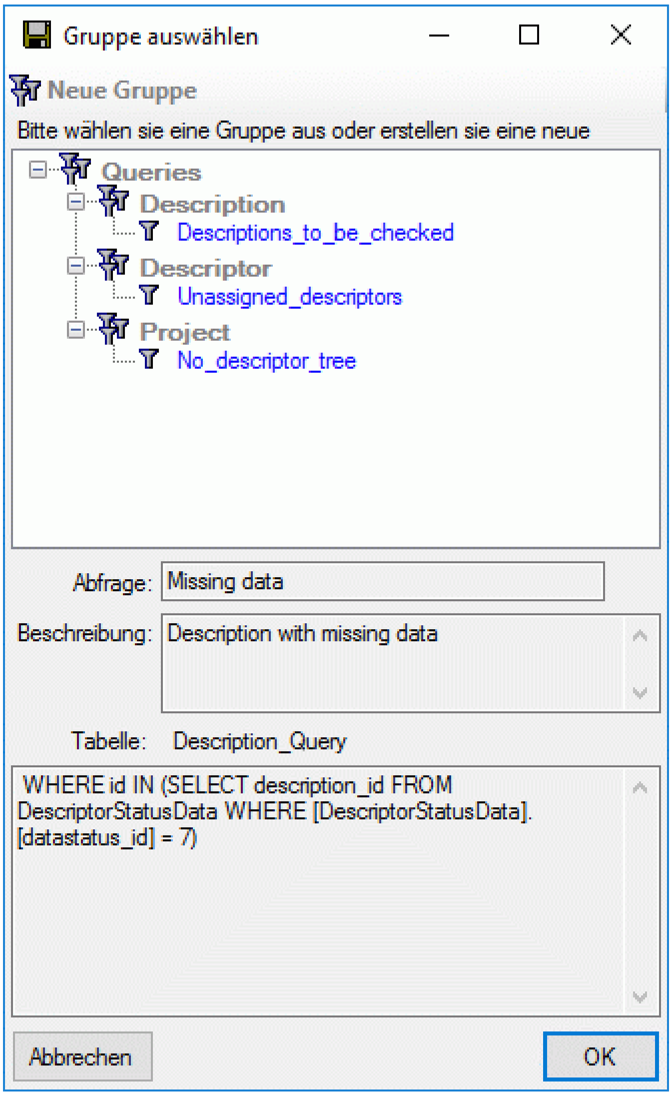
Abfrage: Missing data

Beschreibung: Descriptions with missing data

Tabelle: Description_Query

```
WHERE id IN (SELECT description_id FROM
DescriptorStatusData WHERE [DescriptorStatusData].
[datastatus_id] = 7)
```

After you entered title and description of the query, click OK to specify the query group. A window as shown below will open.



Bitte wählen sie eine Gruppe aus oder erstellen sie eine neue

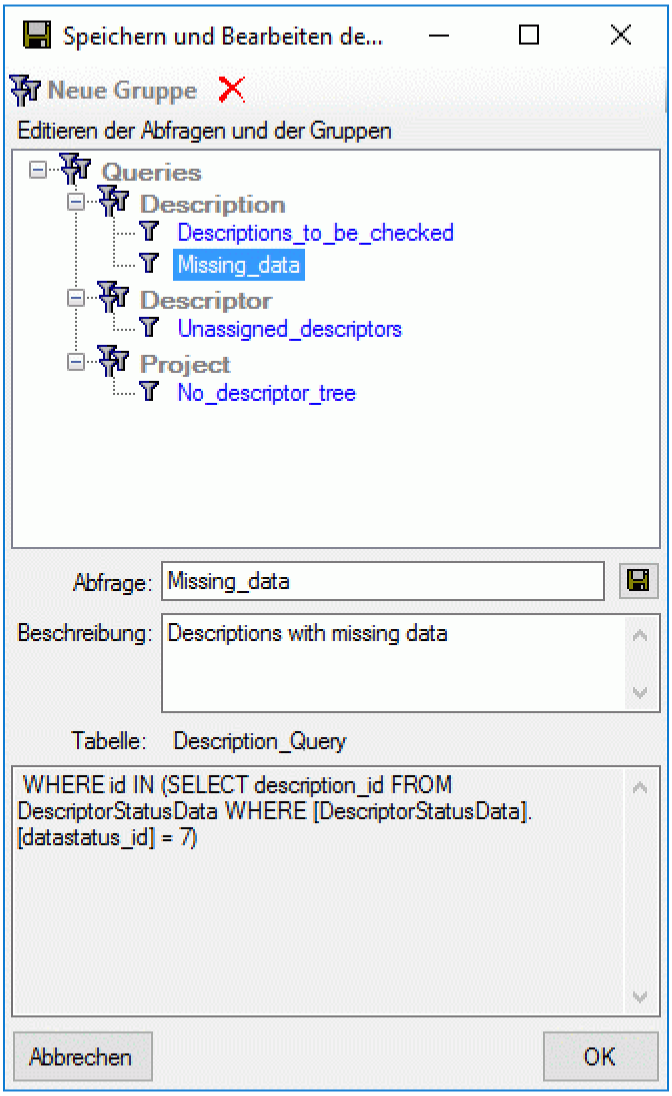
Abfrage: Missing data

Beschreibung: Description with missing data

Tabelle: Description_Query

```
WHERE id IN (SELECT description_id FROM
DescriptorStatusData WHERE [DescriptorStatusData].
[datastatus_id] = 7)
```

Choose a group from the tree or create a new one an click OK. The new query will be included in the selected group.



Editieren der Abfragen und der Gruppen

- Queries
  - Description
    - Descriptions_to_be_checked
    - Missing_data
  - Descriptor
    - Unassigned_descriptors
  - Project
    - No_descriptor_tree

Abfrage: Missing_data

Beschreibung: Descriptions with missing data

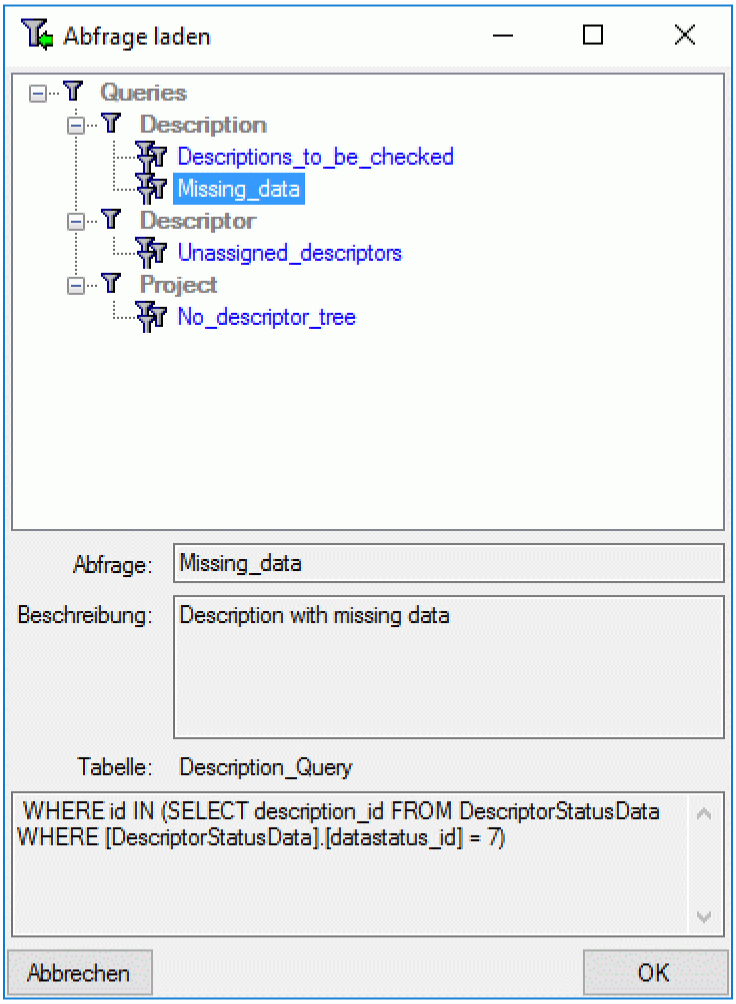
Tabelle: Description_Query

```
WHERE id IN (SELECT description_id FROM
DescriptorStatusData WHERE [DescriptorStatusData].
[datastatus_id] = 7)
```

Finally you can edit the titles and descriptions of the groups an queries. Click the 💾button to store the changes. To delete items from the tree, select it and click on the ✗button. Click OK to save the new query and close the window.

Load query

If you want to load a query that has been stored previously, click on the button. A window as shown below will open.



Abfrage: Missing_data

Beschreibung: Description with missing data

Tabelle: Description_Query

```
WHERE id IN (SELECT description_id FROM DescriptorStatusData
WHERE [DescriptorStatusData].[datastatus_id] = 7)
```

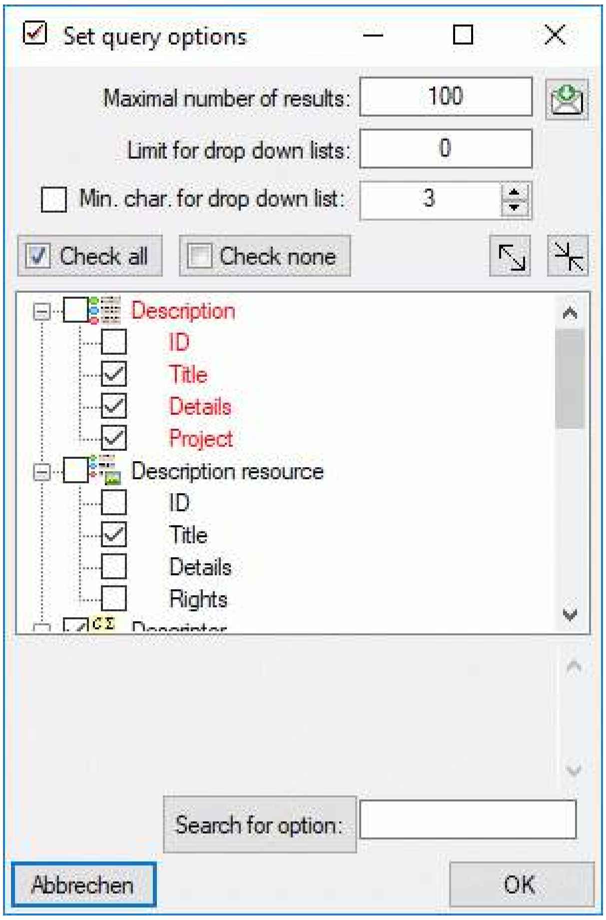
Choose a query from the tree and click OK to close the form and filter the datasets according to the selected query.

Query options

The maximal number of items shown in a query result can be set in the window for the query options. The default value is set to 100. If you have a fast connection to your database or need to see more or less results, you may change this value to any number you like.
To change the displayed search fields click on the ☑ button. This opens a form where you can select and deselect the fields shown for searching specimens. You might also change the maximum number of items that will be shown in the result list.

The limit for the creation of drop down lists is by default set to **0**, that means **no dropdown lists** will be created. If you set the limit to e.g. 1000 and connect to a database, the programm will create drop down list based on the entries in the database to ease the entry in the query. For slow connections you may set this to lower value to speed up the start of the program. If you set the value to 0 no drop down lists will be created.

The minimal numbers of characters for a selection from the drop down list is by default set to 3.



Set query options

Maximal number of results: 100

Limit for drop down lists: 0

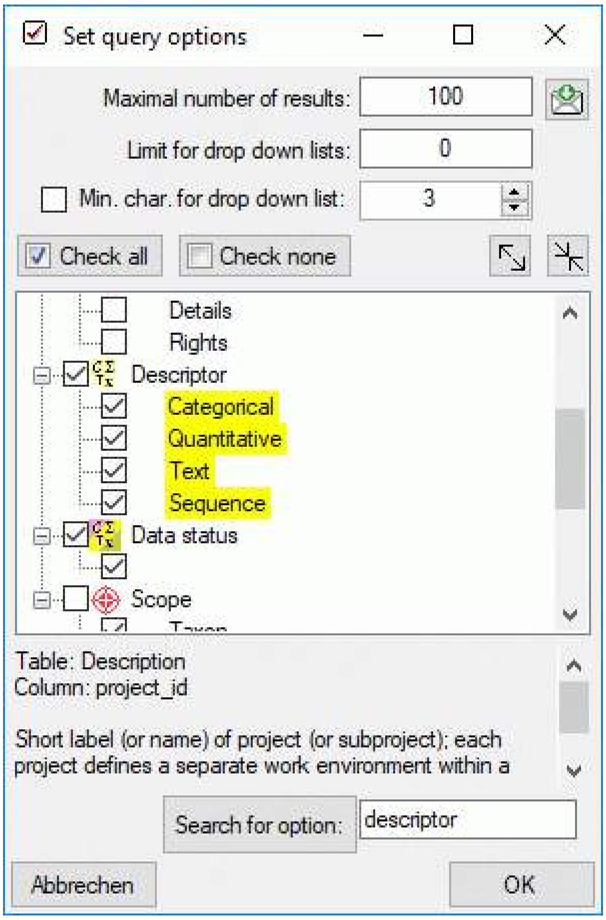
☐ Min. char. for drop down list: 3

- ☐ Description
  - ☐ ID
  - ☑ Title
  - ☑ Details
  - ☑ Project
- ☐ Description resource
  - ☐ ID
  - ☑ Title
  - ☐ Details
  - ☐ Rights

Search for option:

After having edited the query options click OK to store your selection. The new selection will become active for the next query. To ease the selection and deselection of query options you may use the buttons ☑ **Check all**, ☐ **Check none**, ⤡ **Expand** and ⤢ **Collapse**.

To search for a field within the database, use the search function that will check the names and descriptions of the fields and mark them as shown below.



Maximal number of results: 100

Limit for drop down lists: 0

☐ Min. char. for drop down list: 3

Table: Description
Column: project_id

Short label (or name) of project (or subproject); each project defines a separate work environment within a

Search for option: descriptor

After having edited the query options click OK to store you selection. The new selection will become active for the next query.

Wildcards in SQL

There are 4 different possibilities for wildcards in SQL:

% any string consisting of no, one or many characters, e.g. Pinus **%** will find anything like Pinus, Pinus sylvestris, Pinus strobus etc.

***** any string consisting of no, one or many characters, e.g. Pinus ***** will find anything like Pinus, Pinus sylvestris, Pinus strobus etc.

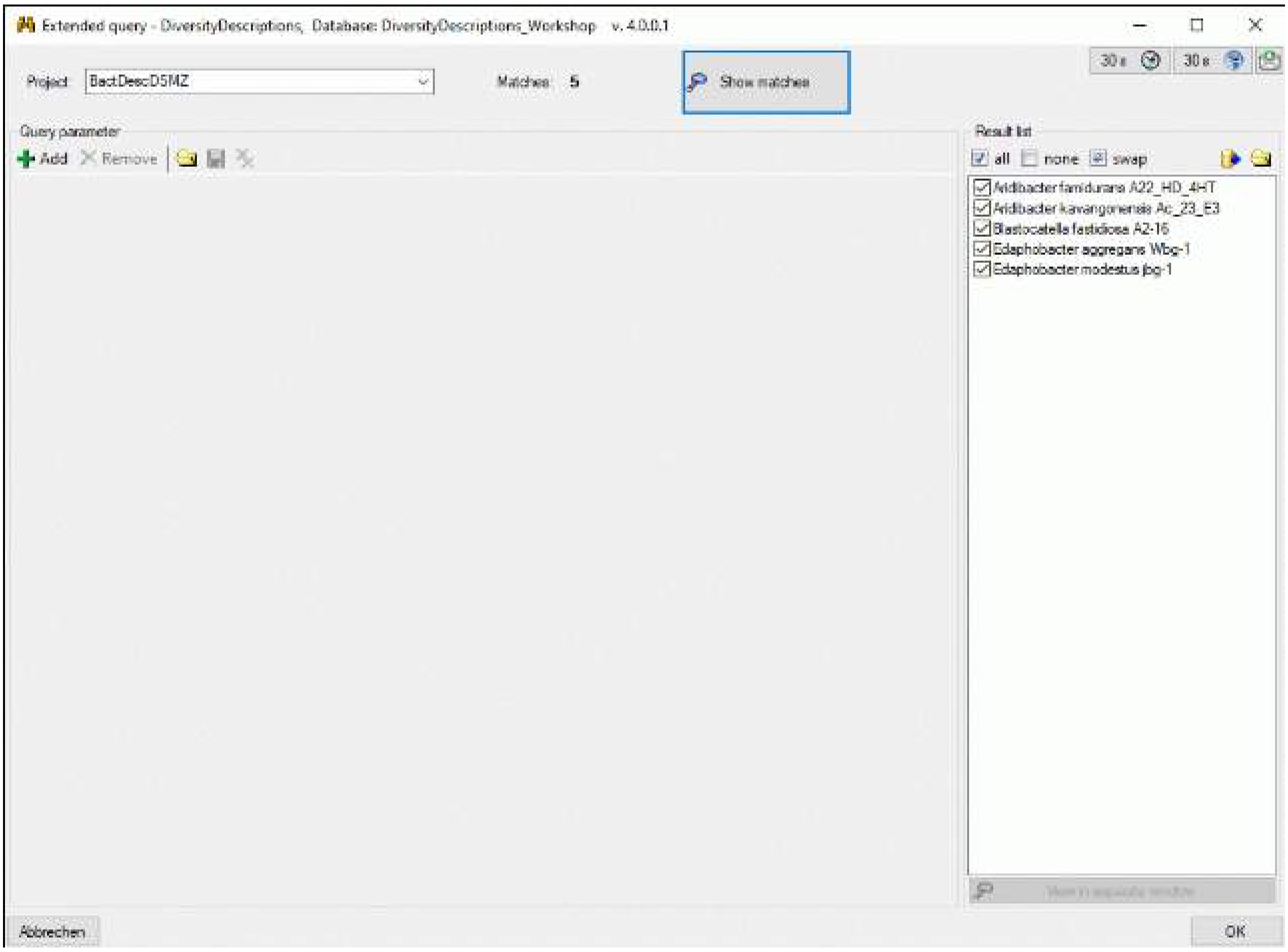
_ a single character, e.g. Pinus s**_**lvestris will find Pinus s**y**lvestris and Pinus s**i**lvestris etc.

[] any character out of a given range like **[abcde]** or **[a-e]**, e.g. Pinus s**[iy]**lvestris will find Pinus sylvestris and Pinus silvestris.

[^] any character not in a given range like **[^abcde]** or **[^a-e]**, e.g. Pinus s**[^i]**lvestris will find Pinus sylvestris but not Pinus silvestris.

Extended query - introduction

With this form you can search description data from the database that match specific descriptor values. Choose **Query -> Extended query ...** from the menu to open the extended query window. With the button you can set the timeout for critical database queries, with button you can set the timeout for the web access to resource data. Feedbacks can be sent with the button .


Extended query - DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 4.0.0.1

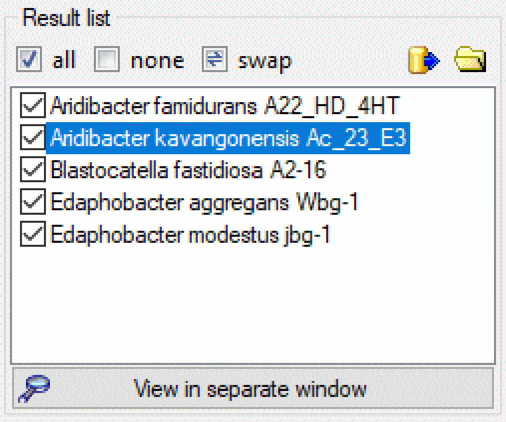
Project: BactDescDSMZ

Matches: 5

Result list

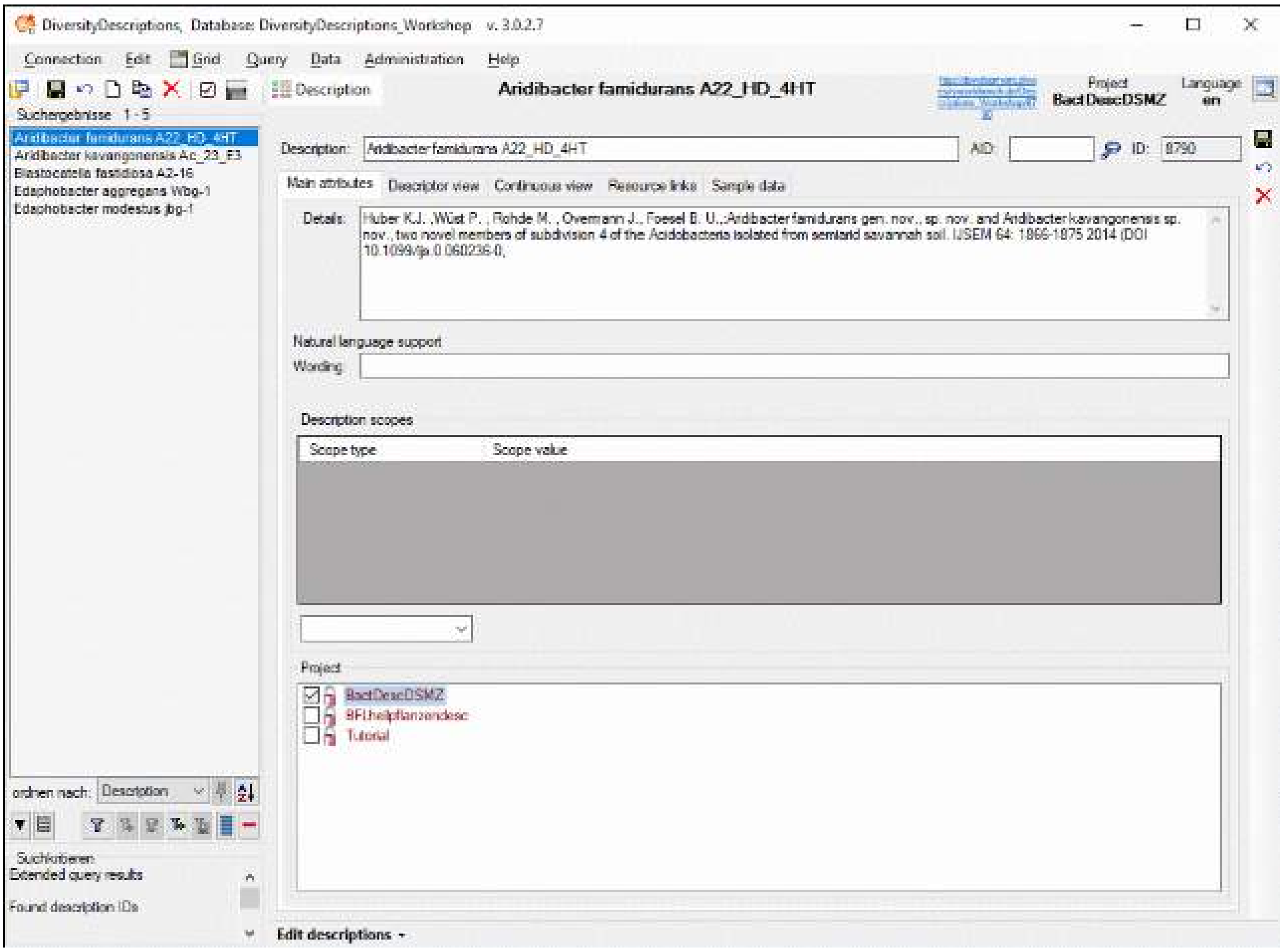
- ☑ Aridibacter famidurans A22_HD_4HT
- ☑ Aridibacter kavangonensis Ac_23_E3
- ☑ Blastocatella fastidiosa A2-16
- ☑ Edaphobacter aggregans Wbg-1
- ☑ Edaphobacter modestus jbg-1

First the **Project** must be selected from the combo box in the upper window area. The **Matches:** field shows the number of available description datasets. If any matches are available, the **Show matches** button is available and by clicking it the datasets are listed in the **Result list** section (see image below).


Result list

- ☑ Aridibacter famidurans A22_HD_4HT
- ☑ Aridibacter kavangonensis Ac_23_E3
- ☑ Blastocatella fastidiosa A2-16
- ☑ Edaphobacter aggregans Wbg-1
- ☑ Edaphobacter modestus jbg-1

If you want to view a single entry of the result list, you may select it by a single click on the entry and press the **View in separate window** button. You may check all entries by clicking the ☑ **all** button, uncheck all entries by clicking the ☐ **none** button or toggle the check marks by clicking the **swap** button. You may export the checked results to a tab-separated text file by clicking the button and view the exported list by clicking .
When you close the window by a click on the **OK** button, the checked entries are passed to the main window of Diversity Descriptions (see below). If you do not want to take over the query results to the main window, close the extended query by pressing the **Cancel** button.



DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.2.7

Suchergebnisse 1 - 5

- Aridibacter famidurans A22_HD_4HT
- Aridibacter kavangonensis Ac_23_E3
- Blastocatella fastidiosa A2-16
- Edaphobacter aggregans Wbg-1
- Edaphobacter modestus jbg-1

Aridibacter famidurans A22_HD_4HT

Project: BactDescDSMZ

Language: en

Description: Aridibacter famidurans A22_HD_4HT

ID: 8790

Details: Huber K.J., Wüst P., Rohde M., Overmann J., Foesel B. U.,:Aridibacter famidurans gen. nov., sp. nov. and Aridibacter kavangonensis sp. nov., two novel members of subdivision 4 of the Acidobacteria isolated from semiarid savannah soil. IJSEM 64: 1866-1875 2014 (DOI 10.1099/ijs.0.060236-0,

Project:

- ☑ BactDescDSMZ
- ☐ BFLheilpflanzendesc
- ☐ Tutorial

ordnen nach: Description

Suchkriterien: Extended query results

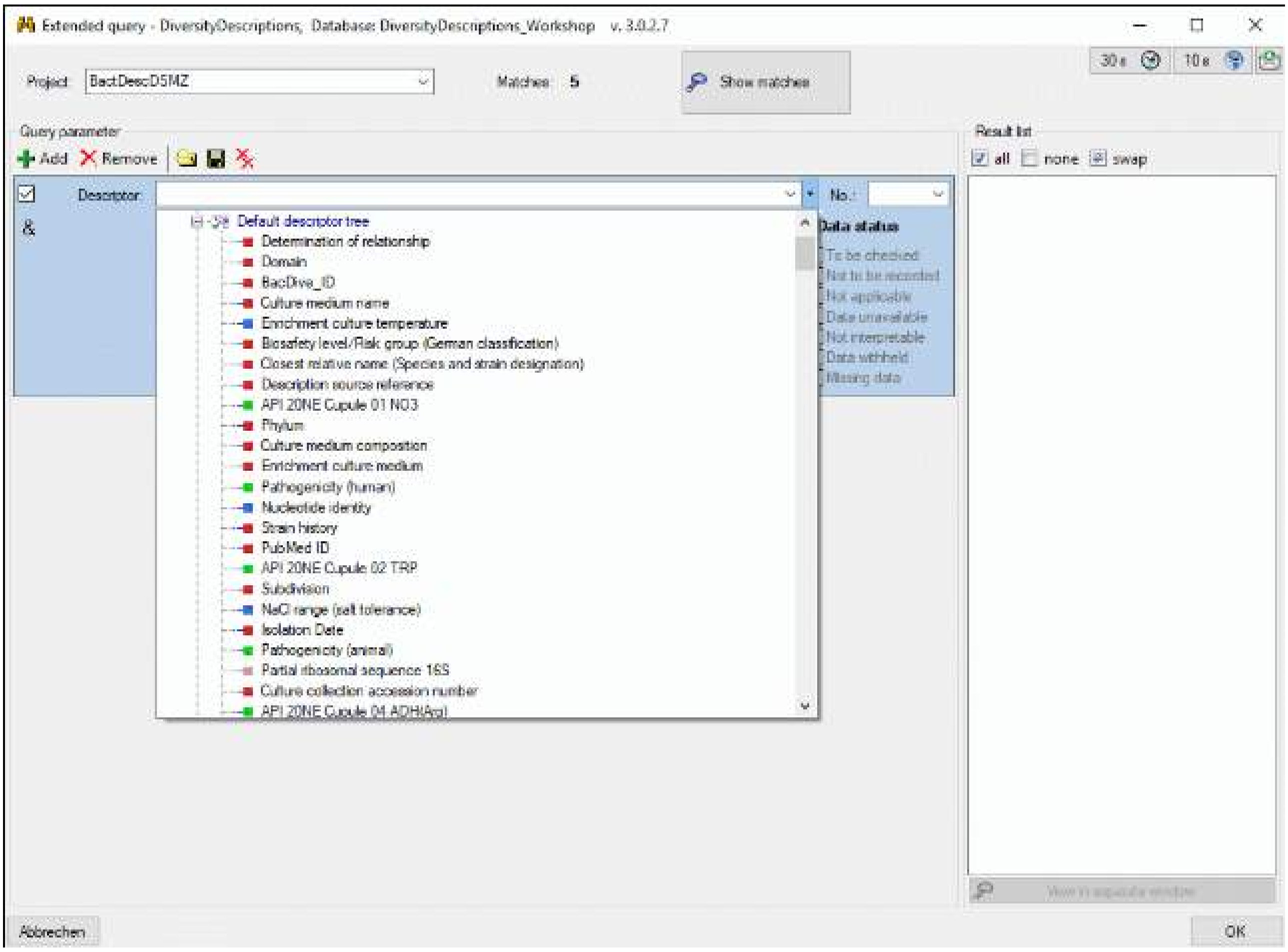
Found description IDs

Continue with:

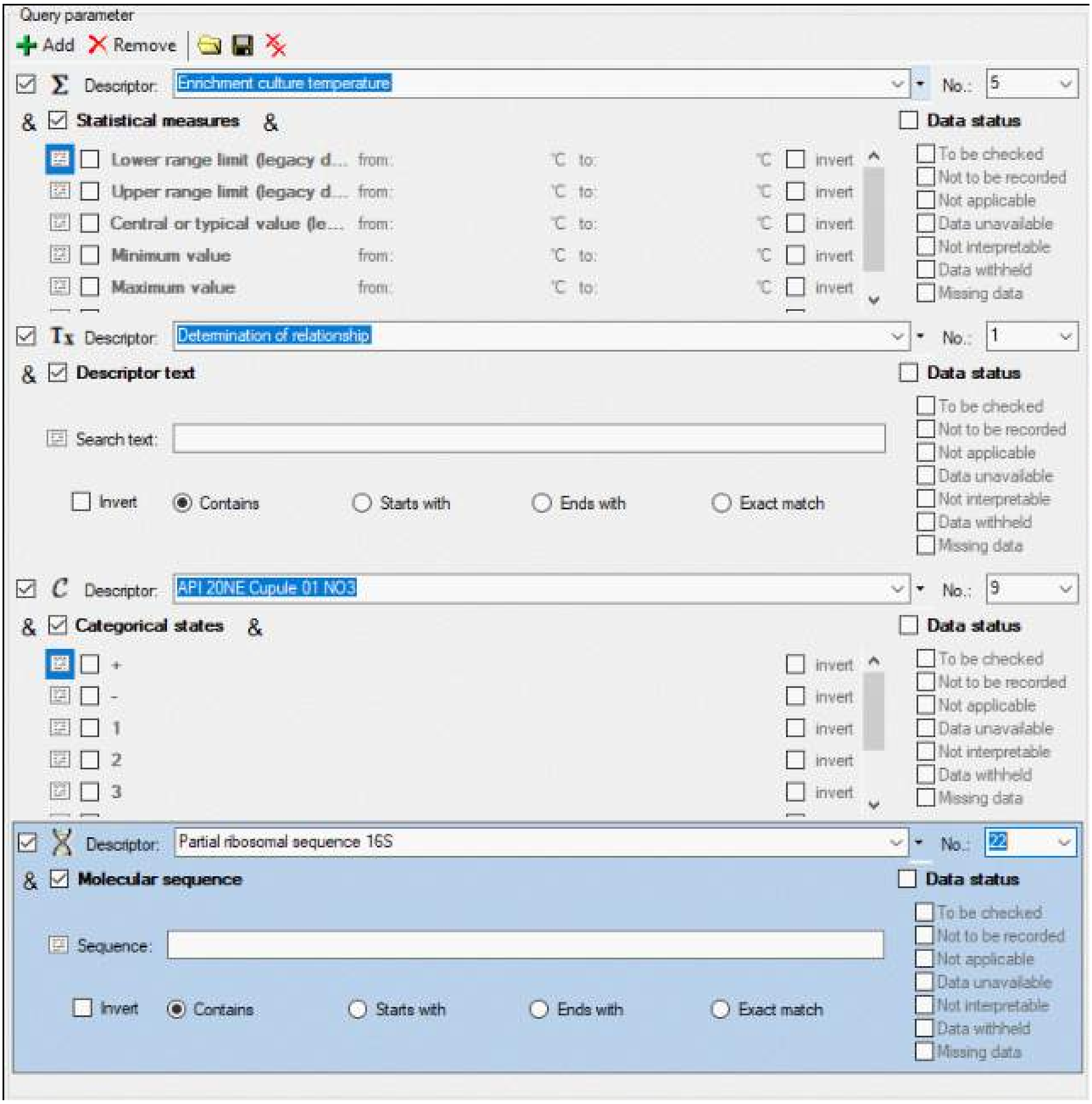
- [Extended query parameter]()
- [Save and load extended query]()

Extended query parameter

Press button **Add** in the **Query parameter** tool strip to insert a new query parameter. A control representing a single descriptor filter will be added at the end of the query parameter list. Now you have to select the descriptor that shall be included in the search filter. This can be done by selecting the descriptor's sequence number with combo box **No.:**, from an alphabetical descriptor list with combo box **Descriptor:** or by selecting from the descriptor tree with button ▾ (see picture below).



After selecting the descriptor the query control shows query parameters depending on the descriptor type (see below). The currently marked parameter control is shown with light blue background. You can delete the current query control by clicking on button **Remove** or all query controls by clicking on button in the **Query parameter** tool strip.



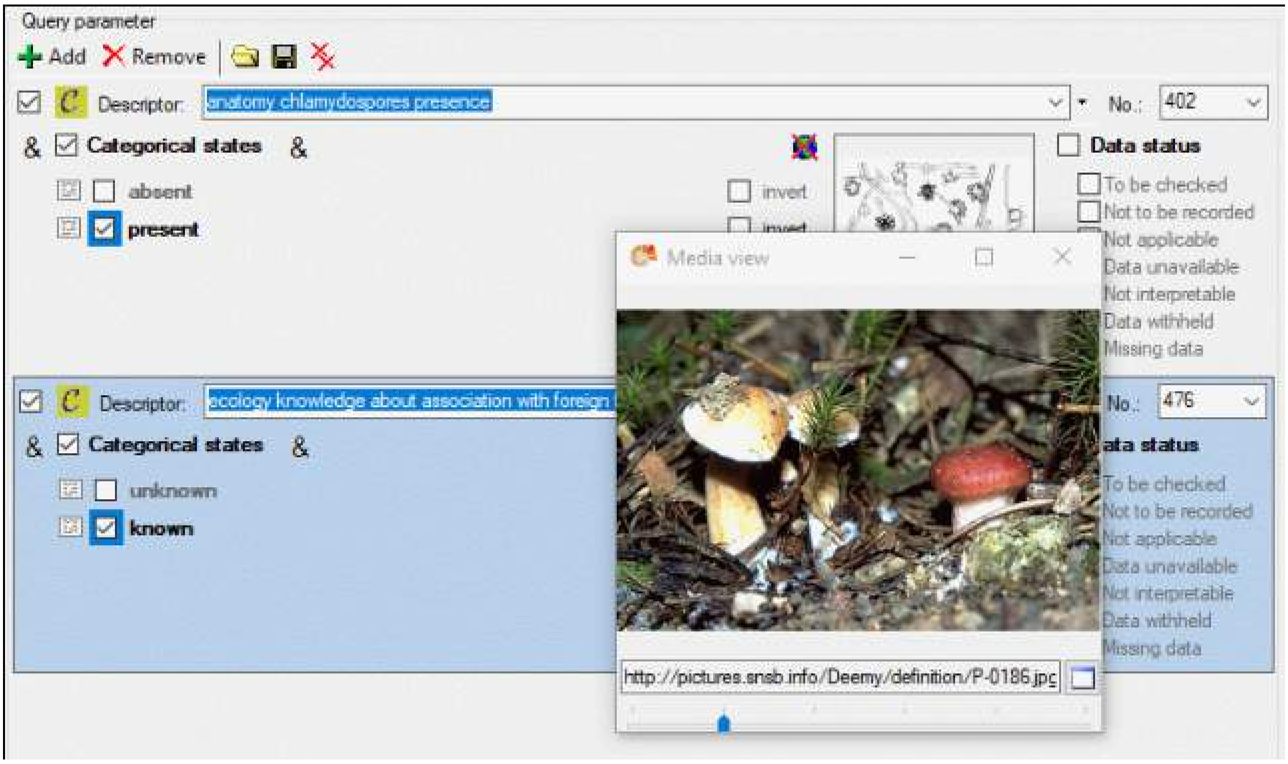
☑ Σ Descriptor: Enrichment culture temperature No.: 5

☑ Tx Descriptor: Determination of relationship No.: 1

☑ C Descriptor: API 20NE Cupule 01 NO3 No.: 9

☑ Descriptor: Partial ribosomal sequence 16S No.: 22

In the parameter control the descriptor type is indicated by symbols in the beginning of the first line (C categorical, Σ quantitive, Tx text or sequence). If additional information for the descriptor are available in the database, you can show them as bubble help by moving the mouse cursor over the symbol. If resource data are available for a descriptor, the symbol is displayed with coloured background and you can view them by double-clicking the it (see image below).



☑ Descriptor: anatomy chlamydospores presence No.: 402

☑ present

☑ Descriptor: ecology knowledge about association with foreign No.: 476

☑ known

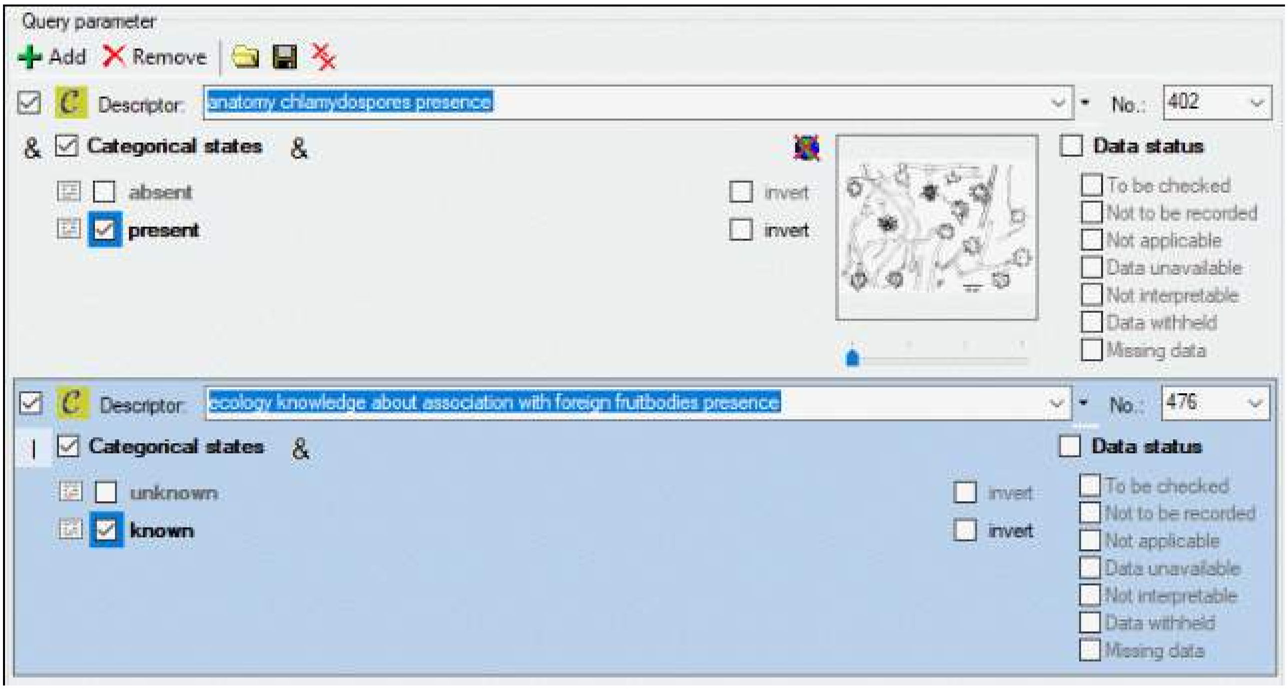
http://pictures.snsb.info/Deemy/definition/P-0186.jpg

Each parameter control has two main sections:

- At the left you find the section for the descriptor parameter, depending on its type (**Categorical states**, **Statistical measures**, **Descriptor text** or **Molecular sequence**). If this section is checked and no other data have been entered, the query filters for all descriptions that include any value for that descriptor, e.g. any descriptor text or any categorical state. By entering additional query data, the filter becomes more restrictive.
- At the right you find the section for the descriptor **Data status**. If this section is checked and no status value has been selected, the query filters for all descriptions that include any status data for that descriptor. By checking dedicated data status values, the filter becomes more restrictive.

If both sections have been checked, matching descriptors must fulfill both conditions, i.e. the value must be present and the data status must be set. If you remove the check mark in the first line of the query parameter, the whole condition will be ignored. Below this check box you find by default the symbol &, which means that "logical AND". If you specify several query parameter controls, which are all adjusted to &, matching description must fulfill all entered query conditions simultaneously.

You may click on the & symbol to change it to | (see image below), which means "logical OR". In this case the result list will include all descriptions that fulfill the first descriptor condition and additionally all descriptions, which fulfill the second condition. I.e. each "AND" condition will reduce the list of matching descriptions and each "OR" condition will add its matching descriptions to the result list.


Query parameter

☑ Descriptor: anatomy chlamydospores presence — No.: 402

& ☑ Categorical states &

- ☐ absent — ☐ invert
- ☑ present — ☐ invert

☐ Data status

- ☐ To be checked
- ☐ Not to be recorded
- ☐ Not applicable
- ☐ Data unavailable
- ☐ Not interpretable
- ☐ Data withheld
- ☐ Missing data

☑ Descriptor: ecology knowledge about association with foreign fruitbodies presence — No.: 476

| ☑ Categorical states &

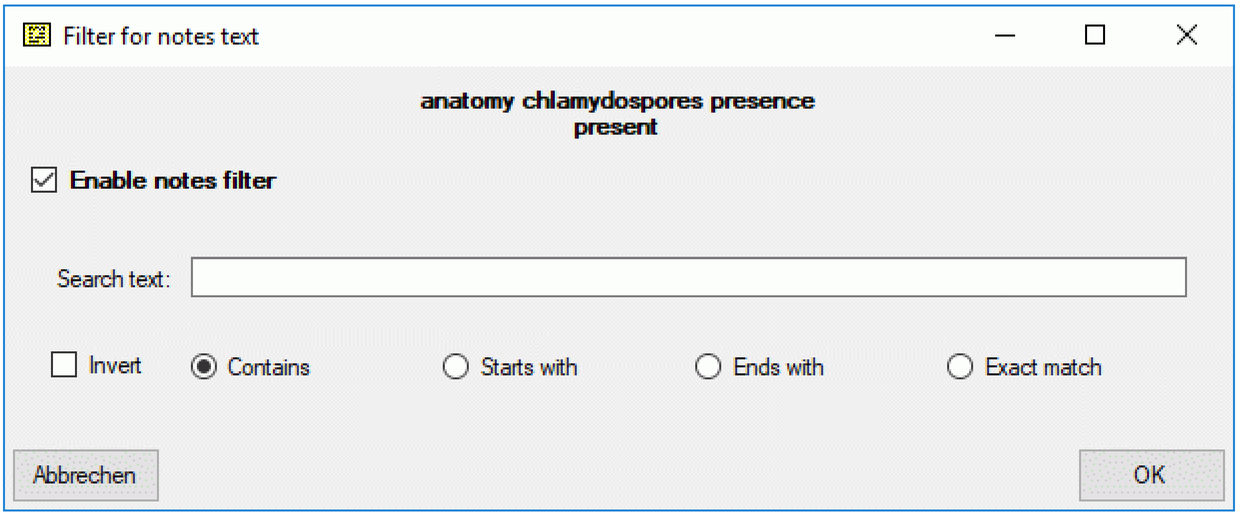
- ☐ unknown — ☐ invert
- ☑ known — ☐ invert

☐ Data status

- ☐ To be checked
- ☐ Not to be recorded
- ☐ Not applicable
- ☐ Data unavailable
- ☐ Not interpretable
- ☐ Data withheld
- ☐ Missing data

Notes

In the descriptive data you may enter free text notes to all text and sequence data. Furthermore individual notes may be entered for every categorical state and statistical measure. You may include additional query contitions for each of those notes, therefore the symbol ▤ is included at the appropriate places. To enter a query condition, click the button and a window as shown below will be opened.


Filter for notes text

anatomy chlamydospores presence
present

☑ Enable notes filter

Search text:

☐ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match

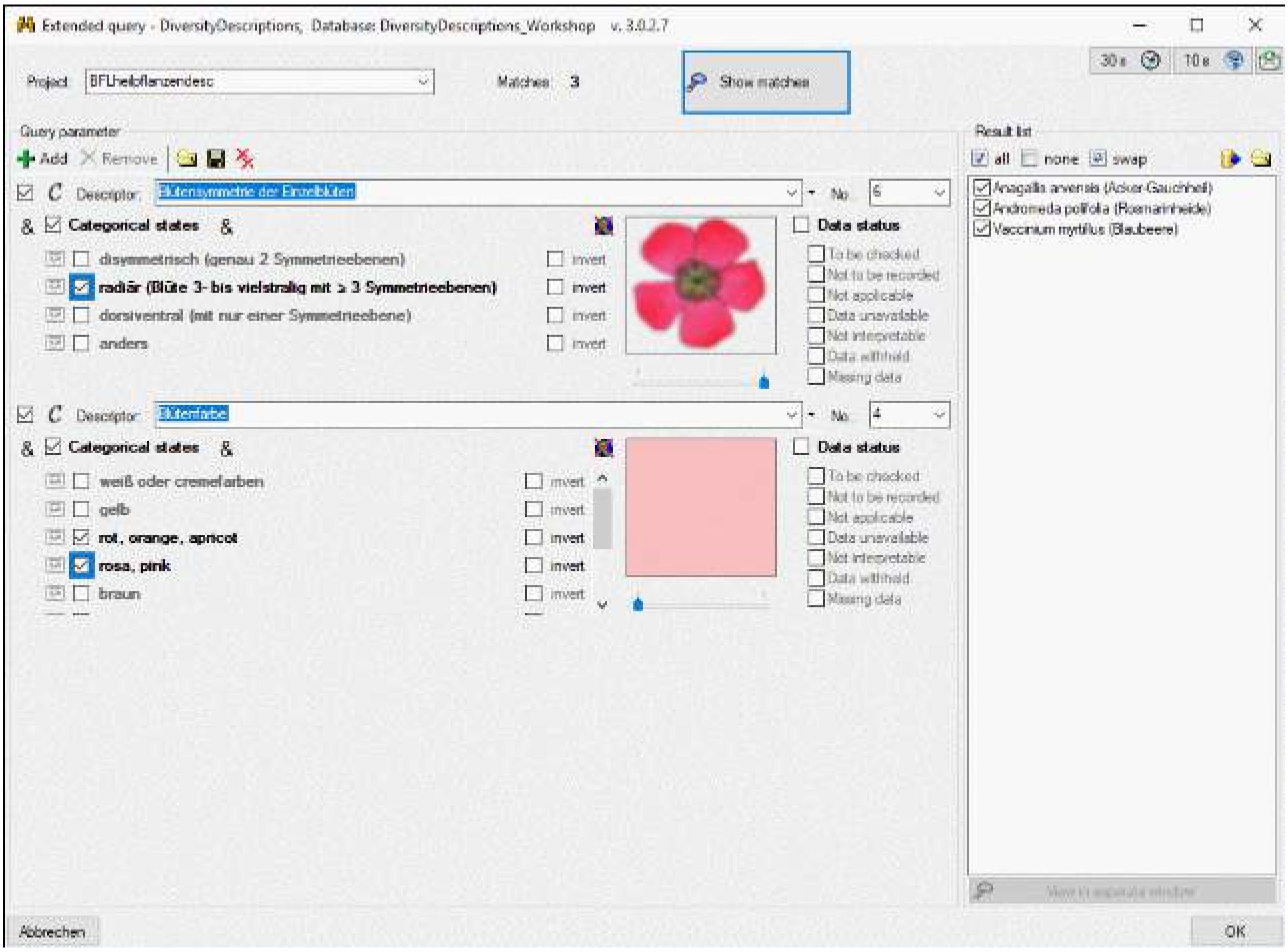
You may enter a **Search text** that shall be part of the notes text. Capitalization is not taken into account. For option **Contains** the descriptor text must contain the search string (see image below). The options **Starts with** and **Ends with** only check the descriptor text begin rsp. end for a match. Finally option **Exact match** requires identical texts. Check the option **invert** to invert the search criteria. When you click **OK** the additional query condition will be active and the icon changes to ▤. If you want to remove the query condition, open the notes form, uncheck the **Enable notes filter** option and click **OK**.

Continue with:

- Extended query parameter - Categorical states
- Extended query parameter - Statistical measures
- Extended query parameter - Descriptor text
- Extended query parameter - Molecular sequence
- Save and load extended query

Extended query parameter - Categorical states

In this query control the categorical states are listed. If pictures of colours are assigned to the categorical states, they can be viewed by clicking on the state name (see picture below). You may switch off automatic loading of the resource view by clicking the button ("no web"), which will be indicated by a yellow symbol background. If this "no web" option is activated, only local resources, e.g. colours, will be shown. If during loading of remote resources an error occurs, e.g. due to a timeout, the "no web" option will automatically be activated.



Project: BFLheilpflanzendesc
Matches: 3

☑ Descriptor: Blütensymmetrie der Einzelblüten — No. 6
& ☑ **Categorical states** &
- ☐ disymmetrisch (genau 2 Symmetrieebenen) — ☐ invert
- ☑ **radiär (Blüte 3- bis vielstrahlig mit ≥ 3 Symmetrieebenen)** — ☐ invert
- ☐ dorsiventral (mit nur einer Symmetrieebene) — ☐ invert
- ☐ anders — ☐ invert

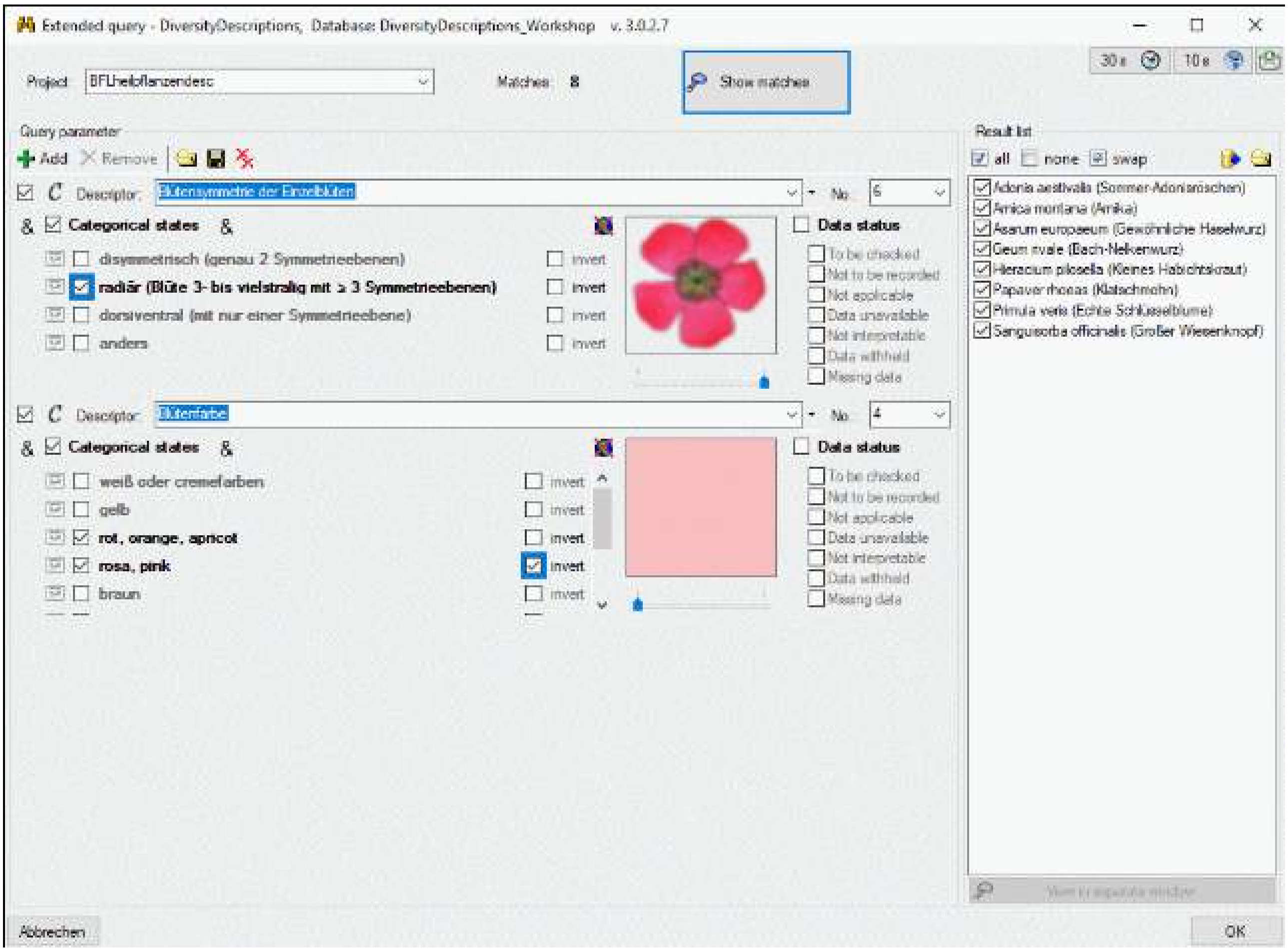
☐ **Data status**
- ☐ To be checked
- ☐ Not to be recorded
- ☐ Not applicable
- ☐ Data unavailable
- ☐ Not interpretable
- ☐ Data withheld
- ☐ Missing data

☑ Descriptor: Blütenfarbe — No. 4
& ☑ **Categorical states** &
- ☐ weiß oder cremefarben — ☐ invert
- ☐ gelb — ☐ invert
- ☑ **rot, orange, apricot** — ☐ invert
- ☑ **rosa, pink** — ☐ invert
- ☐ braun — ☐ invert

☐ **Data status**
- ☐ To be checked
- ☐ Not to be recorded
- ☐ Not applicable
- ☐ Data unavailable
- ☐ Not interpretable
- ☐ Data withheld
- ☐ Missing data

Result list:
- ☑ Anagallis arvensis (Acker-Gauchheil)
- ☑ Andromeda polifolia (Rosmarinheide)
- ☑ Vaccinium myrtillus (Blaubeere)

Categorical states that are not checked are not relevant for the filter. If you want to search for a categorical state that is **NOT** present, check the option **invert** behind the categorical state name (see picture below).


Extended query - DiversityDescriptions; Database: DiversityDescriptions_Workshop v. 3.0.2.7

Project: BFLheilpflanzendesc

Matches: 8

Query parameter

☑ Descriptor: Blütensymmetrie der Einzelblüten No. 6

& ☑ Categorical states &

☐ disymmetrisch (genau 2 Symmetrieebenen) ☐ invert
☑ **radiär (Blüte 3- bis vielstralig mit ≥ 3 Symmetrieebenen)** ☐ invert
☐ dorsiventral (mit nur einer Symmetrieebene) ☐ invert
☐ anders ☐ invert

☐ Data status
☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

☑ Descriptor: Blütenfarbe No. 4

& ☑ Categorical states &

☐ weiß oder cremefarben ☐ invert
☐ gelb ☐ invert
☑ **rot, orange, apricot** ☐ invert
☑ **rosa, pink** ☑ invert
☐ braun ☐ invert

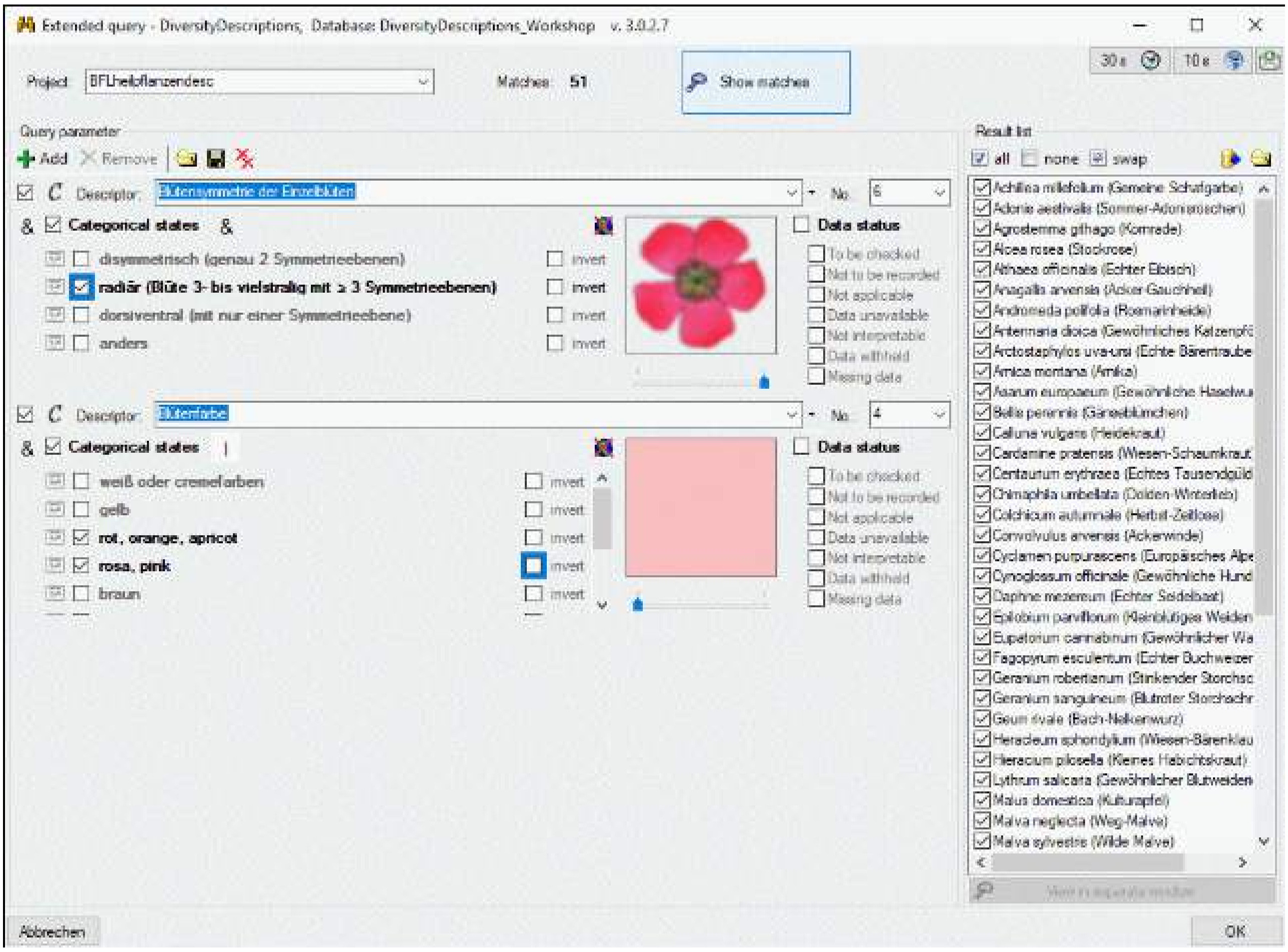
☐ Data status
☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Result list

☑ all ☐ none swap

☑ Adonis aestivalis (Sommer-Adonisröschen)
☑ Arnica montana (Arnika)
☑ Asarum europaeum (Gewöhnliche Haselwurz)
☑ Geum rivale (Bach-Nelkenwurz)
☑ Hieracium pilosella (Kleines Habichtskraut)
☑ Papaver rhoeas (Klatschmohn)
☑ Primula veris (Echte Schlüsselblume)
☑ Sanguisorba officinalis (Großer Wiesenknopf)

By default all categorical states of a descriptor that are selected must be present in the matching descriptions. You may change this logical AND to a logical OR by clicking on the symbol & **behind** the **Categorical state** check box, which will change to symbol | (see picture below). Now all descriptions will match, which include one of the selected states.



Project: BFLheilpflanzendesc

Matches: 51

☑ Descriptor: Blütensymmetrie der Einzelblüten No.: 6

& ☑ Categorical states &

☐ disymmetrisch (genau 2 Symmetrieebenen) ☐ invert
☑ radiär (Blüte 3- bis vielstrahlig mit ≥ 3 Symmetrieebenen) ☐ invert
☐ dorsiventral (mit nur einer Symmetrieebene) ☐ invert
☐ anders ☐ invert

☐ Data status
☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

☑ Descriptor: Blütenfarbe No.: 4

& ☑ Categorical states |

☐ weiß oder cremefarben ☐ invert
☐ gelb ☐ invert
☑ rot, orange, apricot ☐ invert
☑ rosa, pink ☐ invert
☐ braun ☐ invert

☐ Data status
☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Result list: ☑ all ☐ none ☒ swap

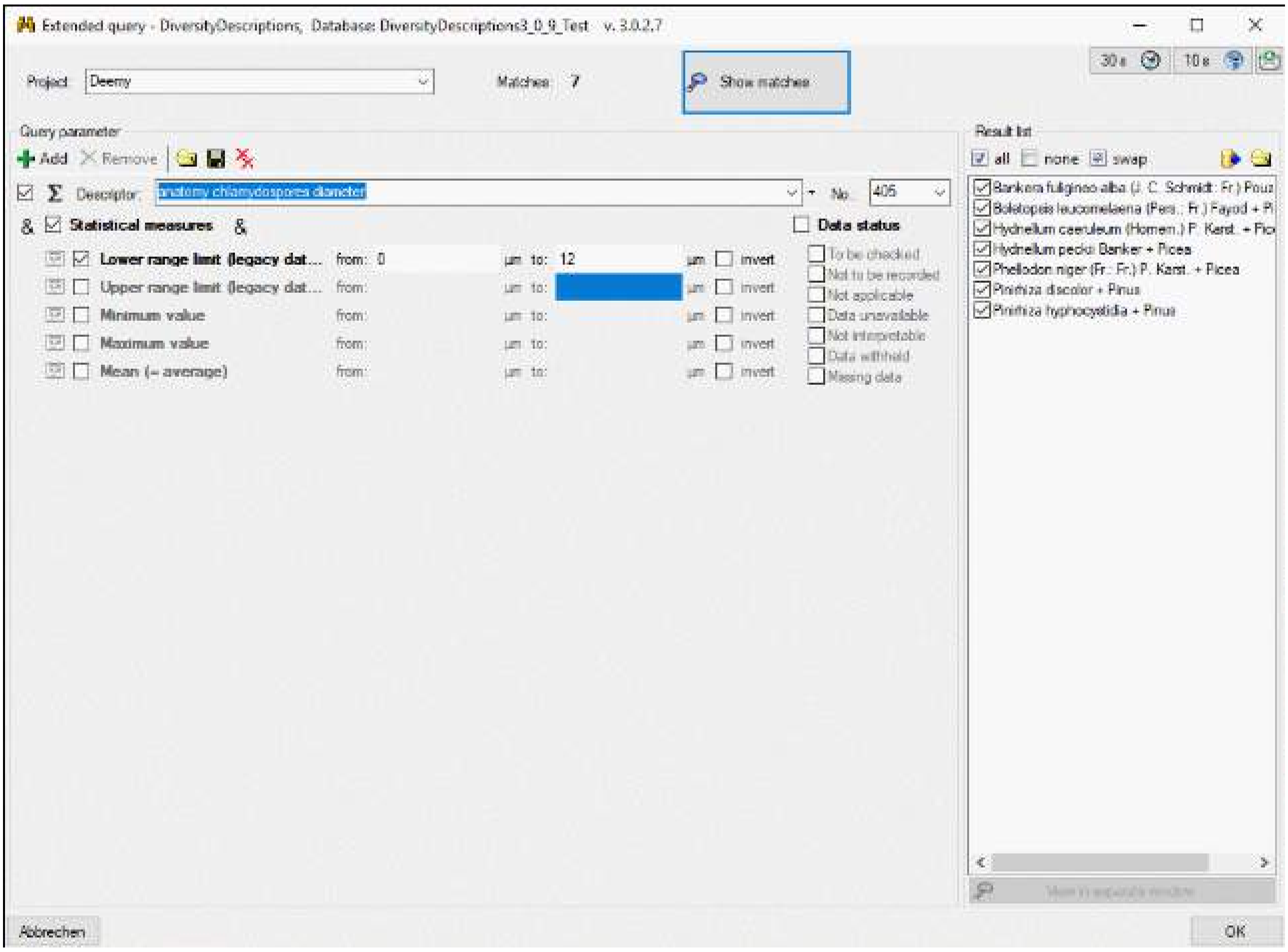
☑ Achillea millefolium (Gemeine Schafgarbe)
☑ Adonis aestivalis (Sommer-Adonisröschen)
☑ Agrostemma githago (Kornrade)
☑ Alcea rosea (Stockrose)
☑ Althaea officinalis (Echter Eibisch)
☑ Anagallis arvensis (Acker-Gauchheil)
☑ Andromeda polifolia (Rosmarinheide)
☑ Antennaria dioica (Gewöhnliches Katzenpfö
☑ Arctostaphylos uva-ursi (Echte Bärentraube
☑ Arnica montana (Arnika)
☑ Asarum europaeum (Gewöhnliche Haselwu
☑ Bellis perennis (Gänseblümchen)
☑ Calluna vulgaris (Heidekraut)
☑ Cardamine pratensis (Wiesen-Schaumkraut
☑ Centaurium erythraea (Echtes Tausendgüld
☑ Chimaphila umbellata (Dolden-Winterlieb)
☑ Colchicum autumnale (Herbst-Zeitlose)
☑ Convolvulus arvensis (Ackerwinde)
☑ Cyclamen purpurascens (Europäisches Alpe
☑ Cynoglossum officinale (Gewöhnliche Hund
☑ Daphne mezereum (Echter Seidelbast)
☑ Epilobium parviflorum (Kleinblütiges Weiden
☑ Eupatorium cannabinum (Gewöhnlicher Wa
☑ Fagopyrum esculentum (Echter Buchweizen
☑ Geranium robertianum (Stinkender Storchsc
☑ Geranium sanguineum (Blutroter Storchschn
☑ Geum rivale (Bach-Nelkenwurz)
☑ Heracleum sphondylium (Wiesen-Bärenklau
☑ Hieracium pilosella (Kleines Habichtskraut)
☑ Lythrum salicaria (Gewöhnlicher Blutweiden
☑ Malus domestica (Kulturapfel)
☑ Malva neglecta (Weg-Malve)
☑ Malva sylvestris (Wilde Malve)

Continue with:

- Extended query parameter - Statistical measures
- Extended query parameter - Descriptor text
- Extended query parameter - Molecular sequence
- Save and load extended query

Extended query parameter - Statistical measures

In this query control the recommended statistical measures are listed. You may enter a single value for an exact match in the **from:** field or a value range in **from:** and **to:** (see picture below). If you want to exclude the specified value range from the query, check the **invert** option. If you do not enter a value, the statistical measure is checked for presence.



Extended query - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Project: Deemy

Matches: 7

☑ Σ Descriptor: anatomy chlamydospores diameter No: 405

& ☑ Statistical measures &

☑ Lower range limit (legacy dat... from: 0 µm to: 12 µm ☐ invert

☐ Upper range limit (legacy dat... from: µm to: µm ☐ invert

☐ Minimum value from: µm to: µm ☐ invert

☐ Maximum value from: µm to: µm ☐ invert

☐ Mean (= average) from: µm to: µm ☐ invert

☐ Data status

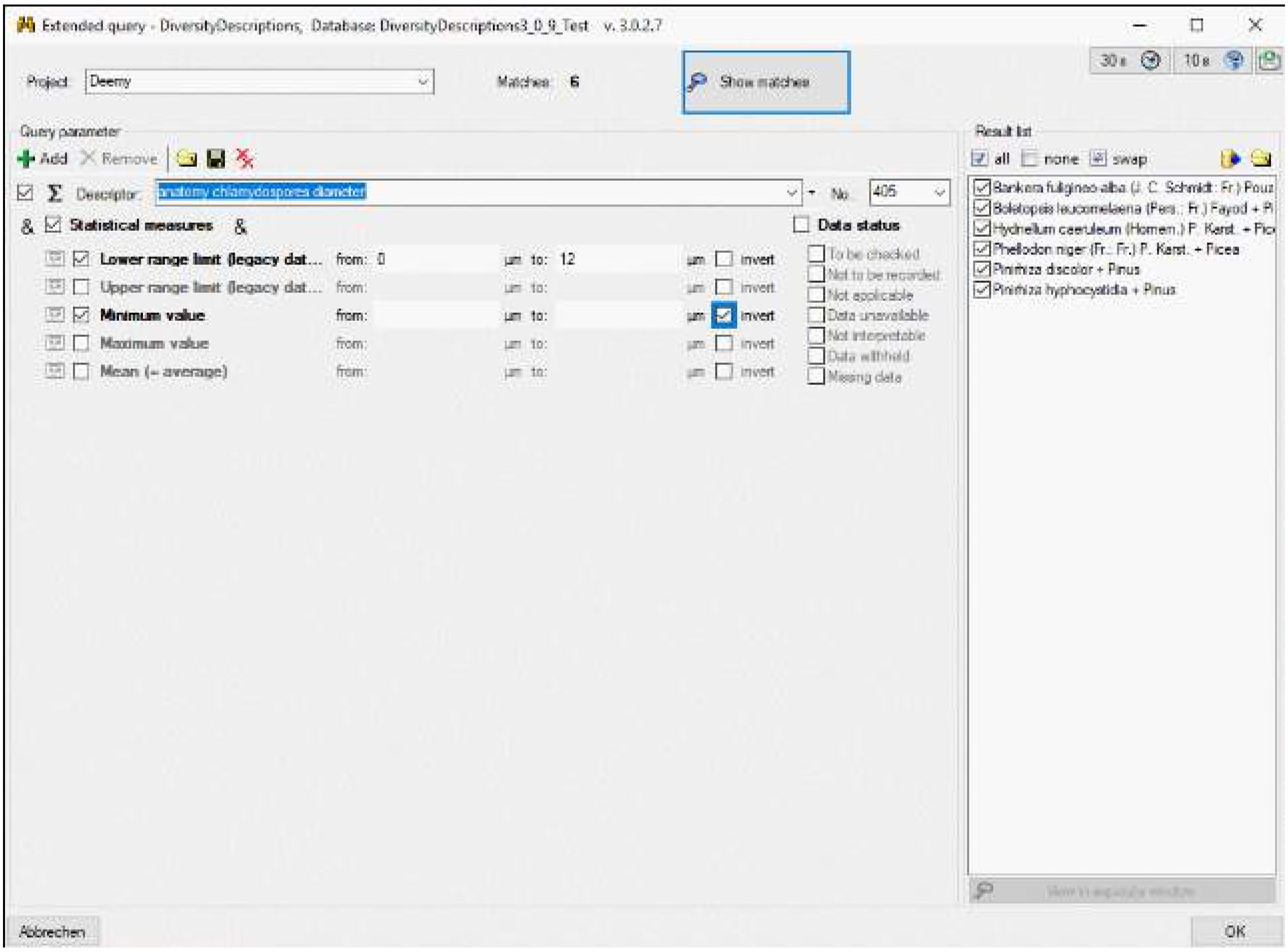
☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Result list

☑ all ☐ none swap

☑ Bankera fuligineo alba (J. C. Schmidt : Fr.) Pouz
☑ Boletopsis leucomelaena (Pers.: Fr.) Fayod + Pi
☑ Hydnellum caeruleum (Hornem.) P. Karst. + Pic
☑ Hydnellum peckii Banker + Picea
☑ Phellodon niger (Fr.: Fr.) P. Karst. + Picea
☑ Pinirhiza discolor + Pinus
☑ Pinirhiza hyphocystidia + Pinus

Statistical measures that are not checked are not relevant for the filter. If you want to search for a statistical measure that is **NOT** present, check the option **invert** and do not enter any values (see picture below).



Project: Deemy

Matches: 6

☑ Σ Descriptor: anatomy chlamydospores diameter No. 405

& ☑ **Statistical measures** &

☐ **Data status**

☑ **Lower range limit (legacy dat…** from: 0 µm to: 12 µm ☐ invert

☐ Upper range limit (legacy dat… from: µm to: µm ☐ invert

☑ **Minimum value** from: µm to: µm ☑ invert

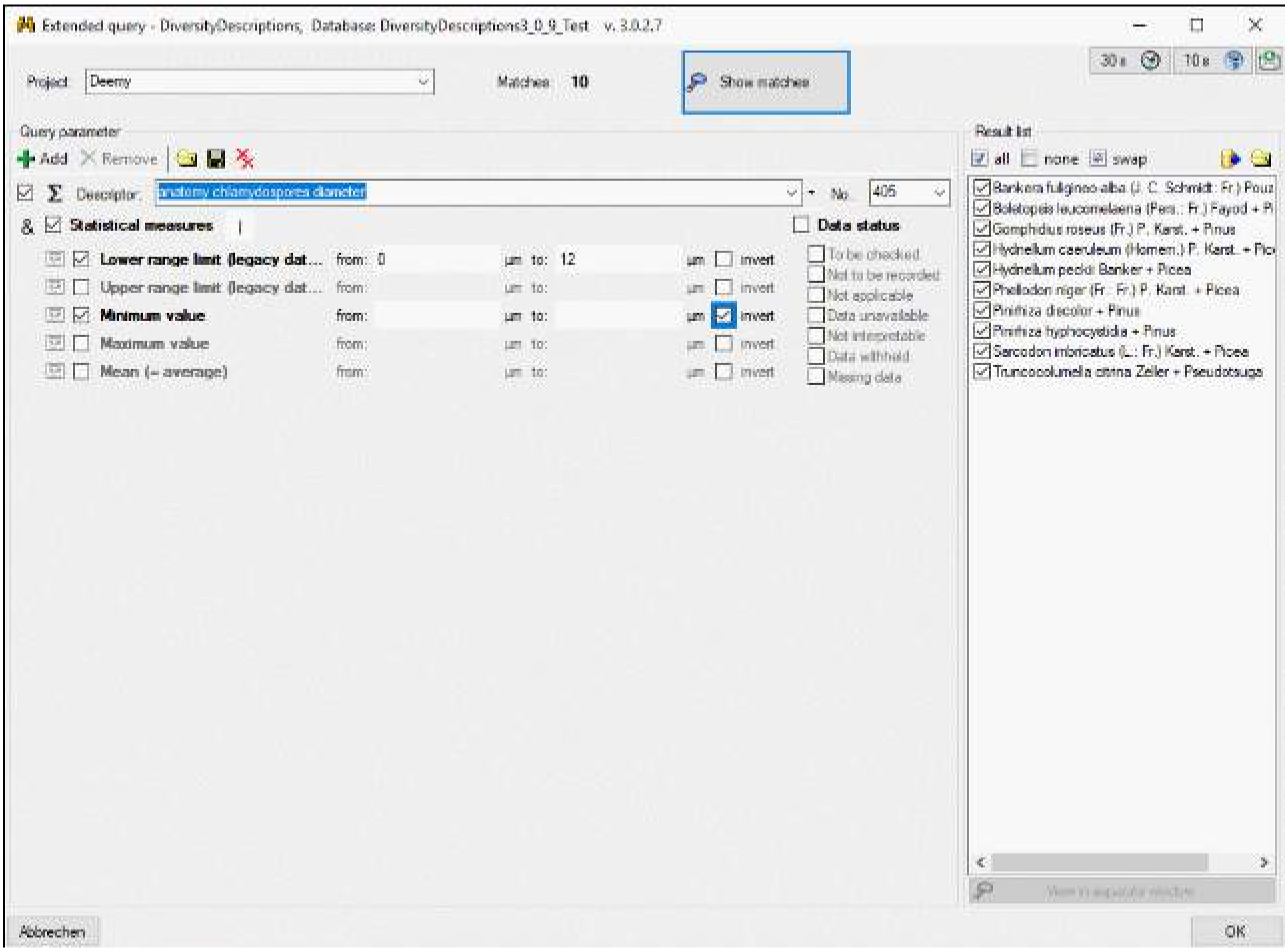
☐ Maximum value from: µm to: µm ☐ invert

☐ Mean (= average) from: µm to: µm ☐ invert

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

☑ Bankera fuligineo-alba (J. C. Schmidt : Fr.) Pouz
☑ Boletopsis leucomelaena (Pers. : Fr.) Fayod + Pi
☑ Hydnellum caeruleum (Hornem.) P. Karst. + Pic
☑ Phellodon niger (Fr. : Fr.) P. Karst. + Picea
☑ Pinirhiza discolor + Pinus
☑ Pinirhiza hyphocystidia + Pinus

By default all statistical measure conditions of a descriptor that are selected must be fulfilled in the matching descriptions. You may change this logical AND to a logical OR by clicking on the symbol & **behind** the **Statistical measure** check box, which will change to symbol | (see picture below). Now all descriptions will match, which include one of the selected measure conditions.



Extended query - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Project: Deemy

Matches 10

Query parameter

☑ Σ Descriptor: anatomy chlamydospores diameter No. 405

& ☑ **Statistical measures**

	Measure						
☑	**Lower range limit (legacy dat…**	from: 0	µm	to: 12	µm	☐	invert
☐	Upper range limit (legacy dat…	from:	µm	to:	µm	☐	invert
☑	**Minimum value**	from:	µm	to:	µm	☑	invert
☐	Maximum value	from:	µm	to:	µm	☐	invert
☐	Mean (= average)	from:	µm	to:	µm	☐	invert

☐ **Data status**

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Result list

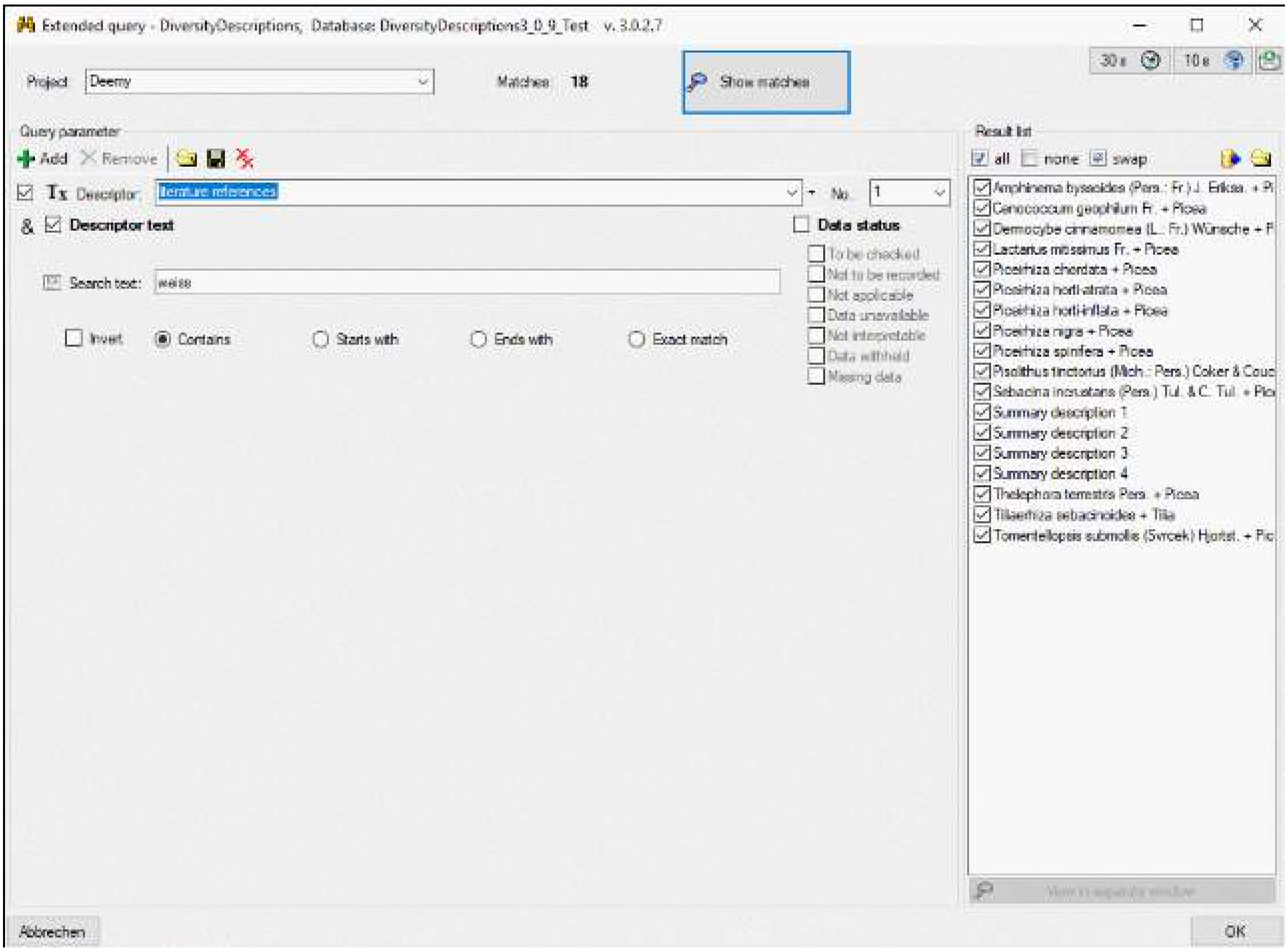
☑ Bankera fuligineo-alba (J. C. Schmidt : Fr.) Pouz
☑ Boletopsis leucomelaena (Pers.: Fr.) Fayod + Pi
☑ Gomphidius roseus (Fr.) P. Karst. + Pinus
☑ Hydnellum caeruleum (Hornem.) P. Karst. + Pic
☑ Hydnellum peckii Banker + Picea
☑ Phellodon niger (Fr.: Fr.) P. Karst. + Picea
☑ Piniriza discolor + Pinus
☑ Piniriza hyphocystidia + Pinus
☑ Sarcodon imbricatus (L.: Fr.) Karst. + Picea
☑ Truncocolumella citrina Zeller + Pseudotsuga

Continue with:

- Extended query parameter - Descriptor text
- Extended query parameter - Molecular sequence
- Save and load extended query

Extended query parameter - Descriptor text

In this query control you may enter a **Search text** that shall be part of the text descriptor data. Capitalization is not taken into account. For option **Contains** the descriptor text must contain the search string (see image below). The options **Starts with** and **Ends with** only check the descriptor text begin rsp. end for a match. Finally option **Exact match** requires identical texts.



Extended query - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Project: Deemy

Matches 18

Query parameter

☑ Descriptor: literature references No. 1

& ☑ **Descriptor text**

Search text: weiss

☐ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match

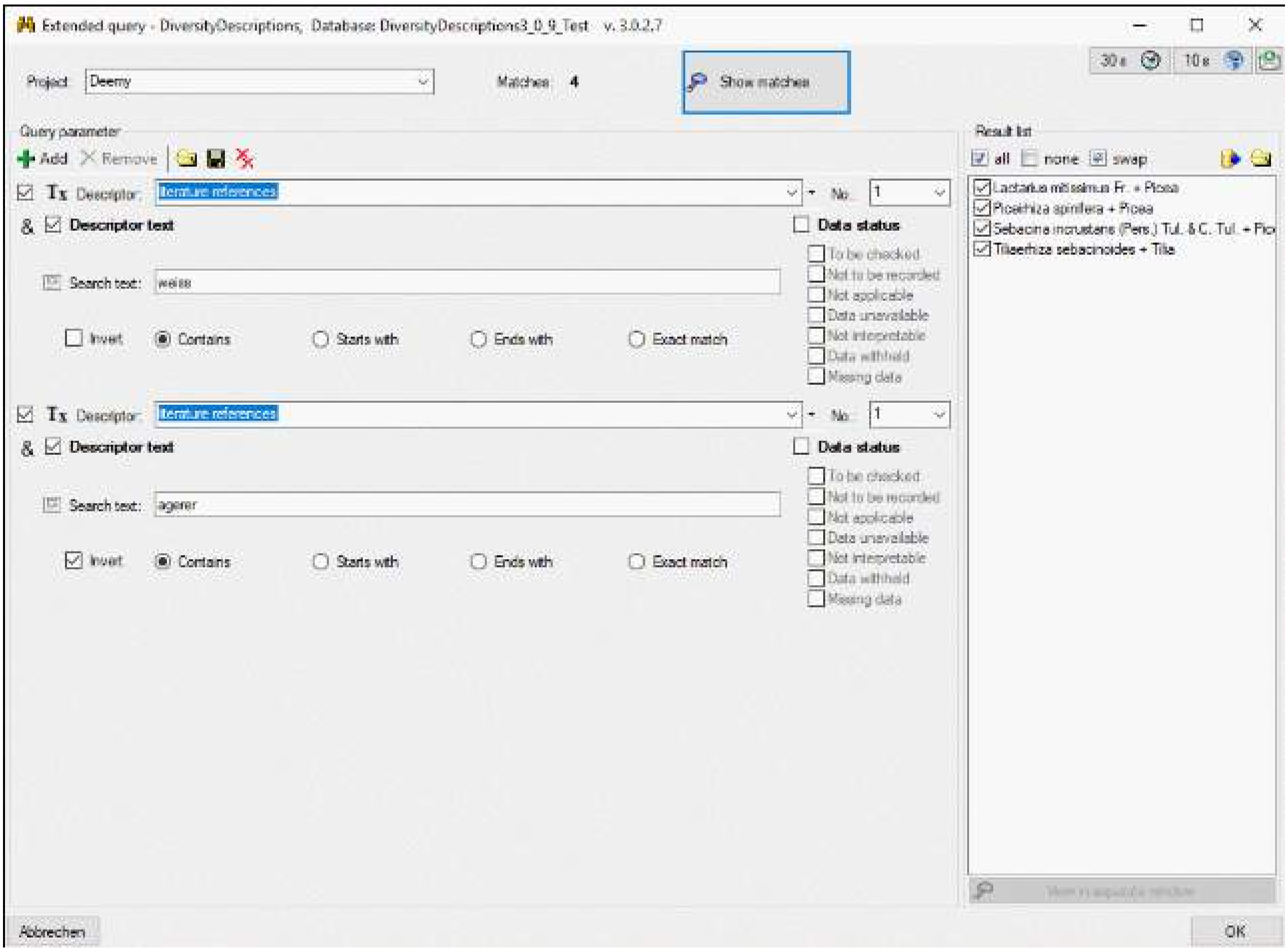
☐ **Data status**

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

☑ all ☐ none ☑ swap

☑ Amphinema byssoides (Pers.: Fr.) J. Erikss. + Pi
☑ Cenococcum geophilum Fr. + Picea
☑ Dermocybe cinnamomea (L.: Fr.) Wünsche + P
☑ Lactarius mitissimus Fr. + Picea
☑ Piceirhiza chordata + Picea
☑ Piceirhiza horti-atrata + Picea
☑ Piceirhiza horti-inflata + Picea
☑ Piceirhiza nigra + Picea
☑ Piceirhiza spinifera + Picea
☑ Pisolithus tinctorius (Mich.: Pers.) Coker & Couc
☑ Sebacina incrustans (Pers.) Tul. & C. Tul. + Pic
☑ Summary description 1
☑ Summary description 2
☑ Summary description 3
☑ Summary description 4
☑ Thelephora terrestris Pers. + Picea
☑ Tiliaerhiza sebacinoides + Tilia
☑ Tomentellopsis submollis (Svrcek) Hjortst. + Pic

Check the option **invert** to invert the search criteria (see picture below).



Extended query - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Project: Deemy

Matches: 4

Query parameter

☑ Descriptor: literature references No.: 1
& ☑ Descriptor text
Search text: weiss
☐ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match
☐ Data status

☑ Descriptor: literature references No.: 1
& ☑ Descriptor text
Search text: agerer
☑ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match
☐ Data status

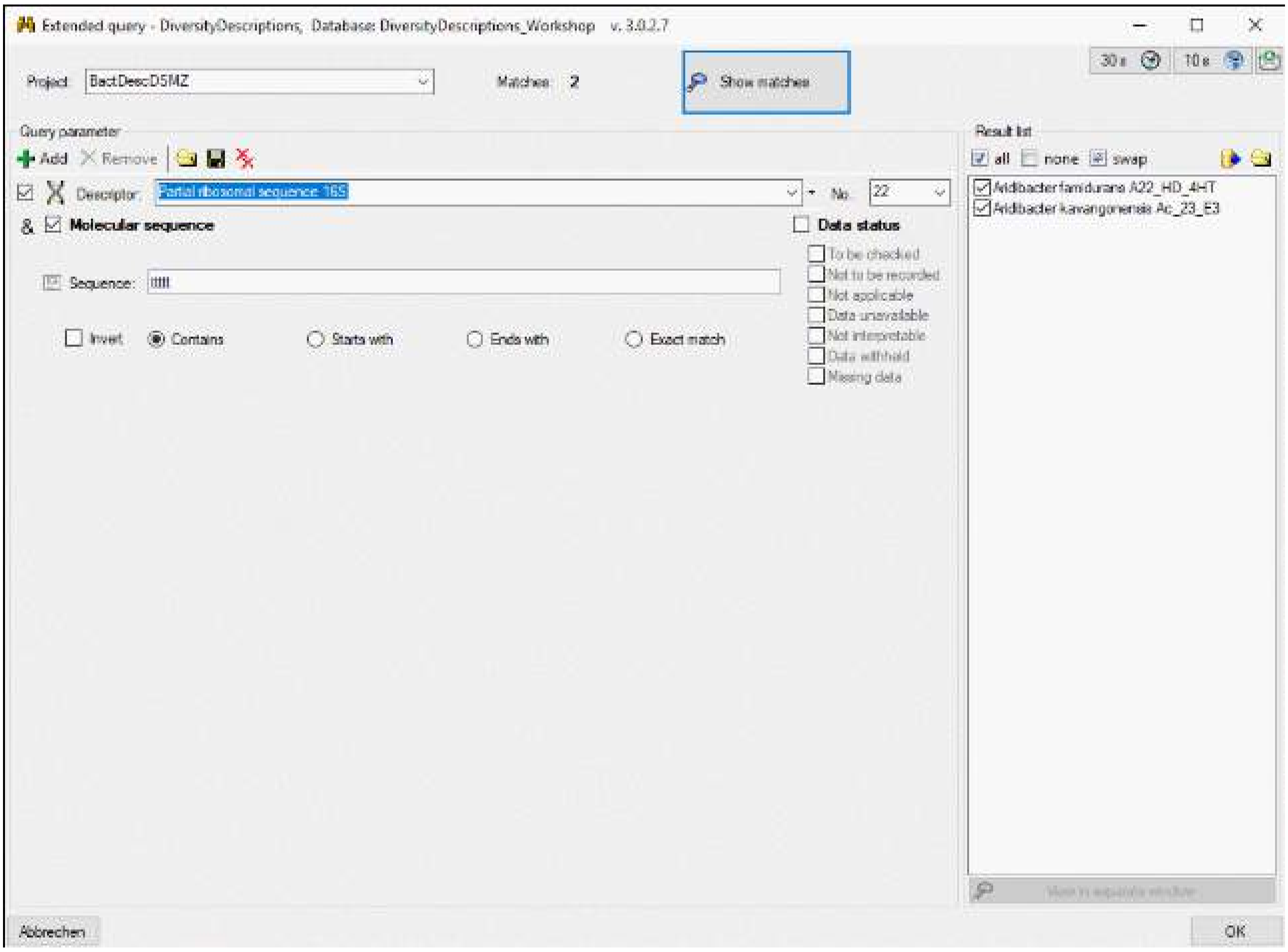
Result list
☑ Lactarius mitissimus Fr. + Picea
☑ Piceirhiza spinifera + Picea
☑ Sebacina incrustans (Pers.) Tul. & C. Tul. + Pic
☑ Tilaerhiza sebacinoides + Tilia

Continue with:

- Extended query parameter - Molecular sequence
- Save and load extended query

Extended query parameter - Molecular sequence

In this query control you may enter a **Sequence** that shall be part of the molecular sequence data. Capitalization is not taken into account. For option **Contains** the sequence text must contain the search string (see image below). The options **Starts with** and **Ends with** only check the descriptor text begin rsp. end for a match. Finally option **Exact match** requires identical texts.



Project: BactDescDSMZ

Matches: 2

☑ Descriptor: Partial ribosomal sequence 16S No. 22

& ☑ **Molecular sequence**

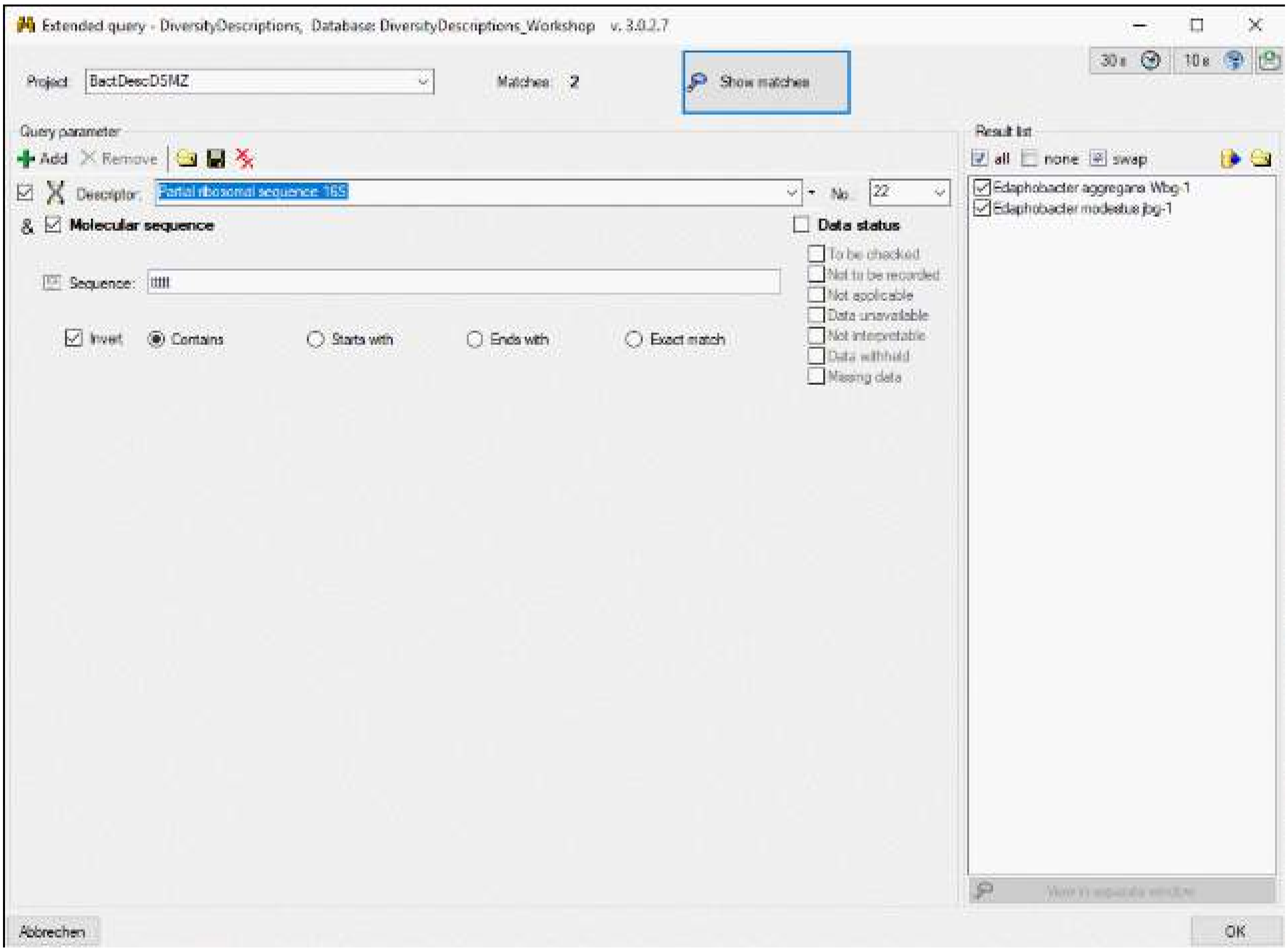
Sequence: ttttt

☐ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match

☑ Aridibacter famidurans A22_HD_4HT

☑ Aridibacter kavangonensis Ac_23_E3

Check the option **invert** to invert the search criteria (see picture below).



Project: BactDescDSMZ

Matches: 2

☑ Descriptor: Partial ribosomal sequence: 16S

No.: 22

& ☑ **Molecular sequence**

Sequence: ttttt

☑ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match

☐ **Data status**

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

☑ Edaphobacter aggregans Wbg-1
☑ Edaphobacter modestus Jbg-1

Continue with:

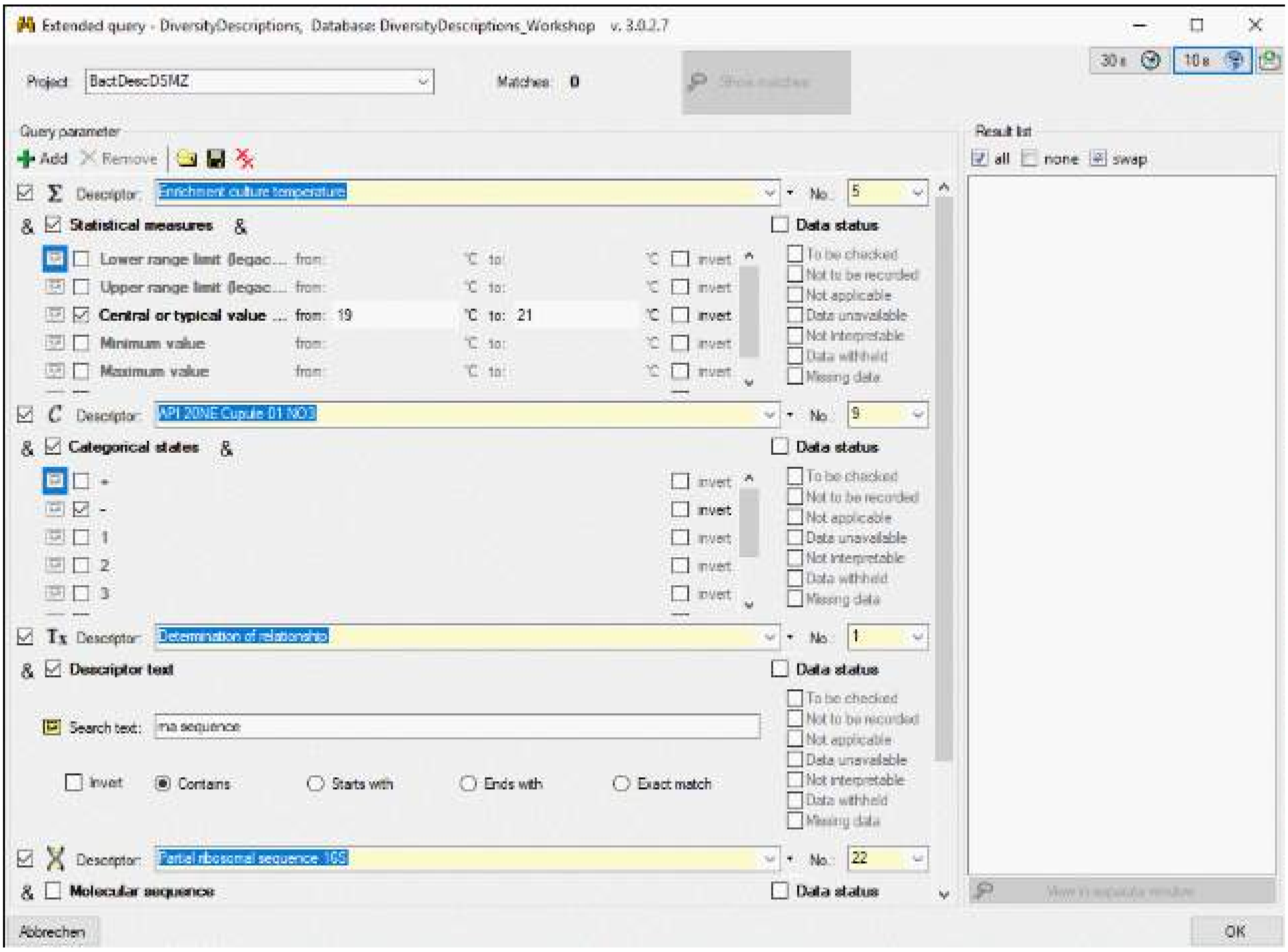
- Save and load extended query

Save and load extended query

The complete query schema may be saved into an XML file using the button 💾, which opens a dialog window to enter the file name and location. By default the schema file name is generated as:

<working directory>\ExtendedQuery\DescriptionQuery_<Database name>_<Project>.xml

The XML schema file includes information concerning the database, the project and the query parameter. By pressing the 📂button in the **Query parameter** section, a query schema file can be opened. If the schema does not meet the active database you will be informed by a message box. In the query file all relevant parameter are identified by the database internal numeric IDs. If no matching values are found, it is tried to get them by their names. Since the names might be ambigious, the corresponding element are displayed with a yellow background colour (see image below).



Extended query - DiversityDescriptions, Database: DiversityDescriptions_Workshop v. 3.0.2.7

Project: BactDescDSMZ Matches: 0

☑ Descriptor: Enrichment culture temperature No.: 5

& ☑ Statistical measures &

☑ Central or typical value ... from: 19 °C to: 21 °C ☐ invert

☑ Descriptor: API 20NE Cupule 01 NO3 No.: 9

& ☑ Categorical states &

☑ -

☑ Descriptor: Determination of relationship No.: 1

& ☑ Descriptor text

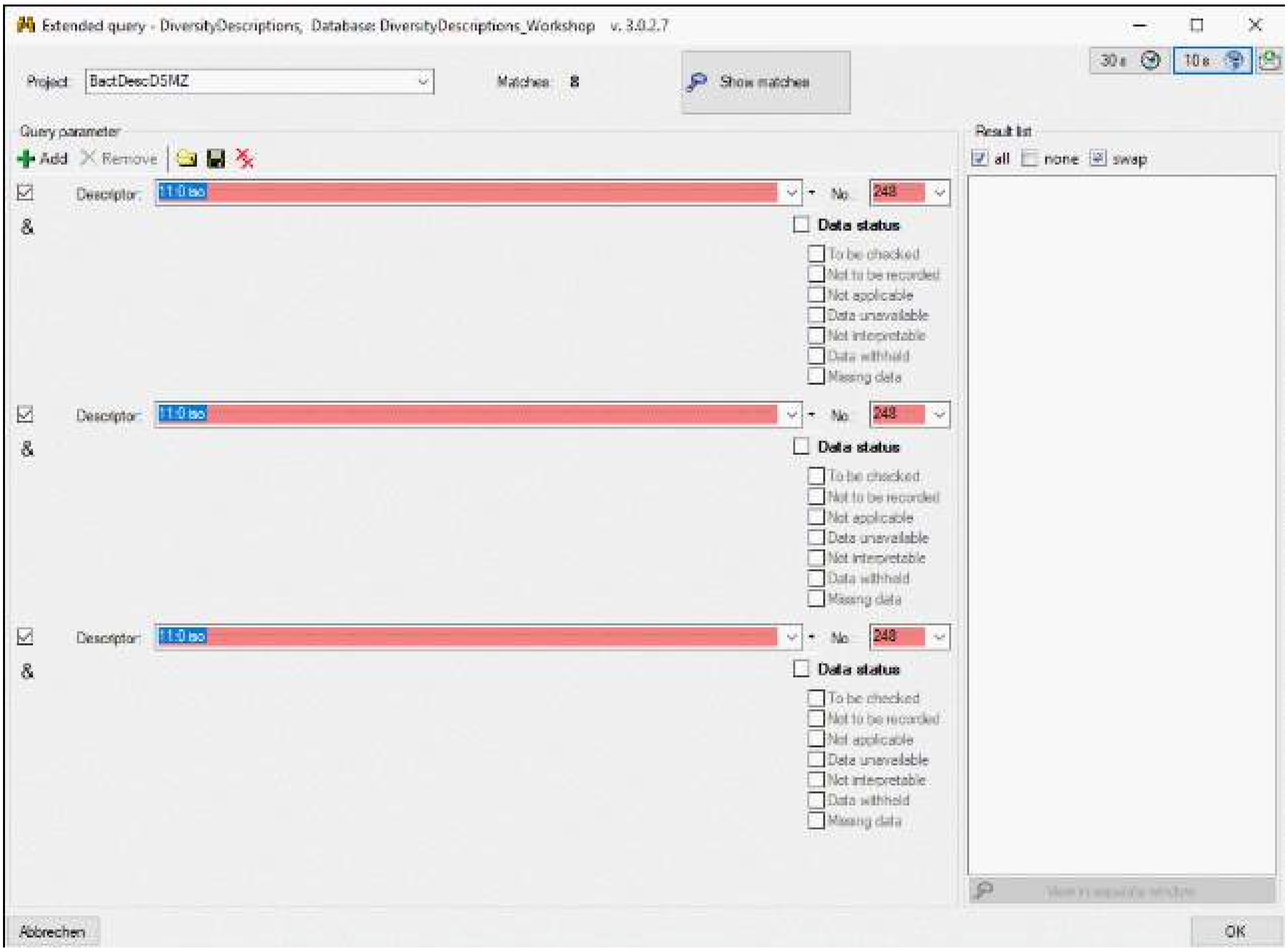
Search text: rna sequence

☐ Invert ● Contains ○ Starts with ○ Ends with ○ Exact match

☑ Descriptor: Partial ribosomal sequence 16S No.: 22

& ☐ Molecular sequence ☐ Data status

If the parameter could not even be assigned by their names, this is indicated by a red background color (see picture below).



Project: BactDescDSMZ

Matches: 8

☑ all ☐ none ☑ swap

☑ Descriptor: 11:0 iso · No: 248
&
☐ Data status

☑ Descriptor: 11:0 iso · No: 248
&
☐ Data status

☑ Descriptor: 11:0 iso · No: 248
&
☐ Data status

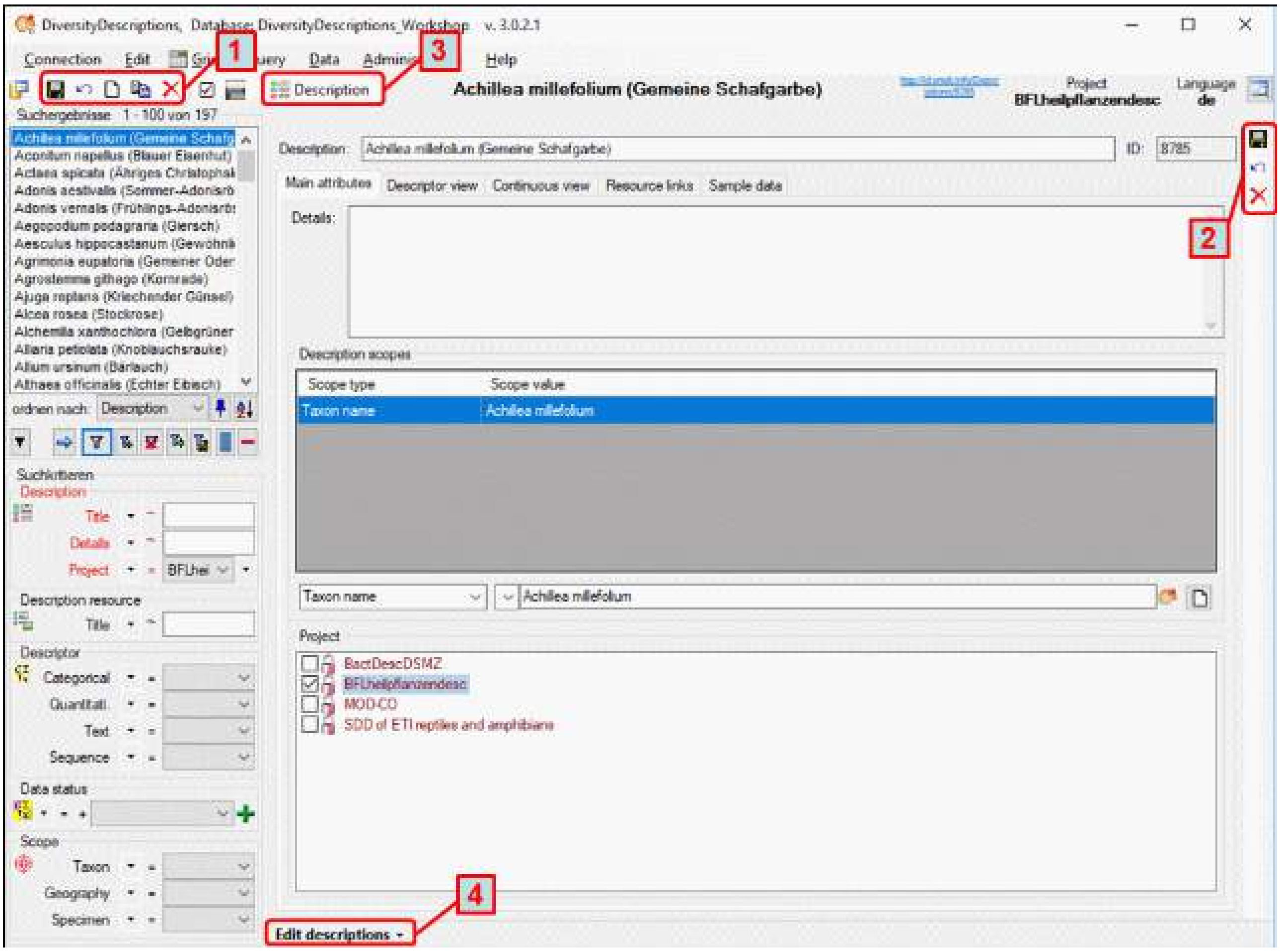
Editing the data

The database of DiversityDescriptions consists of three major areas:

- The descriptive data (descriptions) reference elements of the descriptive terminology and add specific data, e.g. numeric values.
- The descriptive terminology, consisting of descriptors, categorical states, statistical measures and modifiers.
- The project data build the administrative frame for terminology and descriptions. Each description belongs to exactly one project. By additional entities (descriptor tress) it is possible to restrict the descriptors, statistical measures and modifier that shall be used in a certain project.

In almost all forms an Extended text editor can be opened for single text fields that provides additional editing features.

Corresponding with that three major sections of the data model, the DiversityDewscriptions application provide three edit modes. The edit mode is diplayed at the bottom of the main window (see picture below). After the first start the edit mode is preselected to **"Edit descriptions"**. You can switch the edit mode using the menu **Edit-> Descriptions**, **Edit-> Descriptors** or **Edit-> Projects**. Alternatively you may switch the edit mode by click the mode button in the upper left corner of the header area (item 3 in picture below) or on the tiny triangle besides the edit mode display in the status line at the bottom (see item 4 in picture below).



Description: Achillea millefolium (Gemeine Schafgarbe)
ID: 8785

Achillea millefolium (Gemeine Schafg
Aconitum napellus (Blauer Eisenhut)
Actaea spicata (Ähriges Christophsk
Adonis aestivalis (Sommer-Adonisrö
Adonis vernalis (Frühlings-Adonisrö
Aegopodium podagraria (Giersch)
Aesculus hippocastanum (Gewöhnli
Agrimonia eupatoria (Gemeiner Oder
Agrostemma githago (Kornrade)
Ajuga reptans (Kriechender Günsel)
Alcea rosea (Stockrose)
Alchemilla xanthochlora (Gelbgrüner
Alliaria petiolata (Knoblauchsrauke)
Allium ursinum (Bärlauch)
Althaea officinalis (Echter Eibisch)

Scope type	Scope value
Taxon name	Achillea millefolium

Taxon name: Achillea millefolium

Project:
☐ BactDescDSMZ
☑ BFUheilpflanzendesc
☐ MOD-CO
☐ SDD of ETI reptiles and amphibians

Suchkriterien
Description: Title, Details, Project BFUhei
Description resource: Title
Descriptor: Categorical, Quantitati., Text, Sequence
Data status
Scope: Taxon, Geography, Specimen

The main window of the DiversityDescriptions client contains two main areas. At the left you find the query and the results of this query. In the right part the data of the dataset selected in the result list is shown.

Basic operations

In each edit mode there are some common functions for storing and reloading data, to create a new dataset or delete or copy the actual dataset. On top of the query results (item 1 in image above) there is button 💾to store the actual dataset, button ✗to delete the actual dataset and button 🗋to create a new dataset. By pressing button ↶ the actual dataset is reloaded, i.e. changes that have been made will be dropped. Finally, button ⎘copies the data of the actual dataset to a new one.

Some of those buttons can be found in the tool bar at the right side of the edit window (item 2), too.

Additionally to explicit saving by pressing the 💾button, an automatic saving of the dataset is done, if an entry in the query result list is selected or a new query is performed. If a dataset has been modified without saving, a message window will appear and ask if changes shall be saved for several actions, e.g. change of edit mode, connetion to a database or if the application is closed.

Translations

For many database tables the text columns may be translated into different languages. To enter, modify or view the translated texts, use the translations editor. For an overview on multilingualism in Diversity Descriptions see chapter translations.

Description grid view

An alternate form for editing or viewing the data of several descriptions in a grid is provided by the description grid view. It provides a simplified user interface for access to a subset of the description data.

Sample data grid view

An alternate form for editing or viewing the sample data of several descriptions in a grid is provided by the sample data grid view.

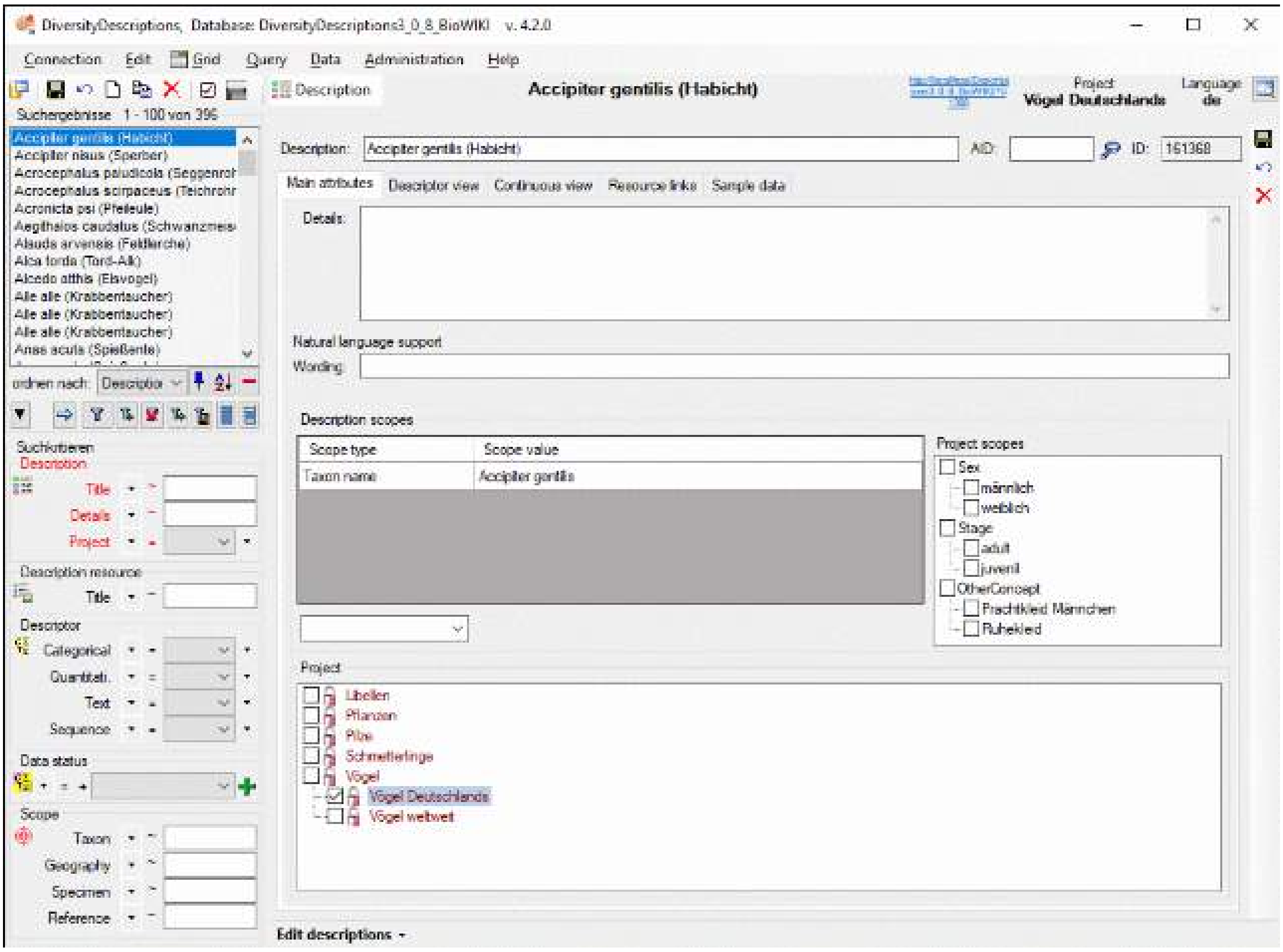
Table editors

For a selected set of database tables a direct data editing in a grid is provided by the table editors.

Editing the description

After starting a database query and selecting an entry in the result list the dataset is diplayed in the edit window. In the header area the dataset name, the default project language and the URI of the current dataset are show (see picture below). Below the header area the description name may be edited in a text box. Changes of the description data, e.g. the name, will be visible in the header after saving the dataset. To check dataset changes, click on the button to open the history.

The main description data may be accessed in the first **Main attributes** tab, which is described below. Click on one of the other tabs in the picture below to go directly to the appropriate manual chapter.



Description: Accipiter gentilis (Habicht)

ID: 161368

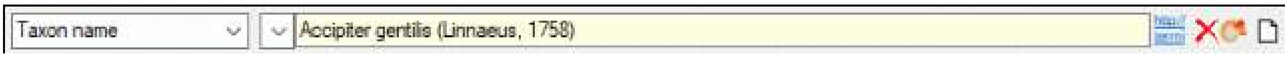
Scope type	Scope value
Taxon name	Accipiter gentilis

Main attributes tab

The main attributes tab provides in the upper area a field to enter additional description details and a wording for natural language support. The optional filed **AID** may keep an alpha-numeric alternate ID of the dataset. If used, it should be unambigious within the project, but this is not checked by the program. Click on to get an overview of the used keys.

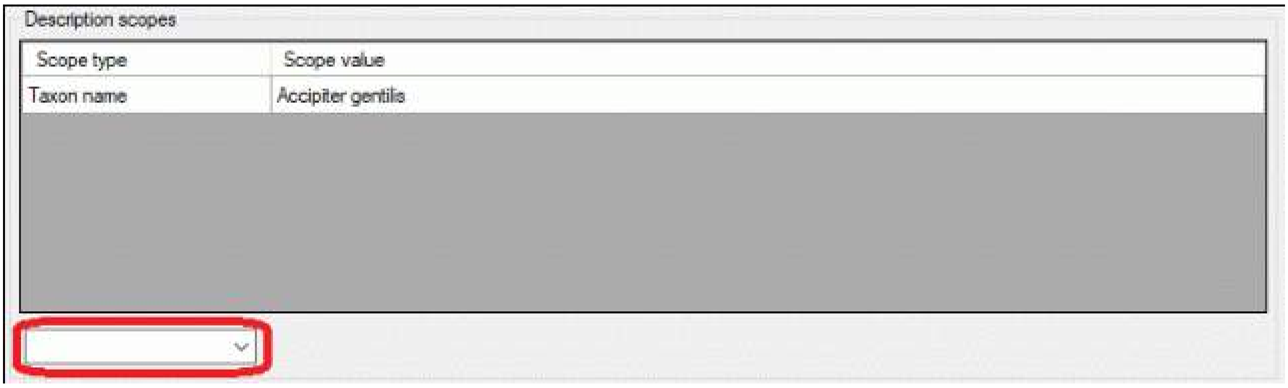
Scopes

The next section **Description scopes** allows specification of description scopes. This sections consists of the scope table with scope type and value and a edit section to modify a seleted scope entry or to enter e new scope. The scope types **Geographic ares**, **Reference**, **Specimen**, **Observation** and **Taxon name** allow input of a free-form text or reference to the corresponding DiversityWorkbench module or a web service. The connection to to a module or web service is done using the button . After selecting the entry in the referenced database the text will be taken over and the backround colour of the scope value field changes to yellow. A further editing of the text will not be possible (see below).


Taxon name
Accipiter gentilis (Linnaeus, 1758)

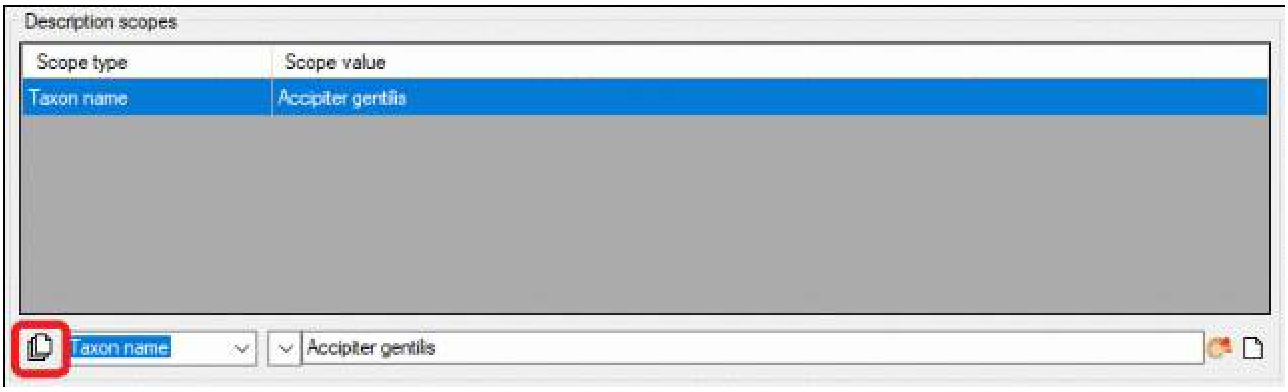
Additionally the edit section now shows the buttons to view the database link and ✕ to remove the database link. In the latter case editing of the scope value will be possible again.

If a scope entry has been selected in the scope table, it can be modified in the edit section. If you want to enter a new scope value instead, press the button at the end of the edit line. The scope entry in the scope table will be deselected and a selection box for the scope type appears in the edit section (see below).



Scope type	Scope value
Taxon name	Accipiter gentilis

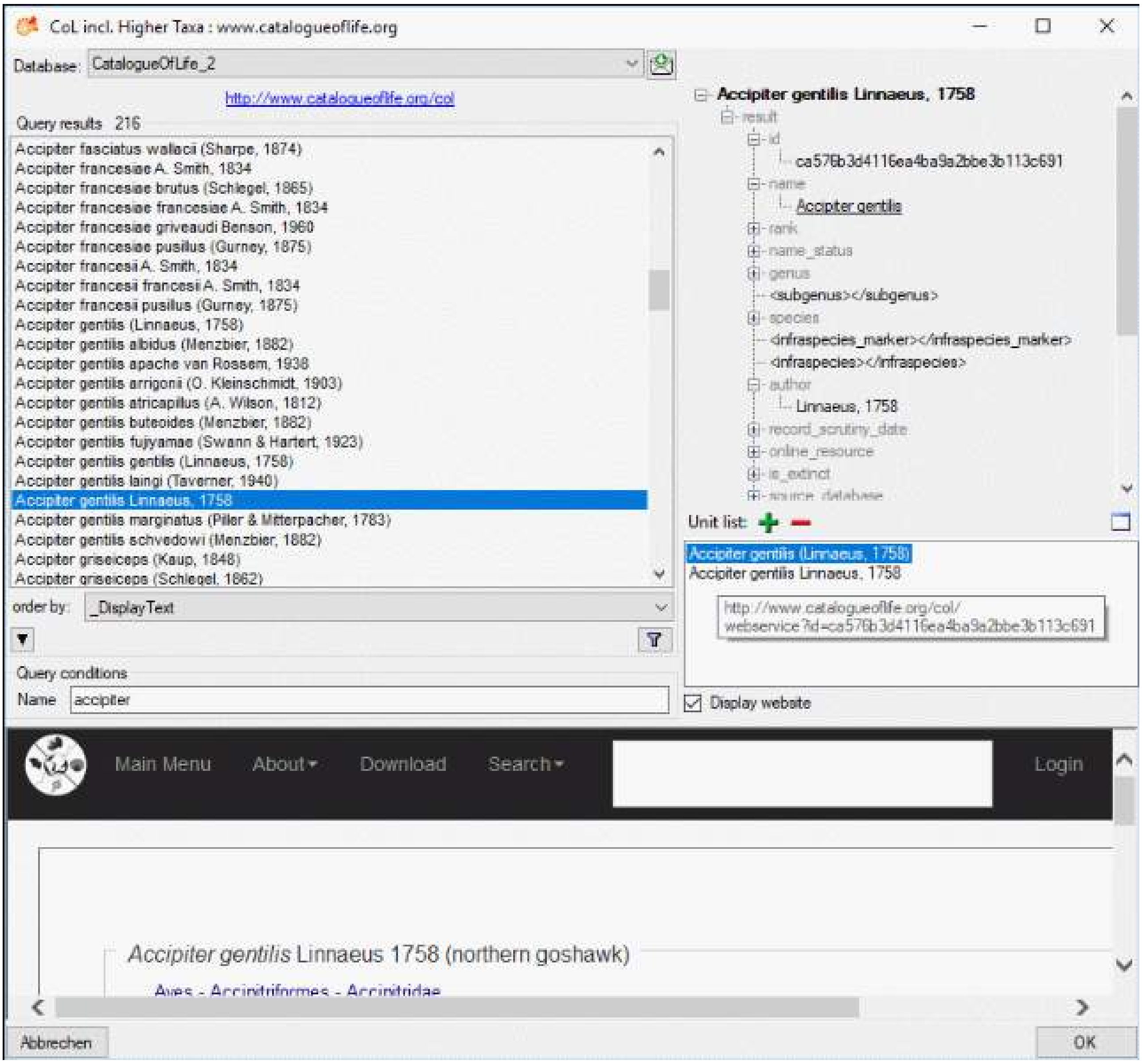
You may insert mutiple scope values with links to a DiversityWorkbench module or a webservice. Therfore enter a new scope value with scope type **Geographic ares**, **Reference** , **Specimen**, **Observation** and **Taxon name** (or select one, which is not yet linked). Besides the scope type dropdown box the button is shown, which allows insert of multiple scopes (see image below).



Scope type	Scope value
Taxon name	Accipiter gentilis

Taxon name
Accipiter gentilis

You may insert mutiple scope values with links to a DiversityWorkbench module or a webservice. Therfore enter a new scope value with scope type **Geographic ares**, **Reference** , **Specimen**, **Observation** and **Taxon name** (or select one, which is not yet linked). Besides the scope type dropdown box the button is shown, which allows insert of multiple scopes (see image below).



Database: CatalogueOfLife_2

Query results 216

Accipiter fasciatus wallacii (Sharpe, 1874)
Accipiter francesiae A. Smith, 1834
Accipiter francesiae brutus (Schlegel, 1865)
Accipiter francesiae francesiae A. Smith, 1834
Accipiter francesiae griveaudi Benson, 1960
Accipiter francesiae pusillus (Gurney, 1875)
Accipiter francesii A. Smith, 1834
Accipiter francesii francesii A. Smith, 1834
Accipiter francesii pusillus (Gurney, 1875)
Accipiter gentilis (Linnaeus, 1758)
Accipiter gentilis albidus (Menzbier, 1882)
Accipiter gentilis apache van Rossem, 1938
Accipiter gentilis arrigonii (O. Kleinschmidt, 1903)
Accipiter gentilis atricapillus (A. Wilson, 1812)
Accipiter gentilis buteoides (Menzbier, 1882)
Accipiter gentilis fujiyamae (Swann & Hartert, 1923)
Accipiter gentilis gentilis (Linnaeus, 1758)
Accipiter gentilis laingi (Taverner, 1940)
Accipiter gentilis Linnaeus, 1758
Accipiter gentilis marginatus (Piller & Mitterpacher, 1783)
Accipiter gentilis schvedowi (Menzbier, 1882)
Accipiter griseiceps (Kaup, 1848)
Accipiter griseiceps (Schlegel, 1862)

order by: _DisplayText

Name: accipiter

Accipiter gentilis Linnaeus, 1758
- result
  - id
    - ca576b3d4116ea4ba9a2bbe3b113c691
  - name
    - Accipiter gentilis
  - rank
  - name_status
  - genus
  - <subgenus></subgenus>
  - species
  - <infraspecies_marker></infraspecies_marker>
  - <infraspecies></infraspecies>
  - author
    - Linnaeus, 1758
  - record_scrutiny_date
  - online_resource
  - is_extinct
  - source_database

Unit list:

Accipiter gentilis (Linnaeus, 1758)
Accipiter gentilis Linnaeus, 1758

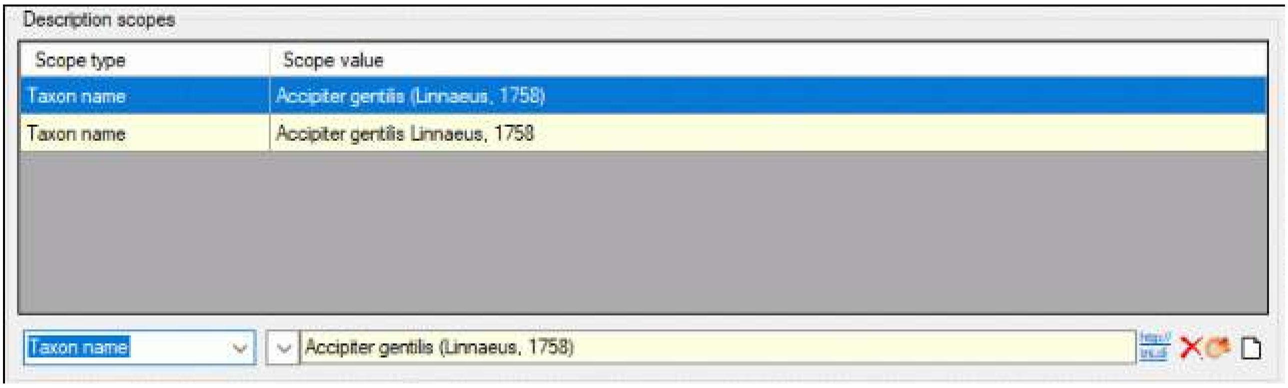
http://www.catalogueoflife.org/col/webservice?id=ca576b3d4116ea4ba9a2bbe3b113c691

☑ Display website

Accipiter gentilis Linnaeus 1758 (northern goshawk)

Aves - Accipitriformes - Accipitridae

In the remote query panel you find the section **Unit list**, where you may add the currently selected query result by clicking the ➕button. When you select an entry in the **Unit list**, you may remove it by clicking ➖or view the data in a separate window by clicking ☐. When you have collected all query results click the **OK** button and the scopes are inserted for the description (see below).

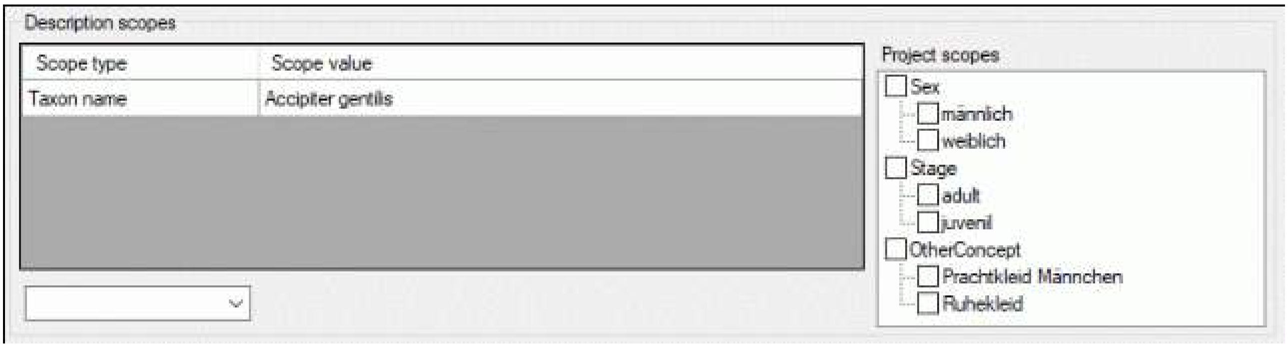


Scope type	Scope value
Taxon name	Accipiter gentilis (Linnaeus, 1758)
Taxon name	Accipiter gentilis Linnaeus, 1758

Taxon name | Accipiter gentilis (Linnaeus, 1758)

Project scopes

Besides the already mentioned scope types that allow input of a free text or reference to a database entry, the scope types **Sex**, **Stage**, **Part** and **Other scope** provide pre-defined scope values. The values can be administrated as described in the "Editing the Project" chapter. For each project a different set of values can be selected as "recommended" values. If for the current description project scope values are defined/assigned, they are shown in the right part of the description scopes as **Project scopes** (see below).



Description scopes

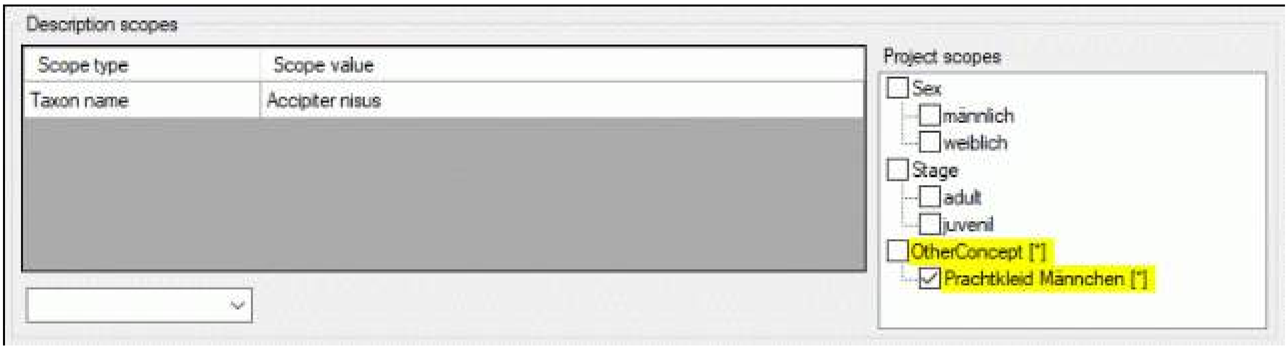
Scope type	Scope value
Taxon name	Accipiter gentilis

Project scopes

- ☐ Sex
  - ☐ männlich
  - ☐ weiblich
- ☐ Stage
  - ☐ adult
  - ☐ juvenil
- ☐ OtherConcept
  - ☐ Prachtkleid Männchen
  - ☐ Ruhekleid

Selecting or deleting of a scope entry can be easily done by selecting clickin on the check box before the scope value. You may select rsp. deselect all scope values of a certain scope type (Sex, State, Part or Other scope) by clicking the check box of the category. If for a scope value a detailled description text has been stored, you may view it as bubble help by moving the mous cursor over the values.

If for a description a scope value is selected, that is not assigned to its project, the value ist show with yellow background (see below). Such a situation can occur, if the scope value has been removed for the project or if a description has been moved to a different project.



Description scopes

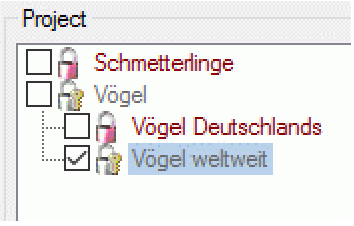
Scope type	Scope value
Taxon name	Accipiter nisus

Project scopes

- ☐ Sex
  - ☐ männlich
  - ☐ weiblich
- ☐ Stage
  - ☐ adult
  - ☐ juvenil
- ☐ OtherConcept [*]
  - ☑ Prachtkleid Männchen [*]

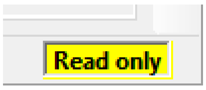
Project

The last section **Project** of the main attributes tab allows selection of the (local) project the description is assigned to. This adjustment has influence of the available values of scope types Sex, Stage and Other scope, the available descriptors and recommended modifier/frequency values and statistical measures of the description. The access rights for a certain user to the projects are contolled by the workbench project associated with the local project (see chapter "Editing the Project") and the login settings (see chapter "Login administration").



Project

☐ Schmetterlinge
☐ Vögel
☐ Vögel Deutschlands
☑ Vögel weltweit

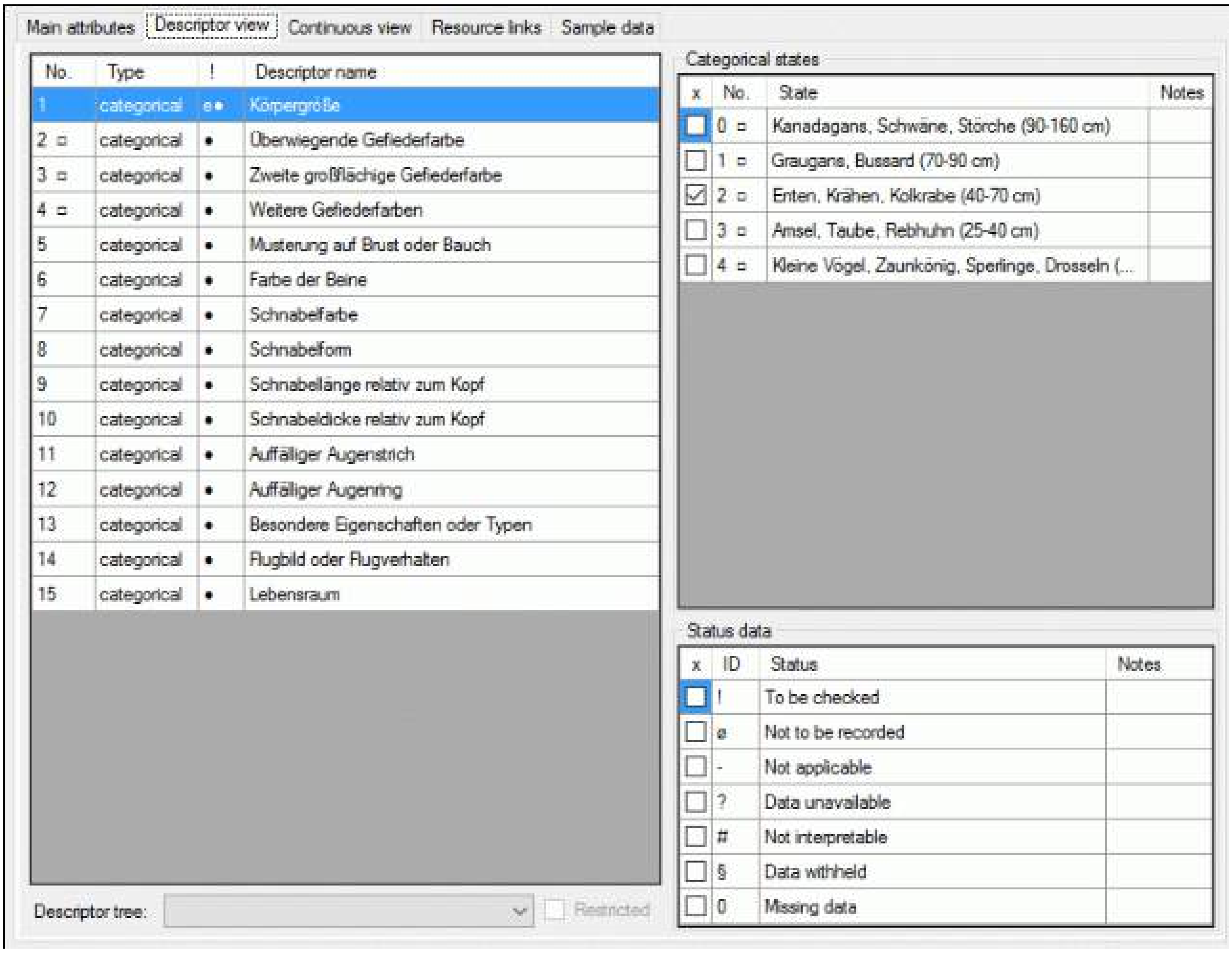


If access to a certain project is restricted to "read only", it is displayed with grey colour and symbol in the **Project** section (see picture above left). A "read only" project cannot be selected for the actual description. If the selected description has already been assigned to a "read only" project by another user with appropriate rights, this is indicated at the right bottom corner of the application window (see above below right).

Continue with:

- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Descriptor view tab



No.	Type	!	Descriptor name
1	categorical	e●	Körpergröße
2 ◻	categorical	•	Überwiegende Gefiederfarbe
3 ◻	categorical	•	Zweite großflächige Gefiederfarbe
4 ◻	categorical	•	Weitere Gefiederfarben
5	categorical	•	Musterung auf Brust oder Bauch
6	categorical	•	Farbe der Beine
7	categorical	•	Schnabelfarbe
8	categorical	•	Schnabelform
9	categorical	•	Schnabellänge relativ zum Kopf
10	categorical	•	Schnabeldicke relativ zum Kopf
11	categorical	•	Auffälliger Augenstrich
12	categorical	•	Auffälliger Augenring
13	categorical	•	Besondere Eigenschaften oder Typen
14	categorical	•	Flugbild oder Flugverhalten
15	categorical	•	Lebensraum

Descriptor tree: ☐ Restricted

Categorical states

x	No.	State	Notes
☐	0 ◻	Kanadagans, Schwäne, Störche (90-160 cm)	
☐	1 ◻	Graugans, Bussard (70-90 cm)	
☑	2 ◻	Enten, Krähen, Kolkrabe (40-70 cm)	
☐	3 ◻	Amsel, Taube, Rebhuhn (25-40 cm)	
☐	4 ◻	Kleine Vögel, Zaunkönig, Sperlinge, Drosseln (...	

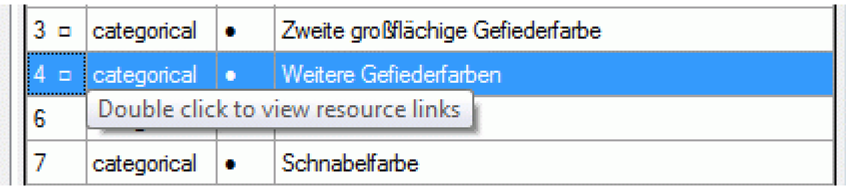
Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

The left part of the descriptor view tab shows all descriptors available for the description's project. The entries in column "!" indicate some additional information about the descriptor:

- Descriptor is referenced in the summary data (•)
- Descriptor is referenced in the status data (○)
- Descriptor is mandatory, values must be specified (!)
- Descriptor is inapplicable because of other specified descriptors/categorical states (x)
- Descriptor is exclusive, only one categorical states shall be selected (e)

If resources are linked to a descriptor, the entry is marked by a square (◻) behind its sequency number and a tool tip appears when the mouse cursor is moved over the "No." column (see below). By double-clicking the sequence number a "Media view" window can be opened to view the resources.

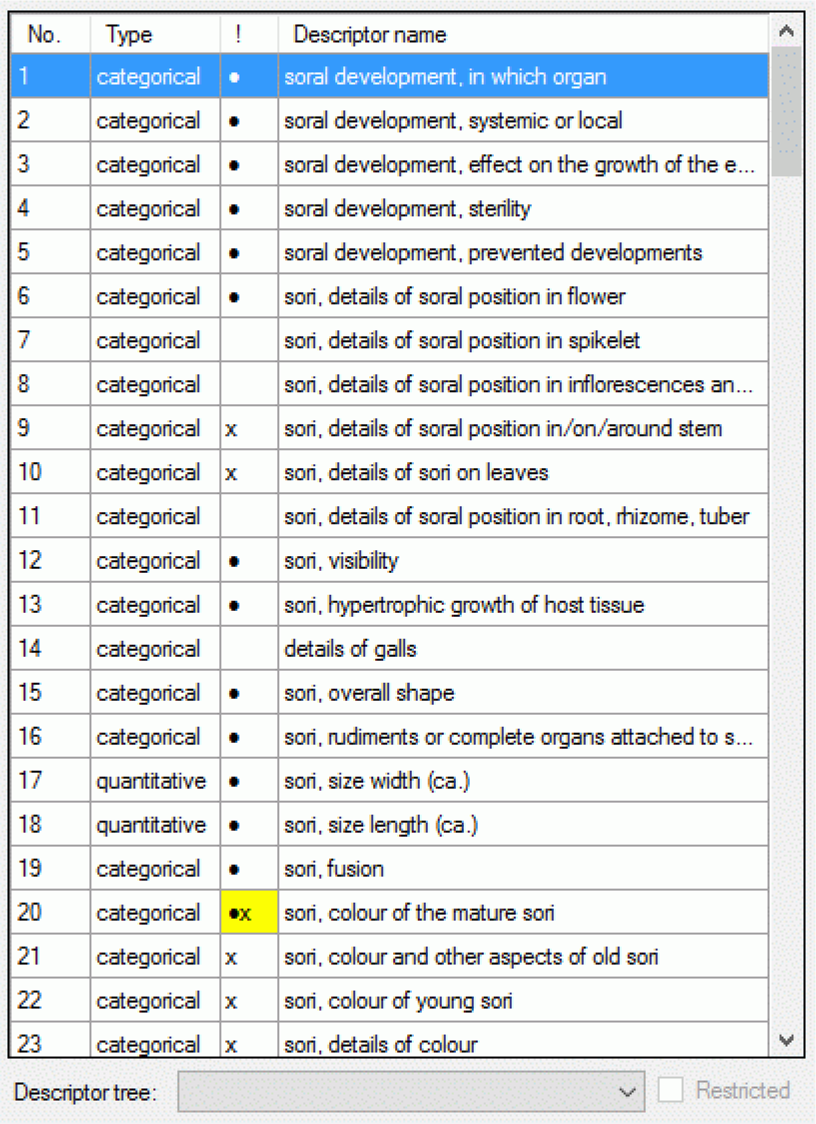


3 ◻	categorical	•	Zweite großflächige Gefiederfarbe
4 ◻	categorical	•	Weitere Gefiederfarben
6			
7	categorical	•	Schnabelfarbe

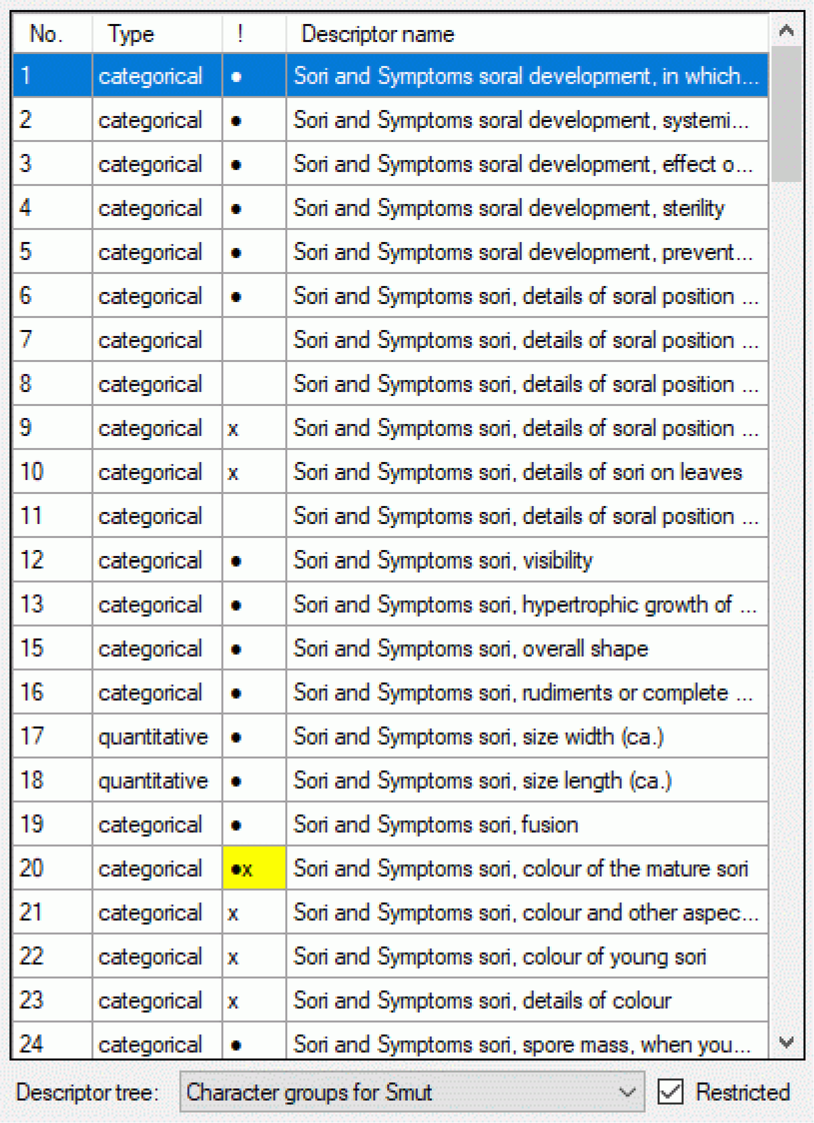
Double click to view resource links

If for the project descriptor trees are defined, the **Descriptor tree:** drop-down list and **Restricted** check box are shown below the descriptor list (see image below left). If a descriptor tree is selected, the names of the descriptor tree node hierarchy is included in the descriptor names (see image below right). This feature is useful, if several descriptors with ambigious names exist the can now be distinguished. E.g. two descriptors "colour", one at descriptor tree node "Leaf", the other at descriptor tree node "Blossom" will become "Leaf colour" and "Blossom colour". If the descriptor name already includes the hierarchy, the duplicate parts will be filtered. In the mentioned example the descriptor names "Leaf colour" and "Blossom colour" will not be changed, if the descriptor tree is selected.

If additionally the **Restricted** option is set, only the descriptors included in the selected descriptor tree are displayed (see image below right, missing descriptor number 14). So you have the option to create several descriptor trees that include only special aspects of the description's property (e.g. morphology, molecular biology and so on) to get a clearly arranged descriptor list.



No.	Type	!	Descriptor name
1	categorical	•	soral development, in which organ
2	categorical	•	soral development, systemic or local
3	categorical	•	soral development, effect on the growth of the e...
4	categorical	•	soral development, sterility
5	categorical	•	soral development, prevented developments
6	categorical	•	sori, details of soral position in flower
7	categorical		sori, details of soral position in spikelet
8	categorical		sori, details of soral position in inflorescences an...
9	categorical	x	sori, details of soral position in/on/around stem
10	categorical	x	sori, details of sori on leaves
11	categorical		sori, details of soral position in root, rhizome, tuber
12	categorical	•	sori, visibility
13	categorical	•	sori, hypertrophic growth of host tissue
14	categorical		details of galls
15	categorical	•	sori, overall shape
16	categorical	•	sori, rudiments or complete organs attached to s...
17	quantitative	•	sori, size width (ca.)
18	quantitative	•	sori, size length (ca.)
19	categorical	•	sori, fusion
20	categorical	•x	sori, colour of the mature sori
21	categorical	x	sori, colour and other aspects of old sori
22	categorical	x	sori, colour of young sori
23	categorical	x	sori, details of colour



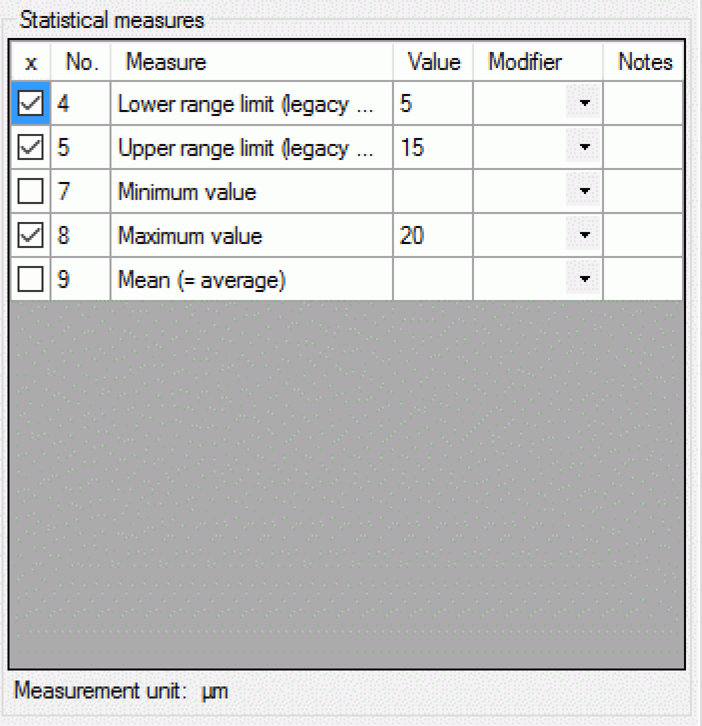
No.	Type	!	Descriptor name
1	categorical	•	Sori and Symptoms soral development, in which...
2	categorical	•	Sori and Symptoms soral development, systemi...
3	categorical	•	Sori and Symptoms soral development, effect o...
4	categorical	•	Sori and Symptoms soral development, sterility
5	categorical	•	Sori and Symptoms soral development, prevent...
6	categorical	•	Sori and Symptoms sori, details of soral position ...
7	categorical		Sori and Symptoms sori, details of soral position ...
8	categorical		Sori and Symptoms sori, details of soral position ...
9	categorical	x	Sori and Symptoms sori, details of soral position ...
10	categorical	x	Sori and Symptoms sori, details of sori on leaves
11	categorical		Sori and Symptoms sori, details of soral position ...
12	categorical	•	Sori and Symptoms sori, visibility
13	categorical	•	Sori and Symptoms sori, hypertrophic growth of ...
15	categorical	•	Sori and Symptoms sori, overall shape
16	categorical	•	Sori and Symptoms sori, rudiments or complete ...
17	quantitative	•	Sori and Symptoms sori, size width (ca.)
18	quantitative	•	Sori and Symptoms sori, size length (ca.)
19	categorical	•	Sori and Symptoms sori, fusion
20	categorical	•x	Sori and Symptoms sori, colour of the mature sori
21	categorical	x	Sori and Symptoms sori, colour and other aspec...
22	categorical	x	Sori and Symptoms sori, colour of young sori
23	categorical	x	Sori and Symptoms sori, details of colour
24	categorical	•	Sori and Symptoms sori, spore mass, when you...

Descriptor tree: Character groups for Smut ☑ Restricted

Editing summary data

The right part of the descriptor view tab shows at the bottom the **Status data** values of the selected descriptor. It is possible to select several values for each descriptor. In the "Notes" column additional information concerning the selected data status may be entered. By a double click on the "Notes" entry a separate edit window can be opened.

Depending on the descriptor type you can find at the top either **Categorical states** (see large picture above), **Statistical measures**, **Descriptive text** or **Molecular sequence** (see pictures below). In the "Notes" columns additional information concerning the specific categorical state rsp. statistical measure may be entered. By a double click on the "Notes" entry a separate edit window can be opened.



Statistical measures

x	No.	Measure	Value	Modifier	Notes
☑	4	Lower range limit (legacy ...	5		
☑	5	Upper range limit (legacy ...	15		
☐	7	Minimum value			
☑	8	Maximum value	20		
☐	9	Mean (= average)			

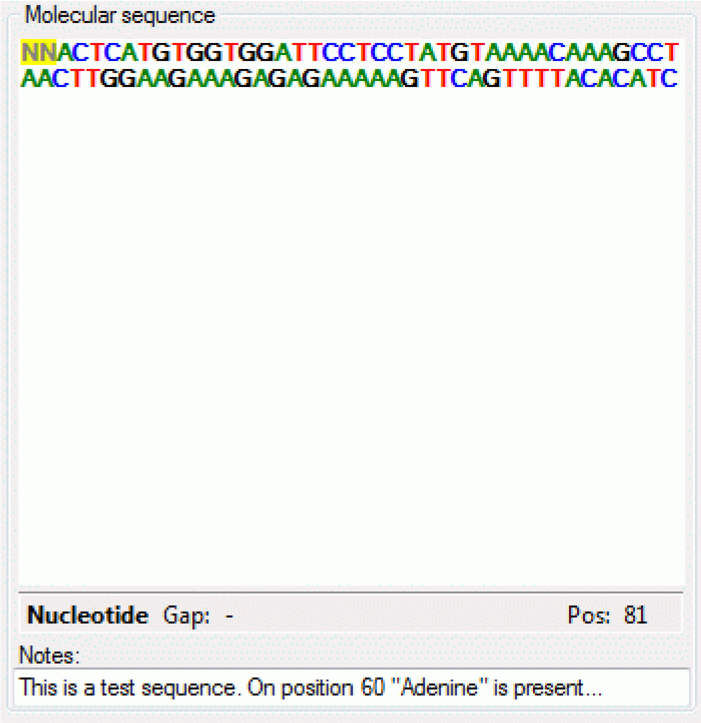
Measurement unit: µm

Descriptive text

Homo sapiens mRNQA for prepro cortistatin like peptide, complete cds

Notes:

Here are notes ...


Molecular sequence

NNACTCATGTGGTGGATTCCTCCTATGTAAAACAAAGCCT
AACTTGGAAGAAAGAGAGAAAAAGTTCAGTTTTACACATC

Nucleotide Gap: - Pos: 81

Notes:

This is a test sequence. On position 60 "Adenine" is present...

To enter a **statistical measure** value click in the "Value" field and enter the value, the check mark in field "x" will be set automatically. If recommended modifier values are defined (see "Editing the Descriptor" and "Editing the Project"), a value may be selected from the drop down list "Modifier". If no modifier values are available, the appropriate table column may be hidden. In the "Notes" field an additional text may be added. By double-clicking the "Notes" field the Extended text editor can be opened.

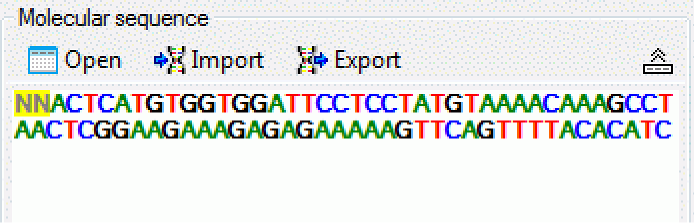
The **descriptive text** may be edited diretly in the window, which shows the pure text without any formatting. In the notes field an additional text may be entered. By double-clicking the text fields the Extended text editor can be opened.

The **molecular sequence** window displays in the status line below the edit area the sequence type ("Nucleotide" or "Protein"), the symbol length ("Len:") in case of proteine sequences, the gap symbol ("Gap:") if defined, the long text of the actual element and the position ("Pos:") (see image below). In case of three-letter proteine symbols the position is the number of the amino acid symbol, not the character position. By pressing the **TAB** key the cursor jumps to the next symbol.

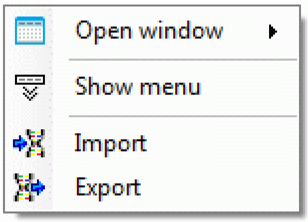

Protein Len: 3 Gap: --- Histidine Pos: 11

When characters are entered in the edit area that are recognized as valid symbols, they will automatically be formatted. One-letter symbols are converted to upper case characters, three-letter symbols are converted according the "Xxx" schema, e.g. "Ala" for "Alanine". The sybols for the nucleotide bases **"Adenine**", "**Cytosine**", **"Guanine"**, "**Thymine**" and **"Uracil**" are dispayed with different colors. Ambiguity symbols and gap symbols are shown in **grey** color. If the ambiguity symbols have not been enabled in the descriptor data, they will be displayed with **yellow** background. Symbols that have not been recognized are displayed with **red** background.

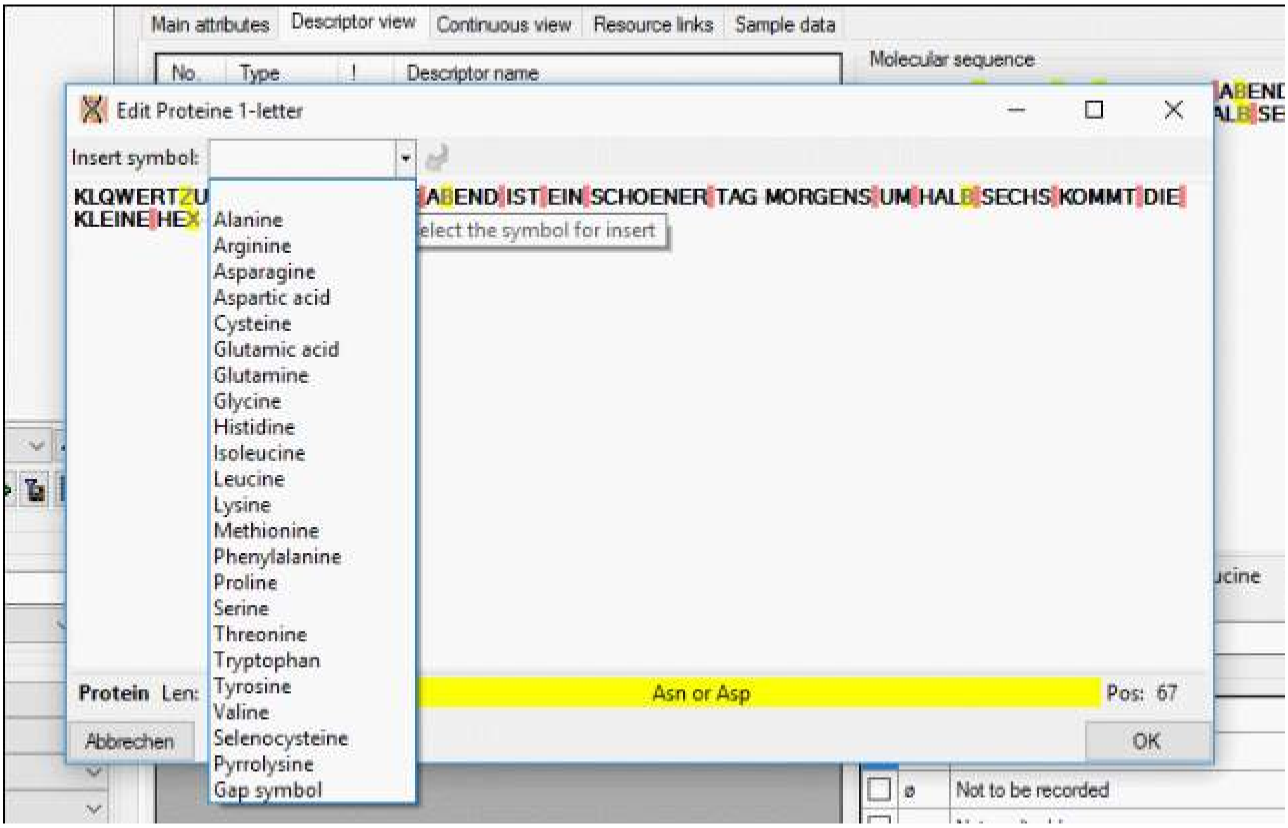
The molecular sequence window offers some additional functions available in the **sequence menu**. It may be opened by moving the mouse cursor over the control header ("Molecular sequence", see window below left) or from the context menu (right-click on the sequence edit area, see windows below right). With menu item **Import** you may read the seqeunce data from a file and insert them to the description. With menu item **Export** you may export the actual sequence data to a file.



NNACTCATGTGGTGGATTCCTCCTATGTAAAACAAAGCCT
AACTCGGAAGAAAGAGAGAAAAAGTTCAGTTTTACACATC



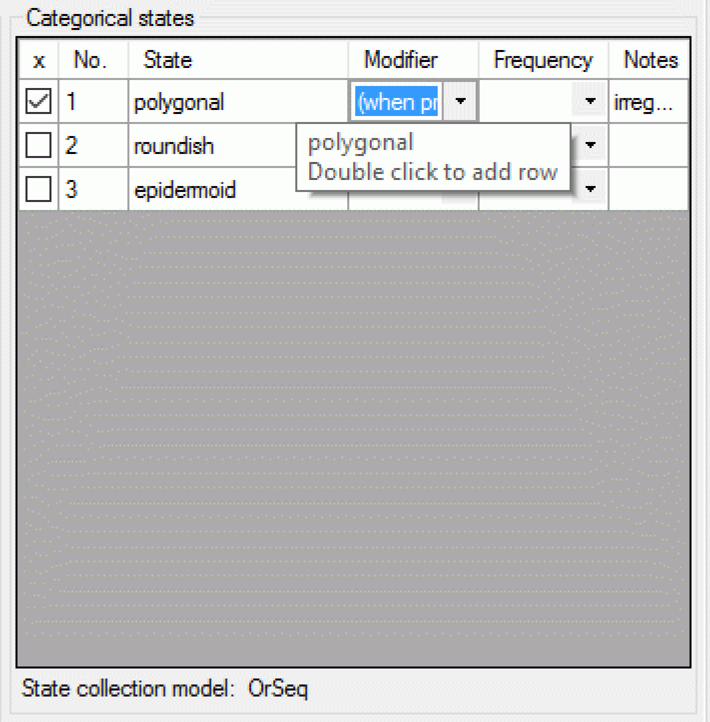
By double-clicking the molecular sequence area or from sequence menu **Open ->** **Sequence** a separate edit window may be opened (see image below). On the top of the window there is the drop-down menu **Insert symbol:** where a value may be selected from a list. After selecting the value press the [ENTER] key or click on to insert the selected symbol at the cursor position.



KLQWERTZU ABEND IST EIN SCHOENER TAG MORGENS UM HALB SECHS KOMMT DIE
KLEINE HEX

To select a **categorical state** set a check mark in field "x" with a mouse click. If recommended modifier or frequency values are defined (see Editing the Descriptor and Editing the Project), values may be selected from the drop down lists "Modifier" rsp. "Frequency". If no modifier or frequency values are available, the appropriate table column may be hidden. In the "Notes" field an additional text may be added. By double-clicking the "Notes" field the Extended text editor can be opened.

If a "Modifier" or "Frequency" value is selected, the multiple specification of a dedicated categorical state is possible. A tool tip offers to add a row by doouble-click, if mouse cursor is moved over the "State" field (left picture below, picture in the midddle after double click). Multiple specifications of one categorical state are only allowed if they have been assigned different modifier and frequency values. Inputs offending these restrictions will be ignored an a cell error will indicate the problem (right picture below).

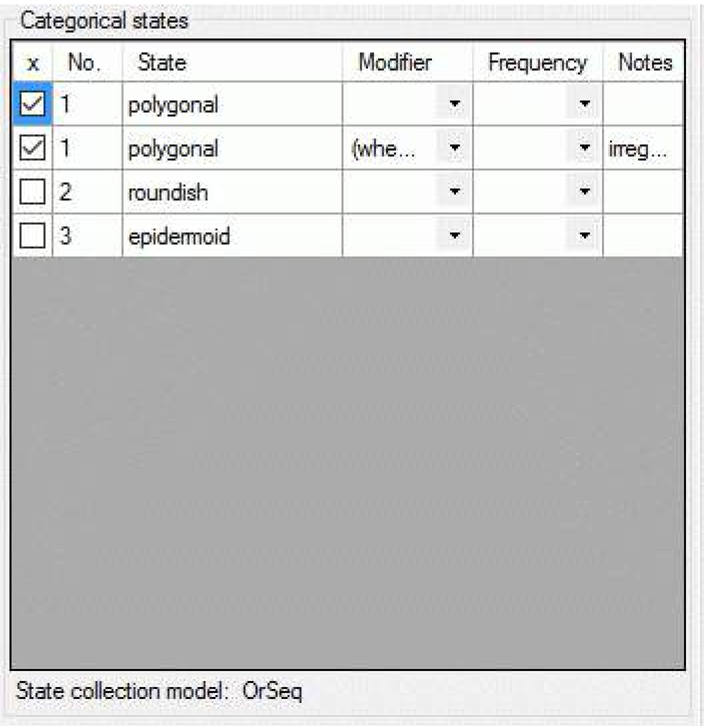


Categorical states

x	No.	State	Modifier	Frequency	Notes
☑	1	polygonal	(when pr		irreg...
☐	2	roundish			
☐	3	epidermoid			

polygonal
Double click to add row

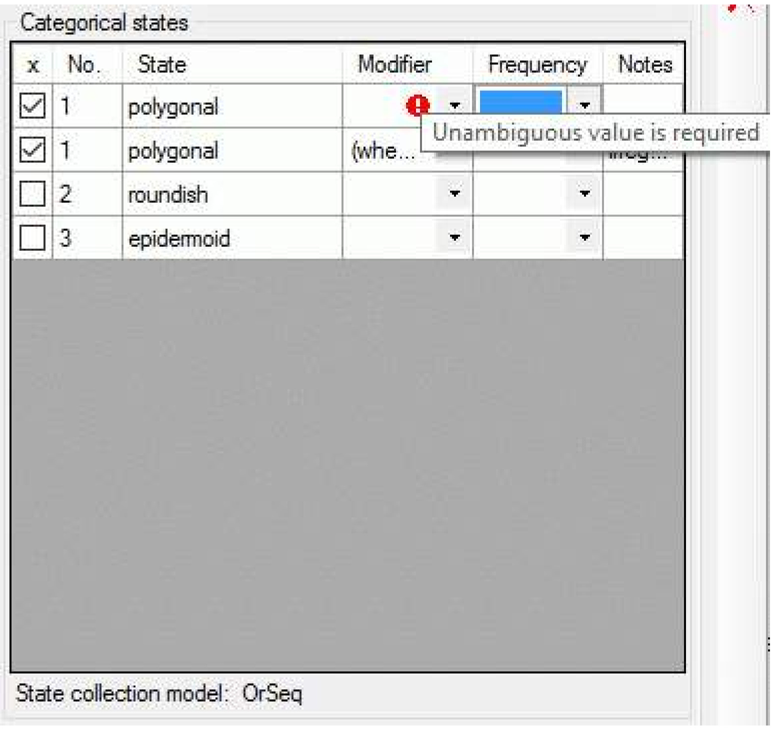
State collection model: OrSeq



Categorical states

x	No.	State	Modifier	Frequency	Notes
☑	1	polygonal			
☑	1	polygonal	(whe...		irreg...
☐	2	roundish			
☐	3	epidermoid			

State collection model: OrSeq



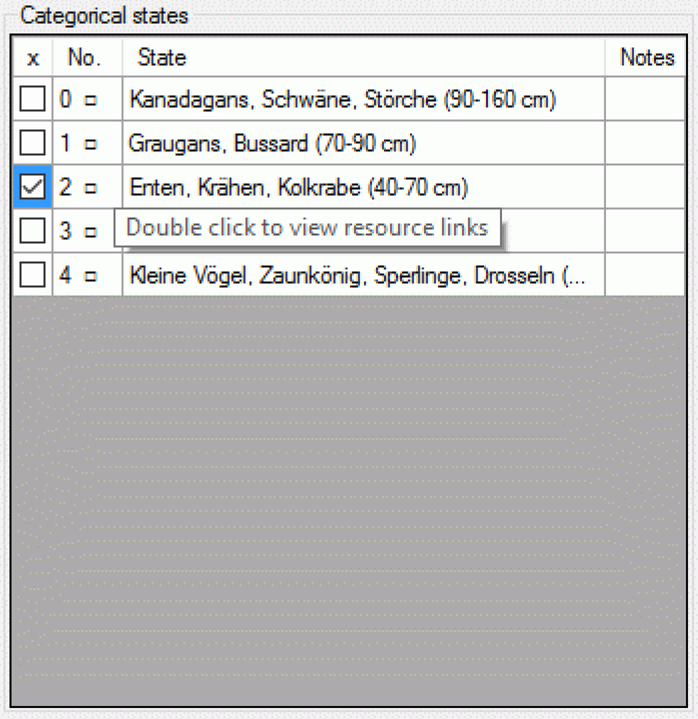
Categorical states

x	No.	State	Modifier	Frequency	Notes
☑	1	polygonal			
☑	1	polygonal	(whe...		irreg...
☐	2	roundish			
☐	3	epidermoid			

Unambiguous value is required

State collection model: OrSeq

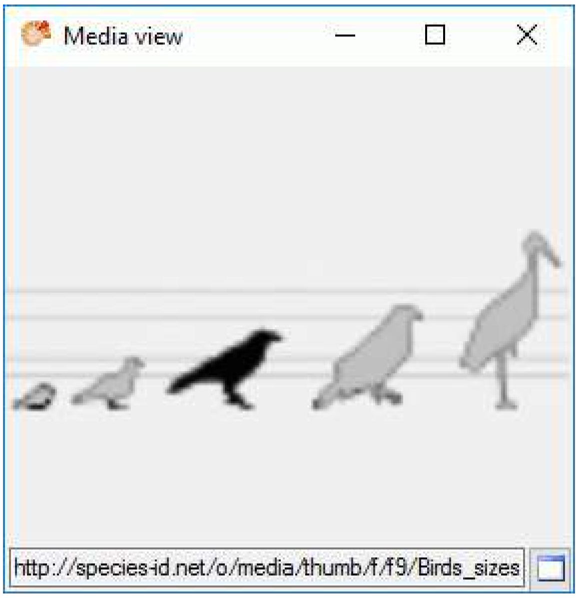
If resources are linked to a categorical state a tool tip appears when the mouse cursor is moved over the ID (left picture below). By double-clicking the ID a "Media view" window can be opened to view the resources (right picture below).



Categorical states

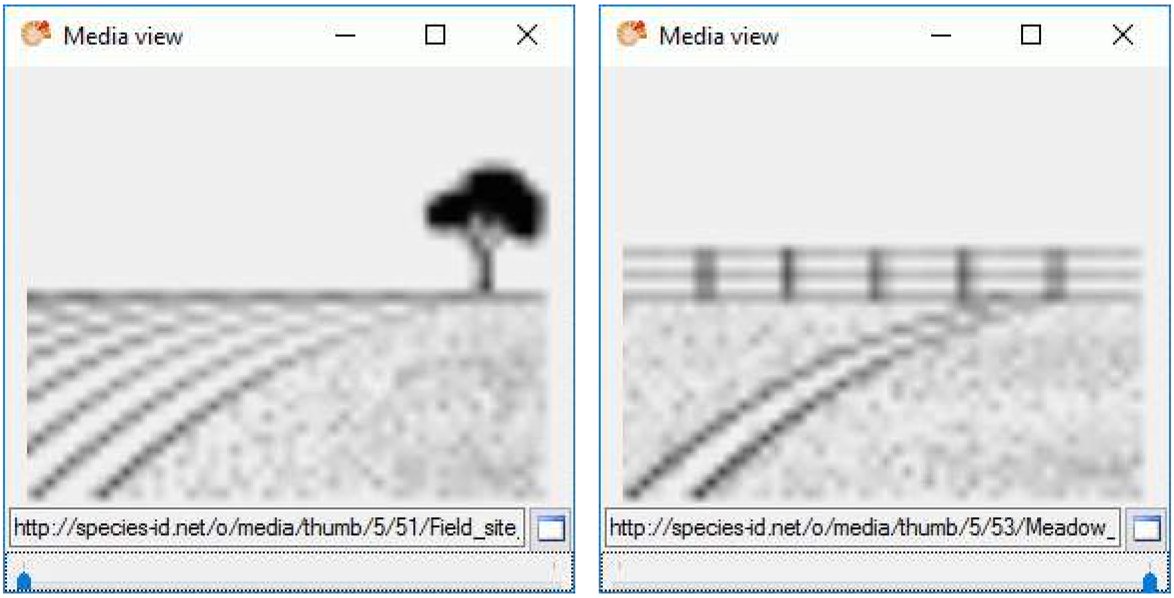
x	No.	State	Notes
☐	0	Kanadagans, Schwäne, Störche (90-160 cm)	
☐	1	Graugans, Bussard (70-90 cm)	
☑	2	Enten, Krähen, Kolkrabe (40-70 cm)	
☐	3		
☐	4	Kleine Vögel, Zaunkönig, Sperlinge, Drosseln (...	

Double click to view resource links



http://species-id.net/o/media/thumb/f/f9/Birds_sizes

If more than one resources have been assigned to one entry, a slider will be visible at the bottom of the "Media view" window. To switch through the available resources the slider can be moved using the mouse or the **right** and **left** arrow keys (see below).



http://species-id.net/o/media/thumb/5/51/Field_site

http://species-id.net/o/media/thumb/5/53/Meadow_

Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Molecular sequence symbols

The editor for sequence data recognizes predefined symbols for nucleotide and protein sequences according the IUPAC definitions.

Nucleic acid symbols

Symbol	Name
A	**A**denine
C	**C**ytosine
G	**G**uanine
T	**T**hymine
U	**U**racile
W	**W**eak (A or T)
S	**S**trong (G or C)
M	a**M**ino (A or C)
K	**K**eto (G or T)
R	pu**R**ine (G or A)
Y	p**Y**rimidine (C or T)
B	not A (**B** comes after A)
D	not C (**D** comes after C)
H	not G (**H** comes after G)
V	not T (**V** comes after T and U)
N	**N**o idea (not a gap)

The symbols with grey background are ambiguity symbols. The difference between "N" and a gap symbol (usually "-", but any other symbol may be defined in the descriptor) is that a gap symbol represents an unspecified number of unknown symbols but "N" stands for exatly one nucleic acid.

Amino acid symbols

Name	1-letter sybmol	3-letter sybmol
Alanine	**A**	**Ala**
Arginine	**R**	**Arg**
Asparagine	**N**	**Asn**
Aspartic acid	**S**	**Asp**
Cysteine	**C**	**Cys**
Glutamic acid	**E**	**Glu**
Glutamine	**Q**	**Gln**
Glycine	**G**	**Gly**
Histidine	**H**	**His**
Isoleucine	**I**	**Ile**

Leucine	**L**	**Leu**
Lysine	**K**	**Lys**
Methionine	**M**	**Met**
Phenylalanine	**F**	**Phe**
Proline	**P**	**Pro**
Serine	**S**	**Ser**
Threonine	**T**	**Thr**
Tryptophan	**W**	**Trp**
Tyrosine	**Y**	**Tyr**
Valine	**V**	**Val**
Selenocysteine	**U**	**Sec**
Pyrrolysine	**O**	**Pyl**
Asparagine or aspartic acid	**B**	**Asx**
Glutamine or glutamic acid	**Z**	**Glx**
Leucine or Isoleucine	**J**	**Xle**
Unspecified or unknown amino acid	**X**	**Xaa**

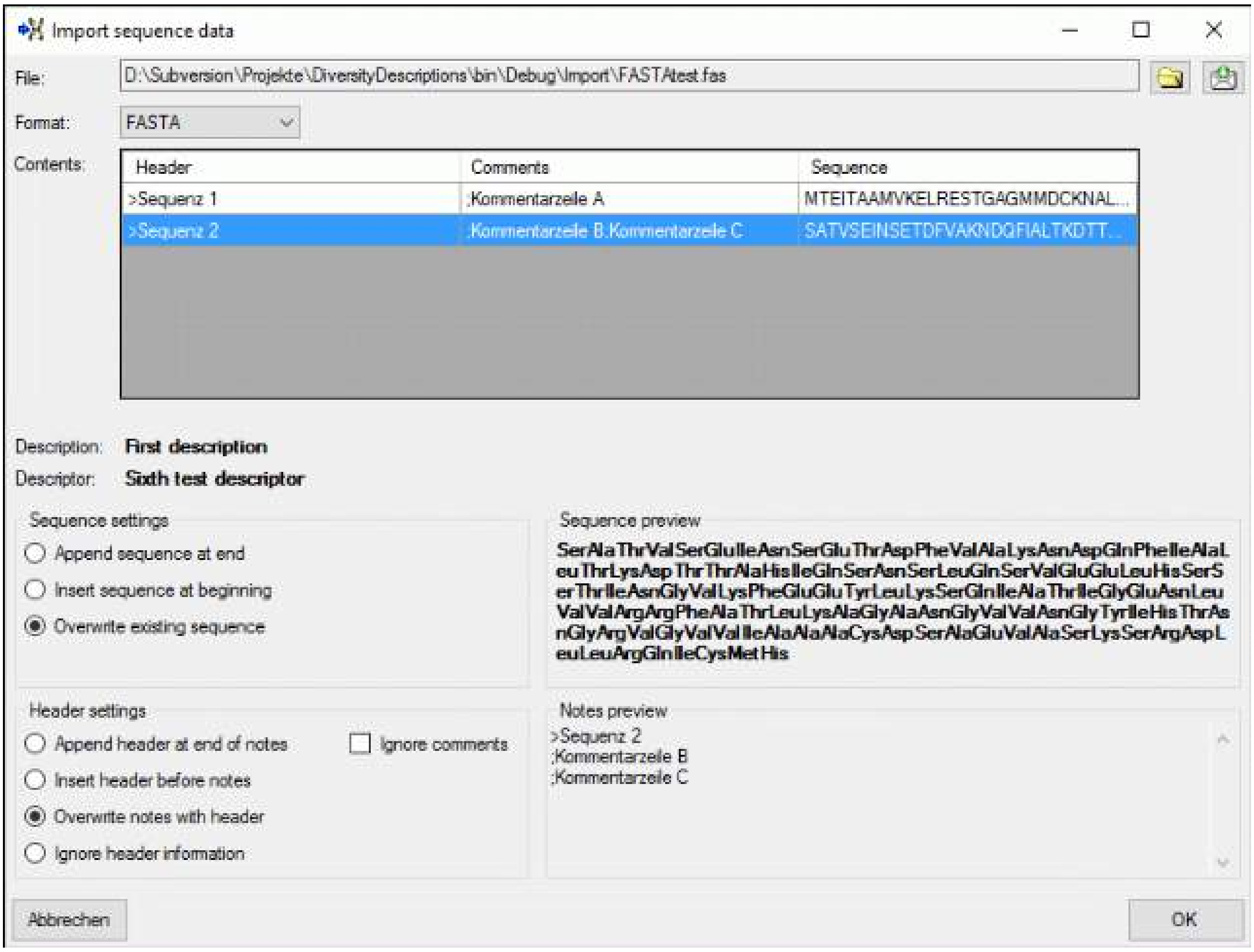
The symbols with grey background are ambiguity symbols. The difference between "X" rsp. "Xaa" and a gap symbol (e.g. "---", but any other symbol may be defined in the descriptor) is that a gap symbol represents an unspecified number of unknown symbols but "X" rsp. "Xaa" stand for exatly one nucleic acid. The amino acids "Selenocysteine" and Pyrrolysine" are non-standard amino acids that only occur in certain species.

Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Import sequence data

With this form you can import sequence data from a file into the database. Choose **Import** from the sequence menu to open the window for the import. **Format** specifies the file format, currently **FASTA** and **FASTQ** are supported. Click on the button to select the file with the data you want to import.



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\FASTAtest.fas

Format: FASTA

Contents:

Header	Comments	Sequence
>Sequenz 1	;Kommentarzeile A	MTEITAAMVKELRESTGAGMMDCKNAL...
>Sequenz 2	;Kommentarzeile B;Kommentarzeile C	SATVSEINSETDFVAKNDQFIALTKDTT...

Description: **First description**

Descriptor: **Sixth test descriptor**

Sequence settings
- ○ Append sequence at end
- ○ Insert sequence at beginning
- ● Overwrite existing sequence

Sequence preview

SerAlaThrValSerGluIleAsnSerGluThrAspPheValAlaLysAsnAspGlnPheIleAlaLeuThrLysAspThrThrAlaHisIleGlnSerAsnSerLeuGlnSerValGluGluLeuHisSerSerThrIleAsnGlyValLysPheGluGluTyrLeuLysSerGlnIleAlaThrIleGlyGluAsnLeuValValArgArgPheAlaThrLeuLysAlaGlyAlaAsnGlyValValAsnGlyTyrIleHisThrAsnGlyArgValGlyValValIleAlaAlaAlaCysAspSerAlaGluValAlaSerLysSerArgAspLeuLeuArgGlnIleCysMetHis

Header settings
- ○ Append header at end of notes
- ○ Insert header before notes
- ● Overwrite notes with header
- ○ Ignore header information

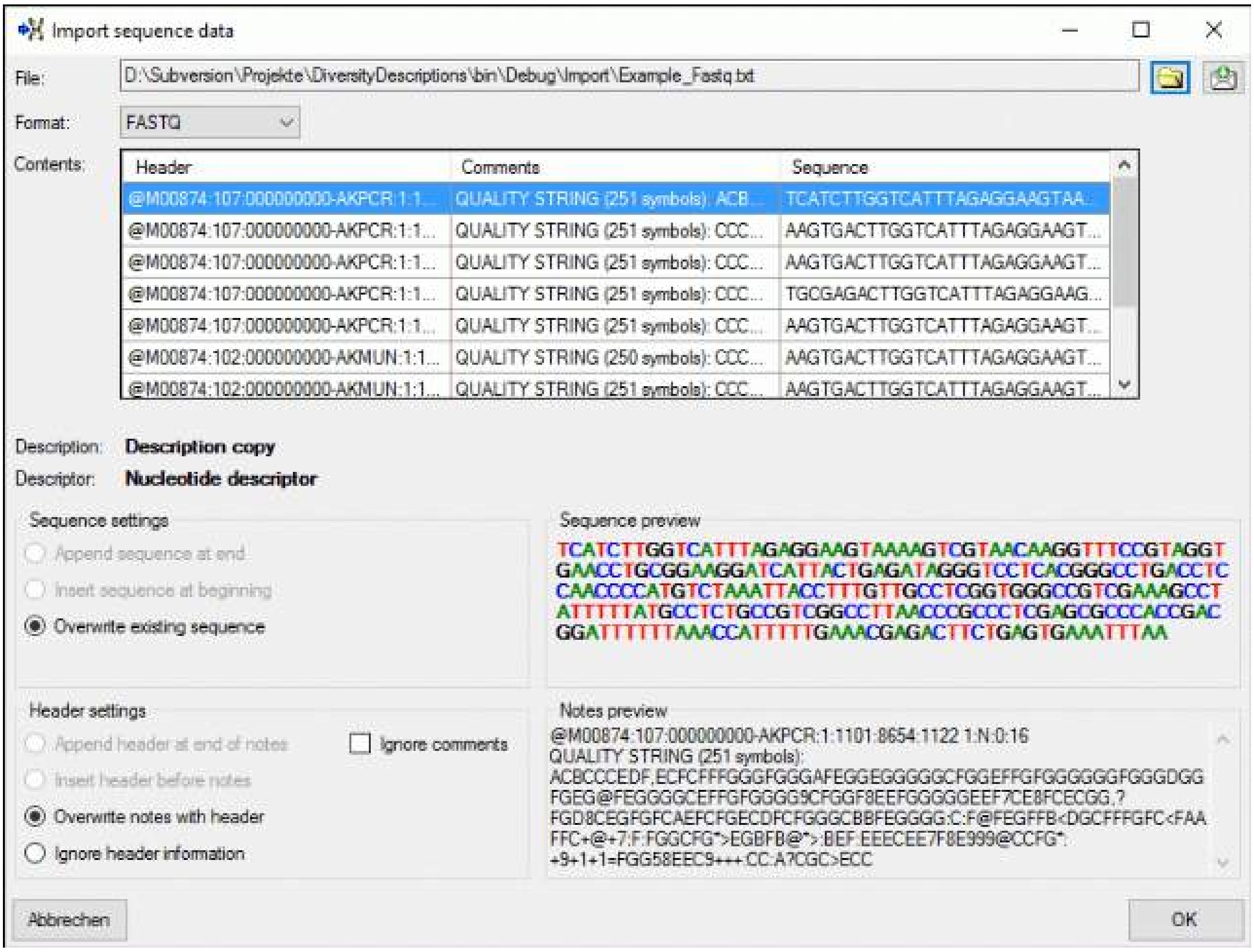
☐ Ignore comments

Notes preview

>Sequenz 2
;Kommentarzeile B
;Kommentarzeile C

The **Contents** of the file will be shown in the upper part of the window. For each seqeunce of the file a separate data row is visible. Select the row you want to import and the selected sequence will be visible in the **Sequence preview** section. Since in FASTA always a one-letter coding is used, the sequence will be converted to the three-letter coding if the descriptor requires this format (see image above). In the **Sequence settings** you may specify if an already existing sequence of the descriptor shall be replaced or if the imported data shall be inserted before or after the sequence. The **Header settings** determine the handling of the FASTA header and comment lines. You have the choice to replace the notes by the header and command lines, to insert them at the beginning or the end or ignore them. If option **Ignore comments** is checked, only the header line will be inserted into the notes. In the **Notes preview** section you can see the resulting notes.

The **FASTQ** format contains a quality string, which specifies each symbol's reliablility. Unless you select one of the **Ignore** options of the **Header settings** section the quality string is inserted int the notes. There the title "QUALITY STRING" marks the start of the quality string to allow a later data export to FASTQ (see image below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Example_Fastq.txt

Format: FASTQ

Contents:

Header	Comments	Sequence
@M00874:107:000000000-AKPCR:1:1...	QUALITY STRING (251 symbols): ACB...	TCATCTTGGTCATTTAGAGGAAGTAA...
@M00874:107:000000000-AKPCR:1:1...	QUALITY STRING (251 symbols): CCC...	AAGTGACTTGGTCATTTAGAGGAAGT...
@M00874:107:000000000-AKPCR:1:1...	QUALITY STRING (251 symbols): CCC...	AAGTGACTTGGTCATTTAGAGGAAGT...
@M00874:107:000000000-AKPCR:1:1...	QUALITY STRING (251 symbols): CCC...	TGCGAGACTTGGTCATTTAGAGGAAG...
@M00874:107:000000000-AKPCR:1:1...	QUALITY STRING (251 symbols): CCC...	AAGTGACTTGGTCATTTAGAGGAAGT...
@M00874:102:000000000-AKMUN:1:1...	QUALITY STRING (250 symbols): CCC...	AAGTGACTTGGTCATTTAGAGGAAGT...
@M00874:102:000000000-AKMUN:1:1...	QUALITY STRING (251 symbols): CCC...	AAGTGACTTGGTCATTTAGAGGAAGT...

Description: **Description copy**

Descriptor: **Nucleotide descriptor**

Sequence settings
- ○ Append sequence at end
- ○ Insert sequence at beginning
- ● Overwrite existing sequence

Sequence preview

```
TCATCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGT
GAACCTGCGGAAGGATCATTACTGAGATAGGGTCCTCACGGGCCTGACCTC
CAACCCCATGTCTAAATTACCTTTGTTGCCTCGGTGGGCCGTCGAAAGCCT
ATTTTTATGCCTCTGCCGTCGGCCTTAACCCGCCCTCGAGCGCCCACCGAC
GGATTTTTTAAACCATTTTTGAAACGAGACTTCTGAGTGAAATTTAA
```

Header settings
- ○ Append header at end of notes
- ○ Insert header before notes
- ● Overwrite notes with header
- ○ Ignore header information
- ☐ Ignore comments

Notes preview

```
@M00874:107:000000000-AKPCR:1:1101:8654:1122 1:N:0:16
QUALITY STRING (251 symbols):
ACBCCCEDF,ECFCFFFGGGFGGGAFEGGEGGGGGCFGGEFFGFGGGGGGFGGGDGG
FGEG@FEGGGGCEFFGFGGGG9CFGGF8EEFGGGGGEEF7CE8FCECGG,?
FGD8CEGFGFCAEFCFGECDFCFGGGCBBFEGGGG:C:F@FEGFFB<DGCFFFGFC<FAA
FFC+@+7:F:FGGCFG*>EGBFB@*>:BEF:EEECEE7F8E999@CCFG*:
+9+1+1=FGG58EEC9+++CC:A?CGC>ECC
```

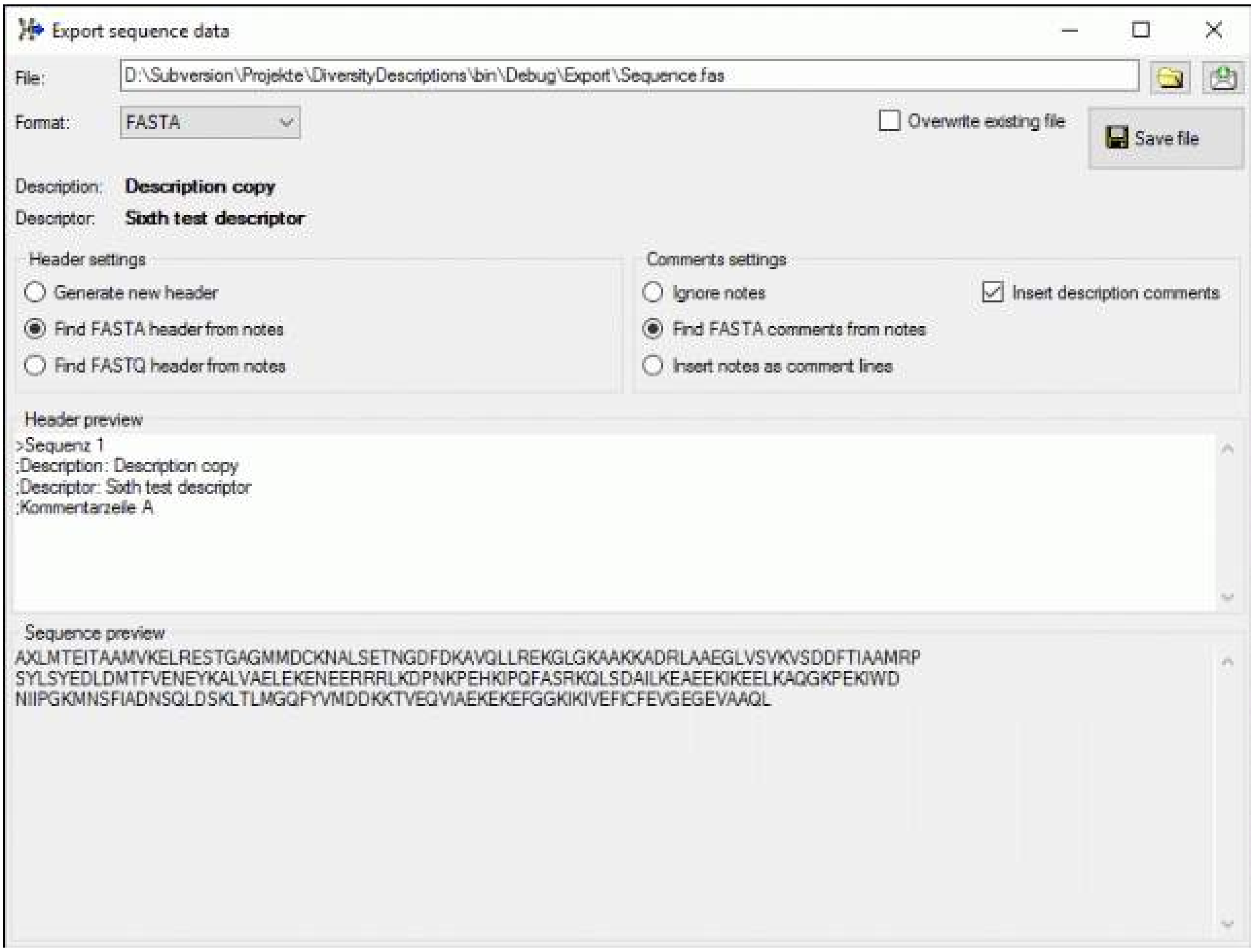
Finally click button **OK** to perform the import of **Cancel** to abort.

Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Export sequence data

With this form you can export data from the database to a file. Choose **Export** from the sequence menu to open the window for the export. **Format** specifies the file format, currently **FASTA** and **FASTQ** are supported.



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\Sequence.fas

Format: FASTA

☐ Overwrite existing file

Description: **Description copy**

Descriptor: **Sixth test descriptor**

Header settings
- ○ Generate new header
- ● Find FASTA header from notes
- ○ Find FASTQ header from notes

Comments settings
- ○ Ignore notes
- ● Find FASTA comments from notes
- ○ Insert notes as comment lines
- ☑ Insert description comments

Header preview

```
>Sequenz 1
;Description: Description copy
;Descriptor: Sixth test descriptor
;Kommentarzeile A
```

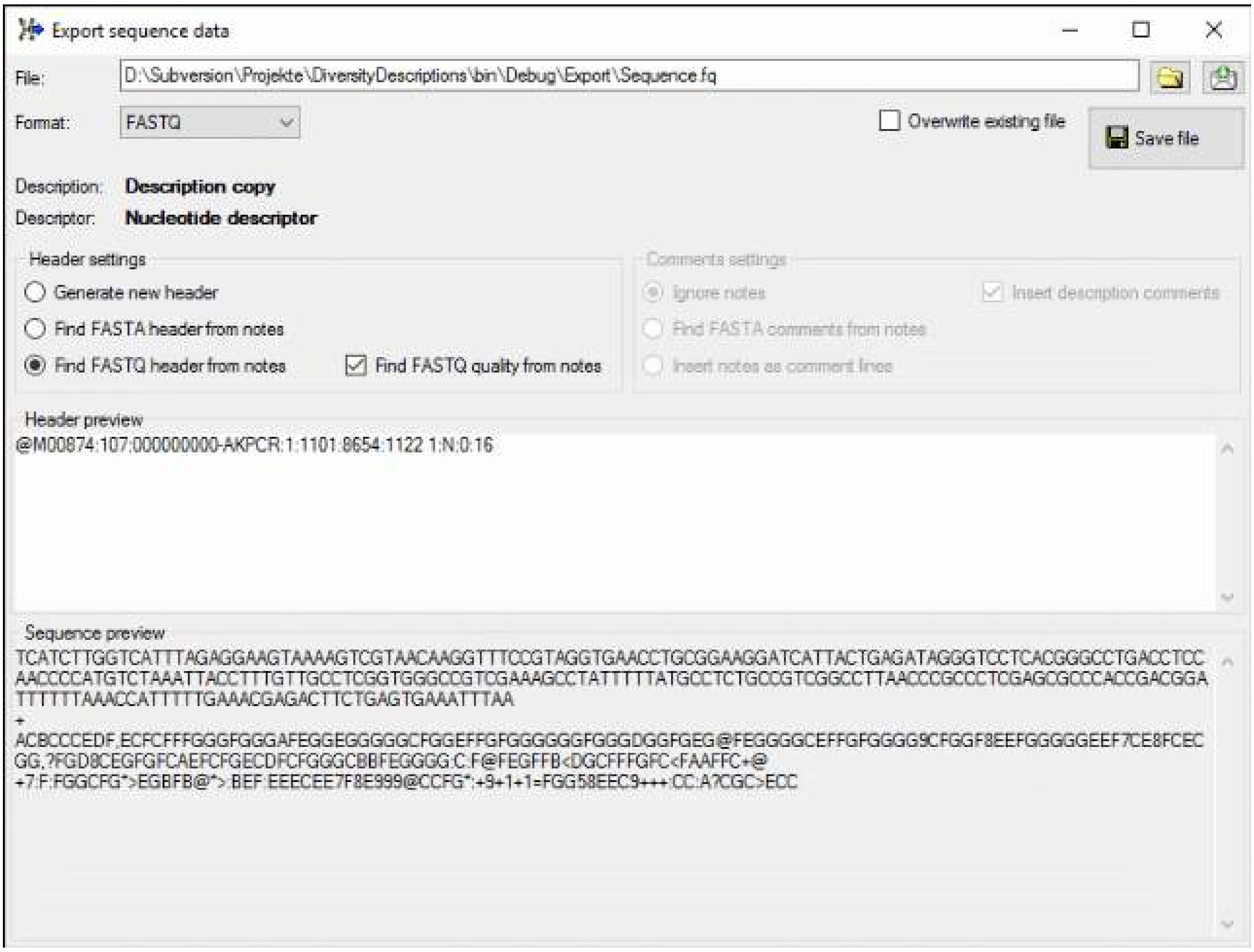
Sequence preview

```
AXLMTEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEGLVSVKVSDDFTIAAMRP
SYLSYEDLDMTFVENEYKALVAELEKENEERRRLKDPNKPEHKIPQFASRKQLSDAILKEAEEKIKEELKAQGKPEKIWD
NIIPGKMNSFIADNSQLDSKLTLMGQFYVMDDKKTVEQVIAEKEKEFGGKIKIVEFICFEVGEGEVAAQL
```

In the **Header settings** you may specify if a new header shall be generated or if the notes shall be searched for a FASTA rsp. FASTQ header. In case of **FASTA** export you may specify in the **Comments settings** section if FASTA comment lines from the notes (starting with ";") shall be inserted after the header, the whole notes shall be inserted as FASTA comments or if the notes shall be ignored. If **Insert description comments** is checked, two comment linsed wit the description and descriptor title will be generated.

In the **Header preview** section you may check and edit the resulting header, in the **Sequence preview** section the converted sequence in one-letter notation is displayed.

In case of **FASTQ** export the Comments settings are irrelevant. If the notes include a QUALITY STRING sections, it is inserted in the FASTQ output (see image below). If no quality string can be found or the **Find FASTQ quality from notes** has been unchecked, the lowest quaality value "!" is inserted.



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\Sequence.fq

Format: FASTQ

☐ Overwrite existing file

Description: **Description copy**

Descriptor: **Nucleotide descriptor**

Header settings
- ○ Generate new header
- ○ Find FASTA header from notes
- ● Find FASTQ header from notes
- ☑ Find FASTQ quality from notes

Comments settings
- ● Ignore notes
- ○ Find FASTA comments from notes
- ○ Insert notes as comment lines
- ☑ Insert description comments

Header preview

```
@M00874:107:000000000-AKPCR:1:1101:8654:1122 1:N:0:16
```

Sequence preview

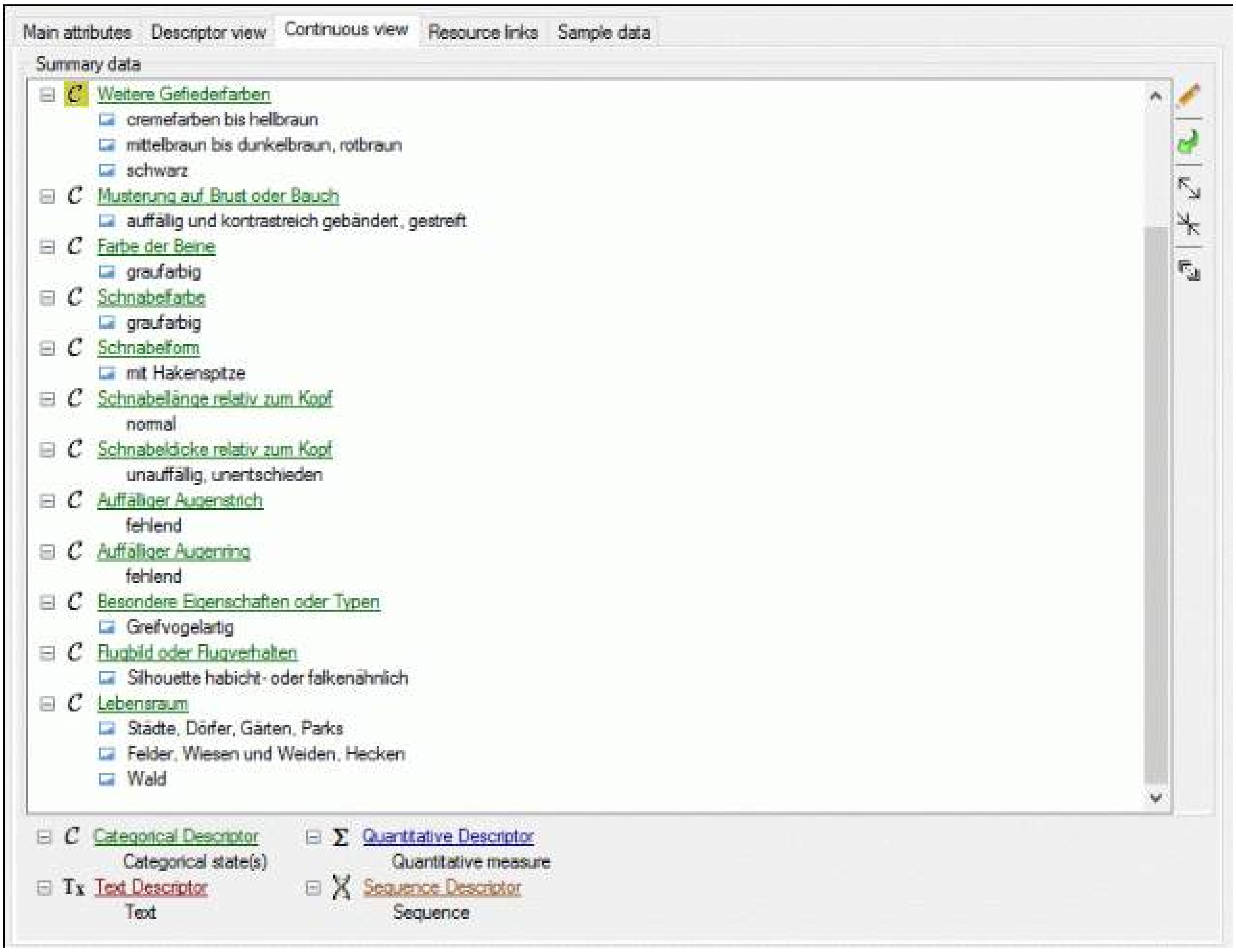
```
TCATCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGAGATAGGGTCCTCACGGGCCTGACCTCC
AACCCCATGTCTAAATTACCTTTGTTGCCTCGGTGGGCCGTCGAAAGCCTATTTTTATGCCTCTGCCGTCGGCCTTAACCCGCCCTCGAGCGCCCACCGACGGA
TTTTTTAAACCATTTTTGAAACGAGACTTCTGAGTGAAATTTAA
+
ACBCCCEDF,ECFCFFFGGGFGGGAFEGGEGGGGGCFGGEFFGFGGGGGGFGGGDGGFGEG@FEGGGGCEFFGFGGGG9CFGGF8EEFGGGGGEEF7CE8FCEC
GG,?FGD8CEGFGFCAEFCFGECDFCFGGGCBBFEGGGG:C:F@FEGFFB<DGCFFFGFC<FAAFFC+@
+7:F:FGGCFG*>EGBFB@*>:BEF:EEECEE7F8E999@CCFG*:+9+1+1=FGG58EEC9+++:CC:A?CGC>ECC
```

Click on the button to select the file where the data shall be exported. By default the data are appended at the end of the selected file, check the **Overwrite existing file** option to overwrite it. Finally click the **Save file** button to write the data.

Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Continuous view tab



C Weitere Gefiederfarben
- cremefarben bis hellbraun
- mittelbraun bis dunkelbraun, rotbraun
- schwarz

C Musterung auf Brust oder Bauch
- auffällig und kontrastreich gebändert, gestreift

C Farbe der Beine
- graufarbig

C Schnabelfarbe
- graufarbig

C Schnabelform
- mit Hakenspitze

C Schnabellänge relativ zum Kopf
- normal

C Schnabeldicke relativ zum Kopf
- unauffällig, unentschieden

C Auffälliger Augenstrich
- fehlend

C Auffälliger Augenring
- fehlend

C Besondere Eigenschaften oder Typen
- Greifvogelartig

C Flugbild oder Flugverhalten
- Silhouette habicht- oder falkenähnlich

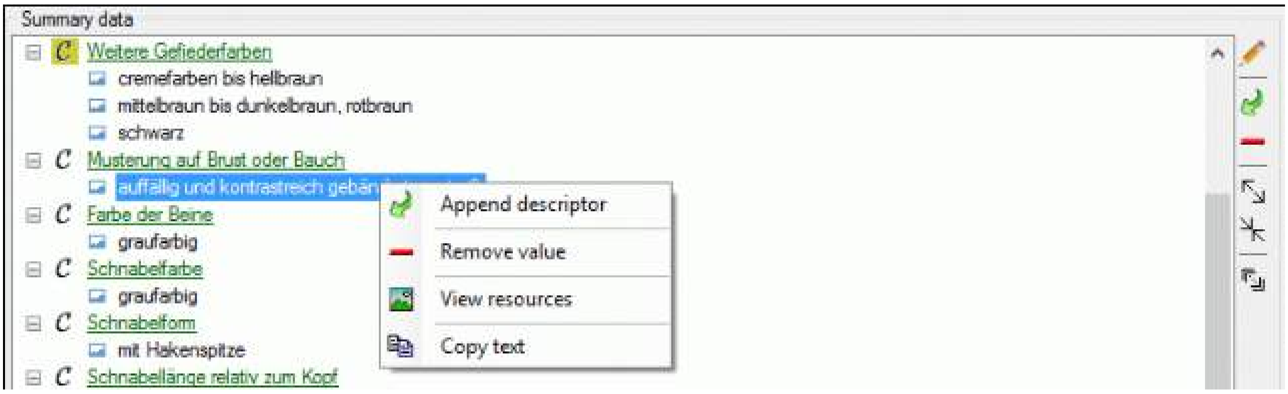
C Lebensraum
- Städte, Dörfer, Gärten, Parks
- Felder, Wiesen und Weiden, Hecken
- Wald

C Categorical Descriptor — Categorical state(s)
Σ Quantitative Descriptor — Quantitative measure
Tx Text Descriptor — Text
Sequence Descriptor — Sequence

The continuous view tab provides an alternate view on the descriptive data. In the **Summary data** only the descriptors are included where data have been entered. At the right side there is a tool strip. The displayed buttons will change depending on the selected entry. The descriptor types C **categorical**, Σ **quantitive**, Tx **text** and **sequence** are indicated by different colours and icons as shown in the example at the bottom. By pressing the button on the tool strip this example may be hidden. Descriptors that are marked as mandatory are displayed with **light red** text, descriptors that are inapplicable are **greyed out**. Additionally coloured background indicated possible problems, e.g. if an **inapplicability rule** has been ignored or a **not allowed descriptor** has been used. A tool tip text shows the error or warning reason when the mouse curser is moved over the element.

By pressing the button the tree view may be expanded to display the contained categorical states, quantitative measures or texts. By pressing the button the tree will be collapsed to descriptor level.

To insert a descriptor press , to delete a descriptor select the entry and press ✕. If only a single value shall be removed, select the entry and use the button. All these functions can alternatively be accessed by the context menu by a right-click on the tree node.



Summary data

Weitere Gefiederfarben
- cremefarben bis hellbraun
- mittelbraun bis dunkelbraun, rotbraun
- schwarz

Musterung auf Brust oder Bauch
- auffällig und kontrastreich gebän

Farbe der Beine
- graufarbig

Schnabelfarbe
- graufarbig

Schnabelform
- mit Hakenspitze

Schnabellänge relativ zum Kopf

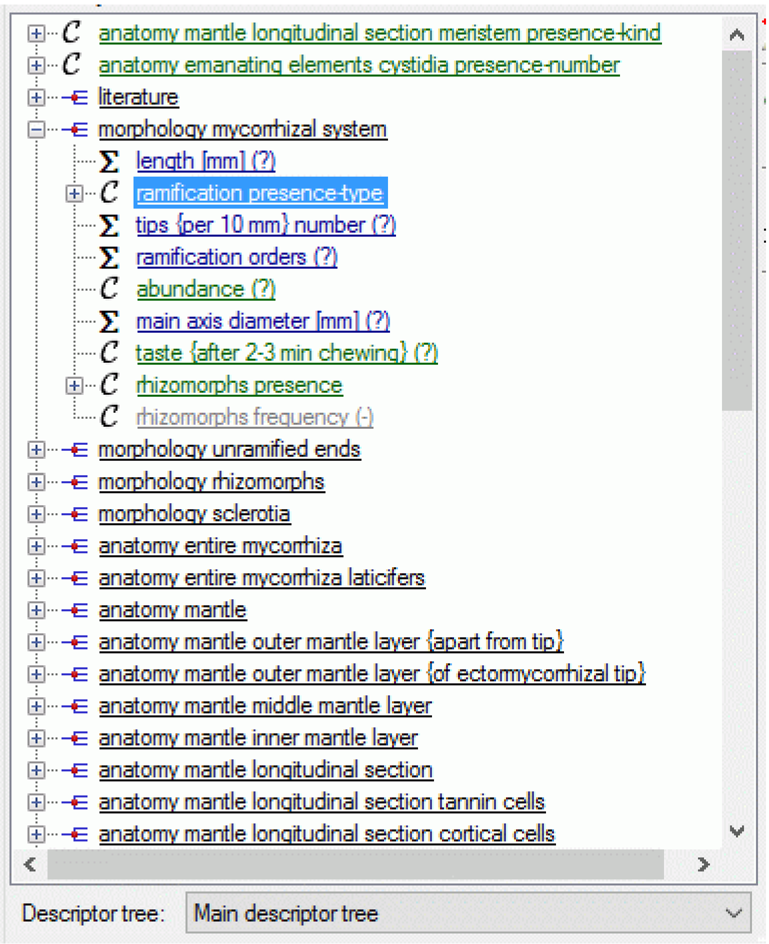
If for a descriptor resources, e.g. pictures, are avaialble, this is indicated by the background color of the descriptor icon. Categorical states with resources are marked with icon 🖼 (see first entries in picture above). The resources may be accessed by a right-click on the tree node and selecting context menu item 🖼 **View resources** (see picture above).

Structured descriptor view

If for the project a structured descriptor tree is defined, i.e. a descriptor tree that contains at least one descriptor tree node, the **Descriptor tree:** drop-down list is shown below the descriptor tree (see image below left). If a descriptor tree is selected, the descriptor tree node hierarchy will be included in the output and the descriptors will be arranged accordingly. The names of the descriptor tree nodes and the descriptors will be reduced by parts contained in the supriour hierarchy nodes (see image below right).

literature references
morphology mycorrhizal system length [mm] (?)
morphology mycorrhizal system ramification presence-type
morphology mycorrhizal system tips {per 10 mm} number (?)
morphology mycorrhizal system ramification orders (?)
morphology mycorrhizal system abundance (?)
morphology mycorrhizal system main axis diameter [mm] (?)
morphology mycorrhizal system taste {after 2-3 min chewing} (?)
morphology mycorrhizal system rhizomorphs presence
morphology mycorrhizal system rhizomorphs frequency (-)
morphology unramified ends mantle hydrophobicity presence (?)
morphology unramified ends shape (?)
morphology unramified ends shape {of distal end} (?)
morphology unramified ends length [mm] (?)
morphology unramified ends diameter [mm] (?)
morphology unramified ends colour
morphology unramified ends very tip colour (?)
morphology unramified ends older parts colour (?)
morphology unramified ends mantle cortical cells visibility (?)
morphology unramified ends mantle {distinct} surface visibility
morphology unramified ends mantle transparency (?)
morphology unramified ends mantle laticifers visibility
morphology unramified ends mantle secreted latex {after scratchin
morphology unramified ends mantle secreted latex {after scratchin
morphology unramified ends mantle dots presence-colour (?)
morphology unramified ends mantle carbonizing presence

Descriptor tree:



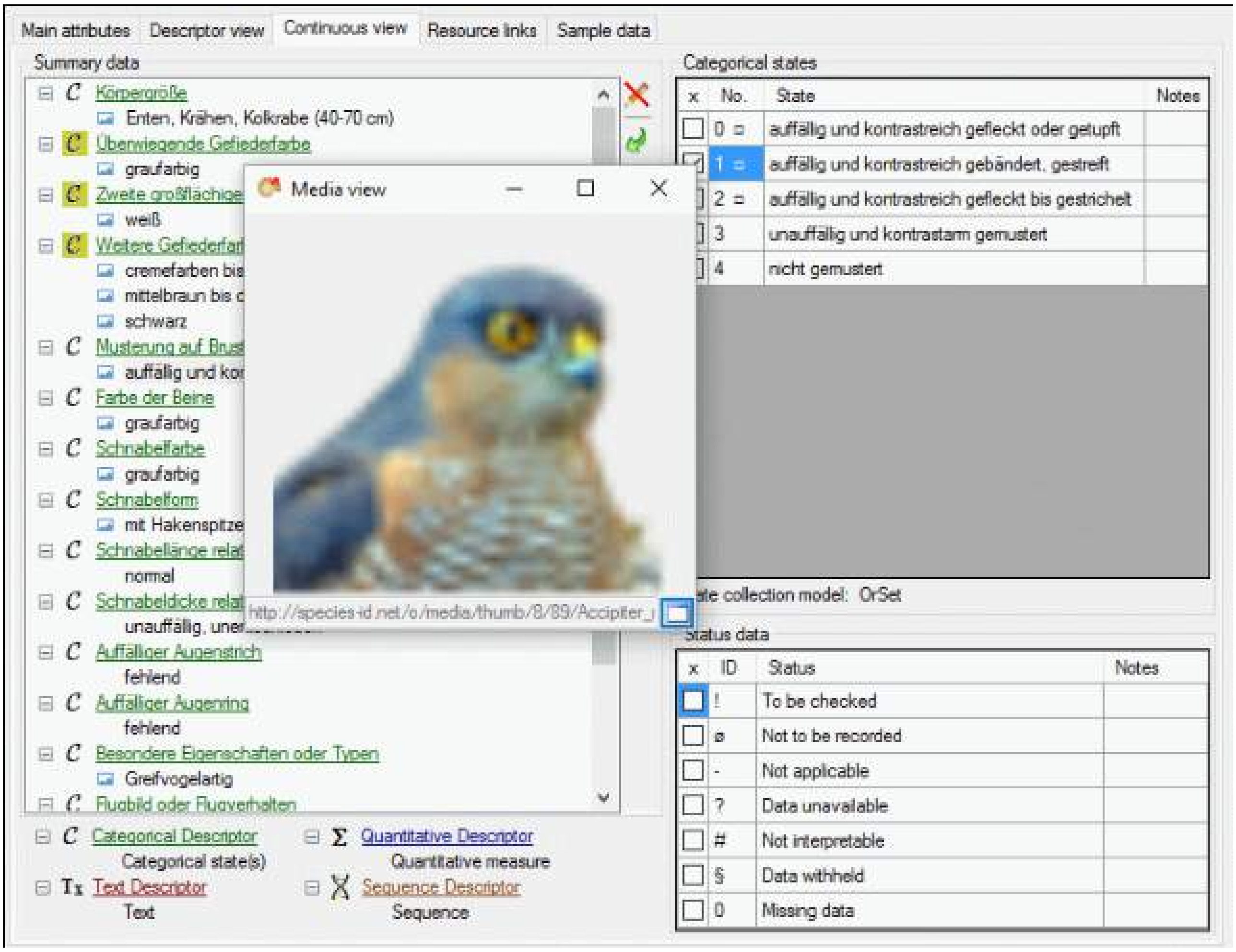
anatomy mantle longitudinal section meristem presence-kind
anatomy emanating elements cystidia presence-number
literature
morphology mycorrhizal system
  length [mm] (?)
  ramification presence-type
  tips {per 10 mm} number (?)
  ramification orders (?)
  abundance (?)
  main axis diameter [mm] (?)
  taste {after 2-3 min chewing} (?)
  rhizomorphs presence
  rhizomorphs frequency (-)
morphology unramified ends
morphology rhizomorphs
morphology sclerotia
anatomy entire mycorrhiza
anatomy entire mycorrhiza laticifers
anatomy mantle
anatomy mantle outer mantle layer {apart from tip}
anatomy mantle outer mantle layer {of ectomycorrhizal tip}
anatomy mantle middle mantle layer
anatomy mantle inner mantle layer
anatomy mantle longitudinal section
anatomy mantle longitudinal section tannin cells
anatomy mantle longitudinal section cortical cells

Descriptor tree: Main descriptor tree

If for a descriptor tree node resources are available, this is indicated by the grey background color of the descriptor tree icon. The resources may be accessed by a right-click on the tree node and selecting context menu item **View resources**. Additional descriptor tree node information, e.g. an optional abbreviation or details text can be viewed as bubble help by placing the mouse cursor over the item.

Editing summary data

A click on opens an edit window at the right part of the tab. This window provides the same functions as available in the descriptor view tab. The picture below shows the resource linked to a categorical state that can be opened by doule-clicking the state ID in the **Categorical states** section.



Summary data

- Körpergröße
  - Enten, Krähen, Kolkrabe (40-70 cm)
- Überwiegende Gefiederfarbe
  - graufarbig
- Zweite großflächige
  - weiß
- Weitere Gefiederfar
  - cremefarben bis
  - mittelbraun bis c
  - schwarz
- Musterung auf Brus
  - auffällig und kor
- Farbe der Beine
  - graufarbig
- Schnabelfarbe
  - graufarbig
- Schnabelform
  - mit Hakenspitze
- Schnabellänge relat
  - normal
- Schnabeldicke relat
  - unauffällig, uner
- Auffälliger Augenstrich
  - fehlend
- Auffälliger Augenring
  - fehlend
- Besondere Eigenschaften oder Typen
  - Greifvogelartig
- Flugbild oder Flugverhalten

http://species-id.net/o/media/thumb/8/89/Accipiter_

Categorical Descriptor
Categorical state(s)

Quantitative Descriptor
Quantitative measure

Text Descriptor
Text

Sequence Descriptor
Sequence

Categorical states

x	No.	State	Notes
☐	0 =	auffällig und kontrastreich gefleckt oder getupft	
☑	1 =	auffällig und kontrastreich gebändert, gestreift	
☐	2 =	auffällig und kontrastreich gefleckt bis gestrichelt	
☐	3	unauffällig und kontrastarm gemustert	
☐	4	nicht gemustert	

ate collection model: OrSet

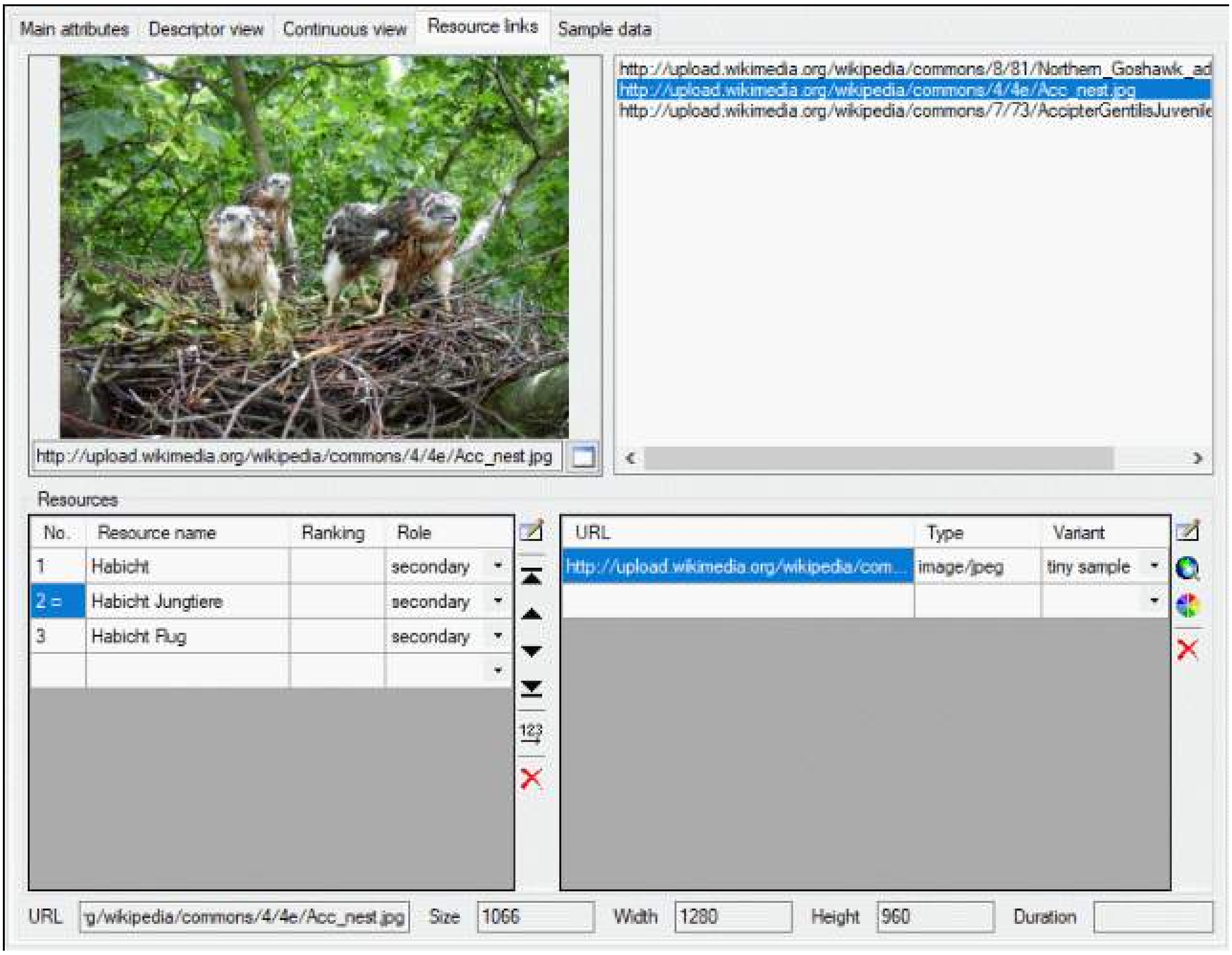
Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	⌀	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Resource links tab
- Edit descriptions - Sample data tab

Editing the description - Resource links tab



http://upload.wikimedia.org/wikipedia/commons/8/81/Northern_Goshawk_ad
http://upload.wikimedia.org/wikipedia/commons/4/4e/Acc_nest.jpg
http://upload.wikimedia.org/wikipedia/commons/7/73/AccipterGentilisJuvenile

http://upload.wikimedia.org/wikipedia/commons/4/4e/Acc_nest.jpg

No.	Resource name	Ranking	Role
1	Habicht		secondary
2	Habicht Jungtiere		secondary
3	Habicht Flug		secondary

URL	Type	Variant
http://upload.wikimedia.org/wikipedia/com...	image/jpeg	tiny sample

URL: g/wikipedia/commons/4/4e/Acc_nest.jpg Size: 1066 Width: 1280 Height: 960 Duration:

The resouce links tab allows assigment and inspection of resource links for the description. In the lower **Resources** part of the tab there are two tables. Ar the left the "Resource" table specifies the single resources, at the right the "Resource variant" table contains the associated URLs to images, video or sound resources.

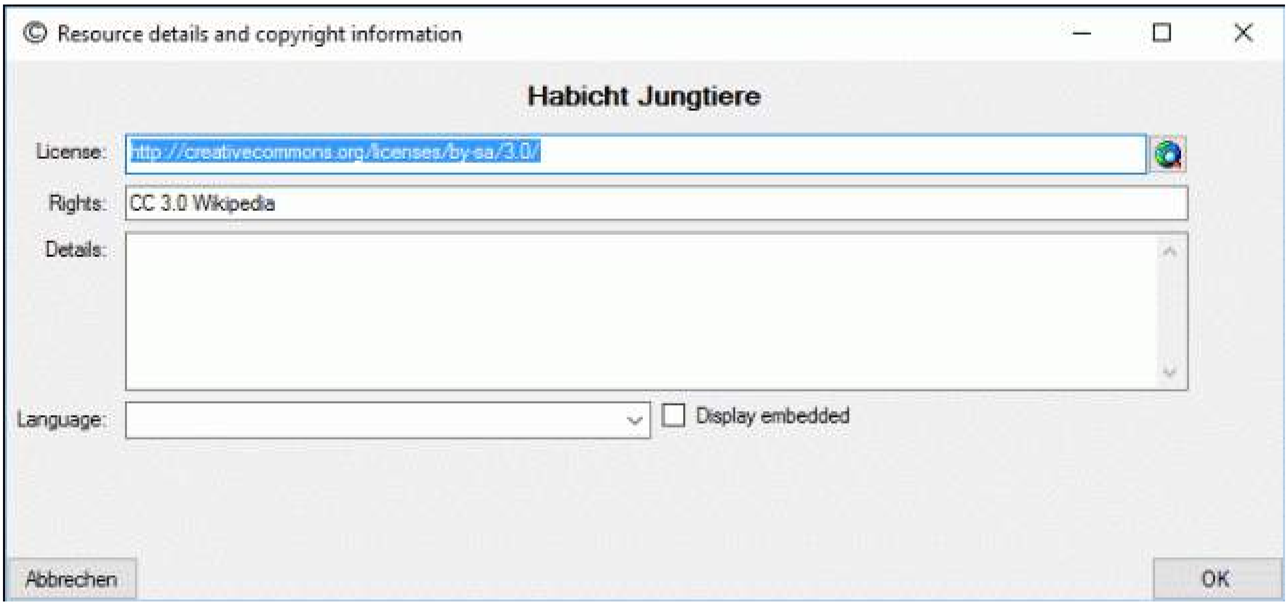
To enter a new resource select the empty line at the end of the "Resource" table and click on the "Resource name" field. After entering the "Resource name" (leave the cell by pressing the **TAB** key) automatically a new value for the sequence number ("No.") is initialized. The sequence number determines the display order in tables and may be changed manually. You may order the resource entries by clicking on the column header or by using the arrow buttons in the left tool strip (▲ and ▼for up and down, ⤒and ⤓to shift the selected entry to top or bottom). After ordering the resources click button 123→to renumber the entries starting with "1" and make the changes effective. In field "Ranking" you may enter a numeric value in range 0 ... 10 expressing the suitability of the resource. In field "Role" you may select one of the offered values.

If you want to **delete** a resource, you have three choices:

1. Select the resource and press the ✕button in the left tool strip.
2. Select the resource and press the **Delete** key on the keyboard.
3. Enter the sequence number column ("No.") and remove the value. After leaving the cell the entry will be deleted.

In any case you will be asked if you want to delete the data row, if resource links are present.

To view or edit the additional resource data and copyright information press on the button besides the resource table. In field **License:** and a link to the license text in the web may be entered, in field **Rights:** you may enter a copyright text. By pressing the button a browser window can be opened to navigate to the license page in the web. Furthermore you may enter a detailled text (field **Details:**), the resource language (field **Language:**) and set the **Display embedded** flag (see picture below). If any additional resource data have been entered, this will be indicated by a square (□) behind the resource name's sequence number (see picture above).



Resource details and copyright information

Habicht Jungtiere

License: http://creativecommons.org/licenses/by-sa/3.0/

Rights: CC 3.0 Wikipedia

Details:

Language:

☐ Display embedded

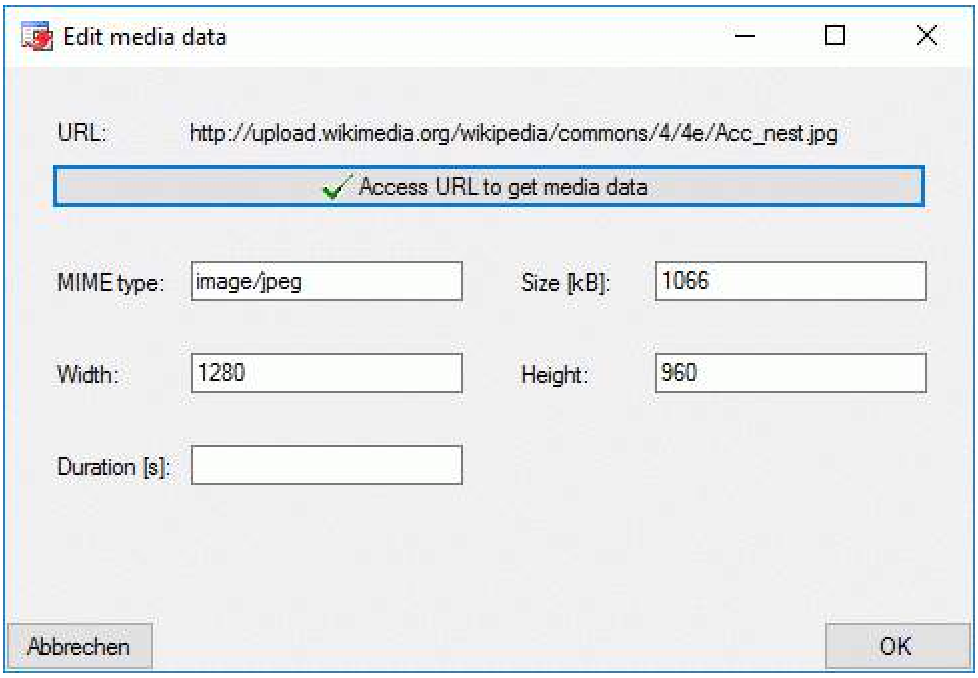
To enter a resource link, first select the entry in the "Resource" table, then select the empty line at the end of the "Resource variant table". By clicking on the "URL" field a web address may be entered. By double-clicking the "URL" field a browser window opens to navigate to the resource. For each resource several URLs to resource variants with different quality levels, e.g. different resolution, may be inserted. For each entry in the URL table a different value of "Variant" must be selected.

As an alternative to a resource URL a colour may be spcified in the format "color://#rrggbb" where "rrggbb" specifies a hexadecimal colour code. The colour can simply be seleced by clicking the button besides the resource variant table.

To remove a resource variant, select the entry and press the button in the right tool strip or the **Delete** key on the keyboard. Alternatively you may delete the "URL" entry in the resource variant table.

The upper part of the resource links tab consists of a preview window on the left side and the complete list of resource links. By selecting one of the links the preview is shown on the preview window. If you press button in the preview window, the resource is opened in a separate viewer window.

At the bottom of the resource links tab the media data of a selected URL are displayed. These data can be edited by double-clicking the "Type" entry in the resource variant table, by clicking at one of the media data value fields or the button. The edit dialog provides the possibility to access the URL to get available data. Additionally the values may be edited manually.



URL: http://upload.wikimedia.org/wikipedia/commons/4/4e/Acc_nest.jpg

MIME type: image/jpeg

Size [kB]: 1066

Width: 1280

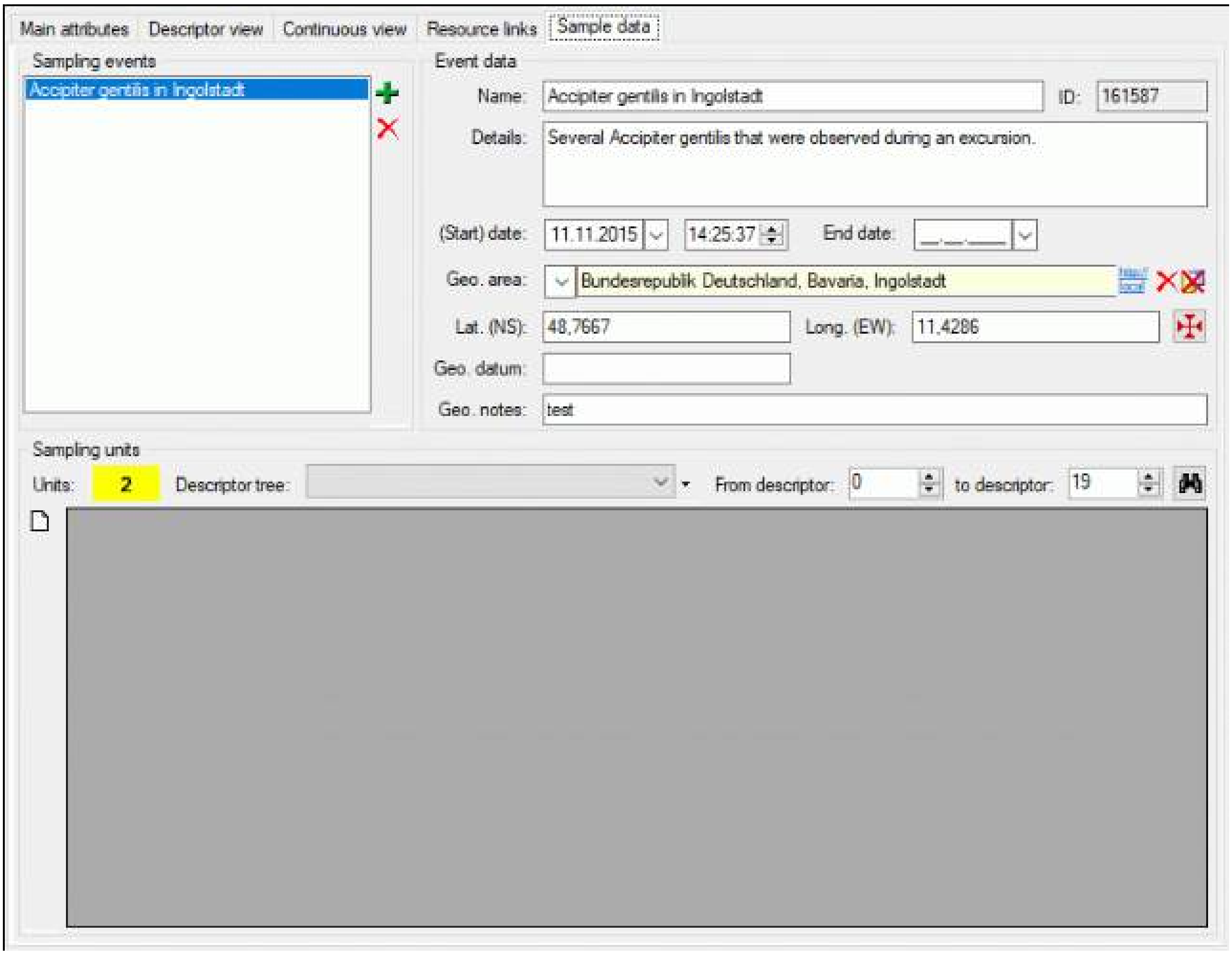
Height: 960

Duration [s]:

Continue with::

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Sample data tab

Editing the description - Sample data tab



Sampling events: Accipiter gentilis in Ingolstadt

Name: Accipiter gentilis in Ingolstadt
ID: 161587
Details: Several Accipiter gentilis that were observed during an excursion.
(Start) date: 11.11.2015 14:25:37
End date: __.__.____
Geo. area: Bundesrepublik Deutschland, Bavaria, Ingolstadt
Lat. (NS): 48,7667
Long. (EW): 11,4286
Geo. datum:
Geo. notes: test

Units: 2
From descriptor: 0
to descriptor: 19

The sample data tab allows assigment and inspection of sampling events and associated sampling units for the description. In the upper left **Sampling events** part of the tab there is a list of the sampling events stored for the description. By selecting a sampling event entry the **Event data** are shown in the upper right part of the tab. Here you may edit the event name, a detailled description, the date and time rsp. a date and time span and geographic data. To insert a new sampling event click on the + button in the **Sampling events** section, to delete the selected sampling event and all stored sampling unit data press the − button (see image above).

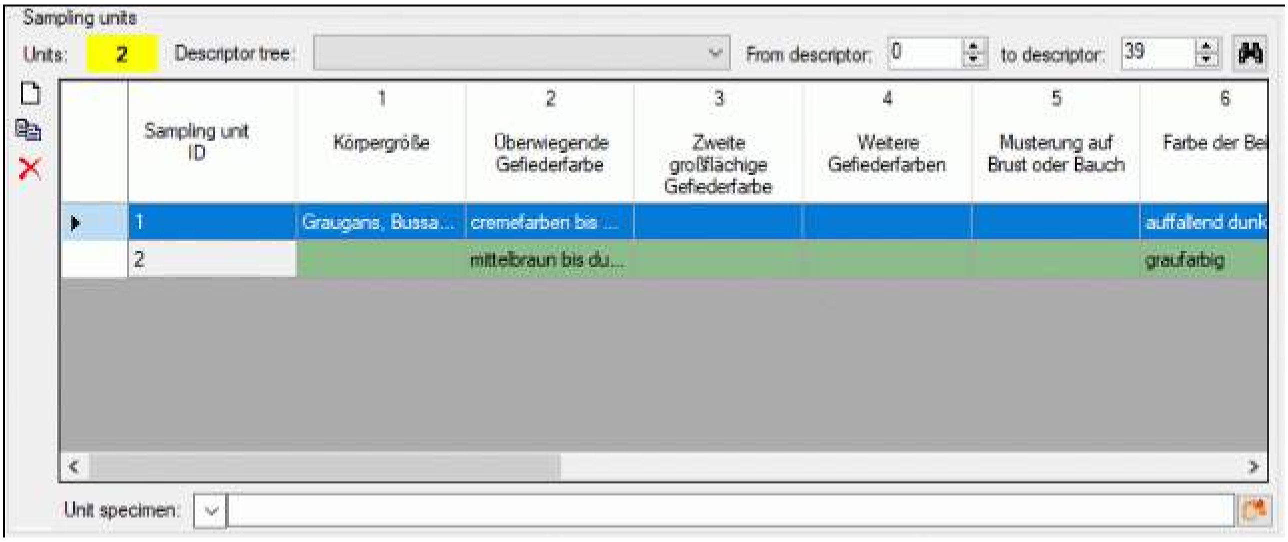
The geographic area may be linked to an entry of a DiversityGazetteers database (see section Module related entry). If latitiude and longituede have not yet been entered, the coordinates of the selected DiversityGazetteers entry will be inserted. By pressing the ✠ button a window to select the coordinates by Google maps will be opened. Field **Geo. datum** allows entering short text concerning the geodetic datum. If coordinates are entered using Google maps a remark that WGS84 coordinates are used will be inserted.

Editing sampling unit data

For each sampling events one or several **Sampling units** may be entered. A sampling unit represents a tuple of values that belong together, e.g. because they represent a single specimen. For each descriptor, which is represented by the table column, a value may be entered in a sampling unit, which builds a single table line. The background colour of each table column indicates the type of sample data: categorical, quantitative, text or sequence . If the number of sampling units is displayed in field **Units** of the **Sampling units** section in the lower part of the tab. If sampling units are present, the number is displayed with **yellow** background (see image below).

To view the unit data, select a **Descriptor tree** and choose the descriptor sequence range (**From descriptor ... to descriptor**) to restrict the number of columns displayed in the unit table. Finally press button and the sampling untis will be displayed (see image below). If you prefer to display the present sampling units automatically whenever you select a sampling event, click on the number behind **Units.** The background changes from **yellow** to **red** to indicate this mode. When you select a cell and resources are available for the selected descriptor column, the button will be shown. You may click it to view the descriptor resources.

To insert a new sampling unit press button 🗋. By clicking on the free space at the beginning of a table line you mark the whole sampling unit (see picture below). Now you have the additional options to delete the unit by pressing button ✕or to copy the data to a new sampling unit by pressing the button. Keep in mind that **all** unit data will be copied, even if you do not see all descriptor columns due to the display restrictions.



Sampling units

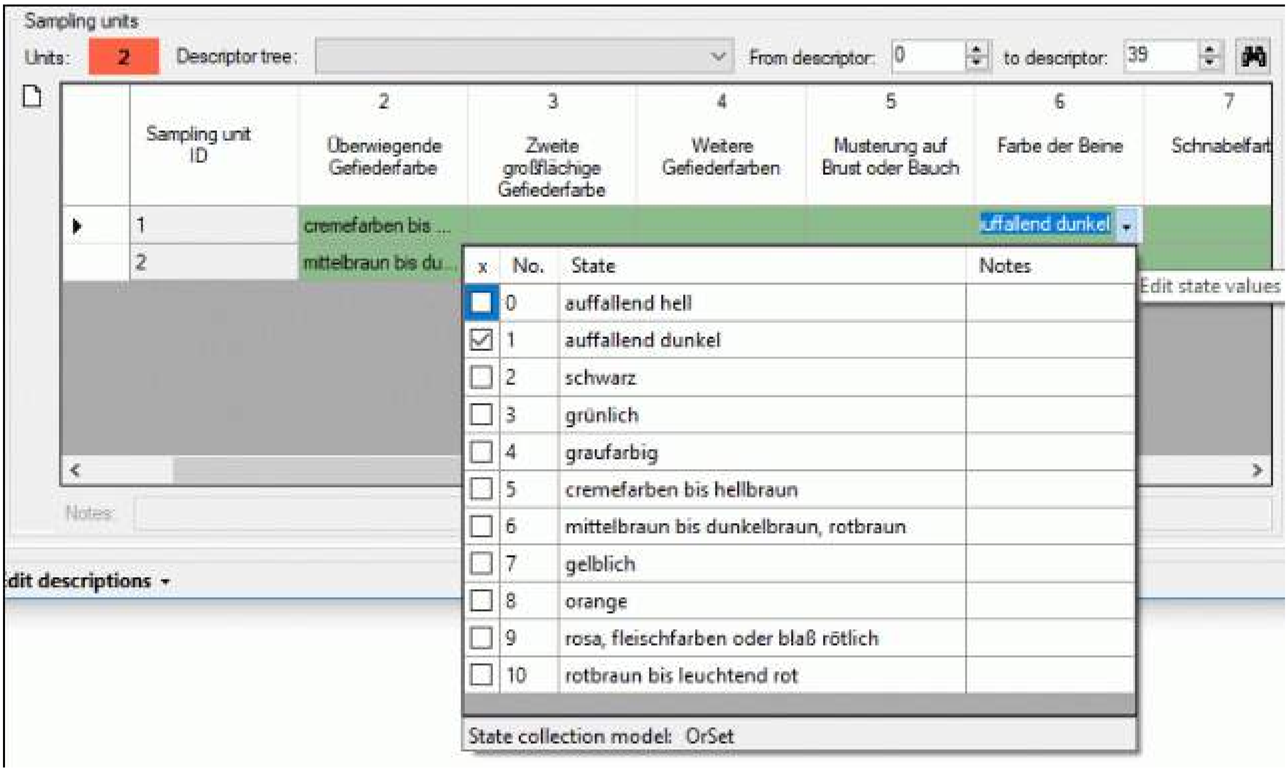
Units: 2 | Descriptor tree: | From descriptor: 0 | to descriptor: 39

Sampling unit ID	1 Körpergröße	2 Überwiegende Gefiederfarbe	3 Zweite großflächige Gefiederfarbe	4 Weitere Gefiederfarben	5 Musterung auf Brust oder Bauch	6 Farbe der Bei
1	Graugans, Bussa...	cremefarben bis ...				auffallend dunk
2		mittelbraun bis du...				graufarbig

Unit specimen:

When you select the **Sampling unit ID** cell you may enter a collection specimen in the **Unit specimen** control below the units table. By clicking the button (see section [Module related entry](#)) you can link it to an entry in a DiversityCollection database. If the sampling unit is linked to a database entry in DiversityCollection, the text of the **Unit specimen:** control is shown with light yellow background. You may view the linked data by clicking the button or double clicking the **Sampling unit ID** cell.

To modify categorical sampling data enter the table cell and press the ▾ button within the cell. A control will be opened where you can select the categorical states and enter notes or modifier values (if defined) for each single state (see image below).



Sampling units

Units: 2

Descriptor tree:

From descriptor: 0

to descriptor: 39

	Sampling unit ID	2 Überwiegende Gefiederfarbe	3 Zweite großflächige Gefiederfarbe	4 Weitere Gefiederfarben	5 Musterung auf Brust oder Bauch	6 Farbe der Beine	7 Schnabelfar
▶	1	cremefarben bis ...				uffallend dunkel	
	2	mittelbraun bis du...					

x	No.	State	Notes
☐	0	auffallend hell	
☑	1	auffallend dunkel	
☐	2	schwarz	
☐	3	grünlich	
☐	4	graufarbig	
☐	5	cremefarben bis hellbraun	
☐	6	mittelbraun bis dunkelbraun, rotbraun	
☐	7	gelblich	
☐	8	orange	
☐	9	rosa, fleischfarben oder blaß rötlich	
☐	10	rotbraun bis leuchtend rot	

State collection model: OrSet

For all other sampling data the value can be entered directly in the table cell. Notes for the selected table cell are entered in the **Notes:** text box directly below the units table. For categorical, text and molecular sequence sample data a separate edit window can be opened by double-clicking the table cell. For molecular sequence data the tool strip buttons (import) and (export) allow import and export from rsp. to dedicated file formats as described in sections **Import sequence data** and **Export sequence data**.

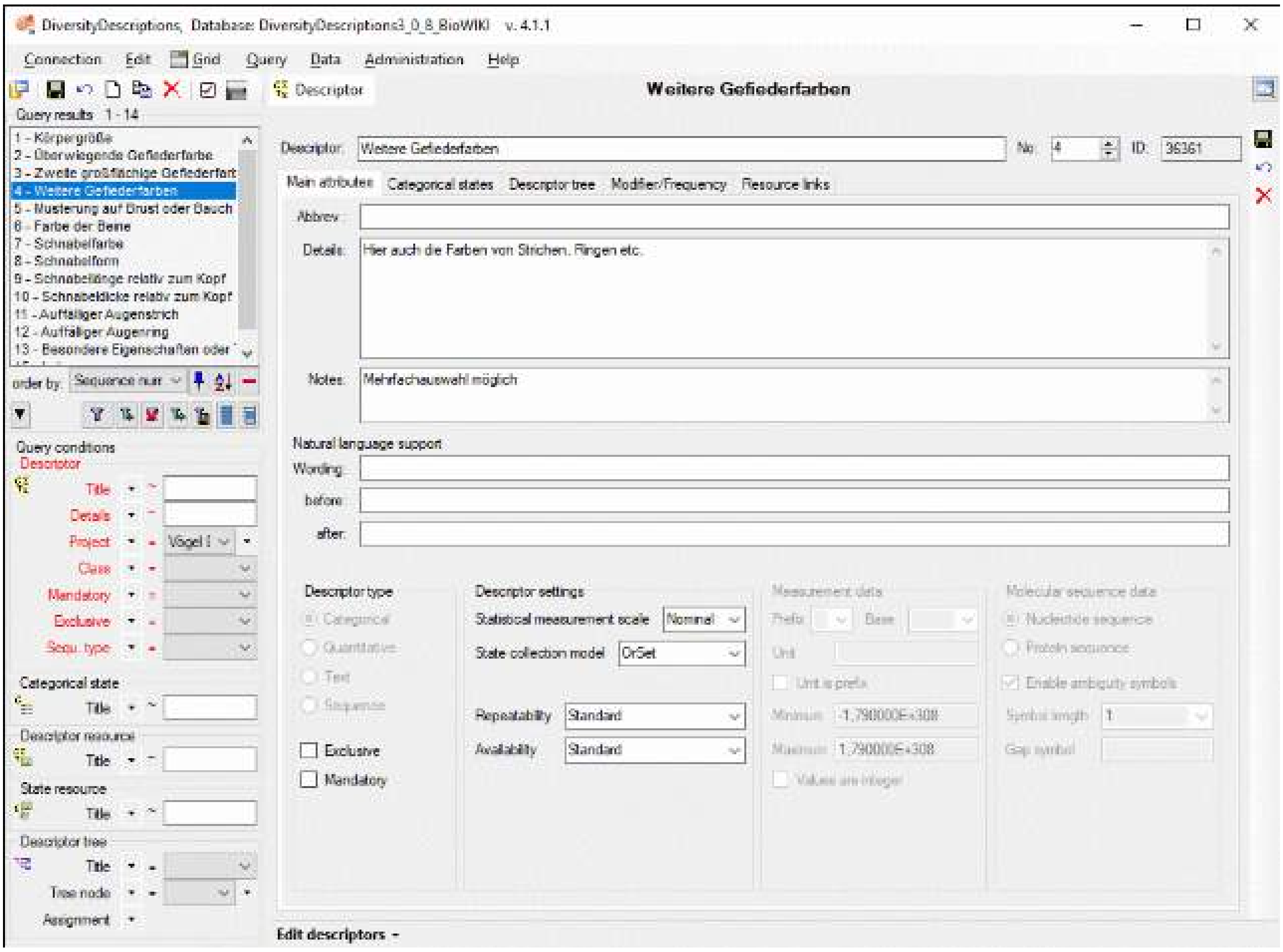
Continue with:

- Edit descriptions - Main attributes tab
- Edit descriptions - Descriptor view tab
- Edit descriptions - Molecular sequence symbols
- Edit descriptions - Import sequence data
- Edit descriptions - Export sequence data
- Edit descriptions - Continuous view tab
- Edit descriptions - Resource links tab

Editing the descriptor

After starting a database query and selecting an entry in the result list the dataset is diplayed in the edit window. In the header area the dataset name is shown (see picture below). Below the header area the descriptor name may be edited in a text box and the sequence number (No.) can be set, which determines the display order in descriptor lists. Changes of the descriptor name will be visible in the header after saving the dataset. To check dataset changes, click on the button to open the history.

The main descriptor data may be accessed in the first **Main attributes** tab, which is described below. Click on one of the other tabs in the picture below to go directly to the appropriate manual chapter.



Query results 1 - 14

1 - Körpergröße
2 - Überwiegende Gefiederfarbe
3 - Zweite großflächige Gefiederfarb
4 - Weitere Gefiederfarben
5 - Musterung auf Brust oder Bauch
6 - Farbe der Beine
7 - Schnabelfarbe
8 - Schnabelform
9 - Schnabellänge relativ zum Kopf
10 - Schnabeldicke relativ zum Kopf
11 - Auffälliger Augenstrich
12 - Auffälliger Augenring
13 - Besondere Eigenschaften oder

order by: Sequence num

Project: Vögel I

Descriptor: Weitere Gefiederfarben No: 4 ID: 36361

Abbrev:

Details: Hier auch die Farben von Strichen, Ringen etc.

Notes: Mehrfachauswahl möglich

Wording:

before:

after:

Descriptor type
● Categorical
○ Quantitative
○ Text
○ Sequence

☐ Exclusive
☐ Mandatory

Descriptor settings
Statistical measurement scale: Nominal
State collection model: OrSet
Repeatability: Standard
Availability: Standard

Minimum: -1,790000E+308
Maximum: 1,790000E+308

Symbol length: 1

Main attributes tab

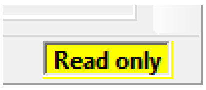
The main attributes tab provides access to an abbreviation, a detailled descriptor text, notes and wording information for natural laguage descriptions. In the bottom area the **Descriptor type**, **Descriptor settings, Measurement data** (only for quantitative descriptors) and **Molecular sequence data** (only for sequence descriptors) can be adjusted. The descriptor type can only be modified, if the descriptor is not referenced by any description. If the descriptor type "Categorical" is changed, already entered categorical states will be deleted.

The check box **Exclusive** (only for categorical descriptors) indicates that only one state shall be specified in a description. Check box **Mandatory** indicates that for this descriptor always data shall be specified. **Statistical measurement scale** specifies for categorical descriptors, if the states are unordered (e.g. red/green/blue) of ordered (e.g. bad/medium/good). For quantitative descriptors it specifies if intervals or ratios are measured. **Repeatability** and **Availability** specify how reliable (different measurements or scorings by different observers) and accessible the descriptor is, e.g. for identification.

For quantitative descriptors the **Unit** of the measurement values my be specified either by directly entering the string or alternatively by selecting a **Prefix** (e.g. "k" for "kilo" = 1000) and the **Base** unit (e.g. "g" for "gramm"). **Unit is prefix** indicates that the measurement unit preceeds the measurement value. **Minimum** and **Maximum** specify the absolute range limits expected for the measurement values. If in a description specific values, e.g. "Mean", exceed these limits, a warning will be shown. **Values are integer** indicates that dedicated values, e.g. "Min" or "Max", are expected to be integer values. Take care that statisical measures like "Mean" certainly may be real numbers. If this condition is violated in the description data, a warning will be displayed.

For sequence descriptors the sequence type **Nucleodide sequence** or **Proteine sequence** must be selected. **Enable ambiguity symbols** determines if in the sequence data ambiguity symbols like "S" for "C or G" in nucleotide sequences, are allowed. In case of protein sequences the **Symbol length** may be chosen from one letter sybols (e.g. "A" for "Alanine") and three letter symbols (e.g. "Ala" for "Alanine). The **Gap symbol** is a symbol that indicates gaps of unspecified length and must meet the selected symbol length.

Descriptors are not directly assigned to a project, instead descriptor trees are used. One descriptor may be included in several descriptor trees and therefore belong to several projects or it might be unassigned. You can easily find descriptors that are not included in any descriptor tree by setting "Descriptor tree" -> "Assignment" to "Ø" in the search criteria. By opening the **Descriptor tree tab** these descriptors may be easily inserted into a tree by selecting the tree (node) and clicking .

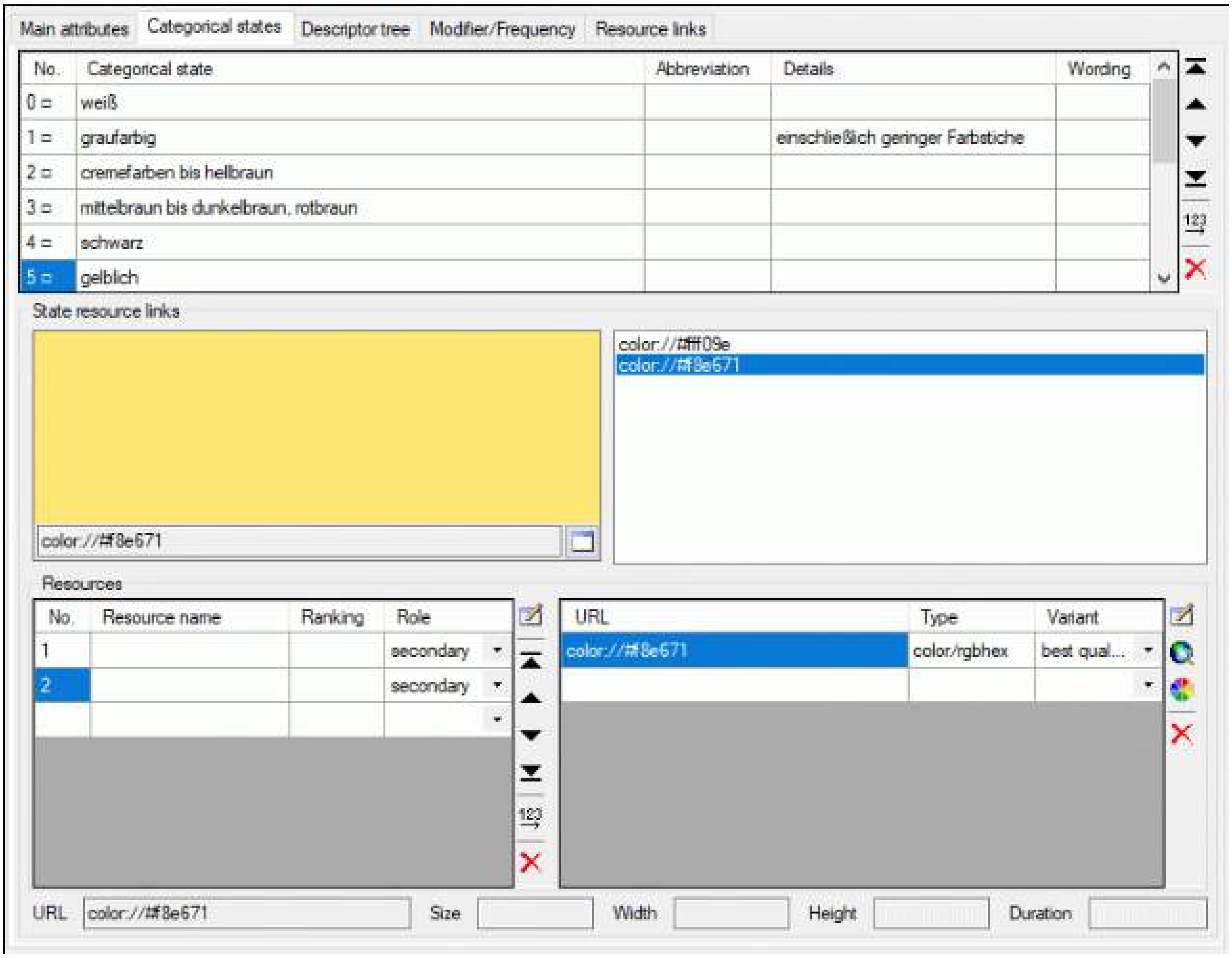


If the actually selected descriptor is referenced by more than ony project and not all of the projects can be modified by the actual user, the descriptor data cannot be changed, which will be indicated at the lower right corner of the application window (see above).

Continue with:

- Edit descriptors - Categorical states tab
- Edit descriptors - Descriptor tree tab
- Edit descriptors - Modifier/Frequency tab
- Edit descriptors - Resource links tab

Editing the descriptor - Categorical states tab



No.	Categorical state	Abbreviation	Details	Wording
0 □	weiß			
1 □	graufarbig		einschließlich geringer Farbstiche	
2 □	cremefarben bis hellbraun			
3 □	mittelbraun bis dunkelbraun, rotbraun			
4 □	schwarz			
5 □	gelblich			

color://#f8e671

color://#fff09e
color://#f8e671

No.	Resource name	Ranking	Role
1			secondary
2			secondary

URL	Type	Variant
color://#f8e671	color/rgbhex	best qual...

URL color://#f8e671 Size Width Height Duration

The **Categorical states** tab is only enabled, if the descriptor type has been set to "Categorical". The upper part of the state tab shows the table of categorical states. To enter a new state select the empty line at the end of the table and click on the "Categorical state" field. After entering the "Categorical state" name (leave the cell by pressing the **TAB** key) automatically a new value for the sequence number ("No.") is initialized. The sequence number determines the display order in tables and may be changed manually. You may order the state entries by clicking on the column header or by using the arrow buttons in the tool strip right besides the states (▲ and ▼for up and down, ⤒and ⤓to shift the selected entry to top or bottom). After ordering the states click button 123→to renumber the entries starting with "1" and make the changes effective.

If you want to **delete** a categorical state, you have three choices:

1. Select the state and press the ✕button in the tool strip right besides the states.
2. Select the state and press the **Delete** key on the keyboard.
3. Enter the sequence number column ("No.") and remove the value. After leaving the cell the entry will be deleted.

In any case you will be asked if you want to delete the data row. If the categorical state is already used in any description items, the number of affected entries will be shown and you have the option to abort the action.

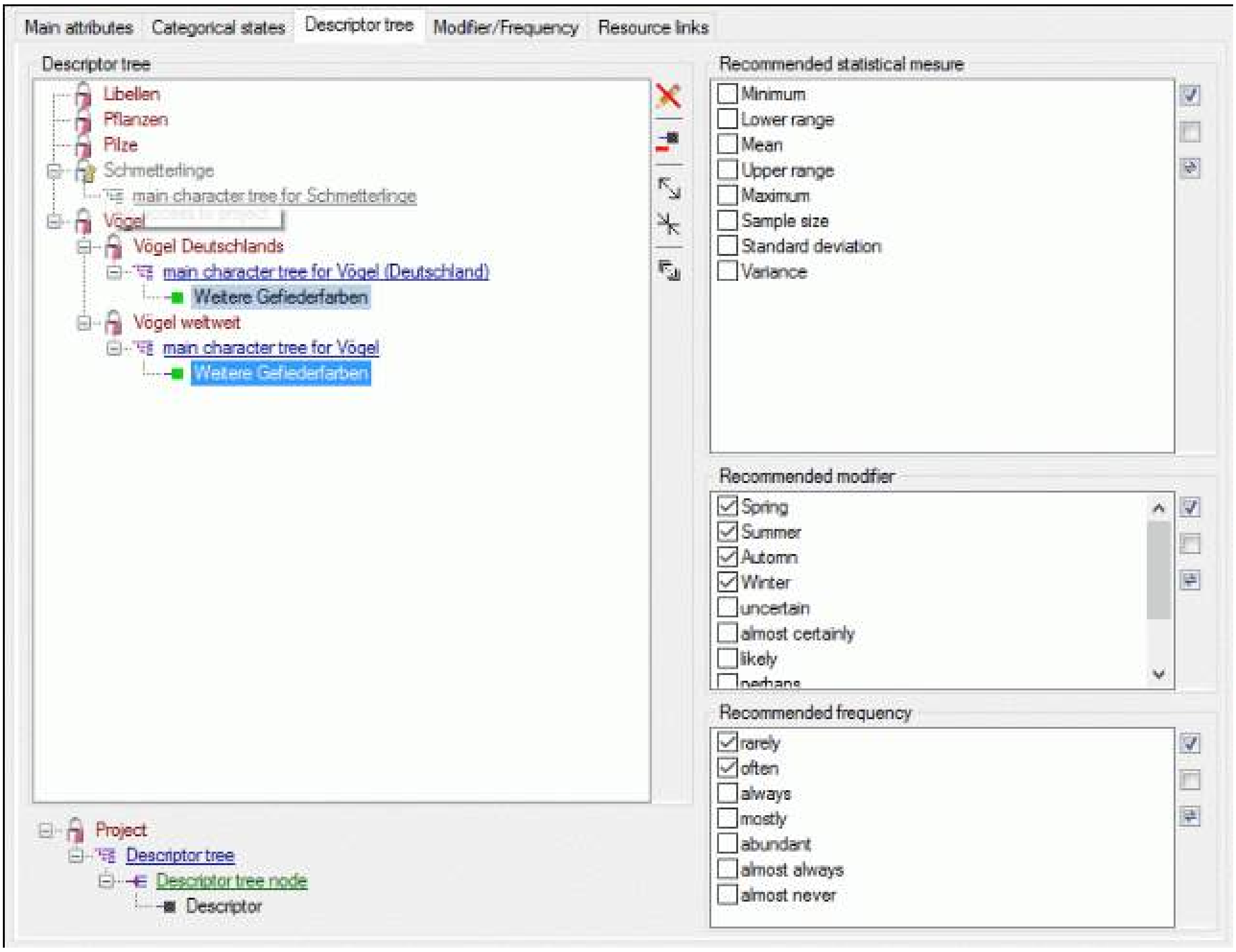
If for a state at least one assigned resource is present, the state is marked by a square (□) behind its sequence number (see image above). After selecting the categorical state its assigned resources ar displayed in the lower part of the state tab, the **State resource links**.

It allows management of resources linked to a categorical state marked in the upper table. For a detailled description take a look at the Resource links tab section.

Continue with:

- Edit descriptors - Main attributes tab
- Edit descriptors - Descriptor tree tab
- Edit descriptors - Modifier/Frequency tab
- Edit descriptors - Resource links tab

Editing the descriptor - Descriptor tree tab



Recommended statistical mesure:

☐ Minimum
☐ Lower range
☐ Mean
☐ Upper range
☐ Maximum
☐ Sample size
☐ Standard deviation
☐ Variance

Recommended modifier:

☑ Spring
☑ Summer
☑ Automn
☑ Winter
☐ uncertain
☐ almost certainly
☐ likely
☐ perhaps

Recommended frequency:

☑ rarely
☑ often
☐ always
☐ mostly
☐ abundant
☐ almost always
☐ almost never

The **Descriptor tree** tab provides the possibility for a structured assignment of the descriptors to the projects. The **Descriptor tree** consists of three node types, which show the administered **projects**, **descriptor trees**, **descriptor tree nodes** and **descriptors**. The tree parts' colours are shown in the example at the bottom. By pressing the button on the tool stipe at the right side the example may be hidden. The buttons displayed on the too strip will change depending on the selected entry.

Descriptor trees are the root of a tree and may only be appended at a project. To insert a new descriptor tree select a project and press . **Descriptor tree nodes** may be appended at a descriptor tree or another descriptor tree node. To insert a new descriptor tree node, select the parent and press . **Descriptors** may be appended to a descriptor tree or a descriptor tree node. To append a descriptor select the parent and press , to remove it select the descriptor and press . All these functions can alternatively be accessed by the context menu by a right click on the entry. The descriptor type is indicated by different icons. Categorical descriptors are marked as 🟩, quantitative descriptors as 🟦, text descriptors as 🟥 and sequence descriptors as 🟧.

You may change the name of a **Descriptor tree** or a **Descriptor tree node** in three different ways:

1. Select the tree element (single click) and then click once on it.
2. Select the tree element (single click) and click on button in the tool bar on the right.
3. Right-click the tree element and select item **Edit name** from the context menu.

You may edit the name of the selected node within the tree. The **Descriptor tree** must be globally unique. The **Descriptor tree node** names must be unique with respect to their tree position, i.e. all nodes with the same parent within a descriptor tree must have distinguished names.

If a **Descriptor tree** or a **Descriptor tree node** does not contain any other element, it may be deleted by pressing (delete descriptor tree) rsp. (delete descriptor tree node). Please be aware that in edit mode "Descriptor" the descriptor tree shows only the descriptor that as actually selected in the query panel! To get a complete overview of all descriptors assigned to a certain descriptor tree and to delete trees or nodes with all included objects, select edit mode "Project" (see Edit projects).

If projects and their associated descriptor trees cannot be changed, because the project has been set to "read-only" state, these parts are displayed with **grey** text color (see project "Schmetterlinge" in picture above).

Descriptor trees can be marked as "tree complete", to indicate that they should contain all descriptors of the project. In this case the symbol of the descriptor tree changes from to . Setting and resetting the "tree complete" flag is described in the Edit projects section, where additional edit options are availabe.

When a new descriptor tree or descriptor tree node is inserted it gets a numeric name, which may be changed by clicking on the node or selecting from the context menu. Take care that the names of the discriptor trees must be unambiguous within the whole database! The names of the descriptor tree nodes must only be unambiguous within one parent.

The descriptor trees support three main functions:

- Assignment of descriptors to a certain project
- Selection of recommended **Frequency/Modifier** values and **Statistical measures** for a certain descriptor
- Structured arragement of the descriptors, e.g. for hierarchical selection lists and definition of descriptor subsets for description editing and export

If no descriptor tree is installed for a certain project, all descriptors, modifier/frequency values and statistical measures will be usable in the project's descriptions. If a project contains several descriptor trees, the available descriptors are the superset of the descriptors assigned to all contained trees.

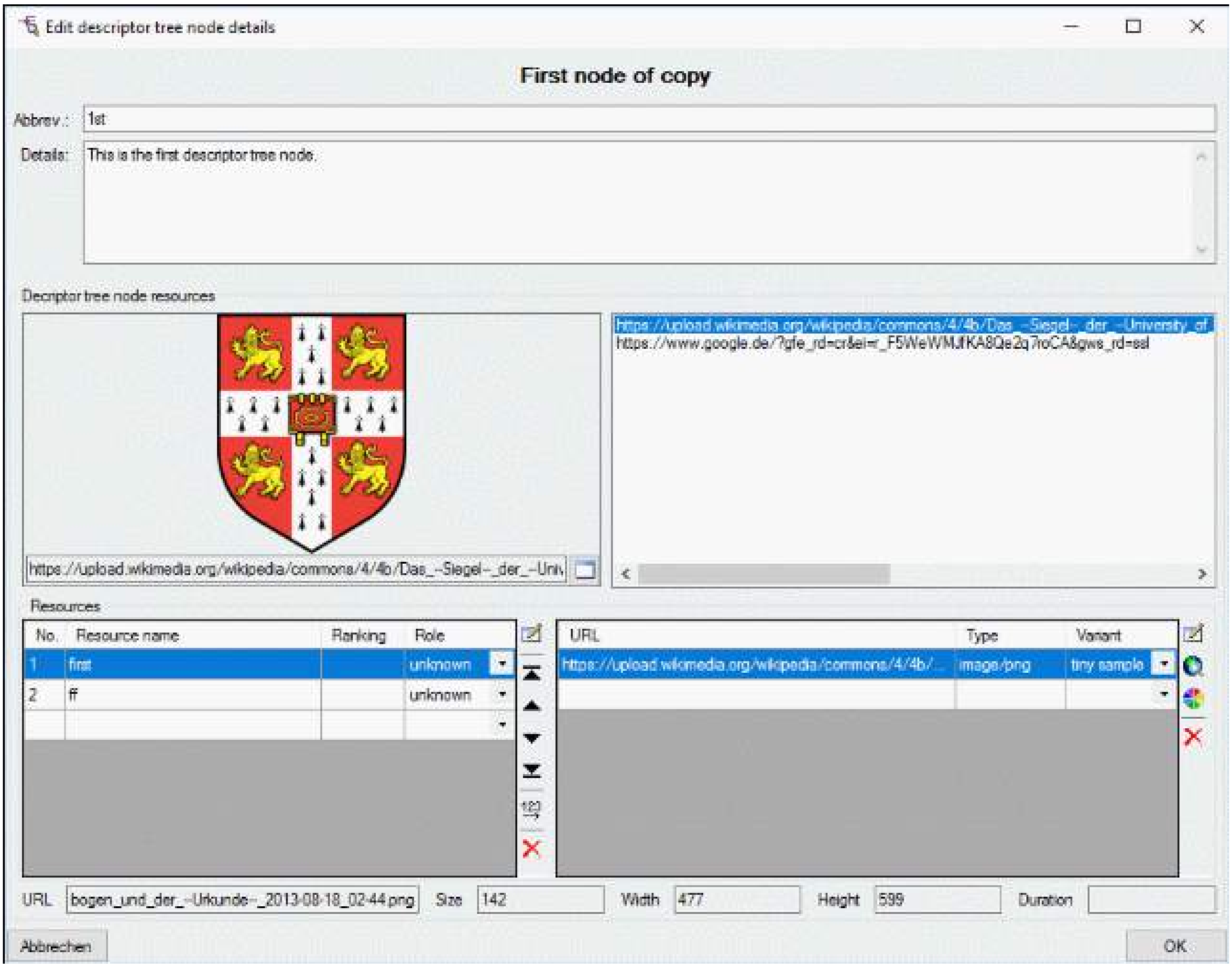
Sorting of descriptor tree elements

By pressing the button you can expand the tree view to display all elements, by pressing the tree will be collapsed to descriptor tree level. With the arrow buttons (▲ ▼rsp. ⏶ ⏷) you can move descriptor tree nodes up or down rsp. to the top or the bottom. An additional ordering option is to select the descriptor tree node you want to move and click the button. The button's back color changes to red and you may now select the new position in the tree.

In operation mode Edit projects you may take over the descriptor order from a descriptor tree to the descriptor sequence numbers of all project's descriptors. This will affect the descriptor presentation for description data editing or document generation.

Descriptor tree node details etails

For **Descriptor tree nodes** you may enter an abbreviation a details text and assign resource data. Select the **Descriptor tree node** (single click) and click on button in the tool bar on the right. Alternatively you may right-click the **Descriptor tree node** and select **Edit details** from the context menu. An edit window as shown below will be opened.



First node of copy

Abbrev.: 1st

Details: This is the first descriptor tree node.

Decriptor tree node resources

https://upload.wikimedia.org/wikipedia/commons/4/4b/Das_-Siegel-_der_-University_of
https://www.google.de/?gfe_rd=cr&ei=r_F5WeWMJfKA8Qe2q7roCA&gws_rd=ssl

https://upload.wikimedia.org/wikipedia/commons/4/4b/Das_-Siegel-_der_-Univ

Resources

No.	Resource name	Ranking	Role
1	first		unknown
2	ff		unknown

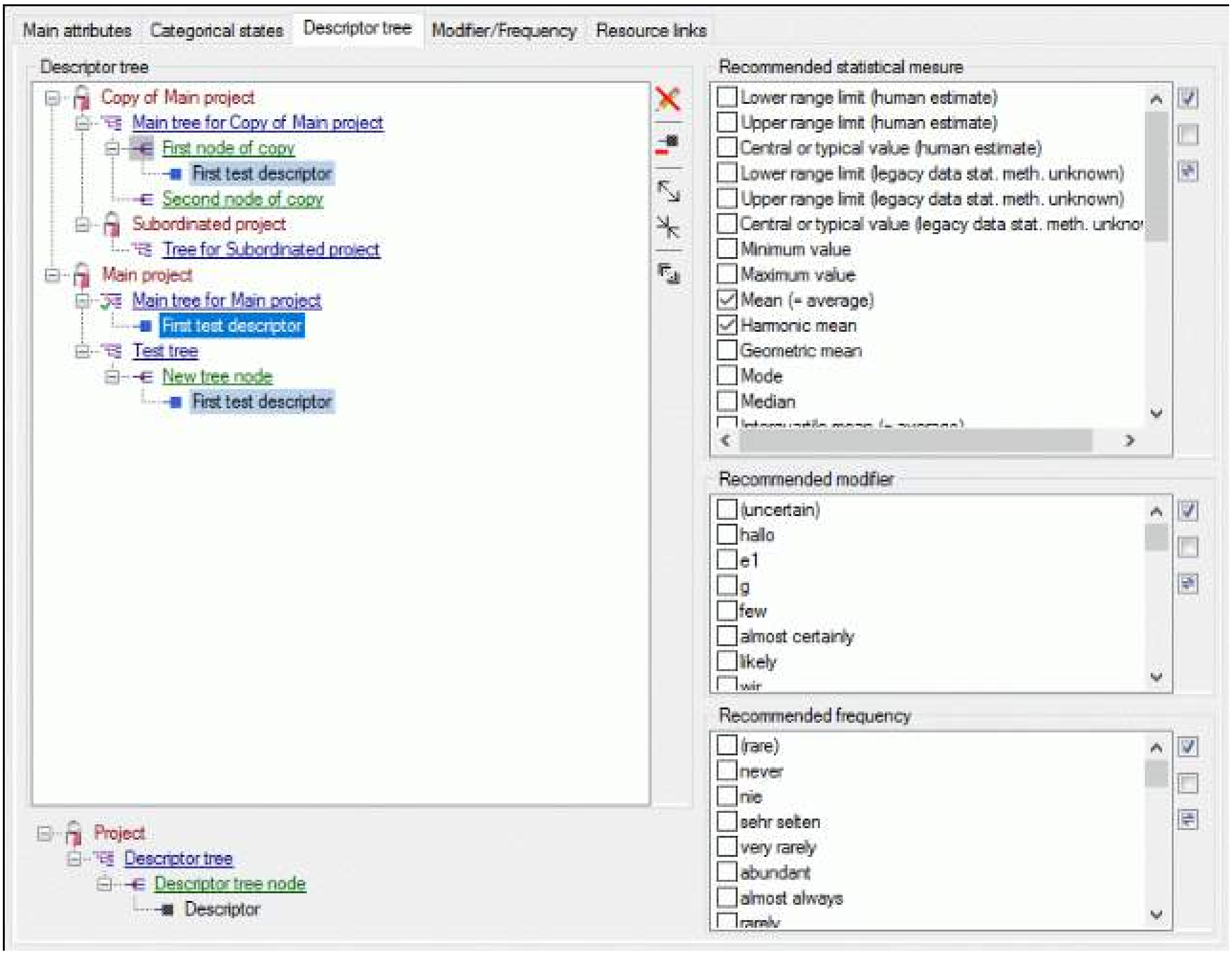
URL	Type	Variant
https://upload.wikimedia.org/wikipedia/commons/4/4b/...	image/png	tiny sample

URL: bogen_und_der_-Urkunde-_2013-08-18_02-44.png
Size: 142
Width: 477
Height: 599
Duration:

If resources are assigned to a **Descriptor tree node**, its symbol is shown with grey background in the descriptor tree. You may view the resources by right-clicking it and selecting **View resources** from the context menu.

Recommended statistical measures, modifiers and frequency values

Click on in the tool bar to close the edit window in the right part of the tab or on to reopen it. In the edit window you can select recommended modifier/frequency values and statistical measures. The recommended values can be administered for a selected descriptor or for a selected descriptor tree node. In the latter case selected values are inherited by all subordinate nodes, which will be indicated by the background colour if a subordinate node is selected in the descriptor tree.



Descriptor tree

- Copy of Main project
  - Main tree for Copy of Main project
    - First node of copy
      - First test descriptor
    - Second node of copy
  - Subordinated project
    - Tree for Subordinated project
- Main project
  - Main tree for Main project
    - First test descriptor
  - Test tree
    - New tree node
      - First test descriptor

- Project
  - Descriptor tree
    - Descriptor tree node
      - Descriptor

Recommended statistical mesure

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unkno
☐ Minimum value
☐ Maximum value
☑ Mean (= average)
☑ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

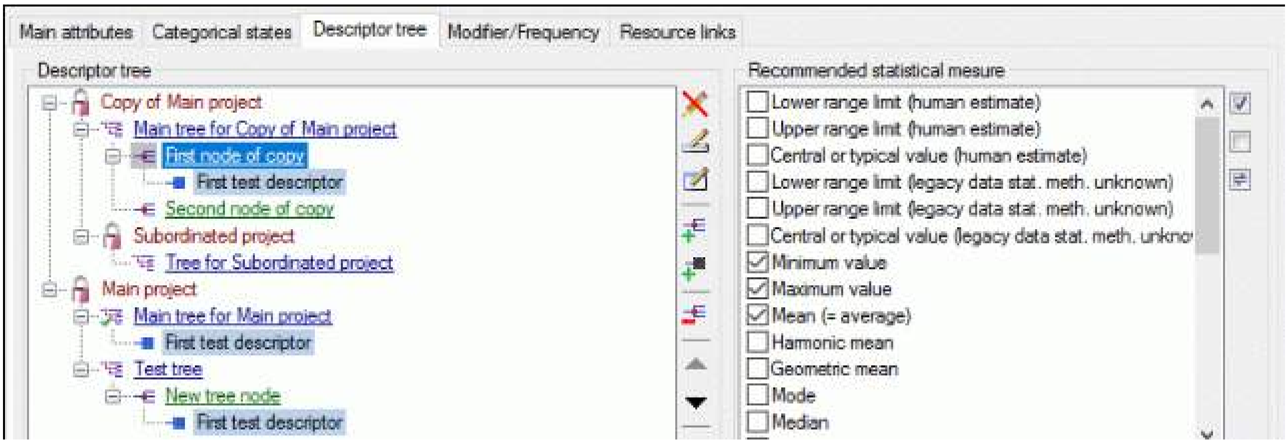
Recommended modifier

☐ (uncertain)
☐ hallo
☐ e1
☐ g
☐ few
☐ almost certainly
☐ likely

Recommended frequency

☐ (rare)
☐ never
☐ nie
☐ sehr selten
☐ very rarely
☐ abundant
☐ almost always

The picture below shows an example for a descriptor where the recommended statistical measures **Minimum value**, **Maximum value** and **Mean** are inherited by the superior node.



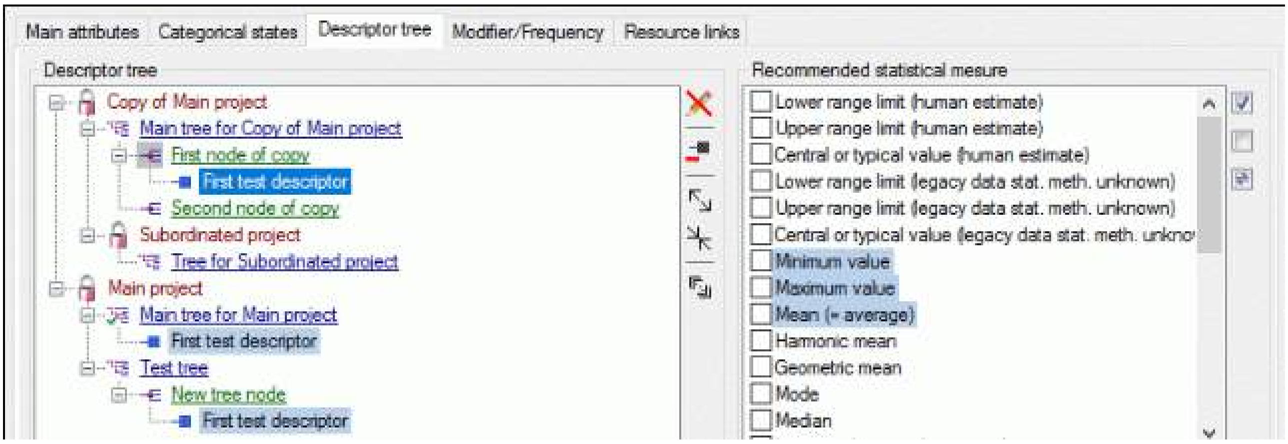
Descriptor tree

- Copy of Main project
  - Main tree for Copy of Main project
    - First node of copy
      - First test descriptor
    - Second node of copy
  - Subordinated project
    - Tree for Subordinated project
- Main project
  - Main tree for Main project
    - First test descriptor
  - Test tree
    - New tree node
      - First test descriptor

Recommended statistical mesure

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unkno
☑ Minimum value
☑ Maximum value
☑ Mean (= average)
☐ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

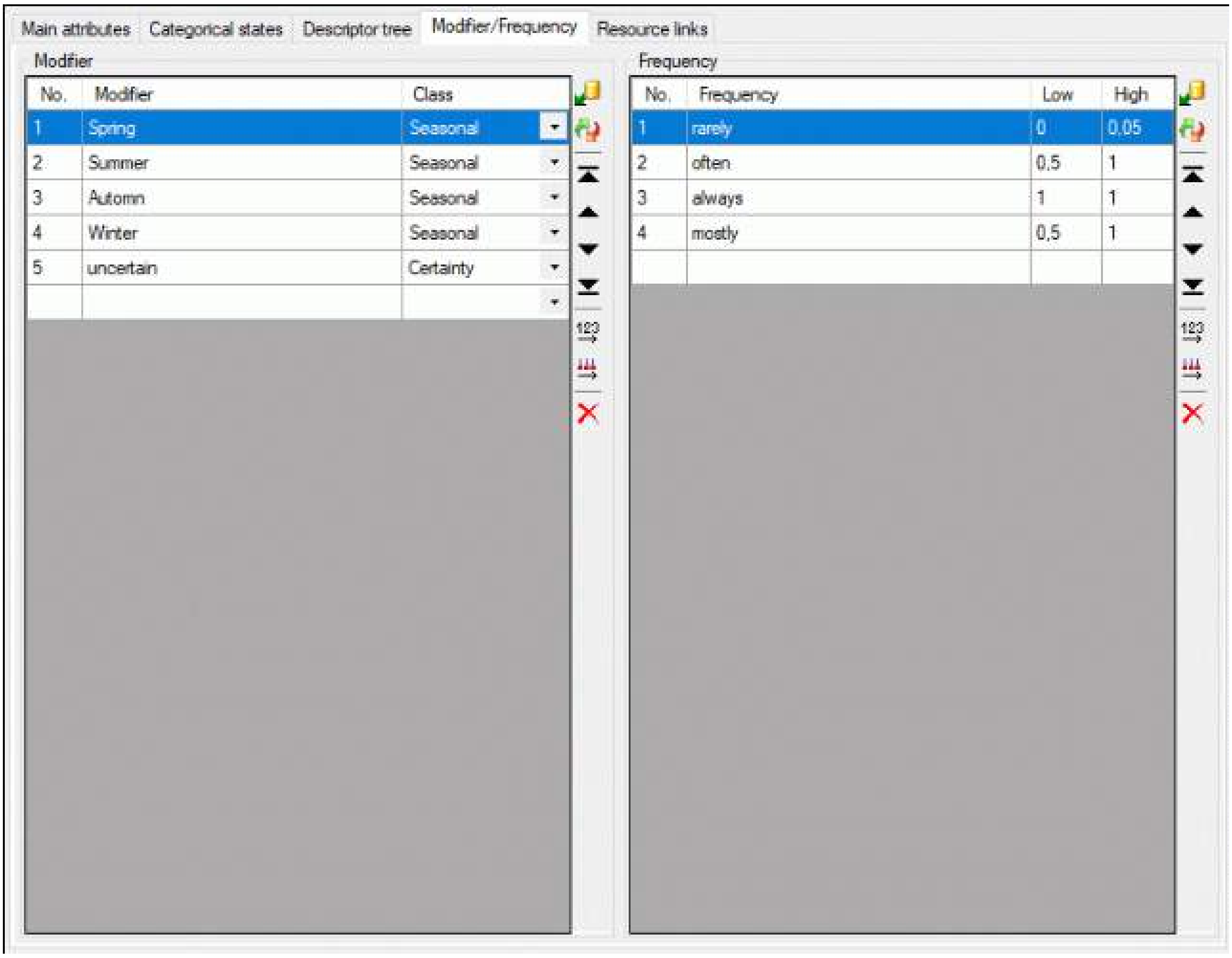
For the contained descriptor only additional values may be selected, but the inherited values cannot be de-selected.



Continue with:

- Edit descriptors - [Main attributes tab]
- Edit descriptors - [Categorical states tab]
- Edit descriptors - [Modifier/Frequency tab]
- Edit descriptors - [Resource links tab]

Editing the descriptor - Modifier/Frequency tab



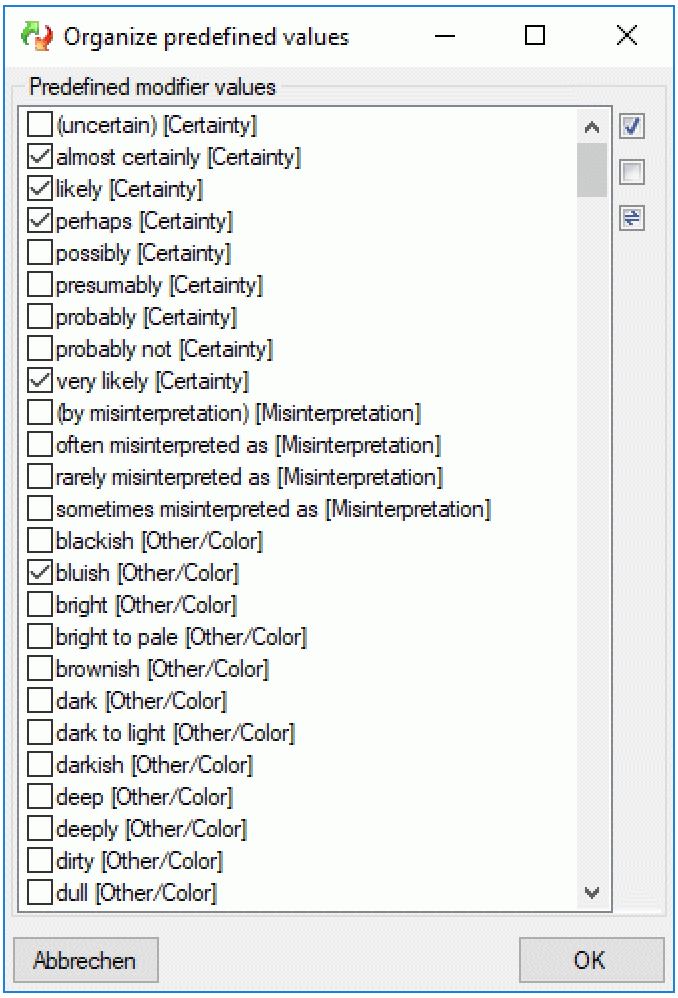
No.	Modifier	Class
1	Spring	Seasonal
2	Summer	Seasonal
3	Automn	Seasonal
4	Winter	Seasonal
5	uncertain	Certainty

No.	Frequency	Low	High
1	rarely	0	0,05
2	often	0,5	1
3	always	1	1
4	mostly	0,5	1

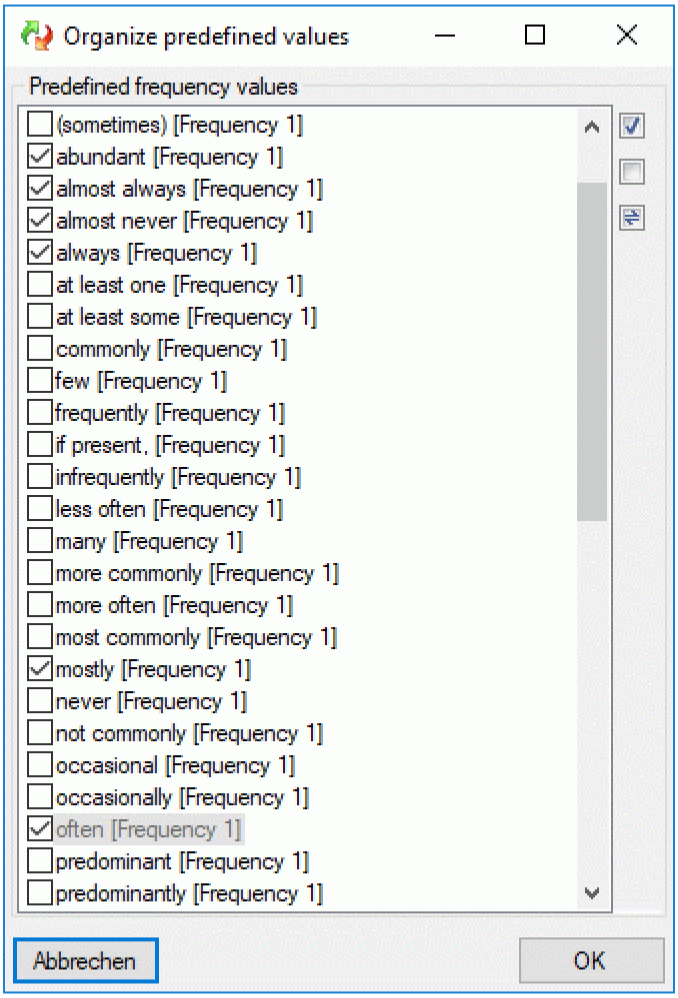
The **Modifier/Frequency** tab allows definition of modifier and frequency values. The sequence number column ("No.") determines the display sequence in selection lists. You may order the entries by clicking on a column header. With the arrow buttons (▲ ▼) you can move the selected entries up or down within the table, clicking button ⤒or ⤓shifts the selected entries to the top respective bottom of the table. After ordering the entries click button 123→to renumber the table entries (starting with "1" for the first table entry) and make the changes effective. After pressing button ⛁column "Use" shows the number of references in the database for each modifier rsp. frequency value.

To enter a new modifier or frequency value, select the empty line on the end of the table and click on the "Modifier" rsp. "Frequency" field to enter the new values. After entering the new entry name automatically a new value for "No." is initialized. To delete an entry, select the entry and press the ✕tool strip button, the **Delete** key or remove the value in the sequence number column ("No.").

There is a number of predefined modifier and frequency values commonly used. These values can be accessed by pressing the 🔄 button, which opens one of the windows shown below.

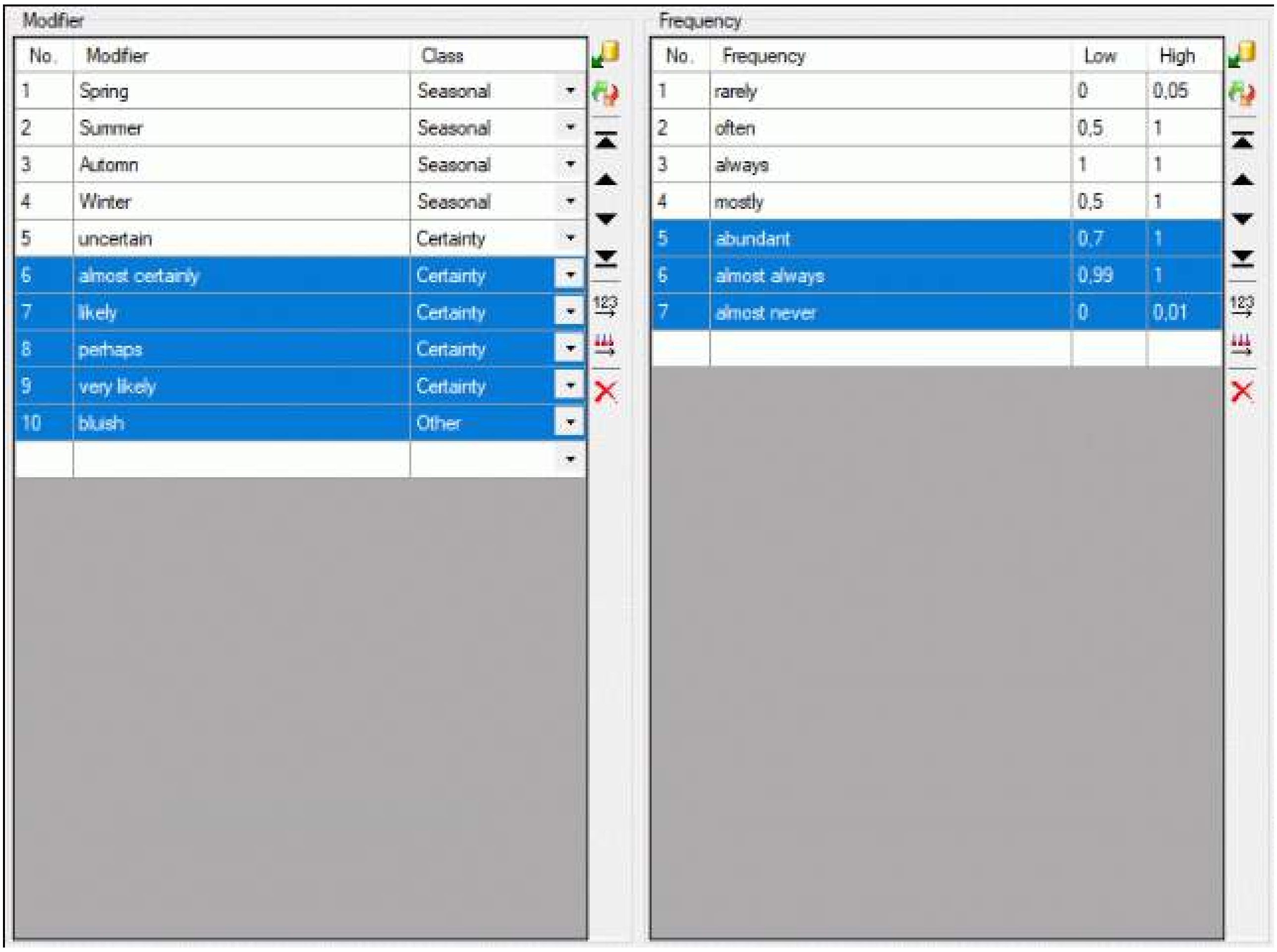


- ☐ (uncertain) [Certainty]
- ☑ almost certainly [Certainty]
- ☑ likely [Certainty]
- ☑ perhaps [Certainty]
- ☐ possibly [Certainty]
- ☐ presumably [Certainty]
- ☐ probably [Certainty]
- ☐ probably not [Certainty]
- ☑ very likely [Certainty]
- ☐ (by misinterpretation) [Misinterpretation]
- ☐ often misinterpreted as [Misinterpretation]
- ☐ rarely misinterpreted as [Misinterpretation]
- ☐ sometimes misinterpreted as [Misinterpretation]
- ☐ blackish [Other/Color]
- ☑ bluish [Other/Color]
- ☐ bright [Other/Color]
- ☐ bright to pale [Other/Color]
- ☐ brownish [Other/Color]
- ☐ dark [Other/Color]
- ☐ dark to light [Other/Color]
- ☐ darkish [Other/Color]
- ☐ deep [Other/Color]
- ☐ deeply [Other/Color]
- ☐ dirty [Other/Color]
- ☐ dull [Other/Color]



- ☐ (sometimes) [Frequency 1]
- ☑ abundant [Frequency 1]
- ☑ almost always [Frequency 1]
- ☑ almost never [Frequency 1]
- ☑ always [Frequency 1]
- ☐ at least one [Frequency 1]
- ☐ at least some [Frequency 1]
- ☐ commonly [Frequency 1]
- ☐ few [Frequency 1]
- ☐ frequently [Frequency 1]
- ☐ if present, [Frequency 1]
- ☐ infrequently [Frequency 1]
- ☐ less often [Frequency 1]
- ☐ many [Frequency 1]
- ☐ more commonly [Frequency 1]
- ☐ more often [Frequency 1]
- ☐ most commonly [Frequency 1]
- ☑ mostly [Frequency 1]
- ☐ never [Frequency 1]
- ☐ not commonly [Frequency 1]
- ☐ occasional [Frequency 1]
- ☐ occasionally [Frequency 1]
- ☑ often [Frequency 1]
- ☐ predominant [Frequency 1]
- ☐ predominantly [Frequency 1]

By checking of uncecking the values, they can easily be inserted or deleted from the modifier rsp. frequency list. Values that are already used in the database are marked by a grey text colour. When these values are marked to be removed from the list, you will be asked for each single value if it really shall be deleted after pressing **OK**. New values are inserted at the end of the list (see below).



Modifier

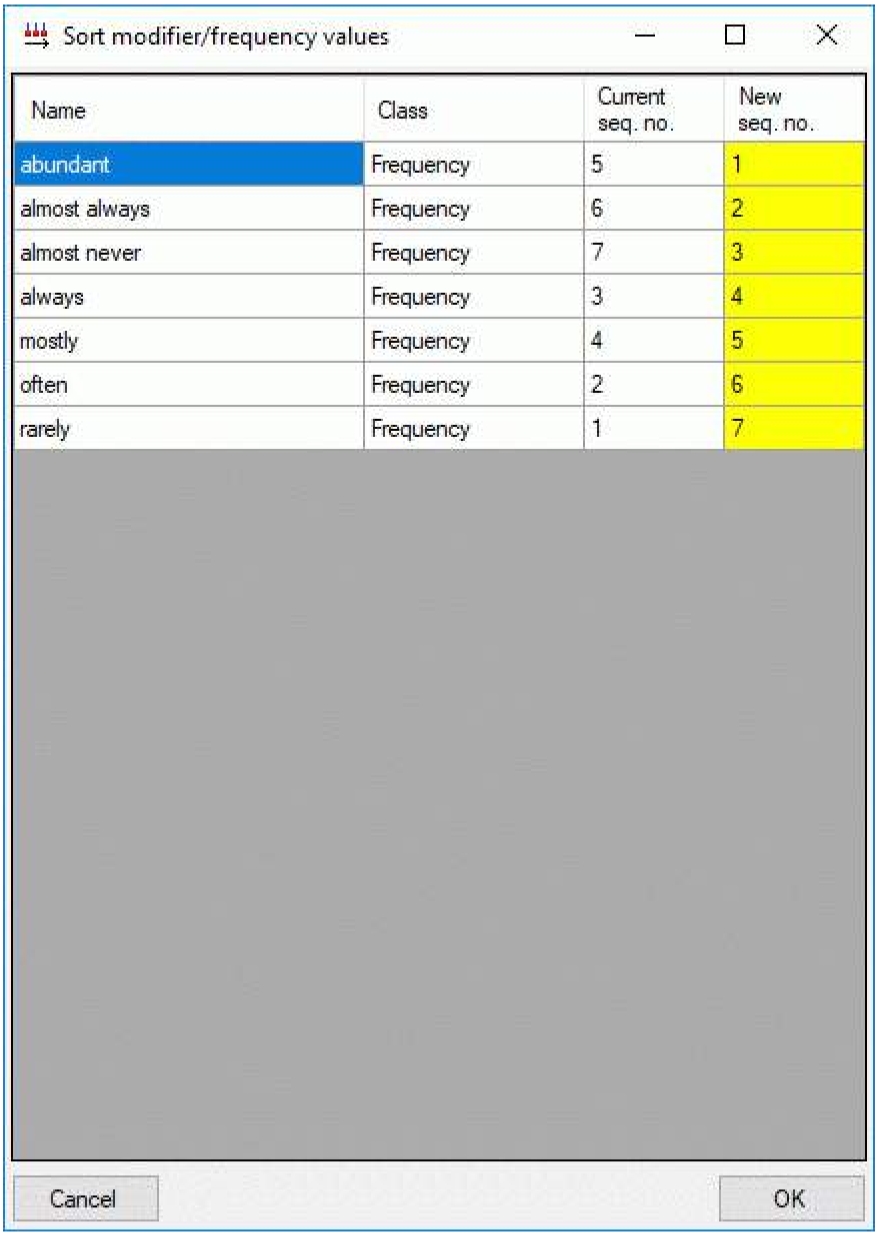
No.	Modifier	Class
1	Spring	Seasonal
2	Summer	Seasonal
3	Automn	Seasonal
4	Winter	Seasonal
5	uncertain	Certainty
6	almost certainly	Certainty
7	likely	Certainty
8	perhaps	Certainty
9	very likely	Certainty
10	bluish	Other

Frequency

No.	Frequency	Low	High
1	rarely	0	0,05
2	often	0,5	1
3	always	1	1
4	mostly	0,5	1
5	abundant	0,7	1
6	almost always	0,99	1
7	almost never	0	0,01

You may order the modifier and frequency values according the sequence of the predefined values by pressing the ⇉ button, which opens one of the windows shown below. Values that are not in the predefined lists will be shifted to the end of the list.

Name	Class	Current seq. no.	New seq. no.
almost certainly	Certainty	6	1
likely	Certainty	7	2
perhaps	Certainty	8	3
very likely	Certainty	9	4
bluish	Other	10	5
Spring	Seasonal	1	6
Summer	Seasonal	2	7
Automn	Seasonal	3	8
Winter	Seasonal	4	9
uncertain	Certainty	5	10

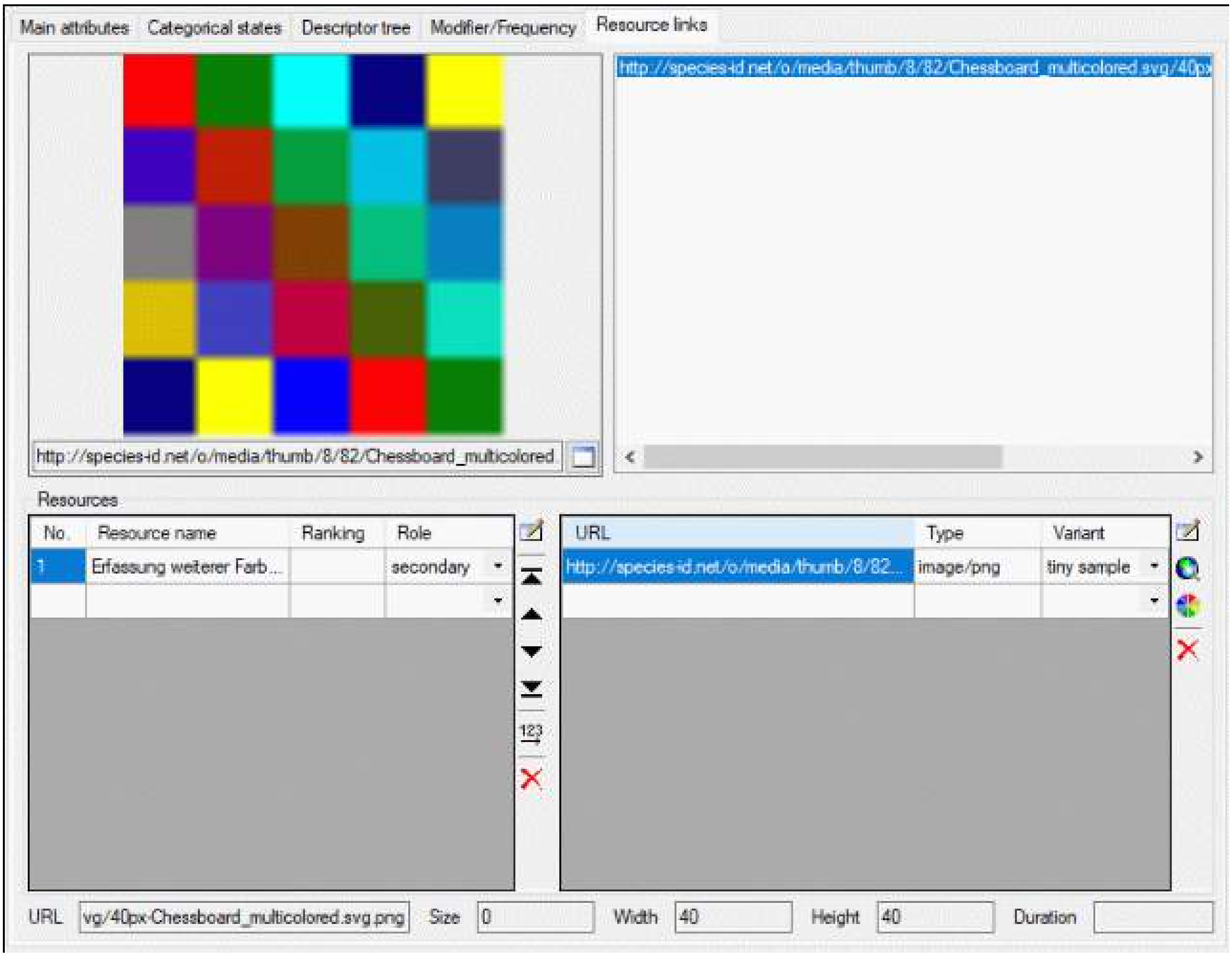


Name	Class	Current seq. no.	New seq. no.
abundant	Frequency	5	1
almost always	Frequency	6	2
almost never	Frequency	7	3
always	Frequency	3	4
mostly	Frequency	4	5
often	Frequency	2	6
rarely	Frequency	1	7

Continue with:

- Edit descriptors - Main attributes tab
- Edit descriptors - Categorical states tab
- Edit descriptors - Descriptor tree tab
- Edit descriptors - Resource links tab

Editing the descriptor - Resource links tab



http://species-id.net/o/media/thumb/8/82/Chessboard_multicolored.svg/40px

http://species-id.net/o/media/thumb/8/82/Chessboard_multicolored

No.	Resource name	Ranking	Role
1	Erfassung weiterer Farb...		secondary

URL	Type	Variant
http://species-id.net/o/media/thumb/8/82...	image/png	tiny sample

URL: vg/40px-Chessboard_multicolored.svg.png
Size: 0
Width: 40
Height: 40
Duration:

The resouce links tab allows assigment and inspection of resource links for the descriptor. In the lower **Resources** part of the tab there are two tables. Ar the left the "Resource" table specifies the single resources, at the right the "Resource variant" table contains the associated URLs to images, video or sound resources.

To enter a new resource select the empty line at the end of the "Resource" table and click on the "Resource name" field. After entering the "Resource name" (leave the cell by pressing the **TAB** key) automatically a new value for the sequence number ("No.") is initialized. The sequence number determines the display order in tables and may be changed manually. You may order the resource entries by clicking on the column header or by using the arrow buttons in the left tool strip (▲ and ▼for up and down, ⤒and ⤓to shift the selected entry to top or bottom). After ordering the resources click button ¹²³→to renumber the entries starting with "1" and make the changes effective. In field "Ranking" you may enter a numeric value in range 0 ... 10 expressing the suitability of the resource. In field "Role" you may select one of the offered values.

If you want to **delete** a resource, you have three choices:

1. Select the resource and press the ✗button in the left tool strip.
2. Select the resource and press the **Delete** key on the keyboard.
3. Enter the sequence number column ("No.") and remove the value. After leaving the cell the entry will be deleted.

In any case you will be asked if you want to delete the data row, if resource links are present.

To view or edit the additional resource data and copyright information press on the button besides the resource table. In field **License:** and a link to the license text in the web may be entered, in field **Rights:** you may enter a copyright text. By pressing the button a browser window can be opened to navigate to the license page in the web. Furthermore you may enter a detailled text (field **Details:**), the resource language (field **Language:**) and set the **Display embedded** flag (see picture below). If any additional resource data have been entered, this will be indicated by a square (□) behind the resource name's sequence number.

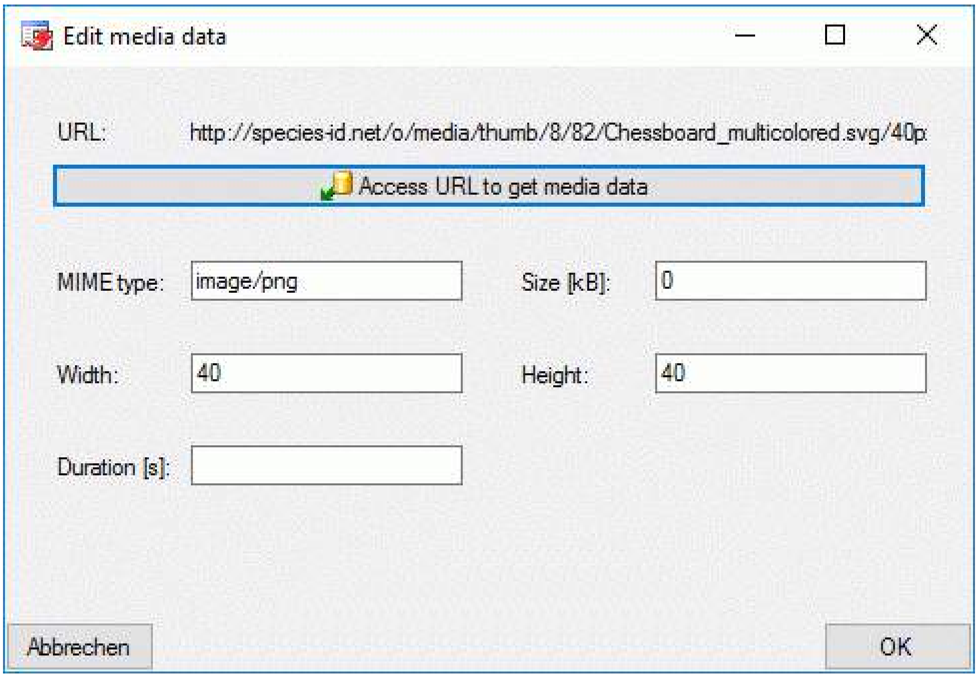
To enter a resource link, first select the entry in the "Resource" table, then select the empty line at the end of the "Resource variant table". By clicking on the "URL" field a web address may be entered. By double-clicking the "URL" field a browser window opens to navigate to the resource. For each resource several URLs to resource variants with different quality levels, e.g. different resolution, may be inserted. For each entry in the URL table a different value of "Variant" must be selected.

As an alternative to a resource URL a colour may be spcified in the format "color://#rrggbb" where "rrggbb" specifies a hexadecimal colour code. The colour can simply be seleced by clicking the button besides the resource variant table.

To remove a resource variant, select the entry and press the button in the right tool strip or the **Delete** key on the keyboard. Alternatively you may delete the "URL" entry in the resource variant table.

The upper part of the resource links tab consists of a preview window on the left side and the complete list of resource links. By selecting one of the links the preview is shown on the preview window. If you press button in the preview window, the resource is opened in a separate viewer window.

At the bottom of the resource links tab the media data of a selected URL are displayed. These data can be edited by double-clicking the "Type" entry in the resource variant table, by clicking at one of the media data value fields or the button. The edit dialog provides the possibility to access the URL to get available data. Alternatively the values may be edited manually.



URL: http://species-id.net/o/media/thumb/8/82/Chessboard_multicolored.svg/40p

MIME type: image/png

Size [kB]: 0

Width: 40

Height: 40

Duration [s]:

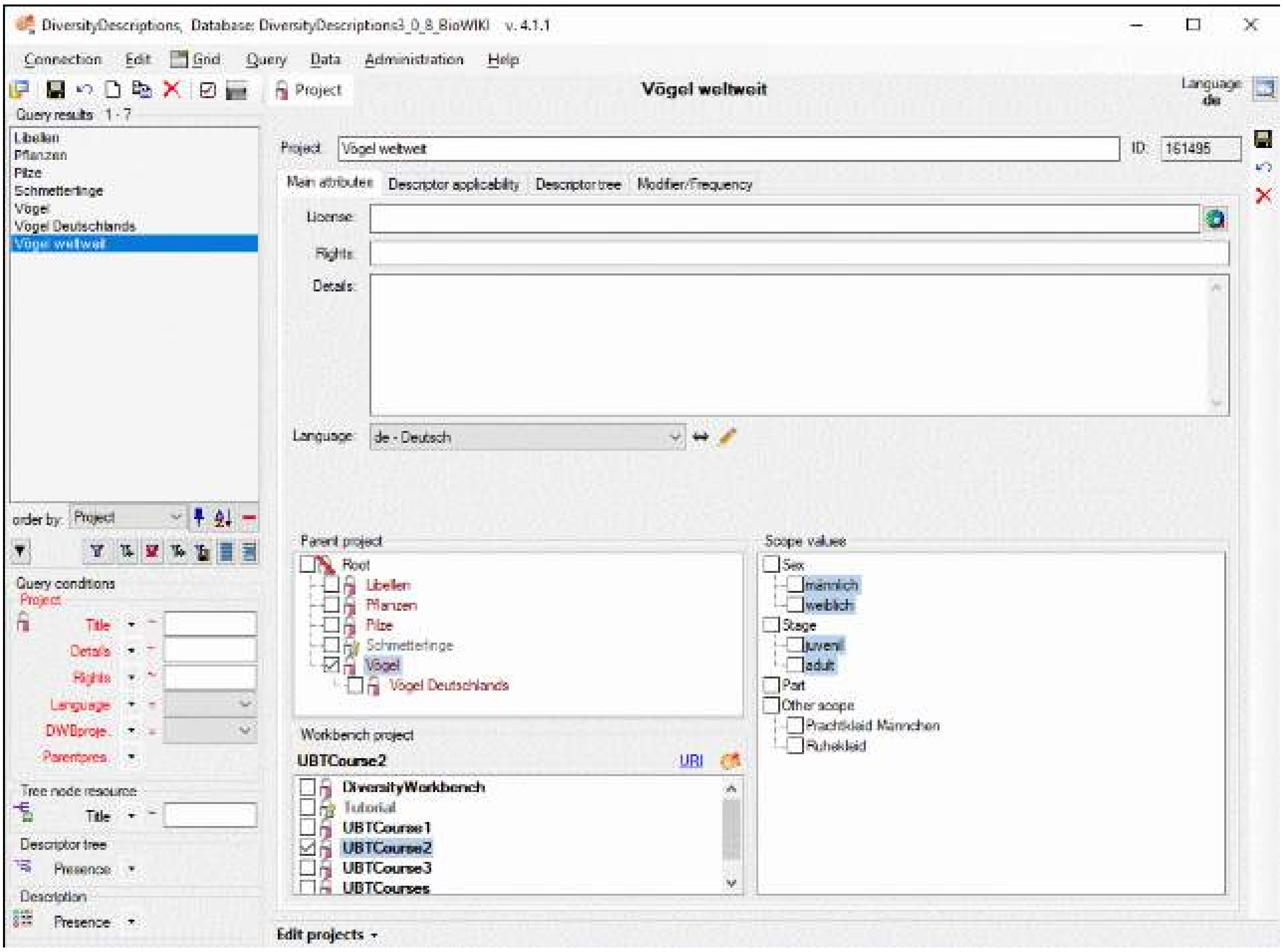
Continue with:

- Edit descriptors - Main attributes tab
- Edit descriptors - Categorical states tab
- Edit descriptors - Descriptor tree tab
- Edit descriptors - Modifier/Frequency tab

Editing the project

After starting a database query and selecting an entry in the result list the dataset is diplayed in the edit window. In the header area the dataset name and the project language are shown (see picture below). Below the header area the project name may be edited in a text box. Changes of the project name or the project language will be visible in the header after saving the dataset. To check dataset changes, click on the button to open the history.

The main project data may be accessed in the first **Main attributes** tab, which is described below. Click on one of the other tabs in the picture below to go directly to the appropriate manual chapter.



Project: Vögel weltweit

ID: 161495

Language: de - Deutsch

Workbench project: UBTCourse2

Main attributes tab

The main attributes tab provides access to a license URI, a short rights text and a detailled project text. The project language can be selected from a list. In field **Rights** you may enter a copyright text, in field **License** and a link to the license text in the web may be entered. By pressing the button a browser window can be opened to navigate in the web.

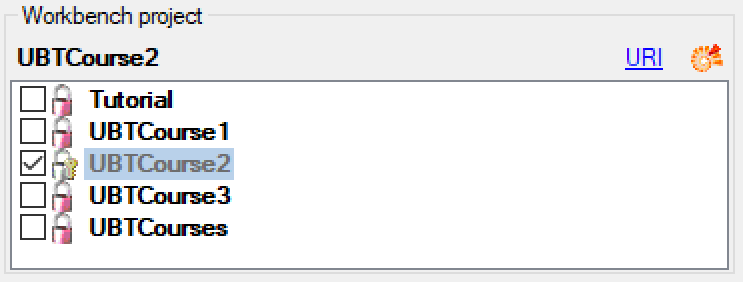
With combo box **Language** you can select the project's default language. You man change the display and sorting of the entries in the **Language** combo box from "<code> - <description>" to "<description> - <code>" (and back) by clicking the button ⇔. If you need language codes that are not included in the list, click the button. For more details see Edit language codes.

In the bottom area at the left side the **Parent project** and **Workbench project** can be adjusted. If the project has no parent, select "Root" (symbol). The **Parent project** adjustment has an influence on the available descriptors, recommended modifier and frequency values and recommended statistical measures, because these adjustments are inherited by the subordinate project. If for a project in the **Parent project** tree no write access is possible, this is indicated by grey text colour and symbol . The missing write rights for a parent project has no influence on accessability of the actually selected project, except that the parent project adjustment cannot be changed.


Parent project

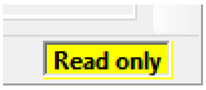
- ☐ Root
  - ☐ Schmetterlinge
  - ☑ Vögel
    - ☐ Vögel Deutschlands

The **Workbench project** (except the dummy value "DiversityDescriptions") references a project entry administered in DiversityProjects. It determins visibility and accessability of the local DiversityDescriptions projects for the database user. Each local project is assigned to exactly one **Workbench project**. When you mark the entry you may view the database link by clicking on URI or view the data stored in DiversityProjects by clicking on symbol at the right (see image balow). For details about access rights administration see section "Data access".


Workbench project

UBTCourse2

- ☐ Tutorial
- ☐ UBTCourse1
- ☑ UBTCourse2
- ☐ UBTCourse3
- ☐ UBTCourses

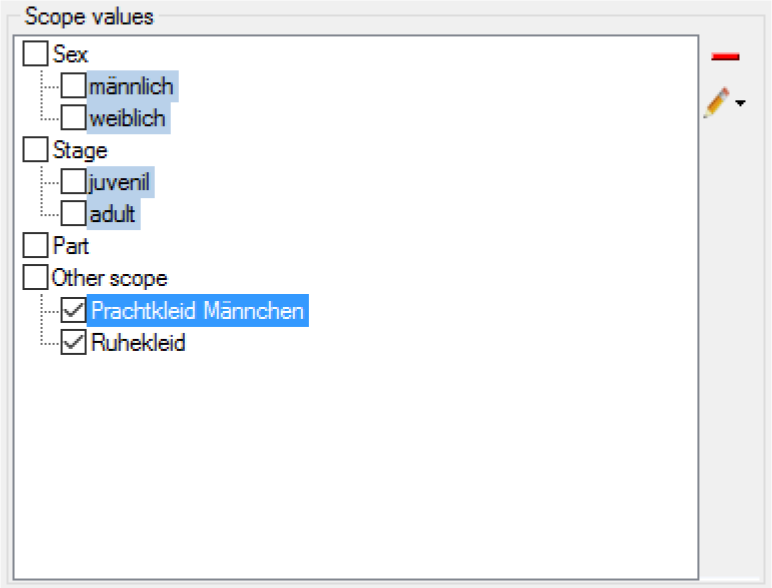

Read only

Fully accessible workbench projects are marked with the symbol . If only read access is allowed, the workbench project is shown with grey text and symbol (see picture above). If the actually selected project has been assigned to a "read only" workbench project, e.g. by another user with appropriate rights, this is indicated at the right bottom corner of tha application window (see picture below right).

In the **Scope values** section at the right the values for scope types "Sex", "Stage" and "Other scope" may defined. When you mark one of the entries, a tool strip with the available operations is shown at the right border of the control. To insert a new value, select the scope type and press button ✚. In case of "Sex" one of the predefined "sex status" values derived from the SDD standard has to be selected. In all other cases a new value with a numeric key is appended, that can be renamed by pressing the button and selecting **Edit scope name** or by clicking at the name.

In case of "Sex" scope the "Edit" menu offers the additional menu items **Reset scope name** , which appears if the name differs from the original "sex status". Further the "sex status" value may be changed with menu item **Set sex status**. For the other scope types you may enter a details text by pressing the button and selecting **Edit scope details**.

To remove a scope value, select it and press the ━ button. To make a value available for the project, the check box must be checked. If the selected project has a parent and a value has already been checked in the parent project, this is indicated by the background colour (see image below).

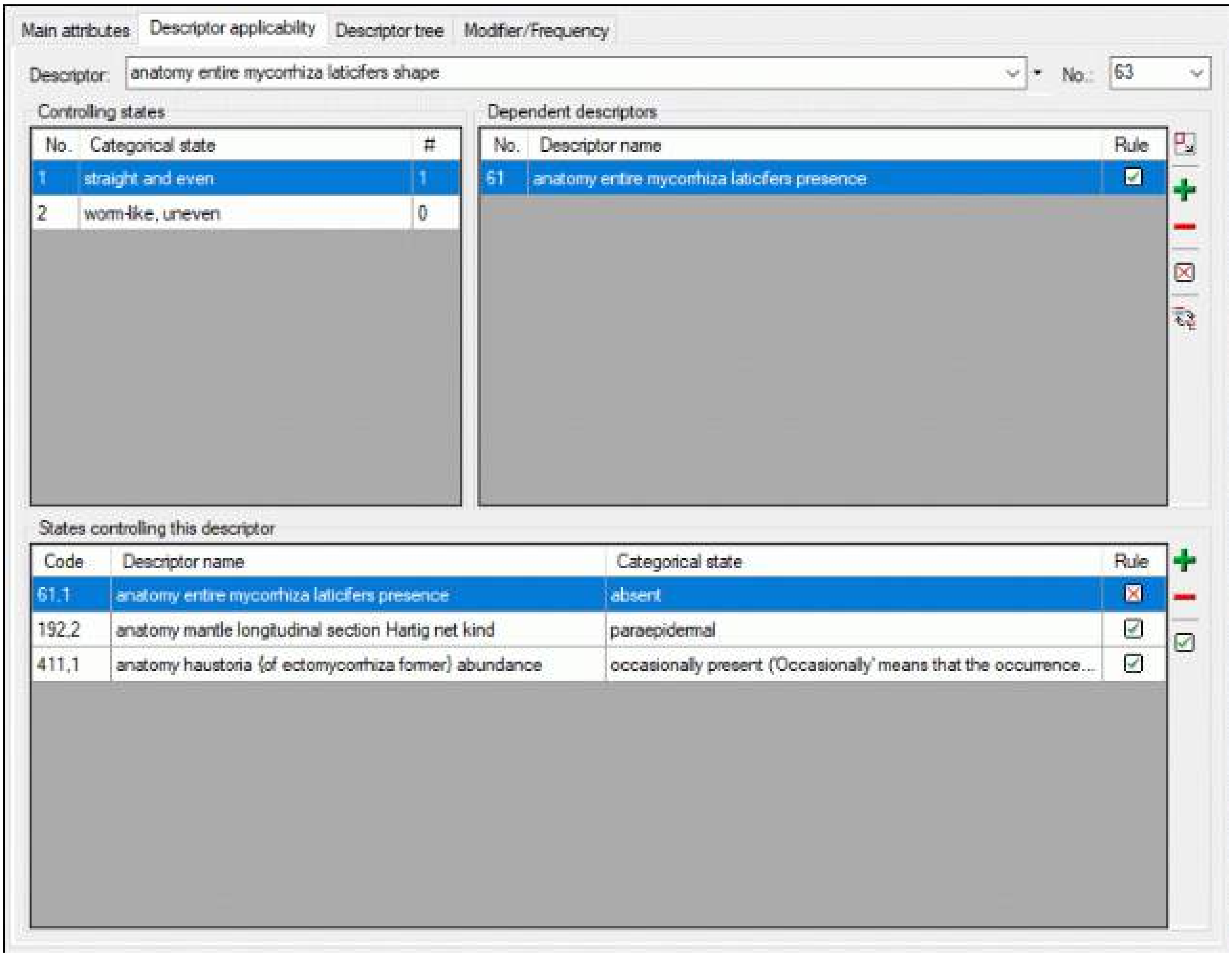


- ☐ Sex
  - ☐ männlich
  - ☐ weiblich
- ☐ Stage
  - ☐ juvenil
  - ☐ adult
- ☐ Part
- ☐ Other scope
  - ☑ Prachtkleid Männchen
  - ☑ Ruhekleid

Continue with:

- Edit projects - Descriptor applicability tab
- Edit projects - Descriptor tree tab
- Edit projects - Move/Copy descriptor trees
- Edit projects - Modifier/Frequency tab

Editing the project - Descriptor applicability tab



Descriptor: anatomy entire mycorrhiza laticifers shape No.: 63

Controlling states

No.	Categorical state	#
1	straight and even	1
2	worm-like, uneven	0

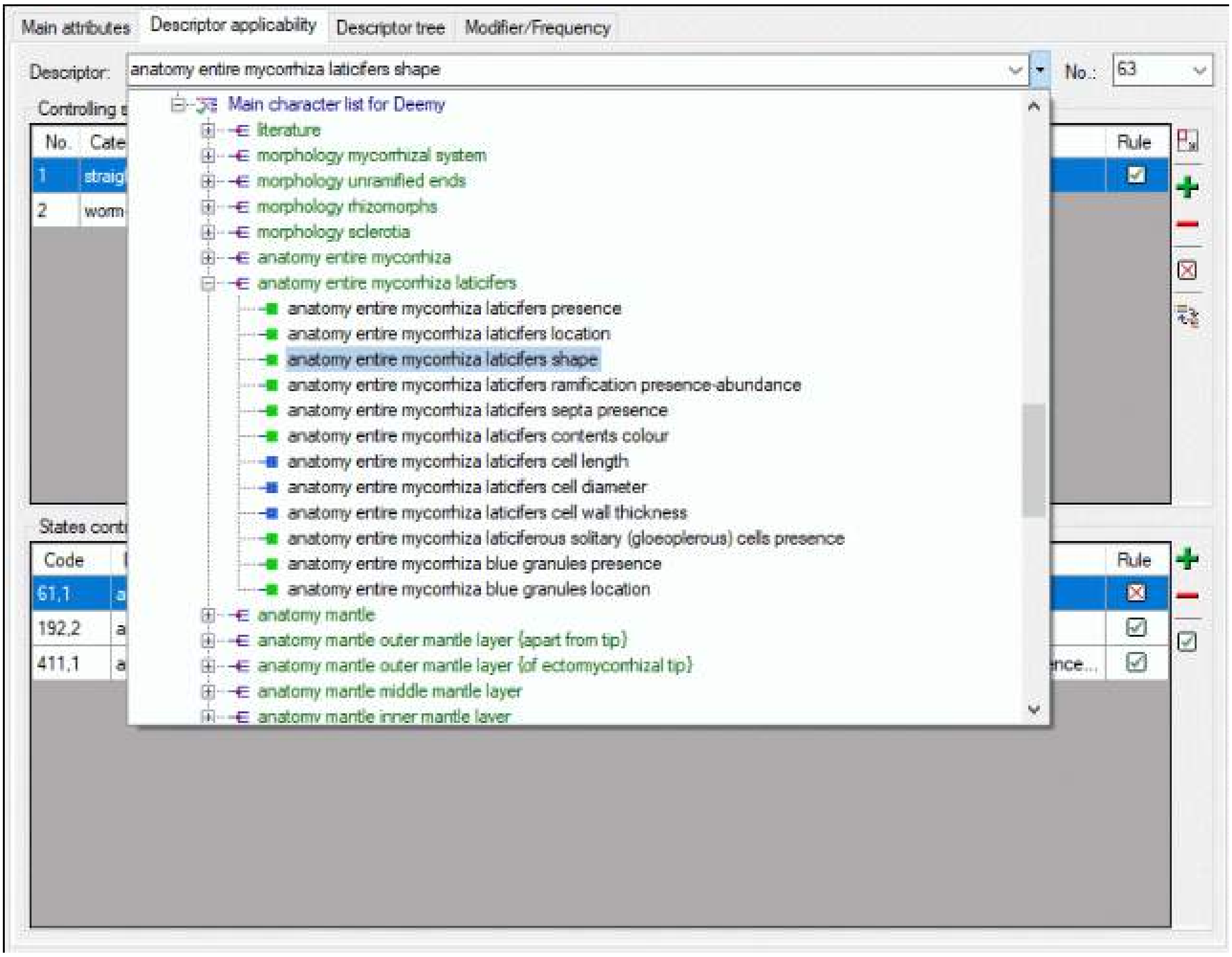
Dependent descriptors

No.	Descriptor name	Rule
61	anatomy entire mycorrhiza laticifers presence	☑

States controlling this descriptor

Code	Descriptor name	Categorical state	Rule
61.1	anatomy entire mycorrhiza laticifers presence	absent	☒
192.2	anatomy mantle longitudinal section Hartig net kind	paraepidermal	☑
411.1	anatomy haustoria (of ectomycorrhiza former) abundance	occasionally present ('Occasionally' means that the occurrence...	☑

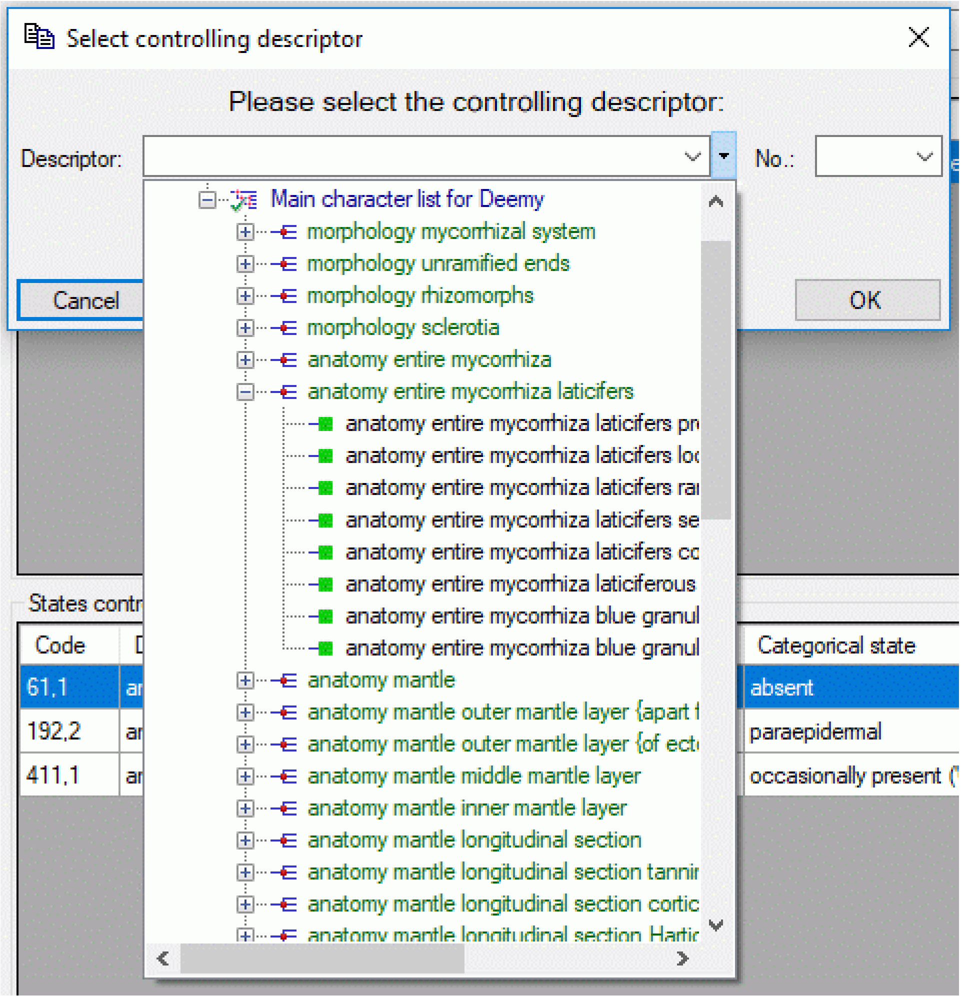
The **Descriptor applicability** tab serves the administration of dependencies between categorical states and dependent descriptors. First a descriptor has to be selected either by its name in the alphabetically ordered drop down list or its sequence number ("No.") in the first line of the descriptor dependencies tab. If for the selected project a descriptor tree is present, the ▾ button allows selecting the descriptor form the descriptor tree (see picture below).



Descriptor: anatomy entire mycorrhiza laticifers shape

No.: 63

The table **Controlling states** in the upper left part of the tab shows the categorical states if a categorical descriptor has been selected. When you have adusted the restrichted descriptor view, visible by the button in the toolbar of the **Dependent descriptor** section, only the actually set dependent descriptors are displayed here. You can switch to an alternate **Full descriptor view** as described below. For each categorical state **Dependent descriptors** can be inserted by pressing the + button. A dialog window opens to select the descriptor either by its name, sequence number or using the descriptor tree (see picture below).



Code	D	Categorical state
61,1	ar	absent
192,2	ar	paraepidermal
411,1	ar	occasionally present ('

In column "Rule" the symbol ☒ indicates that the dependent descriptor is inapplicable if the controlling state is present in a description. The symbol ☑ indicates that the controlling state must be present in a description if the controlled descriptor shall be applicable. The rule can be toggled by clicking the symbol in the table or by pressing the corresponding button (☒ rsp. ☑) at the right. To remove a dependent descriptor select it and press the − button.

In the lower part of the tab you find the **States controlling this descriptor**. You may double-click on the item to select navigate to it for editing. Alternatively you may edit the controlling descriptor states using the control buttons of the tool strip at the right. By double-clicking an entry in **Dependent descriptors** or in **States controlling this descriptor** you may navigate forwards and backwards in the chain of dependent descriptors.

If you want to get an overview of all the project's descriptor dependencies or want to delete all dependencies, take a look at the **Applicability tree** section below.

Calculation of the descriptor applicability

To decide if a descriptor is applicable in a description, the following conditions are evaluated:

- **Inapplicable-if rule:** If only controlling states are present in a description, these make the controlled descriptor inapplicable. The character remains applicable if either no state at all, or any non-controlling states are present.
- **Applicable-if rule:** If any controlling state is present in a description, these make the

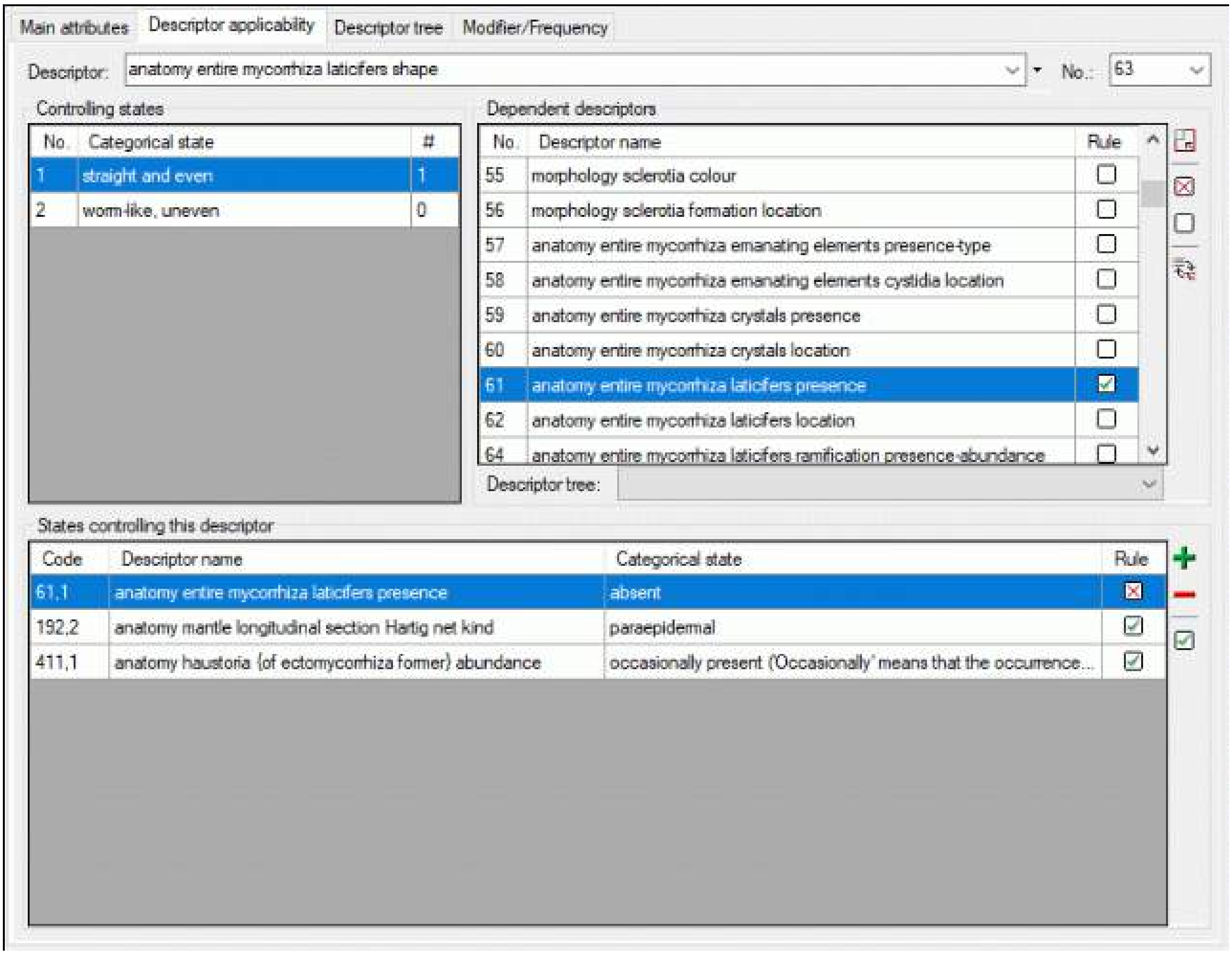
controlled descriptor applicable. It is inapplicable if only non-controlling states are present.

- **Special condition 1:** If the controlling descriptor is inapplicable (through another applicability rule, or through an explicit "Not applicable" data status value), the controlled descriptor is always inapplicable as well.
- **Special condition 2:** If no data for the controlling character are present in a description (data completely missing or only status is "Missing data" or "Not to be recorded"), the controlled character always remains applicable.

Full descriptor view

By clicking the button ⇲ in the toolbar of the **Dependent descriptor** section, you can chenge to the full descriptor view (see image below). In section **Dependent descriptors** all available project descriptors are shown. You may set a dependency by selecting the descriptor and clicking the button ☒ rsp. ☑. To remove the dependency, click on button ☐. Alternatively you may click on they symbol in the table column "Rule" to change the values in the sequence ☒ -> ☑ -> ☐.

If you select a values for the **Descriptor tree**, the descriptor list is restricted to the values included in that descriptor tree. Please be aware that existing dependencies might be hidden by such a selection!



Descriptor: anatomy entire mycorrhiza laticifers shape

No.: 63

Controlling states

No.	Categorical state	#
1	straight and even	1
2	worm-like, uneven	0

Dependent descriptors

No.	Descriptor name	Rule
55	morphology sclerotia colour	☐
56	morphology sclerotia formation location	☐
57	anatomy entire mycorrhiza emanating elements presence-type	☐
58	anatomy entire mycorrhiza emanating elements cystidia location	☐
59	anatomy entire mycorrhiza crystals presence	☐
60	anatomy entire mycorrhiza crystals location	☐
61	anatomy entire mycorrhiza laticifers presence	☑
62	anatomy entire mycorrhiza laticifers location	☐
64	anatomy entire mycorrhiza laticifers ramification presence-abundance	☐

Descriptor tree:

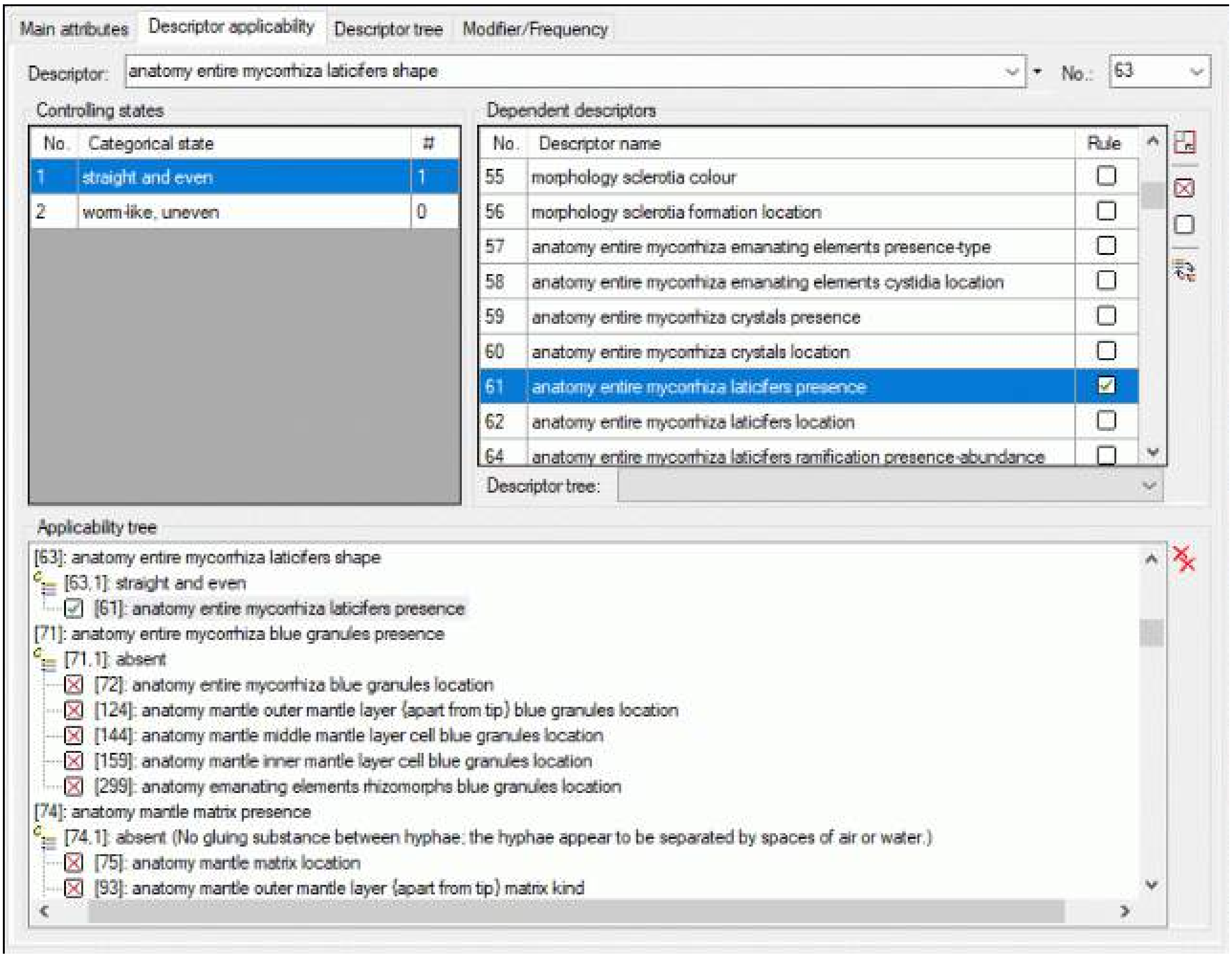
States controlling this descriptor

Code	Descriptor name	Categorical state	Rule
61,1	anatomy entire mycorrhiza laticifers presence	absent	☒
192,2	anatomy mantle longitudinal section Hartig net kind	paraepidermal	☑
411,1	anatomy haustoria (of ectomycorrhiza former) abundance	occasionally present ('Occasionally' means that the occurrence...	☑

You can return to the restricted descriptor view by clicking on button ⇱.

Applicability tree

Instead of the **States controlling this descriptor** you may display a complete overview of the descriptor applicability rules by pressing the button in the **Dependent descriptors** section (see image below). By double-clicking an item in the **Applicability tree** you can open it for editing.



Descriptor: anatomy entire mycorrhiza laticifers shape No.: 63

Controlling states

No.	Categorical state	#
1	straight and even	1
2	worm-like, uneven	0

Dependent descriptors

No.	Descriptor name	Rule
55	morphology sclerotia colour	☐
56	morphology sclerotia formation location	☐
57	anatomy entire mycorrhiza emanating elements presence-type	☐
58	anatomy entire mycorrhiza emanating elements cystidia location	☐
59	anatomy entire mycorrhiza crystals presence	☐
60	anatomy entire mycorrhiza crystals location	☐
61	anatomy entire mycorrhiza laticifers presence	☑
62	anatomy entire mycorrhiza laticifers location	☐
64	anatomy entire mycorrhiza laticifers ramification presence-abundance	☐

Descriptor tree:

Applicability tree

[63]: anatomy entire mycorrhiza laticifers shape
- [63.1]: straight and even
  - ☑ [61]: anatomy entire mycorrhiza laticifers presence

[71]: anatomy entire mycorrhiza blue granules presence
- [71.1]: absent
  - ☒ [72]: anatomy entire mycorrhiza blue granules location
  - ☒ [124]: anatomy mantle outer mantle layer (apart from tip) blue granules location
  - ☒ [144]: anatomy mantle middle mantle layer cell blue granules location
  - ☒ [159]: anatomy mantle inner mantle layer cell blue granules location
  - ☒ [299]: anatomy emanating elements rhizomorphs blue granules location

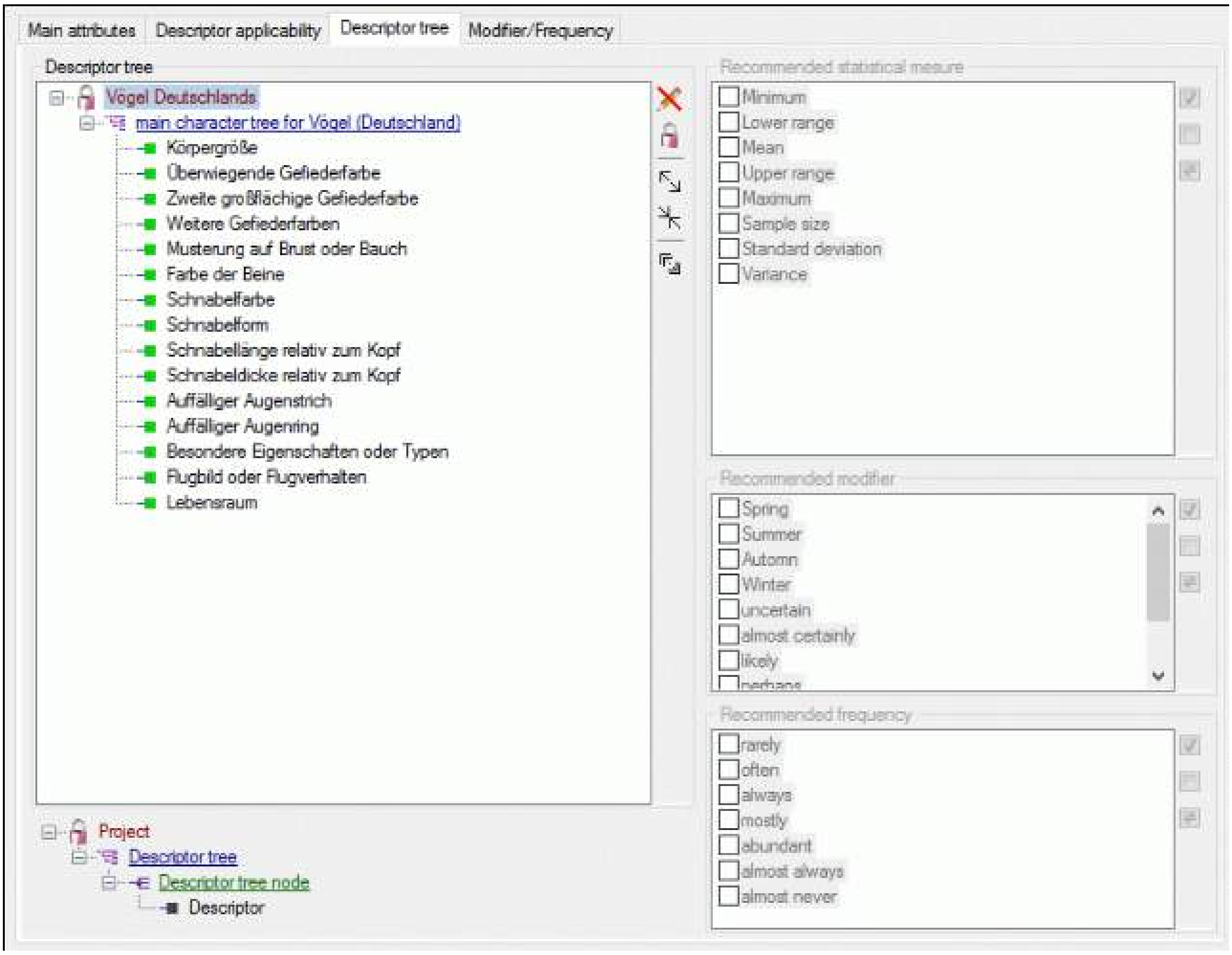
[74]: anatomy mantle matrix presence
- [74.1]: absent (No gluing substance between hyphae; the hyphae appear to be separated by spaces of air or water.)
  - ☒ [75]: anatomy mantle matrix location
  - ☒ [93]: anatomy mantle outer mantle layer (apart from tip) matrix kind

By pressing the button in the **Applicability tree** section you can delete all dependencies shown in the tree.

Continue with::

- Edit projects - Main attributes tab
- Edit projects - Descriptor tree tab
- Edit projects - Move/Copy descriptor trees
- Edit projects - Modifier/Frequency tab

Editing the project - Descriptor tree tab



The **Descriptor tree** tab provides the possibility for a structured assignment of the descriptors to the projects. The **Descriptor tree** consists of three node types, which show the administered **projects**, **descriptor trees**, **descriptor tree nodes** and **descriptors**. The tree parts' colours are shown in the example at the bottom. By pressing the ⧉ button on the tool stip at the right side the example may be hidden. The buttons displayed on the too strip will change depending on the selected entry.

By default only the selected project. its subordinated projects and their descriptor trees are displayed. You may select the "Show all projects" option by clicking the button 🔒 in the tool strip to show alle projects. To indicate that this option is active, the icon background will be changed to red color (see images below). Be aware that this option might slow down data loading.

Descriptor trees are the root of a tree and may only be appended at a project. To insert a new descriptor tree select a project and press ➕, to delete it select the descriptor tree and press ➖. **Descriptor tree nodes** may be appended at a descriptor tree or another descriptor tree node. To insert a new descriptor tree node, select the parent and press ➕, to remove it select the descriptor tree node and press ➖. **Descriptors** may be appended to a descriptor tree or a descriptor tree node. To append a descriptor select the parent and press ➕, to remove it select the descriptor and press ➖. All these functions can alternatively be accessed by the context menu by a right click on the entry. The descriptor type is indicated by different icons. Categorical descriptors are marked as 🟩, quantitative descriptors as 🟦, text descriptors as 🟥 and sequence descriptors as 🟧.

You may change the name of a **Descriptor tree** or a **Descriptor tree node** in three different ways:

1. Select the tree element (single click) and then click once on it.
2. Select the tree element (single click) and click on button in the tool bar on the right.
3. Right-click the tree element and select item **Edit name** from the context menu.

You may edit the name of the selected node within the tree. The **Descriptor tree** must be globally unique. The **Descriptor tree node** names must be unique with respect to their tree position, i.e. all nodes with the same parent within a descriptor tree must have distinguished names.

If projects and their associated descriptor trees cannot be changed, because the project has been set to "read-only" state, these parts are displayed with **grey** text color (see project "Schmetterlinge" in picture above).

When a new descriptor tree or descriptor tree node is inserted it gets numeric name, which may be changed by clicking on the node or selecting from the context menu. Take care that the names of the discriptor trees must be unambiguous within the whole database! The names of the descriptor tree nodes must only be unambiguous within one parent.

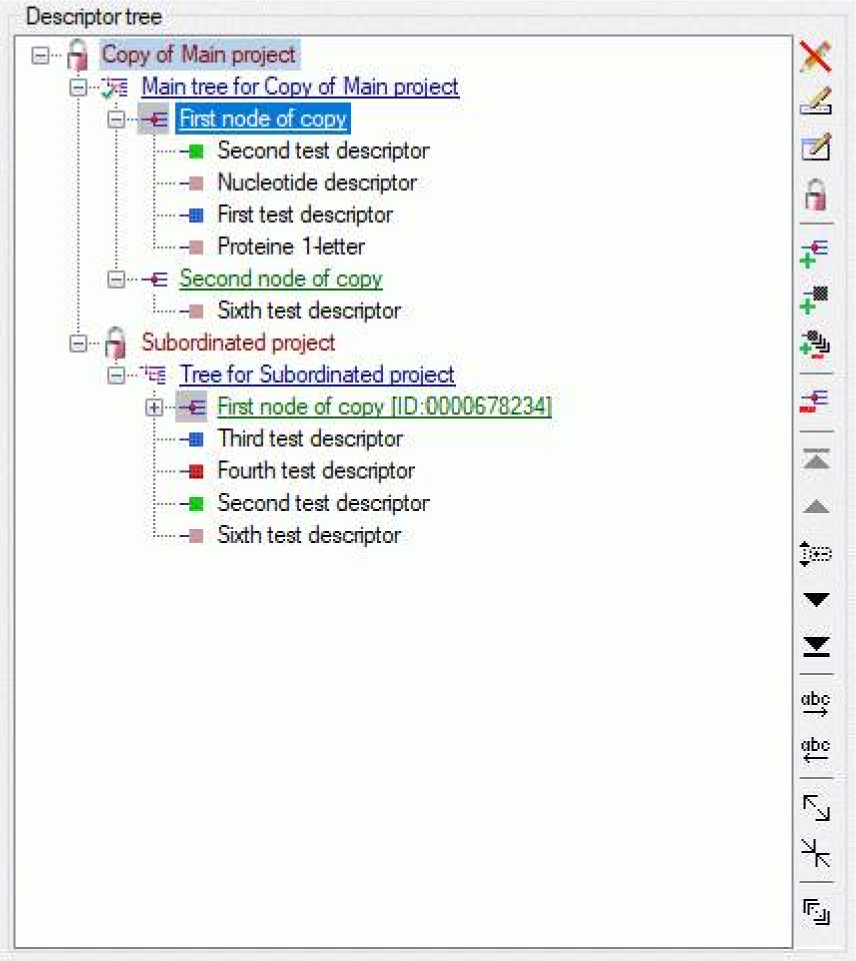
The descriptor trees support three main functions:

- Assignment of descriptors to a certain project
- Selection of recommended **Frequency/Modifier** values and **Statistical measures** for a certain descriptor
- Structured arragement of the descriptors, e.g. for hierarchical selection lists and definition of descriptor subsets for description editing and export

If no descriptor tree is installed for a certain project, all descriptors, modifier/frequency values and statistical measures will be usable in the project's descriptions. If a project contains several descriptor trees, the available descriptors are the superset of the descriptors assigned to all contained trees.

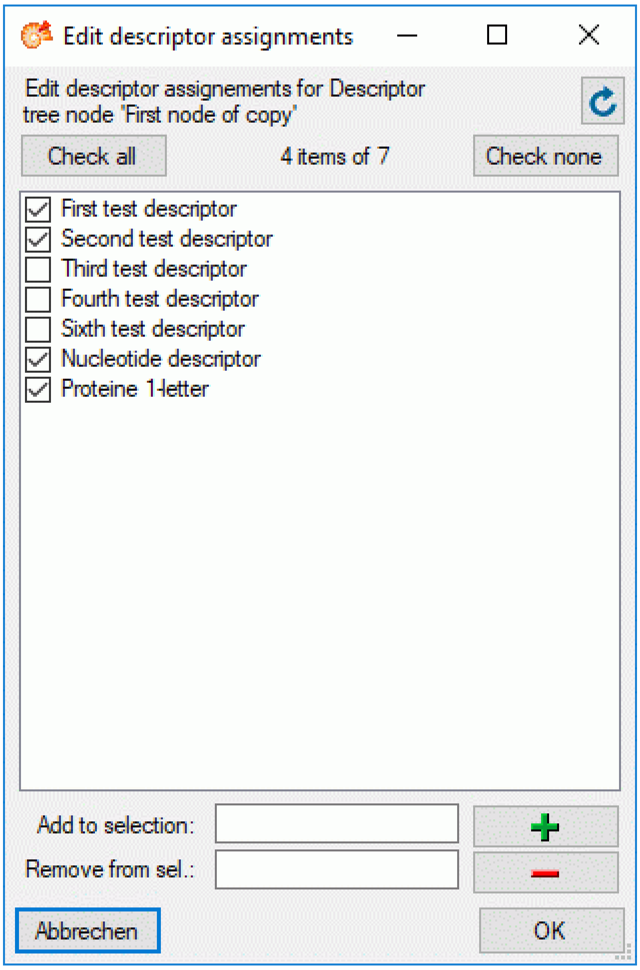
Editing the project descriptor assignemnts for a tree node

When you use button to append a descriptor to a tree node, you will be offered all accessible descriptors in the database. In many cases, when you have already assigned all required descriptors to the project, you may wish to build some additional structured descriptor trees. If you select a descriptor tree or a descriptor tree node, the button is shown (see image below left). After clicking this button you will get a selection list with all descriptors assigned to the project. Descriptors that are included in the tree node are selected in the list (see image below right). You may easily change the selection and click "OK" to make the changes effective.



Descriptor tree

- Copy of Main project
  - Main tree for Copy of Main project
    - First node of copy
      - Second test descriptor
      - Nucleotide descriptor
      - First test descriptor
      - Proteine 1-letter
    - Second node of copy
      - Sixth test descriptor
  - Subordinated project
    - Tree for Subordinated project
      - First node of copy [ID:0000678234]
      - Third test descriptor
      - Fourth test descriptor
      - Second test descriptor
      - Sixth test descriptor



Edit descriptor assignements for Descriptor tree node 'First node of copy'

☑ First test descriptor
☑ Second test descriptor
☐ Third test descriptor
☐ Fourth test descriptor
☐ Sixth test descriptor
☑ Nucleotide descriptor
☑ Proteine 1-letter

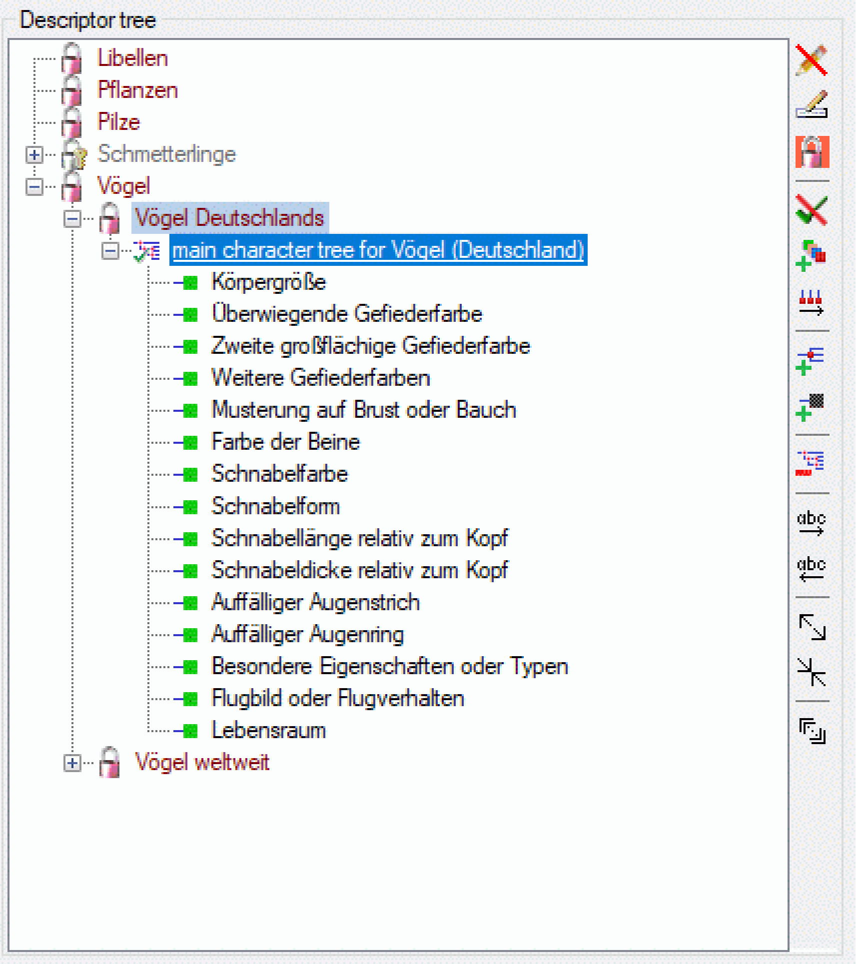
Add to selection:

Remove from sel.:

Sorting of descriptor tree elements

By pressing the button you can expand the tree view to display all elements, by pressing the tree will be collapsed to descriptor tree level. With the arrow buttons (▲ ▼ rsp.) you can move descriptors or descriptor tree nodes up or down rsp. to the top or the bottom. An additional ordering option is to select the descriptor tree node you want to move and click the button. The button's back color changes to red and you may now select the new position in the tree. If you select a descriptor tree or a descriptor tree node, you may arrange the contained descriptors in alphabedical order by clicking the buttons (ascending) or (descending).

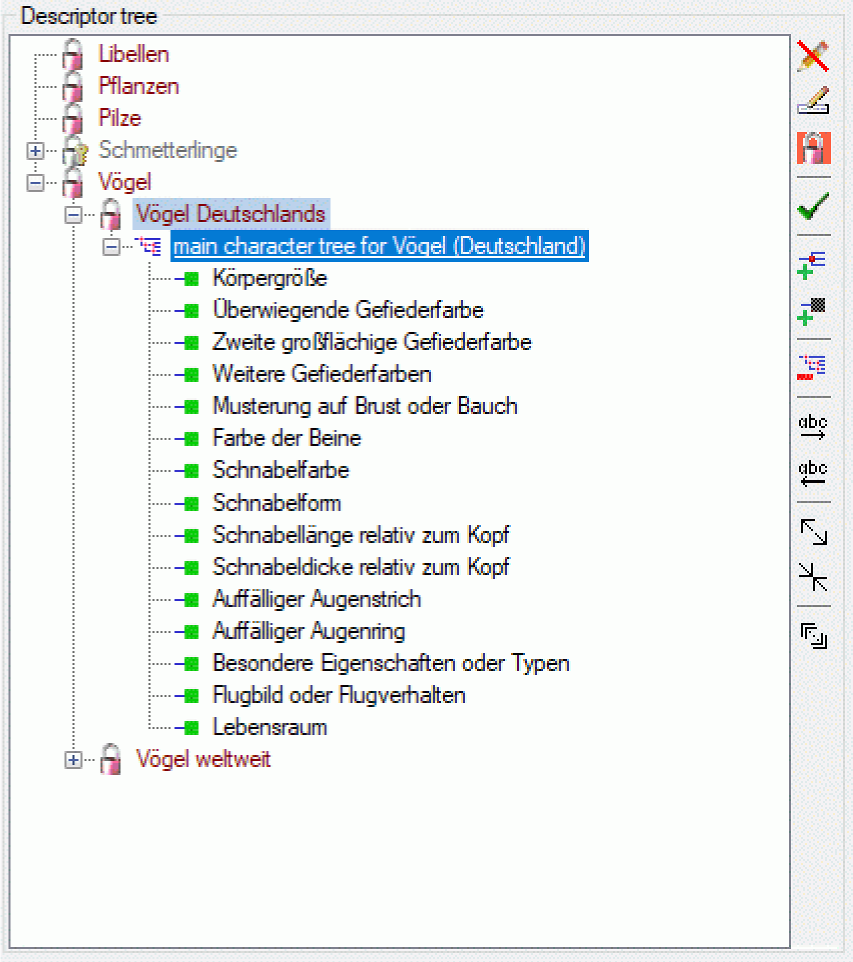
A descriptor tree may be marked as "tree complete" to indicate that this tree shall contain all descriptors for the project. This is done by selecting the descriptor tree node and clicking the button ✓. To indicate that the tree is marked as complete the tree icon changes to (see picture below).



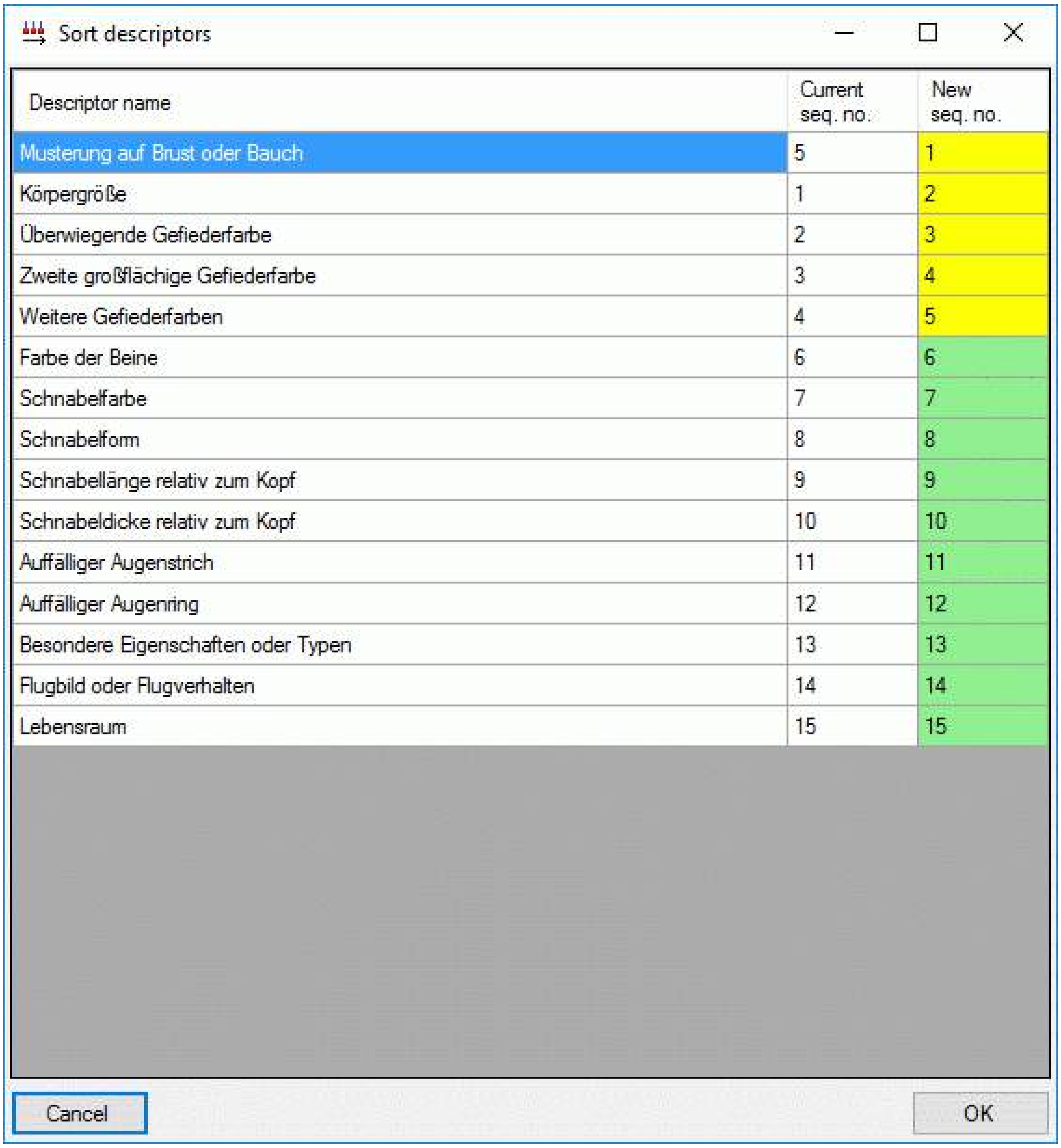
Descriptor tree

- Libellen
- Pflanzen
- Pilze
- Schmetterlinge
- Vögel
  - Vögel Deutschlands
    - main character tree for Vögel (Deutschland)
      - Körpergröße
      - Überwiegende Gefiederfarbe
      - Zweite großflächige Gefiederfarbe
      - Weitere Gefiederfarben
      - Musterung auf Brust oder Bauch
      - Farbe der Beine
      - Schnabelfarbe
      - Schnabelform
      - Schnabellänge relativ zum Kopf
      - Schnabeldicke relativ zum Kopf
      - Auffälliger Augenstrich
      - Auffälliger Augenring
      - Besondere Eigenschaften oder Typen
      - Flugbild oder Flugverhalten
      - Lebensraum
  - Vögel weltweit

The "tree complete" flag may be removed by clicking the button ✓and the tree icon will be changed back to ☰(see picture below).



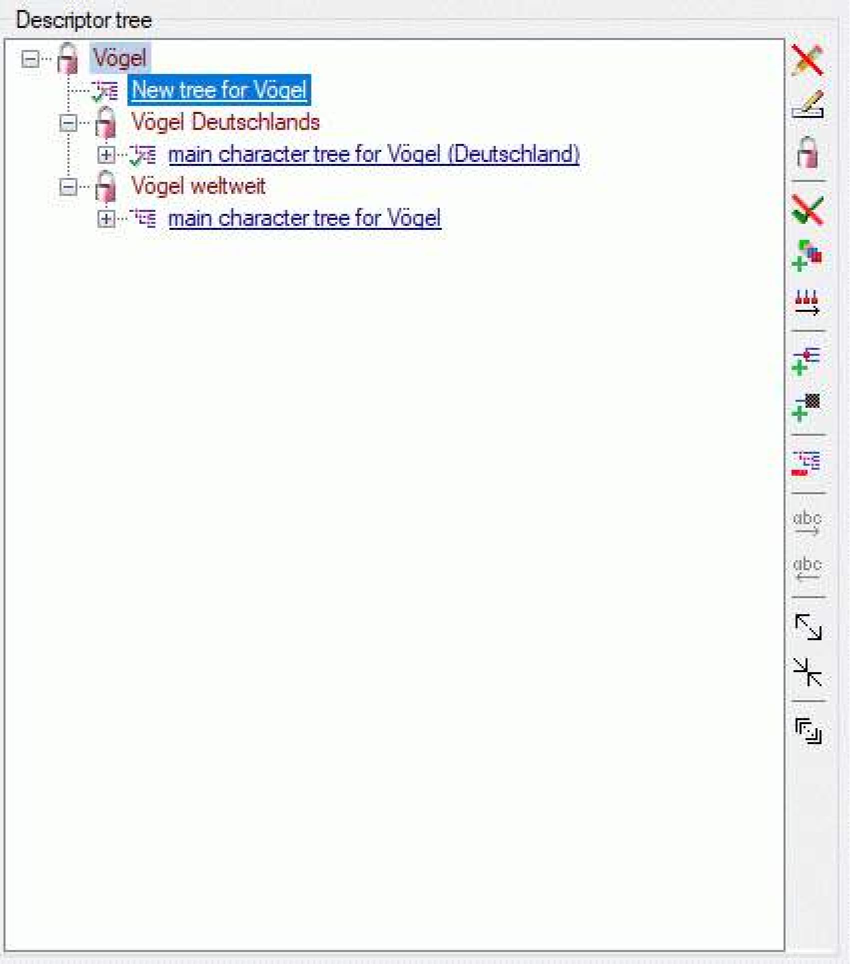
If a descriptor tree is marked as "tree complete", it can be used to take over the sorting of the descriptor nodes to the sequence number of the descriptors. But you must be aware that the descriptor's sequence number (field "No." in "Edit descriptor" main panel) is not project or tree dependent, i.e. that this operations will have influence on the dispolay sequence of all descriptions using these descriptors. Click on button (see picture above) to open the descriptor sorting window below.



Descriptor name	Current seq. no.	New seq. no.
Musterung auf Brust oder Bauch	5	1
Körpergröße	1	2
Überwiegende Gefiederfarbe	2	3
Zweite großflächige Gefiederfarbe	3	4
Weitere Gefiederfarben	4	5
Farbe der Beine	6	6
Schnabelfarbe	7	7
Schnabelform	8	8
Schnabellänge relativ zum Kopf	9	9
Schnabeldicke relativ zum Kopf	10	10
Auffälliger Augenstrich	11	11
Auffälliger Augenring	12	12
Besondere Eigenschaften oder Typen	13	13
Flugbild oder Flugverhalten	14	14
Lebensraum	15	15

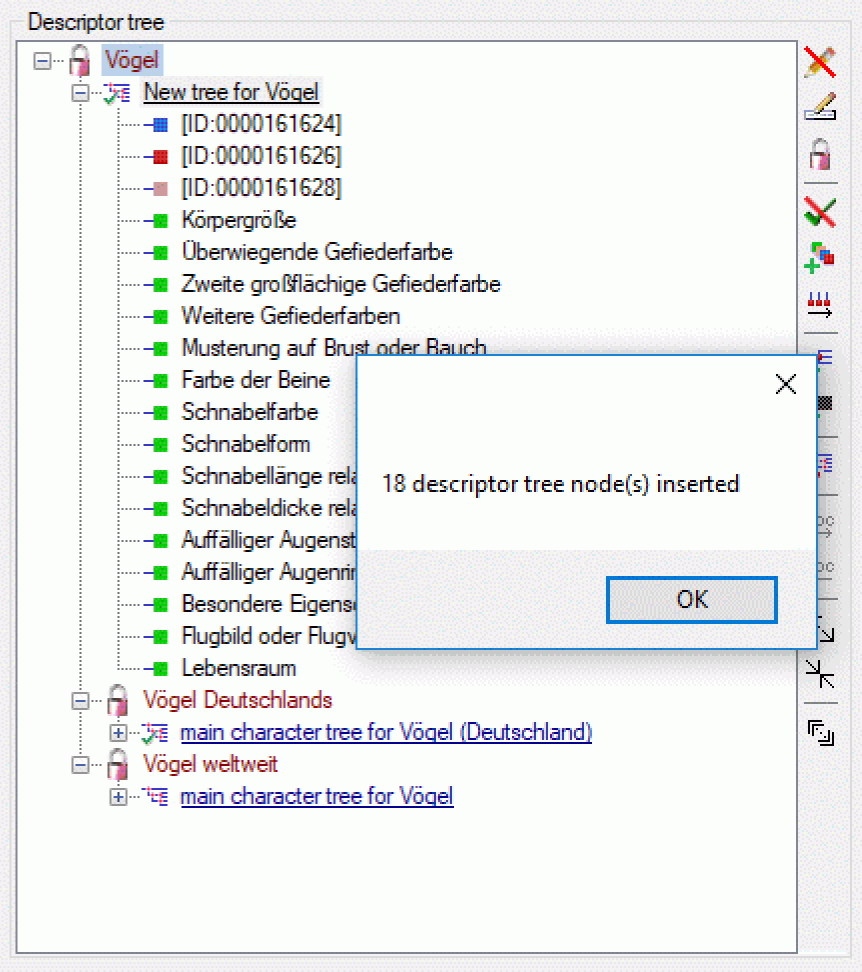
The first column shows the descriptor names as sorted in the descriptor tree, the second column shows the current sequence number int the database and the last column shows the new sequence number. If the sequence number stays unchanged, the new sequence number is displayed with green background, otherwise with yellow background. You may click on a new sequence number and change its value manually. By clicking on the table headers, you may sort the table display according descriptor names, old or new sequence numbers. If a descriptor may not be changed, because it is assigned to a project where the user has no write access, the whole line is displayed with grey backgound and cannot be changed. Finally click on **OK** to accept or **Cancel** to reject the changes.

An additional option available for complete trees is to copy missing descriptors with button . The descriptors available for a certain project include all descriptors assigned to all descriptor trees of the project and its sub-projects. In our example a new descriptor tree has been assigned to the upmost project (see image below left). After clicking the button all valid descriptors are inserted to the descriptor tree (see image below right).



Descriptor tree

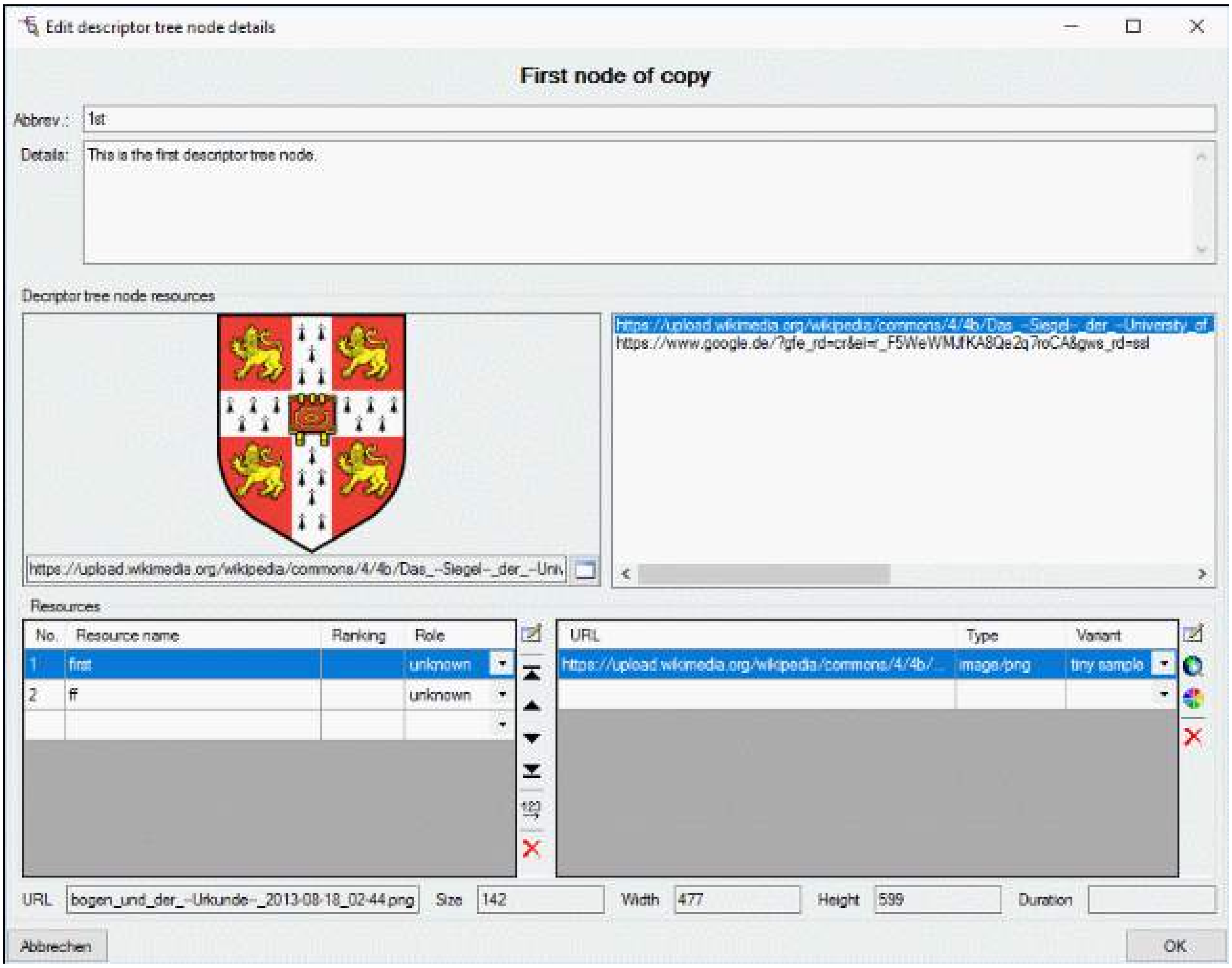
- Vögel
  - New tree for Vögel
  - Vögel Deutschlands
    - main character tree for Vögel (Deutschland)
  - Vögel weltweit
    - main character tree for Vögel



18 descriptor tree node(s) inserted

Descriptor tree node details

For **Descriptor tree nodes** you may enter an abbreviation a details text and assign resource data. Select the **Descriptor tree node** (single click) and click on button ✎in the tool bar on the right. Alternatively you may right-click the **Descriptor tree node** and select ✎**Edit details** from the context menu. An edit window as shown below will be opened.



First node of copy

Abbrev.: 1st

Details: This is the first descriptor tree node.

Decriptor tree node resources

https://upload.wikimedia.org/wikipedia/commons/4/4b/Das_-Siegel-_der_-Univ

https://upload.wikimedia.org/wikipedia/commons/4/4b/Das_-Siegel-_der_-University_of
https://www.google.de/?gfe_rd=cr&ei=r_F5WeWMJfKA8Qe2q7roCA&gws_rd=ssl

Resources

No.	Resource name	Ranking	Role
1	first		unknown
2	ff		unknown

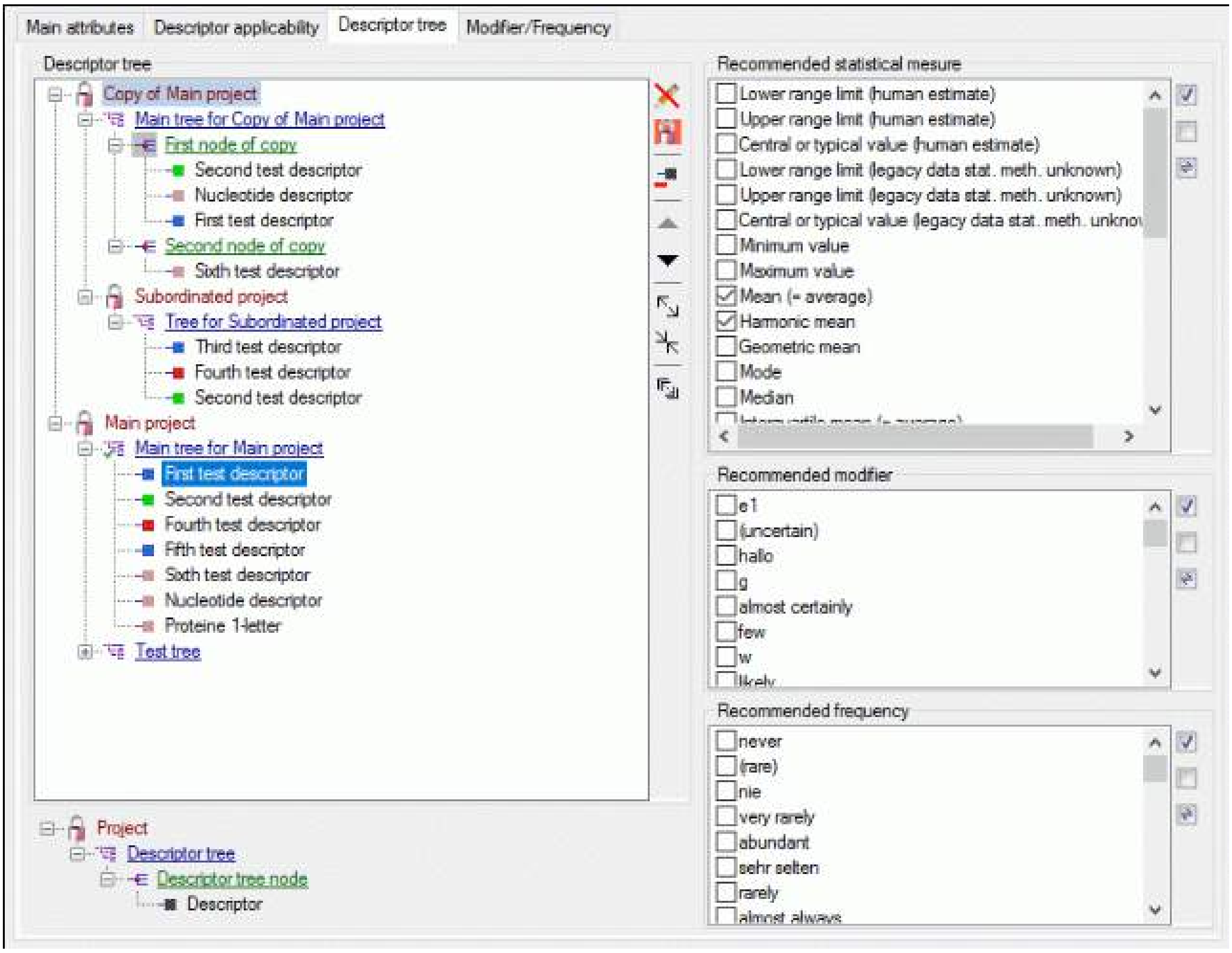
URL	Type	Variant
https://upload.wikimedia.org/wikipedia/commons/4/4b/...	image/png	tiny sample

URL: bogen_und_der_-Urkunde-_2013-08-18_02-44.png Size: 142 Width: 477 Height: 599 Duration:

If resources are assigned to a **Descriptor tree node**, its symbol is shown with grey background in the descriptor tree. You may view the resources by right-clicking it and selecting **View resources** from the context menu.

Recommended statistical measures, modifiers and frequency values

Click on in the tool bar to close the edit window in the right part of the tab or on to reopen it. In the edit window you can select recommended modifier/frequency values and statistical measures. The recommended values can be administered for a selected descriptor or for a selected descriptor tree node. In the latter case selected values are inherited by all subordinate nodes, which will be indicated by the background colour if a subordinate node is selected in the descriptor tree.



Recommended statistical mesure

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unknow
☐ Minimum value
☐ Maximum value
☑ Mean (= average)
☑ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median
☐ Interquartile mean (= average)

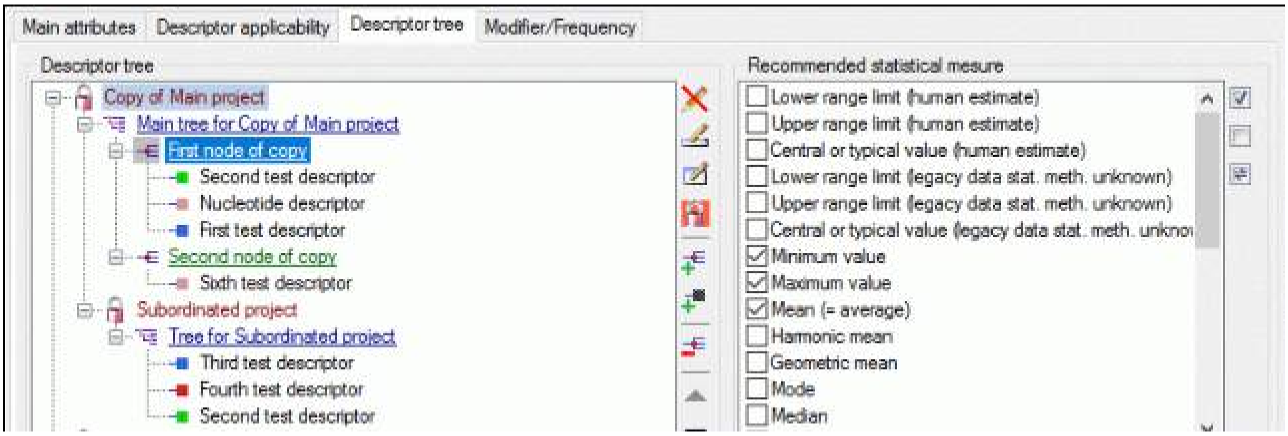
Recommended modifier

☐ e1
☐ (uncertain)
☐ hallo
☐ g
☐ almost certainly
☐ few
☐ w
☐ likely

Recommended frequency

☐ never
☐ (rare)
☐ nie
☐ very rarely
☐ abundant
☐ sehr selten
☐ rarely
☐ almost always

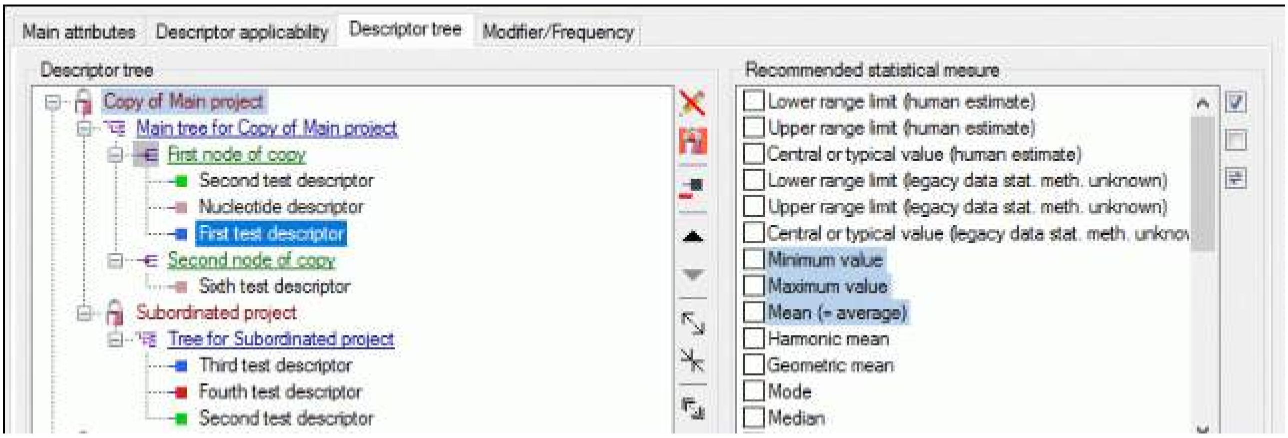
The picture below shows an example for a descriptor where the recommended statistical measures **Minimum value**, **Maximum value** and **Mean** are inherited by the superior node.



Recommended statistical mesure

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unknow
☑ Minimum value
☑ Maximum value
☑ Mean (= average)
☐ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

For the contained descriptor only additional values may be selected, but the inherited values cannot be de-selected.



- Copy of Main project
  - Main tree for Copy of Main project
    - First node of copy
      - Second test descriptor
      - Nucleotide descriptor
      - First test descriptor
    - Second node of copy
      - Sixth test descriptor
  - Subordinated project
    - Tree for Subordinated project
      - Third test descriptor
      - Fourth test descriptor
      - Second test descriptor

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estimate)
☐ Lower range limit (legacy data stat. meth. unknown)
☐ Upper range limit (legacy data stat. meth. unknown)
☐ Central or typical value (legacy data stat. meth. unknow
☐ Minimum value
☐ Maximum value
☐ Mean (= average)
☐ Harmonic mean
☐ Geometric mean
☐ Mode
☐ Median

Continue with:

- Edit projects - Main attributes tab
- Edit projects - Descriptor applicability tab
- Edit projects - Move/Copy descriptor trees
- Edit projects - Modifier/Frequency tab

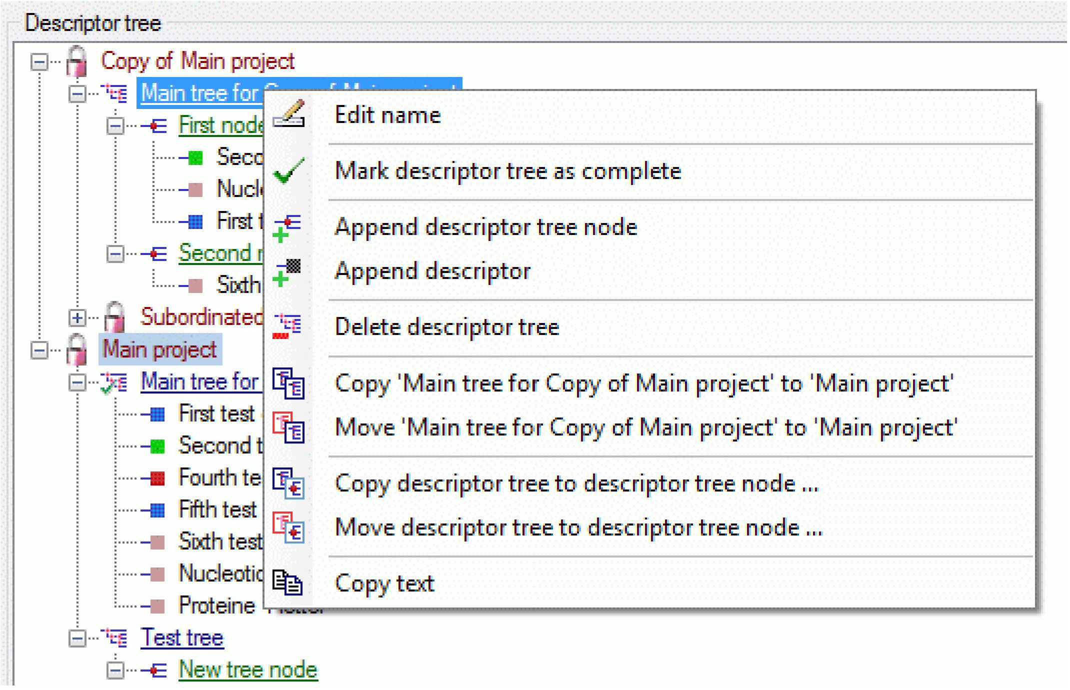
Editing the project - Move or copy descriptor trees

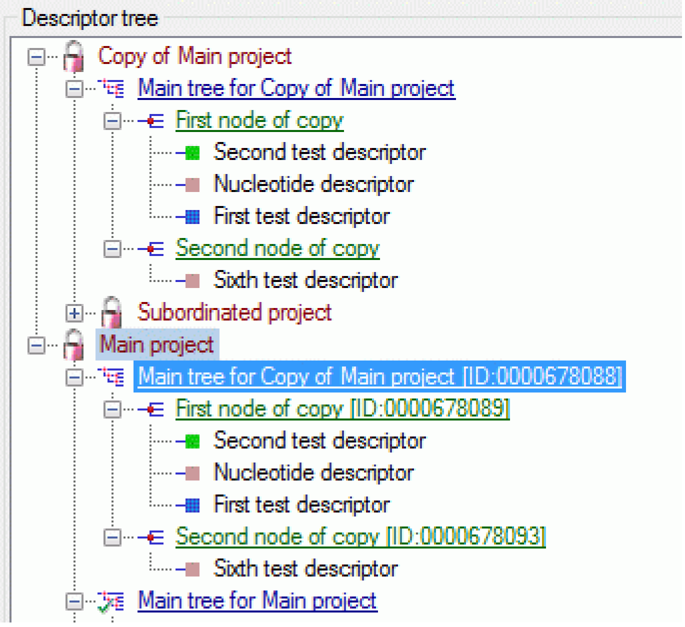
Using the context menue, you may move or copy parts of a descriptor tree to other branches. Please note that for the move and copy operations the selected project, marked by its background colour in the descriptor tree, is assumed as the target project. You may copy descriptor trees or parts of projects with read-only access to your selected project. The move operation is certainly not possible in those cases. Note that by the copy operations only the tree structures will be copied, associated recommended statistical measures, modifiers and frequencies will not be copied! The move operations preserve those adjustments.

Remark: If you want to move or copy element from an other than the selected project, activate the "Show all projects" option by clicking the button in the tool strip. The icon background will be changed to red color to indicate that this option is active.

1. Move or copy a descriptor tree

Right click on the descriptor tree you want to move/copy. A context menu opens, that offers the options **Copy '<tree name>' to '<project name>'** rsp. **Move '<tree name>' to 'project name'** (see picture below left). If you selected "Move", the descriptor tree is removed from the original project and appended to your selected project. If you selected "Copy", a copy of the tree will be appended to the selected project. In this case numeric IDs are appended to generate unique tree and tree node names (see picture below right). The copy function can be used to generate a clone of a descriptor tree in the selected project.

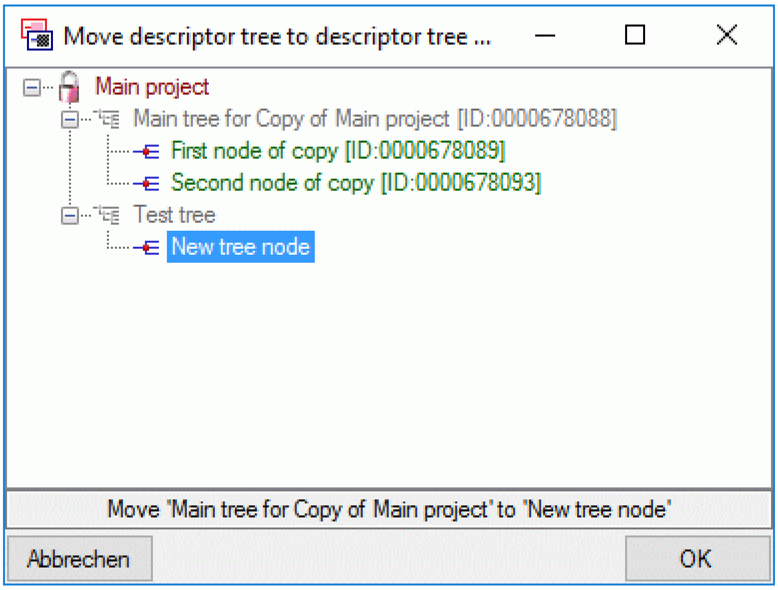




Descriptor tree

- Copy of Main project
  - Main tree for Copy of Main project
    - First node of copy
      - Second test descriptor
      - Nucleotide descriptor
      - First test descriptor
    - Second node of copy
      - Sixth test descriptor
  - Subordinated project
- Main project
  - Main tree for Copy of Main project [ID:0000678088]
    - First node of copy [ID:0000678089]
      - Second test descriptor
      - Nucleotide descriptor
      - First test descriptor
    - Second node of copy [ID:0000678093]
      - Sixth test descriptor
  - Main tree for Main project

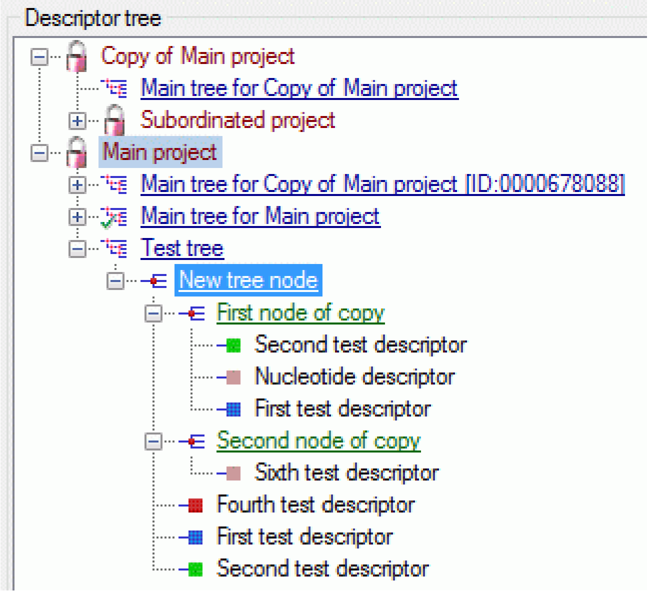
Additionally you may copy the contents of a descriptor tree to a descriptor tree node by clicking selecting the option **Copy descriptor tree to descriptor tree node ...** rsp. **Move descriptor tree to descriptor tree node ...** (see picture above left). A separate window opens to select the target node (see picture below left). Find the move result in the right picture below. Since the tree has been moved, the tree node names have not been changed. One duplicate descriptor has not been moved to the target node.



Move descriptor tree to descriptor tree ...

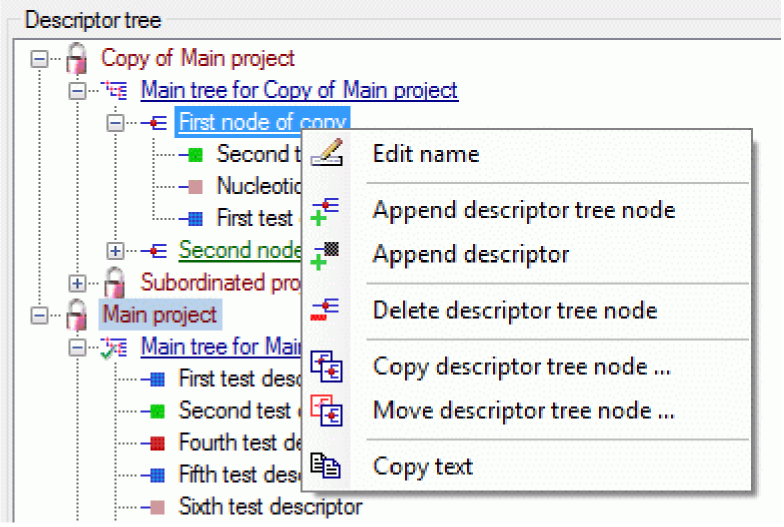
- Main project
  - Main tree for Copy of Main project [ID:0000678088]
    - First node of copy [ID:0000678089]
    - Second node of copy [ID:0000678093]
  - Test tree
    - New tree node

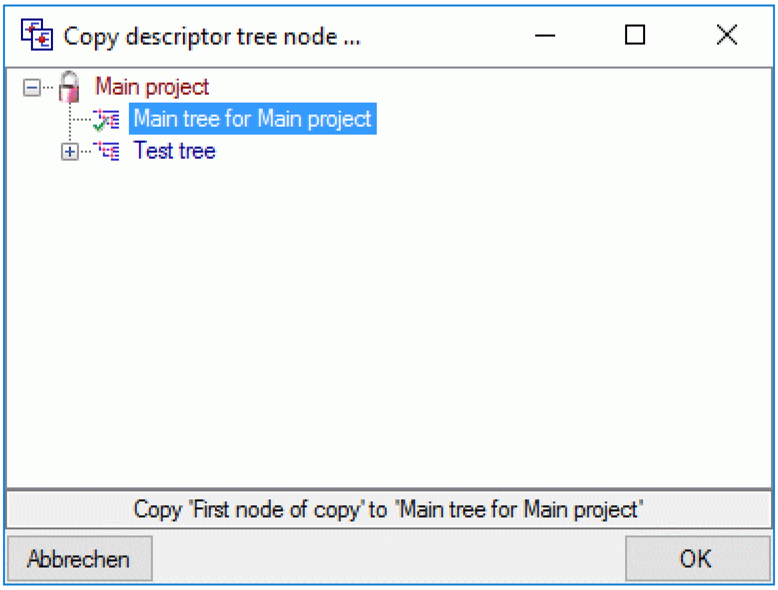
Move 'Main tree for Copy of Main project' to 'New tree node'



2. Move or copy a descriptor tree node

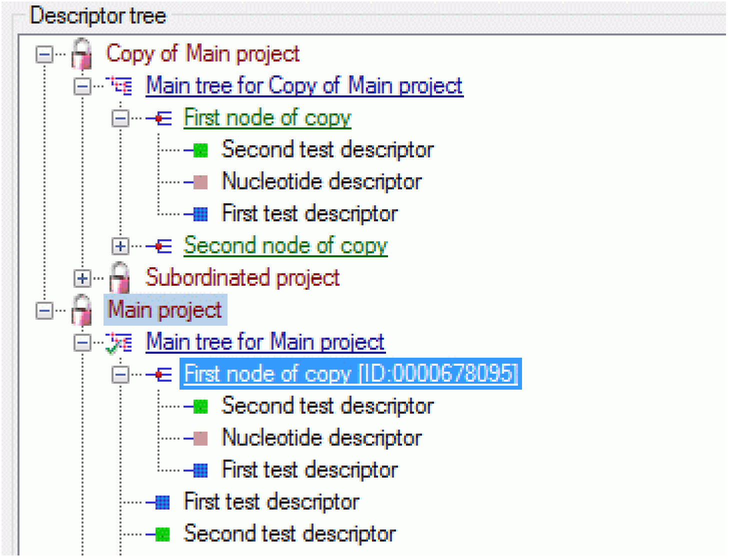
Right click on the descriptor tree node you want to move/copy. A context menu opens, that offers the options **Copy descriptor tree node ...** rsp. **Move descriptor tree node ...** (see picture below left). After selecting one of there items a dialog windows opens where you may select the target descriptor tree or descriptor tree node (see picture below right).





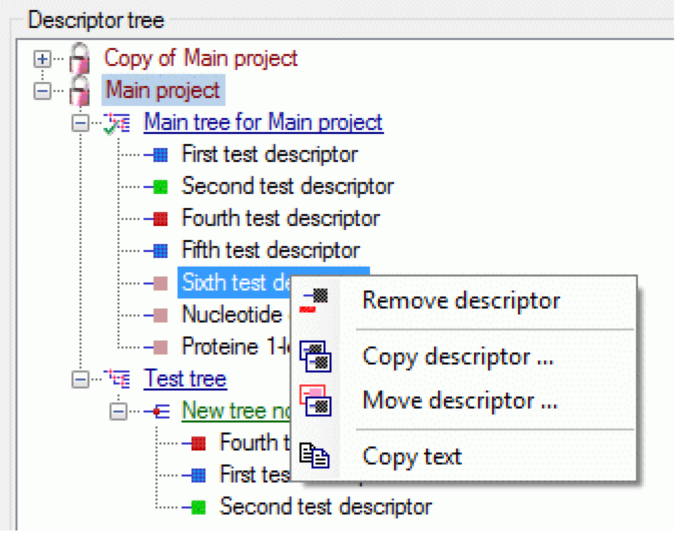
Copy 'First node of copy' to 'Main tree for Main project'

If you selected "Move", the descriptor tree node is removed from the original position and appended to the selected tree position. If you selected "Copy", a copy of the tree node will be appended to the selected tree position. In this case numeric IDs are appended to generate unique tree node names (see picture below). The copy function can also be used to generate a clone of a descriptor tree node in the selected project.



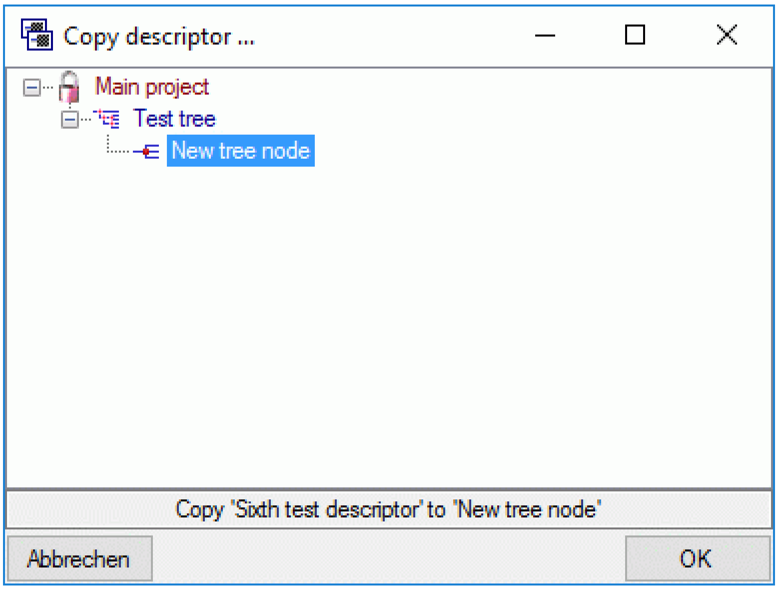
3. Move or copy a descriptor

Right click on the descriptor you want to move/copy. A context menu opens, that offers the options **Copy descriptor ...** rsp. **Move descriptor ...** (see picture below left). After selecting one of there items a dialog windows opens where you may select the target descriptor tree or descriptor tree node (see picture below right).



Descriptor tree

Copy of Main project
Main project
Main tree for Main project
First test descriptor
Second test descriptor
Fourth test descriptor
Fifth test descriptor
Sixth test de
Nucleotide
Proteine 1-l
Test tree
New tree no
Fourth t
First tes
Second test descriptor

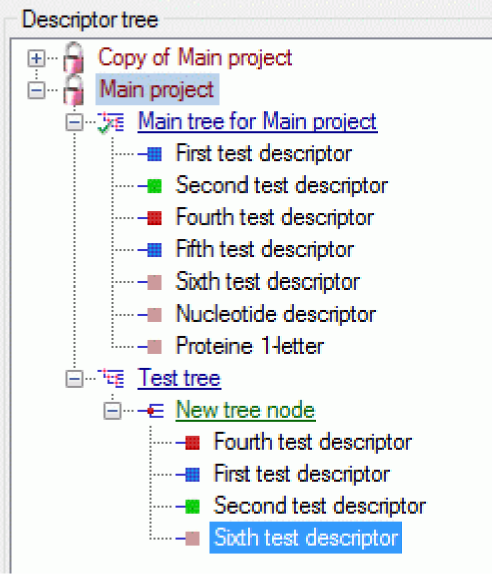


Copy descriptor ...

Main project
Test tree
New tree node

Copy 'Sixth test descriptor' to 'New tree node'

If you selected "Move", the descriptor is removed from the original position and appended to the selected tree position. If you selected "Copy", a new descriptor node will be appended to the selected tree position (see picture below).



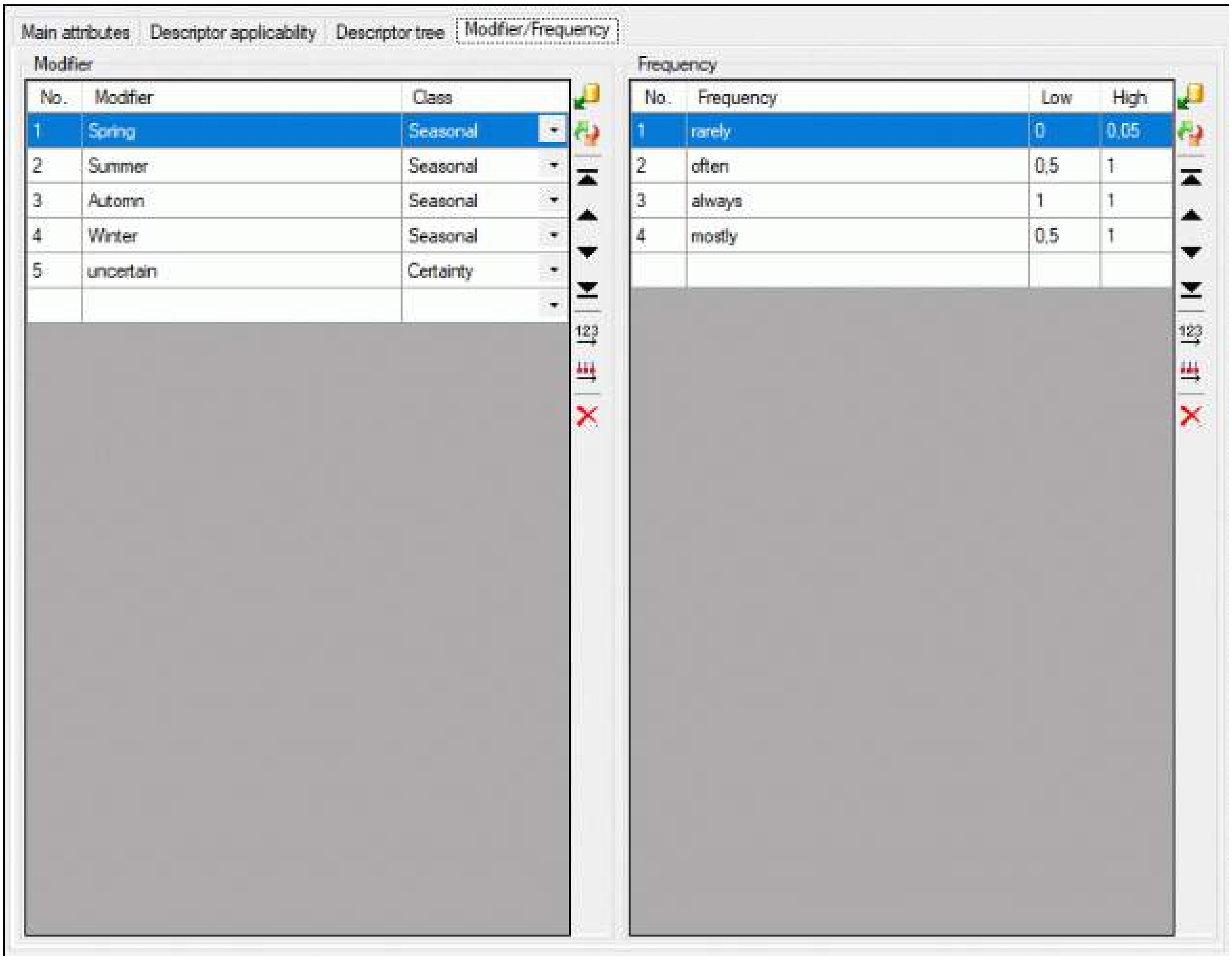
Descriptor tree

Copy of Main project
Main project
Main tree for Main project
First test descriptor
Second test descriptor
Fourth test descriptor
Fifth test descriptor
Sixth test descriptor
Nucleotide descriptor
Proteine 1-letter
Test tree
New tree node
Fourth test descriptor
First test descriptor
Second test descriptor
Sixth test descriptor

Continue with:

- Edit projects - Main attributes tab
- Edit projects - Descriptor applicability tab
- Edit projects - Descriptor tree tab
- Edit projects - Modifier/Frequency tab

Editing the project - Modifier/Frequency tab



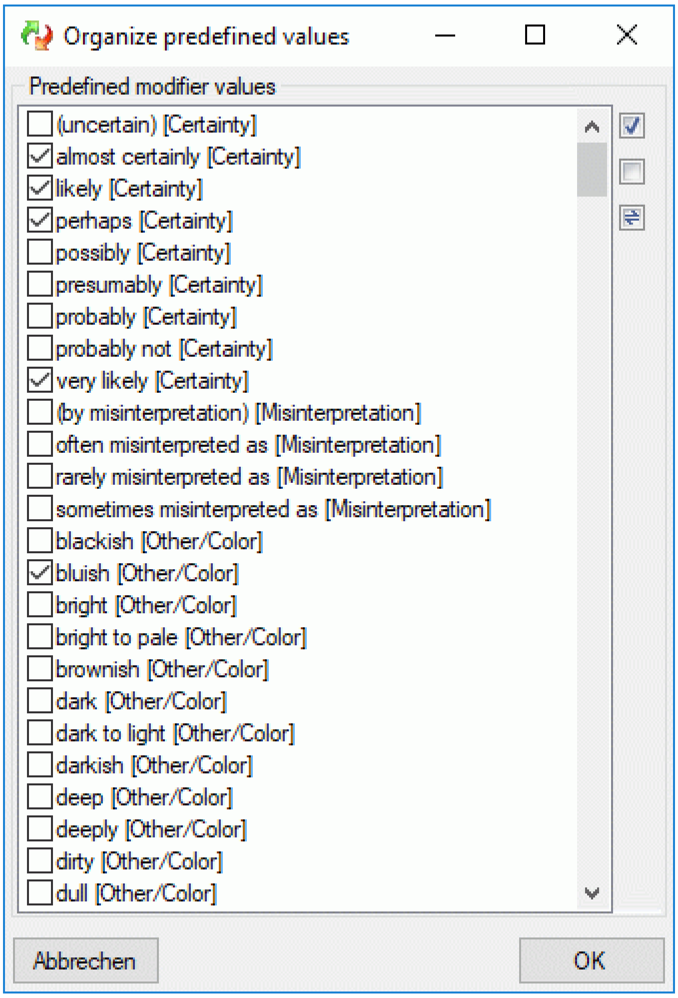
No.	Modifier	Class
1	Spring	Seasonal
2	Summer	Seasonal
3	Automn	Seasonal
4	Winter	Seasonal
5	uncertain	Certainty

No.	Frequency	Low	High
1	rarely	0	0,05
2	often	0,5	1
3	always	1	1
4	mostly	0,5	1

The **Modifier/Frequency** tab allows definition of modifier and frequency values. The sequence number column ("No.") determines the display sequence in selection lists. You may order the entries by clicking on a column header. With the arrow buttons (▲ ▼) you can move the selected entries up or down within the table, clicking button ⤒or ⤓shifts the selected entries to the top respective bottom of the table. After ordering the entries click button 123to renumber the table entries (starting with "1" for the first table entry) and make the changes effective. After pressing button ⛁column "Use" shows the number of references in the database for each modifier rsp. frequency value.

To enter a new modifier or frequency value, select the empty line on the end of the table and click on the "Modifier" rsp. "Frequency" field to enter the new values. After entering the new entry name automatically a new value for "No." is initialized. To delete an entry, select the entry and press the ✕tool strip button, the **Delete** key or remove the value in the sequence number column ("No.").

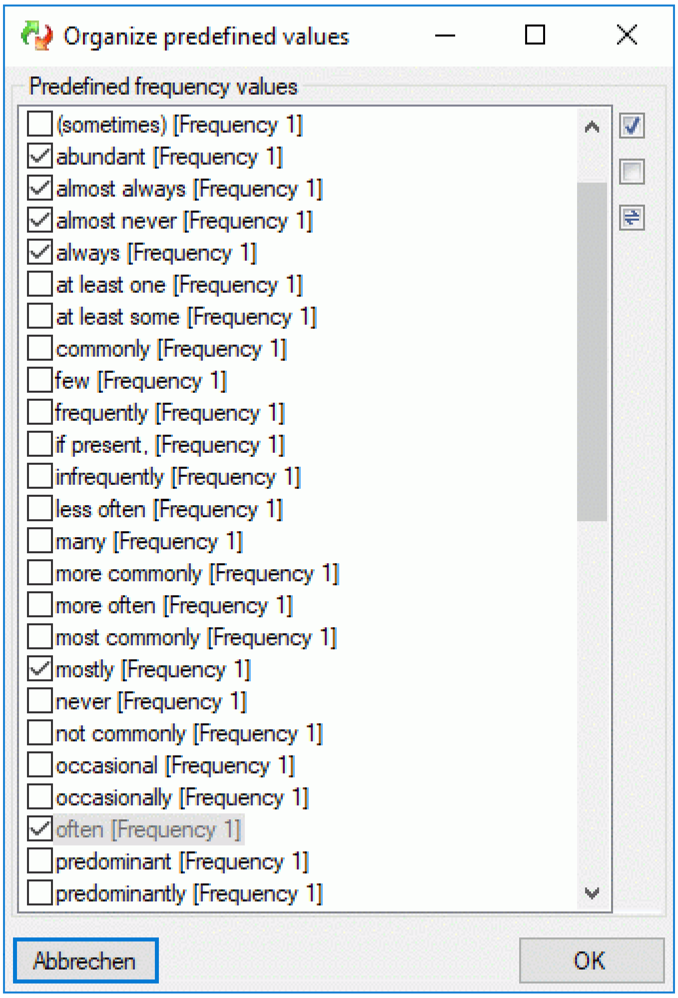
There is a number of predefined modifier and frequency values commonly used. These values can be accessed by pressing the 🔄 button, which opens one of the windows shown below.



Organize predefined values

Predefined modifier values

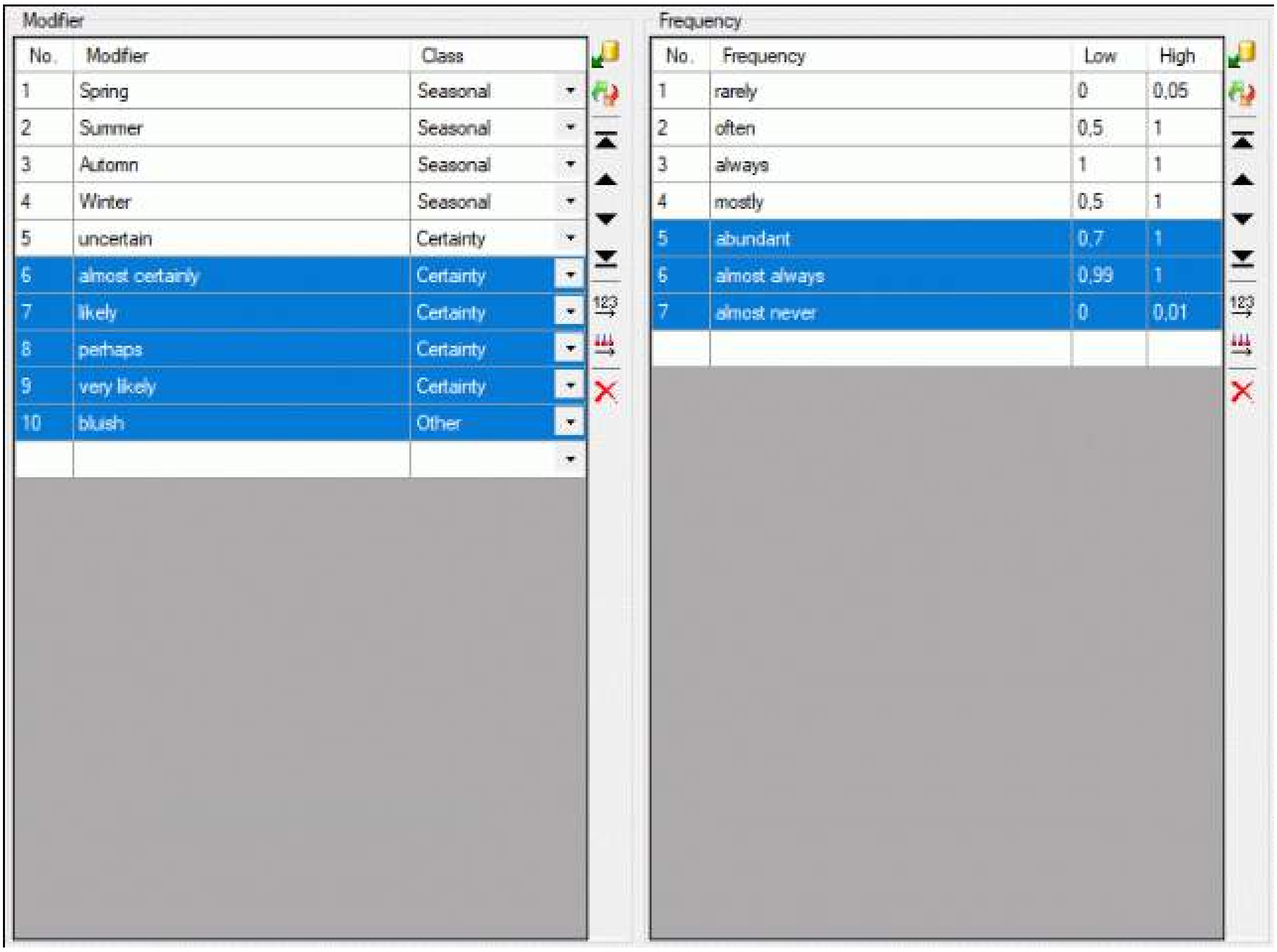
- ☐ (uncertain) [Certainty]
- ☑ almost certainly [Certainty]
- ☑ likely [Certainty]
- ☑ perhaps [Certainty]
- ☐ possibly [Certainty]
- ☐ presumably [Certainty]
- ☐ probably [Certainty]
- ☐ probably not [Certainty]
- ☑ very likely [Certainty]
- ☐ (by misinterpretation) [Misinterpretation]
- ☐ often misinterpreted as [Misinterpretation]
- ☐ rarely misinterpreted as [Misinterpretation]
- ☐ sometimes misinterpreted as [Misinterpretation]
- ☐ blackish [Other/Color]
- ☑ bluish [Other/Color]
- ☐ bright [Other/Color]
- ☐ bright to pale [Other/Color]
- ☐ brownish [Other/Color]
- ☐ dark [Other/Color]
- ☐ dark to light [Other/Color]
- ☐ darkish [Other/Color]
- ☐ deep [Other/Color]
- ☐ deeply [Other/Color]
- ☐ dirty [Other/Color]
- ☐ dull [Other/Color]



Predefined frequency values

☐ (sometimes) [Frequency 1]
☑ abundant [Frequency 1]
☑ almost always [Frequency 1]
☑ almost never [Frequency 1]
☑ always [Frequency 1]
☐ at least one [Frequency 1]
☐ at least some [Frequency 1]
☐ commonly [Frequency 1]
☐ few [Frequency 1]
☐ frequently [Frequency 1]
☐ if present, [Frequency 1]
☐ infrequently [Frequency 1]
☐ less often [Frequency 1]
☐ many [Frequency 1]
☐ more commonly [Frequency 1]
☐ more often [Frequency 1]
☐ most commonly [Frequency 1]
☑ mostly [Frequency 1]
☐ never [Frequency 1]
☐ not commonly [Frequency 1]
☐ occasional [Frequency 1]
☐ occasionally [Frequency 1]
☑ often [Frequency 1]
☐ predominant [Frequency 1]
☐ predominantly [Frequency 1]

By checking of uncecking the values, they can easily be inserted or deleted from the modifier rsp. frequency list. Values that are already used in the database are marked by a grey text colour. When these values are marked to be removed from the list, you will be asked for each single value if it really shall be deleted after pressing **OK**. New values are inserted at the end of the list (see below).



Modifier

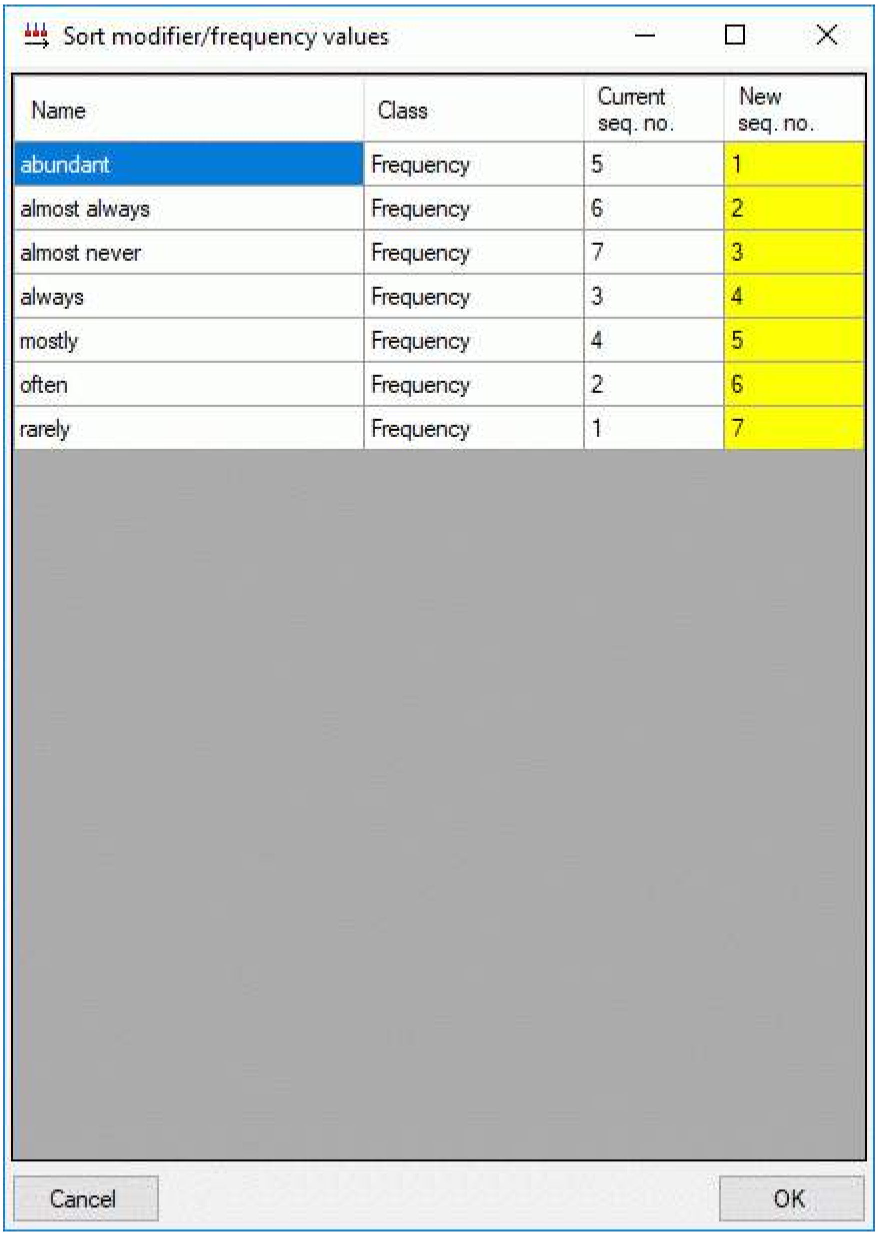
No.	Modifier	Class
1	Spring	Seasonal
2	Summer	Seasonal
3	Automn	Seasonal
4	Winter	Seasonal
5	uncertain	Certainty
6	almost certainly	Certainty
7	likely	Certainty
8	perhaps	Certainty
9	very likely	Certainty
10	bluish	Other

Frequency

No.	Frequency	Low	High
1	rarely	0	0,05
2	often	0,5	1
3	always	1	1
4	mostly	0,5	1
5	abundant	0,7	1
6	almost always	0,99	1
7	almost never	0	0,01

You may order the modifier and frequency values according the sequence of the predefined values by pressing the ⇉ button, which opens one of the windows shown below. Values that are not in the predefined lists will be shifted to the end of the list.

Name	Class	Current seq. no.	New seq. no.
almost certainly	Certainty	6	1
likely	Certainty	7	2
perhaps	Certainty	8	3
very likely	Certainty	9	4
bluish	Other	10	5
Spring	Seasonal	1	6
Summer	Seasonal	2	7
Automn	Seasonal	3	8
Winter	Seasonal	4	9
uncertain	Certainty	5	10



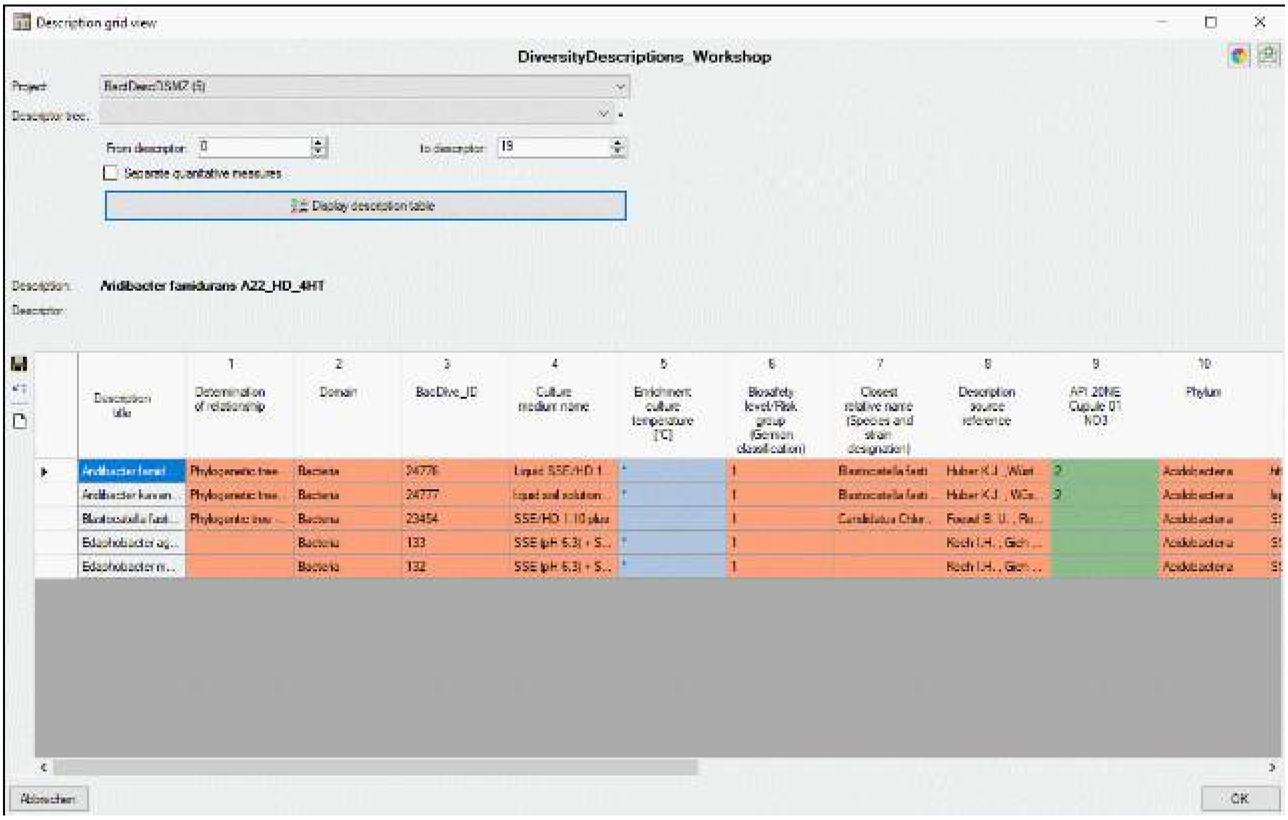
Name	Class	Current seq. no.	New seq. no.
abundant	Frequency	5	1
almost always	Frequency	6	2
almost never	Frequency	7	3
always	Frequency	3	4
mostly	Frequency	4	5
often	Frequency	2	6
rarely	Frequency	1	7

Continue with:

- Edit projects - Main attributes tab
- Edit projects - Descriptor applicability tab
- Edit projects - Descriptor tree tab
- Edit projects - Move/Copy descriptor trees

Description grid view

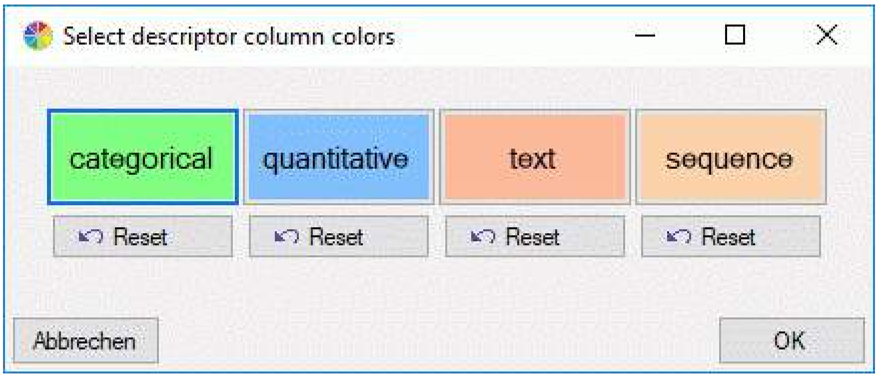
After starting a database query for descriptions select **Grid -> Description grid view ...** from the menu. The query result list is passed to the description grid view form and a window as shown below opens (click the button **Display description table** to build the table output). In the first line the database name is displayed. If you move the mouse cursor over the database name, a tooltip shows the actual connection paramter.



Project: BactDescDSMZ (5)
Descriptor tree:
From descriptor: 0 to descriptor: 19
☐ Separate quantitative measures
Description: Aridibacter famidurans A22_HD_4HT
Descriptor:

	Description title	1 Determination of relationship	2 Domain	3 BacDive_ID	4 Culture medium name	5 Enrichment culture temperature [°C]	6 Biosafety level/Risk group (German classification)	7 Closest relative name (Species and strain designation)	8 Description source reference	9 API 20NE Cupule 01 NO3	10 Phylum
▸	Aridibacter famid...	Phylogenetic tree ...	Bacteria	24776	Liquid SSE/HD 1...	*	1	Blastocatella fasti...	Huber K.J., Wüst ...	2	Acidobacteria
	Aridibacter kaven...	Phylogenetic tree ...	Bacteria	24777	liquid soil solution ...	*	1	Blastocatella fasti...	Huber K.J., WÜs...	2	Acidobacteria
	Blastocatella fasti...	Phylogenetic tree ...	Bacteria	23454	SSE/HD 1:10 plus		1	Candidatus Chlo...	Foesel B. U., Ro...		Acidobacteria
	Edaphobacter ag...		Bacteria	133	SSE (pH 6.3) + S...	*	1		Koch I.H., Gich ...		Acidobacteria
	Edaphobacter m...		Bacteria	132	SSE (pH 6.3) + S...	*	1		Koch I.H., Gich ...		Acidobacteria

The table in the lower part of the window shows the description titles in the first column and the summary data in the other columns. Each summary column holds the data of a certain descriptor. If a cell with summary data is selected, the summary details and the descriptor status data are displayed in the upper right part of the window. The upper left part of the window shows the selection parameters that are used for building the description table. You may change the table colors by clicking the button . A form as shown below will be opened.

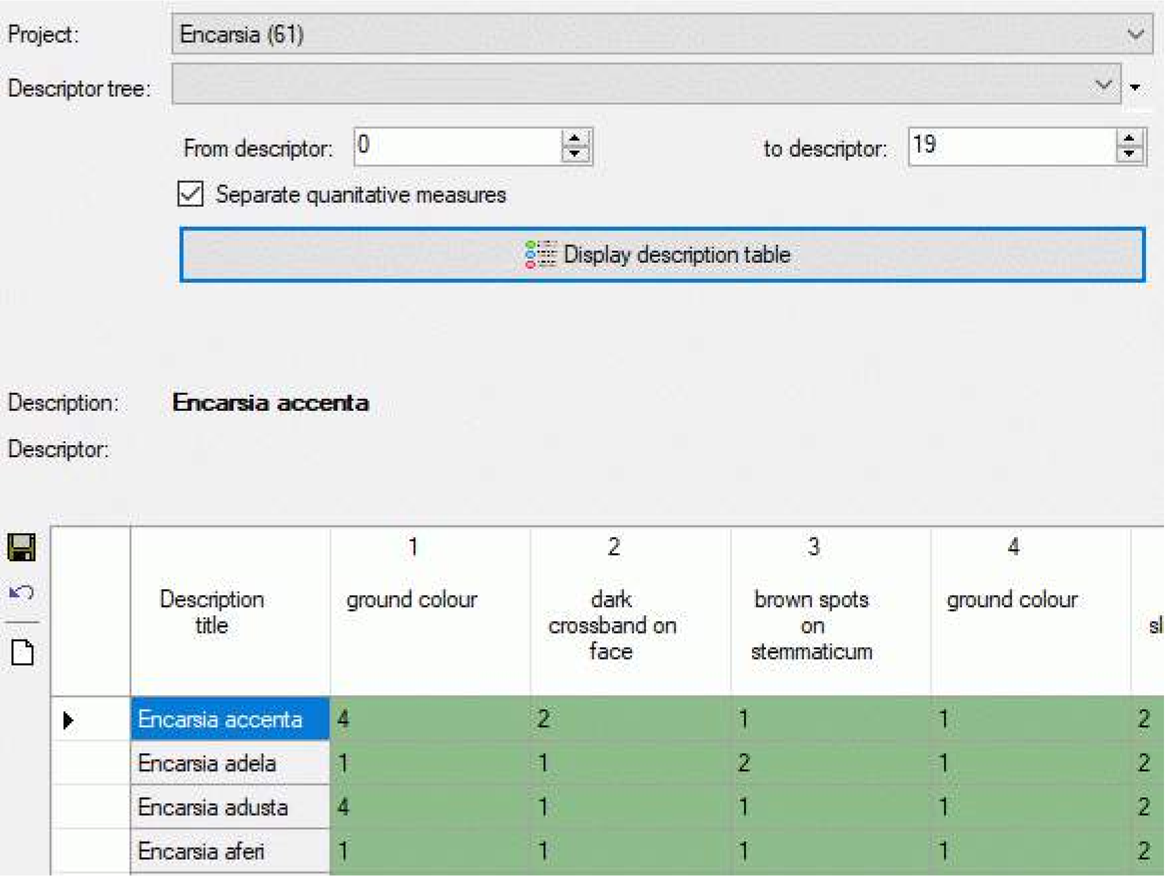


Click on buttons **categorical**, **quanitative**, **text** or **sequence** to select the corresponding table colors. By clicking the **Reset** button below the color, the corresponding default value will be selected. After changing the table colors by a click on the **OK** button, you must re-draw the table.

Selection parameters

In the upper left part of the parameters for the description table can be adjusted. If in the query list passed to the form descriptions of different projects are present, the displayed project can be selected with the **Project:** drop-down box. The entries in the drow-down list include the project name, followed by the number of descriptions for that project in brackets and an asterisk (*****) if the user has only read access for that project.

The **Descriptor tree** drop-down box restricts the descriptor columns to the descriptors contained in the selected tree. Furthermore the tree hierarchy is included in the descriptor names if a structured descriptor tree is selected (see images below).



Project: Encarsia (61)

Descriptor tree:

From descriptor: 0

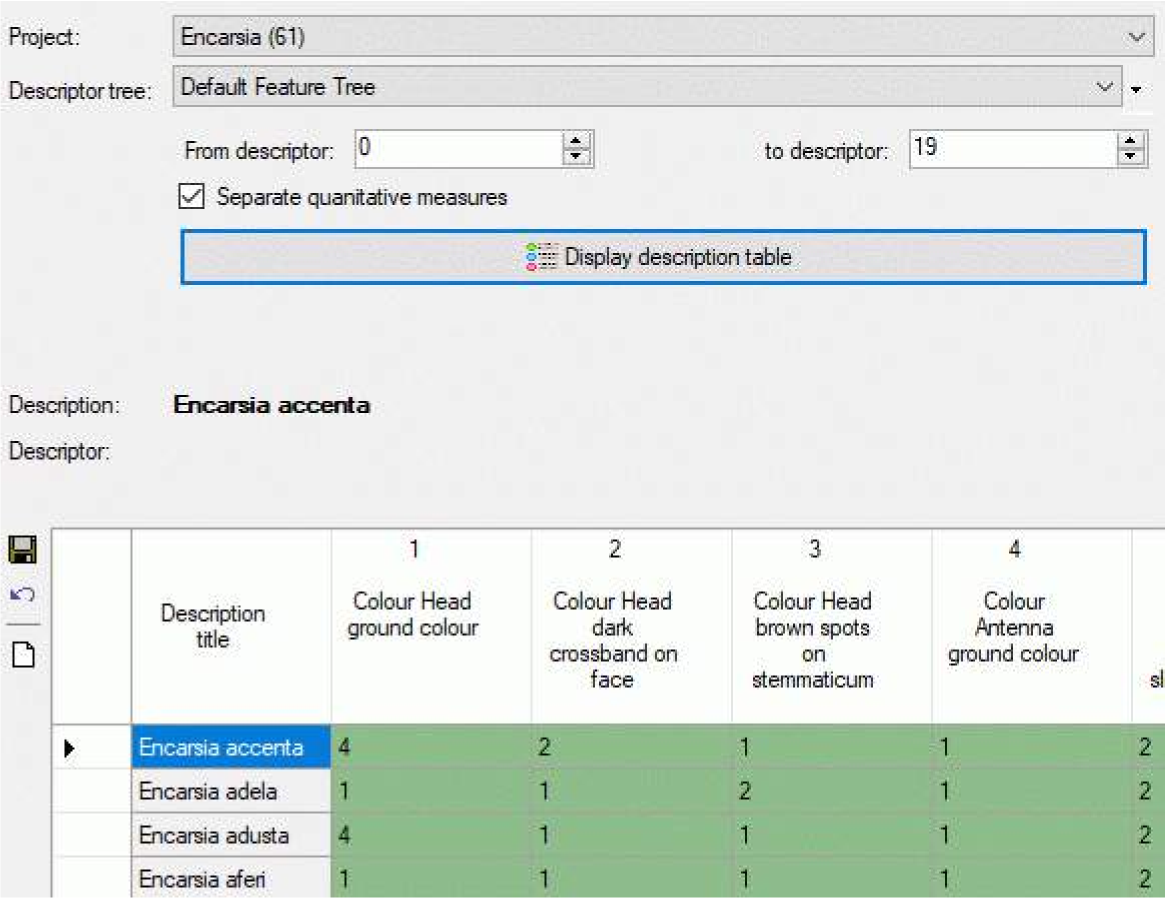
to descriptor: 19

☑ Separate quanitative measures

Description: **Encarsia accenta**

Descriptor:

	Description title	1 ground colour	2 dark crossband on face	3 brown spots on stemmaticum	4 ground colour	sl
▸	Encarsia accenta	4	2	1	1	2
	Encarsia adela	1	1	2	1	2
	Encarsia adusta	4	1	1	1	2
	Encarsia aferi	1	1	1	1	2



Project: Encarsia (61)

Descriptor tree: Default Feature Tree

From descriptor: 0 to descriptor: 19

☑ Separate quanitative measures

Description: **Encarsia accenta**

Descriptor:

Description title	1 Colour Head ground colour	2 Colour Head dark crossband on face	3 Colour Head brown spots on stemmaticum	4 Colour Antenna ground colour	sl
Encarsia accenta	4	2	1	1	2
Encarsia adela	1	1	2	1	2
Encarsia adusta	4	1	1	1	2
Encarsia aferi	1	1	1	1	2

The values **From descriptor** and **to descriptor** limit the range of descriptor sequence numbers that is included in the discription tabe. Be aware that this restiction is additionally effective to a selected desriptor tree! If you want to de-activate this restriction, select "from" value 0 "to" value 999999 by a double-click on the labels **From descriptor** rsp. **to descriptor** . The limitation of the number of descriptor columns makes speeds up the description table generation, especally if many descriptor (e.g. some hundrets) are present.

If you select option **Separate statistical measures**, separate columns will be insterted in the data grid for each quantitative descriptor and its recommended statistical measures. This option may be useful for editing quantitative summary data that use other statistical measures than **Min**, **UMethLower**, **Mean**, **UMethUpper** and **Max** (see section Data editing for details.

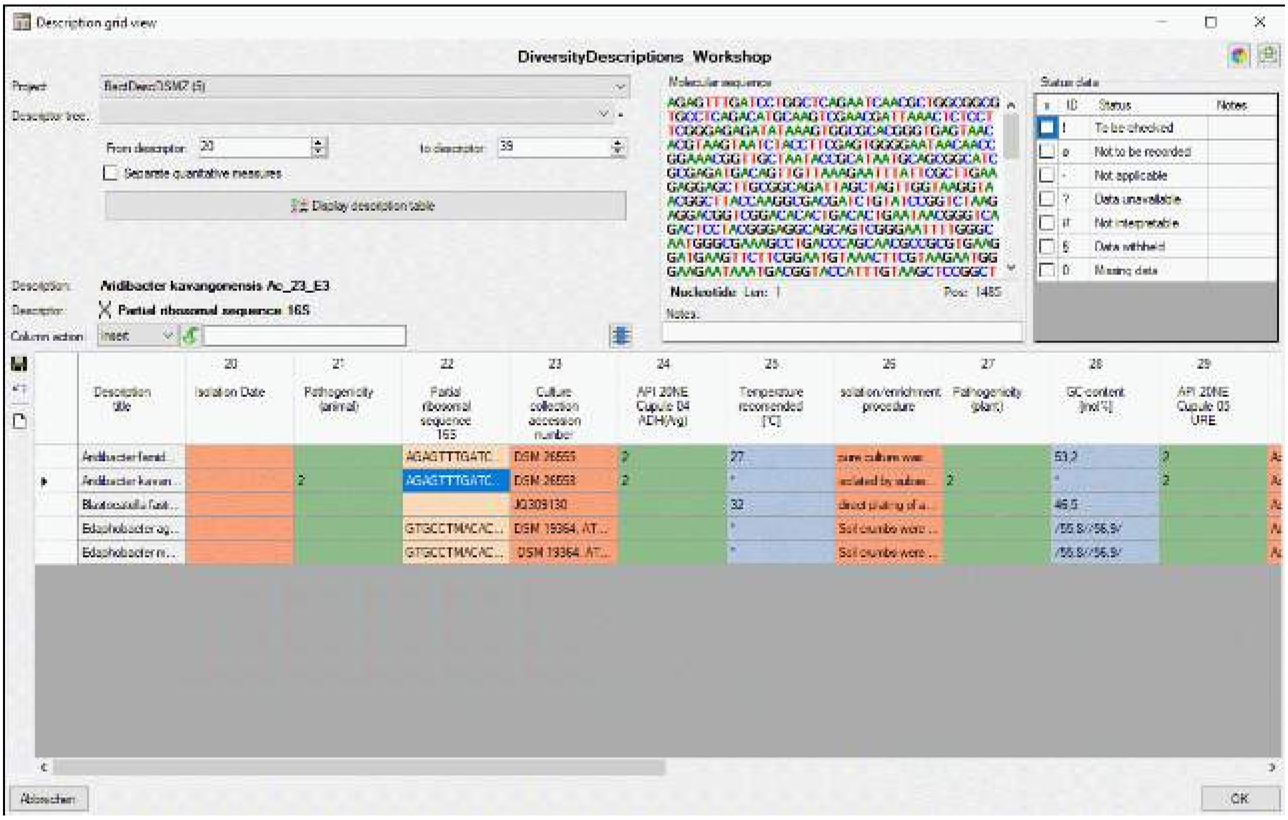
Finally click the button **Display description table** to build a new description table according to your settings. During output of the description table the icon of the button changes to STOP and you may abort processing by clicking the button.

Continue with:

- Description grid view - Data editing
- Description grid view - Copy or create descriptions
- Description grid view - Save or discard changes

Description grid view - Data editing

The first column of the description table shows the description titles, which are fixed. I.e. if you scroll the summary data to the right, the titles are still visible at the left. The other columns show the summary data, where the descriptor type is indicated by the background colour: categorical, quantitative, text or sequence. The column titles include the descriptor name, the mesurement unit in square bracket for quantitative descriptors and the descriptor's sequence number (see image below).



Project: BactDescDSMZ (5)
Descriptor tree:
From descriptor: 20
to descriptor: 39
☐ Separate quantative measures

Description: **Aridibacter kavangonensis Ac_23_E3**
Descriptor: **Partial ribosomal sequence 16S**
Column action: Insert

Molecular sequence
Nucleotide: Len: 1 Pos: 1485
Notes:

Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	//	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

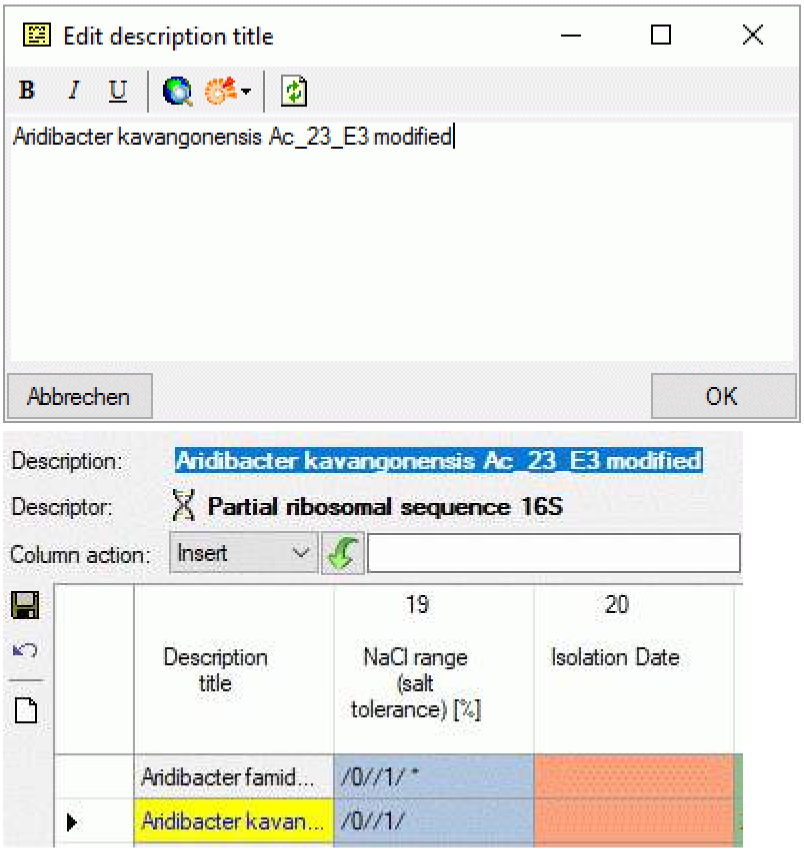
	20	21	22	23	24	25	26	27	28	29
Description title	Isolation Date	Pathogenicity (animal)	Partial ribosomal sequence 16S	Culture collection accession number	API 20NE Cupule 04 ADH(Arg)	Temperature recomended [°C]	isolation/enrichment procedure	Pathogenicity (plant)	GC content [mol %]	API 20NE Cupule 05 URE
Aridibacter famid...			AGAGTTTGATC...	DSM 26555	2	27	pure culture was...		53.2	2
Aridibacter kavan...		2	AGAGTTTGATC...	DSM 26553	2	*	isolated by subse...	2	*	2
Blastocatella fast...				JQ309130		32	direct plating of a...		46.5	
Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/	
Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/	

When a summary cell in the description table is selected, the field **Description:** shows the description title and field **Descriptor:** shows the symbols according the descriptor type (C for categorical, Σ for quantitative, Tx for text and 🧬 for sequence) and the descriptor title. If for a descriptor resources are available, this fact is indicated by a coloured symbol background. You may view them by a double-click on the descriptor title. If for a description resources are available, the symbol 🖼 is displayed before the title. Double click in that symbol to view the resources.

For the selected cell the summary data and the descriptor status data are displayed in the upper right area of the window (see image above). You may edit the data within these controls as described in section Editing the description - Descriptor view tab of this manual. For modified summary cells the text colour changes to blue and the description titles will be shown with yellow background in the table.

Changing the description title

To change the description title, double-click on it in field **Description:** to open a separate edit window. After comitting the changes with "OK" the description will be marked as modified (see images below).



Aridibacter kavangonensis Ac_23_E3 modified

Description: Aridibacter kavangonensis Ac_23_E3 modified

Descriptor: Partial ribosomal sequence 16S

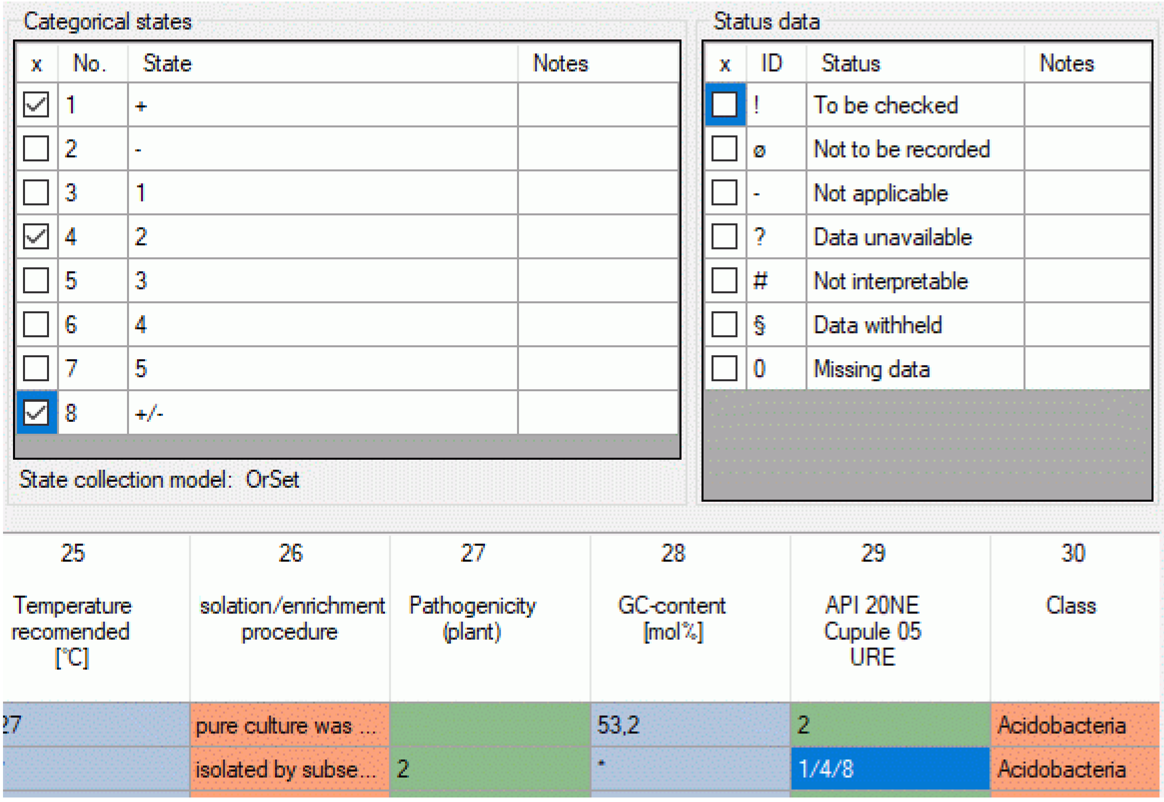
Column action: Insert

Description title	19 NaCl range (salt tolerance) [%]	20 Isolation Date
Aridibacter famid...	/0//1/ *	
Aridibacter kavan...	/0//1/	

Changing the summary data in the table

Categorical summary data

Categorical, states are specified by their sequence number. Multiples are separated by a forward slash ("/", see image below). Existing "notes" will be removed, if the corresponding categorical state is not specified in the input.



Categorical states

x	No.	State	Notes
☑	1	+	
☐	2	-	
☐	3	1	
☑	4	2	
☐	5	3	
☐	6	4	
☐	7	5	
☑	8	+/-	

State collection model: OrSet

Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

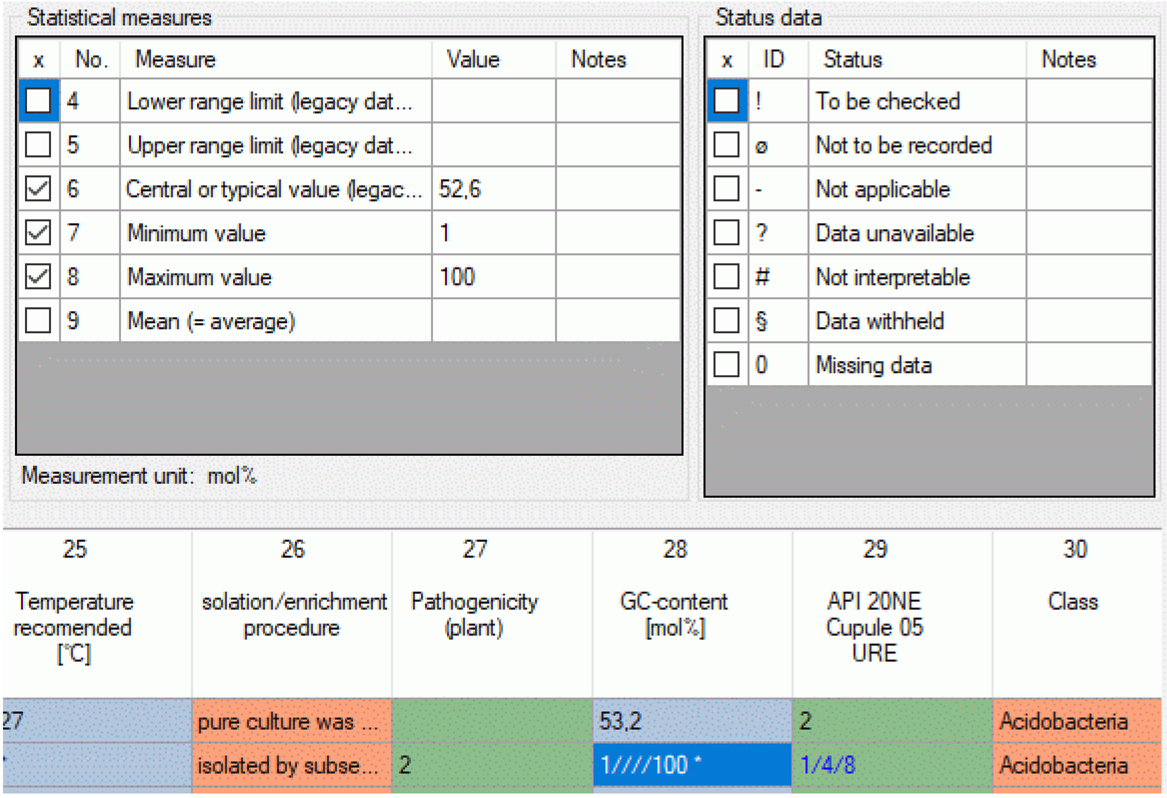
25 Temperature recomended [°C]	26 solation/enrichment procedure	27 Pathogenicity (plant)	28 GC-content [mol%]	29 API 20NE Cupule 05 URE	30 Class
27	pure culture was ...		53,2	2	Acidobacteria
	isolated by subse...	2	*	1/4/8	Acidobacteria

Quantitative summary data

If you did not check the option **Separate quantitative measures**, for quantitative summary data only the five quantitative measures

Min	Minimum value
UMethLower	Lower range limit (legacy data stat. meth. unknown)
Mean	Mean (= average)
UMethUpper	Upper range limit (legacy data stat. meth. unknown)
Max	Maximum value

can be specified within the summary table. The values must be specified in theis given order and separated by a forward slash ("/"). E.g. 1////100 means "Min=1, Max = 100". If only one value without any slashes is entered, it is assumed than only the "Mean" value is specified. To indicate that values for other than the five mentioned statistical measures are present in the data, an asterisk ("*") is appended in the summary table (see image below, cell value 1////100 *).



Statistical measures

x	No.	Measure	Value	Notes
☐	4	Lower range limit (legacy dat...		
☐	5	Upper range limit (legacy dat...		
☑	6	Central or typical value (legac...	52,6	
☑	7	Minimum value	1	
☑	8	Maximum value	100	
☐	9	Mean (= average)		

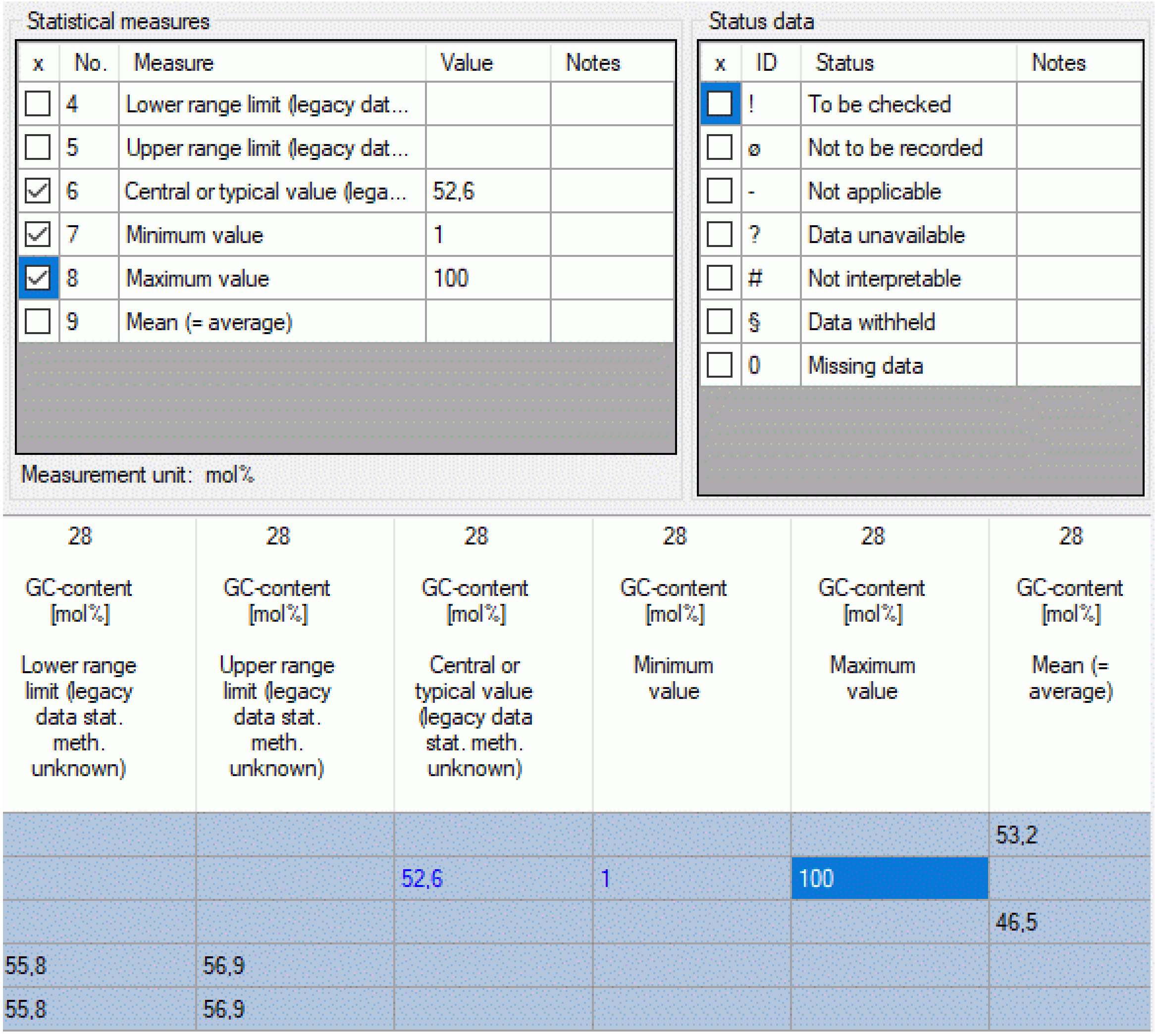
Measurement unit: mol%

Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

25 Temperature recomended [°C]	26 solation/enrichment procedure	27 Pathogenicity (plant)	28 GC-content [mol%]	29 API 20NE Cupule 05 URE	30 Class
27	pure culture was ...		53,2	2	Acidobacteria
	isolated by subse...	2	1////100 *	1/4/8	Acidobacteria

If you checked the option **Separate quantitative measures**, for each statistical measure in the quantitative summary data a separate column will be allocated in the data grid view. I.e. you can direcly enter your values into the table (see image below).



Statistical measures

x	No.	Measure	Value	Notes
☐	4	Lower range limit (legacy dat...		
☐	5	Upper range limit (legacy dat...		
☑	6	Central or typical value (lega...	52,6	
☑	7	Minimum value	1	
☑	8	Maximum value	100	
☐	9	Mean (= average)		

Measurement unit: mol%

Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

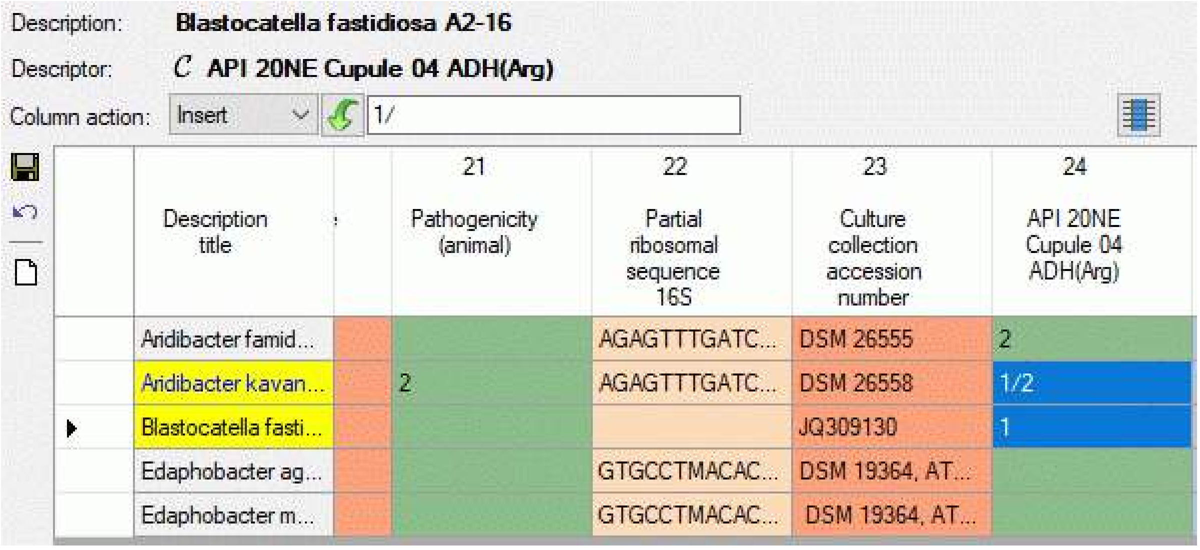
28 GC-content [mol%] Lower range limit (legacy data stat. meth. unknown)	28 GC-content [mol%] Upper range limit (legacy data stat. meth. unknown)	28 GC-content [mol%] Central or typical value (legacy data stat. meth. unknown)	28 GC-content [mol%] Minimum value	28 GC-content [mol%] Maximum value	28 GC-content [mol%] Mean (= average)
					53,2
		52,6	1	100	
					46,5
55,8	56,9				
55,8	56,9				

Text descriptor and Molecular sequence data

For Text and sequence data the texts may be edited directly within the table. The corresponding "notes" will not be affected.

Changing values in a table column

It is possible to modify several values of a single table column. Therefore select the table entries that shall be edited - by selecting an entry and clicking the button in section **Column action** you may select the whole table column (see image below). Then select the required operation: "Insert", "Append", "Replace" or "Clear" and enter the new rsp. new and old value. After clicking the action button - depending on the selected **Column action** this is (Insert), (Append), (Replace) or (Clear). Be aware that this feature performs a pure text operation in the table columns. Especially for quantitative and categorical data columns the resulting data will be interpreted according to the rules described above an might lead to unsexpected results, if not designed ver carefully.



Description: **Blastocatella fastidiosa A2-16**

Descriptor: **API 20NE Cupule 04 ADH(Arg)**

Column action: Insert 1/

	Description title		21 Pathogenicity (animal)	22 Partial ribosomal sequence 16S	23 Culture collection accession number	24 API 20NE Cupule 04 ADH(Arg)
	Aridibacter famid...			AGAGTTTGATC...	DSM 26555	2
	Aridibacter kavan...		2	AGAGTTTGATC...	DSM 26558	1/2
▶	Blastocatella fasti...				JQ309130	1
	Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT...	
	Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...	

Continue with:

- Description grid view - Selection parameters
- Description grid view - Copy or create descriptions
- Description grid view - Save or discard changes

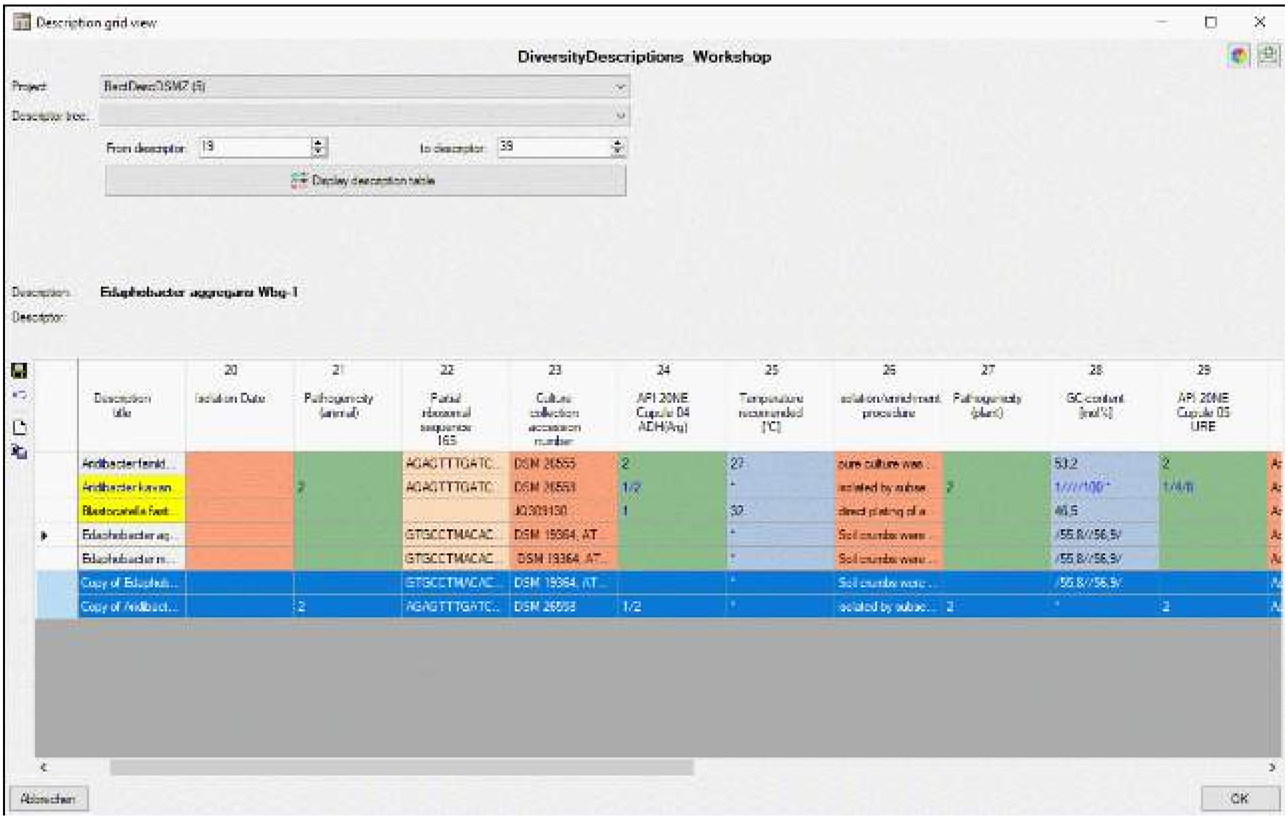
Description grid view - Copy or create descriptions

To copy one or more descriptions select the whole data rows by clicking in the area left from the "Description title" column. In the tool strip the copy button 📋appears (see image below).

Project: BactDescDSMZ (5)
Descriptor tree:
From descriptor: 19
to descriptor: 39
Description: Edaphobacter aggregans Wbg-1
Descriptor:

	20	21	22	23	24	25	26	27	28	29
Description title	Isolation Date	Pathogenicity (animal)	Partial ribosomal sequence 16S	Culture collection accession number	API 20NE Cupule 04 ADH(Arg)	Temperature recommended [°C]	isolation/enrichment procedure	Pathogenicity (plant)	GC content [mol%]	API 20NE Cupule 05 URE
Aridibacter famid...			AGACTTTGATC...	DSM 26555	2	27	pure culture was ...		53.2	2
Aridibacter kavan...		2	AGACTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	1////100 *	1/4/8
Blastocatella fast...				JQ309130	1	30	direct plating of a...		46,5	
Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT		*	Soil crumbs were...		/55.8//56.9/	
Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/	

After clicking the 📋button you may be asked if you want to copy description resources, too. Be aware that the copy operation is directly performed within the database. I.e. that local changes that have been done in the sources desrcriptions will not be included in the targets unless you save your data before copy (see image below, second and last line in descriptors 28 and 29).



Project: BactDescDSMZ (6)

Descriptor tree:

From descriptor: 19 to descriptor: 39

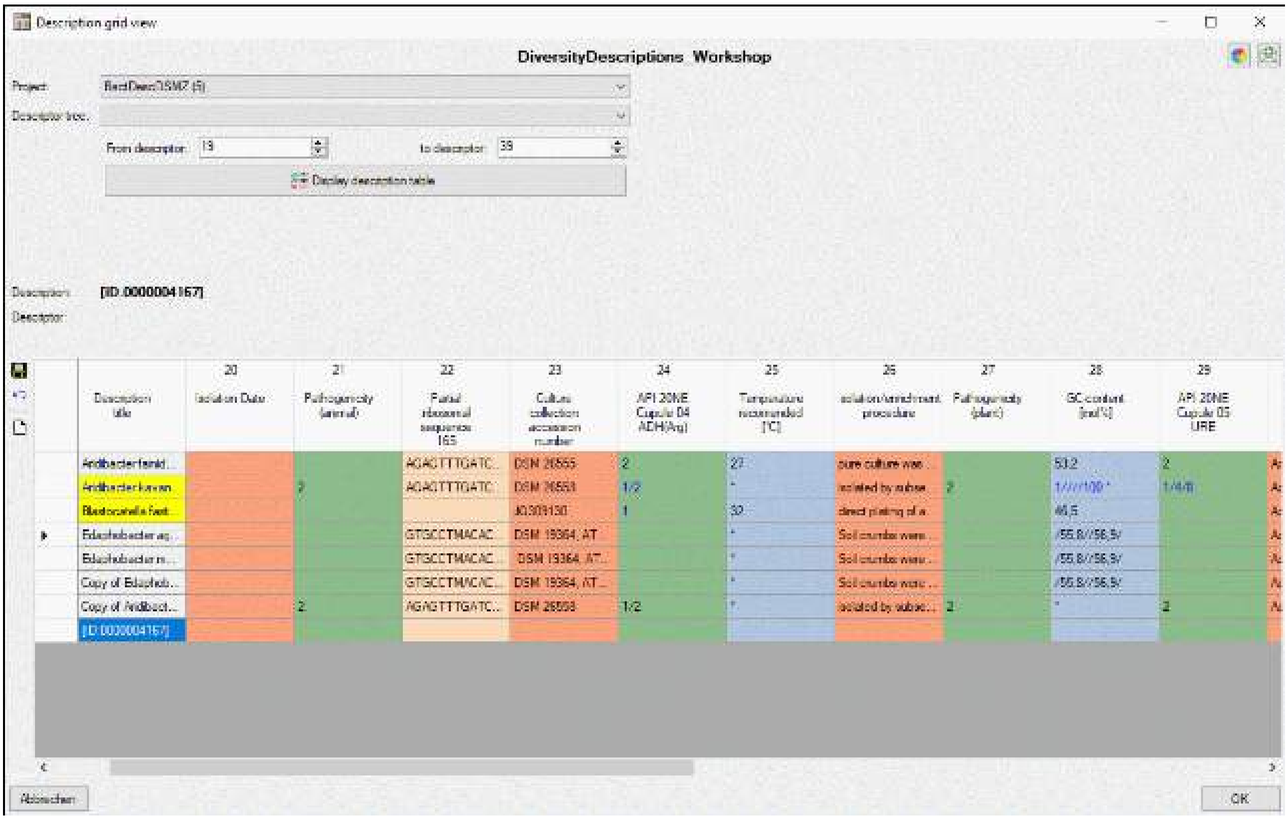
Description: **Edaphobacter aggregans Wbg-1**

Descriptor:

Description title	20 Isolation Date	21 Pathogenicity (animal)	22 Partial ribosomal sequence 16S	23 Culture collection accession number	24 API 20NE Cupule 04 ADH(Arg)	25 Temperature recommended [°C]	26 isolation/enrichment procedure	27 Pathogenicity (plant)	28 GC content [mol%]	29 API 20NE Cupule 05 URE	
Acidibacter ferrid...			AGAGTTTGATC...	DSM 26555	2	27	pure culture was ...		53.2	2	A
Acidibacter kavan...		2	AGAGTTTGATC...	DSM 26553	1/2	*	isolated by subse...	2	1////100*	1/4/8	A
Blastocatella fast...				JQ309130	1	30	direct plating of a ...		46.5		A
Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/		A
Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/		A
Copy of Edaphob...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/		A
Copy of Acidibact...		2	AGAGTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	*	2	A

New description

To enter a new description, click on button ☐ and a new row will be appended (see image below). Same as for copy the new description is created directly within the database.



Project: BactDescDSMZ (6)

Descriptor tree:

From descriptor: 19 to descriptor: 39

Description: **[ID 0000004167]**

Descriptor:

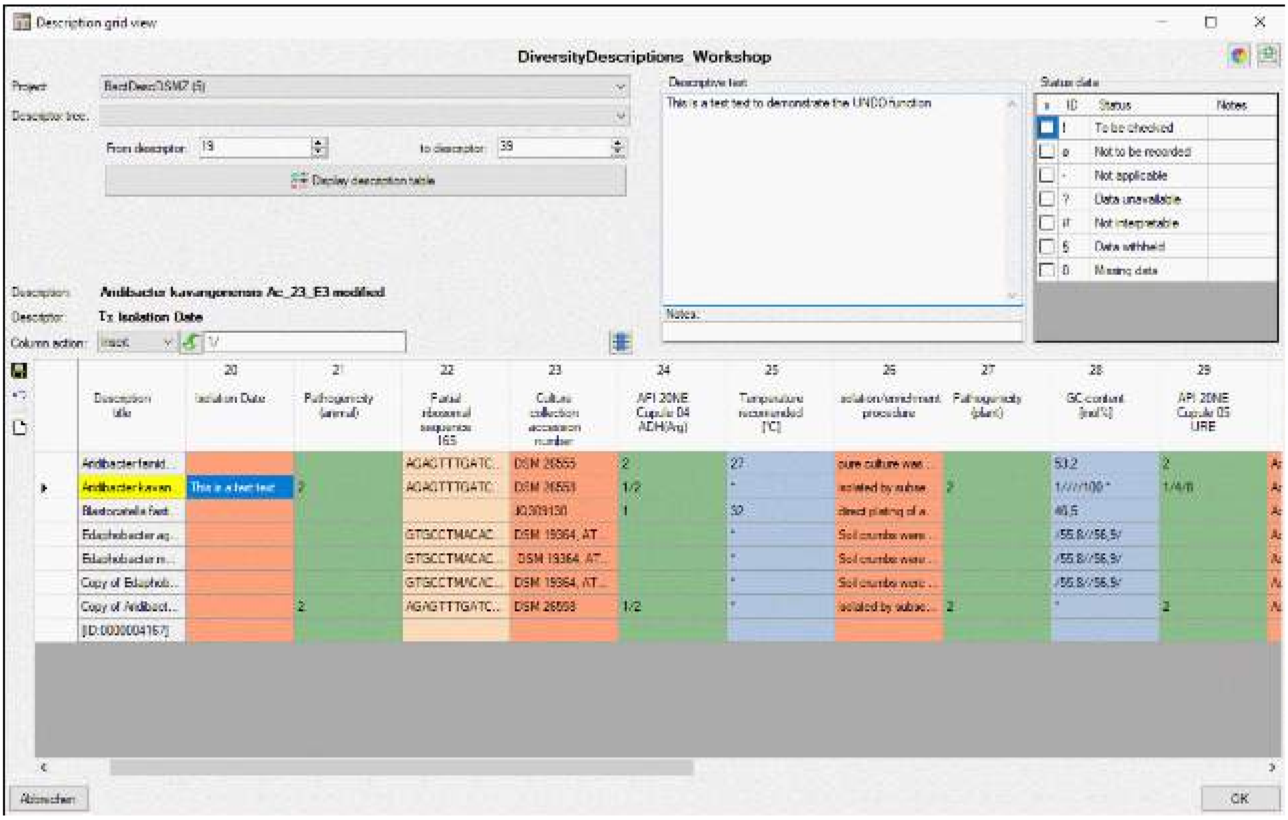
Description title	20 Isolation Date	21 Pathogenicity (animal)	22 Partial ribosomal sequence 16S	23 Culture collection accession number	24 API 20NE Cupule 04 ADH(Arg)	25 Temperature recommended [°C]	26 isolation/enrichment procedure	27 Pathogenicity (plant)	28 GC content [mol%]	29 API 20NE Cupule 05 URE	
Acidibacter ferrid...			AGAGTTTGATC...	DSM 26555	2	27	pure culture was ...		53.2	2	A
Acidibacter kavan...		2	AGAGTTTGATC...	DSM 26553	1/2	*	isolated by subse...	2	1////100*	1/4/8	A
Blastocatella fast...				JQ309130	1	30	direct plating of a ...		46.5		A
Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT		*	Soil crumbs were ...		/55.8//56.9/		A
Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/		A
Copy of Edaphob...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56.9/		A
Copy of Acidibact...		2	AGAGTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	*	2	A
[ID 0000004167]											

Continue with:

- Description grid view - Selection parameters
- Description grid view - Data editing
- Description grid view - Save or discard changes

Description grid view - Save or discard changes

When you click in button "OK" the description grid view is closed and all changes are automatically saved in the database. If you did some changes and want to save them without leaving the form, simply click on 🖫(see image below). If you close the window, e.g. by clicking the "Cancel" button, and still have unsaved changes, you will be asked to save or discard the changes.



Project: BactDescDSMZ (5)
Descriptor tree:
From descriptor: 19
to descriptor: 39

Descriptive text:
This is a test text to demonstrate the UNDO function
Notes:

Status data

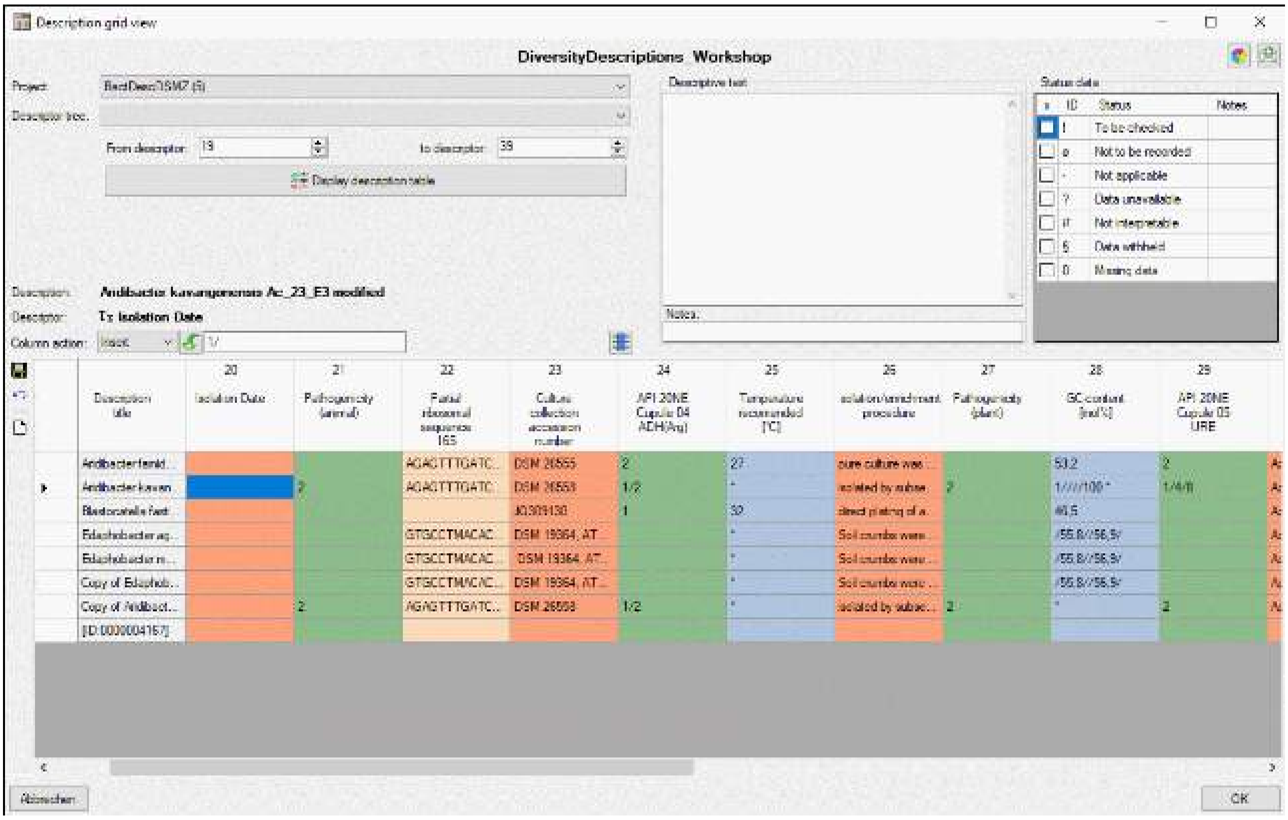
x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	//	Not interpretable	
☐	$	Data withheld	
☐	0	Missing data	

Description: Aridibacter kavangonensis Ac_23_E3 modified
Descriptor: Tx Isolation Date
Column action: Insert \/

Description title	20 Isolation Date	21 Pathogenicity (animal)	22 Partial ribosomal sequence 16S	23 Culture collection accession number	24 API 20NE Cupule 04 ADH(Arg)	25 Temperature recommended [°C]	26 Isolation/enrichment procedure	27 Pathogenicity (plant)	28 GC content [mol%]	29 API 20NE Cupule 05 URE
Aridibacter famid...			AGAGTTTGATC...	DSM 26555	2	27	pure culture was ...		53.2	2
Aridibacter kavan...	This is a test text	2	AGAGTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	1////100 *	1/4/8
Blastocatella fast...				JQ309130	1	30	direct plating of a...		46,5	
Edaphobacter ag...			GTGCCTAACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56,5/	
Edaphobacter m...			GTGCCTAACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56,5/	
Copy of Edaphob...			GTGCCTAACAC...	DSM 19364, AT...		*	Soil crumbs were ...		/55.8//56,5/	
Copy of Aridibact...		2	AGAGTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	*	2
[ID:0000004167]										

Undo all changes

You may discard all unsaved changes without leaving the form by clicking the ↶ button and the data will be reloaded form the database (see image below).



DiversityDescriptions_Workshop

Project: BactDesc/DSMZ (5)

Descriptor tree:

From descriptor: 19 to descriptor: 39

Display description table

Description: **Andibacter kavangonensis Ac_23_E3 modified**

Descriptor: **Tx: Isolation Date**

Column action: Insert \/

Descriptive text

Notes:

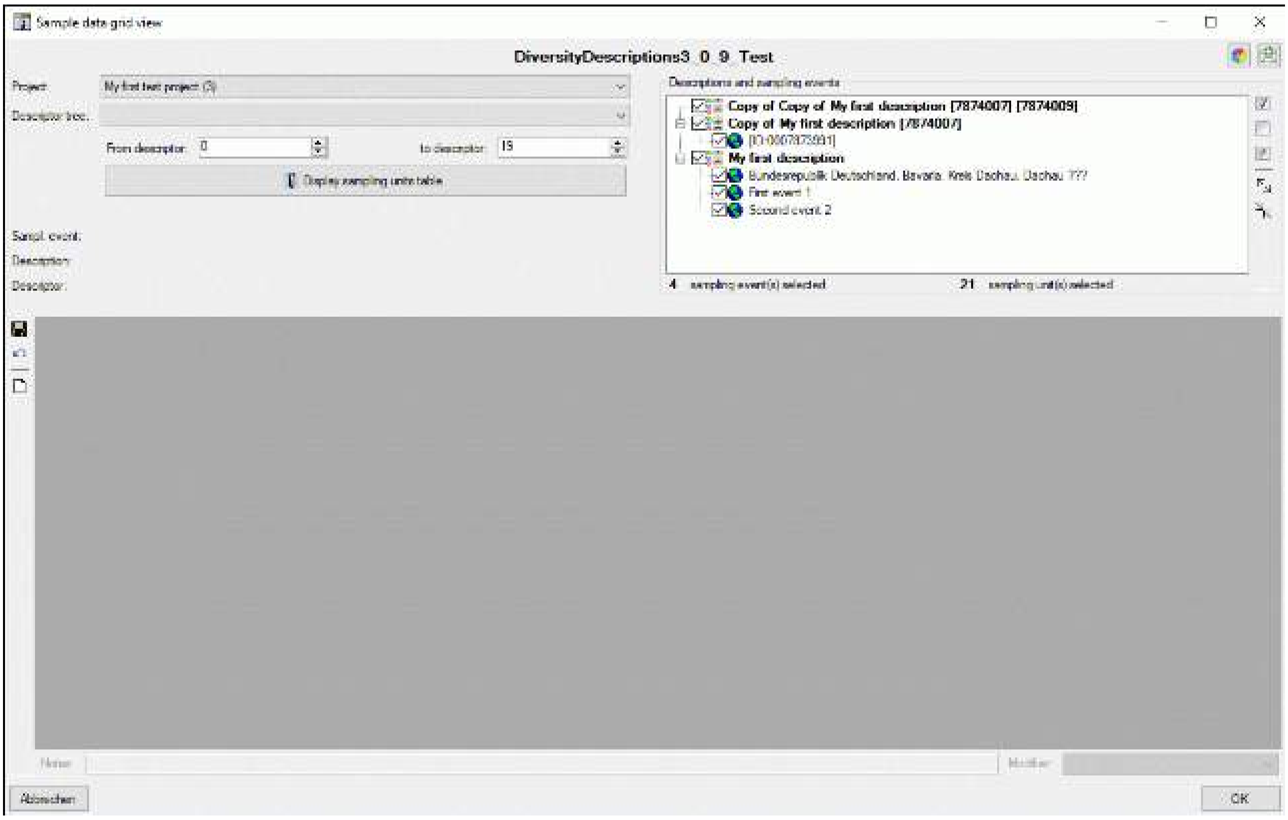
Status data

☐	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	//	Not interpretable	
☐	§	Data withheld	
☐	0	Missing data	

	Description title	20 Isolation Date	21 Pathogenicity (animal)	22 Partial ribosomal sequence 16S	23 Culture collection accession number	24 API 20NE Cupule 04 ADH(Arg)	25 Temperature recommended [°C]	26 isolation/enrichment procedure	27 Pathogenicity (plant)	28 GC content [mol%]	29 API 20NE Cupule 05 URE
	Andibacter famid...			AGAGTTTGATC...	DSM 26555	2	27	pure culture was ...		53.2	2
▸	Andibacter kavan...		2	AGAGTTTGATC...	DSM 26553	1/2	*	isolated by subse...	2	1////100 *	1/4/8
	Bladocorella fast...				JQ309130	1	30	direct plating of a...		46.5	
	Edaphobacter ag...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were...		/55.8//56.9/	
	Edaphobacter m...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were...		/55.8//56.9/	
	Copy of Edaphob...			GTGCCTMACAC...	DSM 19364, AT...		*	Soil crumbs were...		/55.8//56.9/	
	Copy of Andibact...		2	AGAGTTTGATC...	DSM 26558	1/2	*	isolated by subse...	2	*	2
	[ID:0000004167]										

Sample data grid view

After starting a database query for descriptions select **Grid -> Sample data grid view ...** from the menu. The query result list is passed to the description grid view form and a window as shown below opens. In the first line the database name is displayed. If you move the mouse cursor over the database name, a tooltip shows the actual connection paramter.



DiversityDescriptions3_0_9_Test

Project: My first test project (3)

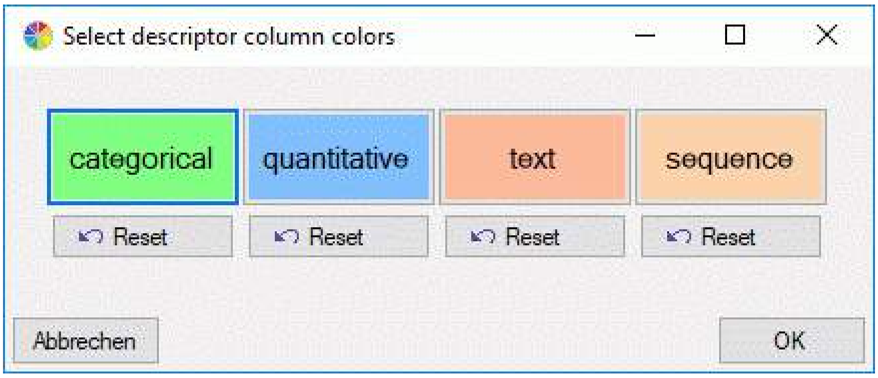
Descriptor tree:

From descriptor: 0 to descriptor: 15

- ☑ **Copy of Copy of My first description [7874007] [7874009]**
- ☑ **Copy of My first description [7874007]**
  - ☑ [ID-0007873991]
- ☑ **My first description**
  - ☑ Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☑ First event 1
  - ☑ Second event 2

4 sampling event(s) selected 21 sampling unit(s) selected

The table in the lower parThe table in the lower part of the window shows the sampling unit IDs in the first column and the sample data in the other columns. Each sample column holds the data of a certain descriptor. The upper part of the window shows the selection parameters that are used for building the sampling unit table. You may change the table colors by clicking the button . A form as shown below will be opened.



Click on buttons **categorical**, **quanitative**, **text** or **sequence** to select the corresponding table colors. By clicking the **Reset** button below the color, the corresponding default value will be selected. After changing the table colors by a click on the **OK** button, you must re-draw the table.

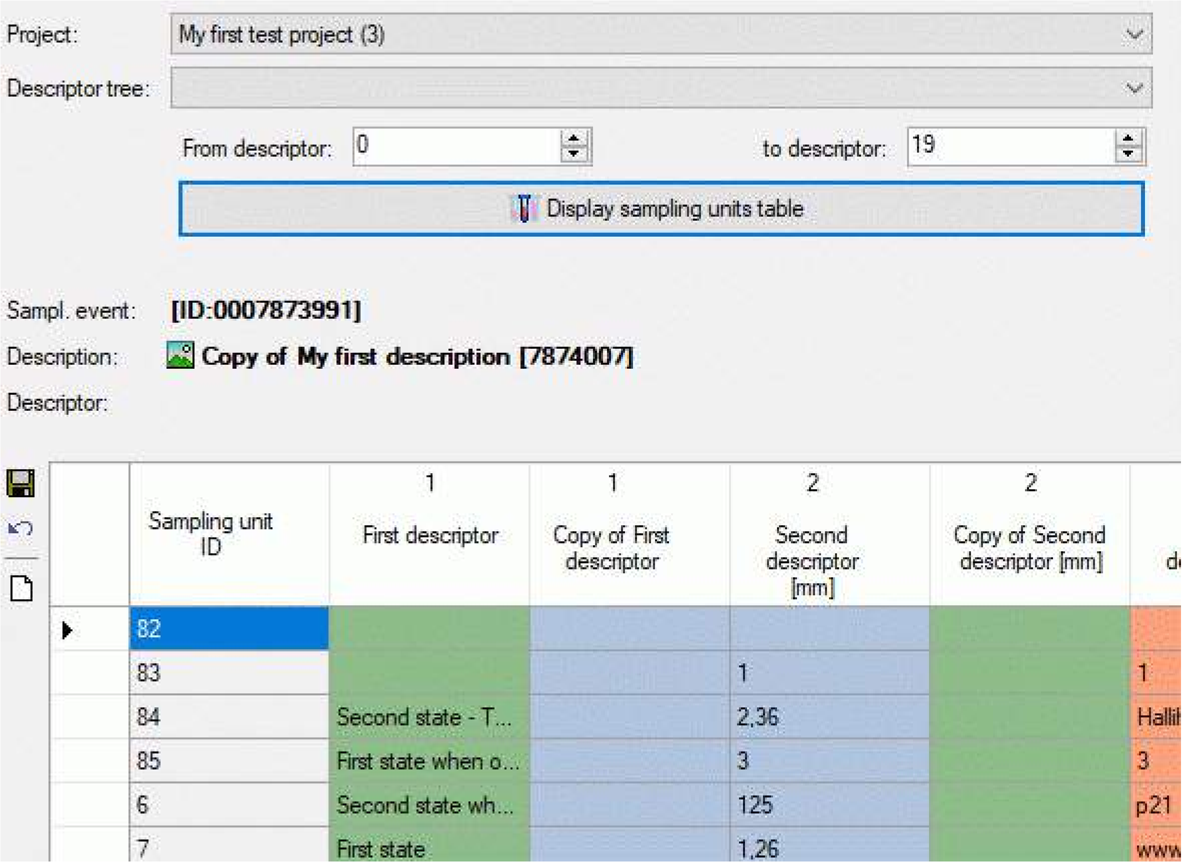
Selection parameters

In the upper left part of the parameters for the samping unit table can be adjusted. If in the query list passed to the form descriptions of different projects are present, the displayed project can be selected with the **Project** drop-down box. The entries in the drow-down list include the project name, followed by the number of descriptions for that project in brackets and an asterisk (*) if the user has only read access for that project.

After selecing a project in section **Descriptions and sampling events** (right upper part of the window) the descriptions and their sampling events are listed. Here you may select the descriptions and sampling events that shall be used for building the sampling unit table. The buttons ☑ **all**, ☐ **none** and **swap** can be used to change the selection of all tree elements. By pressing the button the tree view may be expanded to display the contained sampling events, by pressing the button only the descriptions will be shown. In the bottom of the section the currently selected number of sampling events and sampling units is displayed.

When you click on a single sampling event and more than one description is in the list, the button appears in the tool strip. By clicking this button you can open a description selection window and thus shift the sampling event to a different parent description.

The **Descriptor tree** drop-down box restricts the descriptor columns to the descriptors contained in the selected tree. Furthermore the tree hierarchy is included in the descriptor names if a structured descriptor tree is selected (see images below).



Project: My first test project (3)

Descriptor tree:

From descriptor: 0

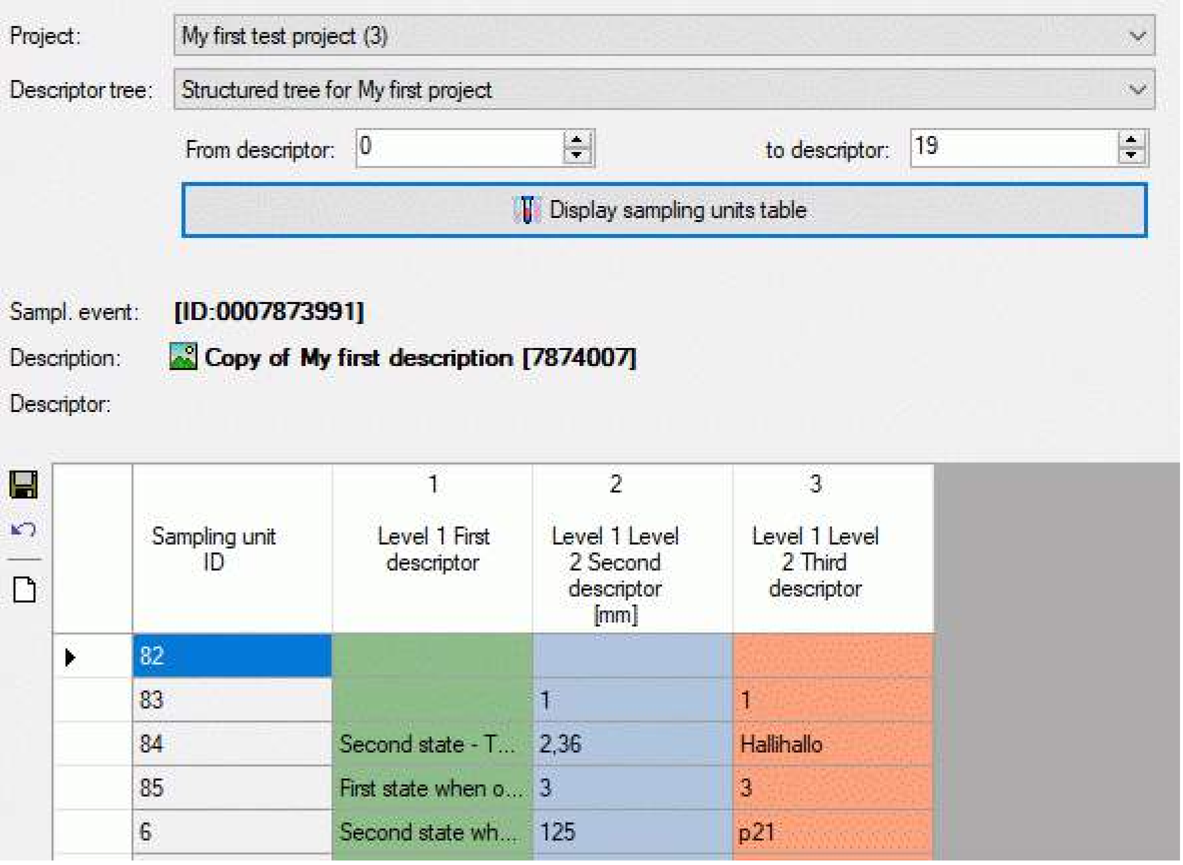
to descriptor: 19

Sampl. event: [ID:0007873991]

Description: Copy of My first description [7874007]

Descriptor:

	Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	d
▶	82					
	83			1		1
	84	Second state - T...		2,36		Halli
	85	First state when o...		3		3
	6	Second state wh...		125		p21
	7	First state		1,26		www



Project: My first test project (3)
Descriptor tree: Structured tree for My first project
From descriptor: 0
to descriptor: 19

Sampl. event: **[ID:0007873991]**
Description: **Copy of My first description [7874007]**
Descriptor:

Sampling unit ID	1 Level 1 First descriptor	2 Level 1 Level 2 Second descriptor [mm]	3 Level 1 Level 2 Third descriptor
82			
83		1	1
84	Second state - T...	2,36	Hallihallo
85	First state when o...	3	3
6	Second state wh...	125	p21

The values **From descriptor** and **to descriptor** limit the range of descriptor sequence numbers that is included in the discription tabe. Be aware that this restiction is additionally effective to a selected desriptor tree! If you want to de-activate this restriction, select "from" value 0 "to" value 999999 by a double-click on the labels **From descriptor** rsp. **to descriptor** . The limitation of the number of descriptor columns makes speeds up the description table generation, especally if many descriptor (e.g. some hundrets) are present.

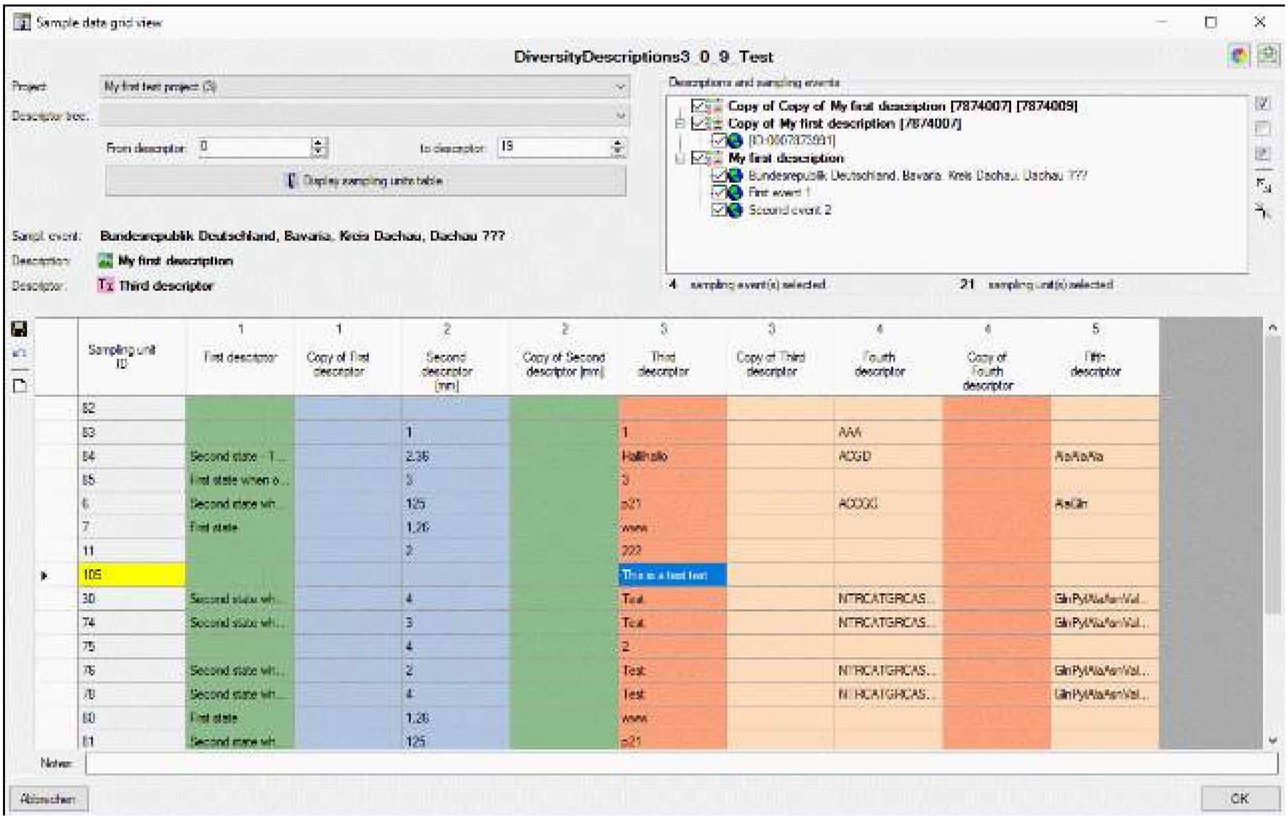
Finally click the button **Display sampling units table** to build a new sampling unit table according to your settings. During output of the sampling unit table the icon of the button changes to 🛑 and you may abort processing by clicking the button.

Continue with:

- Sample data grid view - Data editing
- Sample data grid view - Save or discard changes

Sample data grid view - Data editing

The first column of the sampling unit table shows the sampling unit IDs titles, which are fixed. I.e. if you scroll the sample data to the right, the IDs are still visible at the left. The other columns show the sample data, where the descriptor type is indicated by the background colour: categorical, quantitative, text or sequence. The column titles include the descriptor name, the mesurement unit in square bracket for quantitative descriptors and the descriptor's sequence number (see image below).



DiversityDescriptions3_0_9_Test

Project: My first test project (3)

Descriptor tree:

From descriptor: 0

to descriptor: 19

Sampl. event: Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???

Description: My first description

Descriptor: Tx Third descriptor

- ☑ Copy of Copy of My first description [7874007] [7874009]
- ☑ Copy of My first description [7874007]
  - ☑ 🌍 [ID-0007873991]
- ☑ My first description
  - ☑ 🌍 Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☑ 🌍 First event 1
  - ☑ 🌍 Second event 2

4 sampling event(s) selected

21 sampling unit(s) selected

Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	3 Third descriptor	3 Copy of Third descriptor	4 Fourth descriptor	4 Copy of Fourth descriptor	5 Fifth descriptor
82									
83			1		1		AAA		
84	Second state - 1...		2,36		Hallihallo		ACGD		AlaAlaAla
85	First state when o...		3		3				
6	Second state wh...		125		a21		ACGGG		AlaGln
7	First state		1,26		www				
11			2		222				
105					This is a test text				
30	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
75			4		2				
76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
80	First state		1,26		www				
81	Second state wh...		125		a21				

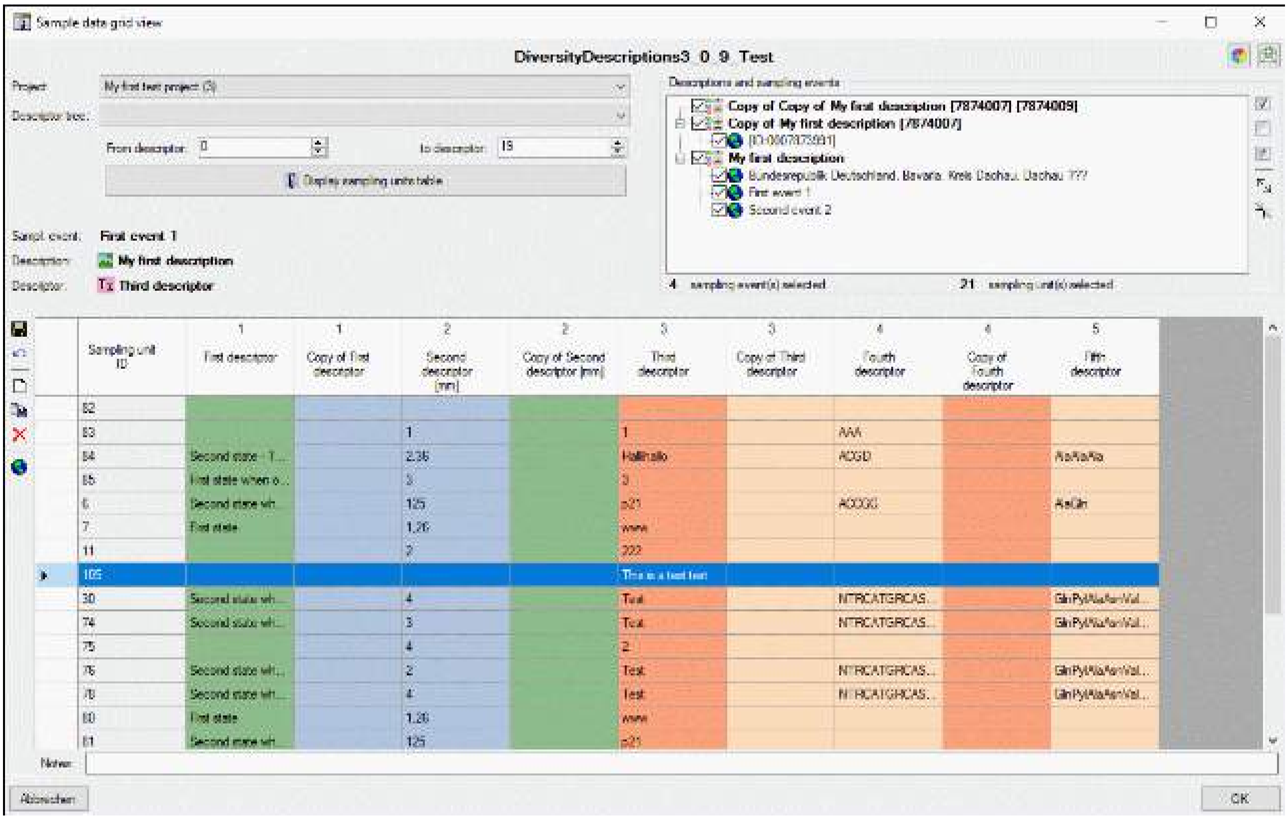
Notes:

When a sample cell in the sampling unit table is selected, the field **Sampl. event:** shows the sampling event titles, field **Description:** shows the description title and field **Descriptor:** shows the symbols according the descriptor type (C for categorical, Σ for quantitative, Tx for text and 🧬 for sequence) and the descriptor title. If for a descriptor resources are available, this fact is indicated by a coloured symbol background. You may view them by a double-click on the descriptor title. If for a description resources are available, the symbol 🖼 is displayed before the title. Double click in that symbol to view the resources.

For the selected cell the sample data may be edited as described in section Editing the description - Sample data tab of this manual. For modified sample cells the text colour changes to blue and the sample unit IDs will be shown with yellow background in the table.

Changing the sampling event

To shift samling units to a different sampling event, select the whole data rows by clicking in the area left from the "Sampling unit ID" column. In the tool strip the set event button 🌍 appears. After clicking the button a window for selecting the new parent sampling event will be opened (see image below).



DiversityDescriptions3_0_9_Test

Project: My first test project (3)

Descriptor tree:

From descriptor: 0 to descriptor: 19

Descriptions and sampling events

- ☑ Copy of Copy of My first description [7874007] [7874009]
- ☑ Copy of My first description [7874007]
  - ☑ [ID:0007873991]
- ☑ My first description
  - ☑ Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☑ First event 1
  - ☑ Second event 2

4 sampling event(s) selected

21 sampling unit(s) selected

Sampl. event: First event 1

Description: My first description

Descriptor: Third descriptor

	Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	3 Third descriptor	3 Copy of Third descriptor	4 Fourth descriptor	4 Copy of Fourth descriptor	5 Fifth descriptor
	82									
	83			1		1		AAA		
	84	Second state - T...		2,36		Hallhallo		ACGD		AlaAlaAla
	85	First state when o...		3		3				
	6	Second state wh...		125		p21		ACCGG		AlaGln
	7	First state		1,26		www				
	11			2		222				
▶	105					This is a test text				
	30	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	75			4		2				
	76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	80	First state		1,26		www				
	81	Second state wh...		125		p21				

Notes:

Copy sampling units

To copy one or more sampling units select the whole data rows by clicking in the area left from the "Sampling unit ID" column. In the tool strip the copy button 📋appears (see image below).

	Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	3 Third descriptor	3 Copy of Third descriptor	4 Fourth descriptor	4 Copy of Fourth descriptor	5 Fifth descriptor
	82									
	83			1		1		AAA		
	84	Second state - T...		2,36		Hallhallo		ACGD		AlaAlaAla
	85	First state when o...		3		3				
▶	6	Second state wh...		125		p21		ACCGG		AlaGln
	7	First state		1,26		www				
	11			2		222				
	105					This is a test text				
	30	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	75			4		2				
	76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	80	First state		1,26		www				
	81	Second state wh...		125		p21				

After clicking the 📋button the copied line are inserte at the end of the tabel (see image below).

	1	1	2	2	3	3	4	4	5
Sampling unit ID	First descriptor	Copy of First descriptor	Second descriptor [mm]	Copy of Second descriptor [mm]	Third descriptor	Copy of Third descriptor	Fourth descriptor	Copy of Fourth descriptor	Fifth descriptor
74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
75			4		2				
76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
80	First state		1,26		www				
81	Second state wh...		125		p21				
1			1		1				
2	Third state when ...		2,252		test text				
64	First state when o...		3		3				
65	Second state - T...		2,36		Hallhallo		ACGG		AlaAlaAla
68			1		1				
77									
115	Second state wh...		125		p21		ACCGG		AlaGln
116					This is a test text				

Delete sampling units

To delete one or more sampling units select the whole data rows by clicking in the area left from the "Sampling unit ID" column. In the tool strip the copy button ✗appears.

New sampling unit

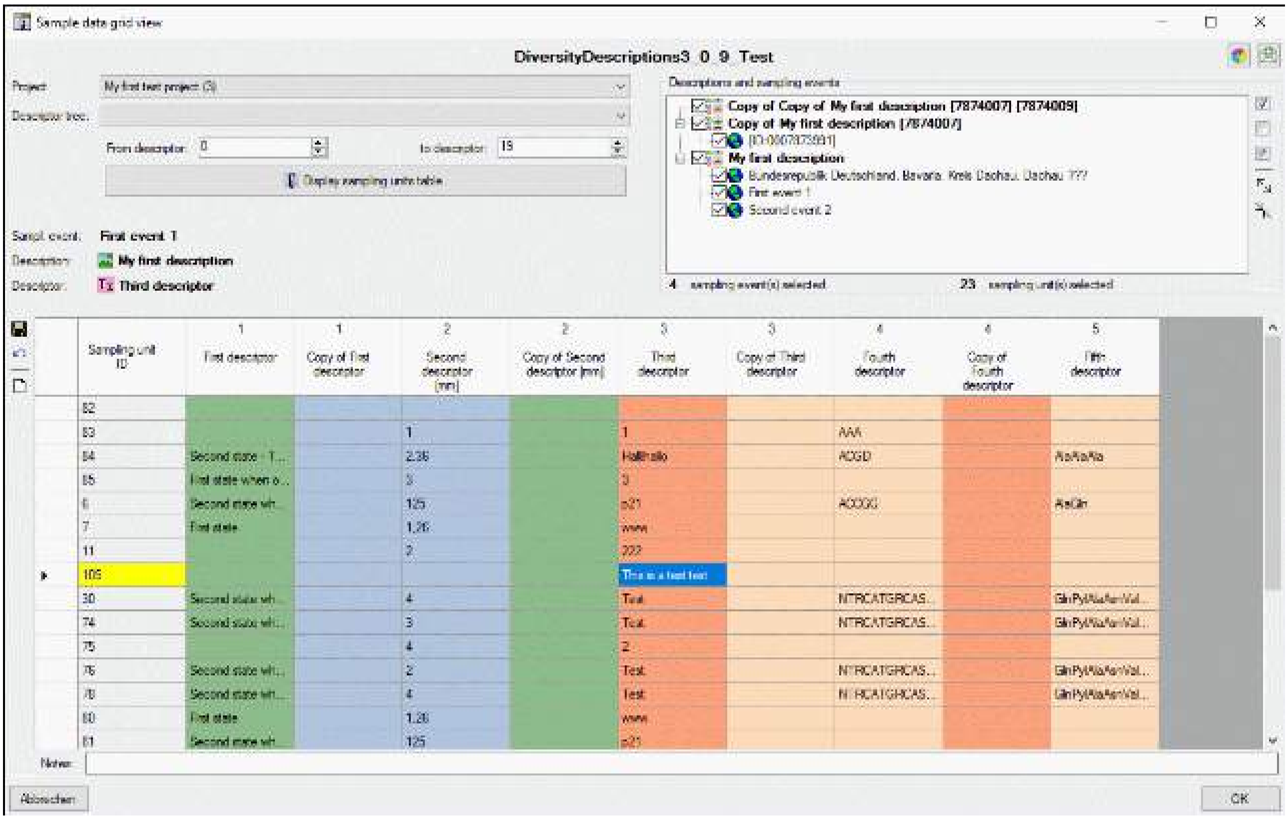
To enter a new sampling, click on button 🗋and a new row will be appended. After clicking the button a window for selecting the sampling event will be opened.

Continue with:

- Sample data grid view - Selection parameters
- Sample data grid view - Save or discard changes

Sample data grid view - Save or discard changes

When you click in button "OK" the sample data grig view is closed and all changes are automatically saved in the database. If you did some changes and want to save them without leaving the form, simply click on 💾(see image below). If you close the window, e.g. by clicking the "Cancel" button, and still have unsaved changes, you will be asked to save or discard the changes.



Project: My first test project (3)
Descriptor tree:
From descriptor: 0
to descriptor: 15

Descriptions and sampling events
- ☑ Copy of Copy of My first description [7874007] [7874009]
- ☑ Copy of My first description [7874007]
  - ☑ [ID-0007873991]
- ☑ My first description
  - ☑ Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☑ First event 1
  - ☑ Second event 2

4 sampling event(s) selected
23 sampling unit(s) selected

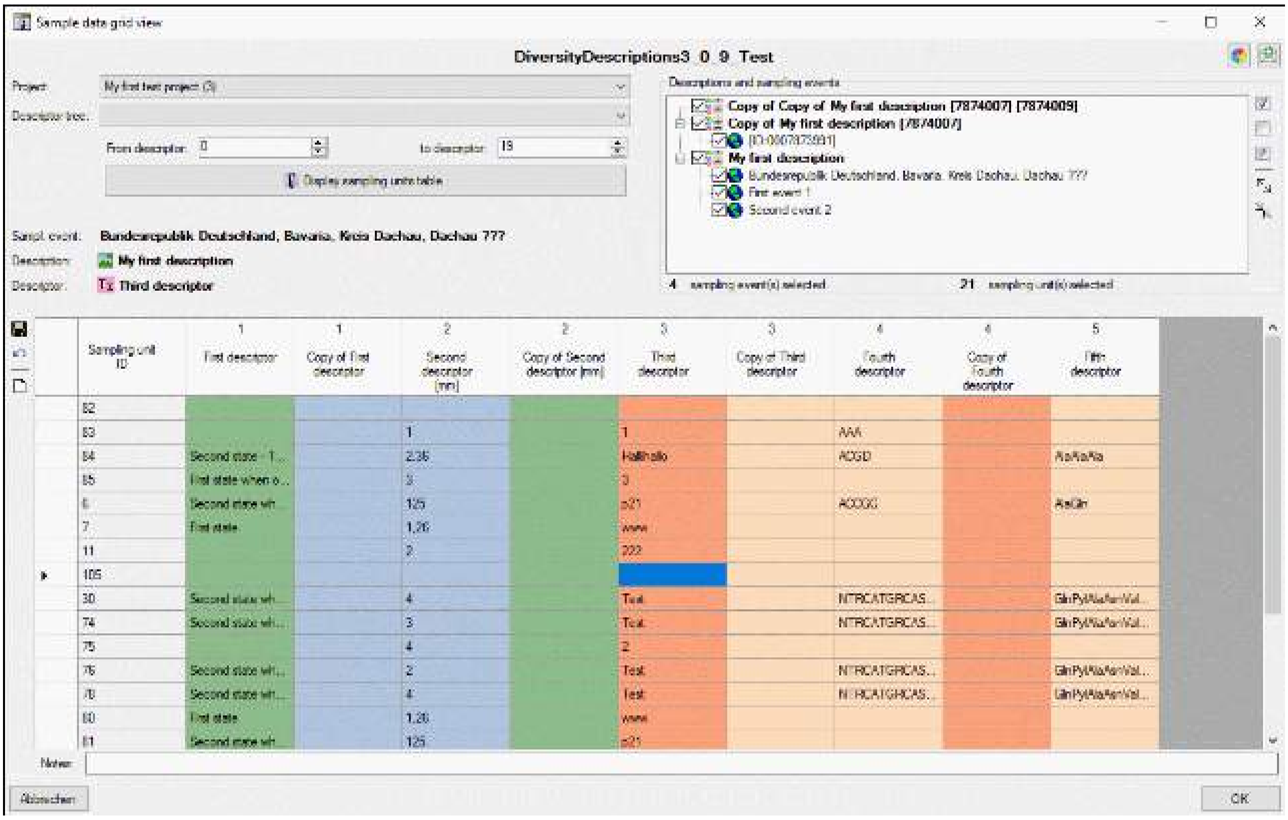
Sampl. event: First event 1
Description: My first description
Descriptor: Third descriptor

Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	3 Third descriptor	3 Copy of Third descriptor	4 Fourth descriptor	4 Copy of Fourth descriptor	5 Fifth descriptor
82									
83			1		1		AAA		
84	Second state - T...		2,36		Hallhallo		ACGD		AlaAlaAla
85	First state when o...		3		3				
6	Second state wh...		125		a21		ACCGG		AlaGln
7	First state		1,26		www				
11			2		222				
105					This is a test text				
30	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
75			4		2				
76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
80	First state		1,26		www				
81	Second state wh...		125		a21				

Notes:

Undo all changes

You may discard all unsaved changes without leaving the form by clicking the ↶ button and the data will be reloaded form the database (see image below).



Project: My first test project (3)

Descriptor tree:

From descriptor: 0 to descriptor: 19

Sampl. event: **Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???**

Description: **My first description**

Descriptor: **Third descriptor**

Descriptions and sampling events

- ☑ **Copy of Copy of My first description [7874007] [7874009]**
- ☑ **Copy of My first description [7874007]**
  - ☑ [ID-0007873991]
- ☑ **My first description**
  - ☑ Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☑ First event 1
  - ☑ Second event 2

4 sampling event(s) selected 21 sampling unit(s) selected

	Sampling unit ID	1 First descriptor	1 Copy of First descriptor	2 Second descriptor [mm]	2 Copy of Second descriptor [mm]	3 Third descriptor	3 Copy of Third descriptor	4 Fourth descriptor	4 Copy of Fourth descriptor	5 Fifth descriptor
	82									
	83			1		1		AAA		
	84	Second state - 1...		2,35		Hallhallo		ACGD		AlaAlaAla
	85	First state when o...		3		3				
	6	Second state wh...		125		a21		ACCGG		AlaGln
	7	First state		1,26		www				
	11			2		222				
▸	105									
	30	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	74	Second state wh...		3		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	75			4		2				
	76	Second state wh...		2		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	78	Second state wh...		4		Test		NTRCATGRCAS...		GlnPylAlaAsnVal...
	80	First state		1,26		www				
	81	Second state wh...		125		a21				

Notes:

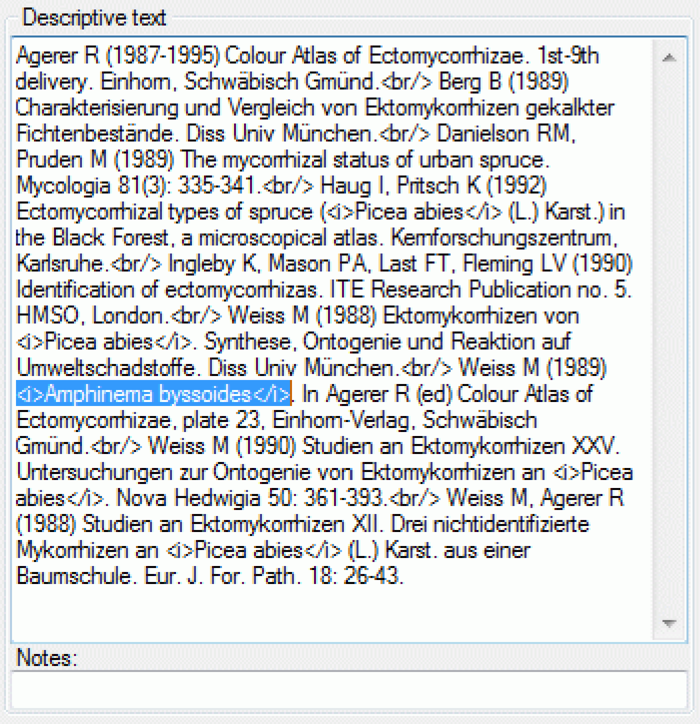
Extended text editor

In the most text fields you can open an extended text editor by double-clicking the text field, whic proviedes the following features:

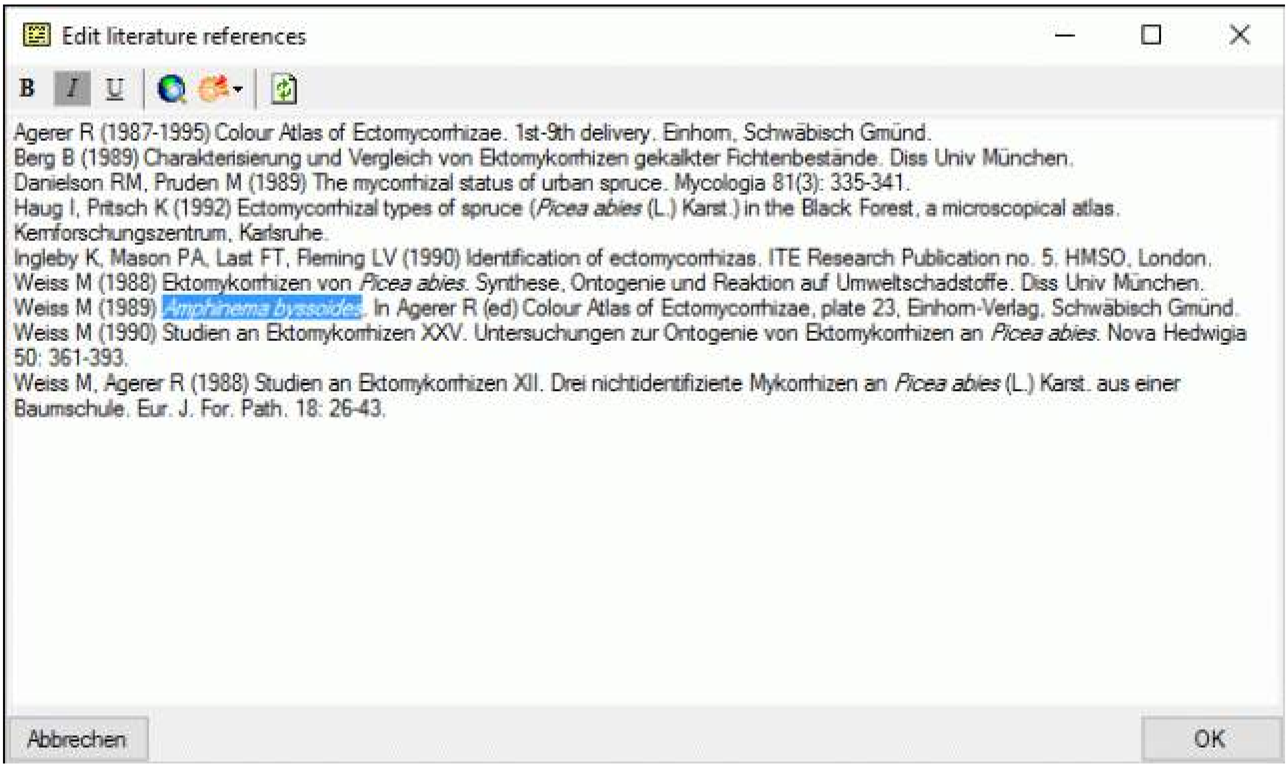
- Text formatting
- RTF-like text formatting
- Inserting text links

Text formatting

In the text fields you may use some HTML mark-ups bold <i>italic</i> and <u>underline</u> for text formatting (see image below left). Additionally the tags <br>, <br/> or <br /> may be inserted to indicate a new text line, but the most common way is to press the ENTER key instead. The format tags will have an effect if documents are generated from the database.



Agerer R (1987-1995) Colour Atlas of Ectomycorrhizae. 1st-9th delivery. Einhorn, Schwäbisch Gmünd.
 Berg B (1989) Charakterisierung und Vergleich von Ektomykorrhizen gekalkter Fichtenbestände. Diss Univ München.
 Danielson RM, Pruden M (1989) The mycorrhizal status of urban spruce. Mycologia 81(3): 335-341.
 Haug I, Pritsch K (1992) Ectomycorrhizal types of spruce (<i>Picea abies</i> (L.) Karst.) in the Black Forest, a microscopical atlas. Kernforschungszentrum, Karlsruhe.
 Ingleby K, Mason PA, Last FT, Fleming LV (1990) Identification of ectomycorrhizas. ITE Research Publication no. 5. HMSO, London.
 Weiss M (1988) Ektomykorrhizen von <i>Picea abies</i>. Synthese, Ontogenie und Reaktion auf Umweltschadstoffe. Diss Univ München.
 Weiss M (1989) <i>Amphinema byssoides</i>. In Agerer R (ed) Colour Atlas of Ectomycorrhizae, plate 23, Einhorn-Verlag, Schwäbisch Gmünd.
 Weiss M (1990) Studien an Ektomykorrhizen XXV. Untersuchungen zur Ontogenie von Ektomykorrhizen an <i>Picea abies</i>. Nova Hedwigia 50: 361-393.
 Weiss M, Agerer R (1988) Studien an Ektomykorrhizen XII. Drei nichtidentifizierte Mykorrhizen an <i>Picea abies</i> (L.) Karst. aus einer Baumschule. Eur. J. For. Path. 18: 26-43.



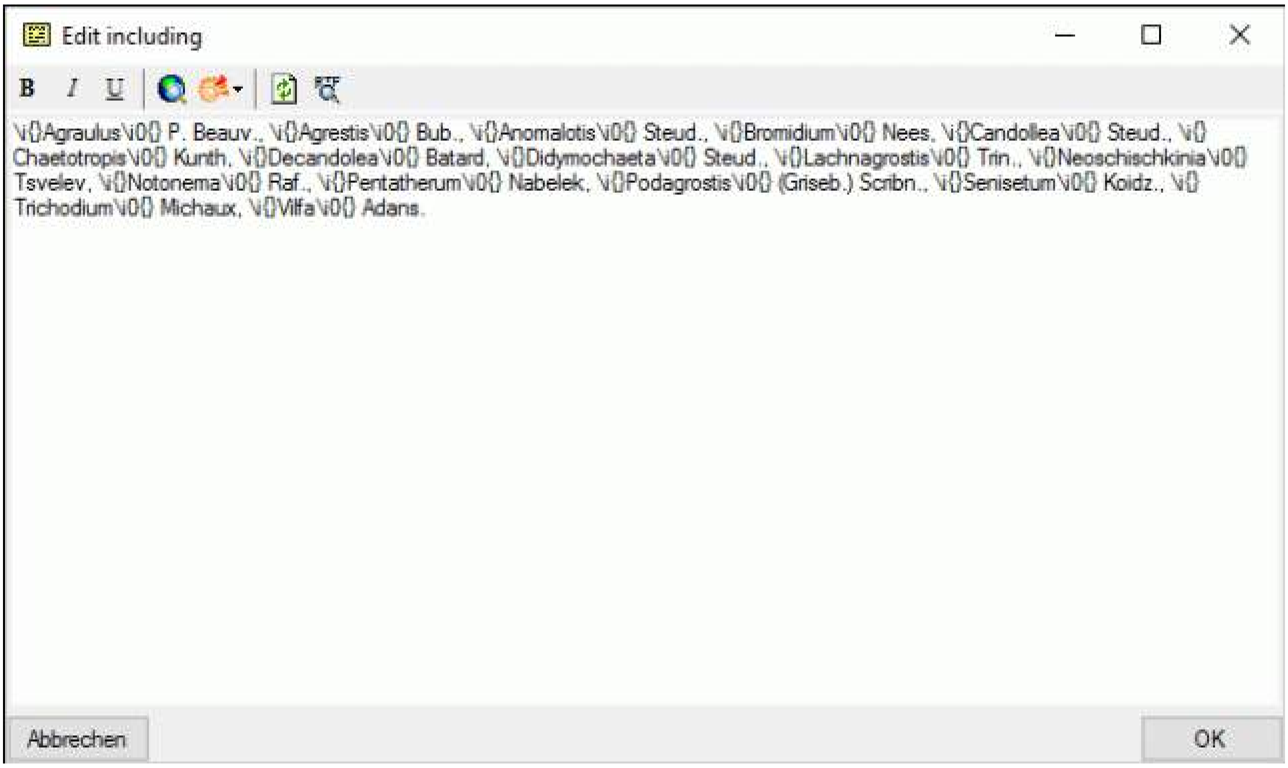
Agerer R (1987-1995) Colour Atlas of Ectomycorrhizae. 1st-9th delivery. Einhorn, Schwäbisch Gmünd.
Berg B (1989) Charakterisierung und Vergleich von Ektomykorrhizen gekalkter Fichtenbestände. Diss Univ München.
Danielson RM, Pruden M (1989) The mycorrhizal status of urban spruce. Mycologia 81(3): 335-341.
Haug I, Pritsch K (1992) Ectomycorrhizal types of spruce (*Picea abies* (L.) Karst.) in the Black Forest, a microscopical atlas. Kernforschungszentrum, Karlsruhe.
Ingleby K, Mason PA, Last FT, Fleming LV (1990) Identification of ectomycorrhizas. ITE Research Publication no. 5. HMSO, London.
Weiss M (1988) Ektomykorrhizen von *Picea abies*. Synthese, Ontogenie und Reaktion auf Umweltschadstoffe. Diss Univ München.
Weiss M (1989) *Amphinema byssoides*. In Agerer R (ed) Colour Atlas of Ectomycorrhizae, plate 23, Einhorn-Verlag, Schwäbisch Gmünd.
Weiss M (1990) Studien an Ektomykorrhizen XXV. Untersuchungen zur Ontogenie von Ektomykorrhizen an *Picea abies*. Nova Hedwigia 50: 361-393.
Weiss M, Agerer R (1988) Studien an Ektomykorrhizen XII. Drei nichtidentifizierte Mykorrhizen an *Picea abies* (L.) Karst. aus einer Baumschule. Eur. J. For. Path. 18: 26-43.

By double-clicking the text field you can open a separate edit window that shows the text formatting (see image above right). You can easily change the formatting by selecting a text and clicking the buttons **B**, *I* or U.

To reload the original text into the edit window click the button. By clicking **OK** the changes are taken over to the text field, to ignore the changes, click the cancel button.

RTF-like text formatting

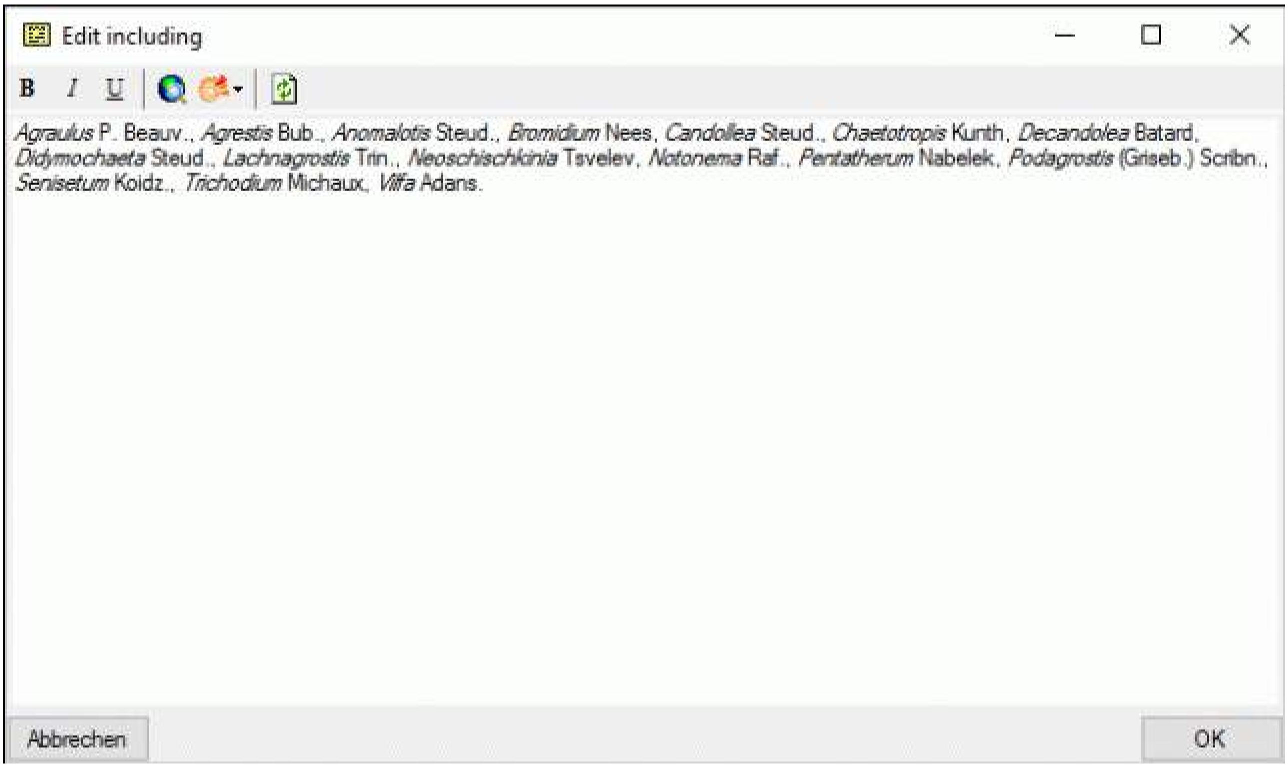
In some projects RTF-like mark-ups are used to indicate text formatting, e.g. \i{}italics\i0{} for *italics*. If you double-click on the text field you can open the separate edit window and button indicates that RTF-like format mark-ups have been detected (see image below).



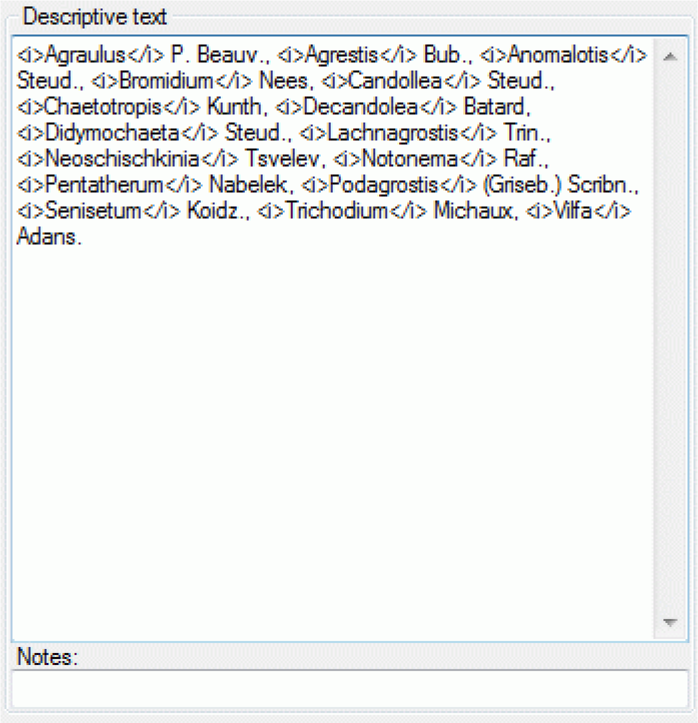
```
\i{}Agraulus\i0{} P. Beauv., \i{}Agrestis\i0{} Bub., \i{}Anomalotis\i0{} Steud., \i{}Bromidium\i0{} Nees, \i{}Candollea\i0{} Steud., \i{}
Chaetotropis\i0{} Kunth, \i{}Decandolea\i0{} Batard, \i{}Didymochaeta\i0{} Steud., \i{}Lachnagrostis\i0{} Trin., \i{}Neoschischkinia\i0{}
Tsvelev, \i{}Notonema\i0{} Raf., \i{}Pentatherum\i0{} Nabelek, \i{}Podagrostis\i0{} (Griseb.) Scribn., \i{}Senisetum\i0{} Koidz., \i{}
Trichodium\i0{} Michaux, \i{}Vilfa\i0{} Adans.
```

<

By clicking the button the edit window will show you the formatted text (see image below left). After clicking **OK** the text will be stored using the HTML mark-ups, which is the standard for DiversityDescriptions (see image below right).



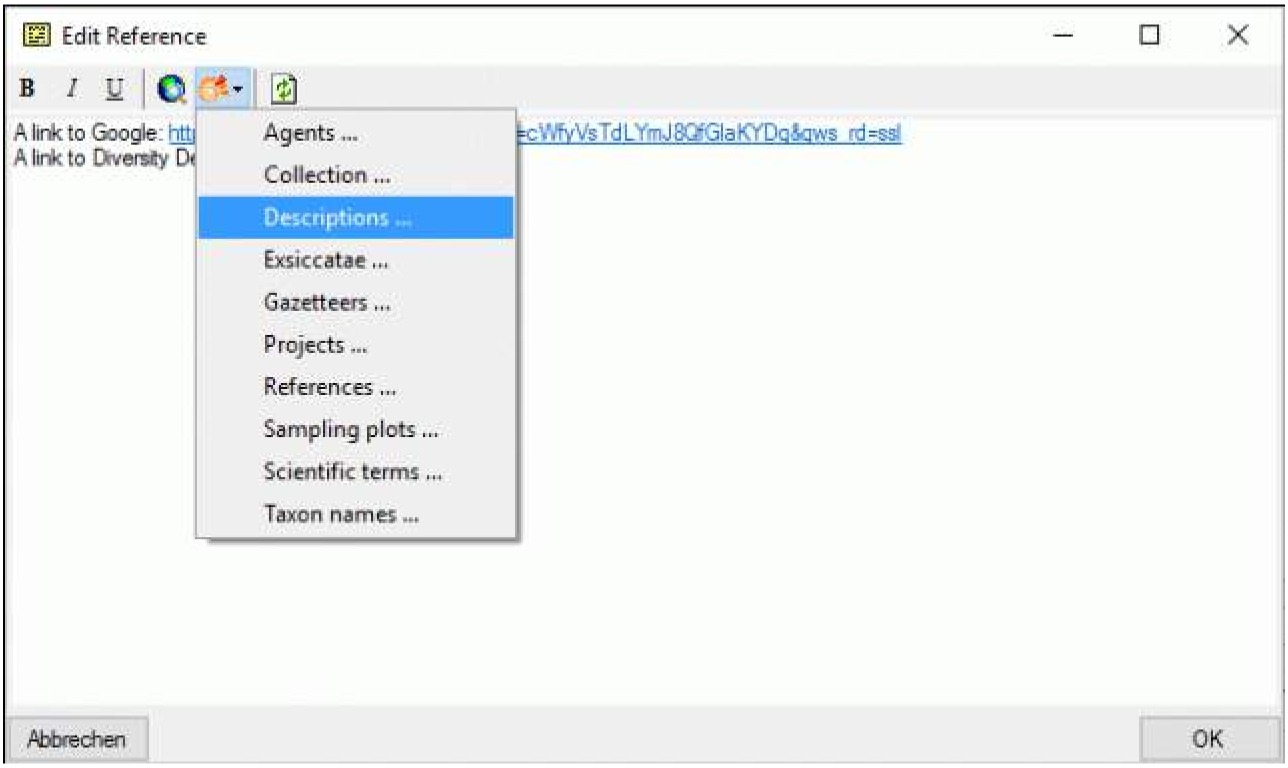
Agraulus P. Beauv., *Agrestis* Bub., *Anomalotis* Steud., *Bromidium* Nees, *Candollea* Steud., *Chaetotropis* Kunth, *Decandolea* Batard, *Didymochaeta* Steud., *Lachnagrostis* Trin., *Neoschischkinia* Tsvelev, *Notonema* Raf., *Pentatherum* Nabelek, *Podagrostis* (Griseb.) Scribn., *Senisetum* Koidz., *Trichodium* Michaux, *Vilfa* Adans.



<i>Agraulus</i> P. Beauv., <i>Agrestis</i> Bub., <i>Anomalotis</i> Steud., <i>Bromidium</i> Nees, <i>Candollea</i> Steud., <i>Chaetotropis</i> Kunth, <i>Decandolea</i> Batard, <i>Didymochaeta</i> Steud., <i>Lachnagrostis</i> Trin., <i>Neoschischkinia</i> Tsvelev, <i>Notonema</i> Raf., <i>Pentatherum</i> Nabelek, <i>Podagrostis</i> (Griseb.) Scribn., <i>Senisetum</i> Koidz., <i>Trichodium</i> Michaux, <i>Vilfa</i> Adans.

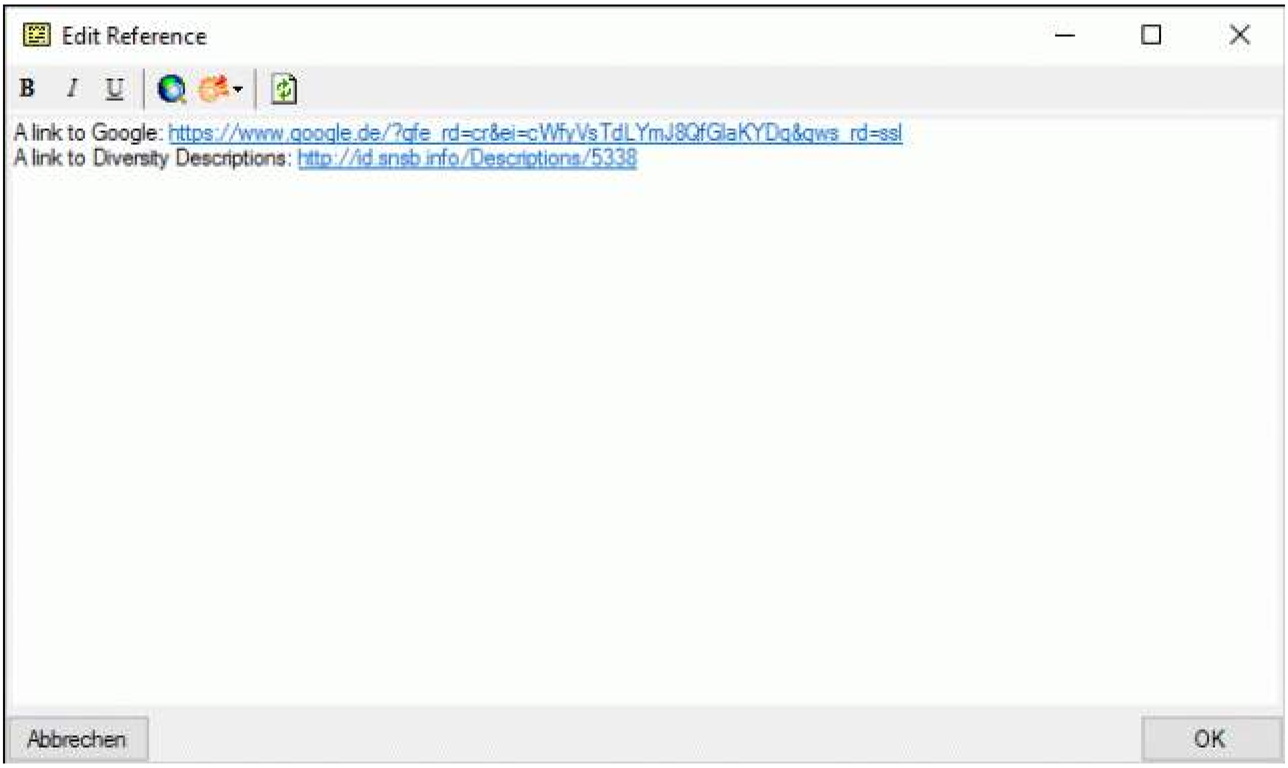
Inserting links into text

You may open an internet browser by klicking the button . After navigating to your target page, click **OK** to insert the link at the current cursor position. By klicking the drop-down button you can select a Diversity Workbench database and search for a certain database entry (see image below).



A link to Google: htt
=cWfyVsTdLYmJ8QfGlaKYDq&gws_rd=ssl
A link to Diversity D

After selecting a found entry and clicking **OK** the database link is inserted at the current cursor position (see image below).



A link to Google: https://www.google.de/?gfe_rd=cr&ei=cWfyVsTdLYmJ8QfGlaKYDg&gws_rd=ssl
A link to Diversity Descriptions: http://id.snsb.info/Descriptions/5338

When the link is clicked either the web browser opens (for regular HTML links) or the Diversity Workbench application to display the databease entry (see image below).

ID: 5338
Description name: Common Frog (Rana temporaria)
Details
Project: SDD of ETI reptiles and amphibians
Rights
License
Taxon name: Common Frog
Observation
Specimen
Geographic area
Stage
Part
Other scope

Table editors

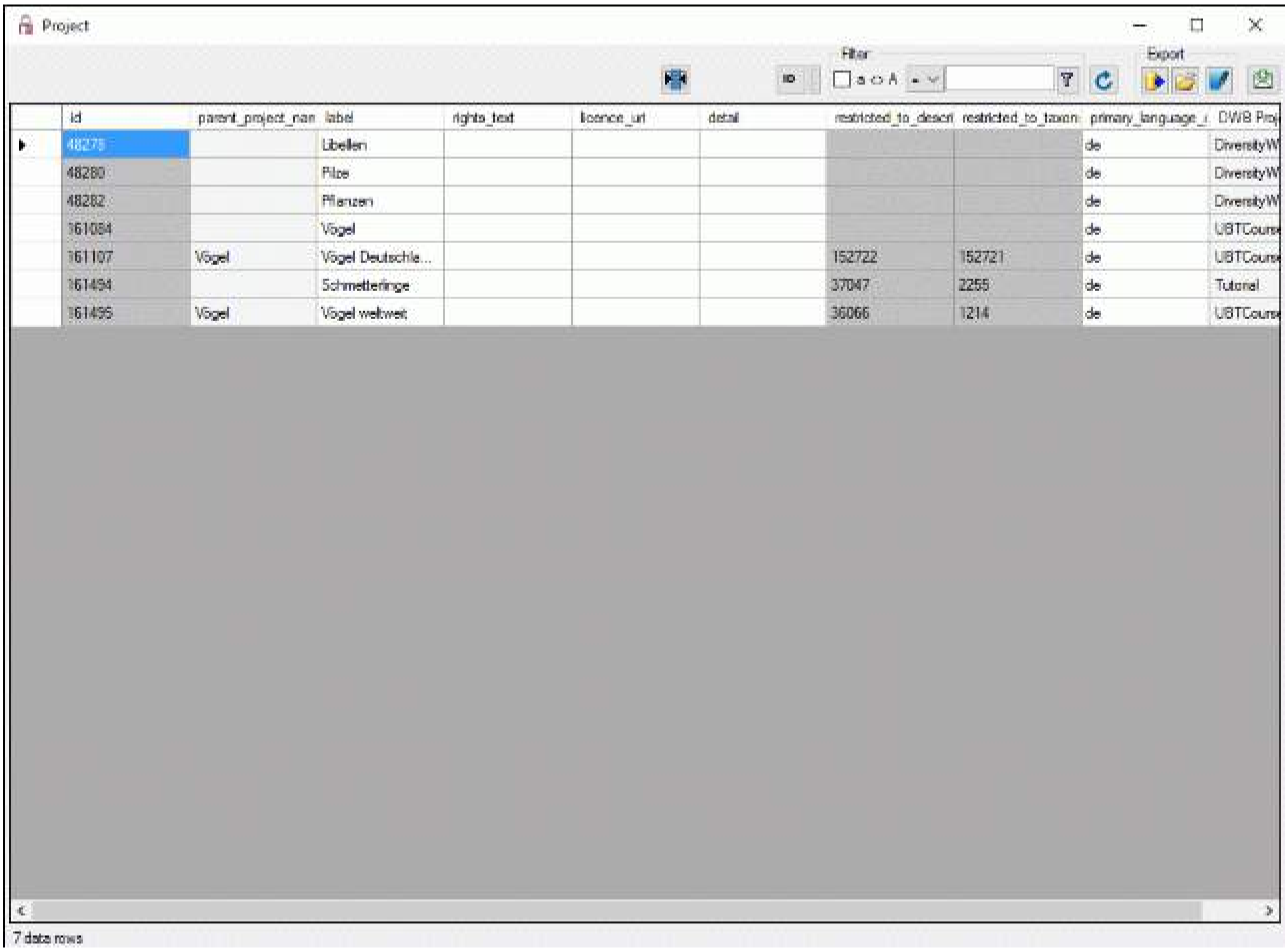
For the data selected in the main window the table editors offer a direct access to the tables of the database. Underneath the menu Grid select one of the Table editors. A window with the content of the table will open. Columns with a gray background can not be edited here. Columns with a light gray background are linked to the contents of lookup tables where you can change according to the contents of these tables. The following tables are included for direct access:

- Project
- SamplingEvent
- Description
- Descriptor
- CategoricalState
- Resource
- ResourceVariant
- Translation

Depending on the edit mode the following options are available in the Table editors menue:

- Edit descriptions
  - **Sampling events** to edit the sampling events of the descriptions in the query result list
  - **Descriptions** to edit the descriptions in the query result list
  - **Description resources** to edit the resource entries for the descriptions in the query result list
  - **Resource variants** to edit the resource variant entries for the descriptions in the query result list
  - **Translations** to edit the translation entries for the descriptions in the query result list
- Edit descriptors:
  - **Descriptors** to edit the descriptors in the query result list
  - **Descriptor resources** to edit the resource entries for the descriptors in the query result list
  - **Categorical states** to edit the categorical states of the descriptors in the query result list
  - **Categorical state resources** to edit the resource entries for the categorical states of the descriptors in the query result list
  - **Resource variants** to edit the resource variant entries for the descriptors and categorical states in the query result list
  - **Translations** to edit the translation entries for the descriptors and categorical states in the query result list
- Edit projects
  - **Project** to edit the projects in the query result list
  - **Descriptor tree node resources** to edit the resource entries for the descriptor tree nodes of the projects in the query result list
  - **Resource variants** to edit the resource variant entries for the descriptor tree nodes of the projects in the query result list
  - **Translations** to edit the translation entries for the projects in the query result list

As an example see below the table editor window for projects.



id	parent_project_nam	label	rights_text	licence_url	detail	restricted_to_descri	restricted_to_taxon	primary_language_	DWB Proj
48278		Libellen						de	DiversityW
48280		Pilze						de	DiversityW
48282		Pflanzen						de	DiversityW
161084		Vögel						de	UBTCours
161107	Vögel	Vögel Deutschla...				152722	152721	de	UBTCours
161494		Schmetterlinge				37047	2255	de	Tutorial
161495	Vögel	Vögel weltweit				36066	1214	de	UBTCours

7 data rows

Read-only

If for parts of the query result no write access exists, the table editor will be opened in read-only mode. Especially for descriptors you should keep in mind that they may belong to more than one project. Therefore the table editors for descriptors, categorical states and their resources or resource variants may be opened for read-only, if you have not write permissions for all projects in the database.

Editing

You can either edit the contents of the table directly or perform changes to any number of marked fields. To mark a whole column use the button. Once you have selected the contents to change, select one of the modes of change that appear in the upper left corner. The modes of change are:

- Insert: Insert the given value at the beginning of the content
- Append: Append the given value at the end of the content
- Replace: Replace a string in the content with the given value
- Clear: Remove the content

After selecting the change mode, enter the text in the field where necessary and click on the corresponding button to perform the changes.

If you want to delete a line in the database, select it by clicking in the space before the line and press the ✕button. Take care that an undo of that action is not possible.

Filtering

To filter the content of the table, click in the column that should be used for filtering. Then choose the mode of comparision:

- = : The content must be exactly like the given value
- ~ : The content must contain the given value
- ≠ : The content must be different to the given value

If you want the filtering to be case sensitive, choose the ☑a<>A option. After all parameters are set, click on the ▼button. To undo the filtering, click on the ↻button. This will reset the data to the last saved version. If you want your changes to be saved, click the 💾button before you reset the filtering. If you close the window all changes so far will be saved automatically. If you do not want to save your changes, click on the 🚪button to close the window without saving.

Export

To export the data as a tab separated text file, click on the 📤button. The file will be automatically saved in the client-folder.

Translations

For each project a default language is selected in the Edit project panel. In Diversity Descriptions for most database entries additionally translated expressions can be stored in the Translation table. Even for the default language adjusted for the project alternate expressions may be entered. In several export and document generation forms it is possible to select an alternate output language, if translations are available. Translatable entities are listed in the following table.

Database table	Database columns
CategoricalState	label, detail, abbreviation, wording
DataStatus_Enum	label, detail, abbreviation
Description	label, detail, wording
Descriptor	label, detail, abbreviation, wording_before, wording_after, wording
DescriptorTree	label
DescriptorTreeNode	label, detail, abbreviation
Frequency	label
Modifier	label
OtherScope	label, detail
Project	label, detail
Resource	label, detail
ResourceVariant_Enum	label, detail
SamplingEvent	label, detail
SexStatus_Enum	label, detail, abbreviation
StatisticalMeasure_Enum	label, abbreviation

All mentioned entities may be edited using the translations editor. If for an output a translation language is specified, a situation may occur that for a certain entity not translation is stored in the database. In those cases automatically the original database values will be used.

As you can see in the table above, no translations are supported for the descriptive data, i.e. summary or sampling data. Concerning categorical data, there is a tranlsation support, because the terminology parts (Descriptor and CategoricalState) my be translated. Quatitative data mainly include numeric values and their statistical measure, where the measure texts themselves can be translated. The same is valid for descriptor status data. Molecular sequence data naturally do not contain any translatable texts. Finally only the contents of text descriptor data and notes, that can be included in any summary or sampling data, are not supported for translation.

Data export

The export format **SDD** is XML based and offers multilingual support. By default the document language ist set to the project default language and the original database entries (labels, detail texts and so on) are included without explicit language tag. If translations are stored in the database, they are included in the SDD output with their specific language tag. As an option translations may be completely excluded from export or the SDD document language may even be switched to one of the available translation languages. Please be aware, that the enumerated values (DataStatus_Enum, StatisticalMeasures_Enum and SexStatus_Enum) are identified by specific tags within SDD. Therefore the translations for these are **not** included in the SDD file!

The export format **DELTA** is text based and does **not** support multilinguality. By default the original database entries are used in the DELTA output. If translations are stored in the database, you may select one of the available languages for the DELTA output.

In both cases the general rule applies that if for a certain term no translated value is present, the original value will be used. For details concerning the data export see here.

Data import

In the **SDD** import form the available languages are displayed. You have the options to omit translations during import or select a different language as the project's default language.

The **DELTA** import form offers the option to import translations for descriptors, categorical states and description items from separate DELTA files with identical structure. In a first step the complete data are imported form a main DELTA file. In subsequent steps the identifier for additional languages may be imported from additional language specific DELTA files.

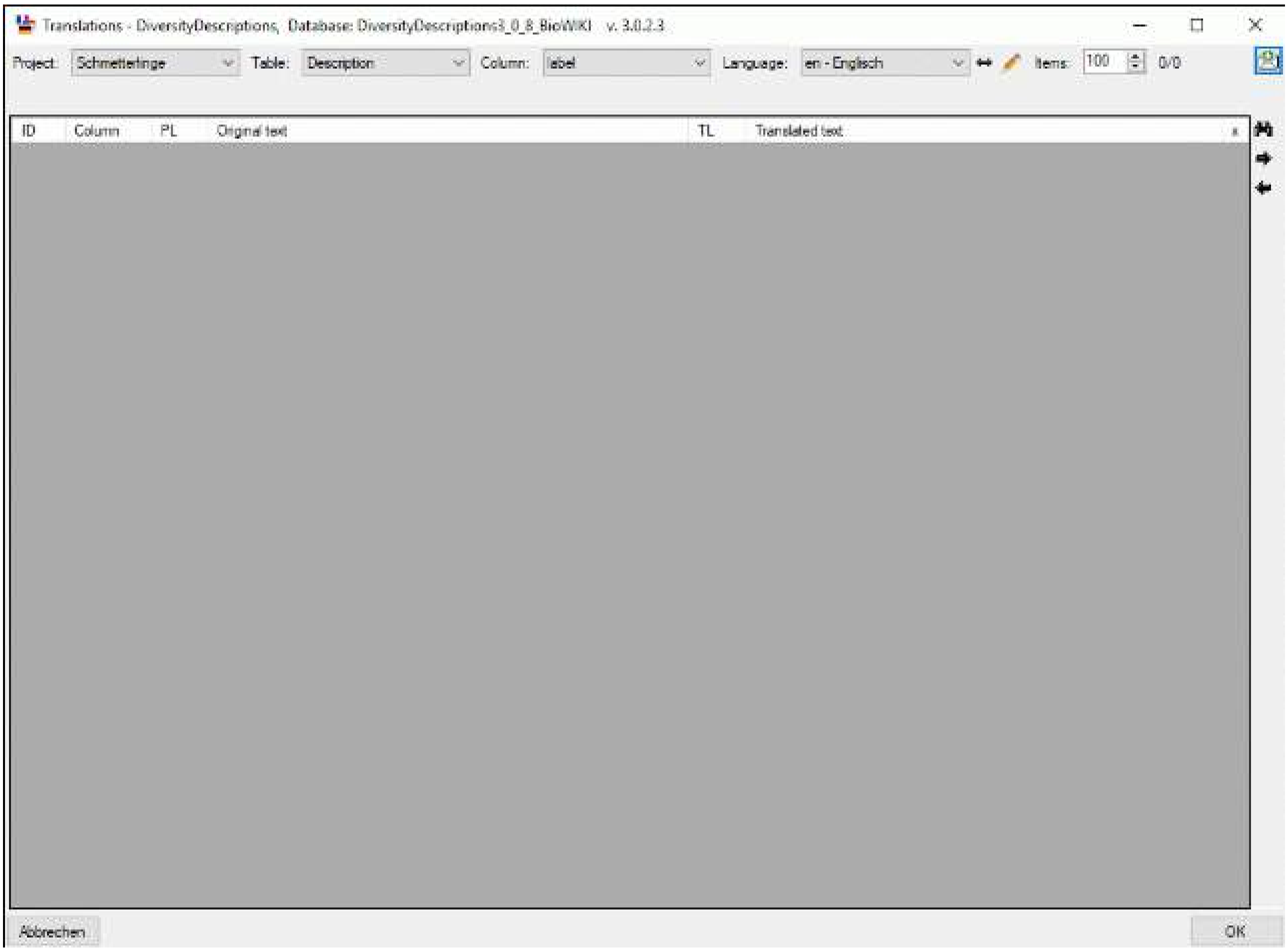
Document generators

The is a number of document generators to generate HTML or Media Wiki output. In this form an "Export language" field is shown if any translations are available in the database. In those cases you have the choice to adjust the default language or one of the offered tranlsations languages. Anyway, there may be some fixed expressions in the generated documents, where currently no mutilingual support is available.

Editing translations

After connecting a database select **Edit -> Translations ...** from the menu (see image below). You have to select the mandatory parameter **Project** and the **Table**. If you want to enter a new translation text, the **Column** and the target **Language** must be selected. If you omit one of those parameters, only existing tranlation texts from the database will be shown.

You man change the display and sorting of the entries in the **Language** combo box from "<code> - <description>" to "<description> - <code>" (and back) by clicking the button ⇔. If you need language codes that are not included in the list, click the ✏ button. For more details see [Edit language codes](#).

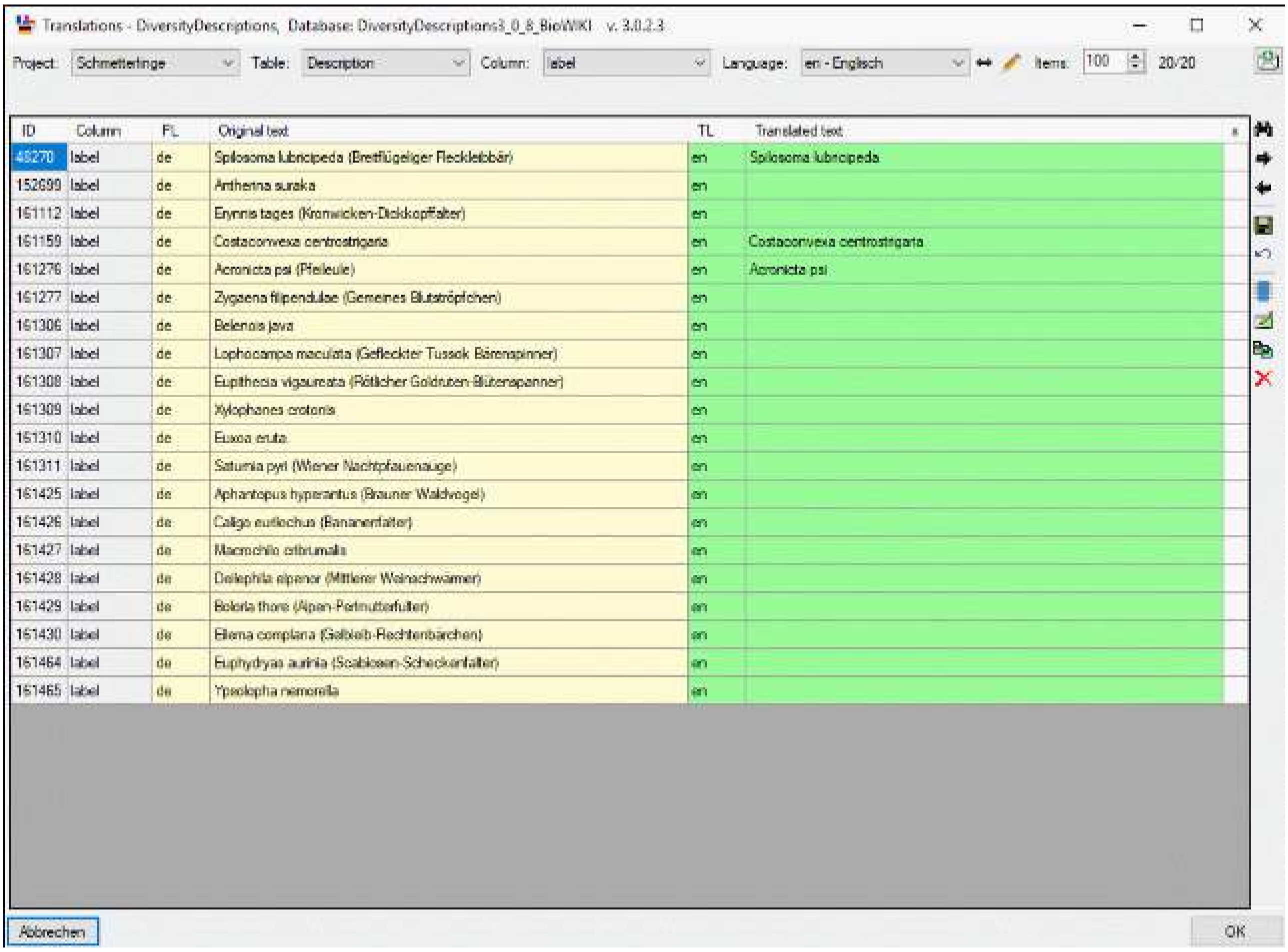


Translations - DiversityDescriptions, Database: DiversityDescriptions3_0_8_BioWIKI v. 3.0.2.3

Project: Schmetterlinge
Table: Description
Column: label
Language: en - Englisch
Items: 100
0/0

With the numeric control **Items** you may adjust how many database items shall be selected for display. After clicking the button the query results are displayed. By clicking the buttons ➡ and ⬅ you can load the next rsp. previous matches.

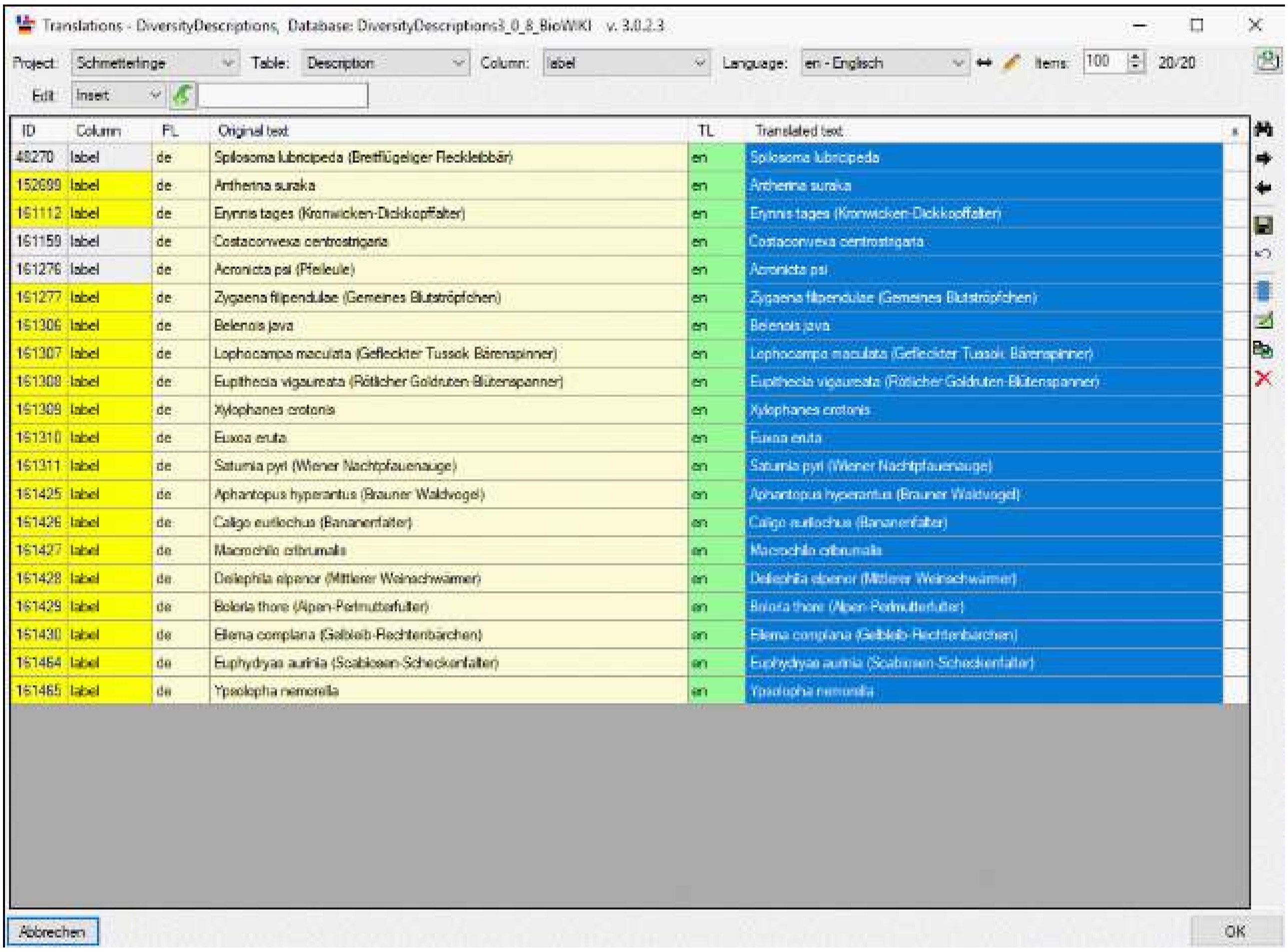
The table lists the internal ID of the data entry ("ID"), the table column ("Column"), the project language ("PL"), the "Original text", the translation language ("TL") and the "Translated text" (see image below). In table column "x" lines without write access will be marked as x. If you have write access, you may enter the tranlated text directly in the table.



Project: Schmetterlinge Table: Description Column: label Language: en - Englisch Items: 100 20/20

ID	Column	FL	Original text	TL	Translated text
40270	label	de	Spilosoma lubricipeda (Breitflügeliger Fleckleibbär)	en	Spilosoma lubricipeda
152699	label	de	Antherina suraka	en	
161112	label	de	Erynnis tages (Kronwicken-Dickkopffalter)	en	
161159	label	de	Costaconvexa centrostrigaria	en	Costaconvexa centrostrigaria
161276	label	de	Acronicta psi (Pfeileule)	en	Acronicta psi
161277	label	de	Zygaena filipendulae (Gemeines Blutströpfchen)	en	
161306	label	de	Belenois java	en	
161307	label	de	Lophocampa maculata (Gefleckter Tussok Bärenspinner)	en	
161308	label	de	Eupithecia virgaureata (Rötlicher Goldruten-Blütenspanner)	en	
161309	label	de	Xylophanes crotonis	en	
161310	label	de	Euxoa eruta	en	
161311	label	de	Saturnia pyri (Wiener Nachtpfauenauge)	en	
161425	label	de	Aphantopus hyperantus (Brauner Waldvogel)	en	
161426	label	de	Caligo eurilochus (Bananenfalter)	en	
161427	label	de	Macrochilo cribrumalis	en	
161428	label	de	Deilephila elpenor (Mittlerer Weinschwärmer)	en	
161429	label	de	Boloria thore (Alpen-Perlmutterfalter)	en	
161430	label	de	Eilema complana (Gelbleib-Flechtenbärchen)	en	
161464	label	de	Euphydryas aurinia (Scabiosen-Scheckenfalter)	en	
161465	label	de	Ypsolopha nemorella	en	

You may copy the original text of selected lines to the translated text by clicking the button 📋or delete the translated text with button ✕. To select all translated texts click on button ☰. In modified lines the background color of the first two columns will be change to yellow (see image below). With button 💾you can save the modified data, with button ↶you can reload the table, i.e. discard the changes.



Translations - DiversityDescriptions, Database: DiversityDescriptions3_0_8_BioWIKI v. 3.0.2.3

Project: Schmetterlinge Table: Description Column: label Language: en - Englisch Items: 100 20/20

Edit: Insert

ID	Column	FL	Original text	TL	Translated text
48270	label	de	Spilosoma lubricipeda (Breitflügeliger Fleckleibbär)	en	Spilosoma lubricipeda
152699	label	de	Antherina suraka	en	Antherina suraka
161112	label	de	Erynnis tages (Kronwicken-Dickkopffalter)	en	Erynnis tages (Kronwicken-Dickkopffalter)
161159	label	de	Costaconvexa centrostrigaria	en	Costaconvexa centrostrigaria
161276	label	de	Acronicta psi (Pfeileule)	en	Acronicta psi
161277	label	de	Zygaena filipendulae (Gemeines Blutströpfchen)	en	Zygaena filipendulae (Gemeines Blutströpfchen)
161306	label	de	Belenois java	en	Belenois java
161307	label	de	Lophocampa maculata (Gefleckter Tussok Bärenspinner)	en	Lophocampa maculata (Gefleckter Tussok Bärenspinner)
161308	label	de	Eupithecia vigaureata (Rötlicher Goldruten Blütenspanner)	en	Eupithecia vigaureata (Rötlicher Goldruten-Blütenspanner)
161309	label	de	Xylophanes crotonis	en	Xylophanes crotonis
161310	label	de	Euxoa eruta	en	Euxoa eruta
161311	label	de	Saturnia pyri (Wiener Nachtpfauenauge)	en	Saturnia pyri (Wiener Nachtpfauenauge)
161425	label	de	Aphantopus hyperantus (Brauner Waldvogel)	en	Aphantopus hyperantus (Brauner Waldvogel)
161426	label	de	Caligo eurilochus (Bananenfalter)	en	Caligo eurilochus (Bananenfalter)
161427	label	de	Macrochilo cribrumalis	en	Macrochilo cribrumalis
161428	label	de	Deilephila elpenor (Mittlerer Weinschwärmer)	en	Deilephila elpenor (Mittlerer Weinschwärmer)
161429	label	de	Boloria thore (Alpen-Perlmutterfalter)	en	Boloria thore (Alpen-Perlmutterfalter)
161430	label	de	Eilema complana (Gelbleib-Flechtenbärchen)	en	Eilema complana (Gelbleib-Flechtenbärchen)
161464	label	de	Euphydryas aurinia (Scabiosen-Scheckenfalter)	en	Euphydryas aurinia (Scabiosen-Scheckenfalter)
161465	label	de	Ypsolopha nemorella	en	Ypsolopha nemorella

If you selected any **Translated text** entries, it is possible to modify several values simultaneously. Therefore select the table entries that shall be edited - by clicking the button ▤ you may select the whole table column. Then select the required operation in the **Edit** section: "Insert", "Append" or "Replace" and enter the new rsp. new and old value. After clicking the action button - depending on the selected operation this is ↶ (Insert), ↷ (Append) or ⟳ (Replace).

By double-clicking the table line or clicking the ✎ button you can open a separate edit window (see image below). This form works almost in the same way as the Extended text editor.

Description label, ID: 48270
Spilosoma lubricipeda (Breitflügeliger Fleckleibbär)

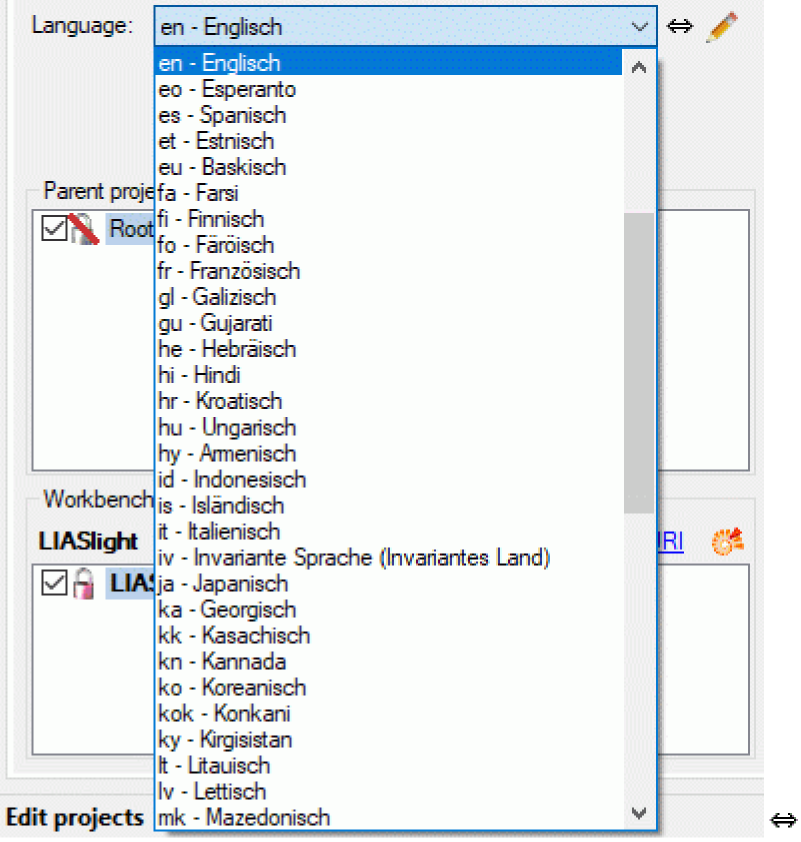
Spilosoma lubricipeda (Breitflügeliger Fleckleibbär)

Spilosoma lubricipeda

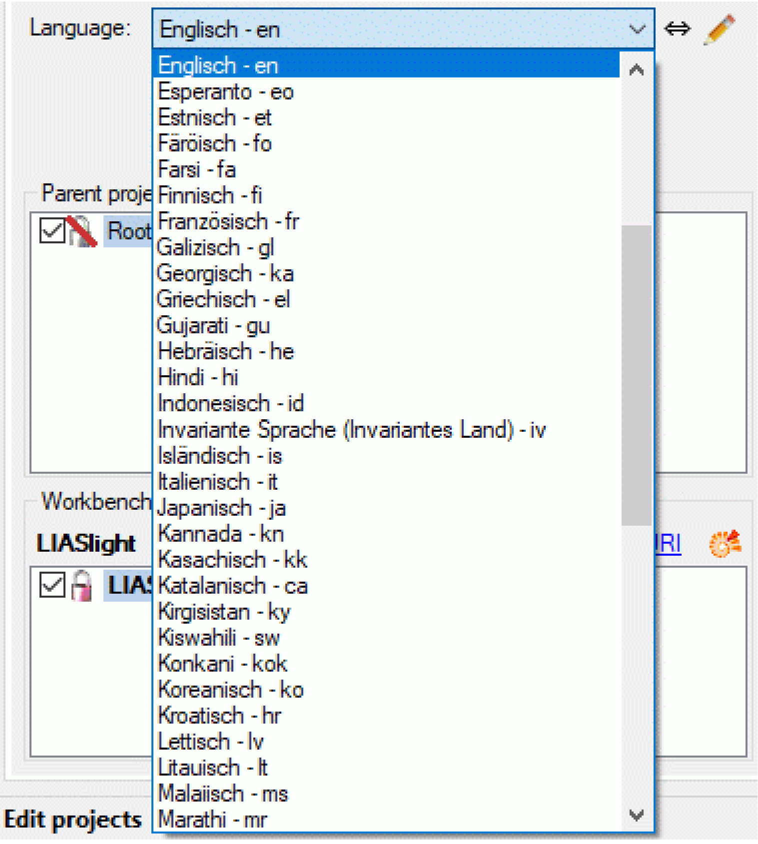
Edit language codes

In the Diversity Descriptions database language codes are used for two purposes: The first one is to indicate the project's default language. Furthermore for the most important parts of the data translations may be entered, which carry a laguage code, too.

By all means the language codes consists of an at most three-letter string. In the application you may select the language code from a drop-down box, which shows the language code - in most cases a two-letter ISO 639-1 code - and the corresponding long name. By clicking the ⇔ button you may change the display sequence (see images below).



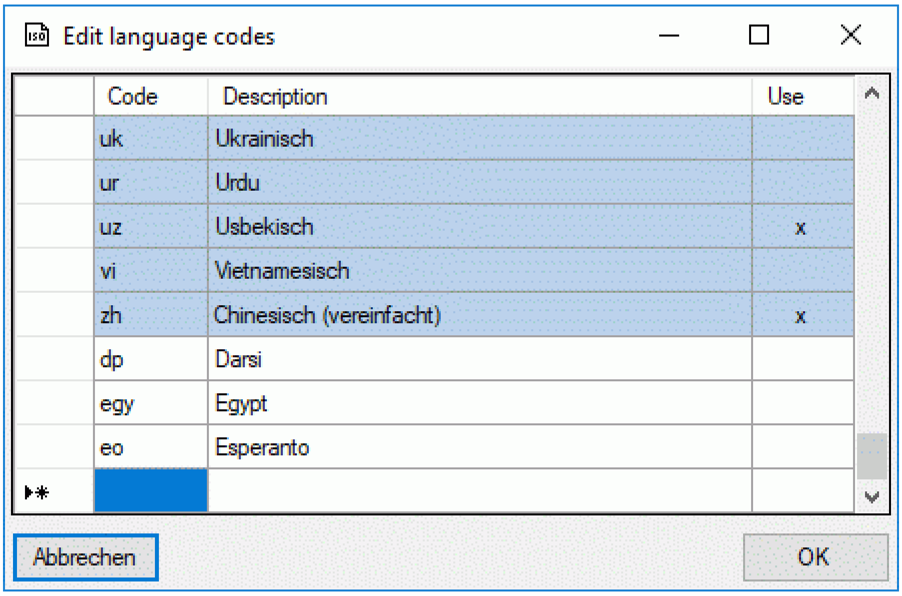
Language: en - Englisch



Language: Englisch - en

Most of the values are provided by the operating system. Anyway there might be the need to include additional values, e.g. "eo" for Esperanto. For those cases as a second source additional language codes may be stored in the application's settings. Finally, language codes that are present in the database but neither included in the operating system's list nor the application settings will be included at the end of the selection list with red background, if neccessary.

To edit the language codes, click the ✏ button and a new window will open (see image below). The operating system's entries are shown with a light blue background and cannot be modified. The language codes that are stored in the application settings are shown with white background and may be edited. To enter a new value, use the empty line at the end of the table. To delete an entry, mark the whole line by clicking on the row header and press the **delete** key on the keyboard.



Edit language codes

Code	Description	Use
uk	Ukrainisch	
ur	Urdu	
uz	Usbekisch	x
vi	Vietnamesisch	
zh	Chinesisch (vereinfacht)	x
dp	Darsi	
egy	Egypt	
eo	Esperanto	

By clicking **OK** the changes will be stored in the settings.

Summarize data

Currently the following functions for summarizing data are available:

Summarize descriptions : Summarize the data of selected descriptions and create a new one or update an existing description.

Summarize sample data : Summarize the sample data of selected descriptions and update their summary data.

Summarizing methods

Depending on the selected summarizing function either the descriptor data of selected descriptions or the sampling data of the selected descriptions build the data source. Summarization of the data is done according their data type.

Categorical summary data

For building of categorical summary data the single categorical states of the data sources are accumulated. In general for each states test notes can be entered. To summarize the text notes, the different notes are accumulated (append in a new line), if they are not yet included in the summary note.

If modifier have to be processed, each combination of a categerical state and a modifier will be treated as separate values. Summarization of notes text will be done separately for each of these tuples. Only modifiers that are assigned to a descriptor as recommended modifier (see Editing the descriptor - Descriptor tree tab) are evaluated, otherwise the modifier values are ignored.

Categorical descriptors may be marked as "exclusive", which means that only on state may be selected. If the approptiate option is set for the summarization, the categorical states that is most often selected in the source data will be used in the target.

Quantitative summary data

For building of quantitative summary data from the numeric values of the data sources all recommended statistical measures (see Editing the descriptor - Descriptor tree tab) for the processed descriptor are calculated. Text notes are accumulated for each statistical measure the same way as described for categorical summary data.

If modifier have to be processed, all the modifier are accumulated for eache statistical measure. Since in the resulting quantitative summary data only one modifier value is allowed for each statistical measure, the most often used modfier is inserted.

Text descriptor data

To summarize the text descriptor data, the different texts are accumulated (append in a new line), if they are note yet included in the summary text. Text notes are accumulated in the same way.

Molecular sequence data

To summarize the moecular sequence data, the different sequences are accumulated (append in a new line), if they are note yet included in the target sequence. Text notes are accumulated in the same way.

Statistical measures

Name	**Abbr.**	**Calculation**
Lower range limit (human estimate)	-	$x_1..x_n$ sorted list: x_1
Upper range limit (human estimate)	+	$x_1..x_n$ sorted list: x_n
Central or typical value (human estimate)	centr.	$x_1..x_n$ sorted list: $x_{n/2}$
Lower range limit (legacy data stat. meth. unknown)	-(?)	$x_1..x_n$ sorted list: x_1
Upper range limit (legacy data stat. meth. unknown)	+(?)	$x_1..x_n$ sorted list: x_n
Central or typical value (legacy data stat. meth. unknown)	centr.(?)	$x_1..x_n$ sorted list: $x_{n/2}$
Minimum value	Min	Absolute smallest value
Maximum value	Max	Absolute largest value
Mean (= average)	μ	$\mu=(^1/_n)\Sigma_{(n)}x_i$
Harmonic mean	hμ	$h\mu=n/(\Sigma_{(n)}(1/x_i))$ $h\mu=0$ if any $x_i=0$
Geometric mean	gμ	$g\mu={}^n\surd\Pi_{(n)}x_i$
Mode	mode	Value that appears most often (ambigious!)
Median	med.	$x_1..x_n$ sorted list n odd: $med=x_{(n+1)/2}$ n even: $med=(x_{n/2}+x_{(n/2+1)})/2$
Interquartile mean (= average)	IQM	$x_1..x_n$ sorted list $IQM=\mu(x_{0.25n+1}..x_{0.75n+1})$
Variance (sample df = n-1)	Var.	$S_{n-1}=(^1/_{n-1})\Sigma_{(n)}(x_i-\mu)^2$
Variance (population; df = n; rarely applicable!)	Var. (pop.)	$S_n=(^1/_n)\Sigma_{(n)}(x_i-\mu)^2$
Standard deviation (sample)	s.d.	$\sigma_{n-1}=\surd S_{n-1}$
Standard deviation (population; df = n; rarely applicable!)	s.d. (pop.)	$\sigma_n=\surd S_n$
Mean deviation	m.d.	$md=(^1/_n)\Sigma_{(n)}\lvert x_i-\mu\rvert$
Mean deviation from median	m.d.m.	$mdm=(^1/_n)\Sigma_{(n)}\lvert x_i-med\rvert$
Coefficient of variation (sample)	CV	$CV=\sigma_n/\mu$
Corrected coefficient of variation (sample)	CVC	$CVC=\sigma_{n-1}/\mu$

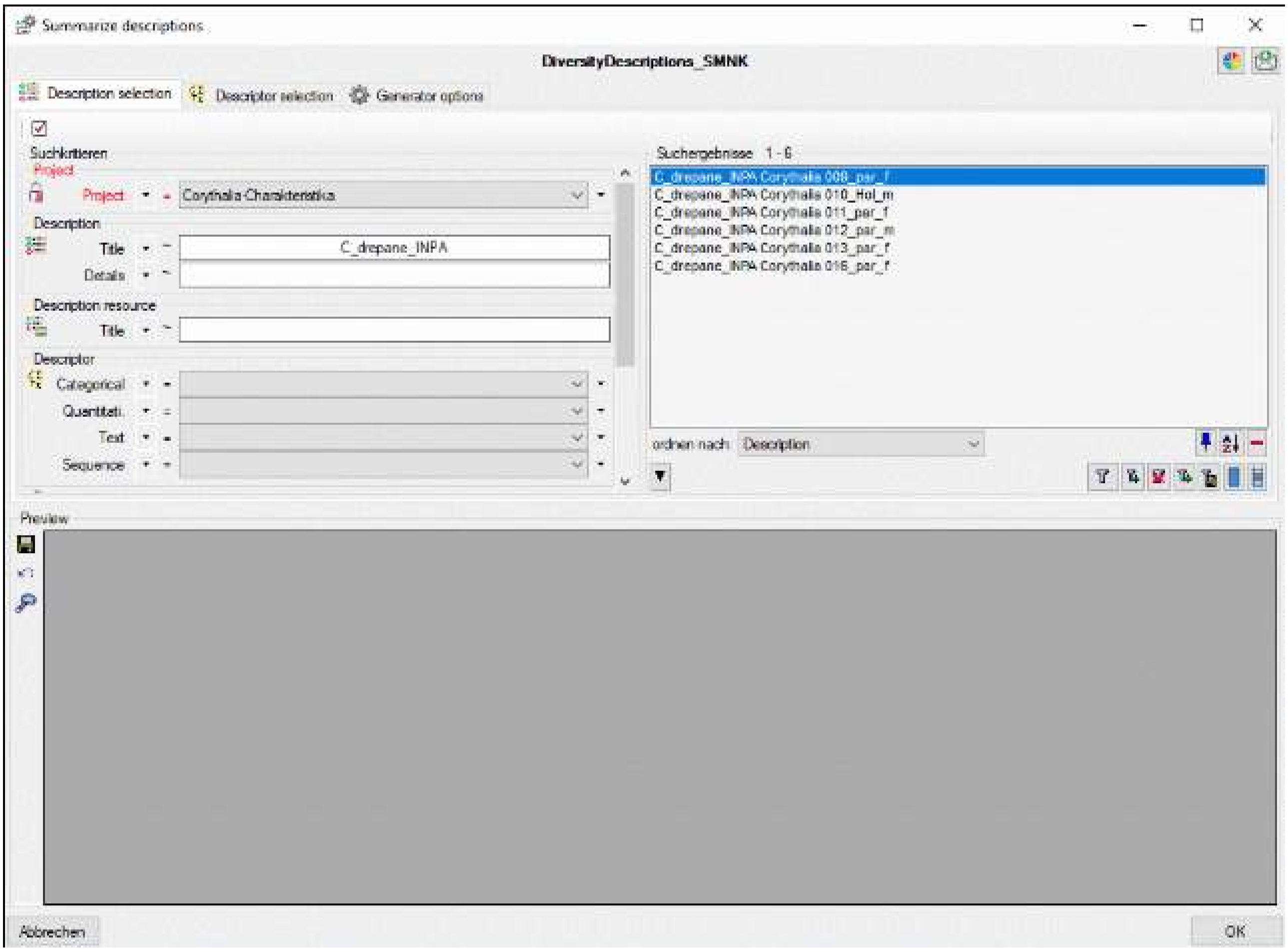
Total range	TR	$x_1..x_n$ sorted list TR=x_n-x_1
Interquartile range	IQR	$x_1..x_n$ sorted list IQR=$x_{0.75n+1}-x_{0.25n+1}$
Standard error of mean	s.e.	$\sigma_x=\sigma_{n-1}/\sqrt{n}$
Standard error of variance (of multiple samples)	s.e.(var.)	$S_x=S_{n-1}/n$
Skewness	Skw.	$\Upsilon_1=(^1/_n)\Sigma_{(n)}((x_i-\mu)/\sigma)^3$
Kurtosis	Kurt.	$\mathrm{Kurt}=(^1/_n)\Sigma_{(n)}((x_i-\mu)/\sigma)^4$
Sample size	n	Number of values

Summarize description data

With this form you can summarize the information of selected descriptions and store the summarized data in a new description or update an existing one. After connecting a database select **Edit -> Summarize descriptions ...** from the menu.

Description selection

In the first tab **Description selection** you search for the **source** descriptions that shall be summarized into a new or an existing **target** description (see image below).



Project = Corythalia Charakteristika

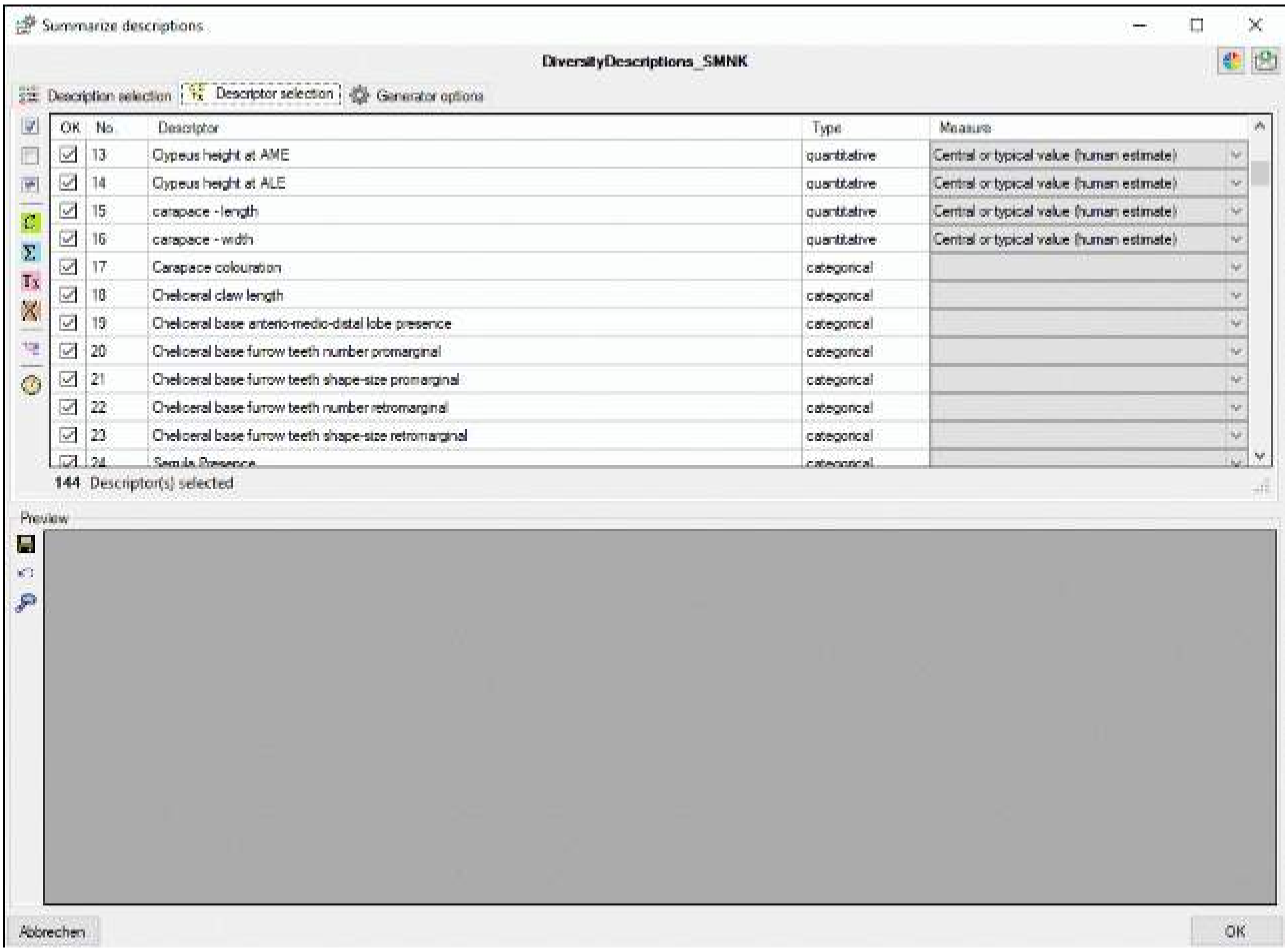
Title ~ C_drepane_INPA

C_drepane_INPA Corythalia 008_par_f
C_drepane_INPA Corythalia 010_Hol_m
C_drepane_INPA Corythalia 011_par_f
C_drepane_INPA Corythalia 012_par_m
C_drepane_INPA Corythalia 013_par_f
C_drepane_INPA Corythalia 016_par_f

You have to select at least the mandatory parameter **Project** and start a query with button . From the result list superfluous entries may be removed with the − button. For a detailled description of the query control please refer to section Query.

Descriptor selection

In tab **Descriptor selection** select the descriptors that shall be summarized in table column **OK** (see image below). You can select rsp. deselect all descriptors with buttons ☑ and ☐. Button inverts all selections. To select all categorical, quantitative, text or sequence descriptors the buttons C, Σ, Tx and are avaiable. With button you may select a descriptor tree rsp. descriptor tree node to select all descriptors assigned to the selected element.



OK	No.	Descriptor	Type	Measure
☑	13	Clypeus height at AME	quantitative	Central or typical value (human estimate)
☑	14	Clypeus height at ALE	quantitative	Central or typical value (human estimate)
☑	15	carapace - length	quantitative	Central or typical value (human estimate)
☑	16	carapace - width	quantitative	Central or typical value (human estimate)
☑	17	Carapace colouration	categorical	
☑	18	Cheliceral claw length	categorical	
☑	19	Cheliceral base anterio-medio-distal lobe presence	categorical	
☑	20	Cheliceral base furrow teeth number promarginal	categorical	
☑	21	Cheliceral base furrow teeth shape-size promarginal	categorical	
☑	22	Cheliceral base furrow teeth number retromarginal	categorical	
☑	23	Cheliceral base furrow teeth shape-size retromarginal	categorical	
☑	24	Serrula Presence	categorical	

144 Descriptor(s) selected

For quantitative descriptors a statistical measure must be specified where the values for summarization are available. When the descriptor table is filled, for each quantitative descriptor the available recommended measures are checked if one of the measures "Mean (= average)", "Central or typical value (human estimate)", "Central or typical value (legacy data stat. meth. unknown)", "Mode" or "Sample size" is available (priority in this sequence), it is pre-selected in colum **Measure**. You may modify this adjustment for each single descriptor or use button ⏲to change the setting for all selected descriptors.

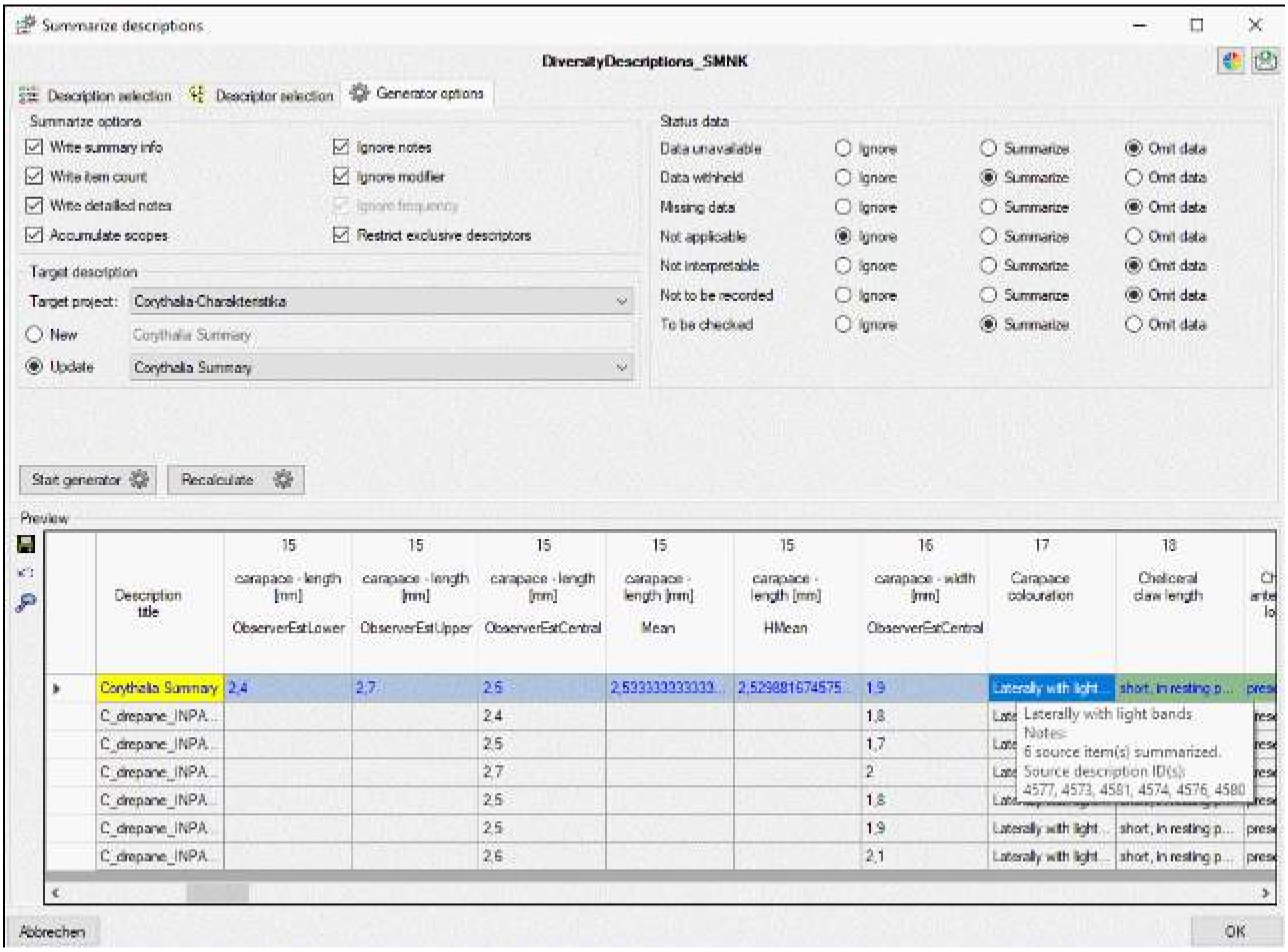
Generator options

In section **Summarize options** you may specify to **Ignore notes** and to **Ignore modfier** values of the source descriptions. If you select **Restrict exclusive descriptors**, the most often selected categorical state of a "exclusive" descriptor will be set instead of accumulating all source values. **Accumulate scopes** will collect all scope values of the source descriptions in the target. **Write item count** will enter notes containing information about the number of collected items in the summary data. If you additionally select **Write detailled notes**, the source description IDs will be listed in the notes. Finally, **Write summary infomation** inserts a summary about summarized descriptions into the target description details (see image below).

In section **Target description** you may select the **Target project** (usually the same as the source description's). You may either create a **New** description and enter the description name or **Update** a description selected form a drop-down list.

In section **Status data** you may control the summarization behaviour for every descriptor data status value:

- **Ignore**
  If in a summarized description the corresponding data status is present for a descriptor value, it will be summarized but the descriptor data status will not be set in the target description.
- **Summarize**
  As for Ignore the descriptor values will be summarized. Additionally the descriptor data status will be set in the target description.
- **Omit data**
  If in a summarized description the corresponding data status is present for a descriptor value, it will not be summarized and the descriptor data status will not be set in the target description.



Summarize options
☑ Write summary info
☑ Write item count
☑ Write detailed notes
☑ Accumulate scopes
☑ Ignore notes
☑ Ignore modifier
☑ Ignore frequency
☑ Restrict exclusive descriptors

Target description
Target project: Corythalia-Charakteristika
○ New Corythalia Summary
● Update Corythalia Summary

Status data
Data unavailable ○ Ignore ○ Summarize ● Omit data
Data withheld ○ Ignore ● Summarize ○ Omit data
Missing data ○ Ignore ○ Summarize ● Omit data
Not applicable ● Ignore ○ Summarize ○ Omit data
Not interpretable ○ Ignore ○ Summarize ● Omit data
Not to be recorded ○ Ignore ○ Summarize ● Omit data
To be checked ○ Ignore ● Summarize ○ Omit data

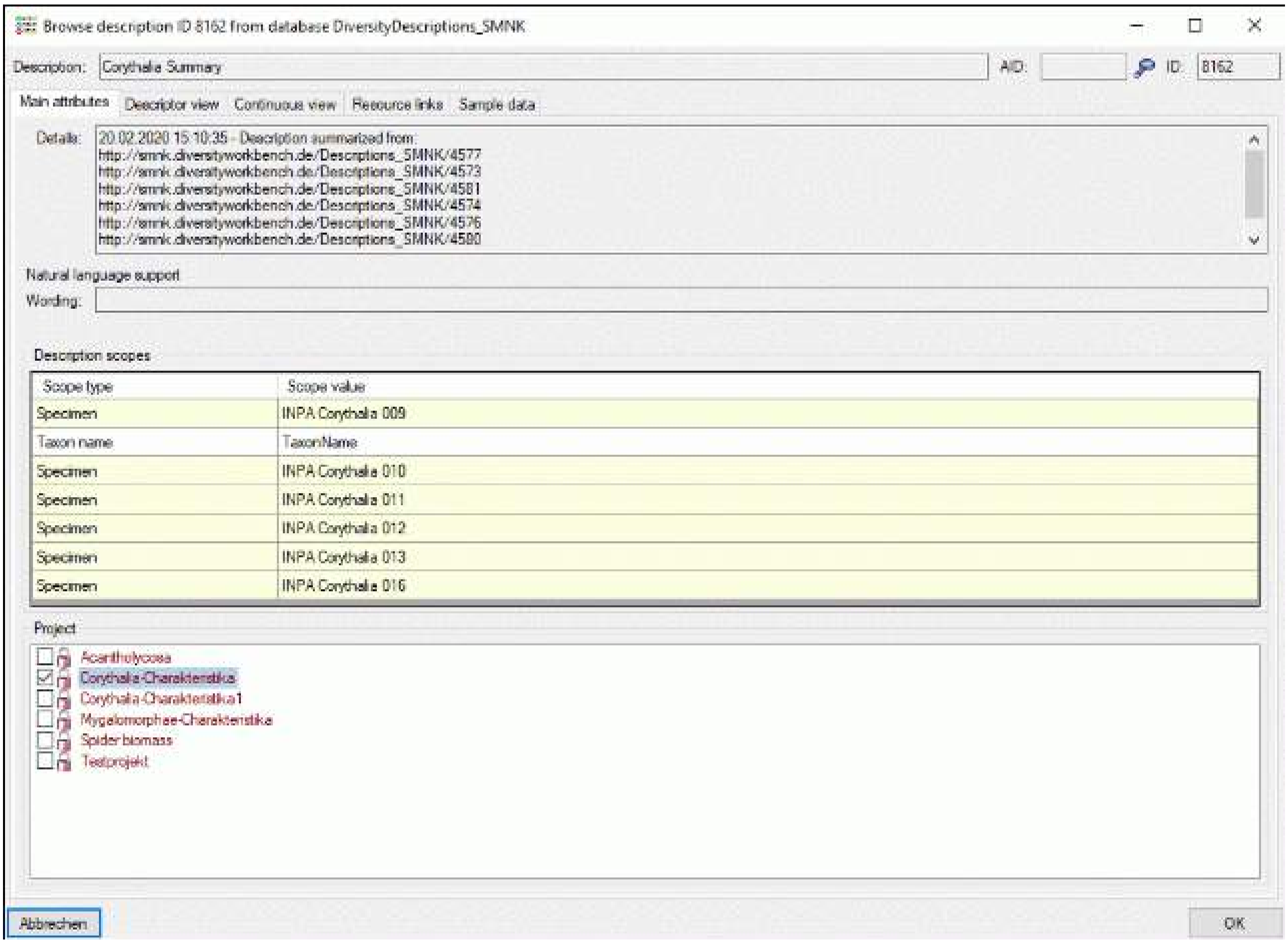
Description title	15 carapace - length [mm] ObserverEstLower	15 carapace - length [mm] ObserverEstUpper	15 carapace - length [mm] ObserverEstCentral	15 carapace - length [mm] Mean	15 carapace - length [mm] HMean	16 carapace - width [mm] ObserverEstCentral	17 Carapace colouration	18 Cheliceral claw length	Ch ante lo
Corythalia Summary	2,4	2,7	2,6	2,533333333333...	2,529881674575	1,9	Laterally with light...	short, in resting p...	pres
C_drepane_INPA...			2,4			1,8	Late		rese
C_drepane_INPA...			2,5			1,7	Late		rese
C_drepane_INPA...			2,7			2	Late		rese
C_drepane_INPA...			2,5			1,8	Late		rese
C_drepane_INPA...			2,5			1,9	Laterally with light...	short, in resting p...	pres
C_drepane_INPA...			2,6			2,1	Laterally with light...	short, in resting p...	pres

Laterally with light bands
Notes:
6 source item(s) summarized.
Source description ID(s):
4577, 4573, 4581, 4574, 4576, 4580

After checking the settings click in button **Start generator** ⚙. During processing the icon of the button changes to STOP and you may abort by clicking the button. In the **Preview** area a table with the generated rsp. updated target description (coloured background, may be change with button) and the summarized source descriptions (grey background) is shown. If the target description has been modified, this is indicated ba a yellow background of the description title (see image above). Updated values are shown as blue text. By double-clicking on a field in the preview table you may view the contents in a separate browser window. To save the updated values and close the window click the **OK** button. To exit without saving click **Abort**. In this case you will be asked if you want to save modified data.

Since building the preview table may take some time, especially if a lot of descriptors have been selected, you may use the button **Recalculate** ⚙for restarting the summary process. In this case the descriptor columns will not be re-built, only the summary data will be calculated and actualized. This feature may be useful, if you change some settings an want to update the data. If you use the **Recalculate** ⚙button with an empty preview table, only the description titles will be displayed. Anyway you can view the summarized data using the button (see below).

You may store all changed entries by clicking the button or omit all changes and reload the data by clicking the button. To view the description details of the currently selected entry click the button and a separate browser window opens (see image below).



Description: Corythalia Summary

AID:

ID: 8162

Details:
20.02.2020 15:10:35 - Description summarized from:
http://smnk.diversityworkbench.de/Descriptions_SMNK/4577
http://smnk.diversityworkbench.de/Descriptions_SMNK/4573
http://smnk.diversityworkbench.de/Descriptions_SMNK/4581
http://smnk.diversityworkbench.de/Descriptions_SMNK/4574
http://smnk.diversityworkbench.de/Descriptions_SMNK/4576
http://smnk.diversityworkbench.de/Descriptions_SMNK/4580

Natural language support

Wording:

Description scopes

Scope type	Scope value
Specimen	INPA Corythalia 009
Taxon name	TaxonName
Specimen	INPA Corythalia 010
Specimen	INPA Corythalia 011
Specimen	INPA Corythalia 012
Specimen	INPA Corythalia 013
Specimen	INPA Corythalia 016

Project

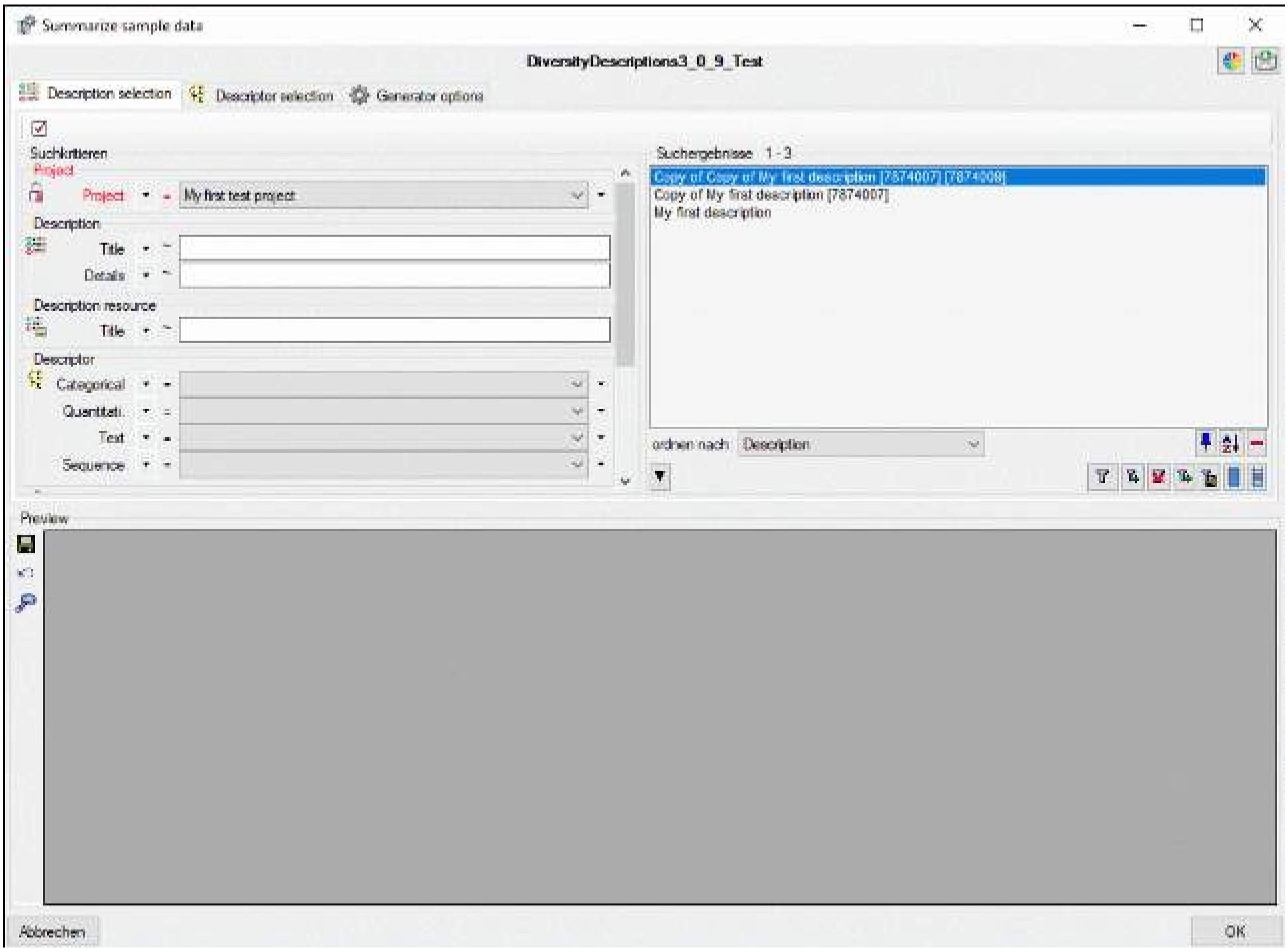
☐ Acantholycosa
☑ Corythalia-Charakteristika
☐ Corythalia-Charakteristika1
☐ Mygalomorphae-Charakteristika
☐ Spider biomass
☐ Testprojekt

Summarize sample data

With this form you can summarize the information of selected descriptions and store the summarized data in a new description or update an existing one. After connecting a database select **Edit -> Summarize sample data ...** from the menu.

Description selection

In the first tab **Description selection** you search for the desriptions that shall be **updated** by their summarized sample data (see image below).



Project: My first test project

Suchergebnisse 1 - 3

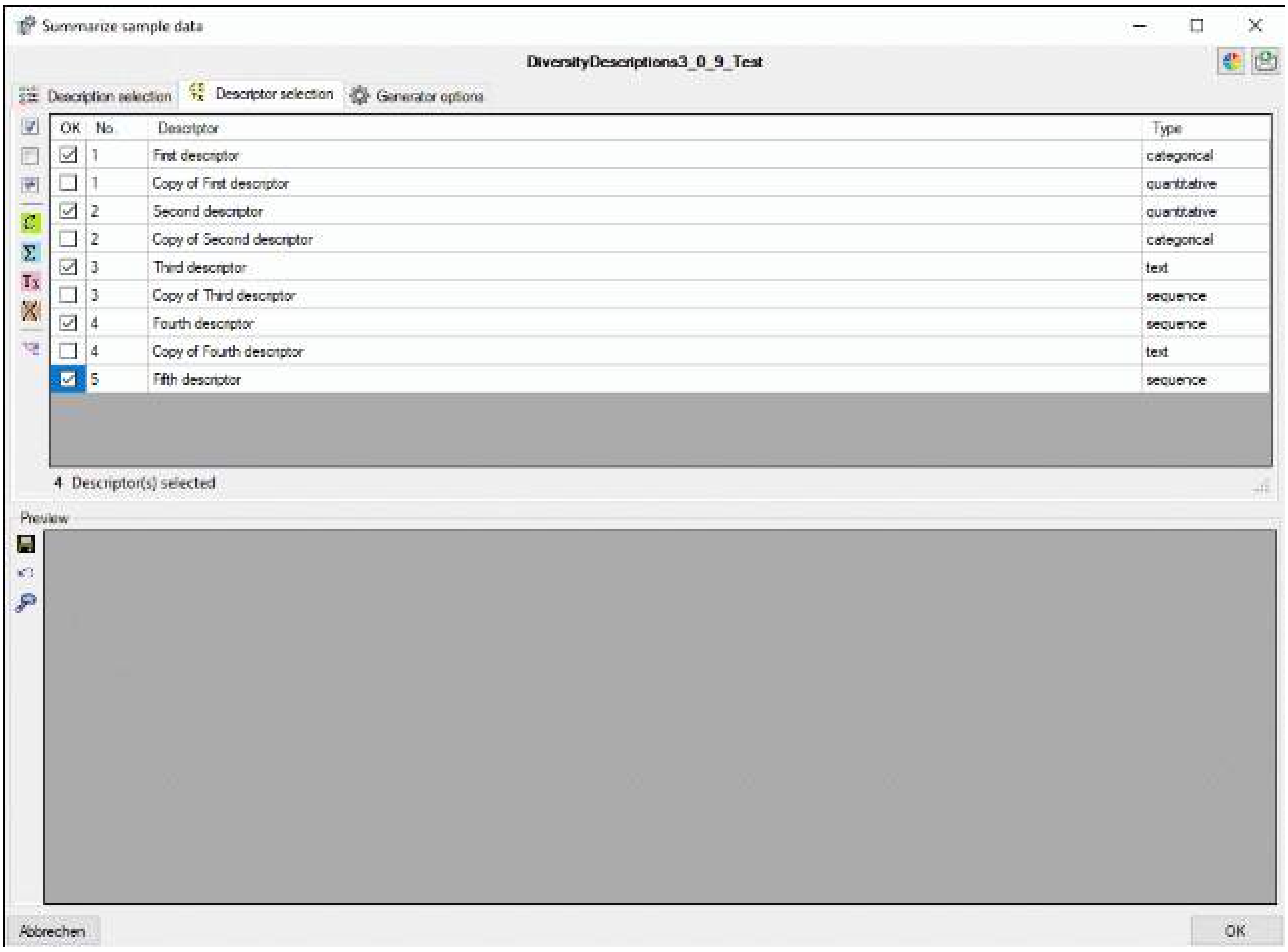
Copy of Copy of My first description [7874007] [7874008]
Copy of My first description [7874007]
My first description

ordnen nach: Description

You have to select at least the mandatory parameter **Project** and start a query with button . From the result list superfluous entries may be removed with the button. For a detailled description of the query control please refer to section Query.

Descriptor selection

In tab **Descriptor selection** select the descriptors that shall be summarized in table column **OK** (see image below). You can select rsp. deselect all descriptors with buttons ☑ and ☐. Button inverts all selections. To select all categorical, quantitative, text or sequence descriptors the buttons , , and are avaiable. With button you may select a descriptor tree rsp. descriptor tree node to select all descriptors assigned to the selected element.



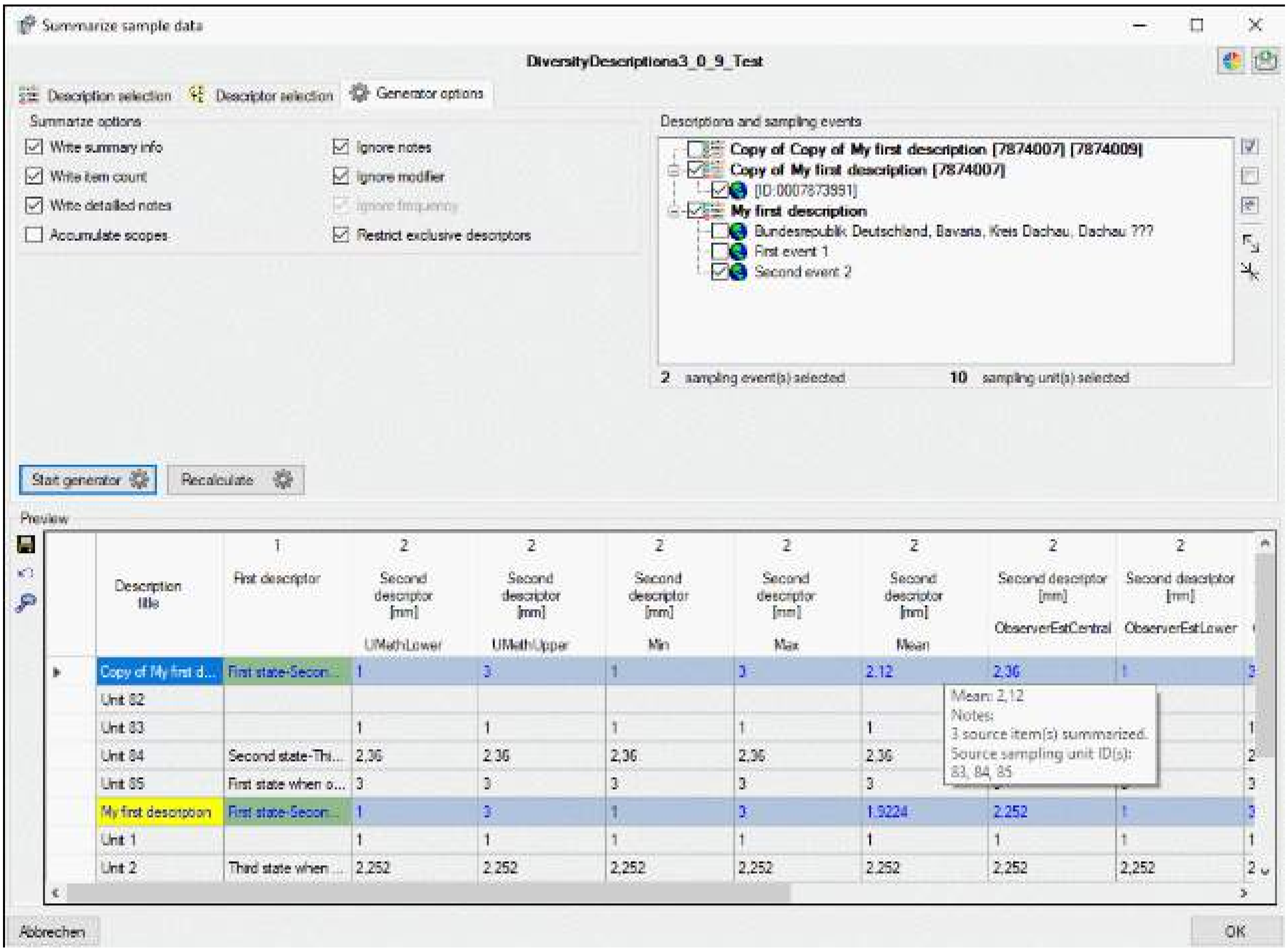
OK	No.	Descriptor	Type
☑	1	First descriptor	categorical
☐	1	Copy of First descriptor	quantitative
☑	2	Second descriptor	quantitative
☐	2	Copy of Second descriptor	categorical
☑	3	Third descriptor	text
☐	3	Copy of Third descriptor	sequence
☑	4	Fourth descriptor	sequence
☐	4	Copy of Fourth descriptor	text
☑	5	Fifth descriptor	sequence

4 Descriptor(s) selected

Generator options

In section **Summarize options** you may specify to **Ignore notes** and to **Ignore modfier** values of the description's sample data. If you select **Restrict exclusive descriptors**, the most often selected categorical state of a "exclusive" descriptor will be set instead of accumulating all source values. **Accumulate scopes** will collect all scope values of the sampling events (geographic areas) and sampling units (specimen) in the description summary. **Write item count** will enter notes containing information about the number of collected items in the summary data. If you additionally select **Write detailled notes**, the source description IDs will be listed in the notes. Finally, **Write summary infomation** inserts a summary about summarized sampling events into the target description details (see image below).

In section **Descriptions and sampling events** you find the descriptions from the query result list in tab **Description selection** and their sampling events. You may exclude single sampling events or even the whole description form the summarization. In the latter case the description data will not be changed.



Summarize options

☑ Write summary info
☑ Write item count
☑ Write detailed notes
☐ Accumulate scopes
☑ Ignore notes
☑ Ignore modifier
☑ Ignore frequency
☑ Restrict exclusive descriptors

Descriptions and sampling events

- ☐ Copy of Copy of My first description [7874007] [7874009]
- ☑ Copy of My first description [7874007]
  - ☑ [ID:0007873991]
- ☑ My first description
  - ☐ Bundesrepublik Deutschland, Bavaria, Kreis Dachau, Dachau ???
  - ☐ First event 1
  - ☑ Second event 2

2 sampling event(s) selected 10 sampling unit(s) selected

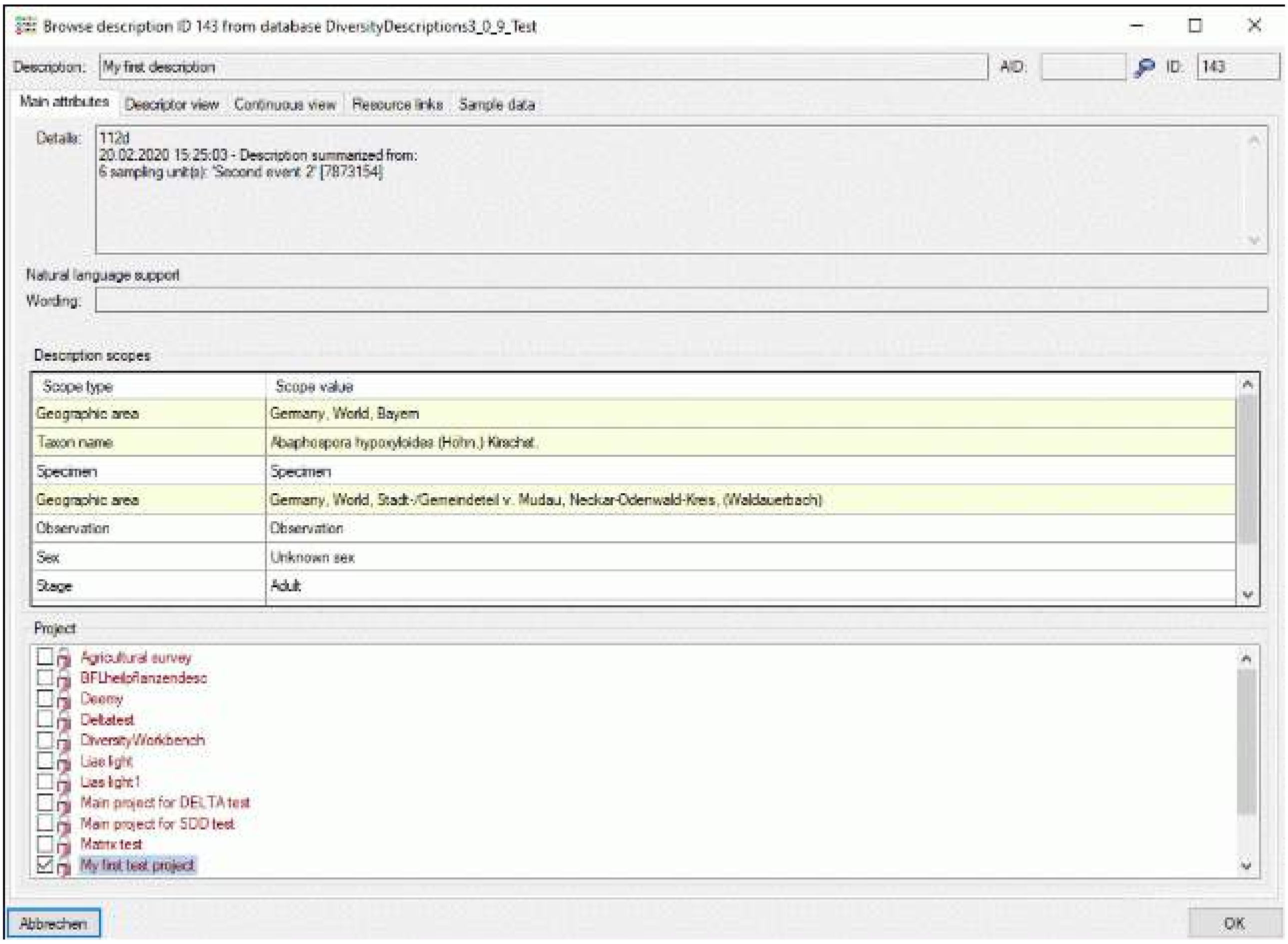
Description title	1 First descriptor	2 Second descriptor [mm] UMethLower	2 Second descriptor [mm] UMethUpper	2 Second descriptor [mm] Min	2 Second descriptor [mm] Max	2 Second descriptor [mm] Mean	2 Second descriptor [mm] ObserverEstCentral	2 Second descriptor [mm] ObserverEstLower	
Copy of My first d...	First state-Secon...	1	3	1	3	2.12	2.36	1	3
Unit 82							[illegible]	[illegible]	
Unit 83		1	1	1	1	1	[illegible]	[illegible]	1
Unit 84	Second state-Thi...	2,36	2.36	2,36	2,36	2,36	[illegible]	[illegible]	2
Unit 85	First state when o...	3	3	3	3	3	[illegible]	[illegible]	3
My first description	First state-Secon...	1	3	1	3	1.9224	2.252	1	3
Unit 1		1	1	1	1	1	1	1	1
Unit 2	Third state when ...	2,252	2.252	2,252	2,252	2,252	2,252	2,252	2

Mean: 2,12
Notes:
3 source item(s) summarized.
Source sampling unit ID(s):
83, 84, 85

After checking the settings click in button **Start generator** . During processing the icon of the button changes to STOP and you may abort by clicking the button. In the **Preview** area a table with the updated target descriptions (coloured background, may be change with button) and the summarized sampling units (grey background) is shown. If the target description has been modified, this is indicated ba a yellow background of the description title (see image above). Updated values are shown as blue text. By double-clicking on a field in the preview table you may view the contents in a separate browser window. To save the updated values and close the window click the **OK** button. To exit without saving click **Abort**. In this case you will be asked if you want to save modified data.

Since building the preview table may take some time, especially if a lot of descriptors have been selected, you may use the button **Recalculate** for restarting the summary process. In this case the descriptor columns will not be re-built, only the summary data will be calculated and actualized. This feature may be useful, if you change some settings an want to update the data. If you use the **Recalculate** button with an empty preview table, only the description titles will be displayed. Anyway you can view the summarized data using the button (see below).

You may store all changed entries by clicking the button or omit all changes and reload the data by clicking the button. To view the description details of the currently selected entry click the button and a separate browser window opens (see image below).



Description: My first description

AID:

ID: 143

Details: 112d
20.02.2020 15:25:03 - Description summarized from:
6 sampling unit(s): 'Second event 2' [7873154]

Natural language support

Wording:

Description scopes

Scope type	Scope value
Geographic area	Germany, World, Bayern
Taxon name	Abaphospora hypoxyloides (Hohn.) Kirschst.
Specimen	Specimen
Geographic area	Germany, World, Stadt-/Gemeindeteil v. Mudau, Neckar-Odenwald-Kreis, (Waldauerbach)
Observation	Observation
Sex	Unknown sex
Stage	Adult

Project

☐ Agricultural survey
☐ BFLheilpflanzendesc
☐ Deemy
☐ Deltatest
☐ DiversityWorkbench
☐ Lias light
☐ Lias light 1
☐ Main project for DELTA test
☐ Main project for SDD test
☐ Matrix test
☑ My first test project

Generate document

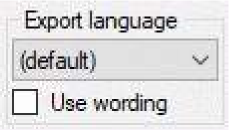
This tool is used to generate a structured documentation of database contents. To use this tool, start a query and choose **Data -> Generate Document ...** from the menu. The entries of the query result will be passed to the form and depending on the query type (description or descriptor) different output options will be provided.

For details check the following pages:

- **Generate a description data document**
- **Generate a descriptor data document**
- **Generate a project data document**

Translations and wording

In most of the forms for document generation a control for adjusting the **Export language** as shown below is included. The drop down box always offers an item "(default)" and language codes for all translation languages available in the database. If you select the default value, the original labels, details a.s.o. is used in the generated document. If you select a specific language code, the corresponding tranlated values are exported. If no tranlation is stored in the database for a specific value, the original value is used instead.



Export language

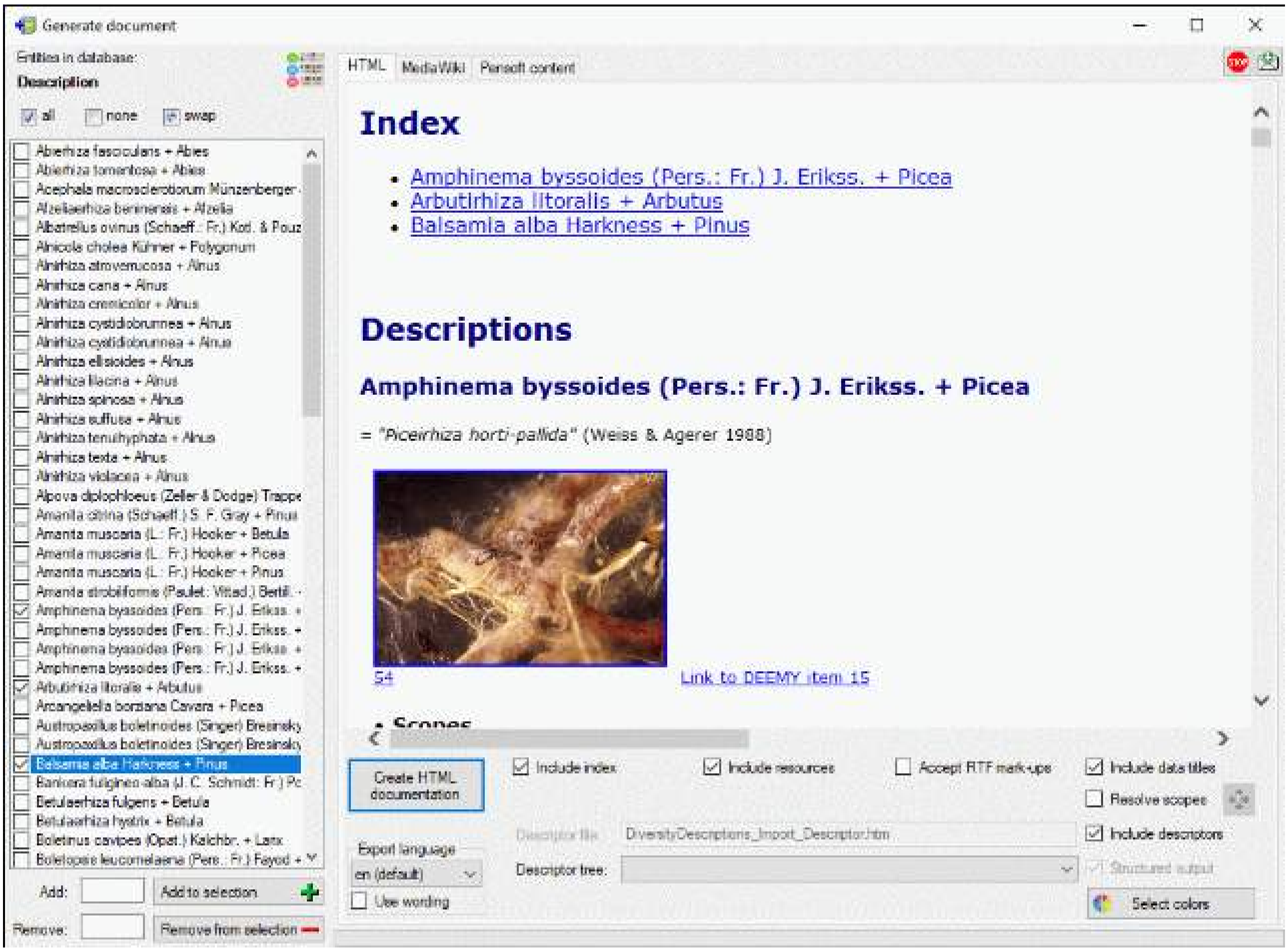
(default)

☐ Use wording

If you select the option **Use wording**, for descriptions, descriptors and categorical states the values of the fields "wording" are exported instead of the names. For summary data additionally the values "wording before" and "wording after", which may be specified for each descriptor, are inserted before and after the values. If no wording is specified, the original name is used.

Generate a description data document

This tool is used to generate a structured documentation of description data stored in the database. To use this tool, start a query for descriptions and choose **Data -> Generate document ...** from the menu. A window with will open as shown below.



Entities in database:
Description

☑ all ☐ none swap

- ☐ Abierhiza fasciculans + Abies
- ☐ Abierhiza tomentosa + Abies
- ☐ Acephala macrosclerotiorum Münzenberger
- ☐ Afzeliaerhiza beninensis + Afzelia
- ☐ Albatrellus ovinus (Schaeff.: Fr.) Kotl. & Pouz
- ☐ Alnicola cholea Kühner + Polygonum
- ☐ Alnirhiza atroverrucosa + Alnus
- ☐ Alnirhiza cana + Alnus
- ☐ Alnirhiza cremicolor + Alnus
- ☐ Alnirhiza cystidiobrunnea + Alnus
- ☐ Alnirhiza cystidiobrunnea + Alnus
- ☐ Alnirhiza ellsioides + Alnus
- ☐ Alnirhiza lilacina + Alnus
- ☐ Alnirhiza spinosa + Alnus
- ☐ Alnirhiza suffusa + Alnus
- ☐ Alnirhiza tenuihyphata + Alnus
- ☐ Alnirhiza texta + Alnus
- ☐ Alnirhiza violacea + Alnus
- ☐ Alpova diplophloeus (Zeller & Dodge) Trappe
- ☐ Amanita citrina (Schaeff.) S. F. Gray + Pinus
- ☐ Amanita muscaria (L.: Fr.) Hooker + Betula
- ☐ Amanita muscaria (L.: Fr.) Hooker + Picea
- ☐ Amanita muscaria (L.: Fr.) Hooker + Pinus
- ☐ Amanita strobiliformis (Paulet: Vittad.) Bertil.
- ☑ Amphinema byssoides (Pers.: Fr.) J. Erikss. +
- ☐ Amphinema byssoides (Pers.: Fr.) J. Erikss. +
- ☐ Amphinema byssoides (Pers.: Fr.) J. Erikss. +
- ☐ Amphinema byssoides (Pers.: Fr.) J. Erikss. +
- ☑ Arbutirhiza litoralis + Arbutus
- ☐ Arcangeliella borziana Cavara + Picea
- ☐ Austropaxillus boletinoides (Singer) Bresinsky
- ☐ Austropaxillus boletinoides (Singer) Bresinsky
- ☑ Balsamia alba Harkness + Pinus
- ☐ Bankera fuligineo-alba (J. C. Schmidt: Fr.) Pc
- ☐ Betulaerhiza fulgens + Betula
- ☐ Betulaerhiza hystrix + Betula
- ☐ Boletinus cavipes (Opat.) Kalchbr. + Larix
- ☐ Boletopsis leucomelaena (Pers.: Fr.) Fayod +

Add: Add to selection

Remove: Remove from selection

Index

- Amphinema byssoides (Pers.: Fr.) J. Erikss. + Picea
- Arbutirhiza litoralis + Arbutus
- Balsamia alba Harkness + Pinus

Descriptions

Amphinema byssoides (Pers.: Fr.) J. Erikss. + Picea

= *"Piceirhiza horti-pallida"* (Weiss & Agerer 1988)

54 Link to DEEMY item 15

- Scopes

Create HTML documentation

☑ Include index ☑ Include resources ☐ Accept RTF mark-ups ☑ Include data titles

☐ Resolve scopes

Export language: en (default)

☐ Use wording

Descriptor file: DiversityDescriptions_Import_Descriptor.htm

☑ Include descriptors

Descriptor tree:

☑ Structured output

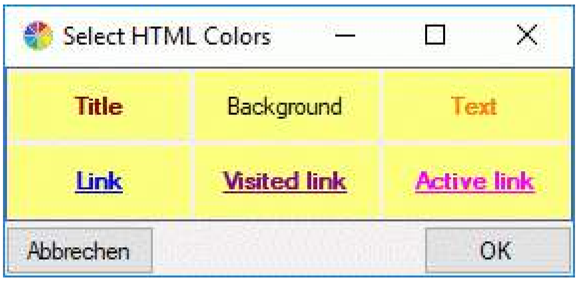
Select colors

You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. Choose among the provided options and click on the button Create ... documentation to create a document in one of the available formats.

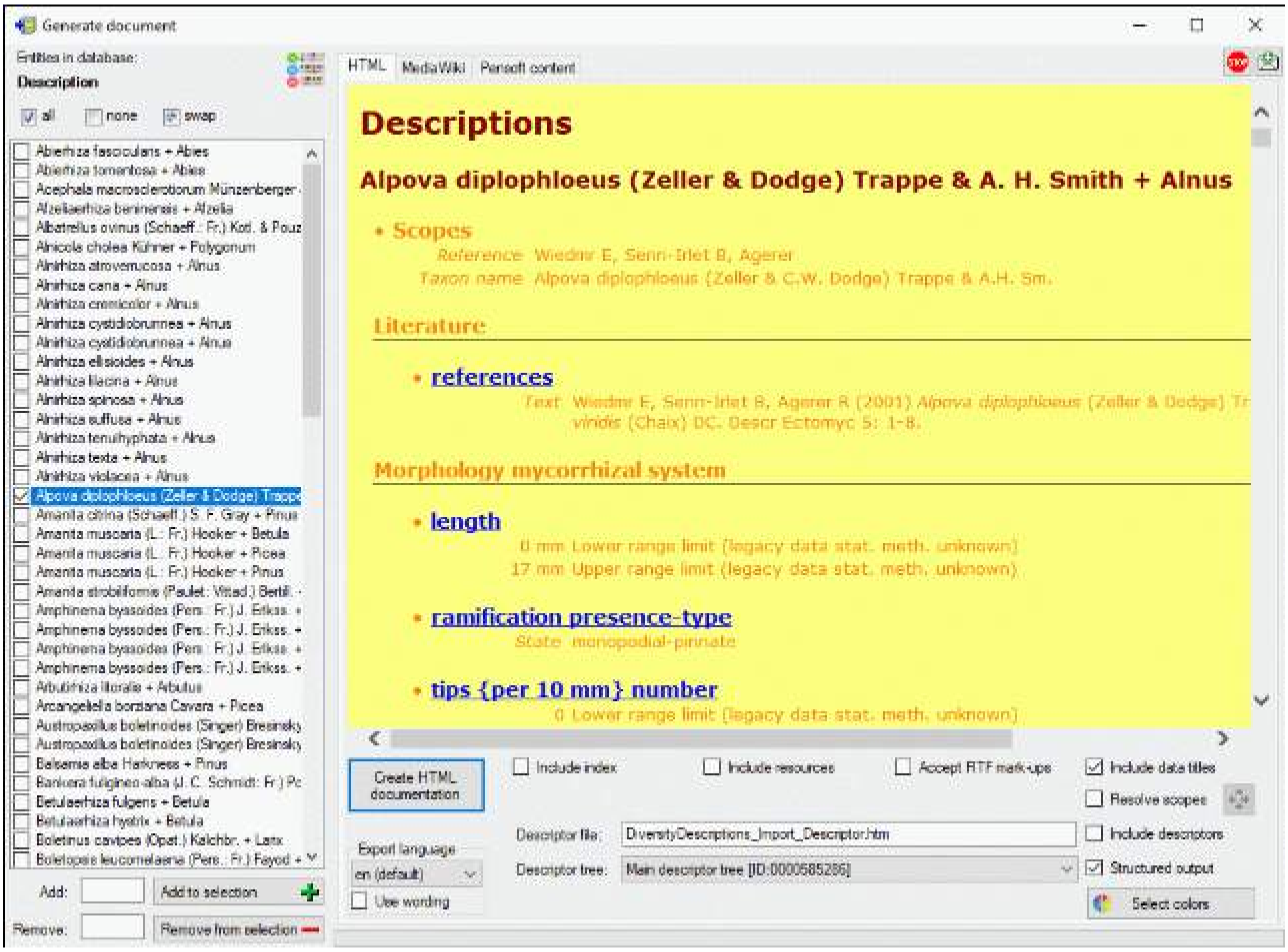
By default no descriptions will be exported that include any descriptor with data status "Data withheld". This is indicated by the STOP button in the upper right corner of the window. You may click on this button to include those descriptions. The button will change to STOP and only the marked descriptor summary data will be excluded from the document.

HTML

If you create a HTML documentation, a local file named **<Database name>_Description.htm** is generated in the application directory, that might be copied and edited for own purposes. If you select option **Include descriptors**, the used descriptors are included at the end of the documents and links to that empedded descriptors are set in the description section. Otherwise the links are set to the entries specified in the **Descriptor file:** text box. By clicking button **Select colors** you may open a dialog window where you can select the colors of different elements (see window below).



If all descriptions in the selection box belong to the same project and a descriptor tree is defined, the **Descriptor tree:** drop-down list is shown in the options (see image below left). If a descriptor tree is selected and the **Structured output** keeps activated, the description data are arranged according the selected descriptor trees. Additionally leading descriptor name parts are omitted, if they are contained in the descriptor tree hierachy. Therefore "literature references" becomes to "references" contained in node "Literature" as shown below. If the selected descriptor tree contains only a subset of descriptors, only this subset will be displayed in the output.



Descriptions

Alpova diplophloeus (Zeller & Dodge) Trappe & A. H. Smith + Alnus

- Scopes
  Reference Wiedmr E, Senn-Irlet B, Agerer
  Taxon name Alpova diplophloeus (Zeller & C.W. Dodge) Trappe & A.H. Sm.

Literature

- references
  Text Wiedmr E, Senn-Irlet B, Agerer R (2001) *Alpova diplophloeus* (Zeller & Dodge) Tr
  viridis (Chaix) DC. Descr Ectomyc 5: 1-8.

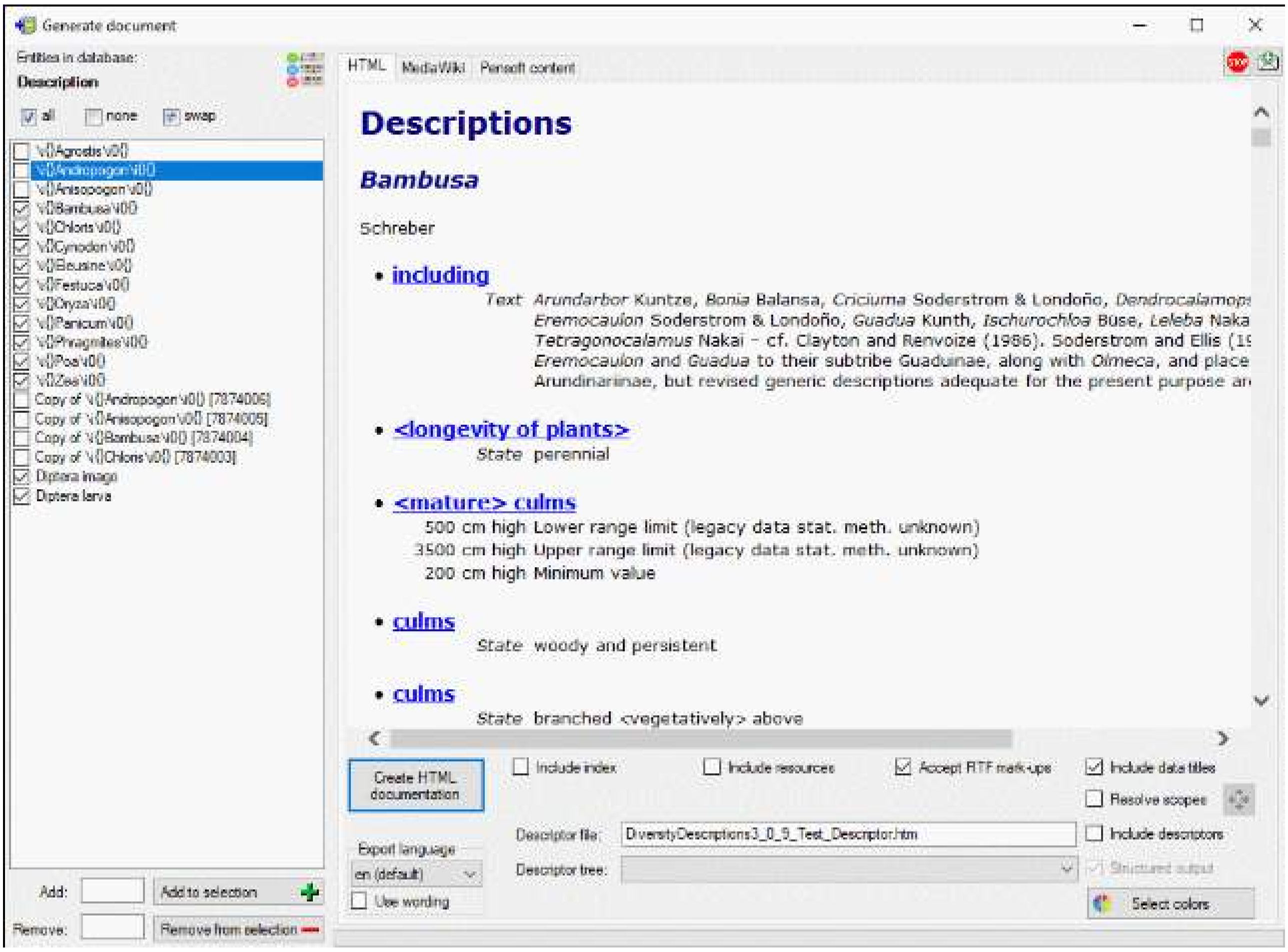
Morphology mycorrhizal system

- length
  0 mm Lower range limit (legacy data stat. meth. unknown)
  17 mm Upper range limit (legacy data stat. meth. unknown)
- ramification presence-type
  State monopodial-pinnate
- tips {per 10 mm} number
  0 Lower range limit (legacy data stat. meth. unknown)

☐ Include index
☐ Include resources
☐ Accept RTF mark-ups
☑ Include data titles
☐ Resolve scopes
☐ Include descriptors
☑ Structured output
Export language: en (default)
☐ Use wording
Descriptor file: DiversityDescriptions_Import_Descriptor.htm
Descriptor tree: Main descriptor tree [ID:000685286]

If the **Structured output** option is deactivated, all descriptors will be included in the output in the standard sequence order. Leading name parts will be reduced if they are already contained in the tree hierarchy as described in the Editing the description - Continuous view tab section. With check box **Include data titles** the output of the titles "State", "Text" and "Sequence" in the descriptor data can be controlled. If you select **Resolve scopes**, for each scope that is linked to a database entry a table with the foreign database values will be inserted. To check and adjust the module connections click on button ✥.

If in the datasets RTF-like formatting tags like **\i{}** or **\sub{}** are included, use option **Accept RTF mark-ups** as shown in the picture below.



Entities in database:
Description

☑ all ☐ none ☑ swap

☐ \i{}Agrostis\i0{}
☐ \i{}Andropogon\i0{}
☐ \i{}Anisopogon\i0{}
☑ \i{}Bambusa\i0{}
☑ \i{}Chloris\i0{}
☑ \i{}Cynodon\i0{}
☑ \i{}Eleusine\i0{}
☑ \i{}Festuca\i0{}
☑ \i{}Oryza\i0{}
☑ \i{}Panicum\i0{}
☑ \i{}Phragmites\i0{}
☑ \i{}Poa\i0{}
☑ \i{}Zea\i0{}
☐ Copy of \i{}Andropogon\i0{} [7874006]
☐ Copy of \i{}Anisopogon\i0{} [7874005]
☐ Copy of \i{}Bambusa\i0{} [7874004]
☐ Copy of \i{}Chloris\i0{} [7874003]
☑ Diptera imago
☑ Diptera larva

Descriptions

Bambusa

Schreber

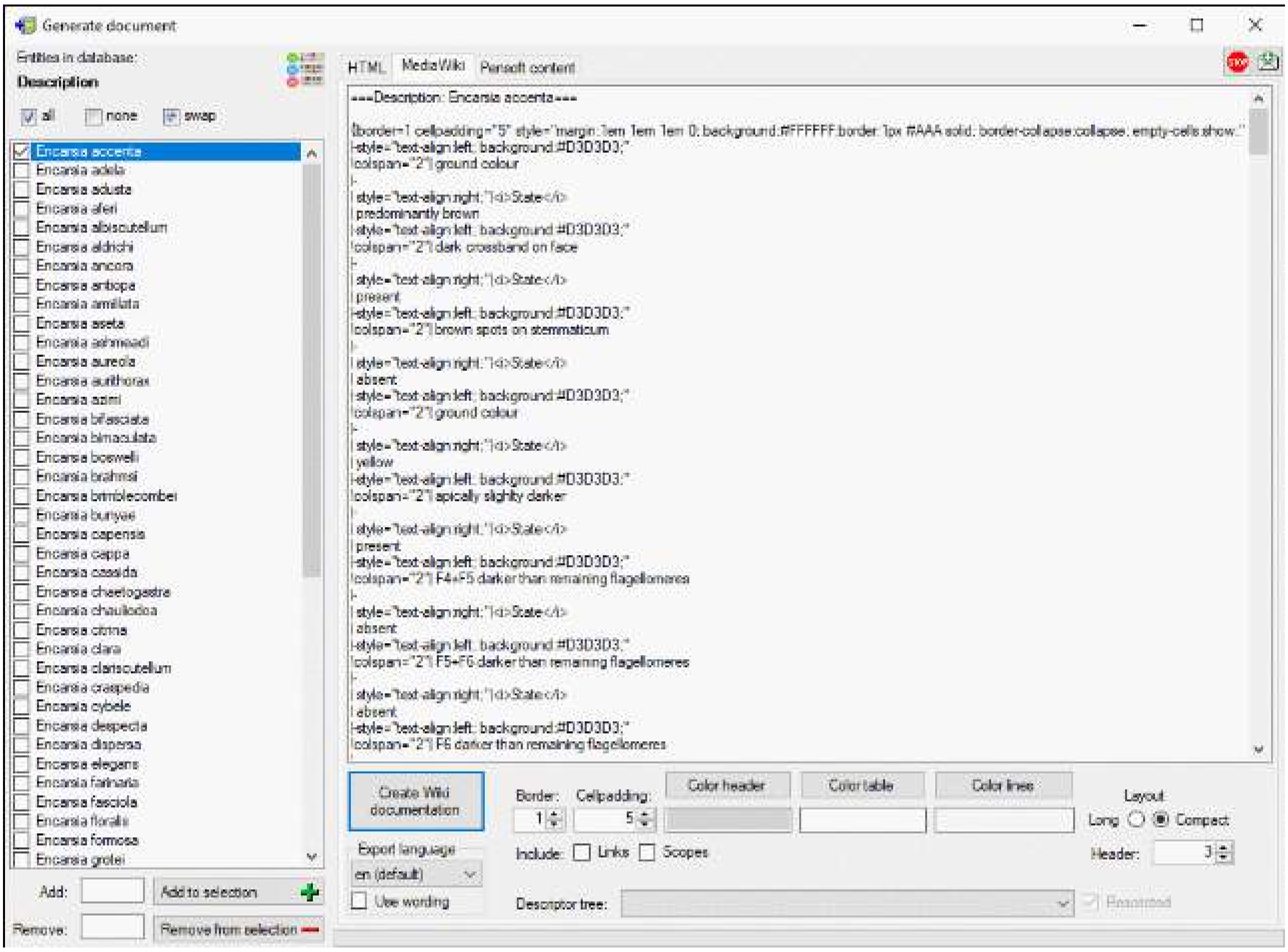
- **including**
  Text *Arundarbor* Kuntze, *Bonia* Balansa, *Criciuma* Soderstrom & Londoño, *Dendrocalamops*
  Eremocaulon Soderstrom & Londoño, *Guadua* Kunth, *Ischurochloa* Büse, *Leleba* Naka
  Tetragonocalamus Nakai - cf. Clayton and Renvoize (1986). Soderstrom and Ellis (1
  Eremocaulon and *Guadua* to their subtribe Guaduinae, along with *Olmeca*, and place
  Arundinarinae, but revised generic descriptions adequate for the present purpose ar
- **<longevity of plants>**
  State perennial
- **<mature> culms**
  500 cm high Lower range limit (legacy data stat. meth. unknown)
  3500 cm high Upper range limit (legacy data stat. meth. unknown)
  200 cm high Minimum value
- **culms**
  State woody and persistent
- **culms**
  State branched <vegetatively> above

☐ Include index ☐ Include resources ☑ Accept RTF mark-ups ☑ Include data titles
☐ Resolve scopes
Descriptor file: DiversityDescriptions3_0_9_Test_Descriptor.htm ☐ Include descriptors
Export language: en (default)
Descriptor tree:
☐ Use wording
☑ Structured output

MediaWiki

If you create a MediaWiki documentation, you may copy the generated text from the output window and insert it in the MediaWiki page. With the **Layout** option you may determine if all data shall be included in a large table or if several tables with additional header lines shall be generated (see image below).

If all descriptions in the selection box belong to the same project and a descriptor tree is defined, the **Descriptor tree:** drop-down list is shown in the options (see image below left). If a descriptor tree is selected and the **Restricted** option is activated, the description data are restricted to the descriptors contained in the selected descriptor tree.



```
===Description: Encarsia accenta===

{|border=1 cellpadding="5" style="margin:1em 1em 1em 0; background:#FFFFFF; border:1px #AAA solid; border-collapse:collapse; empty-cells:show;"
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"|ground colour
|-
| style="text-align:right;"|<i>State</i>
| predominantly brown
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"|dark crossband on face
|-
| style="text-align:right;"|<i>State</i>
| present
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"|brown spots on stemmaticum
|-
| style="text-align:right;"|<i>State</i>
| absent
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"|ground colour
|-
| style="text-align:right;"|<i>State</i>
| yellow
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"|apically slightly darker
|-
| style="text-align:right;"|<i>State</i>
| present
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| F4+F5 darker than remaining flagellomeres
|-
| style="text-align:right;"|<i>State</i>
| absent
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| F5+F6 darker than remaining flagellomeres
|-
| style="text-align:right;"|<i>State</i>
| absent
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| F6 darker than remaining flagellomeres
```

Border: 1

Cellpadding: 5

Include: ☐ Links ☐ Scopes

Layout: Long ○ ● Compact

Header: 3

en (default)

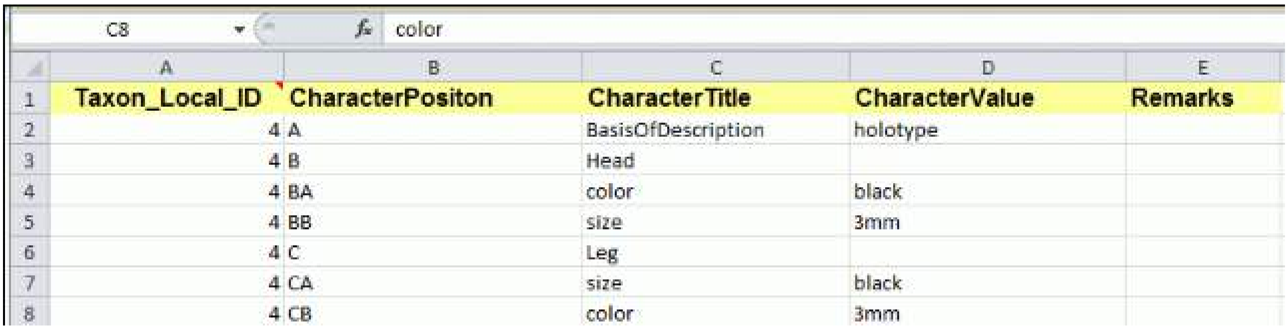
☐ Use wording

☑ Restricted

If the **Restriced** option is deactivated, all descriptor data will be included in the output in the standard sequence order. Only name parts of the descriptor tree hierarchy will be included in the descriptor names as described in the Editing the description - Descriptor view tab section.

Pensoft content

If you like to publish description data in some online media, e.g. the Pensoft "Biodiversity Data Journal", the description data are expected in a dedicated Microsoft Excel format. A template fille as shown below, that includes several tables, is available. DiversityDescriptions allows generating tabulator separated files for tables "Taxa" and "SpeciesDescriptionMatrix" of that template.



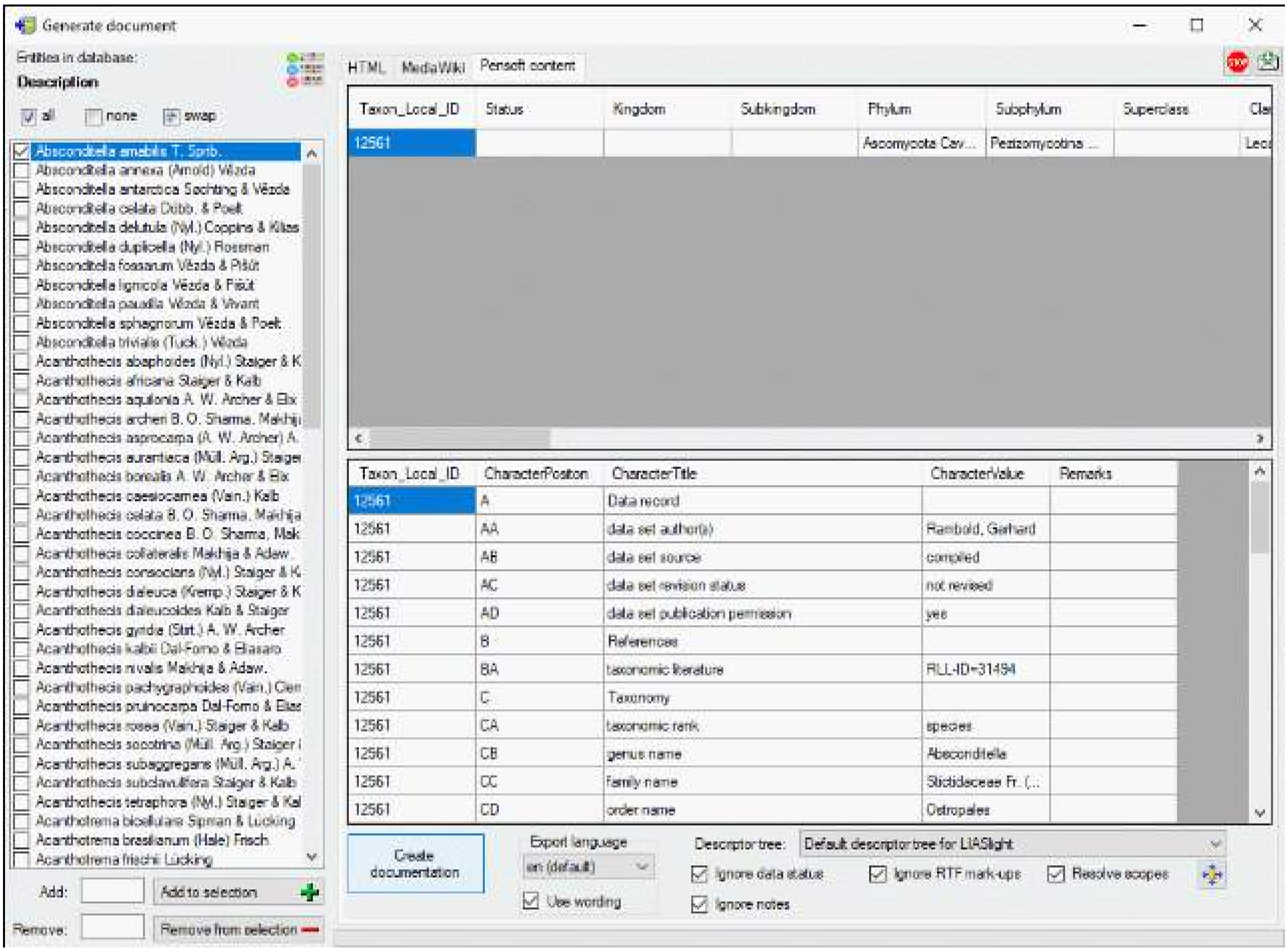
C8 fx color

	A	B	C	D	E
1	Taxon_Local_ID	CharacterPositon	CharacterTitle	CharacterValue	Remarks
2	4	A	BasisOfDescription	holotype	
3	4	B	Head		
4	4	BA	color	black	
5	4	BB	size	3mm	
6	4	C	Leg		
7	4	CA	size	black	
8	4	CB	color	3mm	

If all descriptions in the selection box belong to the same project and a descriptor tree is defined, the **Descriptor tree:** drop-down list is shown in the options (see image below). If a descriptor tree is selected, the description data are arranged with heading according the selected descriptor trees. Additionally leading descriptor name parts are omitted, if they are contained in the descriptor tree hierachy.

When **Ignore data status** ist selected, it will not be included in the "CharacterValue" column. Option **Ignore RTF mark-ups** will remove RTF-like formatting tags like **\i{}** or **\sub{}**. If option **Ignore notes** is de-selected, notes will be inserted in the "Remarks" column of the "SpeciesDescriptionMatrix".

If you select **Resolve scopes** and a scope entry for a taxon name is linked to an entry in DiversityTaxonNames, the corresponding fields of the "Taxa" table will be filled with that data. To check and adjust the module connections click on button ✥. If scope data for a geographic area is available, it will be inserted in the "Distribution" column of the "Taxa" table.



☑ Absconditella amabilis T. Sprib.
☐ Abscondtella annexa (Arnold) Vězda
☐ Abscondtella antarctica Sachting & Vězda
☐ Abscondtella celata Dubb. & Poelt
☐ Abscondtella delutula (Nyl.) Coppins & Kilias
☐ Abscondtella duplicella (Nyl.) Rossman
☐ Abscondtella fossarum Vězda & Pišút
☐ Abscondtella lignicola Vězda & Pišút
☐ Abscondtella paludia Vězda & Vivant
☐ Abscondtella sphagnorum Vězda & Poelt
☐ Abscondtella trivialis (Tuck.) Vězda
☐ Acanthothecis abaphoides (Nyl.) Staiger & K
☐ Acanthothecis africana Staiger & Kalb
☐ Acanthothecis aquilonia A. W. Archer & Elix
☐ Acanthothecis archeri B. O. Sharma, Makhij
☐ Acanthothecis asprocarpa (A. W. Archer) A.
☐ Acanthothecis aurantiaca (Müll. Arg.) Staiger
☐ Acanthothecis borealis A. W. Archer & Elix
☐ Acanthothecis caesiocarnea (Vain.) Kalb
☐ Acanthothecis celata B. O. Sharma, Makhija
☐ Acanthothecis coccinea B. O. Sharma, Mak
☐ Acanthothecis collateralis Makhija & Adaw.
☐ Acanthothecis consocians (Nyl.) Staiger & K
☐ Acanthothecis dialeuca (Kremp.) Staiger & K
☐ Acanthothecis dialeucoides Kalb & Staiger
☐ Acanthothecis gyridia (Stirt.) A. W. Archer
☐ Acanthothecis kalbii Dal-Forno & Eliasaro
☐ Acanthothecis nivalis Makhija & Adaw.
☐ Acanthothecis pachygraphoides (Vain.) Cien
☐ Acanthothecis pruinocarpa Dal-Forno & Elias
☐ Acanthothecis rosea (Vain.) Staiger & Kalb
☐ Acanthothecis socotrina (Müll. Arg.) Staiger
☐ Acanthothecis subaggregans (Müll. Arg.) A.
☐ Acanthothecis subclavulifera Staiger & Kalb
☐ Acanthothecis tetraphora (Nyl.) Staiger & Kal
☐ Acanthotrema bicellularis Sipman & Lücking
☐ Acanthotrema brasilianum (Hale) Frisch
☐ Acanthotrema frischii Lücking

Taxon_Local_ID	Status	Kingdom	Subkingdom	Phylum	Subphylum	Superclass	Cla
12561				Ascomycota Cav...	Pezizomycotina ...		Lec

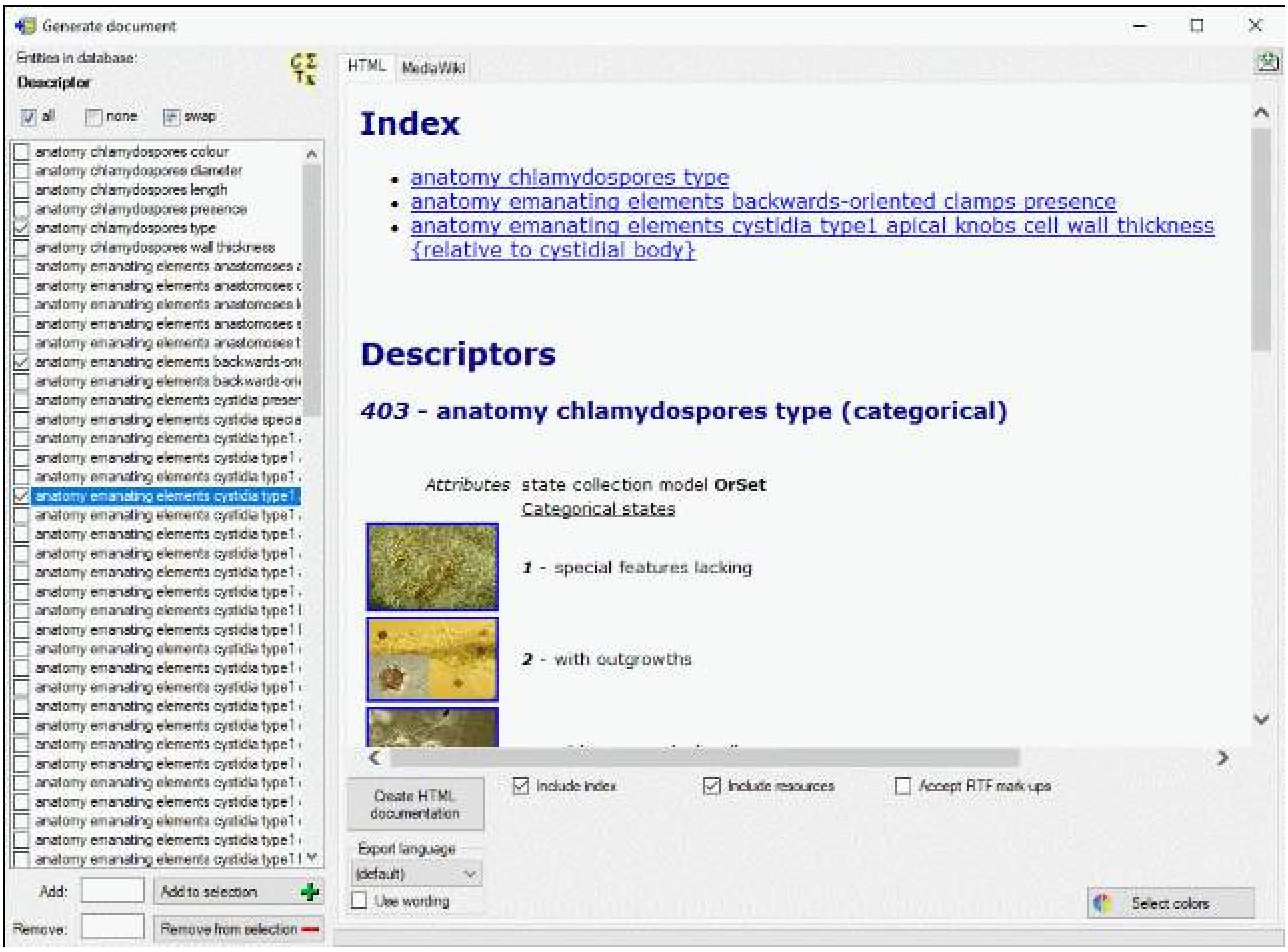
Taxon_Local_ID	CharacterPositon	CharacterTitle	CharacterValue	Remarks
12561	A	Data record		
12561	AA	data set author(s)	Rambold, Gerhard	
12561	AB	data set source	compiled	
12561	AC	data set revision status	not revised	
12561	AD	data set publication permission	yes	
12561	B	References		
12561	BA	taxonomic literature	RLL-ID=31494	
12561	C	Taxonomy		
12561	CA	taxonomic rank	species	
12561	CB	genus name	Abscondritella	
12561	CC	family name	Stictidaceae Fr. (...	
12561	CD	order name	Ostropales	

Export language: en (default)
☑ Use wording
Descriptor tree: Default descriptor tree for LIASlight
☑ Ignore data status
☑ Ignore RTF mark-ups
☑ Resolve scopes
☑ Ignore notes

The results are stored in local files named **<Database name>_Taxa.txt** and **<Database name>_SpeciesDescriptionMatrix.txt**.

Generate a descriptor data document

This tool is used to generate a structured documentation of descriptors stored in the database. To use this tool, start a query for descriptors and choose **Data ->** **Generate Document ...** from the menu. A window will open as shown below.



Index

- anatomy chlamydospores type
- anatomy emanating elements backwards-oriented clamps presence
- anatomy emanating elements cystidia type1 apical knobs cell wall thickness {relative to cystidial body}

Descriptors

***403* - anatomy chlamydospores type (categorical)**

Attributes state collection model **OrSet**

Categorical states

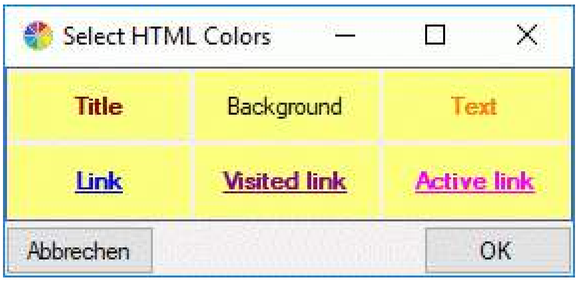
1 - special features lacking

2 - with outgrowths

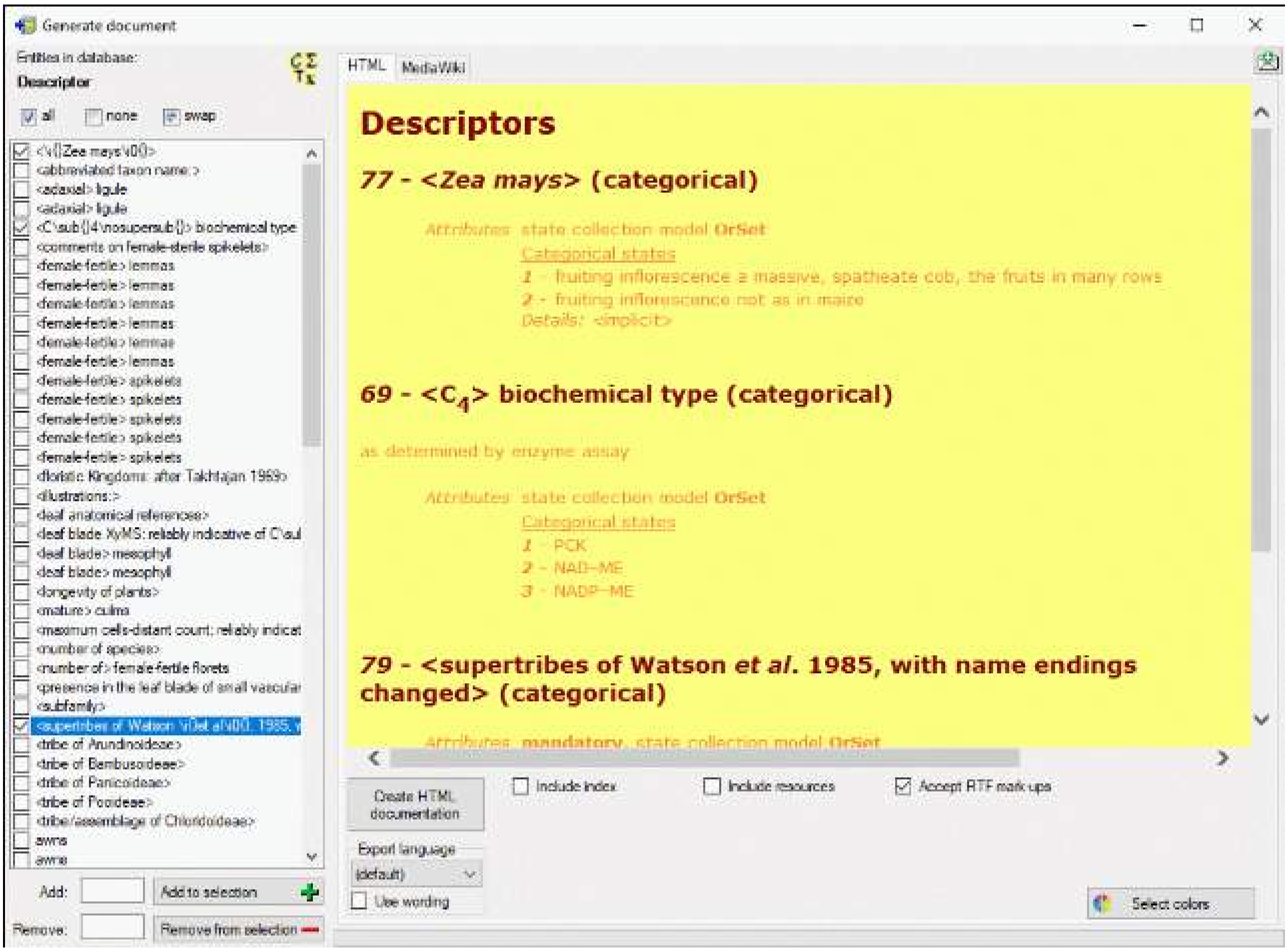
You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. Choose among the provided options and click on the button Create ... documentation to create a document in one of the available formats.

HTML

If you create a HTML documentation, a local file named **<Database name>_Descriptor.htm** is generated in the application directory, that might be copied and edited for own purposes. By clicking button **Select colors** you may open a dialog window where you can select the colors of different elements (see window below).



If in the datasets RTF-like formatting tags like **\i{}** or **\sub{}** are included, use option **Accept RTF mark-ups** as shown in the picture below.



☑ <\i{}Zea mays\i0{}>
☐ <abbreviated taxon name:>
☐ <adaxial> ligule
☐ <adaxial> ligule
☑ <C\sub{}4\nosupersub{}> biochemical type
☐ <comments on female-sterile spikelets>
☐ <female-fertile> lemmas
☐ <female-fertile> lemmas
☐ <female-fertile> lemmas
☐ <female-fertile> lemmas
☐ <female-fertile> lemmas
☐ <female-fertile> lemmas
☐ <female-fertile> spikelets
☐ <female-fertile> spikelets
☐ <female-fertile> spikelets
☐ <female-fertile> spikelets
☐ <female-fertile> spikelets
☐ <floristic Kingdoms: after Takhtajan 1969>
☐ <illustrations:>
☐ <leaf anatomical references>
☐ <leaf blade XyMS: reliably indicative of C\sul
☐ <leaf blade> mesophyll
☐ <leaf blade> mesophyll
☐ <longevity of plants>
☐ <mature> culms
☐ <maximum cells-distant count: reliably indicat
☐ <number of species>
☐ <number of> female-fertile florets
☐ <presence in the leaf blade of small vascular
☐ <subfamily>
☑ <supertribes of Watson \i0et al\i0{}. 1985, v
☐ <tribe of Arundinoideae>
☐ <tribe of Bambusoideae>
☐ <tribe of Panicoideae>
☐ <tribe of Pooideae>
☐ <tribe/assemblage of Chloridoideae>
☐ awns
☐ awns

Descriptors

77 - <*Zea mays*> (categorical)

Attributes state collection model **OrSet**
Categorical states
1 - fruiting inflorescence a massive, spatheate cob, the fruits in many rows
2 - fruiting inflorescence not as in maize
Details: <implicit>

69 - <C_4> biochemical type (categorical)

as determined by enzyme assay

Attributes state collection model **OrSet**
Categorical states
1 - PCK
2 - NAD–ME
3 - NADP–ME

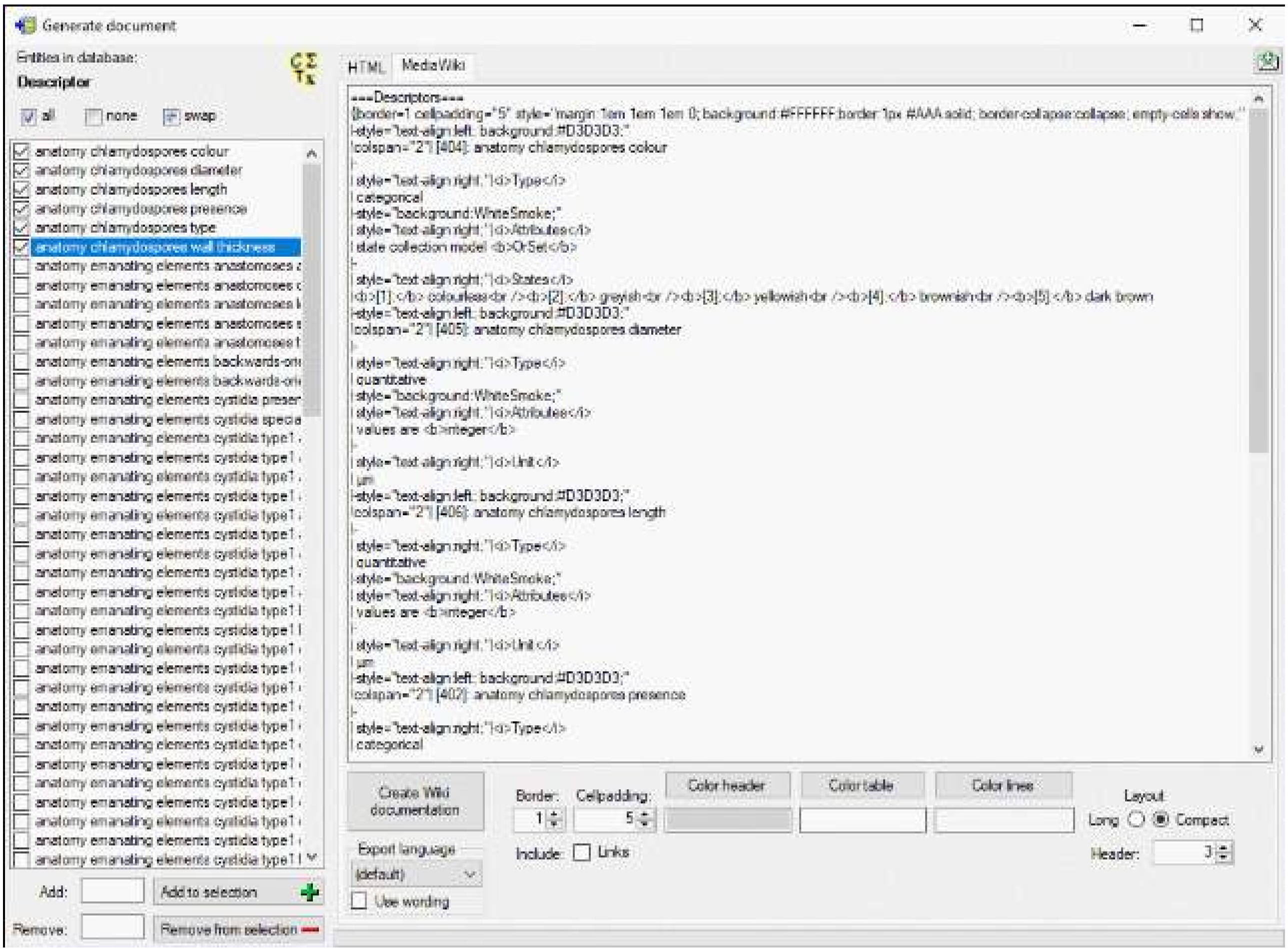
79 - <supertribes of Watson *et al*. 1985, with name endings changed> (categorical)

Attributes **mandatory**, state collection model **OrSet**

☐ Include index
☐ Include resources
☑ Accept RTF mark ups

MediaWiki

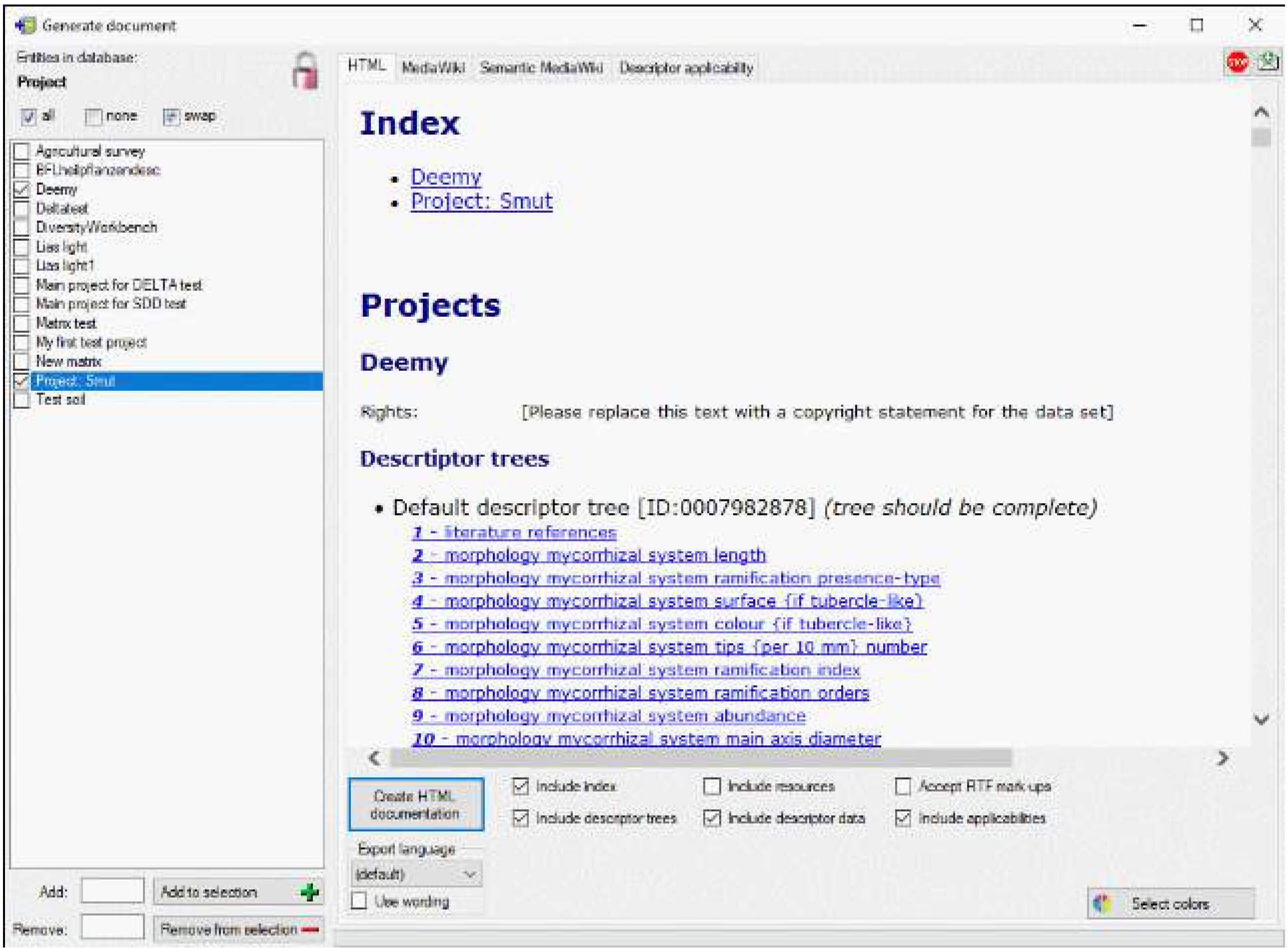
If you create a MediaWiki documentation, you may copy the generated text from the output window and insert it in the MediaWiki page. With the **Layout** option you may determine if all data shall be included in a large table or if several tables with additional header lines shall be generated (see image below).



```
===Descriptors===
{|border=1 cellpadding="5" style="margin:1em 1em 1em 0; background:#FFFFFF;border:1px #AAA solid; border-collapse:collapse; empty-cells:show;"
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [404]: anatomy chlamydospores colour
|-
| style="text-align:right;"|<i>Type</i>
| categorical
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Attributes</i>
| state collection model <b>OrSet</b>
|-
| style="text-align:right;"|<i>States</i>
|<b>[1]:</b> colourless<br /><b>[2]:</b> greyish<br /><b>[3]:</b> yellowish<br /><b>[4]:</b> brownish<br /><b>[5]:</b> dark brown
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [405]: anatomy chlamydospores diameter
|-
| style="text-align:right;"|<i>Type</i>
| quantitative
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Attributes</i>
| values are <b>integer</b>
|-
| style="text-align:right;"|<i>Unit</i>
| µm
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [406]: anatomy chlamydospores length
|-
| style="text-align:right;"|<i>Type</i>
| quantitative
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Attributes</i>
| values are <b>integer</b>
|-
| style="text-align:right;"|<i>Unit</i>
| µm
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [402]: anatomy chlamydospores presence
|-
| style="text-align:right;"|<i>Type</i>
| categorical
```

Generate a project data document

This tool is used to generate a structured documentation of project related data stored in the database. To use this tool, start a query for projects and choose **Data ->** **Generate Document ...** from the menu. A window will open as shown below.



☐ Agricultural survey
☐ BFLheilpflanzendesc
☑ Deemy
☐ Deltatest
☐ DiversityWorkbench
☐ Lias light
☐ Lias light1
☐ Main project for DELTA test
☐ Main project for SDD test
☐ Matrix test
☐ My first test project
☐ New matrix
☑ Project: Smut
☐ Test soil

Index

- Deemy
- Project: Smut

Projects

Deemy

Rights: [Please replace this text with a copyright statement for the data set]

Descrtiptor trees

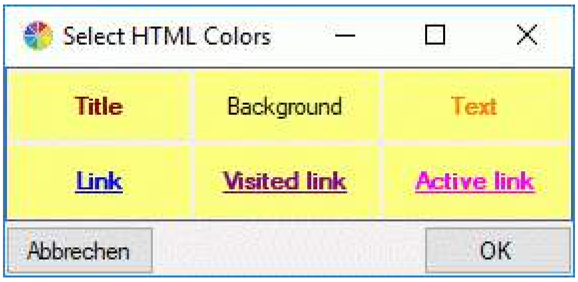
- Default descriptor tree [ID:0007982878] *(tree should be complete)*
  1 - literature references
  2 - morphology mycorrhizal system length
  3 - morphology mycorrhizal system ramification presence-type
  4 - morphology mycorrhizal system surface {if tubercle-like}
  5 - morphology mycorrhizal system colour {if tubercle-like}
  6 - morphology mycorrhizal system tips {per 10 mm} number
  7 - morphology mycorrhizal system ramification index
  8 - morphology mycorrhizal system ramification orders
  9 - morphology mycorrhizal system abundance
  10 - morphology mycorrhizal system main axis diameter

☑ Include index
☐ Include resources
☐ Accept RTF mark-ups
☑ Include descriptor trees
☑ Include descriptor data
☑ Include applicabilities
Export language: (default)
☐ Use wording

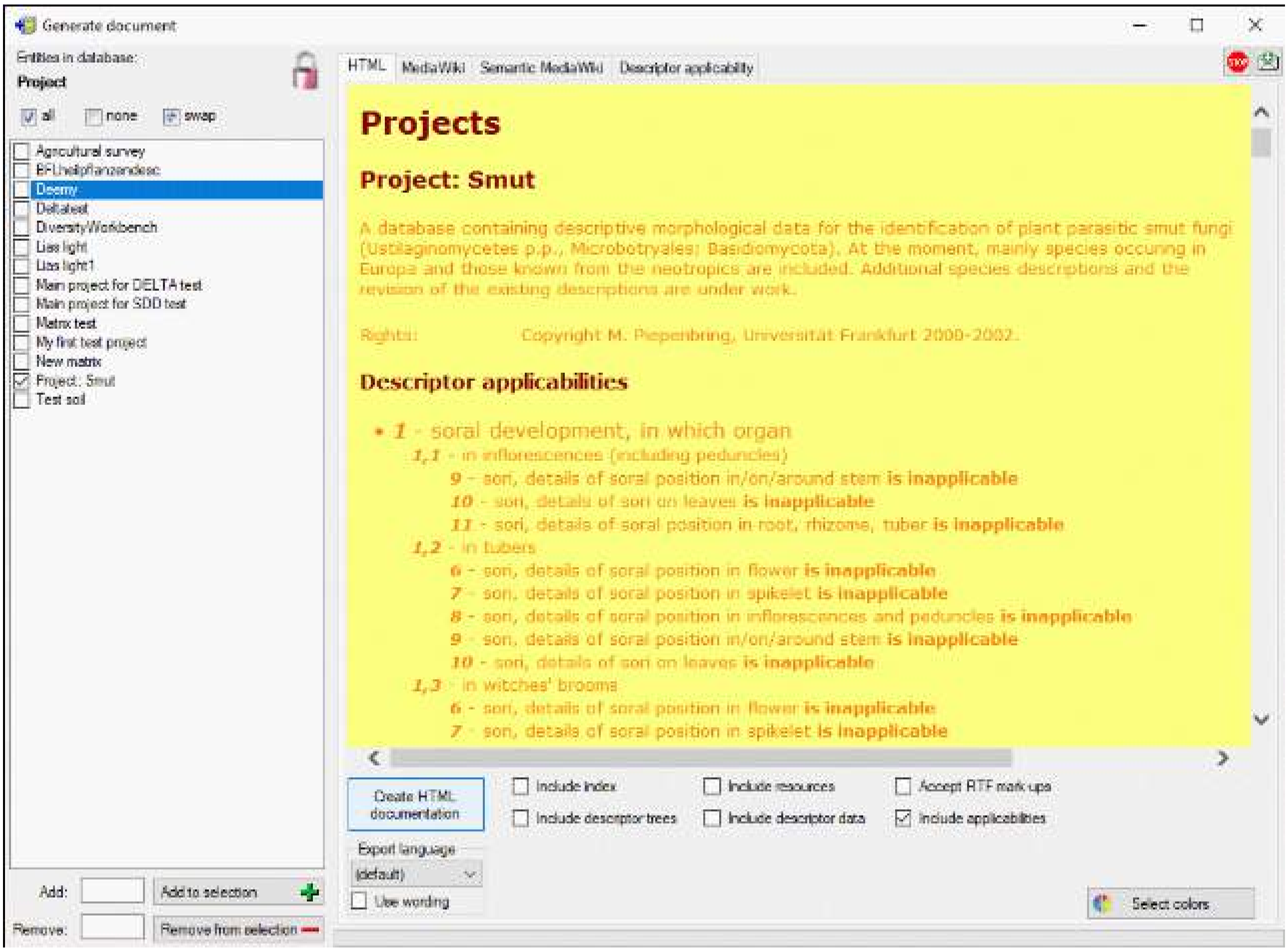
You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. Choose among the provided options and click on the button Create ... documentation to create a document in one of the available formats.

HTML

If you create a HTML documentation, a local file named **<Database name>_Project.htm** is generated in the application directory, that might be copied and edited for own purposes. By clicking button **Select colors** you may open a dialog window where you can select the colors of different elements (see window below).



You have the choice to output additional information besides the basic project data by selection the options **Include descriptor trees**, **Include descriptor data** or **Include applicabilities** (see window below).



☑ Project: Smut

Projects

Project: Smut

A database containing descriptive morphological data for the identification of plant parasitic smut fungi (Ustilaginomycetes p.p., Microbotryales; Basidiomycota). At the moment, mainly species occuring in Europa and those known from the neotropics are included. Additional species descriptions and the revision of the existing descriptions are under work.

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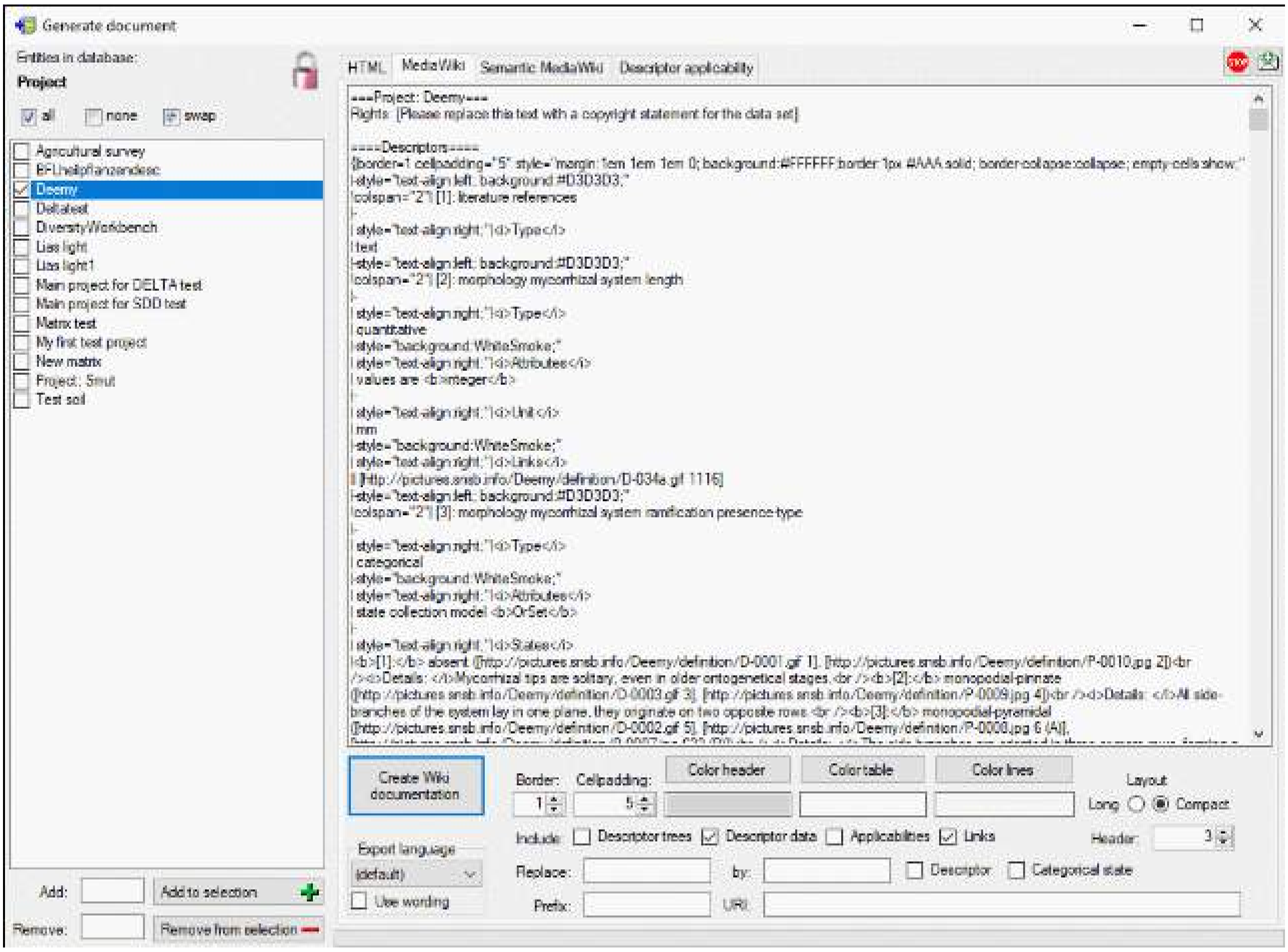
Descriptor applicabilities

- *1* - soral development, in which organ
  - *1,1* - in inflorescences (including peduncles)
    - *9* - sori, details of soral position in/on/around stem **is inapplicable**
    - *10* - sori, details of sori on leaves **is inapplicable**
    - *11* - sori, details of soral position in root, rhizome, tuber **is inapplicable**
  - *1,2* - in tubers
    - *6* - sori, details of soral position in flower **is inapplicable**
    - *7* - sori, details of soral position in spikelet **is inapplicable**
    - *8* - sori, details of soral position in inflorescences and peduncles **is inapplicable**
    - *9* - sori, details of soral position in/on/around stem **is inapplicable**
    - *10* - sori, details of sori on leaves **is inapplicable**
  - *1,3* - in witches' brooms
    - *6* - sori, details of soral position in flower **is inapplicable**
    - *7* - sori, details of soral position in spikelet **is inapplicable**

☐ Include index ☐ Include resources ☐ Accept RTF mark ups
☐ Include descriptor trees ☐ Include descriptor data ☑ Include applicabilities
☐ Use wording

MediaWiki

If you create a MediaWiki documentation, you may copy the generated text from the output window and insert it in the MediaWiki page. With the **Layout** option you may determine if all data shall be included in a large table or if several tables with additional header lines shall be generated (see image below).



```
===Project: Deemy===
Rights: [Please replace this text with a copyright statement for the data set]

====Descriptors====
{|border=1 cellpadding="5" style="margin: 1em 1em 1em 0; background:#FFFFFF;border: 1px #AAA solid; border-collapse:collapse; empty-cells:show;"
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [1]: literature references
|-
| style="text-align:right;"|<i>Type</i>
| text
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [2]: morphology mycorrhizal system length
|-
| style="text-align:right;"|<i>Type</i>
| quantitative
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Attributes</i>
| values are <b>integer</b>
|-
| style="text-align:right;"|<i>Unit </i>
| mm
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Links</i>
| [http://pictures.snsb.info/Deemy/definition/D-034a.gif 1116]
|-style="text-align:left; background:#D3D3D3;"
!colspan="2"| [3]: morphology mycorrhizal system ramification presence-type
|-
| style="text-align:right;"|<i>Type</i>
| categorical
|-style="background:WhiteSmoke;"
| style="text-align:right;"|<i>Attributes</i>
| state collection model <b>OrSet</b>
|-
| style="text-align:right;"|<i>States</i>
|<b>[1]:</b> absent ([http://pictures.snsb.info/Deemy/definition/D-0001.gif 1], [http://pictures.snsb.info/Deemy/definition/P-0010.jpg 2])<br
/><i>Details: </i>Mycorrhizal tips are solitary, even in older ortogenetical stages.<br /><b>[2]:</b> monopodial-pinnate
([http://pictures.snsb.info/Deemy/definition/D-0003.gif 3], [http://pictures.snsb.info/Deemy/definition/P-0009.jpg 4])<br /><i>Details: </i>All side-
branches of the system lay in one plane, they originate on two opposite rows.<br /><b>[3]:</b> monopodial-pyramidal
([http://pictures.snsb.info/Deemy/definition/D-0002.gif 5], [http://pictures.snsb.info/Deemy/definition/P-0008.jpg 6 (A)],
```

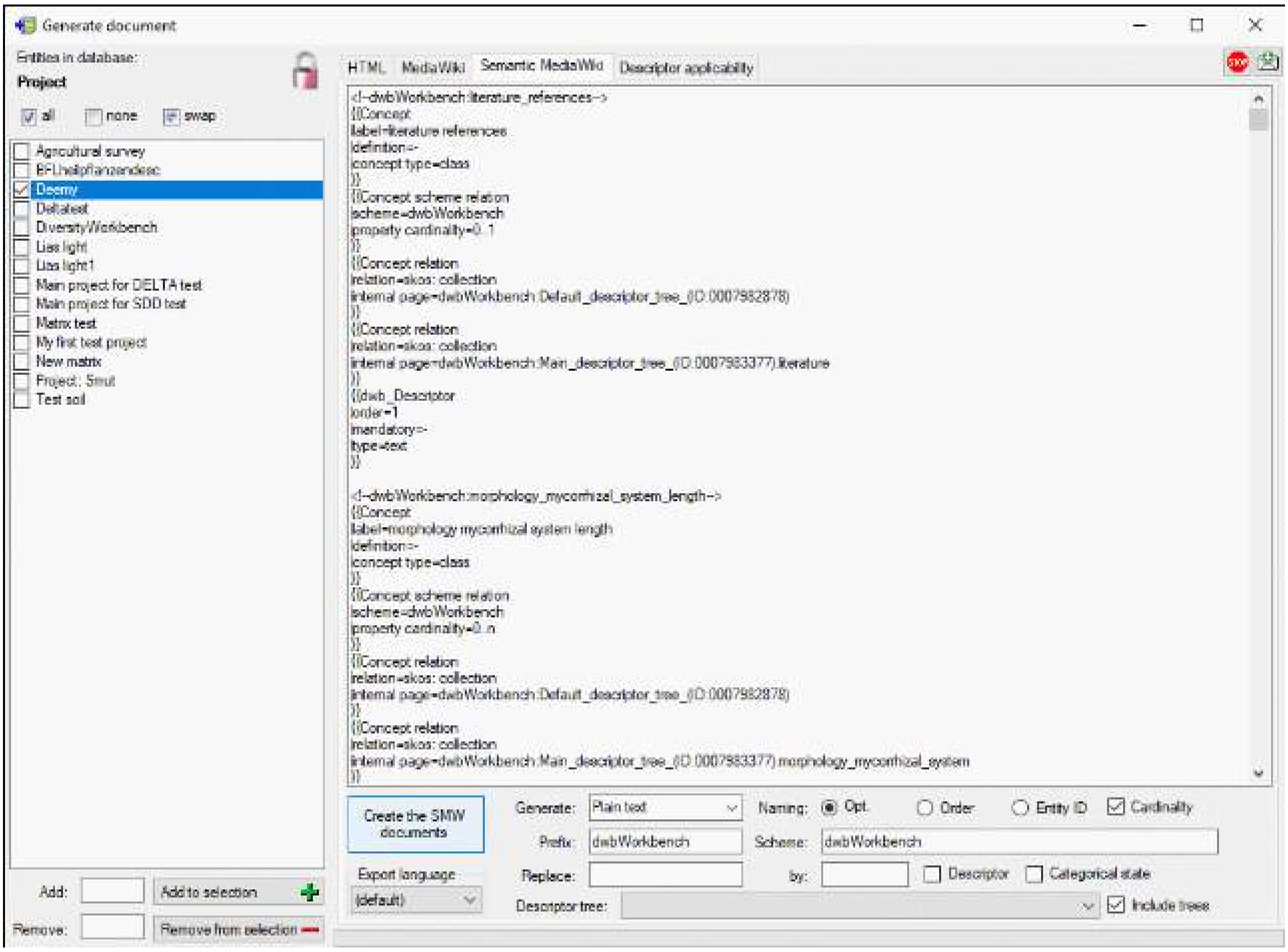
Border: 1
Cellpadding: 5
Layout: Long ○ Compact ●
Include: ☐ Descriptor trees ☑ Descriptor data ☐ Applicabilities ☑ Links
Header: 3
Export language: (default)
☐ Use wording
☐ Descriptor ☐ Categorical state

If you specify values in text fields **Replace:** and **by:** you can perform text replacements for **Descriptor** or **Categorical state** names in the generated output. By specifying a **Prefix:** for a Semantic MediaWiki (see next section) you can generate lokal links to this kind of Wiki pages. Additionally, you may insert the absolute link adresses by entering the base Wiki address in the **URI:** filed.

Semantic MediaWiki

If you create a Semantic MediaWiki documentation, the descriptors, categorical states, descriptor trees and descriptor applicability information are generated in a format that fits to terminology platforms as used e.g by TDWG. In this scheme the most important entities are "Concept" and "Collection". Each "Concept" represents a single descriptor or categorical state value, which is shown on an own page. Each "Collection" represents a single descriptor tree or descriptor tree node, which is shown on an own page. The pages are named according the schema <prefix>:<entity label> [(<number>)], where the <number> parts may be optional, depending on the **Naming:** setting (see image below):

- If **Opt. order** (Optional order) is selected the <number> part is omitted if the name is unambigious. Otherwise it starts with 1 for the first duplicate and is increased for each subsequent one to avoid duplicate page names.
- If **Order** is selected the <number> starts with 1 and is increased for each subsequent duplicate to guarantee unambigious page names.
- If **Entity ID** is selected the <number> contains the database internal ID of each entry to guarantee unambigious page names.



☑ all ☐ none ☑ swap

☐ Agricultural survey
☐ BFLhelpflanzendesc
☑ Deemy
☐ Deltatest
☐ DiversityWorkbench
☐ Lias light
☐ Lias light1
☐ Main project for DELTA test
☐ Main project for SDD test
☐ Matrix test
☐ My first test project
☐ New matrix
☐ Project: Smut
☐ Test soil

```
<!--dwbWorkbench:literature_references-->
{{Concept
|label=literature references
|definition=-
|concept type=class
}}
{{Concept scheme relation
|scheme=dwbWorkbench
|property cardinality=0..1
}}
{{Concept relation
|relation=skos: collection
|internal page=dwbWorkbench:Default_descriptor_tree_(ID:0007982878)
}}
{{Concept relation
|relation=skos: collection
|internal page=dwbWorkbench:Main_descriptor_tree_(ID:0007983377).literature
}}
{{dwb_Descriptor
|order=1
|mandatory=-
|type=text
}}

<!--dwbWorkbench:morphology_mycorrhizal_system_length-->
{{Concept
|label=morphology mycorrhizal system length
|definition=-
|concept type=class
}}
{{Concept scheme relation
|scheme=dwbWorkbench
|property cardinality=0..n
}}
{{Concept relation
|relation=skos: collection
|internal page=dwbWorkbench:Default_descriptor_tree_(ID:0007982878)
}}
{{Concept relation
|relation=skos: collection
|internal page=dwbWorkbench:Main_descriptor_tree_(ID:0007983377).morphology_mycorrhizal_system
}}
```

Create the SMW documents

Generate: Plain text

Naming: ● Opt. ○ Order ○ Entity ID ☑ Cardinality

Prefix: dwbWorkbench

Scheme: dwbWorkbench

Replace: by: ☐ Descriptor ☐ Categorical state

Export language: (default)

Descriptor tree: ☑ Include trees

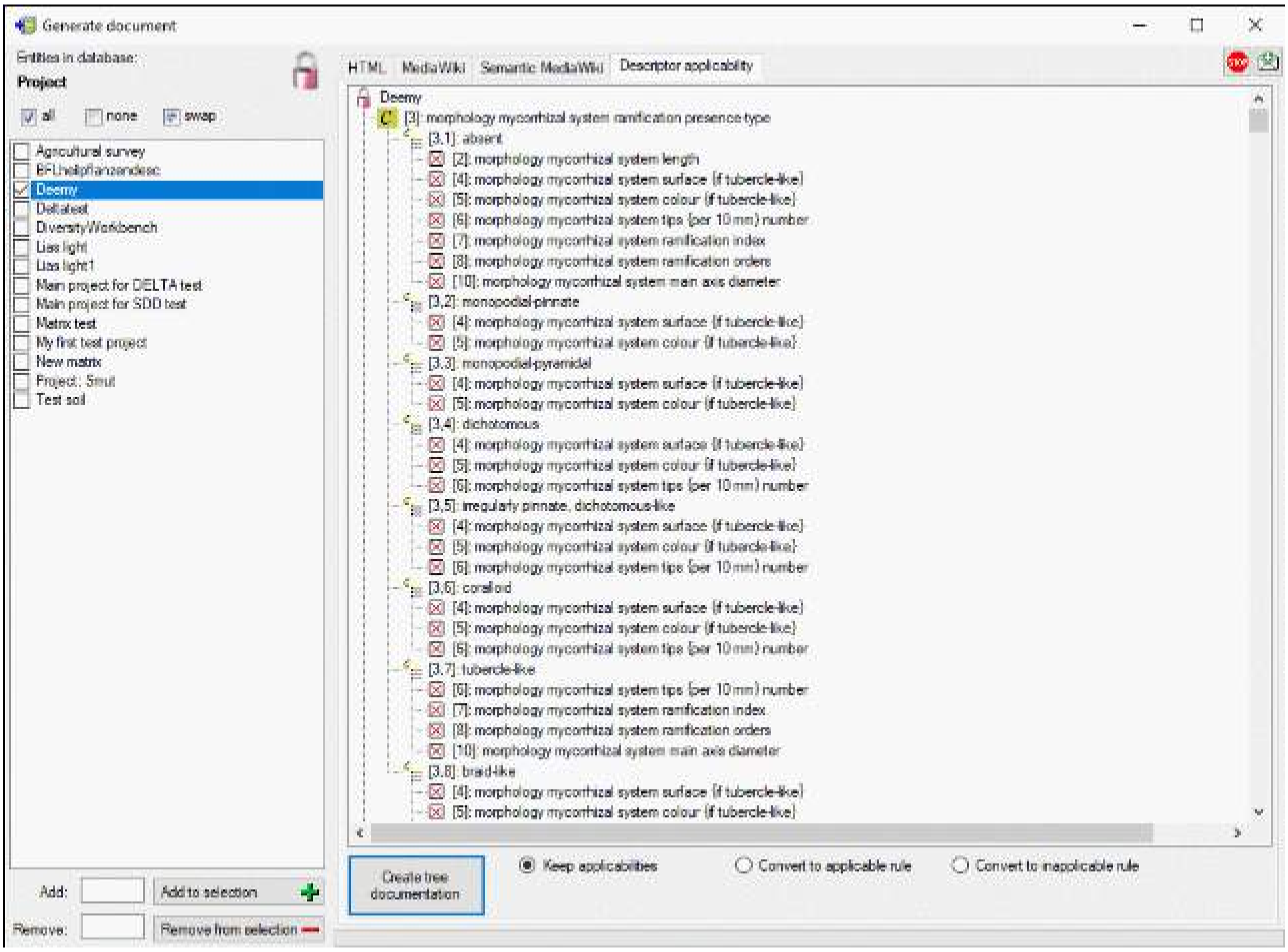
The **Cardinality** option includes information about multiple occurance and the mandatory property in the descriptor concepts. By selecting the **Include trees** option the descriptor trees and the tree structure will be included as collections where subordinated tree nodes are represented by concatenated node names, e.g. <prefix>:<Tree name>.<Node 1 name>.<Node 2 name>. If you specify values in text fields **Replace:** and **by:** you can perform text replacements for **Descriptor** or **Categorical state** names in the generated output.

If **Generate: XML for Wiki import** is selected, the output is generated in an XML format that may be imported to a semantic media wiki. To show all generated data, the two templates "dwb_Descriptor" and "dwb_CategoricalState" must be inserted in the wiki.

If **Generate: XSD/XML document** is selected, an XML schema (XSD) is generated in the main window. If schema generation was ended without problems, a selection list will be shown where description items for the XML document may be selected. For the selected descriptions an XML document structured according the XSD will be shown in a separate window. By default no descriptions will be exported that include any descriptor with data status "Data withheld". This is indicated by the 🛑 button in the upper right corner of the window. You may click on this button to include those descriptions. The button will change to 🛑 and only the marked descriptor summary data will be excluded from the document.

Descriptor applicability

The descriptor applicability tree shows the selected projects 🔒 and as subordinated nodes the categorical descriptors C that control the applicability of dependent descriptors. Contained in the controlling descriptor are their categorical states ☰ and the dependent descriptors with the applicability rule "applicable-if" ☑ or "inapplicable-if" ☒. The descriptor names are prefixed with their sequence number in square brackets, the states with the descriptor's sequence number and their own.

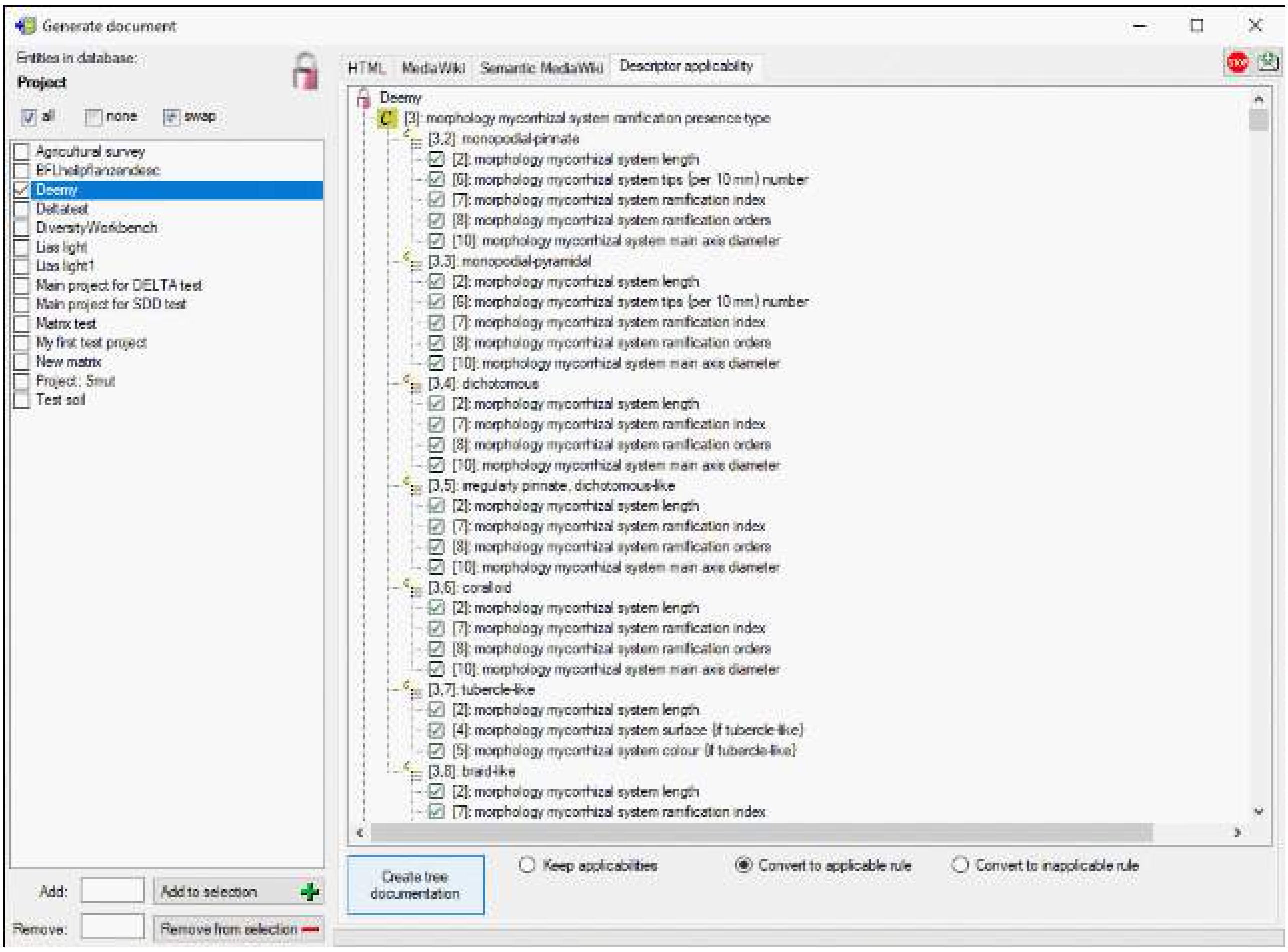


```
Deemy
  [3]: morphology mycorrhizal system ramification presence type
    [3.1]: absent
      ☒ [2]: morphology mycorrhizal system length
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
      ☒ [6]: morphology mycorrhizal system tips (per 10 mm) number
      ☒ [7]: morphology mycorrhizal system ramification index
      ☒ [8]: morphology mycorrhizal system ramification orders
      ☒ [10]: morphology mycorrhizal system main axis diameter
    [3.2]: monopodial-pinnate
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
    [3.3]: monopodial-pyramidal
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
    [3.4]: dichotomous
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
      ☒ [6]: morphology mycorrhizal system tips (per 10 mm) number
    [3.5]: irregularly pinnate, dichotomous-like
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
      ☒ [6]: morphology mycorrhizal system tips (per 10 mm) number
    [3.6]: coralloid
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
      ☒ [6]: morphology mycorrhizal system tips (per 10 mm) number
    [3.7]: tubercle-like
      ☒ [6]: morphology mycorrhizal system tips (per 10 mm) number
      ☒ [7]: morphology mycorrhizal system ramification index
      ☒ [8]: morphology mycorrhizal system ramification orders
      ☒ [10]: morphology mycorrhizal system main axis diameter
    [3.8]: braid-like
      ☒ [4]: morphology mycorrhizal system surface (if tubercle-like)
      ☒ [5]: morphology mycorrhizal system colour (if tubercle-like)
```

● Keep applicabilities

If you create a applicability tree documentation, two local tabulator-separated text files are generated. The first file named **<Database name>_ApplicabilityNodes.txt** contains the node list with columns "Id", "Label" and "Modularity class" ("Project", "Descriptor" or "State"). The second file named **<Database name>_ApplicabilityEdges.txt** contains the edges list with columns "Source", "Target" and "Label" ("Includes" for project-descriptor relations, "Contains" for descriptor-state relations or "Applicable" rsp. "Inapplicable" for state-descriptor relations). You may import those files to a graphic program like "Gephi" to visualize the descriptor applicabilities.

By selecting the option **Convert to applicable rule** or **Convert to inapplicable rule** the applicability settings stored in the database can be converted to the required complatible format (see image below).



Entities in database:
Project

☑ all ☐ none ☐ swap

- ☐ Agricultural survey
- ☐ BFLhelpflanzendesc
- ☑ Deemy
- ☐ Deltatest
- ☐ DiversityWorkbench
- ☐ Lias light
- ☐ Lias light1
- ☐ Main project for DELTA test
- ☐ Main project for SDD test
- ☐ Matrix test
- ☐ My first test project
- ☐ New matrix
- ☐ Project: Smut
- ☐ Test soil

- Deemy
  - [3]: morphology mycorrhizal system ramification presence type
    - [3.2]: monopodial-pinnate
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [6]: morphology mycorrhizal system tips (per 10 mm) number
      - ☑ [7]: morphology mycorrhizal system ramification index
      - ☑ [8]: morphology mycorrhizal system ramification orders
      - ☑ [10]: morphology mycorrhizal system main axis diameter
    - [3.3]: monopodial-pyramidal
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [6]: morphology mycorrhizal system tips (per 10 mm) number
      - ☑ [7]: morphology mycorrhizal system ramification index
      - ☑ [8]: morphology mycorrhizal system ramification orders
      - ☑ [10]: morphology mycorrhizal system main axis diameter
    - [3.4]: dichotomous
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [7]: morphology mycorrhizal system ramification index
      - ☑ [8]: morphology mycorrhizal system ramification orders
      - ☑ [10]: morphology mycorrhizal system main axis diameter
    - [3.5]: irregularly pinnate, dichotomous-like
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [7]: morphology mycorrhizal system ramification index
      - ☑ [8]: morphology mycorrhizal system ramification orders
      - ☑ [10]: morphology mycorrhizal system main axis diameter
    - [3.6]: coralloid
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [7]: morphology mycorrhizal system ramification index
      - ☑ [8]: morphology mycorrhizal system ramification orders
      - ☑ [10]: morphology mycorrhizal system main axis diameter
    - [3.7]: tubercle-like
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [4]: morphology mycorrhizal system surface (if tubercle-like)
      - ☑ [5]: morphology mycorrhizal system colour (if tubercle-like)
    - [3.8]: braid-like
      - ☑ [2]: morphology mycorrhizal system length
      - ☑ [7]: morphology mycorrhizal system ramification index

○ Keep applicabilities ● Convert to applicable rule ○ Convert to inapplicable rule

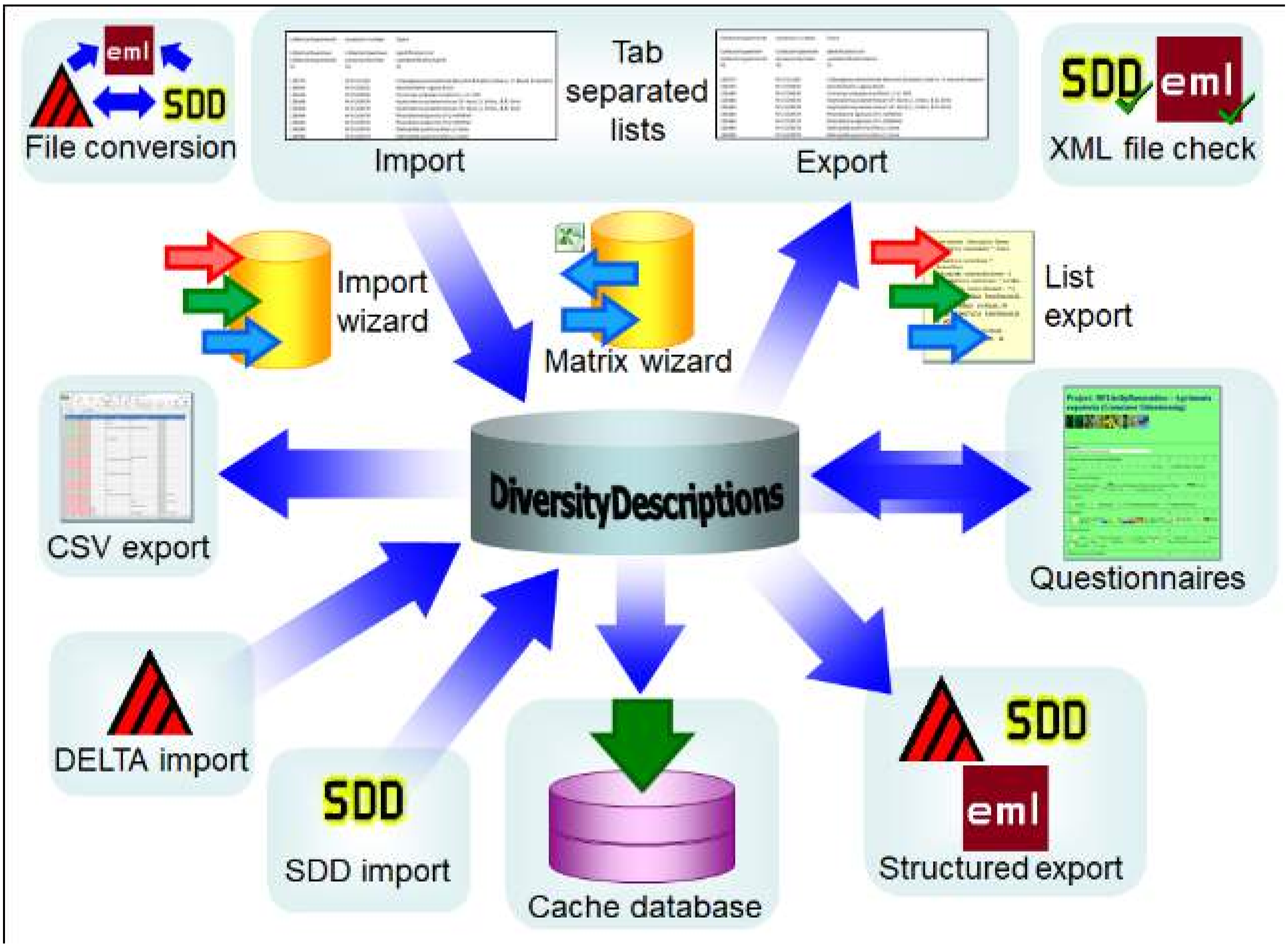
Import / Export

An overview of some options for the import, export and additional file based operations is given in the image below. The import wizard provides a very flexible tool to import data from tab-separated text files, e.g. generated from a foreighn tool or database. With the list export you may generate tab-separated text files from the database. The export and re-import of tab-separated list allows external editing of the data in e.g. spread sheet programs. For this purpose especially the Matrix wizard is very suitable. As an alternative the questionnaires allow editing of data in an HTML form, which can be done with any internet browser. The modified data can be "downloaded" as text files and re-imported into the database. Even new description data may be collected using the questionnaires without the need of a direct database access.

The CSV export provides a direct copy of selected database tables by means of the Microsoft SQL Server. These copies might be used for archiving purposes or if a foreighn application shall be supplied with data.

The most popular genuine formats for storing and exchanging descriptive data are DELTA and SDD, which are both supported for import and export. The structured export additionally allows generation of EML files, that provide metadata as XML and descriptive data as text table. A spin-off of the import and export functions for structured data is the file conversion, which may even be used without any database access. Additionally the SDD and EML structured XML files may be checked for conformance to their XML schemas.

Finally the cache database is providing descriptive data to external partners, e.g. a webportal.



Import

There are several import mechanisms:

Matrix wizard: Import descriptors, descriptions and sample data from tabulator separated text file(s) organized as a matrix.

Import wizard: Import descriptive data from tabulator separated text file(s).

SDD import: Import descriptive data from an XML file according to the SDD schema 1.1 rev 5.

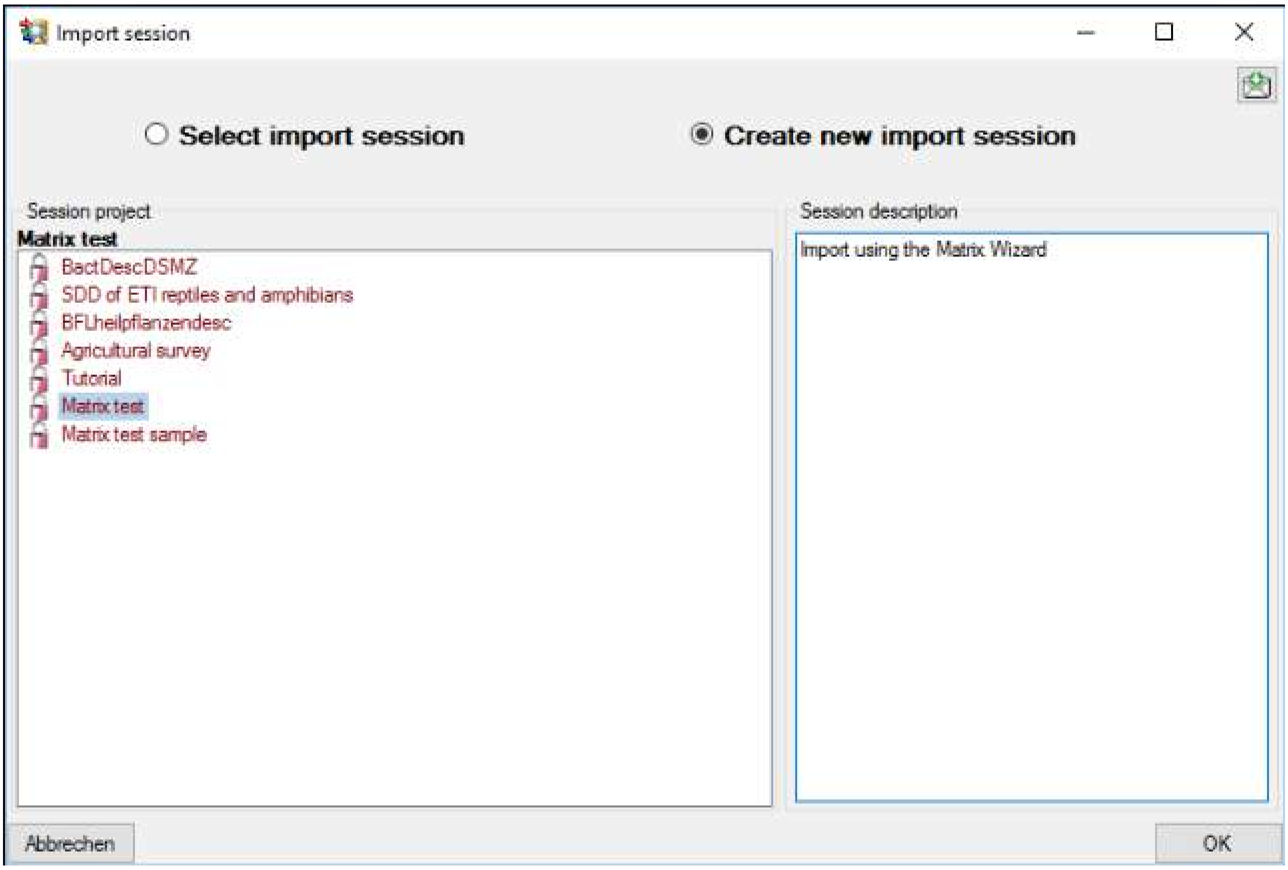
DELTA import: Import descriptive data from DELTA text file(s).

Import questionaires: Import revised data received from HTML forms.

Matrix import wizard for tab separated lists

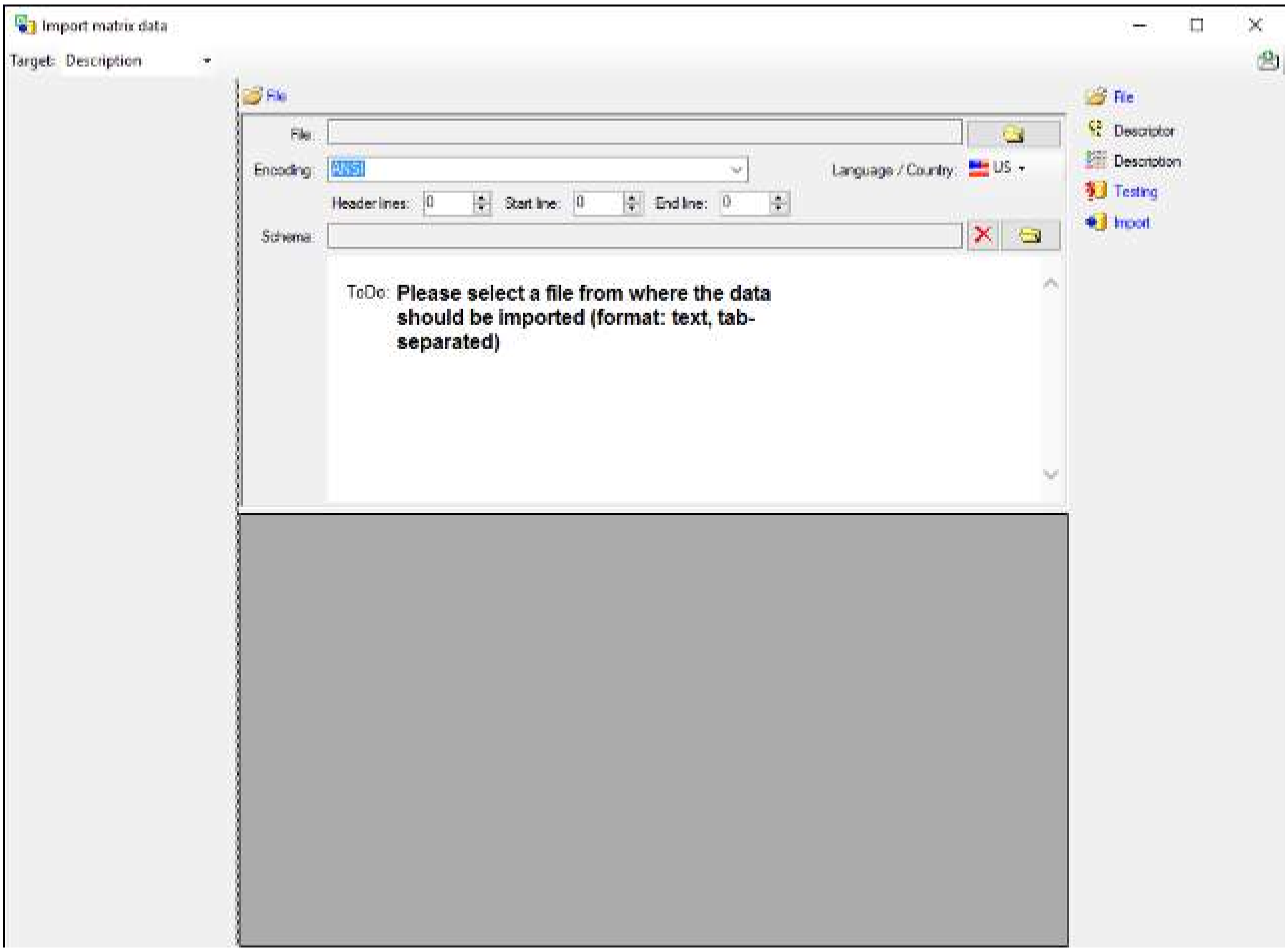
The table oriented import wizard works fine if you have separate lists for descriptor and description data. Usually this type of tables is generated by an export of data from a database. A typical example for that cases is described in the import wizard tutorial. If no dedicated application for collecting description data is available, most commonly a spreadsheet program like MS Excel or Open Office Calc is used to collect the description data. Typically the table columns represent a single character (=descriptor) and the table rows represent the items (=description or sample data). Importing data from such a "matrix" into Diversity Descriptions with the table oriented import wizard usually requires a lot of manual adaptions. Therefore the specialized "Matrix Wizard" was designed to import the most important descriptor and description data in a single import step.

As usual you should create a new project and install a descriptor tree to collect the dedicated descriptors. Then choose **Data -> Import -> Import wizard -> Matrix wizard ...** from the menu. As know from the import wizard, a window to create or select a import session will be shown.



Import using the Matrix Wizard

After selecting or creating an import session a window as shown below will open that will lead you through the import of the data.



Target: Description

File:

Encoding: ANSI

Language / Country: US

Header lines: 0 Start line: 0 End line: 0

Schema:

ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

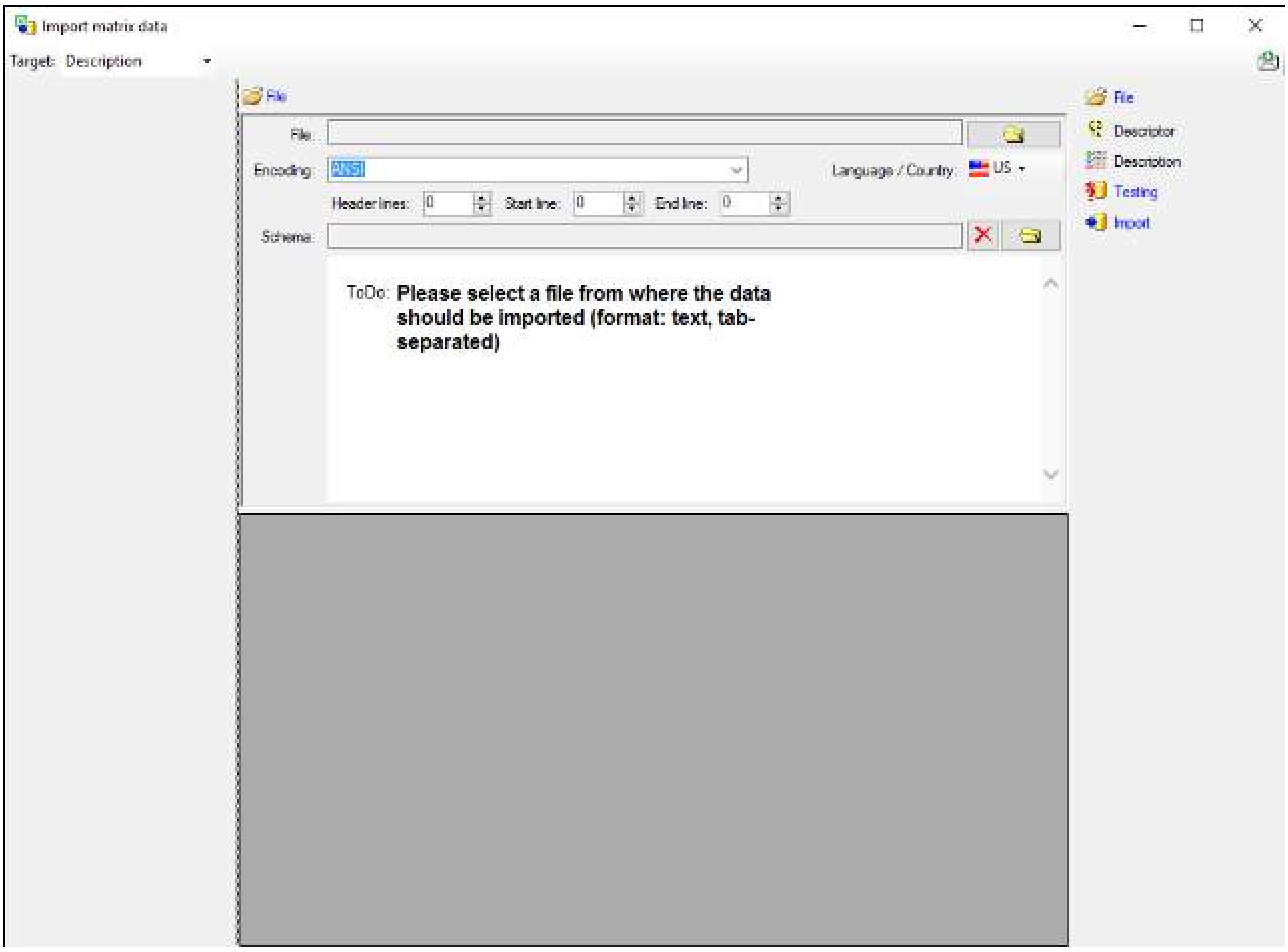
With the selection box **Target:** you may select which data shall be imported:

- Select **Description** to import summary data
- Select **Sampling event** to import sample data

Remark: Example files and XML schemas to import summary or sample data using the matrix wizard may be downloaded from the Diversity Descriptions example file repository.

Matrix import wizard for description data

After selecting **Target: Description** a window as shown below will be displayed. The window is separated in three areas. On the left side you see the descriptor settings for the actual file column (presently not visible). On the right side you see the list of available import steps. In the middle part the details of the selected import steps are shown.



Target: Description

Encoding: ANSI

Language / Country: US

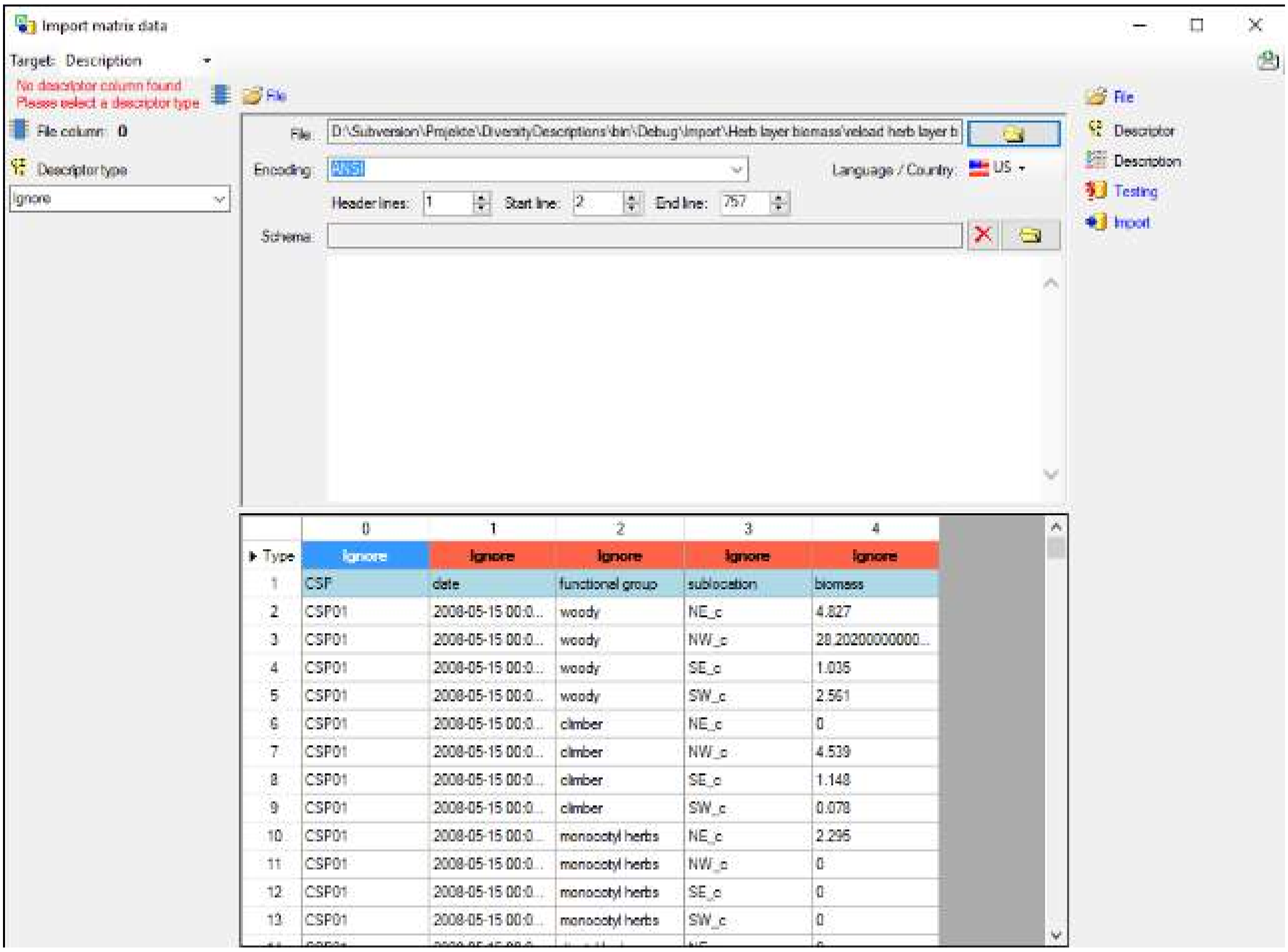
Header lines: 0 Start line: 0 End line: 0

Schema:

ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

Choosing the File

As a first step, choose the File from where the data should be imported. The currently supported format is tab-separated text. Then choose the **Encoding** of the file, e.g. Unicode. The **Header lines** specifies the number of header lines, usually at least the first line which typically contains the descriptor names (see image below). The **Start line** and **End line** will automatically be set according to your data. You may change these to restrict the data lines, i.e. the descriptions/items that shall be imported. The not imported parts in the file are indicated with a gray background. If your data contains e.g. date information or floating point values where notations differ between countries (e.g. 3.14 - 3,13), choose the **Language / Country** to ensure a correct interpretation of your data. Finally you can select a prepared **Schema** (see sections Testing and Import below) for the import.



Target: Description

No descriptor column found
Please select a descriptor type

File column: 0

Descriptor type: Ignore

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Herb layer biomass\reload herb layer b

Encoding: ANSI

Language / Country: US

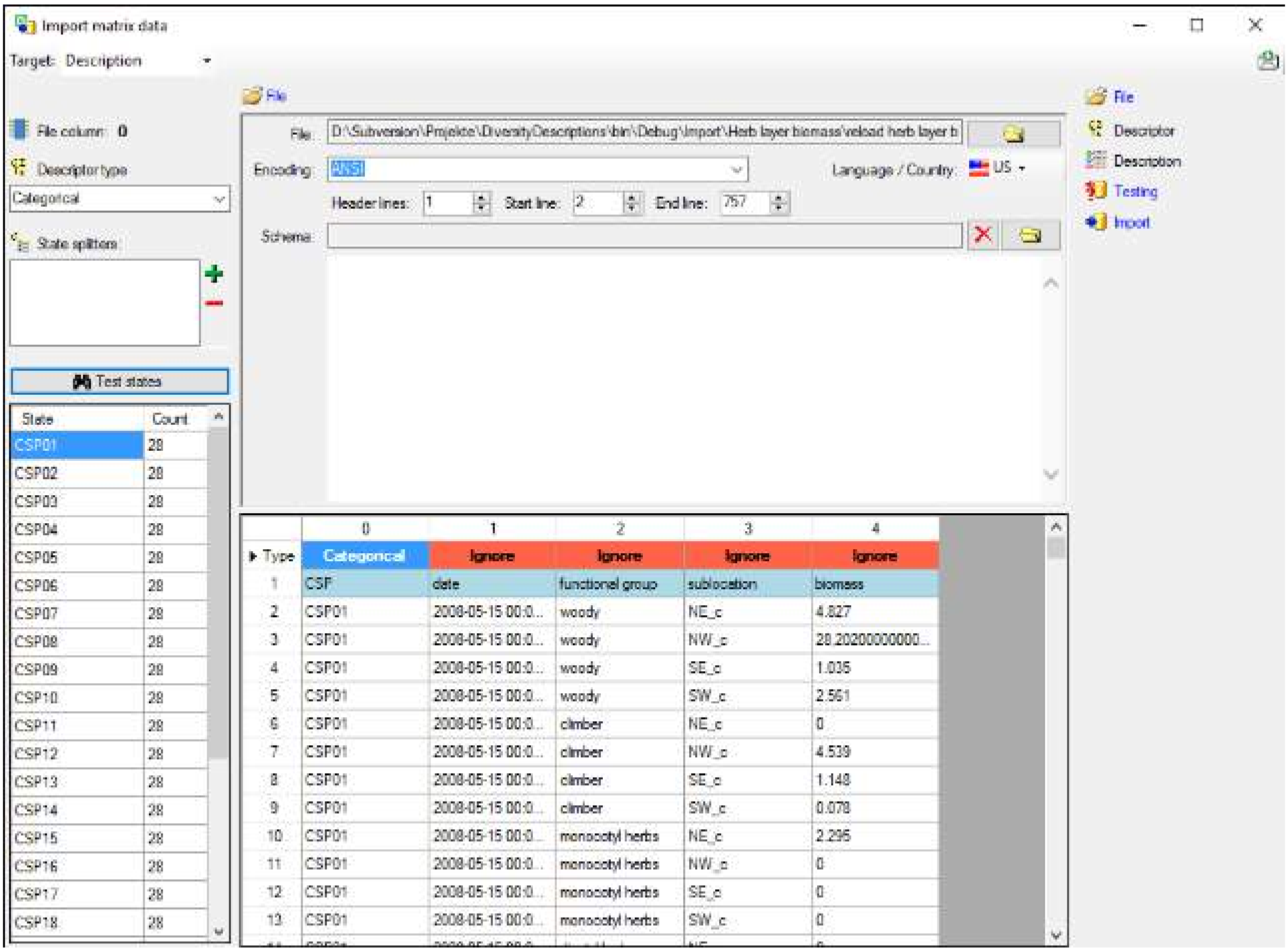
Header lines: 1 Start line: 2 End line: 757

Schema:

	0	1	2	3	4
Type	Ignore	Ignore	Ignore	Ignore	Ignore
1	CSF	date	functional group	sublocation	biomass
2	CSP01	2008-05-15 00:0...	woody	NE_c	4.827
3	CSP01	2008-05-15 00:0...	woody	NW_c	28.20200000000...
4	CSP01	2008-05-15 00:0...	woody	SE_c	1.035
5	CSP01	2008-05-15 00:0...	woody	SW_c	2.561
6	CSP01	2008-05-15 00:0...	climber	NE_c	0
7	CSP01	2008-05-15 00:0...	climber	NW_c	4.539
8	CSP01	2008-05-15 00:0...	climber	SE_c	1.148
9	CSP01	2008-05-15 00:0...	climber	SW_c	0.078
10	CSP01	2008-05-15 00:0...	monocotyl herbs	NE_c	2.295
11	CSP01	2008-05-15 00:0...	monocotyl herbs	NW_c	0
12	CSP01	2008-05-15 00:0...	monocotyl herbs	SE_c	0
13	CSP01	2008-05-15 00:0...	monocotyl herbs	SW_c	0

Choosing the descriptor types

In the first line of the file section the descriptor type of the file columns are displayed. The value **Ignore** indicates that the column shall not be imported. To adjust the descriptor type, select a cell in the file column and chose a **Descriptor type** in the left section of the panel (see image below). Available descriptor types are Categorical, Quantitative, Text and Sequence.



Target: Description

File column: 0

Descriptor type: Categorical

State splitters:

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Herb layer biomass\veload herb layer b

Encoding: ANSI

Language / Country: US

Header lines: 1 Start line: 2 End line: 757

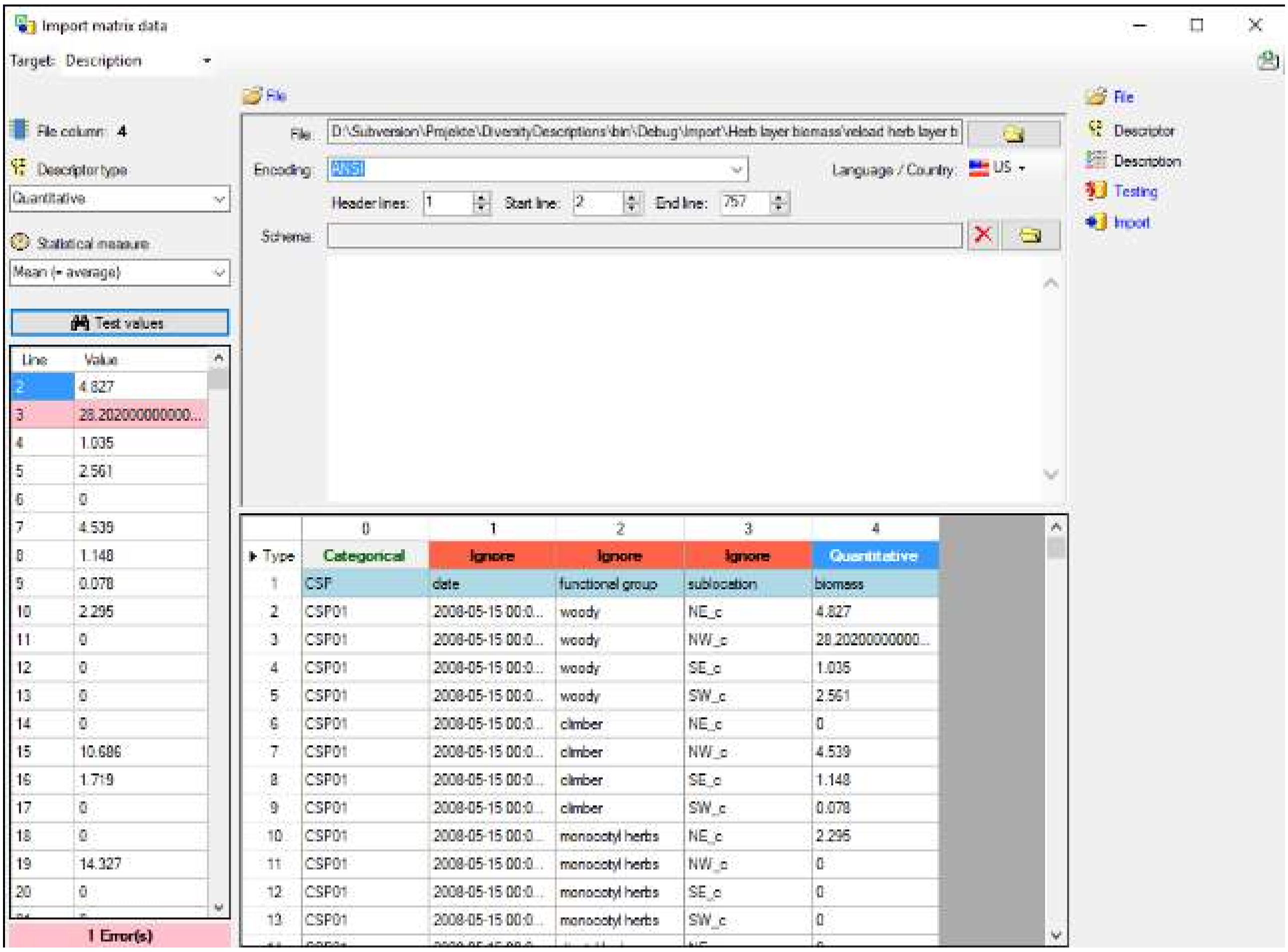
Schema:

State	Count
CSP01	28
CSP02	28
CSP03	28
CSP04	28
CSP05	28
CSP06	28
CSP07	28
CSP08	28
CSP09	28
CSP10	28
CSP11	28
CSP12	28
CSP13	28
CSP14	28
CSP15	28
CSP16	28
CSP17	28
CSP18	28

	0	1	2	3	4
Type	Categorical	Ignore	Ignore	Ignore	Ignore
1	CSF	date	functional group	sublocation	biomass
2	CSP01	2008-05-15 00:0...	woody	NE_c	4.827
3	CSP01	2008-05-15 00:0...	woody	NW_c	28.20200000000...
4	CSP01	2008-05-15 00:0...	woody	SE_c	1.035
5	CSP01	2008-05-15 00:0...	woody	SW_c	2.561
6	CSP01	2008-05-15 00:0...	climber	NE_c	0
7	CSP01	2008-05-15 00:0...	climber	NW_c	4.539
8	CSP01	2008-05-15 00:0...	climber	SE_c	1.148
9	CSP01	2008-05-15 00:0...	climber	SW_c	0.078
10	CSP01	2008-05-15 00:0...	monocotyl herbs	NE_c	2.295
11	CSP01	2008-05-15 00:0...	monocotyl herbs	NW_c	0
12	CSP01	2008-05-15 00:0...	monocotyl herbs	SE_c	0
13	CSP01	2008-05-15 00:0...	monocotyl herbs	SW_c	0

For categorical descriptors you may specify **State splitters**, if one item has more than one categorical state. To add a splitter click on the button, to remove it use the button. By clicking the **Test states** button you get a list of categorical states found in the file between start line and end line and the number of occurrences (field Count, see image above). With this function you may test the effect of the state splitters.

For quantitative descriptors you have to specify the **Statistical measure** that shall be used for the imported values. By clicking the **Test values** button you get a list of values in the file between start line and the line number in the file (see image above).



Target: Description

File column: 4

Descriptor type: Quantitative

Statistical measure: Mean (= average)

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Herb layer biomass\reload herb layer b

Encoding: ANSI

Language / Country: US

Header lines: 1 Start line: 2 End line: 757

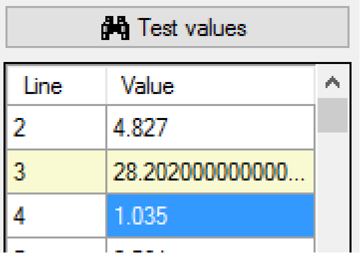
Schema:

Line	Value
2	4.827
3	28.202000000000...
4	1.035
5	2.561
6	0
7	4.539
8	1.148
9	0.078
10	2.295
11	0
12	0
13	0
14	0
15	10.686
16	1.719
17	0
18	0
19	14.327
20	0

1 Error(s)

	0	1	2	3	4
Type	Categorical	Ignore	Ignore	Ignore	Quantitative
1	CSF	date	functional group	sublocation	biomass
2	CSP01	2008-05-15 00:0...	woody	NE_c	4.827
3	CSP01	2008-05-15 00:0...	woody	NW_c	28.20200000000...
4	CSP01	2008-05-15 00:0...	woody	SE_c	1.035
5	CSP01	2008-05-15 00:0...	woody	SW_c	2.561
6	CSP01	2008-05-15 00:0...	climber	NE_c	0
7	CSP01	2008-05-15 00:0...	climber	NW_c	4.539
8	CSP01	2008-05-15 00:0...	climber	SE_c	1.148
9	CSP01	2008-05-15 00:0...	climber	SW_c	0.078
10	CSP01	2008-05-15 00:0...	monocotyl herbs	NE_c	2.295
11	CSP01	2008-05-15 00:0...	monocotyl herbs	NW_c	0
12	CSP01	2008-05-15 00:0...	monocotyl herbs	SE_c	0
13	CSP01	2008-05-15 00:0...	monocotyl herbs	SW_c	0

If a value cannot be interpreted as a number, it is marked with a light red background colour. You may edit the erroneous values in the test result panel (see below).



Line	Value
2	4.827
3	28.202000000000...
4	1.035

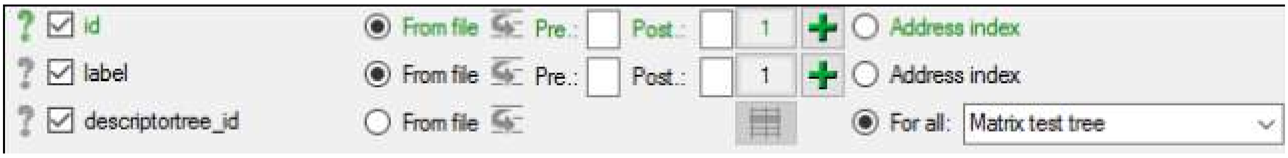
For text and sequence descriptors no additional adjustments are possible. As long as no descriptor columns have been defined, a reminder is visible on top of the left section:

- Please select a descriptor type = At least for one file column a descriptor type is needed.

In our example column 1 (date) will be adjusted as text descriptor and columns 2 (functional group) and 3 (sublocation) as categorical descriptors.

Table data

To set the source for the data columns, select the step of a table listed underneath the File step. Be aware that for the **Descriptor** table not the file columns will be selected but the file rows in the header lines. In the image below you see an example of the descriptor data columns, where the values for id and label are taken from the first line in the file. Additionally the descriptors will be assigned to the descriptor tree "Descriptor tree for matrix".



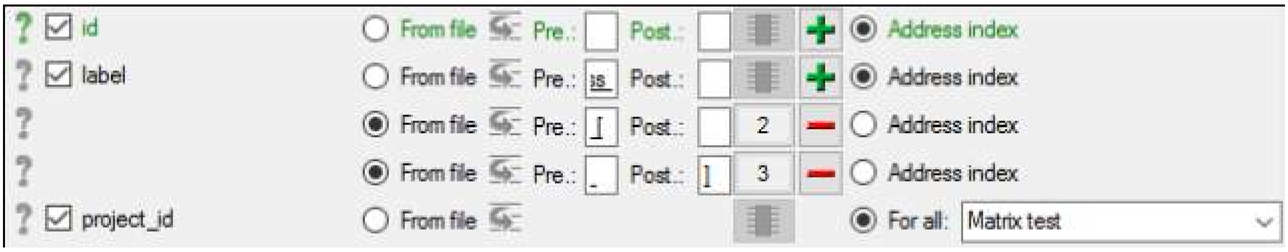
? ☑ id ● From file Pre.: Post.: 1 ○ Address index

? ☑ label ● From file Pre.: Post.: 1 ○ Address index

? ☑ descriptortree_id ○ From file ● For all: Matrix test tree

Remark: Although descriptortree_id is a numeric value in the database, the externally visible descriptor tree name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

The option **Address index** allows the selection of the column number (for descriptor) rsp. the line number (for description) as value. See below an example for the **Description** table data columns. For id the line number has been selected to get an unambigious address value. The label has been composed of the line number, three data columns and some fixed text parts. Finally all description data are assigned to the project "Matrix text".



? ☑ id ○ From file Pre.: Post.: ● Address index

? ☑ label ○ From file Pre.: ss Post.: ● Address index

? ● From file Pre.: [Post.: 2 ○ Address index

? ● From file Pre.: _ Post.:] 3 ○ Address index

? ☑ project_id ○ From file ● For all: Matrix test

Remark: Although project_id is a numeric value in the database, the externally visible project name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

A reminder in the header line will show you what actions are still needed to import the data into the table:

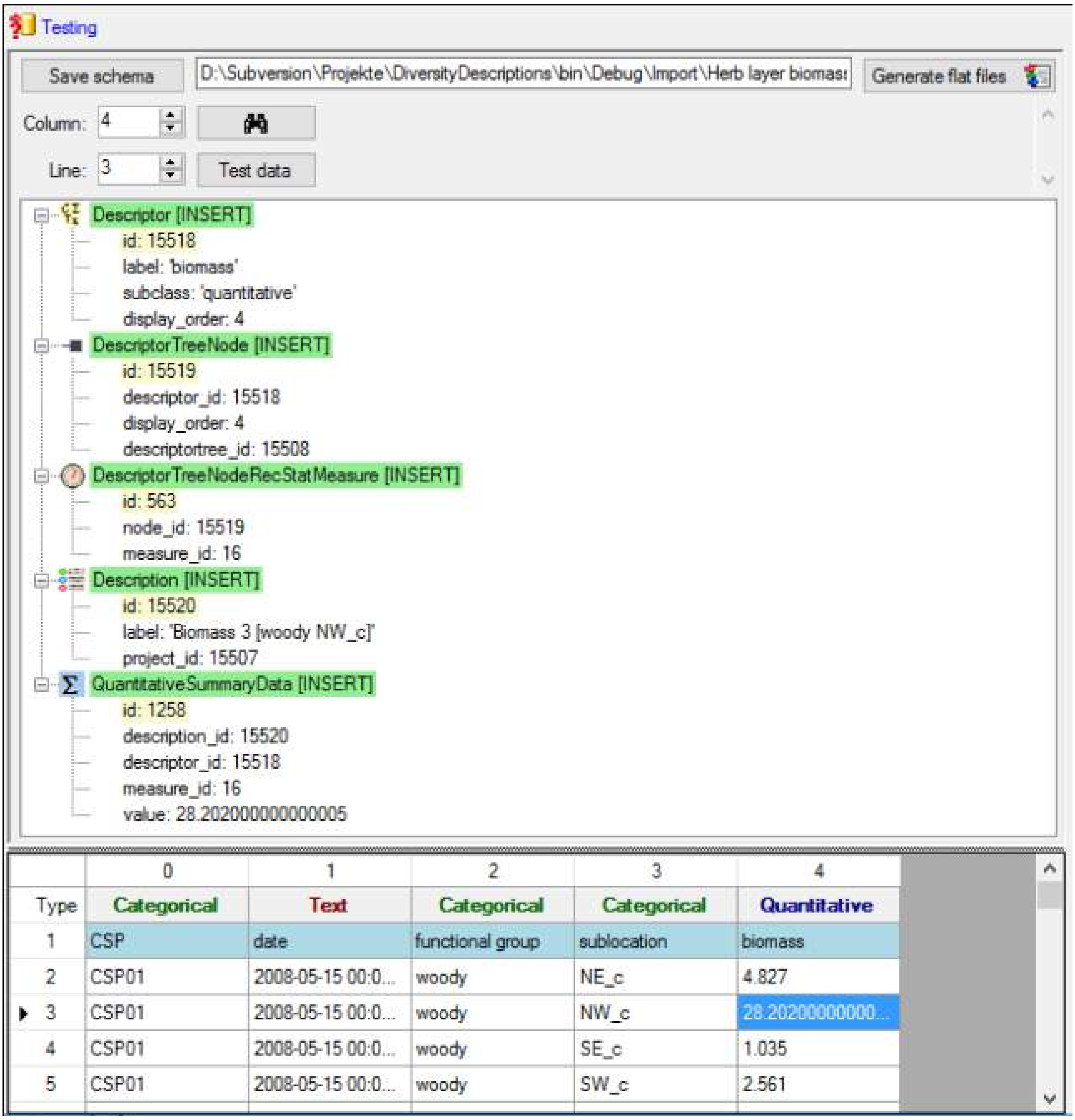
- Please select at least one decisive column ? = If data will be imported depends on the content of decisive colums, so at least one must be selected.
- Please select the position in the file = The position in the file must be given if the data for a column should be taken from the file.
- From file or For all ◉ = For every you have to decide whether the data are taken from the file or a value is entered for all
- Please select a value from the list ▼ = You have to select a value from the provided list

The handling of the columns is almost the same as described in the chapter columns of the table oriented import wizard.

Testing

To test if all requirements for the import are met use the Testing step. You can navigate to a certain data cell by using the **Column:** and **Line:** controls. As an alternative select the data cell ent click on button **.** Finally click on the **Test data** button. If there are still unmet requirements, these will be listed in a window as shown below. In the window below you can see the following test actions:

1. Insert of a quantitative descriptor "biomass"
2. Insert of a descriptor tree node (assignemnt to tree "Matrix test tree")
3. Insert of a recommended statistical measure (measure "Mean") for the descriptor tree node
4. Insert of description "Biomass 3 [CSP01 woody NW_c]" for project "Matrix test"
5. Insert of a statistical measure for "Mean" with value 28.2020000...



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Herb layer biomass

Column: 4

Line: 3

Descriptor [INSERT]
- id: 15518
- label: 'biomass'
- subclass: 'quantitative'
- display_order: 4

DescriptorTreeNode [INSERT]
- id: 15519
- descriptor_id: 15518
- display_order: 4
- descriptortree_id: 15508

DescriptorTreeNodeRecStatMeasure [INSERT]
- id: 563
- node_id: 15519
- measure_id: 16

Description [INSERT]
- id: 15520
- label: 'Biomass 3 [woody NW_c]'
- project_id: 15507

QuantitativeSummaryData [INSERT]
- id: 1258
- description_id: 15520
- descriptor_id: 15518
- measure_id: 16
- value: 28.202000000000005

	0	1	2	3	4
Type	Categorical	Text	Categorical	Categorical	Quantitative
1	CSP	date	functional group	sublocation	biomass
2	CSP01	2008-05-15 00:0...	woody	NE_c	4.827
▸ 3	CSP01	2008-05-15 00:0...	woody	NW_c	28.20200000000...
4	CSP01	2008-05-15 00:0...	woody	SE_c	1.035
5	CSP01	2008-05-15 00:0...	woody	SW_c	2.561

You may save the schema file by a click on button **Save schema**. If you click on button **Generate flat files** according to your adjustments data and matching schema files for the table oriented import wizards will be generated. This option may be used, if you want to import additional data, e.g. a descriptor's measurement unit, that are not supported by the matrix wizard. Since all mapping relevant data are stored in the selected import session, you may import the basic descriptor and description data using the matrix wizard and append additional data with the table oriented import wizards. In this case the generated flat data and schema files might be useful to have a defined starting point.

Import

With the last step you can finally start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).

Schedule for matrix import of tab-separated text files into DiversityDescriptions

Target within DiversityDescriptions: **Description**

Schedule version:	**1**	Database version:	**03.00.17**
Lines:	**2 - 757**	Header lines:	**1**
Encoding:	**ANSI**	Language:	**US**

Tables **Descriptor** (Descriptor) Merge handling: **Merge** **Column in table**	**?**	**Copy**	**Pre**	**Post**	**Feps**
id	**?**				
label					
descriptortree_id					

Description (Description)
Merge handling: **Merge**

Column in table	**?**	**Copy**	**Pre**	**Post**	**File pos.**	**Value**	**Source**
id	**?**						Index
label			Biomass				Index
+			[		0		File
+					2		File
+				]	3		File
project_id						Matrix test	Interface

Descriptor columns

File pos.	**Descriptor type**	**Additional data**
0	Categorical	**Splitters**
1	Text	
2	Categorical	**Splitters**
3	Categorical	**Splitters**

4	Quantitative	**Statistical measure** Mean (= average)	

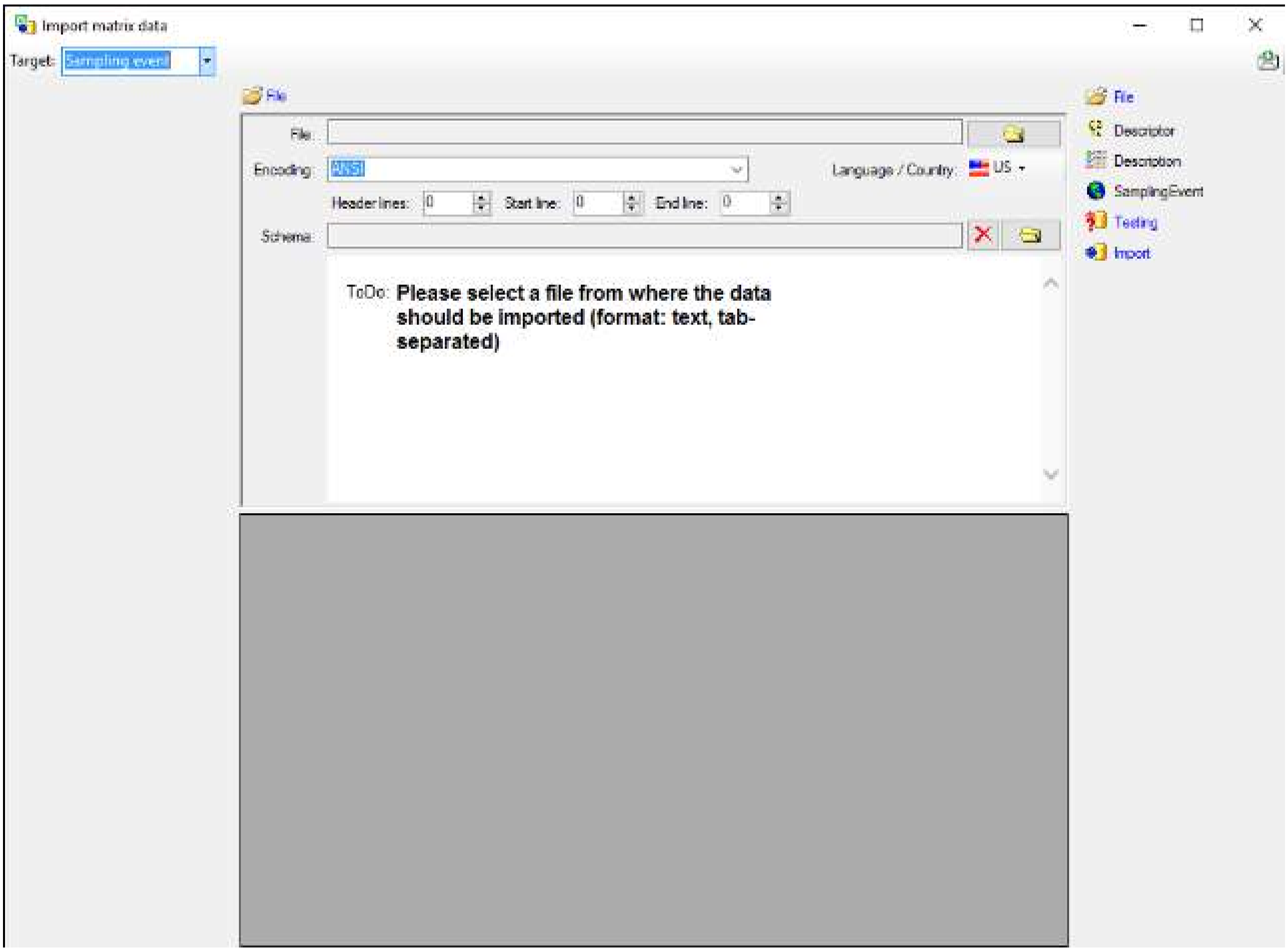
File cells that could not be imported will be marked with a red background while imported lines are marked green. If you want to save lines that produce errors during the import in a separate file, use the Save failed lines option. The protocol of the import will contain all settings acording to the used schema and an overview containing the number of inserted, updated, unchanged and failed lines (see below).

Protocol

Responsible:	**Link**	(DB-User: Workshop)
Date:	**Donnerstag, 20. April 2017, 15:53:24**	
Server:	**training.diversityworkbench.de**	
Database:	**DiversityDescriptions_Workshop**	
Descriptor columns total:	5	
Descriptors imported:	5	
Import lines total:	756	
Descriptions imported:	756	
Cells imported:	3780	

Matrix import wizard for sample data

After selecting **Target: Sampling event** a window as shown below will be displayed. The window is separated in 3 areas. On the left side you see the descriptor settings for the actual file column (presently not visible). On the right side you see the list of available import steps. In the middle part the details of the selected import steps are shown.



Target: Sampling event

Encoding: ANSI

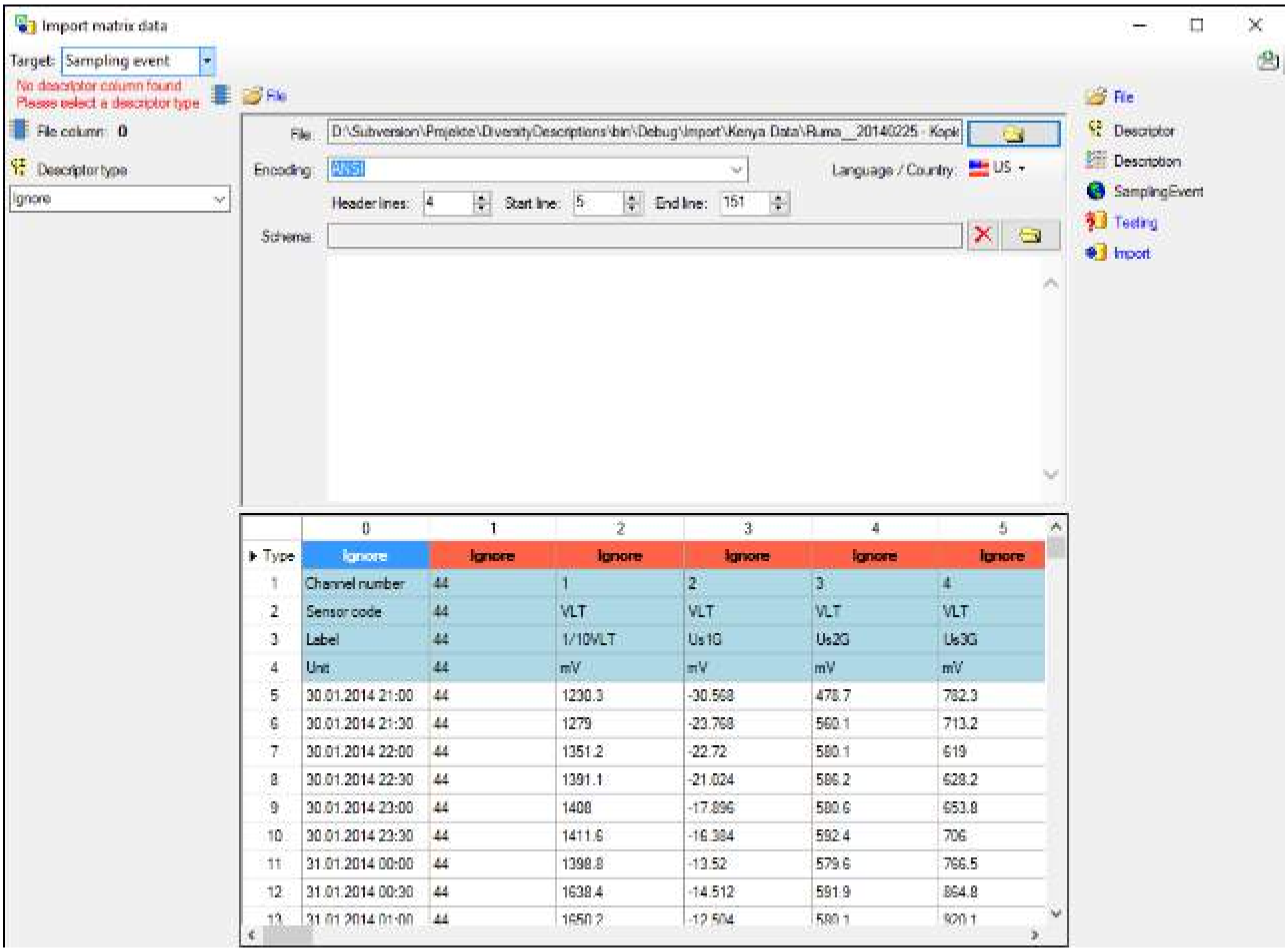
Language / Country: US

Header lines: 0 Start line: 0 End line: 0

ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

Choosing the File

As a first step, choose the File from where the data should be imported. The currently supported format is tab-separated text. Then choose the **Encoding** of the file, e.g. Unicode. The **Header lines** specifies the number of header lines, usually at least the first line which typically contains the descriptor names (see image below). The **Start line** and **End line** will automatically be set according to your data. You may change these to restrict the data lines, i.e. the descriptions/items that shall be imported. The not imported parts in the file are indicated with a gray background. If your data contains e.g. date information or floating point values where notations differ between countries (e.g. 3.14 - 3,13), choose the **Language / Country** to ensure a correct interpretation of your data. Finally you can select a prepared **Schema** (see sections Testing and Import below) for the import.



Target: Sampling event

No descriptor column found
Please select a descriptor type

File column: 0

Descriptor type: Ignore

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Kenya Data\Ruma__20140225 - Kopk

Encoding: ANSI

Language / Country: US

Header lines: 4 Start line: 5 End line: 151

Schema:

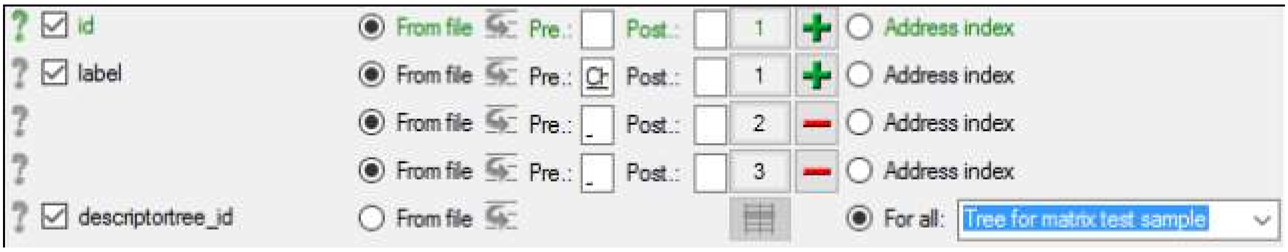
	0	1	2	3	4	5
Type	Ignore	Ignore	Ignore	Ignore	Ignore	Ignore
1	Channel number	44	1	2	3	4
2	Sensor code	44	VLT	VLT	VLT	VLT
3	Label	44	1/10VLT	Us1G	Us2G	Us3G
4	Unit	44	mV	mV	mV	mV
5	30.01.2014 21:00	44	1230.3	-30.568	478.7	782.3
6	30.01.2014 21:30	44	1279	-23.768	560.1	713.2
7	30.01.2014 22:00	44	1351.2	-22.72	580.1	619
8	30.01.2014 22:30	44	1391.1	-21.024	586.2	628.2
9	30.01.2014 23:00	44	1408	-17.896	580.6	653.8
10	30.01.2014 23:30	44	1411.6	-16.384	592.4	706
11	31.01.2014 00:00	44	1398.8	-13.52	579.6	766.5
12	31.01.2014 00:30	44	1638.4	-14.512	591.9	864.8
13	31.01.2014 01:00	44	1650.2	-12.504	580.1	920.1

Choosing the descriptor types

Choosing of the descriptor types is done in exactly the same way as described in section Matrix wizard for description data.

Table data

To set the source for the data columns, select the step of a table listed underneath the File step. Be aware that for the **Descriptor** table not the file columns will be selected but the file rows in the header lines. In the image below you see an example of the descriptor data columns, where the values for id and label are taken from the first line in the file. Additionally the descriptors will be assigned to the descriptor tree "Descriptor tree for matrix".



? ☑ id ● From file Pre.: Post.: 1 ○ Address index

? ☑ label ● From file Pre.: Ch Post.: 1 ○ Address index

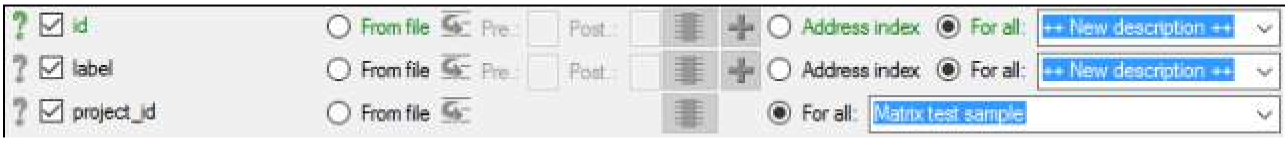
? ● From file Pre.: _ Post.: 2 ○ Address index

? ● From file Pre.: _ Post.: 3 ○ Address index

? ☑ descriptortree_id ○ From file ● For all: Tree for matrix test sample

Remark: Although descriptortree_id is a numeric value in the database, the externally visible descriptor tree name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

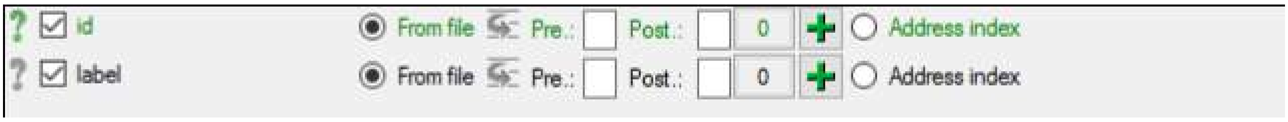
The option **Address index** allows the selection of the column number (for descriptor) rsp. the line number (for description or sampling event) as value. See below an example for the **Description** table data columns. For id and label the **For all:** alue "++ New description ++" was selected to create a single description entry where all sample data are attached. Finally the description is assigned to the project "Matrix text sample".



? ☑ id ○ From file Pre.: Post.: ○ Address index ● For all: ++ New description ++
? ☑ label ○ From file Pre.: Post.: ○ Address index ● For all: ++ New description ++
? ☑ project_id ○ From file ● For all: Matrix test sample

Remark: Although project_id is a numeric value in the database, the externally visible project name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

Finally the source for the **Sampling event** table data columns must be selected. For id and label the file column 0 has been selected (see image below).



? ☑ id ● From file Pre.: Post.: 0 ○ Address index
? ☑ label ● From file Pre.: Post.: 0 ○ Address index

A reminder in the header line will show you what actions are still needed to import the data into the table:

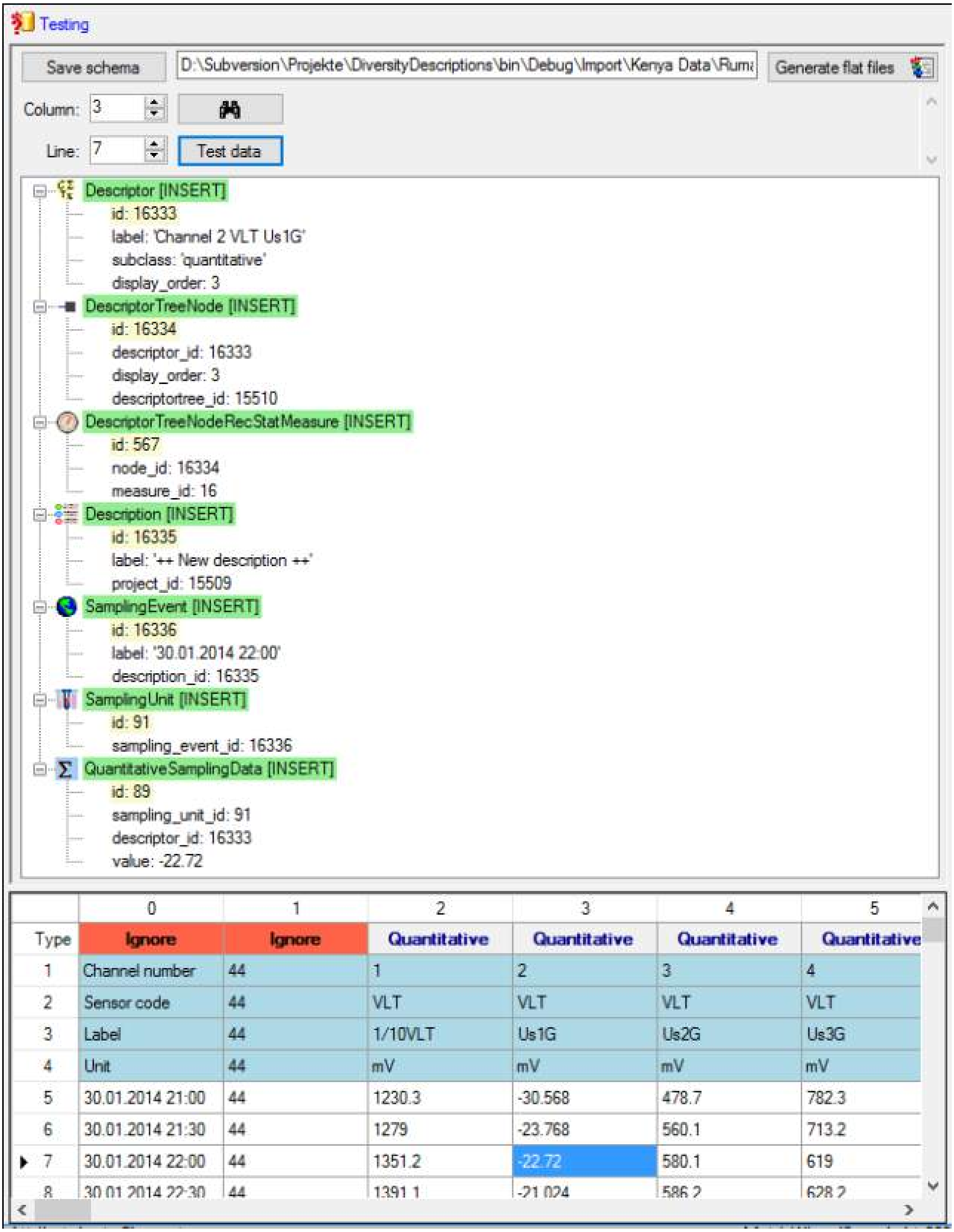
- Please select at least one decisive column ? = If data will be imported depends on the content of decisive colums, so at least one must be selected.
- Please select the position in the file = The position in the file must be given if the data for a column should be taken from the file.
- From file or For all ● = For every you have to decide whether the data are taken from the file or a value is entered for all
- Please select a value from the list ▼ = You have to select a value from the provided list

The handling of the columns is almost the same as described in the chapter columns of the table oriented import wizard.

Testing

To test if all requirements for the import are met use the Testing step. You can navigate to a certain data cell by using the **Column:** and **Line:** controls. As an alternative select the data cell ent click on button **.** Finally click on the **Test data** button. If there are still unmet requirements, these will be listed in a window as shown below. In the window below you can see the following test actions:

1. Insert of a quantitative descriptor "Channel 2 VLT Us1G"
2. Insert of a descriptor tree node (assignemnt to tree "Tree for matrix test sample")
3. Insert of a recommended statistical measure (measure "Mean") for the descriptor tree node
4. Insert of description "++ New description ++" for project "Matrix test sample"
5. Insert of a sampling event "30.01.2014 22:00" for description "++ New description ++"
6. Insert of a sampling unit with id 199 for sampling event "30.01.2014 22:00"
7. Insert of a quantitative value -22.72 to sampling unit 199



Descriptor [INSERT]
- id: 16333
- label: 'Channel 2 VLT Us1G'
- subclass: 'quantitative'
- display_order: 3

DescriptorTreeNode [INSERT]
- id: 16334
- descriptor_id: 16333
- display_order: 3
- descriptortree_id: 15510

DescriptorTreeNodeRecStatMeasure [INSERT]
- id: 567
- node_id: 16334
- measure_id: 16

Description [INSERT]
- id: 16335
- label: '++ New description ++'
- project_id: 15509

SamplingEvent [INSERT]
- id: 16336
- label: '30.01.2014 22:00'
- description_id: 16335

SamplingUnit [INSERT]
- id: 91
- sampling_event_id: 16336

QuantitativeSamplingData [INSERT]
- id: 89
- sampling_unit_id: 91
- descriptor_id: 16333
- value: -22.72

	0	1	2	3	4	5
Type	Ignore	Ignore	Quantitative	Quantitative	Quantitative	Quantitative
1	Channel number	44	1	2	3	4
2	Sensor code	44	VLT	VLT	VLT	VLT
3	Label	44	1/10VLT	Us1G	Us2G	Us3G
4	Unit	44	mV	mV	mV	mV
5	30.01.2014 21:00	44	1230.3	-30.568	478.7	782.3
6	30.01.2014 21:30	44	1279	-23.768	560.1	713.2
▸ 7	30.01.2014 22:00	44	1351.2	-22.72	580.1	619
8	30.01.2014 22:30	44	1391.1	-21.024	586.2	628.2

You may save the schema file by a click on button **Save schema**. If you click on button **Generate flat files** according to your adjustments data and matching schema files for the table oriented import wizards will be generated. This option may be used, if you want to import additional data, e.g. a descriptor's measurement unit, that are not supported by the matrix wizard. Since all mapping relevant data are stored in the selected import session, you may import the basic descriptor and description data using the matrix wizard and append additional data with the table oriented import wizards. In this case the generated flat data and schema files might be useful to have a defined starting point.

Import

With the last step you can finally start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).

Schedule for matrix import of tab-separated text files into DiversityDescriptions

Target within DiversityDescriptions: **SamplingEvent**

Schedule version:	**1**	Database version:	**03.00.17**
Lines:	**5 - 151**	Header lines:	**4**
Encoding:	**ANSI**	Language:	**US**

Tables **Descriptor** (Descriptor) Merge handling: **Merge** **Column in table**	**?**	**Copy**	**Pre**	**Post**	**F e p s**
id	**?**				
label			Channel		
+					
+					
descriptortree_id					

Description (Description)

Merge handling: **Merge**

Column in table	**?**	**Copy**	**Pre**	**Post**	**File pos.**	**Value**	**Source**
id	**?**					++ New description ++	Interface
label						++ New description ++	Interface
project_id						Matrix test sample	Interface

SamplingEvent (SamplingEvent)

Merge handling: **Merge**

Column in table	?	Copy	Pre	Post	File pos.	Value	Source
id	?				0		File
label					0		File

Descriptor columns

File pos.	Descriptor type	Additional data
2	Quantitative	**Statistical measure** Mean (= average)
3	Quantitative	**Statistical measure** Mean (= average)
4	Quantitative	**Statistical measure** Mean (= average)
5	Quantitative	**Statistical measure** Mean (= average)
6	Quantitative	**Statistical measure** Mean (= average)
7	Quantitative	**Statistical measure** Mean (= average)
8	Quantitative	**Stati**

		stical measure Mean (= average)
9	Quantitative	**Statistical measure** Mean (= average)
10	Quantitative	**Statistical measure** Mean (= average)
11	Quantitative	**Statistical measure** Mean (= average)
12	Quantitative	**Statistical measure** Mean (= average)
13	Quantitative	**Statistical measure** Mean (= average)
14	Quantitative	**Statistical measure** Mean (= average)
15	Quantitative	**Statistical measure** Mean

		(= average)	
16	Quantitative	**Statistical measure** Mean (= average)	
17	Quantitative	**Statistical measure** Mean (= average)	
18	Quantitative	**Statistical measure** Mean (= average)	
19	Quantitative	**Statistical measure** Mean (= average)	
20	Quantitative	**Statistical measure** Mean (= average)	
21	Quantitative	**Statistical measure** Mean (= average)	
22	Quantitative	**Statistical measure** Mean (= average)	
23	Quantitative	**Stati**	

		stical measure Mean (= average)	
24	Quantitative	**Statistical measure** Mean (= average)	
25	Quantitative	**Statistical measure** Mean (= average)	
26	Quantitative	**Statistical measure** Mean (= average)	
27	Quantitative	**Statistical measure** Mean (= average)	
28	Quantitative	**Statistical measure** Mean (= average)	
29	Quantitative	**Statistical measure** Mean (= average)	
30	Quantitative	**Statistical measure** Mean	

		(= average)	
31	Quantitative	**Statistical measure** Mean (= average)	
32	Quantitative	**Statistical measure** Mean (= average)	
33	Quantitative	**Statistical measure** Mean (= average)	
34	Quantitative	**Statistical measure** Mean (= average)	
35	Quantitative	**Statistical measure** Mean (= average)	
36	Quantitative	**Statistical measure** Mean (= average)	
37	Quantitative	**Statistical measure** Mean (= average)	
38	Quantitative	**Stati**	

		stical measure Mean (= average)
39	Quantitative	**Statistical measure** Mean (= average)
40	Quantitative	**Statistical measure** Mean (= average)
41	Quantitative	**Statistical measure** Mean (= average)
42	Quantitative	**Statistical measure** Mean (= average)
43	Quantitative	**Statistical measure** Mean (= average)
44	Quantitative	**Statistical measure** Mean (= average)
45	Quantitative	**Statistical measure** Mean

		(= average)	

File cells that could not be imported will be marked with a red background while imported lines are marked green. If you want to save lines that produce errors during the import in a separate file, use the Save failed lines option. The protocol of the import will contain all settings acording to the used schema and an overview containing the number of inserted, updated, unchanged and failed lines (see below).

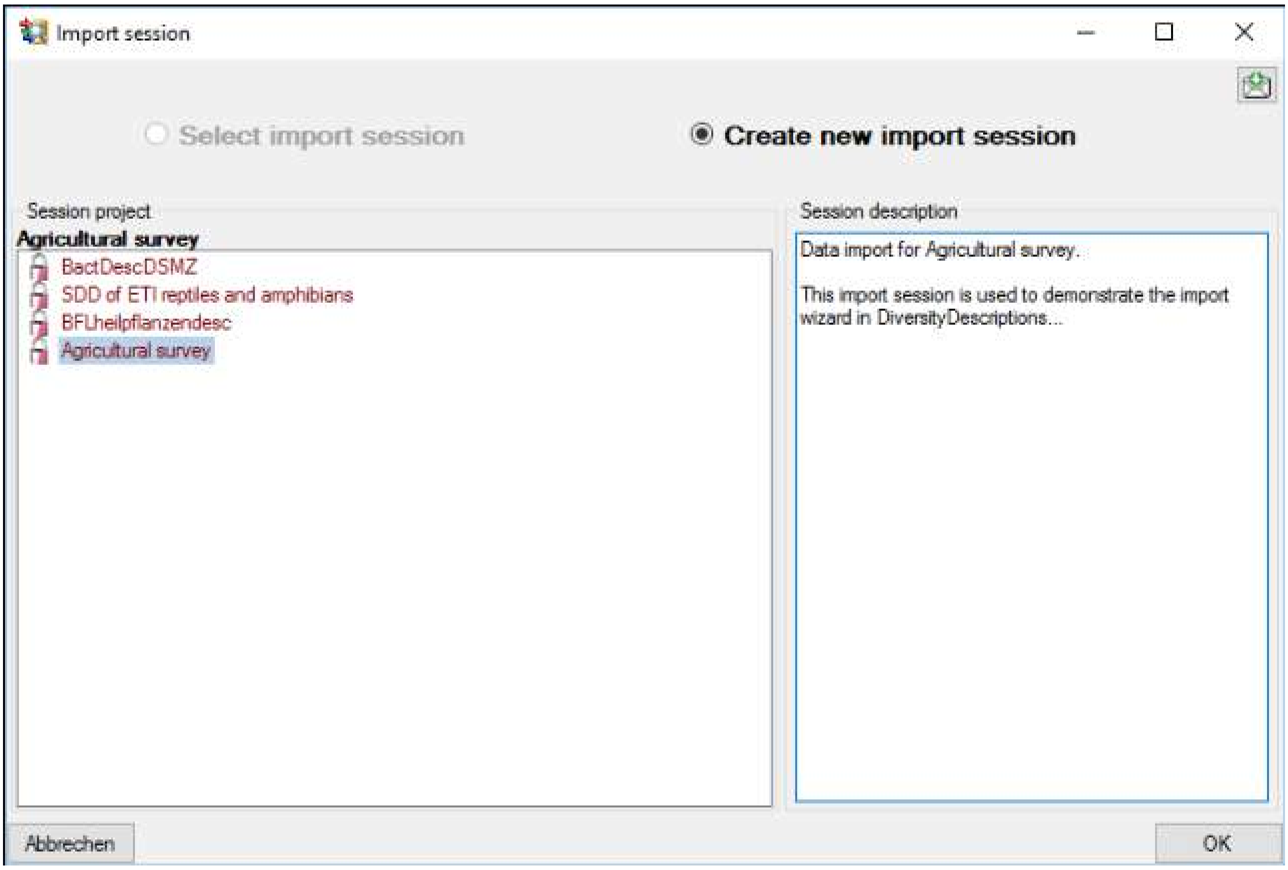
Protocol

Responsible:	**Link**	(DB-User: Workshop)
Date:	**Donnerstag, 20. April 2017, 16:17:42**	
Server:	**training.diversityworkbench.de**	
Database:	**DiversityDescriptions_Workshop**	
Descriptor columns total:	44	
Descriptors imported:	44	
Import lines total:	147	
Descriptions imported:	1	
Samples imported:	147	
Cells imported:	6348	
Cells failed:	120	

Import wizard for tab separated lists

With this import routines, you can import data from text files (as tab-separated lists) into the database. For a comprehensive real-life example that shows many features of the import wizard take a look at the import wizard tutorial.

Choose **Data -> Import -> Import wizard** and then the type of data that should be imported, e.g. **Import descriptors ...** from the menu. If you did not use the import wizard before, the following window is shown to create a new import session.



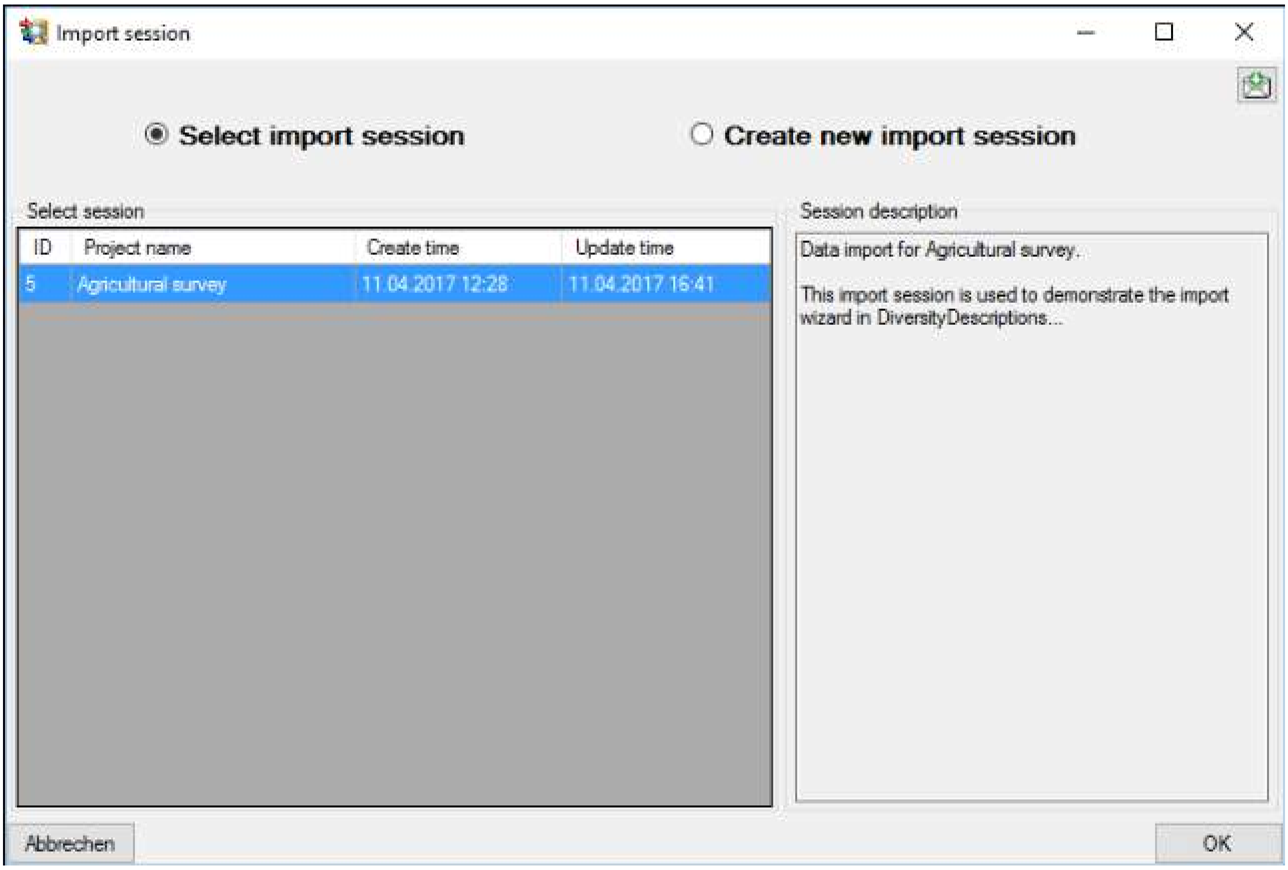
Agricultural survey

- BactDescDSMZ
- SDD of ETI reptiles and amphibians
- BFLheilpflanzendesc
- Agricultural survey

Data import for Agricultural survey.

This import session is used to demonstrate the import wizard in DiversityDescriptions...

In section **Session project** the projects with write access are listed for selection. In section **Session description** you should enter a detailled text description. If already an import session is present in the database, the window below will be shown where you may select the session. You may select one of the offered sessions or create a new one by selecting **Create new import session**.

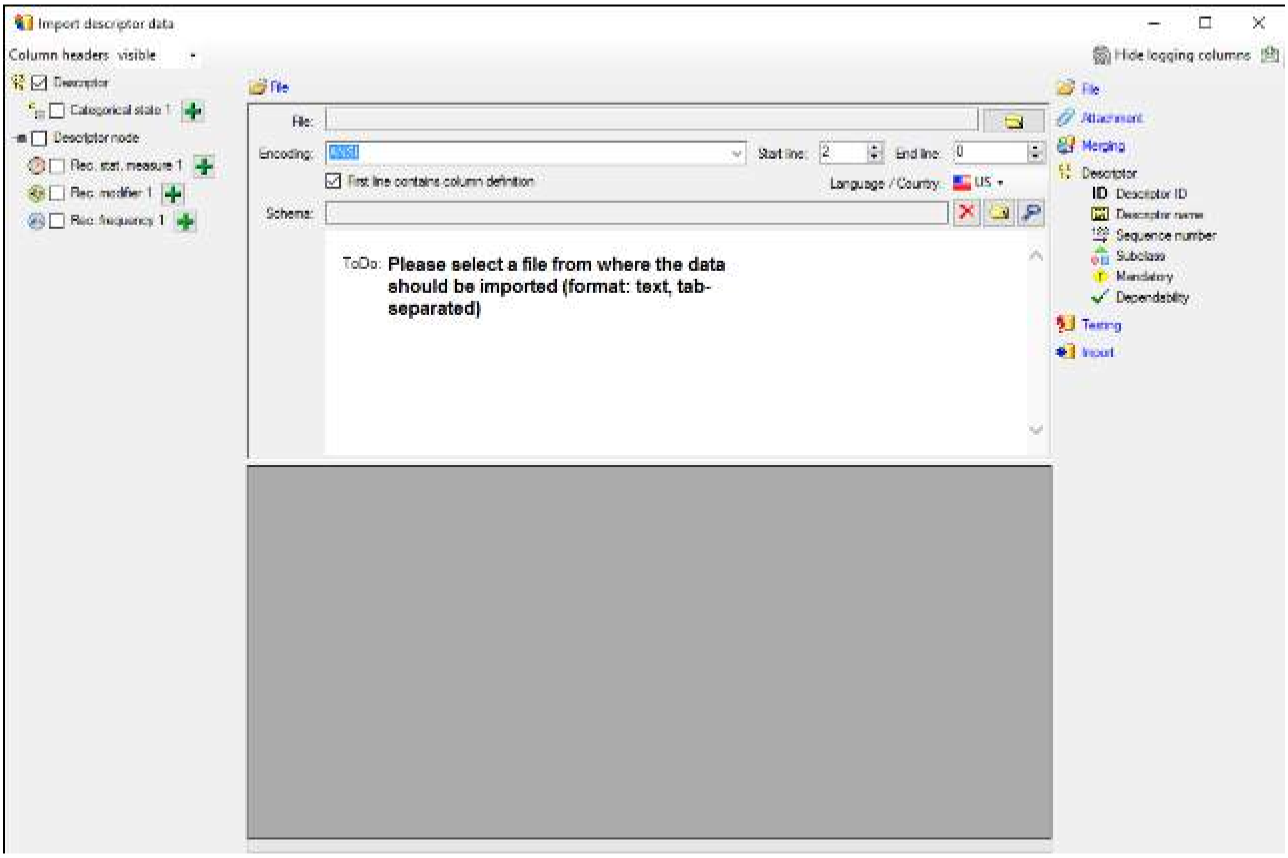


ID	Project name	Create time	Update time
5	Agricultural survey	11.04.2017 12:28	11.04.2017 16:41

Data import for Agricultural survey.

This import session is used to demonstrate the import wizard in DiversityDescriptions...

After selecting or creating an import session a window as shown below will open that will lead you through the import of the data. The window is separated in 3 areas. On the left side you see a list of possible data related import steps according to the type of data you choosed for the import. On the right side you see the list of currently selected import steps. In the middle part the details of the selected import steps are shown.



File:

Encoding: ANSI

Start line: 2

End line: 0

☑ First line contains column definition

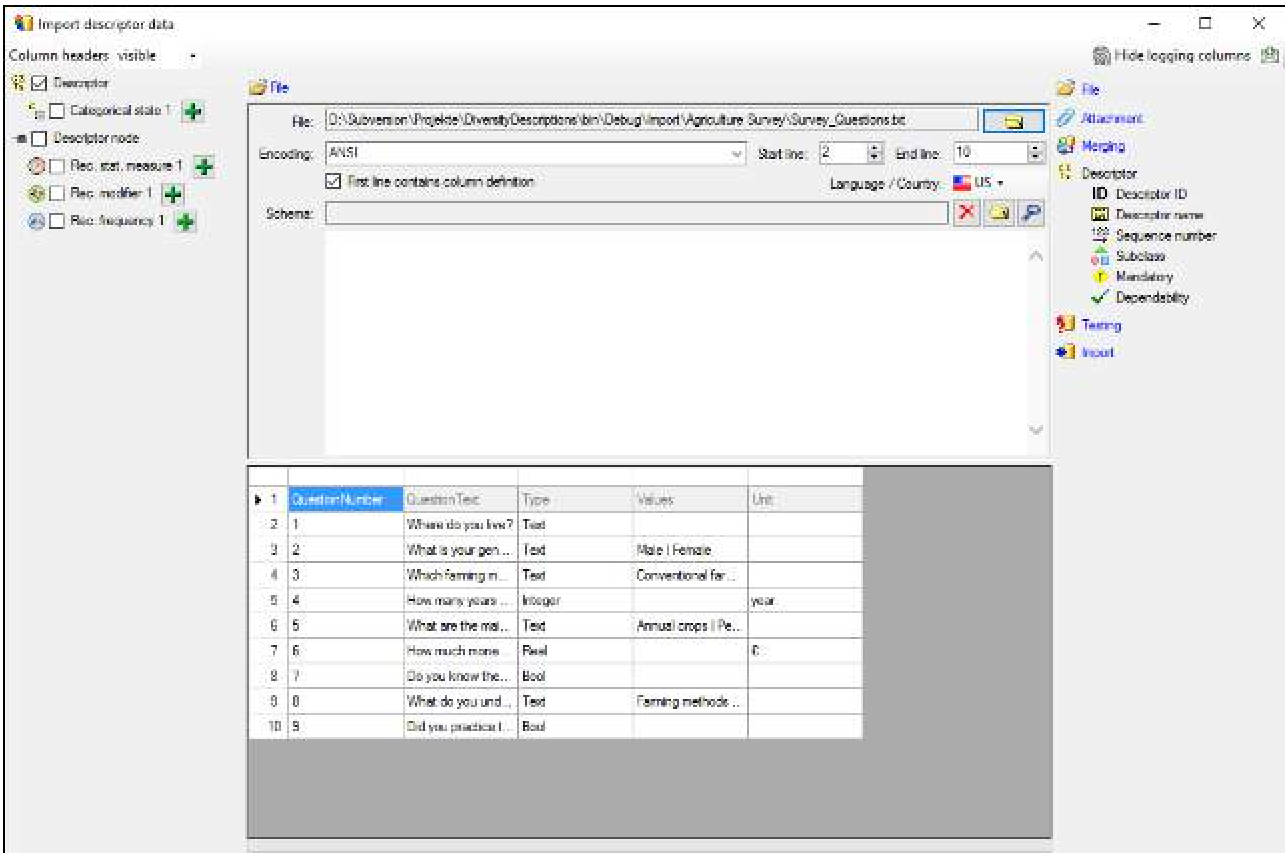
Language / Country: US

Schema:

ToDo: **Please select a file from where the data should be imported (format: text, tab-separated)**

Choosing the File

As a first step, choose the File from where the data should be imported. The currently supported format is tab-separated text. Then choose the **Encoding** of the file, e.g. Unicode. The **Start line** and **End line** will automatically be set according to your data. You may change these to restrict the data lines that should be imported. The not imported parts in the file are indicated as shown below with a gray background. If the ☑ **First line contains the column definition** this line will not be imported as well. If your data contains e.g. date information or floating point values, where notations differ between countries (e.g. 3.14 - 3,14), choose the **Language / Country** to ensure a correct interpretation of your data. Finally you can select a prepared **Schema** (see chapter Schema below) for the import.



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Questions.txt

Encoding: ANSI

Start line: 2

End line: 10

☑ First line contains column definition

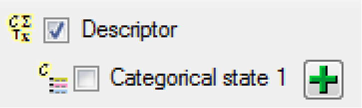
Language / Country: US

Schema:

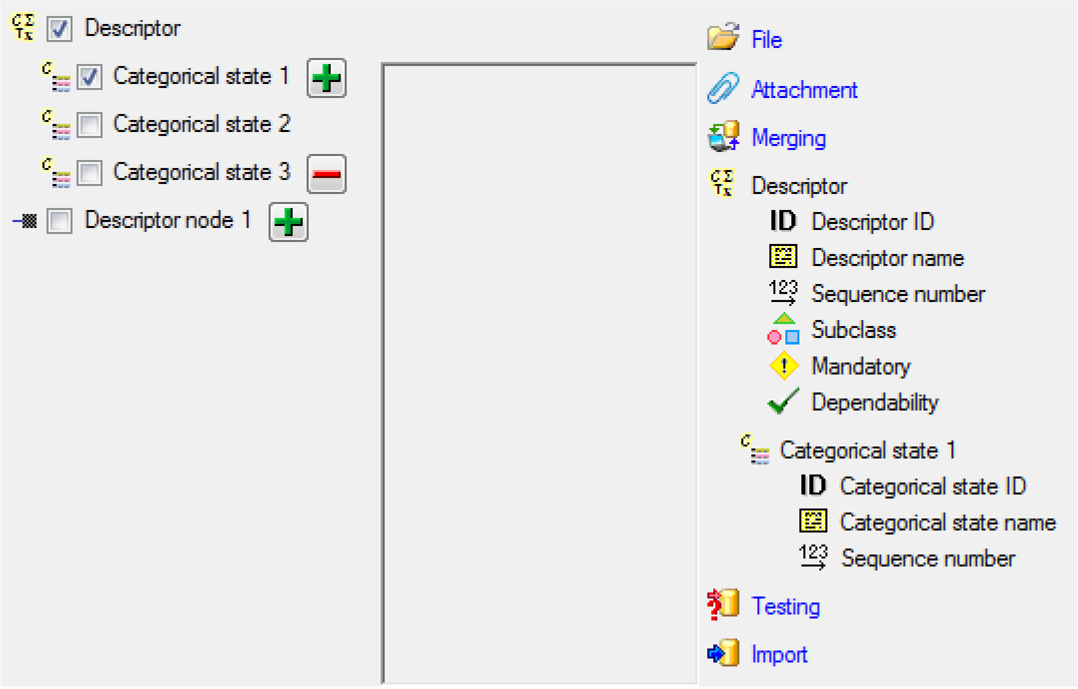
1	Question Number	Question Text	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

Choosing the data ranges

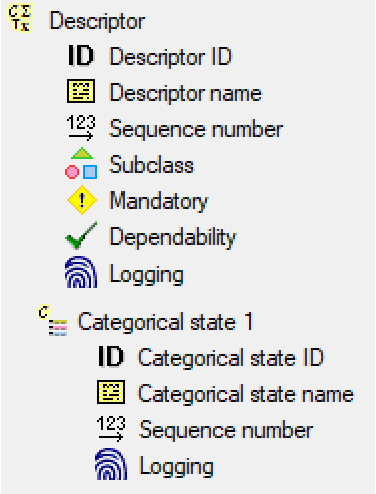
In the selection list on the left side of the window (see below) all possible import steps for the data are listed according to the type of data you want to import.



Certain tables can be imported in parallel. To add parallels click on the ➕button (see below). To remove parallels, use the ➖button. Only selected ranges will appear in the list of the steps on the right (see below).

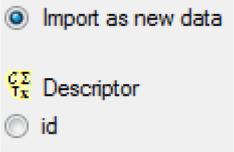


To import information of logging columns like who created and changed the data, click on button in the header line. This will include an additional substeps for every step containing the logging columns (see below). If you do not import these data, they will be automatically filled by default values like the current time and user.

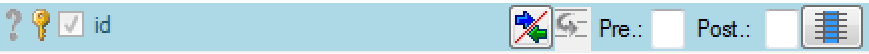


Attaching data

You can either import your data as new data or **Attach** them to data in the database. Select the import step **Attachment** from the list. All tables that are selected and contain columns at which you can attach data are listed (see below). Either choose the first option ● **Import as new data** or one of the columns the attachment columns offered like "id" in the table "Descriptor" in the example below.



If you select a column for attachment, this column will be marked with a blue backgroud (see below and chapter **Table data**).



Merging data

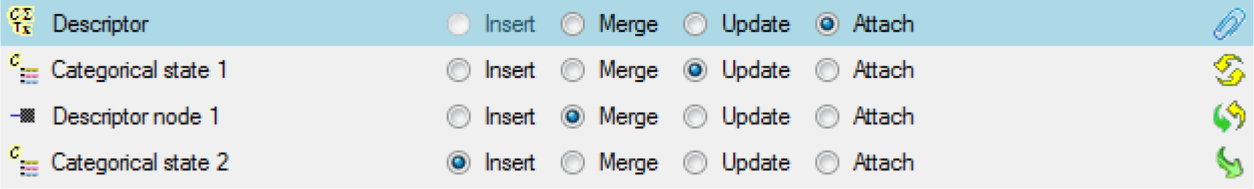
You can either import your data as new data or **Merge** them wih data in the database. Select the import step **Merge** from the list. For every table you can choose between **Insert**, **Merge**, **Update** and **Attach** (see below).

The **Insert** option will import the data from the file independent of existing data in the database.

The **Merge** option will compare the data from the file with those in the database according to the **Key columns** (see below). If no matching data are found in the database, the data from the file will be imported, otherwise the data will be updated..

The **Update** option will compare the data from the file with those in the database according to the **Key columns**. Only matching data found in the database will be updated.

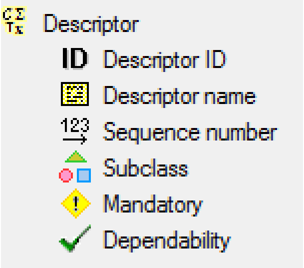
The **Attach** option will compare the data from the file with those in the database according to the **Key columns**. The found data will not be changed, but used as a reference data in depending tables.



Descriptor	○ Insert	○ Merge	○ Update	● Attach
Categorical state 1	○ Insert	○ Merge	● Update	○ Attach
Descriptor node 1	○ Insert	● Merge	○ Update	○ Attach
Categorical state 2	● Insert	○ Merge	○ Update	○ Attach

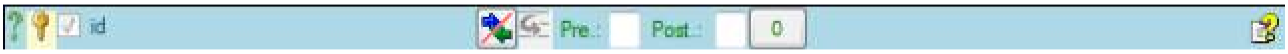
Table data

To set the source for the columns in the file, select the step of a table listed underneath the Merge step. Some columns may be grouped below the table name as shown for the **Descriptor** table.

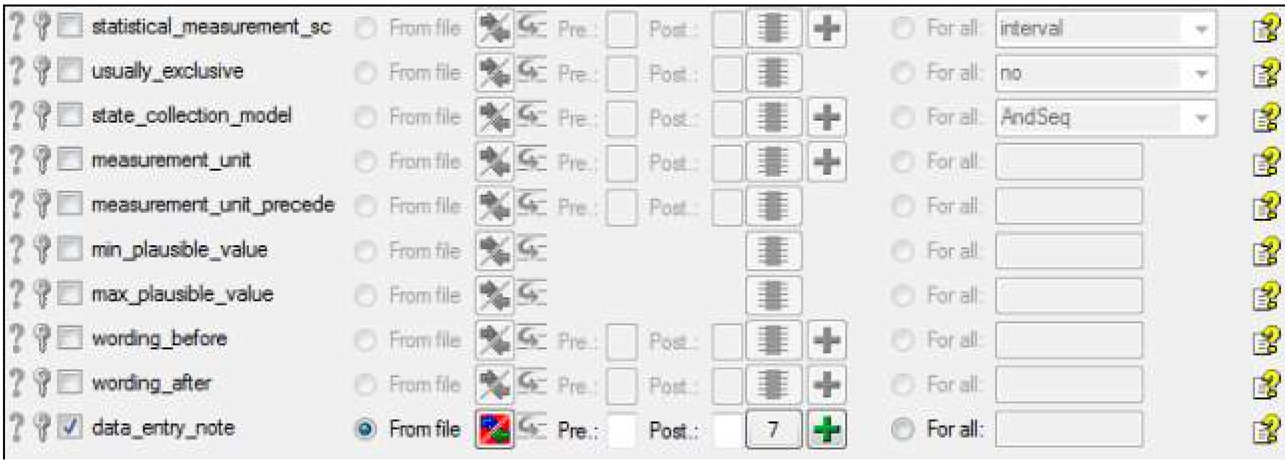


- Descriptor
  - Descriptor ID
  - Descriptor name
  - Sequence number
  - Subclass
  - Mandatory
  - Dependability

Click on one of the subordinated column groups and in the central part of the window the data columns avaialble for importing will be listed in the central part of the window. In the example shown below the column is used to attach the new data to data in the database.



All columns that have not been grouped beneath the table may be accessed by selecting the table ste itself. In the example shown below table **Descriptor** was selected to supply the "data_entry_note" column for import.



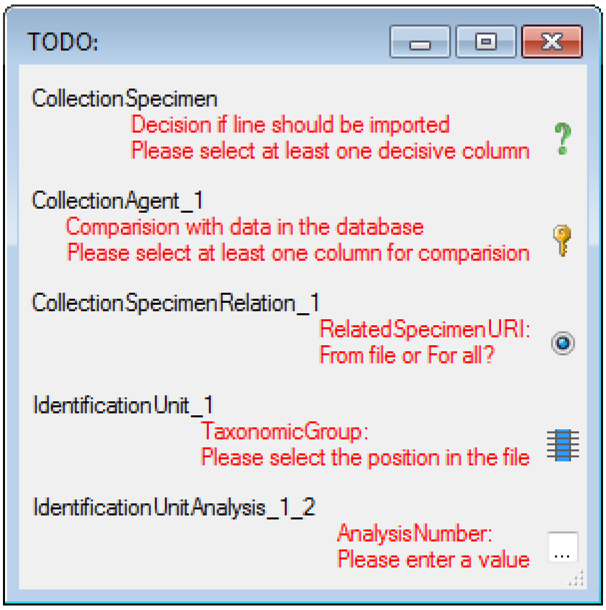
A reminder in the header line will show you what actions are still needed to import the data into the table:

- Please select at least one column ☑ = No column has been selected so far.
- Please select at least one decisive column = If data will be imported depends on the content of decisive colums, so at least one must be selected.
- Please select the position in the file = The position in the file must be given if the data for a column should be taken from the file.
- Please select at least one column for comparision = For all merge types other than insert columns for comparision with data in the database are needed.
- From file or For all ◉ = For every you have to decide whether the data are taken from the file or a value is entered for all
- Please select a value from the list ▼ = You have to select a value from the provided list
- Please enter a value ... = You have to enter a value used for all datasets

The handling of the columns in described in the chapter columns.

Testing

To test if all requirements for the import are met use the Testing step. You can use a certain line in the file for you test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window as shown below.



CollectionSpecimen
Decision if line should be imported
Please select at least one decisive column

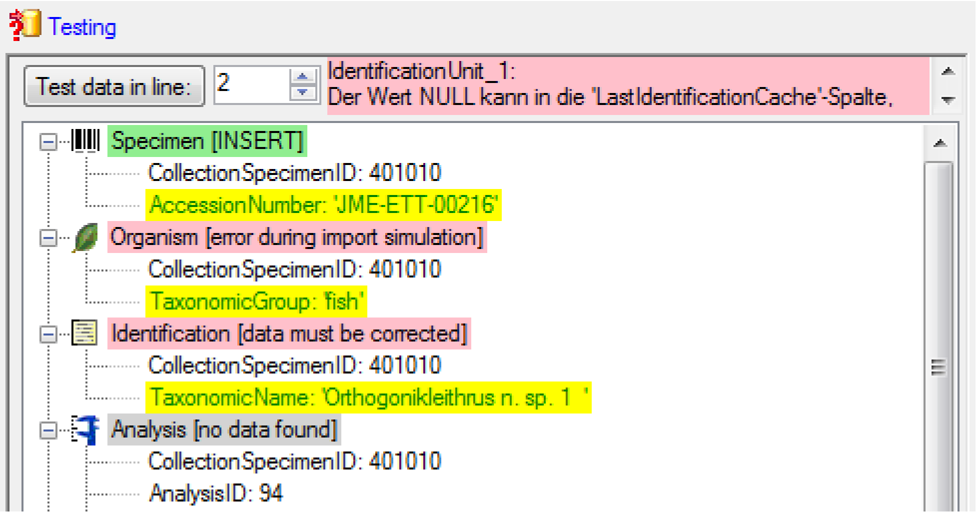
CollectionAgent_1
Comparision with data in the database
Please select at least one column for comparision

CollectionSpecimenRelation_1
RelatedSpecimenURI:
From file or For all?

IdentificationUnit_1
TaxonomicGroup:
Please select the position in the file

IdentificationUnitAnalysis_1_2
AnalysisNumber:
Please enter a value

If finally all requirements are met, the testing function will try to write the data into the database and display you any errors that occurred as shown below. All datasets marked with a red backgroud, produced some error.

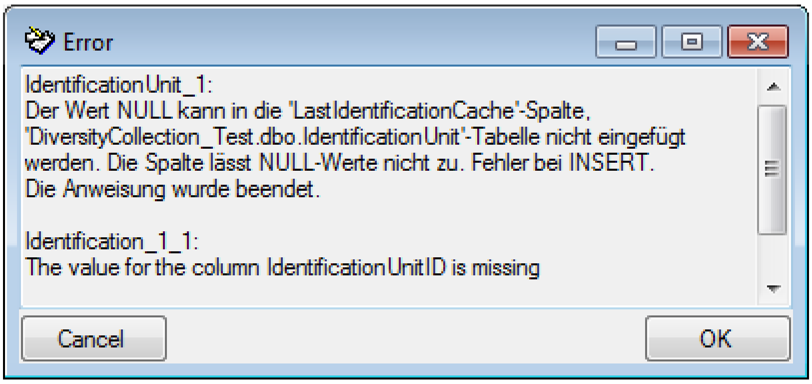


Test data in line: 2

IdentificationUnit_1:
Der Wert NULL kann in die 'LastIdentificationCache'-Spalte,

Specimen [INSERT]
CollectionSpecimenID: 401010
AccessionNumber: 'JME-ETT-00216'
Organism [error during import simulation]
CollectionSpecimenID: 401010
TaxonomicGroup: 'fish'
Identification [data must be corrected]
CollectionSpecimenID: 401010
TaxonomicName: 'Orthogonikleithrus n. sp. 1 '
Analysis [no data found]
CollectionSpecimenID: 401010
AnalysisID: 94

To see the list of all errors, double click in the error list window in the header line (see below).

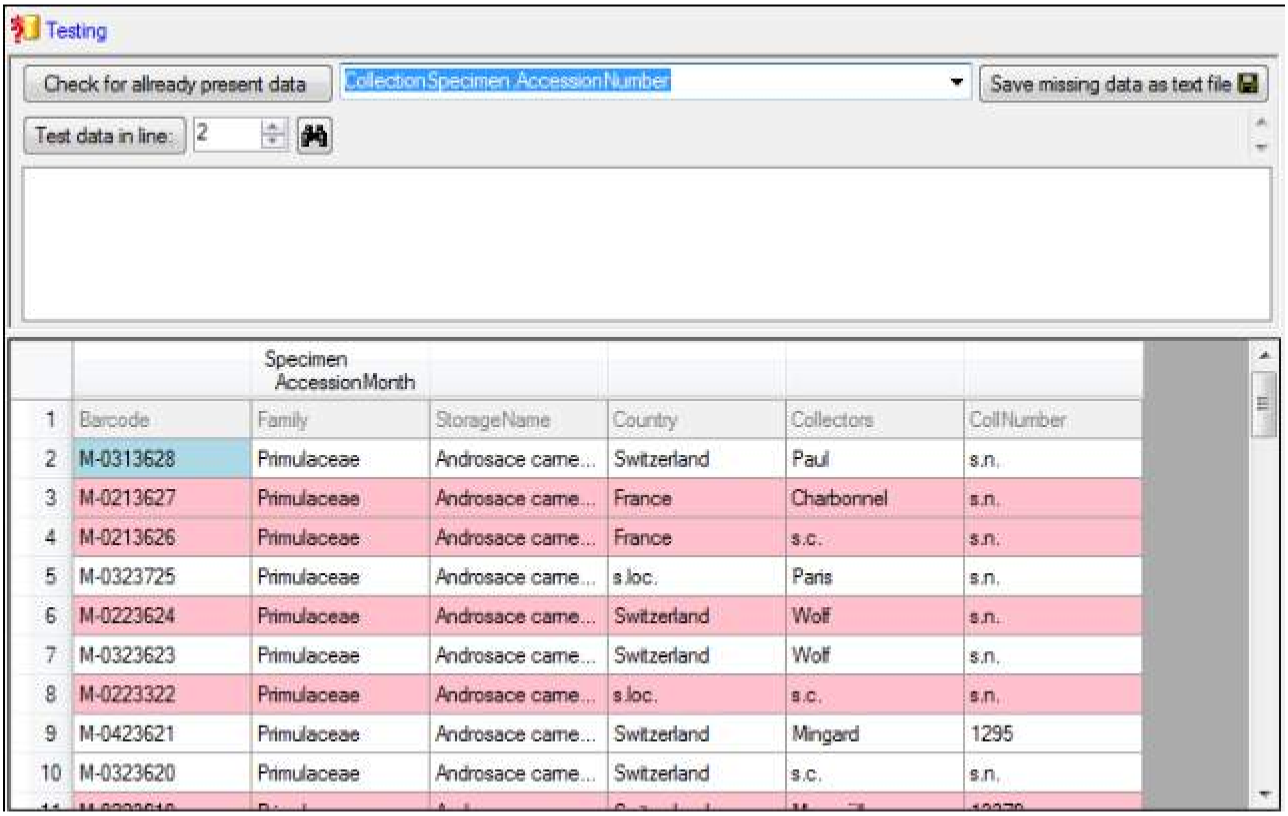


IdentificationUnit_1:
Der Wert NULL kann in die 'LastIdentificationCache'-Spalte, 'DiversityCollection_Test.dbo.IdentificationUnit'-Tabelle nicht eingefügt werden. Die Spalte lässt NULL-Werte nicht zu. Fehler bei INSERT.
Die Anweisung wurde beendet.

Identification_1_1:
The value for the column IdentificationUnitID is missing

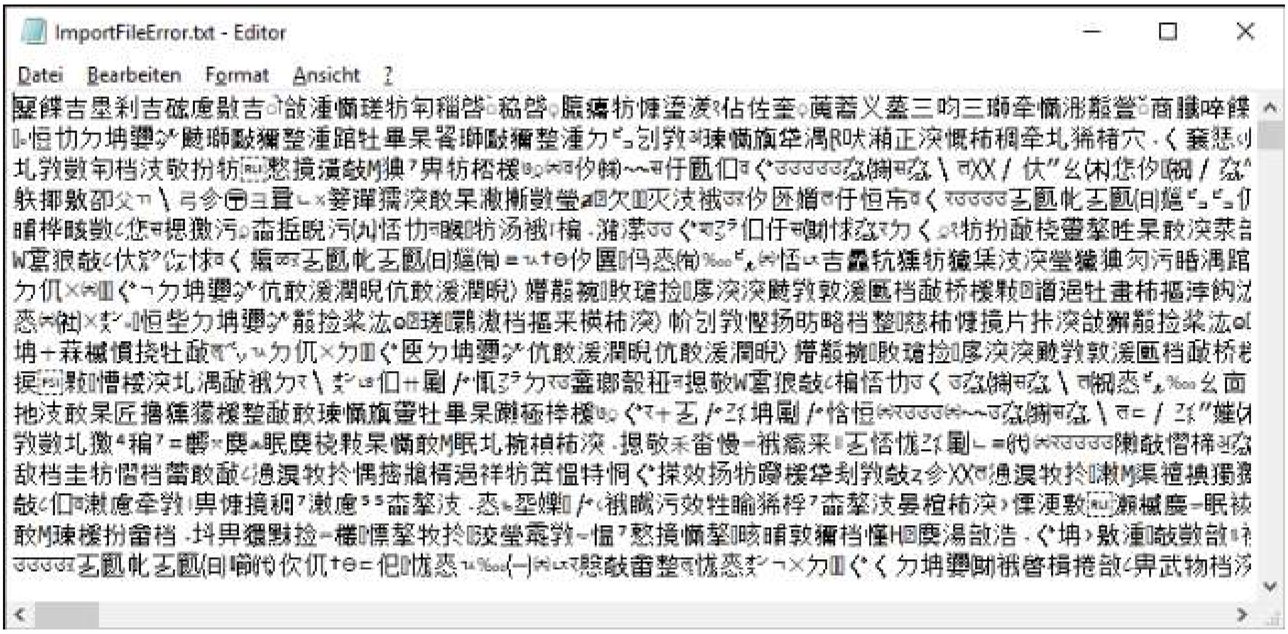
If finally no errors are left, your data are ready for import. The colors in the table nodes in the tree indicate the handling of the datasets: INSERT, MERGE, UPDATE, No difference. Attach, No data. The colors of the table colums indicate whether a colums is decisive , a key column or an attachment column.

If you suspect, that the import file contains data allready present in the database, you may test this an extract only the missing lines in a new file. Choose the attachment column (see chapter Attaching data) and click on the button **Check for allready present data**. The data allready present in the database will be marked red (see below). Click on the button **Save missing data a text file** to store the data not present in the database in a new file for the import.



	Specimen AccessionMonth					
1	Barcode	Family	StorageName	Country	Collectors	CollNumber
2	M-0313628	Primulaceae	Androsace came...	Switzerland	Paul	s.n.
3	M-0213627	Primulaceae	Androsace came...	France	Charbonnel	s.n.
4	M-0213626	Primulaceae	Androsace came...	France	s.c.	s.n.
5	M-0323725	Primulaceae	Androsace came...	s.loc.	Paris	s.n.
6	M-0223624	Primulaceae	Androsace came...	Switzerland	Wolf	s.n.
7	M-0323623	Primulaceae	Androsace came...	Switzerland	Wolf	s.n.
8	M-0223322	Primulaceae	Androsace came...	s.loc.	s.c.	s.n.
9	M-0423621	Primulaceae	Androsace came...	Switzerland	Mingard	1295
10	M-0323620	Primulaceae	Androsace came...	Switzerland	s.c.	s.n.

If you happen to get a file with a content as shown below, you may have seleted the wrong encoding or the encoding is incompatible. Please try to save the original file as UTF8 and select this encoding for the import.



Import

With the last step you can finally start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).

Schedule for import of tab-separated text files into DiversityCollection

Target within DiversityCollection: **Specimen**

Schedule version:	**1**	Database version:	**02.05.41**
Lines:	**2 - 3215**	First line contains column definition:	**?**
Encoding:	**Unicode**	Language:	**de**

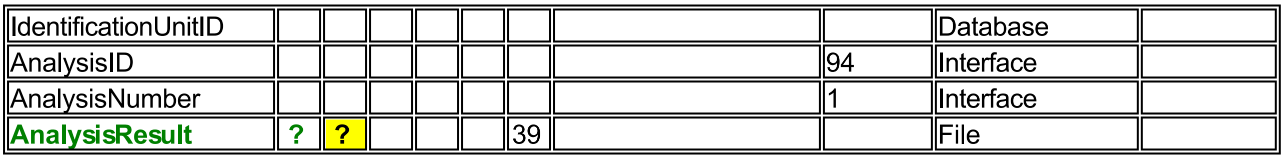
Tables **CollectionSpecimen** (CollectionSpecimen) Parent: CollectionEvent Merge handling: **Insert** **Column in table**	**?**	**Key**	**Copy**	**Pre**	**P s**
CollectionSpecimenID					
AccessionNumber	?	?			

IdentificationUnit_1 (IdentificationUnit)
Parent: CollectionSpecimen
Merge handling: **Merge**

Column in table	?	Key	Copy	Pre	Post	File pos.	Transformations	Value	Source	Table
CollectionSpecimenID									Database	
IdentificationUnitID									Database	
LastIdentificationCache		?				2			File	
+						3			File	
+						4			File	
+						5			File	
TaxonomicGroup	?							fish	Interface	

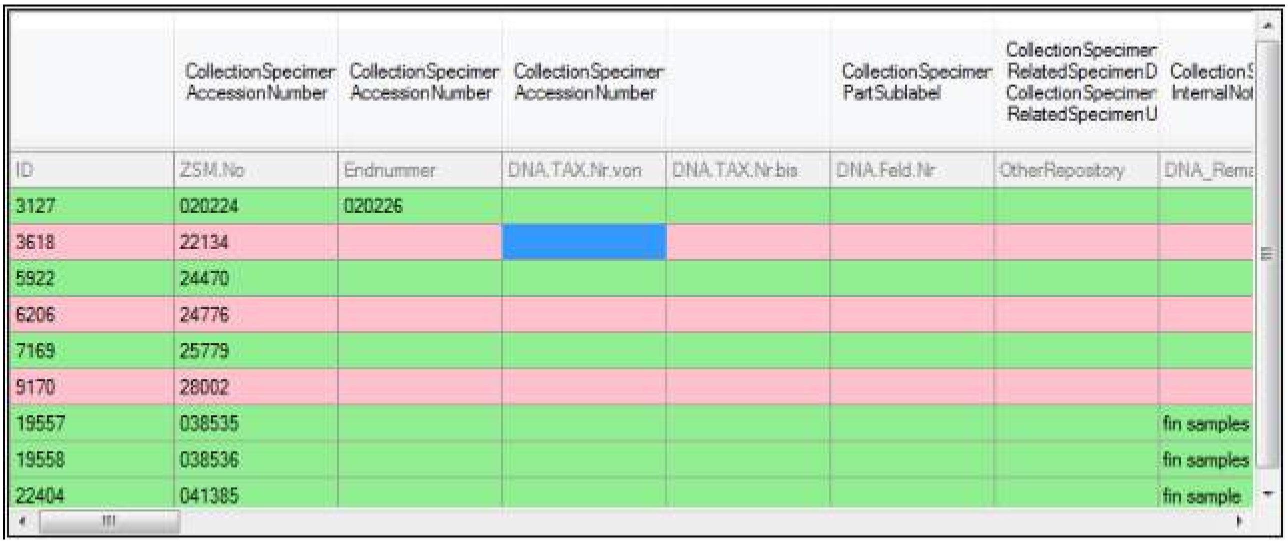
IdentificationUnitAnalysis_1_1 (IdentificationUnitAnalysis)
Parent: IdentificationUnit_1
Merge handling: **Update**

Column in table	?	Key	Copy	Pre	Post	File pos.	Transformations	Value	Source	Table
CollectionSpecimenID									Database	



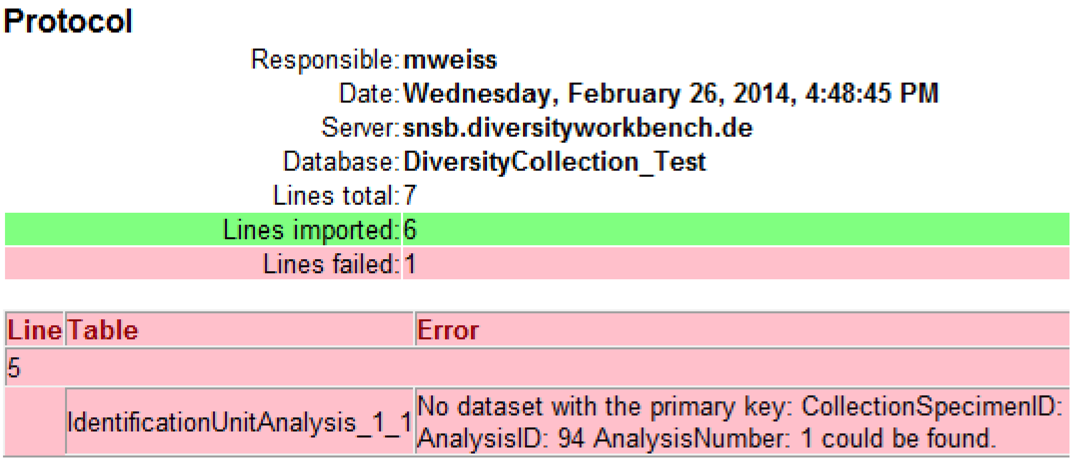
IdentificationUnitID									Database	
AnalysisID								94	Interface	
AnalysisNumber								1	Interface	
AnalysisResult	?	?				39			File	

Lines that could not be imported will be marked with a red background while imported lines are marked green (see below).



	CollectionSpecimer AccessionNumber	CollectionSpecimer AccessionNumber	CollectionSpecimer AccessionNumber		CollectionSpecimer PartSublabel	CollectionSpecimer RelatedSpecimenD CollectionSpecimer RelatedSpecimenU	Collection InternalNot
ID	ZSM.No	Endnummer	DNA.TAX.Nr.von	DNA.TAX.Nr.bis	DNA.Feld.Nr	OtherRepository	DNA_Rema
3127	020224	020226					
3618	22134						
5922	24470						
6206	24776						
7169	25779						
9170	28002						
19557	038535						fin samples
19558	038536						fin samples
22404	041385						fin sample

If you want to save lines that produce errors during the import in a separate file, use the **Save failed lines** option. The protocol of the import will contain all settings acording to the used schema and an overview containing the number of inserted, updated, unchanged and failed lines (see below).



Protocol

Responsible: **mweiss**
Date: **Wednesday, February 26, 2014, 4:48:45 PM**
Server: **snsb.diversityworkbench.de**
Database: **DiversityCollection_Test**
Lines total: 7
Lines imported: 6
Lines failed: 1

Line	Table	Error
5		
	IdentificationUnitAnalysis_1_1	No dataset with the primary key: CollectionSpecimenID: AnalysisID: 94 AnalysisNumber: 1 could be found.

Description

A description of the schema may be included in the schema itself or with a click on the button generated as a separate file. This file will be located in a separate directory Description to avoid confusion with import schemas. An example for a description file is shown below, containing common settings, the treatment of the file columns and interface settings as defined in the schema.

Schedule for import of tab-separated text files into DiversityCollection
Target within DiversityCollection: **Specimen**

Schedule version: **1**

Database version: **02.05.52**

Lines: **2 - 5**

First line contains column definition: **?**

Encoding: **Unicode**

Language: **de**

Description: Import Schema fuer Literaturdaten (Bayernflora) aus Dörr & Lippert mit MTB Daten und max. 4 Sammlern

---

File columns

Merge handling of table				**Co us**
Insert	Merge	Update	Attach	**De isi e**

Pos.	Name	Table	Column	Example	Transformed
0	ID				
		CollectionSpecimen.	**ExternalIdentifier**	1	
1	originalname				
		Identification_1_2.	**TaxonomicName**	Ophioglossum vulgatum	
2	nameautor				
		Identification_1_1.	TaxonomicName	Ophioglossum vulgatum L.	
3	taxnr				
		Identification_1_1.	**NameURI**	3949	
			Prefix:	http://tnt.diversityworkbench.de/TaxonNames_Plants/	
4	mtb				
		CollectionEventLocalisation_6.	**Location1**	8423	
5	qu				
		CollectionEventLocalisation_6.	**Location2**	2	
6	unschärfe				
		CollectionEventLocalisation_6.	**LocationAccuracy**		
7	jahr_von				
		CollectionEvent.	**CollectionYear**	1902	
8	jahr_bis				
		CollectionEvent.	**CollectionDateSupplement**		
			Prefix:	bis?	

9	status			
	IdentificationUnitAnalysis_1_1.	**AnalysisResult**		
10	verwaltungseinheit	**not imported**		
11	fundort	**not imported**		
12	finder	**not imported**		
13	ID_collector1			
	CollectionAgent_1.	**CollectorsAgentURI**	43708	
			Prefix:	http://snsb.diversityworkbench.de/Agents_BayernFlora/
14	ID_collector2			
	CollectionAgent_2.	**CollectorsAgentURI**		
			Prefix:	http://snsb.diversityworkbench.de/Agents_BayernFlora/
15	ID_collector3			
	CollectionAgent_3.	**CollectorsAgentURI**		
			Prefix:	http://snsb.diversityworkbench.de/Agents_BayernFlora/
16	ID_collector4			
	CollectionAgent_4.	**CollectorsAgentURI**		
			Prefix:	http://snsb.diversityworkbench.de/Agents_BayernFlora/
17	primärquelle	**not imported**		
18	ID_primärquelle			
	Annotation_1.	**ReferenceURI**		
			Prefix:	http://id.snsb.info/references/
19	primärquelle_seiten	**not imported**		
20	bestand			
	IdentificationUnitAnalysis_1_2.	**AnalysisResult**		
21	sonstiges			
	CollectionSpecimen.	OriginalNotes		
22	höhe			
	CollectionEventLocalisation_7.	**Location1**		
23	herbar1	**not imported**		
24	herbar2	**not imported**		

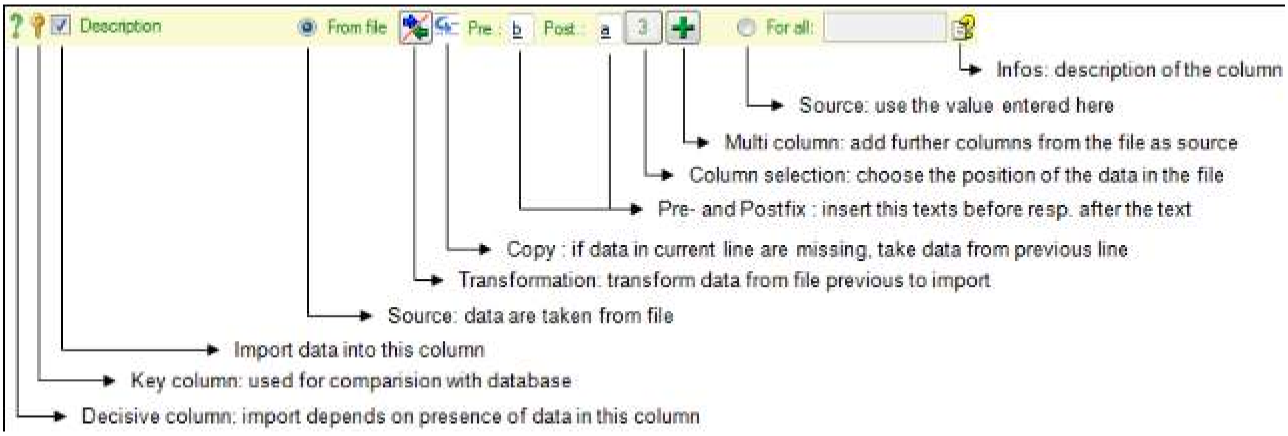
25	herbar3	not imported			
26	ID_herbar1				
	CollectionSpecimenRelation_1.	**RelatedSpecimenCollectionID**			
27	ID_herbar2	not imported			
28	ID_herbar3	not imported			
29	det	not imported			
30	ID_det	not imported			
31	rev	not imported			
32	ID_rev	not imported			
33	datenquelle	not imported			
34	ID_datenquelle				
	CollectionSpecimen.	**ReferenceURI**	135		
		Prefix:	http://id.snsb.info/references/		
35	project1	not imported			
36	project2				
	CollectionSpecimen.	AdditionalNotes	O		Beobachtung
		Transformations:	Reglar express.:		
			O	?	Beobachtung
			Reglar express.:		
			H	?	Herbarauswertung
			Reglar express.:		
			L	?	Literaturauswertung

Interface settings

Table	Table alias	Column	Value
Annotation	Annotation_1	AnnotationType	Reference
	Annotation_1	Annotation	Literaturauswertung: nach Dörr & Lippert (2004)
	Annotation_1	ReferenceDisplayText	Annotation
CollectionAgent	CollectionAgent_1	CollectorsName	Collector1
	CollectionAgent_2	CollectorsName	Collector2
	CollectionAgent_3	CollectorsName	Collector3
	CollectionAgent_4	CollectorsName	Collector4
CollectionEvent		CountryCache	Germany
CollectionProject	CollectionProject_1	ProjectID	37
	CollectionProject_2	ProjectID	149
CollectionSpecimen		ReferenceTitle	Reference
CollectionSpecimenRelation	CollectionSpecimenRelation_1	RelatedSpecimenURI	
	CollectionSpecimenRelation_1	RelatedSpecimenDisplayText	
	CollectionSpecimenRelation_1	Notes	Herbarauswertung: nach Dörr & Lippert (2004)

Identification	Identification_1_1	IdentificationSequence	2
	Identification_1_2	IdentificationSequence	1
	Identification_1_2	Notes	Originalname aus Dörr & Lippert (2004)
IdentificationUnit	IdentificationUnit_1	LastIdentificationCache	plant
	IdentificationUnit_1	TaxonomicGroup	plant
IdentificationUnitAnalysis	IdentificationUnitAnalysis_1_1	AnalysisID	2
	IdentificationUnitAnalysis_1_1	AnalysisNumber	1
	IdentificationUnitAnalysis_1_2	AnalysisID	4
	IdentificationUnitAnalysis_1_2	AnalysisNumber	2

Import wizard - Columns



Infos: description of the column

Source: use the value entered here

Multi column: add further columns from the file as source

Column selection: choose the position of the data in the file

Pre- and Postfix : insert this texts before resp. after the text

Copy : if data in current line are missing, take data from previous line

Transformation: transform data from file previous to import

Source: data are taken from file

Import data into this column

Key column: used for comparision with database

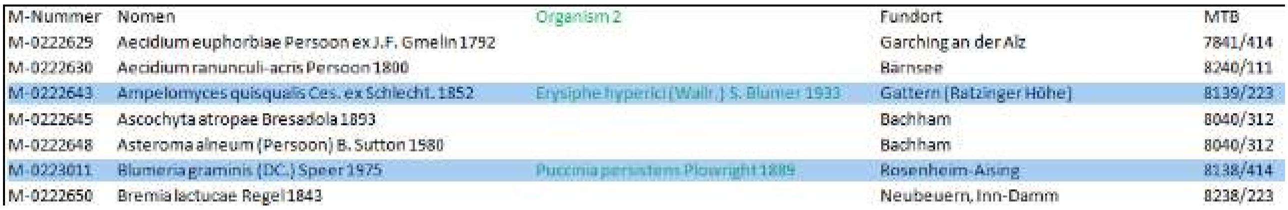
Decisive column: import depends on presence of data in this column

If the content of a file should be imported into a certain column of a table, mark it with the ☑ checkbox.

Decisive columns ?

The import depends upon the data found in the file where certain columns can be choosed as decisive, that means only those lines will be imported where data are found in <u>any</u> of these columns. To mark a column as **decisive**, click on the ? icon at the beginning of the line (see below).

In the example shown below, the file column Organims 2 was marked as decisive. Therefore only the two lines containing content in this column will be imported.



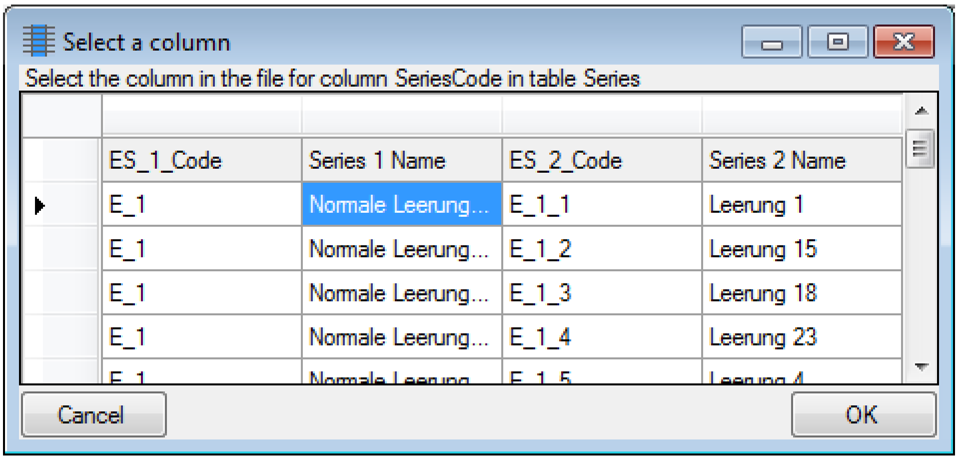
M-Nummer	Nomen	Organism 2	Fundort	MTB
M-0222629	Aecidium euphorbiae Persoon ex J.F. Gmelin 1792		Garching an der Alz	7841/414
M-0222630	Aecidium ranunculi-acris Persoon 1800		Barnsee	8240/111
M-0222643	Ampelomyces quisqualis Ces. ex Schlecht. 1852	Erysiphe hyperici (Wallr.) S. Blumer 1933	Gattern (Ratzinger Höhe)	8139/223
M-0222645	Ascochyta atropae Bresadola 1893		Bachham	8040/312
M-0222648	Asteroma alneum (Persoon) B. Sutton 1980		Bachham	8040/312
M-0223011	Blumeria graminis (DC.) Speer 1975	Puccinia persistens Plowright 1889	Rosenheim-Aising	8138/414
M-0222650	Bremia lactucae Regel 1843		Neubeuern, Inn-Damm	8238/223

Key columns

For the options **Merge**, **Update** and **Attach** the import compares the data from the file with those already present in the database. This comparision is done via key columns. To make a column a key column, click on the icon at the beginning of the line. You can define as many key columns as you need to ensure a valid comparision of the data.

Source ●

The data imported into the database can either be taken ● **From file** or the same value that you enter into the window or select from a list can be used ● **For all** datasets. If you choose the **From file** option, a window as shown below will pop up. Just click in the column where the data for the column should be taken from and click **OK** (see below).



Select a column

Select the column in the file for column SeriesCode in table Series

ES_1_Code	Series 1 Name	ES_2_Code	Series 2 Name
E_1	Normale Leerung...	E_1_1	Leerung 1
E_1	Normale Leerung...	E_1_2	Leerung 15
E_1	Normale Leerung...	E_1_3	Leerung 18
E_1	Normale Leerung...	E_1_4	Leerung 23
E_1	Normale Leerung	E_1_5	Leerung 4

If you choose the ◉**For all** option, you can either enter text, select a value from a list or use a ☑checkbox for YES or NO.

Transformation

The data imported may be transformed e.g. to adapt them to a format demanded by the database. For further details please see the chapter Transformation.

Copy

If data in the source file are missing in subsequent lines as shown below,

13.07.2003	48,2460	12,4567	Carex	firma
				acuta
	48,3453	12,8997		vaginata
			Festuca	ovina
				gigantea
14.07.2003	48,5669	11,9698	Carex	flacca
				acuta
15.07.2003	48,4520	11,2385	Festuca	rubra

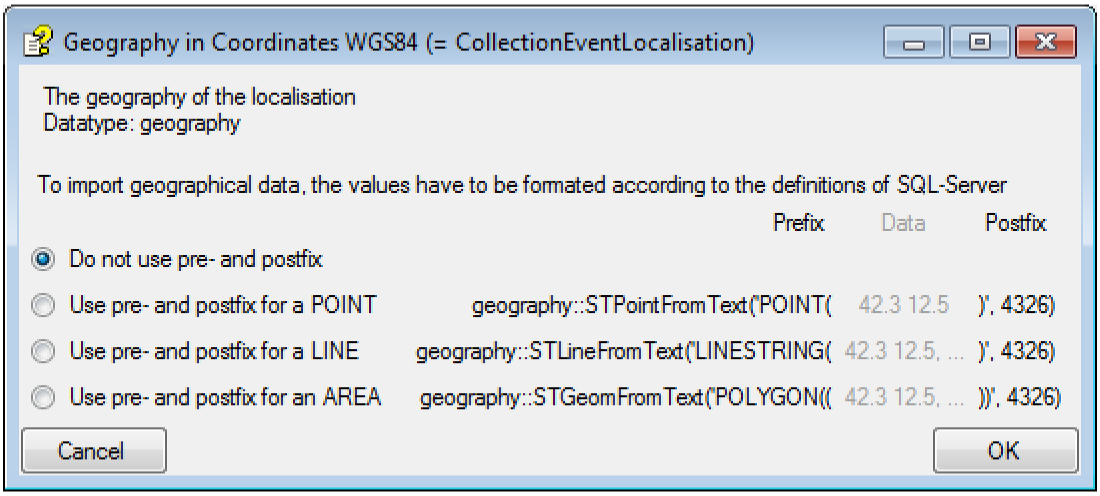
you can use the **Copy line** option to fill in missing data as shown below where the blue values are copied into empty fields during the import. Click on the button to ensure that missing values are filled in from previous lines.

13.07.2003	48,2460	12,4567	Carex	firma
13.07.2003	48,2460	12,4567	Carex	acuta
13.07.2003	48,3453	12,8997	Carex	vaginata
13.07.2003	48,3453	12,8997	Festuca	ovina
13.07.2003	48,3453	12,8997	Festuca	gigantea
14.07.2003	48,5669	11,9698	Carex	flacca
14.07.2003	48,5669	11,9698	Carex	acuta
15.07.2003	48,4520	11,2385	Festuca	rubra

Prefix and Postfix

In addition to the transformation of the values from the file, you may add a pre- and a postfix. These will be added after the transfromation of the text. Double-click in the field to see or edit the content. The pre- and a postfix values will <u>only</u> be used, if the <u>file contains data</u> for the current position.

For the datatype geography the pre- and postfixes will be automatically set to enable the import. The preset values by default are set for points as geographical units. You may change this to predefined types like lines or areas. Click on the button at the end of the line to open the information window. Here you can choose among the types mentioned above (see below).



Geography in Coordinates WGS84 (= CollectionEventLocalisation)

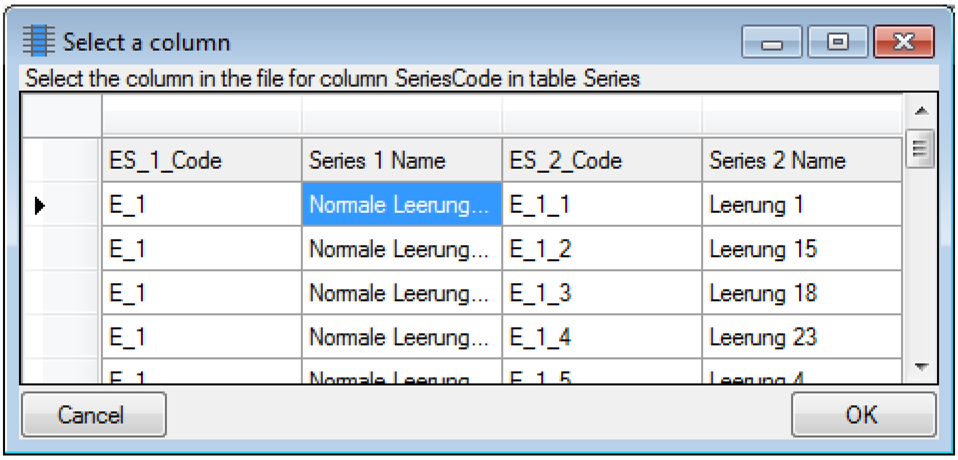
The geography of the localisation
Datatype: geography

To import geographical data, the values have to be formated according to the definitions of SQL-Server

	Prefix	Data	Postfix
● Do not use pre- and postfix			
○ Use pre- and postfix for a POINT	geography::STPointFromText('POINT(	42.3 12.5	)', 4326)
○ Use pre- and postfix for a LINE	geography::STLineFromText('LINESTRING(	42.3 12.5, ...	)', 4326)
○ Use pre- and postfix for an AREA	geography::STGeomFromText('POLYGON((	42.3 12.5, ...	))', 4326)

Column selection

If for any reason, a column that should take its content from the imported file misses the position of the file or you want to change the position click on the button. In case a position ist present, this button will show the number of the column. A window as shown below will pop up where you can select resp. change the position in the file.



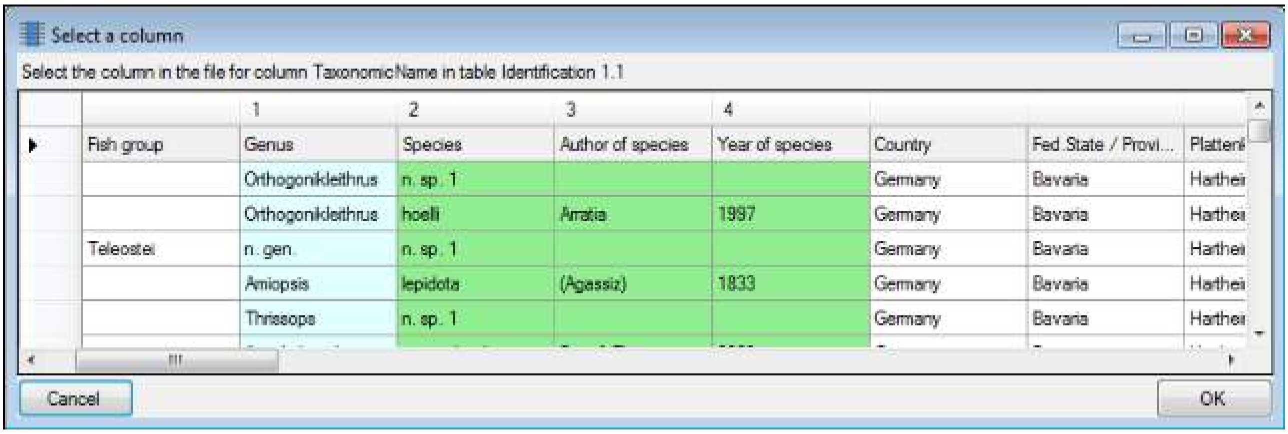
Select a column

Select the column in the file for column SeriesCode in table Series

ES_1_Code	Series 1 Name	ES_2_Code	Series 2 Name
E_1	Normale Leerung...	E_1_1	Leerung 1
E_1	Normale Leerung...	E_1_2	Leerung 15
E_1	Normale Leerung...	E_1_3	Leerung 18
E_1	Normale Leerung...	E_1_4	Leerung 23
E_1	Normale Leerung	E_1_5	Leerung 4

Multi column

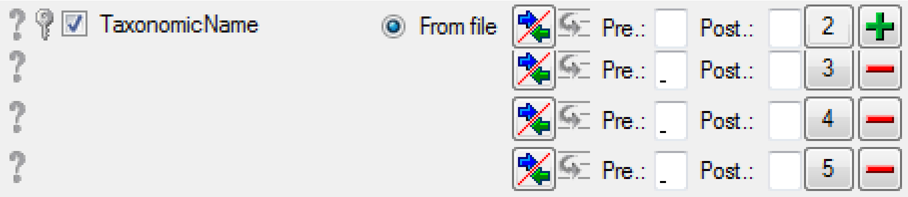
The content of a column can be composed from the content of several columns in the file. To add additional file columns, click on the ✚ button. A window as shown below will pop up, showing you the column selected so far, where the sequence is indicated in the header line. The first colum is marked with a blue background while the added columns are marked with a green background (see below).



Select the column in the file for column TaxonomicName in table Identification 1.1

	1	2	3	4			
Fish group	Genus	Species	Author of species	Year of species	Country	Fed.State / Provi...	Platten
	Orthogonikleithrus	n. sp. 1			Germany	Bavaria	Harthei
	Orthogonikleithrus	hoelli	Arratia	1997	Germany	Bavaria	Harthei
Teleostei	n. gen.	n. sp. 1			Germany	Bavaria	Harthei
	Amiopsis	lepidota	(Agassiz)	1833	Germany	Bavaria	Harthei
	Thrissops	n. sp. 1			Germany	Bavaria	Harthei

To remove a added column, use the ▬ button (see below).



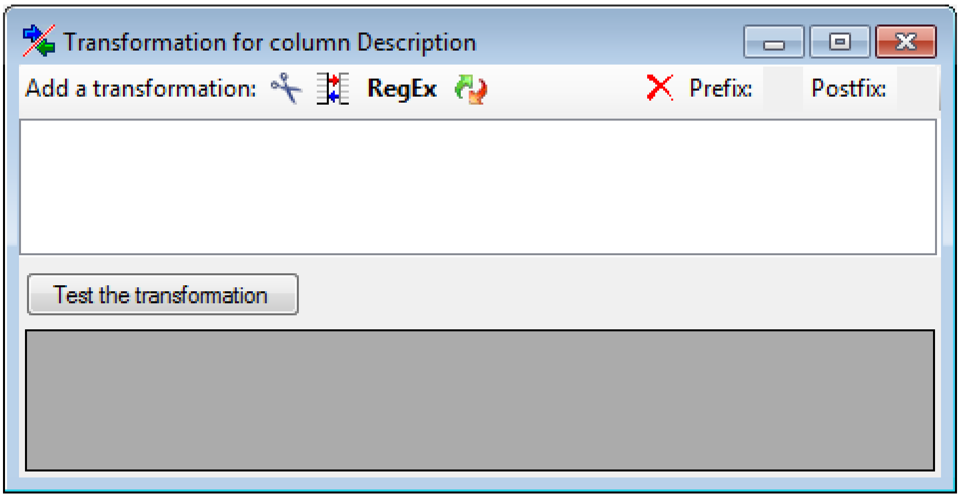
☑ TaxonomicName ● From file Pre.: Post.: 2
Pre.: _ Post.: 3
Pre.: _ Post.: 4
Pre.: _ Post.: 5

Information

The button opens a window displaying the informations about the column. For certain datatypes additional options are included (see Pre- and Postfix).

Import wizard - transformation

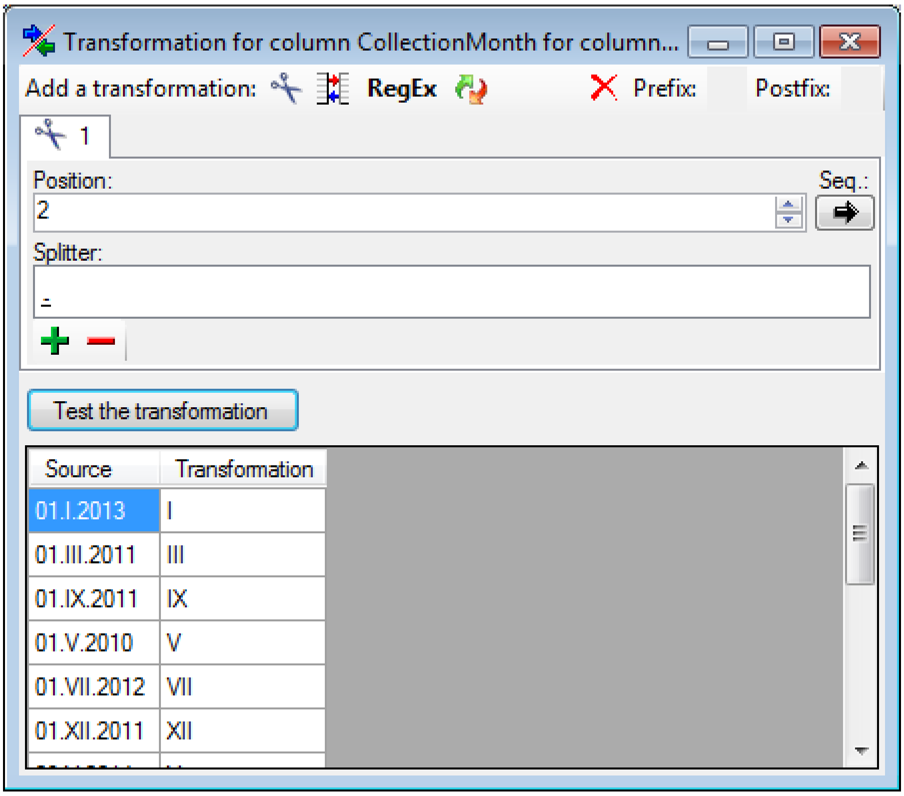
The data imported may be transformed e.g. to adapt them to a format demanded by the database. Click on the button to open a window as shown below.



Here you can enter 4 types of transformation that should be applied to your data. Cut out parts, Translate contents from the file, **RegEx** apply regular expressions or Replace text in the data from the file. All transformations will be applied in the sequence they had been entered. Finally, if a prefix and/or a postfix are defined, these will be added after the transformation. To remove a transformation, select it and click on the ✕button.

Cut

With the cut transformation you can restrict the data taken from the file to a part of the text in the file. This is done by splitters and the position after splitting. In the example below, the month of a date should be extracted from the information. To achieve this, the splitter '.' is added and than the position set to 2. You can change the direction of the sequence with the button ➡Seq starting at the first position and ⬅starting at the last position. Click on the button **Test the transformation** to see the result of your transformation.



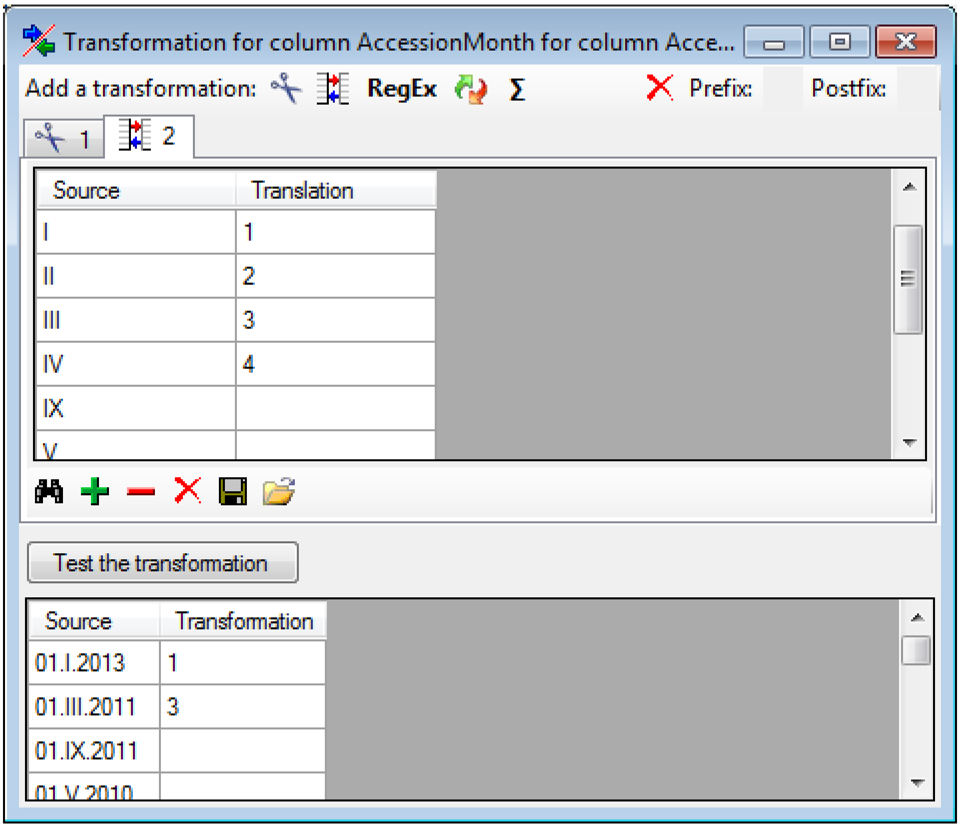
Position: 2

Splitter: .

Source	Transformation
01.I.2013	I
01.III.2011	III
01.IX.2011	IX
01.V.2010	V
01.VII.2012	VII
01.XII.2011	XII

Translate

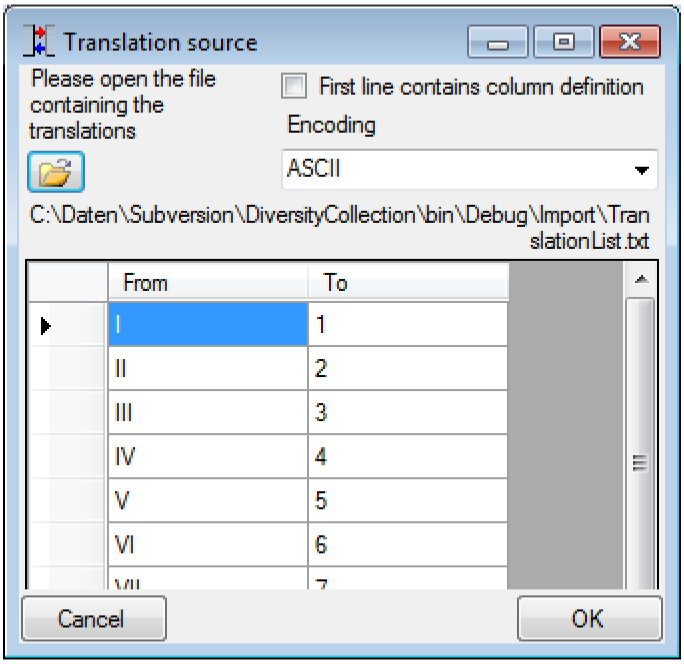
The translate transformation translates values from the file into values entered by the user. In the example above, the values of the month cut out from the date string should be translated from roman into numeric notation. To do this click on the button to add a translation transformation (see below). To list all different values present in the data, click on the button. A list as shown below will be created. You may as well use the ✚ and ▬ buttons to add or remove values from the list or the ✕ button to clear the list. Than enter the translations as shown below. Use the save button to save entries and the **Test the transformation** button to see the result.



Source	Translation
I	1
II	2
III	3
IV	4
IX	
V	

Source	Transformation
01.I.2013	1
01.III.2011	3
01.IX.2011	
01.V.2010	

To load a predefined list for the transformation use the 📂 button. A window as shown below will open. Choose the encoding of the data in you translation source, if the first line contains the column definition and click on the button to open a file. Click OK to use the values from the file for the translation.



☐ First line contains column definition

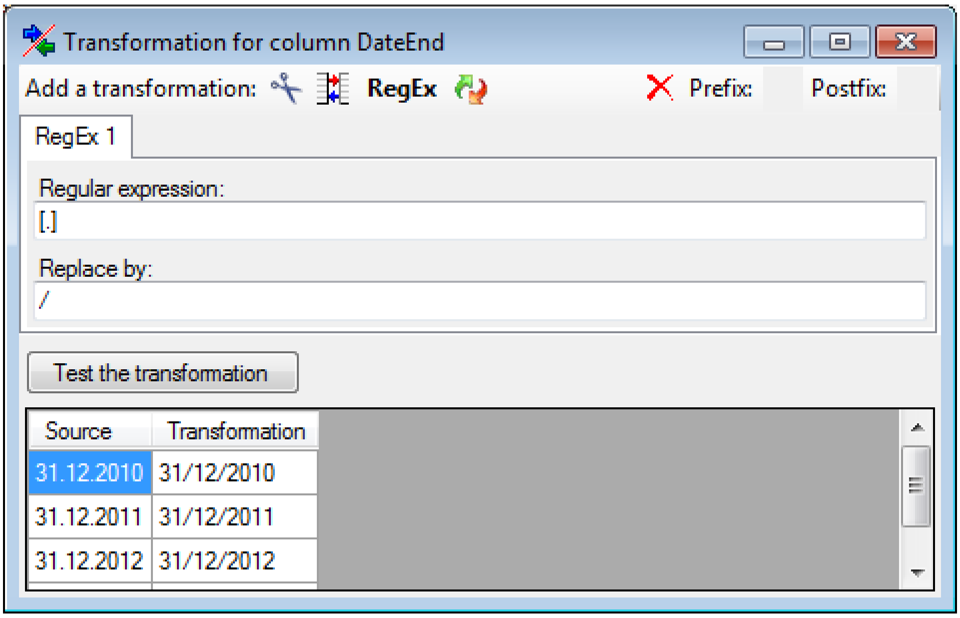
Encoding: ASCII

C:\Daten\Subversion\DiversityCollection\bin\Debug\Import\TranslationList.txt

From	To
I	1
II	2
III	3
IV	4
V	5
VI	6
VII	7

Regular expression

The transformation using regular expressions will transform the values according to the entered **Regular expression** and **Replace by** vales. For more details please see documentations about regular expressions.



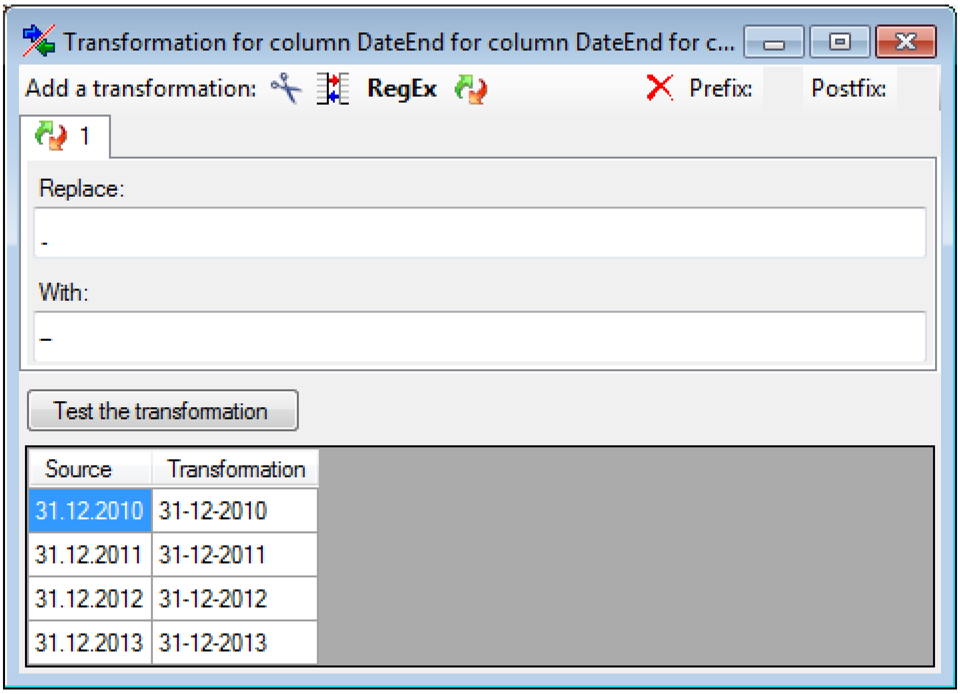
Regular expression:
[.]

Replace by:
/

Source	Transfomation
31.12.2010	31/12/2010
31.12.2011	31/12/2011
31.12.2012	31/12/2012

Replacement

The replacement transformation replaces any text in the data by a text specified by the user. In the example shown below, the text "." is replaced by "-".



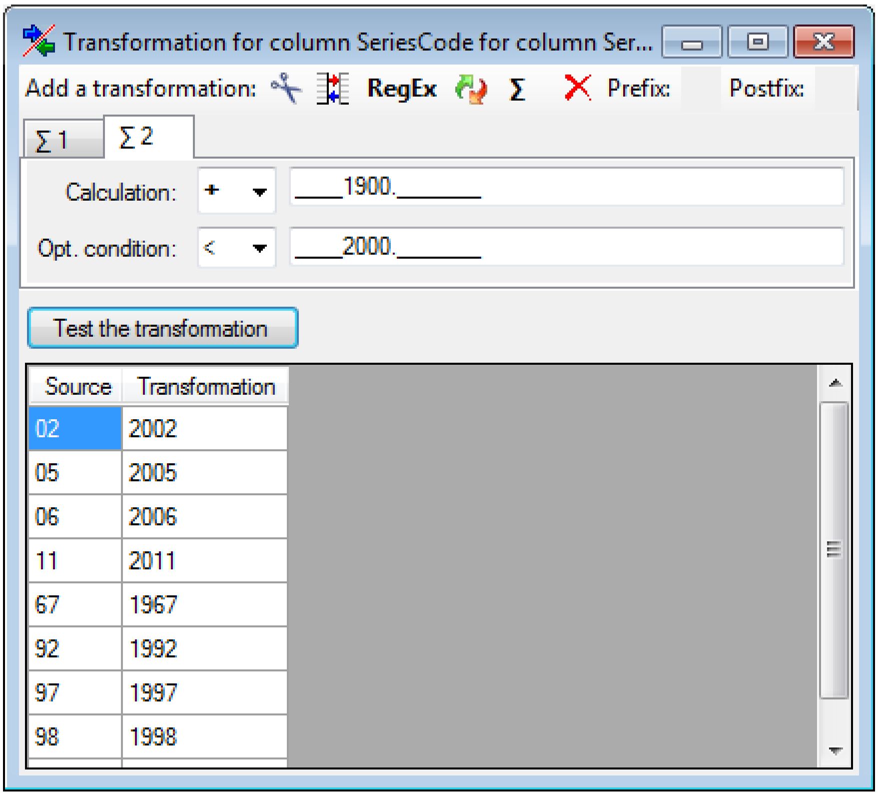
Replace:
-

With:
–

Source	Transfomation
31.12.2010	31-12-2010
31.12.2011	31-12-2011
31.12.2012	31-12-2012
31.12.2013	31-12-2013

Calculation Σ

The calculation transformation performs a calculation on numeric value, dependent on an optional condition. In the example below, 2 calculations were applied to convert 2-digit values into 4 digit years.



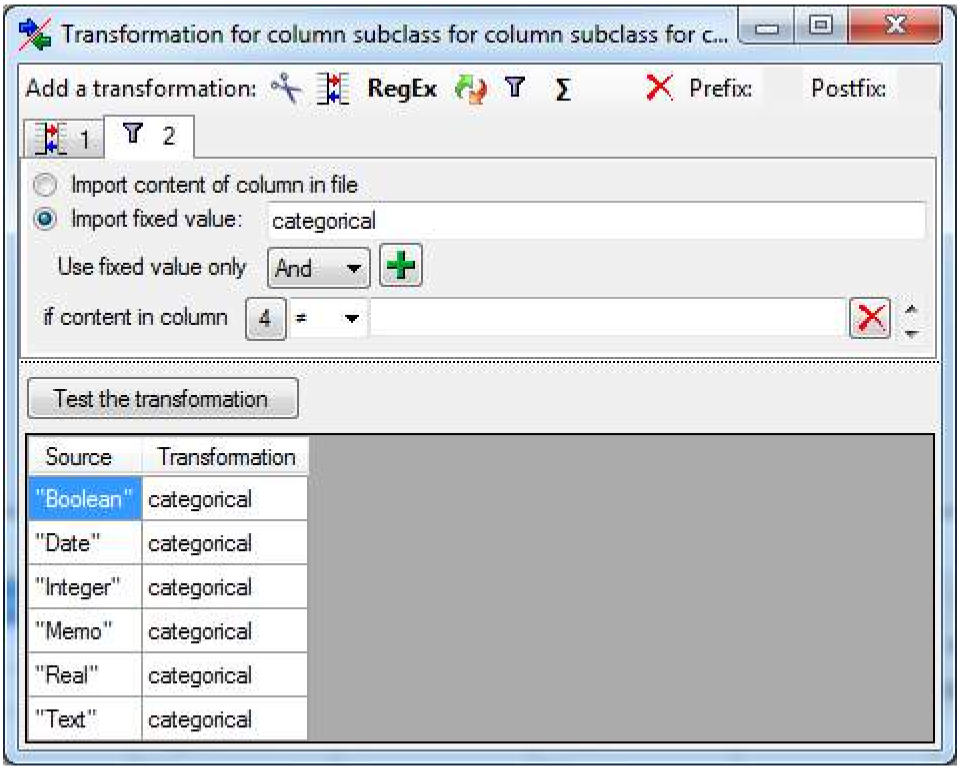
Calculation: + ____1900.______

Opt. condition: < ____2000.______

Source	Transformation
02	2002
05	2005
06	2006
11	2011
67	1967
92	1992
97	1997
98	1998

Filter

The filter transformation compares the values from the file with a value entered by the user. As a result you can either ● **Import content of column in file** or ● **Import a fixed value**. To select another column that should be compared, click on the ☰button and choose a column from the file in the window that will open. If the column that should be compared is not the column of the transformation, the number of the column will be shown instead of the ☰symbol. To add further filter conditions use the +button. For the combination of the conditions you can choose among AND and OR.



○ Import content of column in file

● Import fixed value: categorical

Use fixed value only And

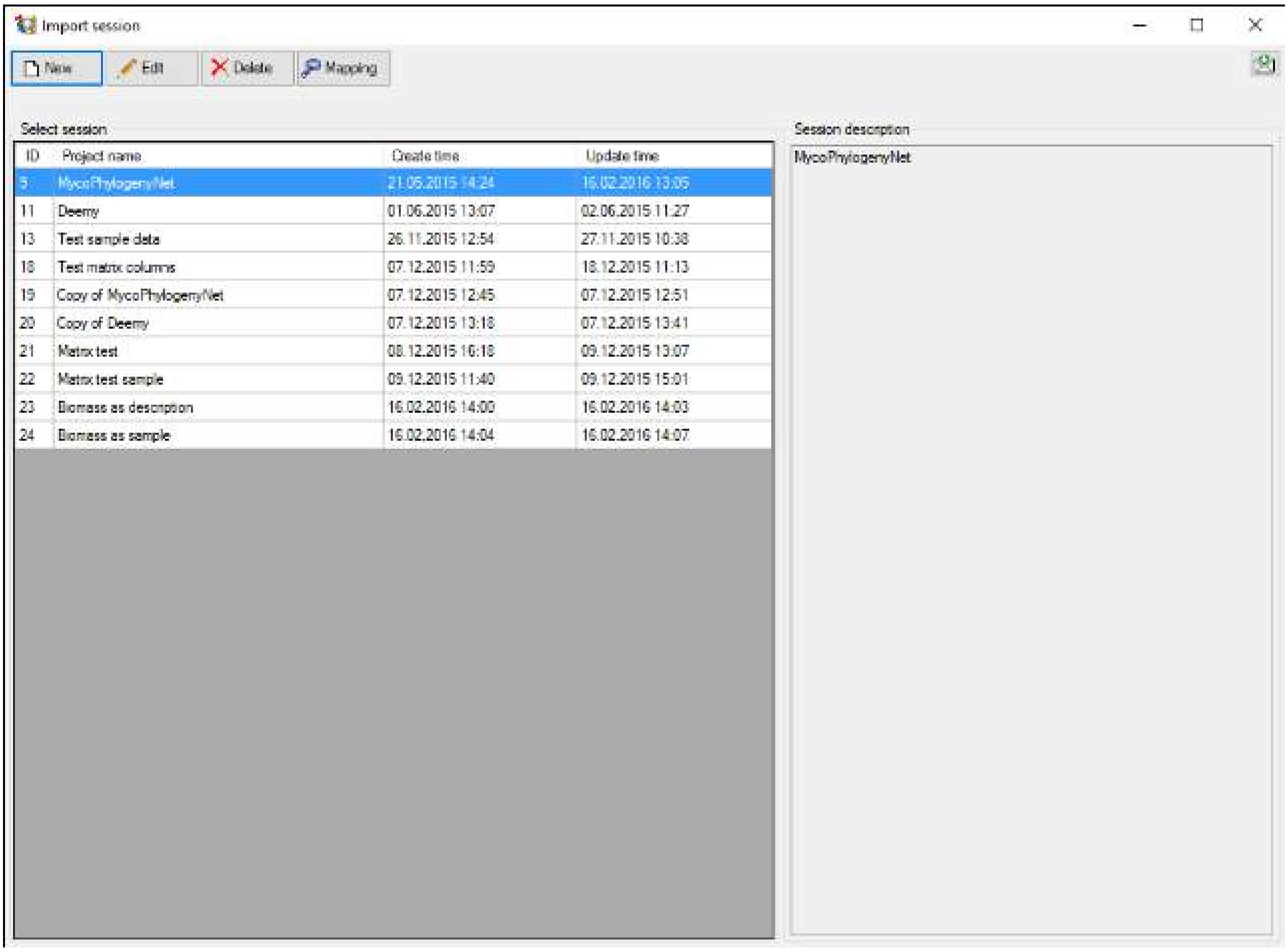
if content in column 4 ≠

Source	Transformation
"Boolean"	categorical
"Date"	categorical
"Integer"	categorical
"Memo"	categorical
"Real"	categorical
"Text"	categorical

Import sessions

Usually the information required for an import into DiversityDescriptions is spread over at least two files, e.g. "terminology" (descriptors/categorical states) and "items" (descriptions data), where the elements of the terminology are referenced to build the item descriptions. Between these files references are usually built using e.g. a descriptor number and/or the categorical state name. Within the DiversityDescriptions database relations are built using automatically generated numbers ("id"). To allow a mapping between the internally generated keys and the external keys, the "Import sessions" are used.

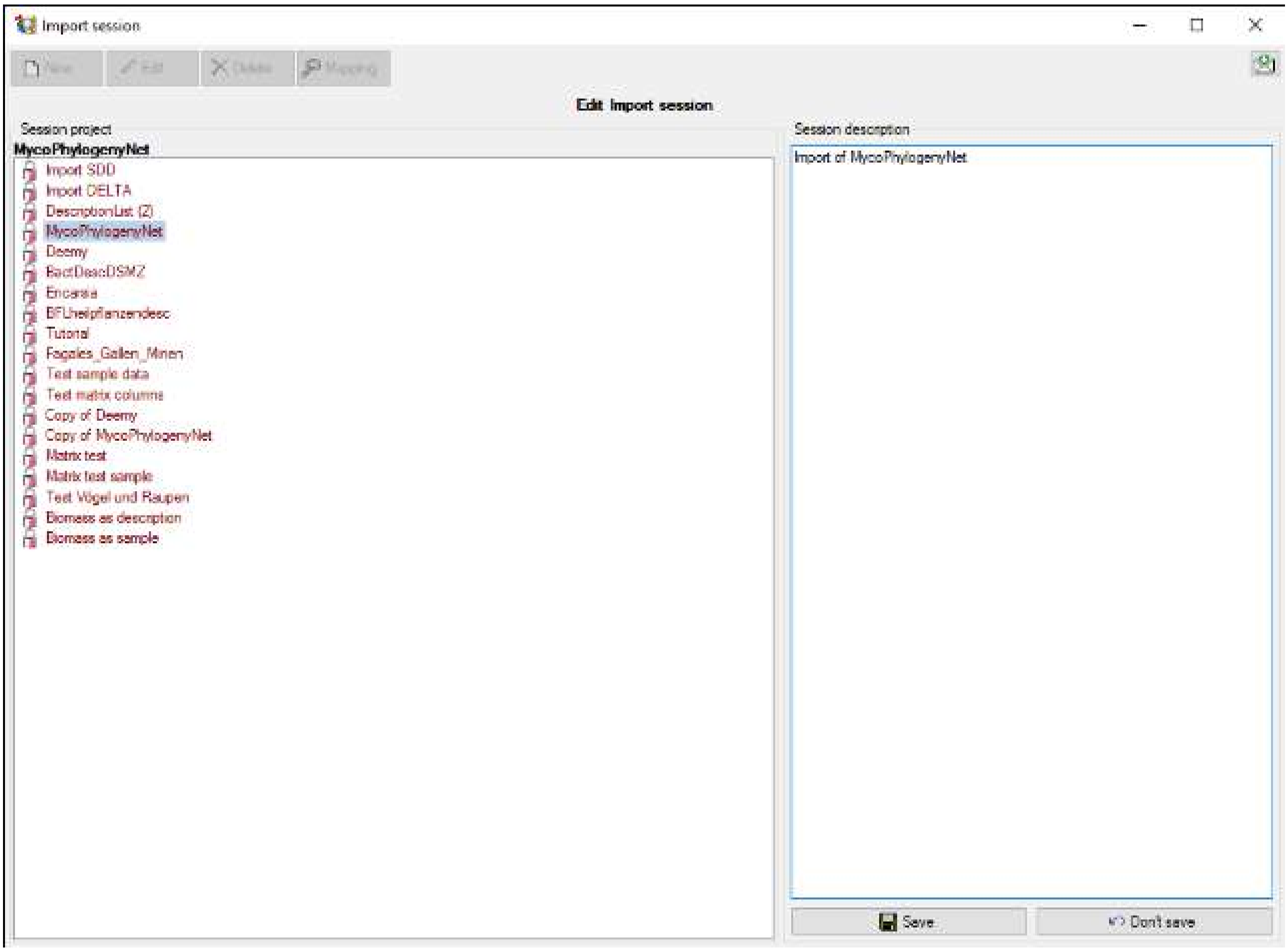
When you start the import wizard you are asked to select rsp. create a new import session. To ge an overview of the present import session or to create, edit and delete import sessiong select **Data -> Import -> Wizard -> Organize sessions ...** and a window as shown below will be shown.



ID	Project name	Create time	Update time
5	MycoPhylogenyNet	21.05.2015 14:24	16.02.2016 13:05
11	Deemy	01.06.2015 13:07	02.06.2015 11:27
13	Test sample data	26.11.2015 12:54	27.11.2015 10:38
18	Test matrix columns	07.12.2015 11:59	18.12.2015 11:13
19	Copy of MycoPhylogenyNet	07.12.2015 12:45	07.12.2015 12:51
20	Copy of Deemy	07.12.2015 13:18	07.12.2015 13:41
21	Matrix test	08.12.2015 16:18	09.12.2015 13:07
22	Matrix test sample	09.12.2015 11:40	09.12.2015 15:01
23	Biomass as description	16.02.2016 14:00	16.02.2016 14:03
24	Biomass as sample	16.02.2016 14:04	16.02.2016 14:07

MycoPhylogenyNet

Click buttoem **New** and a window as shown below will be shown. Select the project of the import session and enter a description text. So save the new import session click **Save** ,to ignore the changes click button **Don't save**. A similar window can be opened by selecting an existing import session and clicking **Edit**.

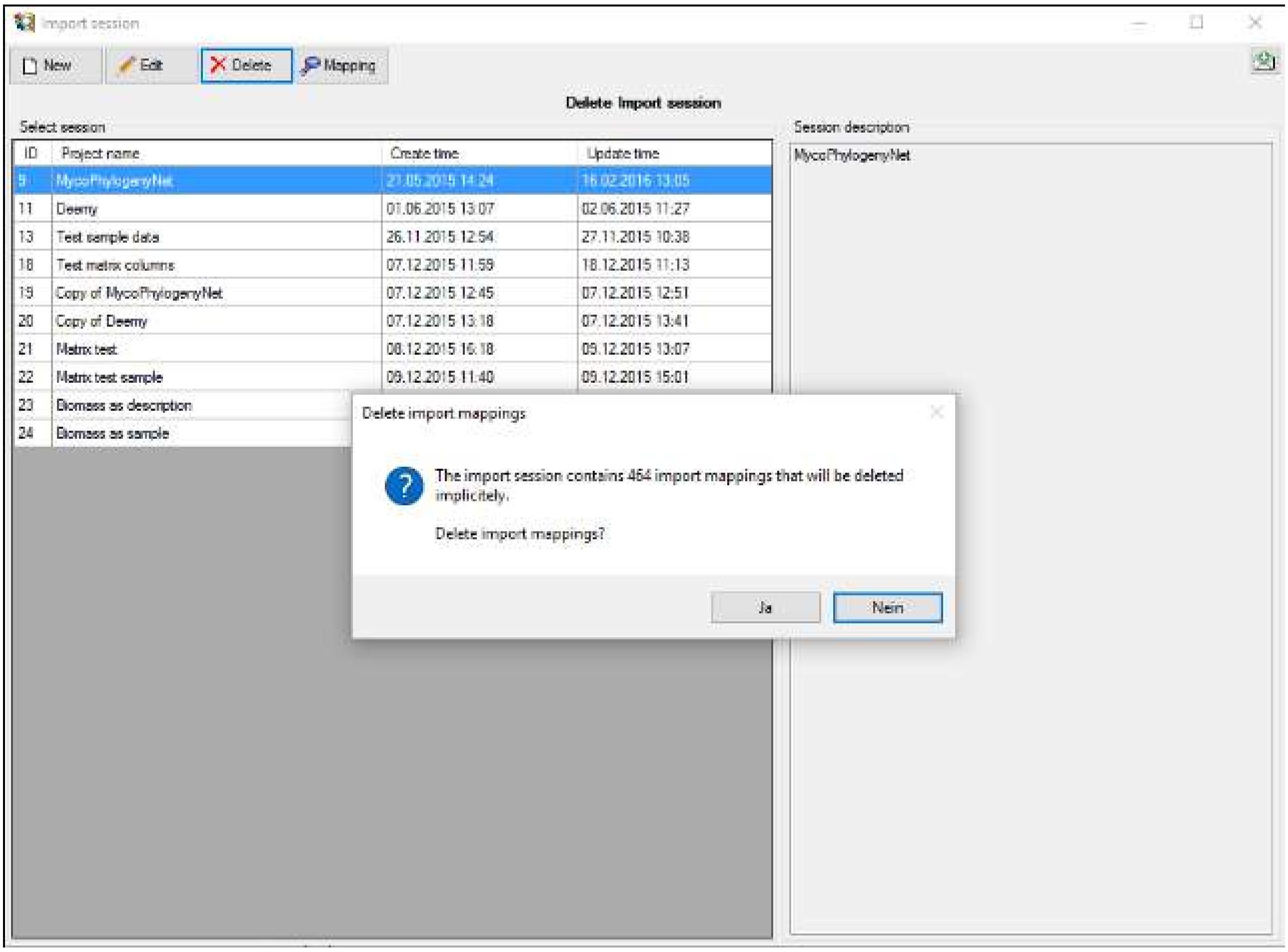


Session project
MycoPhylogenyNet

- Import SDD
- Import DELTA
- DescriptionList (2)
- MycoPhylogenyNet
- Deemy
- BactDescDSMZ
- Encarsia
- BFLheilpflanzendesc
- Tutorial
- Fagales_Gallen_Minen
- Test sample data
- Test matrix columns
- Copy of Deemy
- Copy of MycoPhylogenyNet
- Matrix test
- Matrix test sample
- Test Vögel und Raupen
- Biomass as description
- Biomass as sample

Session description
Import of MycoPhylogenyNet

To delete an import session, select it and click the ✕**Delete** button. If import mapping data are present for the import session, an additional window will be shown that informs you about the number of mappings that will be implicitelx deleted and you have the chance to cancel the delete process (see below).



Delete Import session

Select session

ID	Project name	Create time	Update time
9	MycoPhylogenyNet	21.05.2015 14:24	16.02.2016 13:05
11	Deemy	01.06.2015 13:07	02.06.2015 11:27
13	Test sample data	26.11.2015 12:54	27.11.2015 10:38
18	Test matrix columns	07.12.2015 11:59	18.12.2015 11:13
19	Copy of MycoPhylogenyNet	07.12.2015 12:45	07.12.2015 12:51
20	Copy of Deemy	07.12.2015 13:18	07.12.2015 13:41
21	Matrix test	08.12.2015 16:18	09.12.2015 13:07
22	Matrix test sample	09.12.2015 11:40	09.12.2015 15:01
23	Biomass as description		
24	Biomass as sample		

Session description

MycoPhylogenyNet

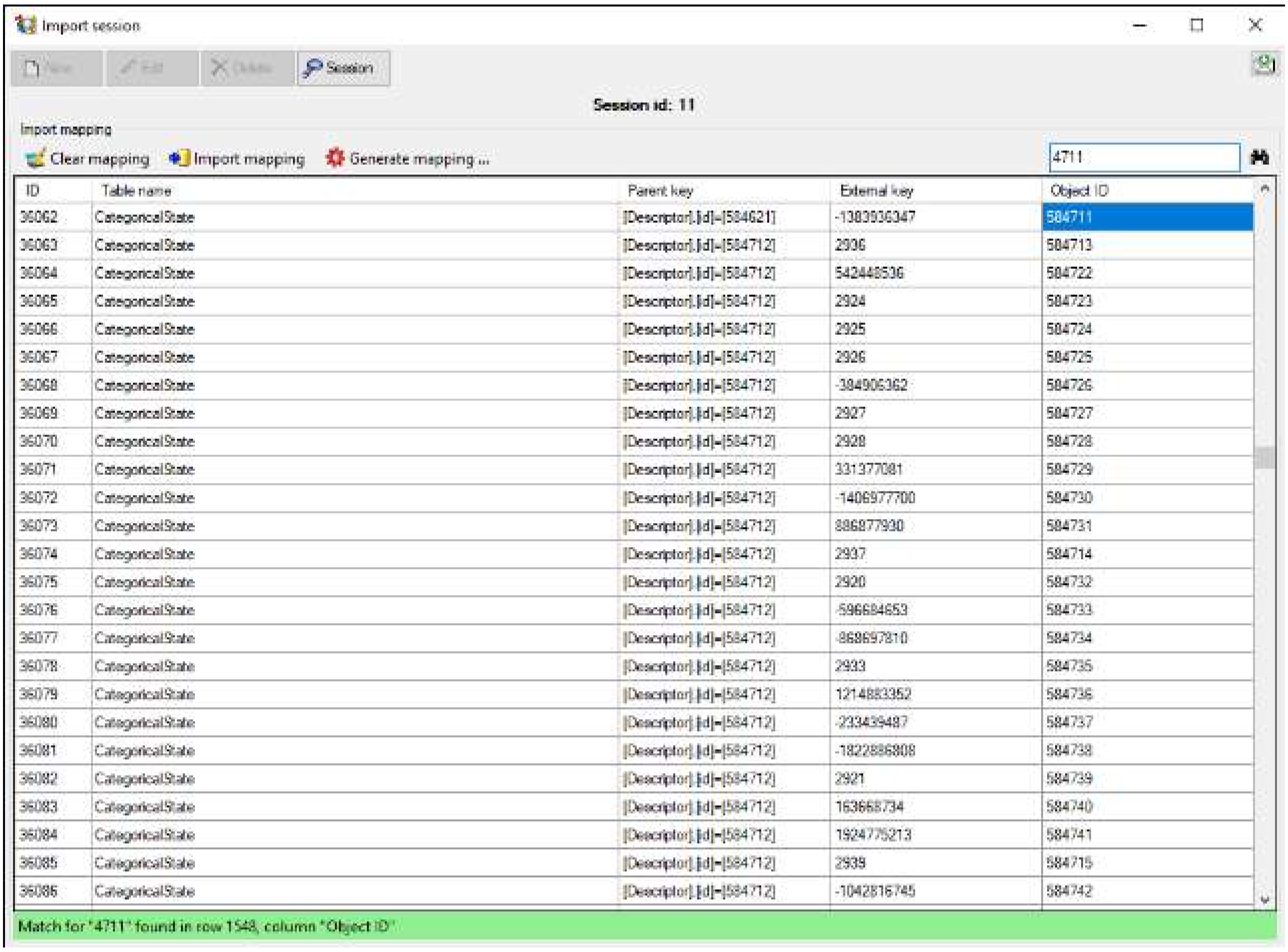
Delete import mappings

The import session contains 464 import mappings that will be deleted implicitely.

Delete import mappings?

Import mapping

To view the mapping information that has been stored for an import session, select it and click the **Mapping** button. If import mapping data are present for the import session, a table with the database "Table name", an optional "Parent key", e.g. the descriptor id in case of categorical states, the "External key" used for import and the database interal key, the "Object ID", is displayed (see below). To go back to the session overview, click the **Session** button.



Session id: 11

Import mapping

ID	Table name	Parent key	External key	Object ID
36062	CategoricalState	[Descriptor].[id]=[584621]	-1383936347	584711
36063	CategoricalState	[Descriptor].[id]=[584712]	2936	584713
36064	CategoricalState	[Descriptor].[id]=[584712]	542448536	584722
36065	CategoricalState	[Descriptor].[id]=[584712]	2924	584723
36066	CategoricalState	[Descriptor].[id]=[584712]	2925	584724
36067	CategoricalState	[Descriptor].[id]=[584712]	2926	584725
36068	CategoricalState	[Descriptor].[id]=[584712]	-384906362	584726
36069	CategoricalState	[Descriptor].[id]=[584712]	2927	584727
36070	CategoricalState	[Descriptor].[id]=[584712]	2928	584728
36071	CategoricalState	[Descriptor].[id]=[584712]	331377081	584729
36072	CategoricalState	[Descriptor].[id]=[584712]	-1406977700	584730
36073	CategoricalState	[Descriptor].[id]=[584712]	886877930	584731
36074	CategoricalState	[Descriptor].[id]=[584712]	2937	584714
36075	CategoricalState	[Descriptor].[id]=[584712]	2920	584732
36076	CategoricalState	[Descriptor].[id]=[584712]	-596684653	584733
36077	CategoricalState	[Descriptor].[id]=[584712]	-868697810	584734
36078	CategoricalState	[Descriptor].[id]=[584712]	2933	584735
36079	CategoricalState	[Descriptor].[id]=[584712]	1214883352	584736
36080	CategoricalState	[Descriptor].[id]=[584712]	-233439487	584737
36081	CategoricalState	[Descriptor].[id]=[584712]	-1822886808	584738
36082	CategoricalState	[Descriptor].[id]=[584712]	2921	584739
36083	CategoricalState	[Descriptor].[id]=[584712]	163668734	584740
36084	CategoricalState	[Descriptor].[id]=[584712]	1924775213	584741
36085	CategoricalState	[Descriptor].[id]=[584712]	2939	584715
36086	CategoricalState	[Descriptor].[id]=[584712]	-1042816745	584742

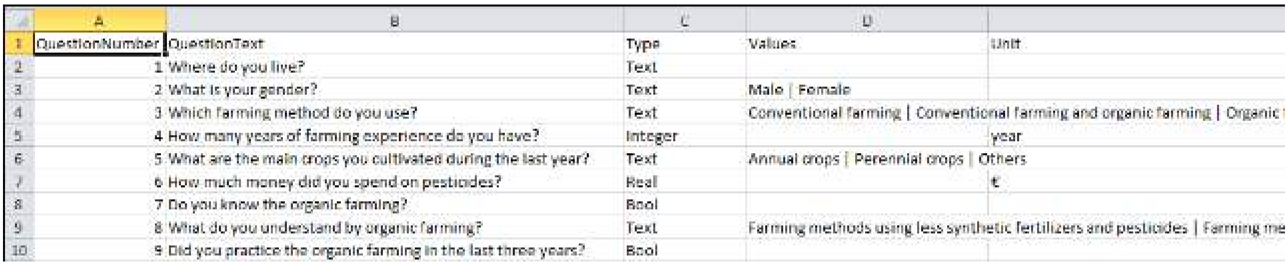
Match for "4711" found in row 1548, column "Object ID"

You may search for specific strings in the mapping table by entering the search string in the upper right text box and clicking the 🔍 button. Menu item **Clear mapping** allows clearing of mapping information for selected tables or all tables. With menu item **Import mapping** an import wizard can be opened to read the mapping information from tab-separated files. A detailled example for using the mapping import is shown in **Import wizard - tutorial for advanced functions.**

If you want to import list data that include the internal database keys, you can generate mapping data that make these internal keys available for import by klicking menu item **Generate mapping ...**. All mappings of the selected import session will be deleted and the internal keys ("Object ID") of descriptors, categorical states, descriptions and their resources will be inserted as external keys. By using this function you can re-import rsp. update data that have been generated with the form Export resource data list and modified with an external program.

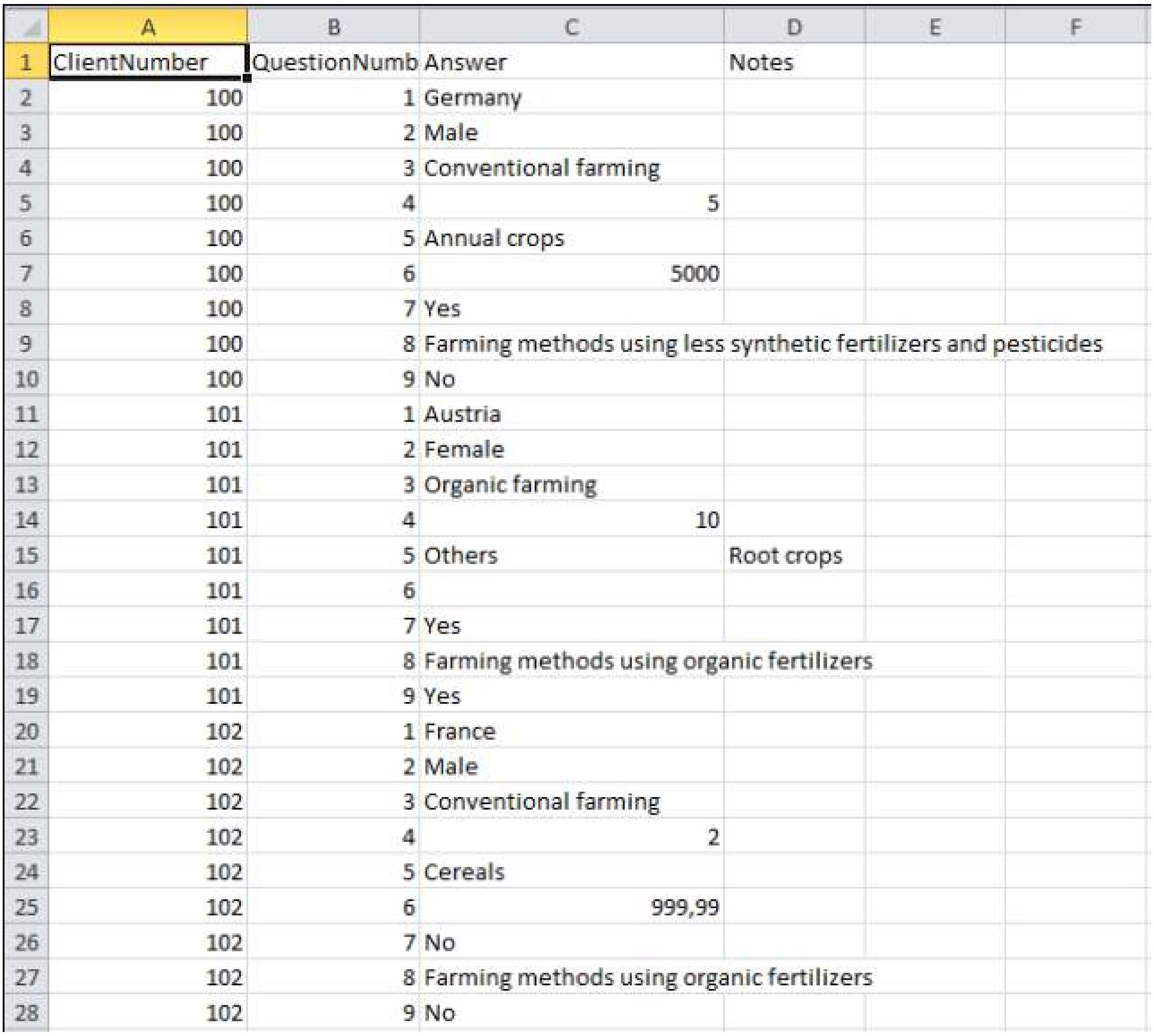
Import wizard - tutorial

This tutorial demostrates the import of descriptors and descriptions from two tabulator separated files into the database. The original data were stored in an MS-Excel sheet with data from an agricultural survey. The first table contains a list of questions and data like expected type of the answer, possible values and the measurement unit in case of numeric values (see image below).



	A	B	C	D	
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gender?	Text	Male | Female	
4	3	Which farming method do you use?	Text	Conventional farming | Conventional farming and organic farming | Organic	
5	4	How many years of farming experience do you have?	Integer		year
6	5	What are the main crops you cultivated during the last year?	Text	Annual crops | Perennial crops | Others	
7	6	How much money did you spend on pesticides?	Real		€
8	7	Do you know the organic farming?	Bool		
9	8	What do you understand by organic farming?	Text	Farming methods using less synthetic fertilizers and pesticides | Farming me	
10	9	Did you practice the organic farming in the last three years?	Bool		

The second table contains the answers of three individuals that are identified by a numeric value (see image below).



	A	B	C	D	E	F
1	ClientNumber	QuestionNumb	Answer	Notes		
2	100	1	Germany			
3	100	2	Male			
4	100	3	Conventional farming			
5	100	4	5			
6	100	5	Annual crops			
7	100	6	5000			
8	100	7	Yes			
9	100	8	Farming methods using less synthetic fertilizers and pesticides			
10	100	9	No			
11	101	1	Austria			
12	101	2	Female			
13	101	3	Organic farming			
14	101	4	10			
15	101	5	Others	Root crops		
16	101	6				
17	101	7	Yes			
18	101	8	Farming methods using organic fertilizers			
19	101	9	Yes			
20	102	1	France			
21	102	2	Male			
22	102	3	Conventional farming			
23	102	4	2			
24	102	5	Cereals			
25	102	6	999,99			
26	102	7	No			
27	102	8	Farming methods using organic fertilizers			
28	102	9	No			

By using the option "Save as unicode text" the tables can easily be exported as tabulator separated text files ("Survey_Questions.txt" and "Survey_Answers.txt"). The import is done in seven steps and demonstrates various features of the import wizard. The tabulator separated text files and import schemas may be downloaded from the Diversity Descriptions example file repository.

Step 1 - Preparations: New local project and descriptor tree

Step 2 - Import of descriptors

Step 3 - Insert recommended values of descriptors

Step 4 - Import of categorical states for boolean data

Step 5 - Import of categorical states and update of descriptor

Step 6 - Import of descriptions

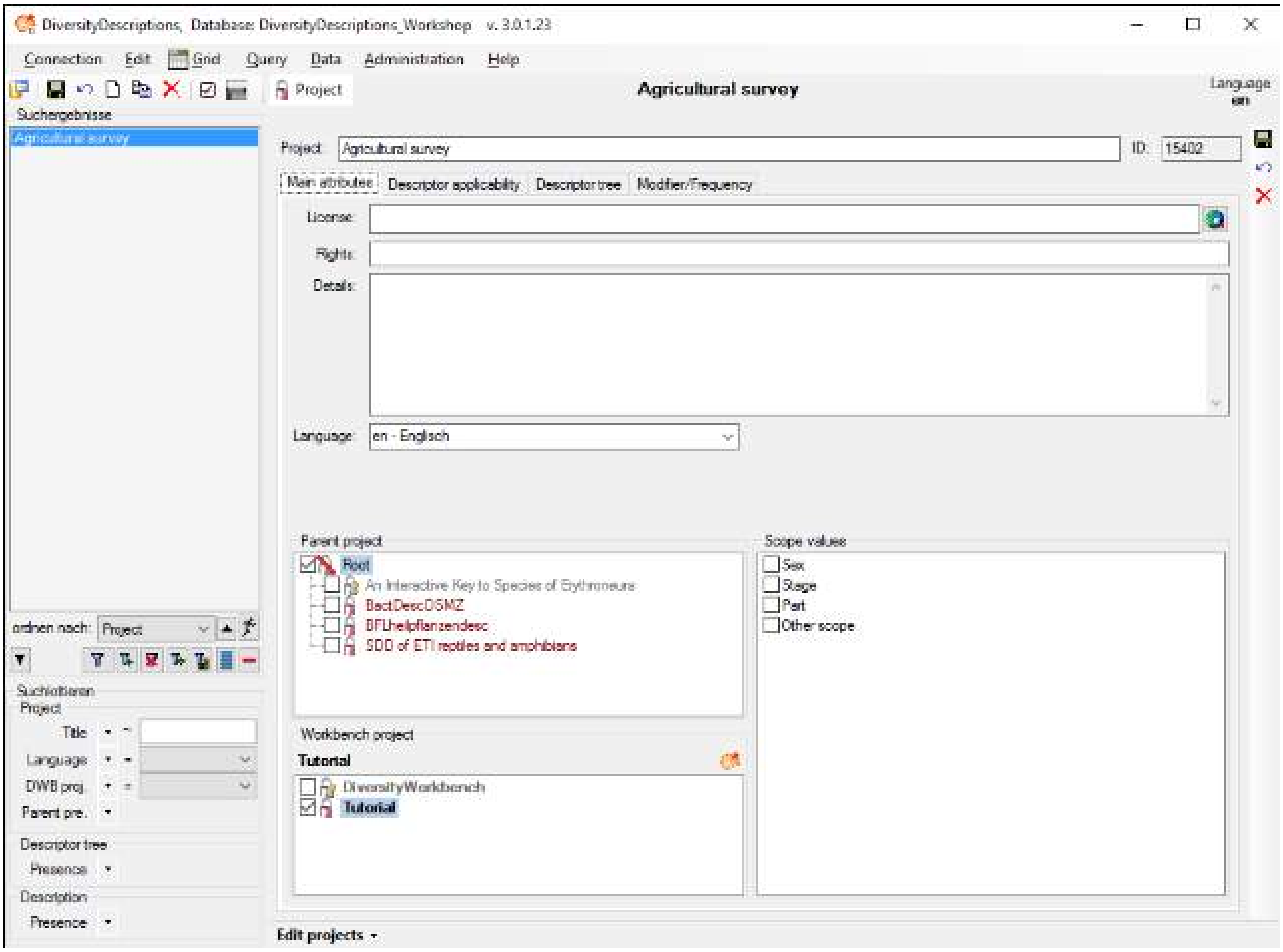
Step 7 - Import of description data

Epilogue

See the **second part of the import wizard tutorial** to learn more about some advanced functions of the import wizard.

Step 1 - Preparations: New local project and descriptor tree

Choose **Edit -> Projects** from the menu and create a new local project by clicking the 🗋 button. If you are asked for a workbench project, select an available one, e.g. DiversityWorkbench and enter the local project name "Agricultural survey". After saving the project by clicking on button 💾 the name in the query list will be updated (see below).



Agricultural survey

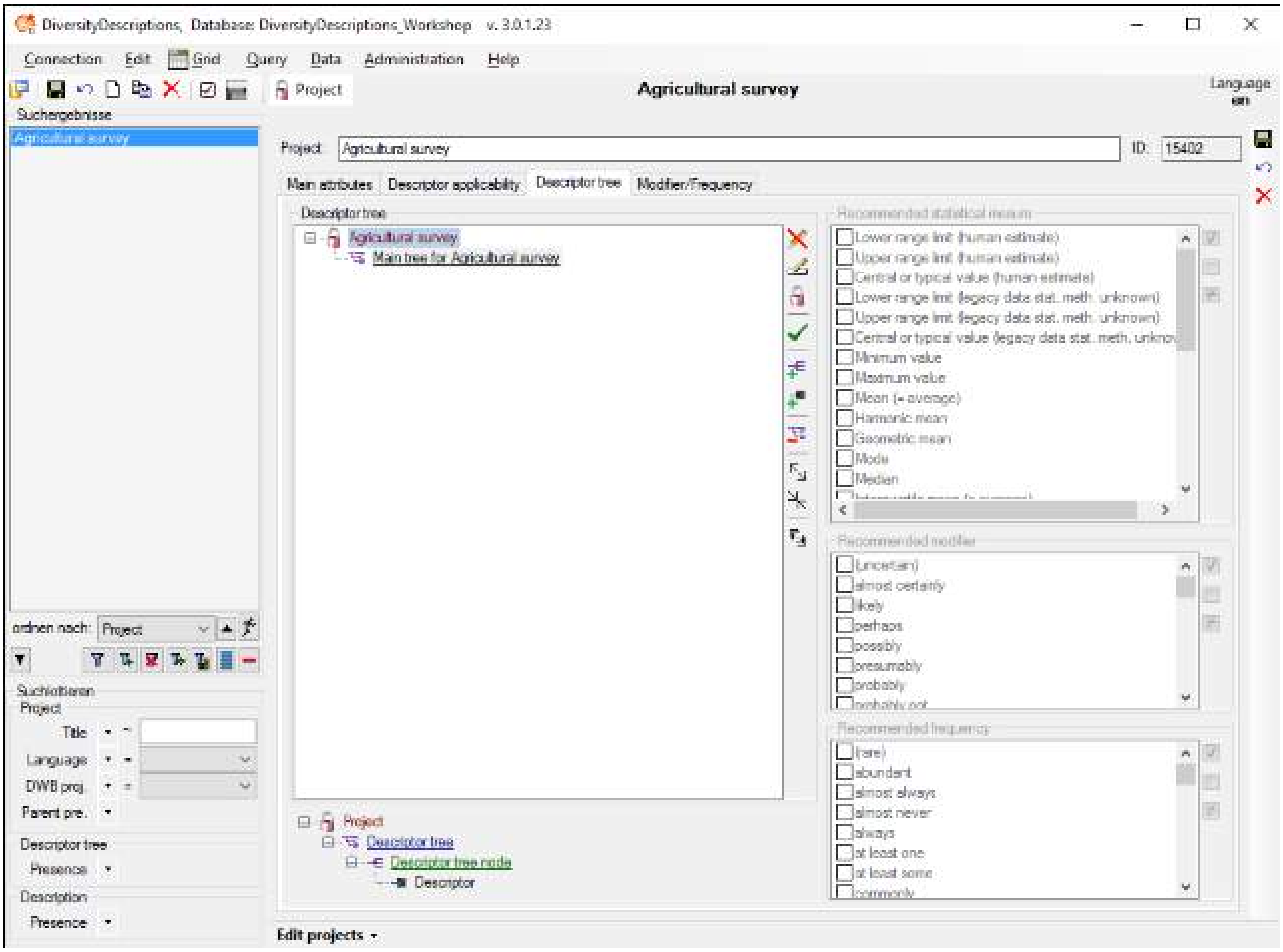
Project: Agricultural survey

ID: 15402

Language: en - Englisch

Workbench project: Tutorial

Change to tab **"Descriptor tree"**, mark project "Agricultural survey" in section "Descriptor tree" and press button to insert a new tree. Change the tree name to "Main tree for Agricultural survey" and again press button 💾 to save all changes (see below).



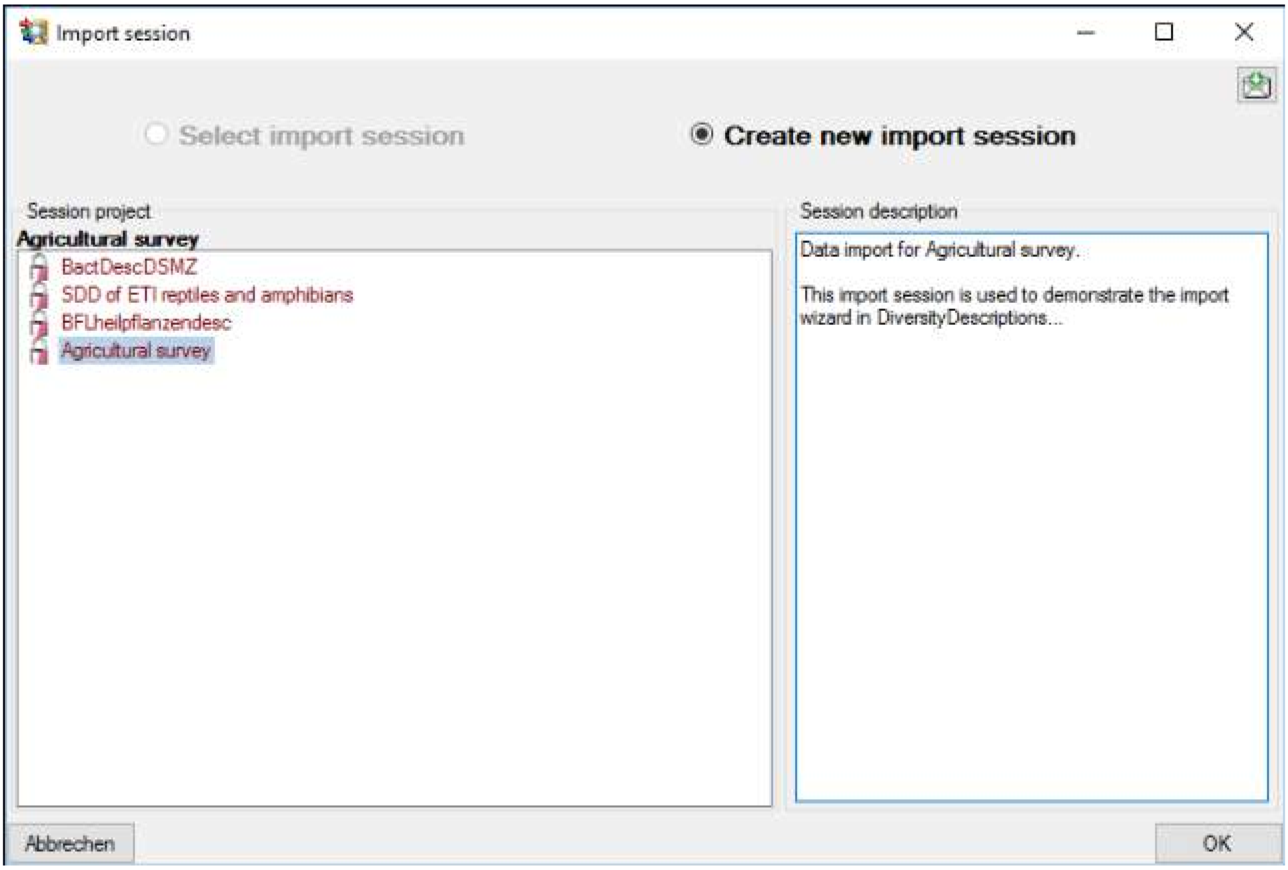
Project: Agricultural survey

ID: 15402

Next: Step 2 - Import of descriptors

Step 2 - Import of descriptors

Choose **Data -> Import -> Import wizard -> Import descriptors ...** from the menu. A window as shown below will open to create a new import session. Select project "MycoPhylogenyNet" and enter a session description.

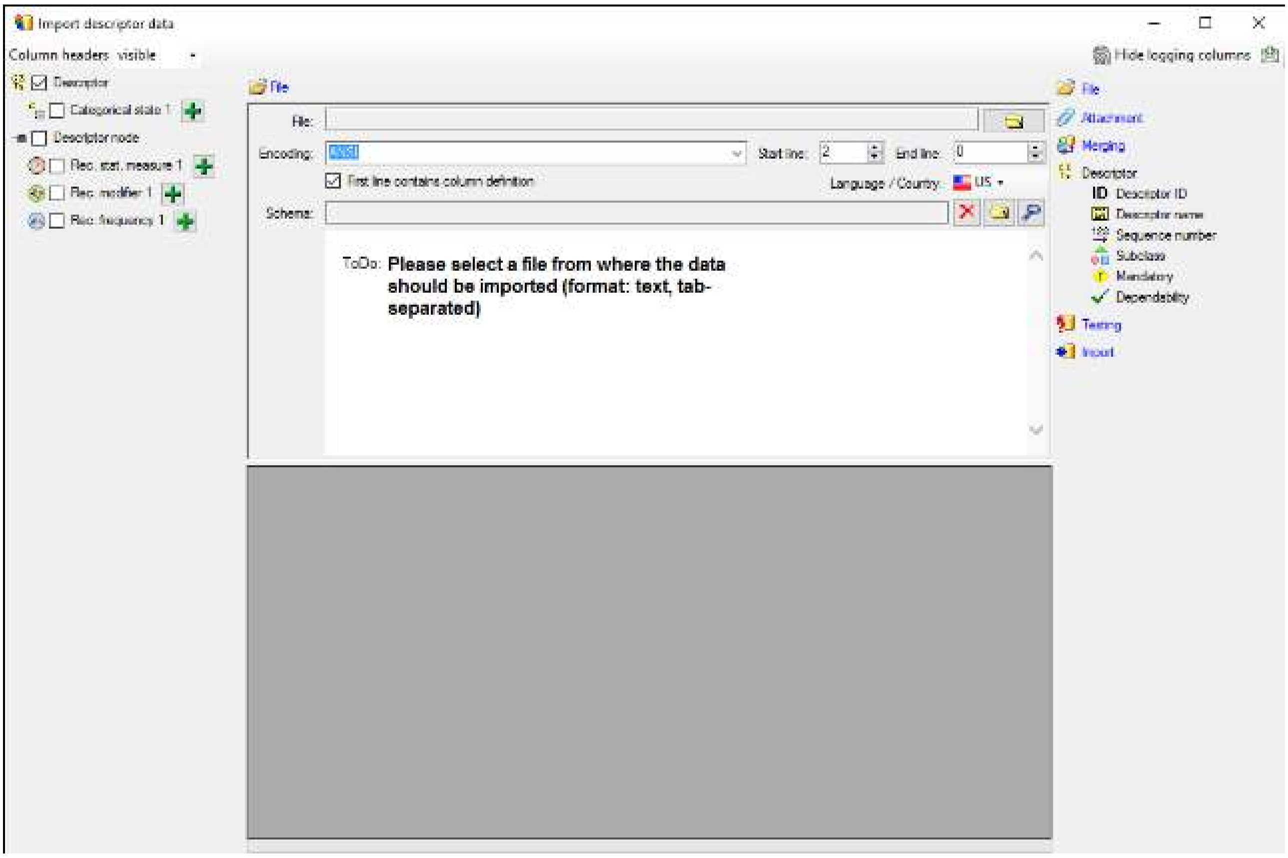


Session project
Agricultural survey
- BactDescDSMZ
- SDD of ETI reptiles and amphibians
- BFLheilpflanzendesc
- Agricultural survey

Session description
Data import for Agricultural survey.

This import session is used to demonstrate the import wizard in DiversityDescriptions...

After clicking **[OK]** the following window opens that will lead you through the import of the descriptor data. The window is separated in three areas. On the left side, you see a list of possible data related import steps according to the type of data you choosed for the import. On the right side you see the list of currently selected import steps. In the center part the details of the selected import step are shown.



Column headers: visible

File:

Encoding: ANSI

Start line: 2

End line: 0

☑ First line contains column definition

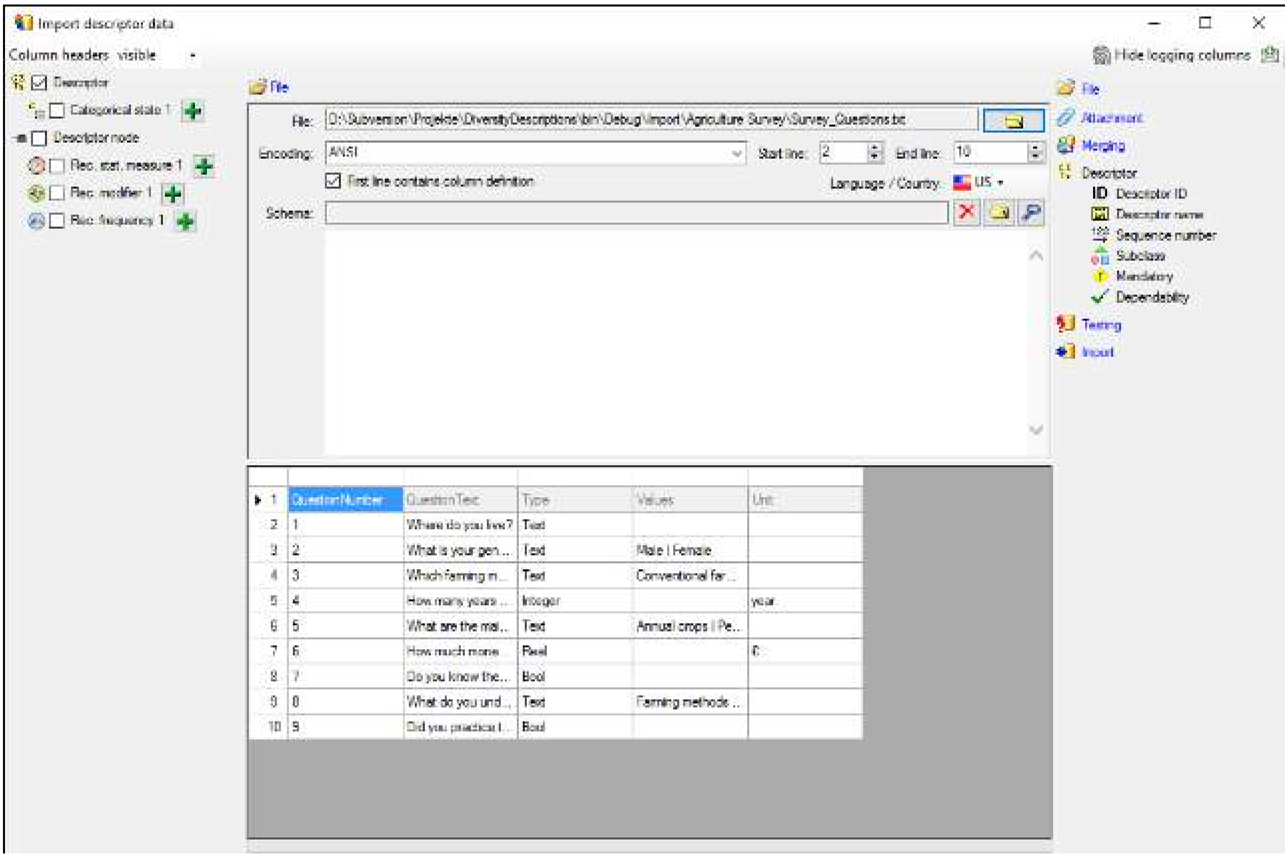
Language / Country: US

Schema:

ToDo: **Please select a file from where the data should be imported (format: text, tab-separated)**

Choosing the File

As a first step, choose the **File** from where the data should be imported. Open file "Survey_Questions.txt". The preselected encoding **ANSI** should be sufficient for our test file. The file column "QuestionText" contains the descriptor names that shall be imported. In file column "QuestionNumber" there is a unique number assigned to each descriptor that will be used by other data tables to reference a certain descriptor. "Type" might give a hint for the descriptor type (categorical, quantitative or text) and "DisplayOrder" may be used to determine the sequence number of the descriptor.



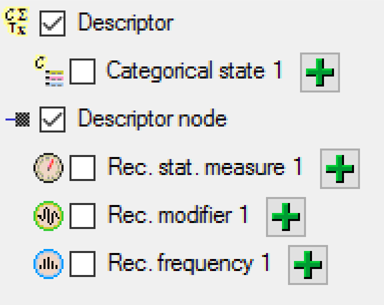
☑ Descriptor
☐ Categorical state 1
☐ Descriptor node
☐ Rec. stat. measure 1
☐ Rec. modifier 1
☐ Rec. frequency 1

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Questions.txt
Encoding: ANSI
Start line: 2
End line: 10
☑ First line contains column definition
Language / Country: US
Schema:

1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import.



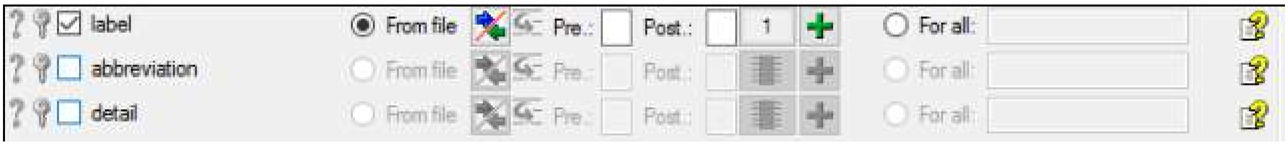
☑ Descriptor
☐ Categorical state 1
☑ Descriptor node
☐ Rec. stat. measure 1
☐ Rec. modifier 1
☐ Rec. frequency 1

The step **Descriptor** is already selected and cannot be de-selected, additionally we select **Descriptor node**, because we want to assign each imported descriptor to a descriptor tree (see above). In the step table at the right side you find the import step **Descriptor** and below the most important data groups of the import step. Click on ID **Descriptor ID** and in the center window the assignemt data for the descriptor id ("id") are displayed. Click on ? to make this the decisive column, further click on **From file** to select the column "QuestionNumber" as data source. After that the column should look as shown below.

☑ id ● From file Pre.: Post.: 0 ○ For all:

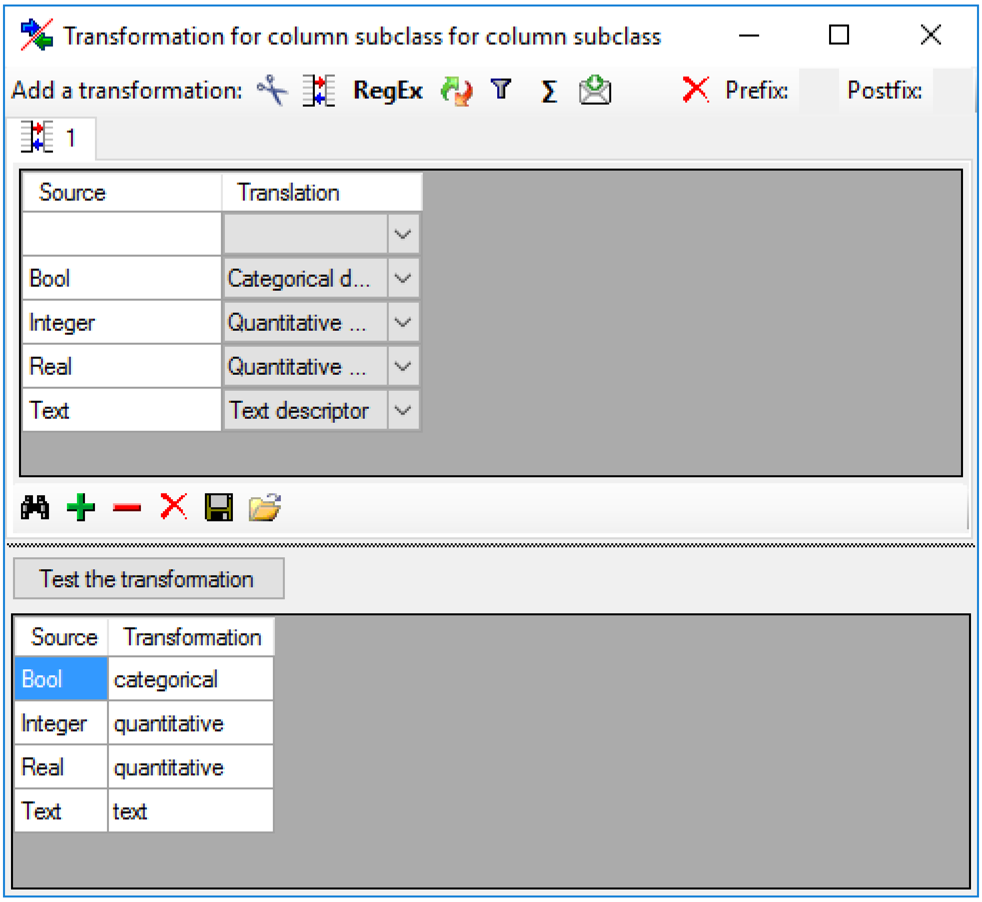
Remark: The ID **Descriptor ID** is a number that is generated automatically from the database when a new descriptor is created. Anyway in the data file there is a field "QuestionNumber" that is linked to a certein descriptor and used in other tables to reference a certain descriptor. The mapping from the "QuestionNumber" values to the internally generated ID **Descriptor ID** values will be stored in a separate import mapping table for the actual import session. In the later import steps this mapping table will allow to find the correct descriptor assigned to a certain "QuestionNumber".

Now the descriptor name must be selected, therefore click on **Descriptor name.** The center window shows three data columns: "label", "abbreviation" and "detail". Click on **From file** in the "label" line to select file column "QuestionText" (see below).



Next click on **Sequence number.** In the center window select the data column "display_order", click on **From file** and select file column "QuestionNumber". (see below).

As already mentioned before the file column "Type" contains information that can be used to determine the descriptor type. Therefore click on **Subclass**, select the "subclass" line, click on **From file** and select the file column "Type". Now click on button to open the transformation window. As only transformation step select to insert a translation table and to list the values contained in the file column. "Bool" shall be converted to "Categorical descriptor", "Integer" and "Real" will become "Quantitative descriptor" and the rest "Text descriptor" (see below).



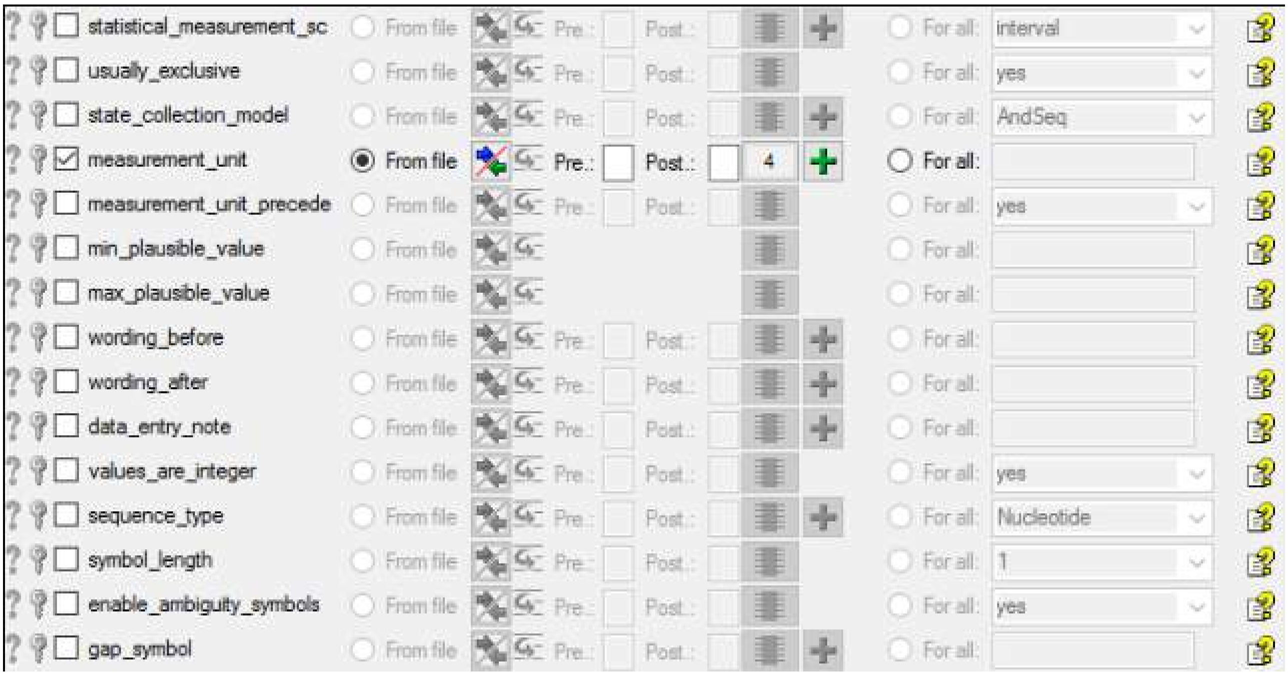
Source	Translation
Bool	Categorical d...
Integer	Quantitative ...
Real	Quantitative ...
Text	Text descriptor

Source	Transformation
Bool	categorical
Integer	quantitative
Real	quantitative
Text	text

The file rows that contain entries in column "Values" seem to specify categorical descriptors but are simply inserted as text characters. We will correct those values when we import the categorical states in a later step. The "subclass" data column now looks as shown below.

	Data column					
☑	subclass	● From file	Pre.:	Post.:	2	○ For all: Categorical descripto

The descriptor step at the right displays the most important data columns grouped in separate steps. Anyway, there are several additional data columns available that can be accessed by clicking on the **Descriptor** step itself. Here we select data column "measurement_unit", choose file column "Unit" (see below).



	Data column					For all:
☐	statistical_measurement_sc	○ From file	Pre.:	Post.:		○ interval
☐	usually_exclusive	○ From file	Pre.:	Post.:		○ yes
☐	state_collection_model	○ From file	Pre.:	Post.:		○ AndSeq
☑	measurement_unit	● From file	Pre.:	Post.:	4	○
☐	measurement_unit_precede	○ From file	Pre.:	Post.:		○ yes
☐	min_plausible_value	○ From file				○
☐	max_plausible_value	○ From file				○
☐	wording_before	○ From file	Pre.:	Post.:		○
☐	wording_after	○ From file	Pre.:	Post.:		○
☐	data_entry_note	○ From file	Pre.:	Post.:		○
☐	values_are_integer	○ From file	Pre.:	Post.:		○ yes
☐	sequence_type	○ From file	Pre.:	Post.:		○ Nucleotide
☐	symbol_length	○ From file	Pre.:	Post.:		○ 1
☐	enable_ambiguity_symbols	○ From file	Pre.:	Post.:		○ yes
☐	gap_symbol	○ From file	Pre.:	Post.:		○

To do the assignment of the imported descriptors to the descriptor tree that was created in the preparation step, select **Descriptor node ID** from step **Descriptor node** and supply it exactly the samy way as the **Descriptor ID**. (Don't forget to click on ? to make it the decision column.) Furthermore supply the **Sequence number** in the same way as described above.

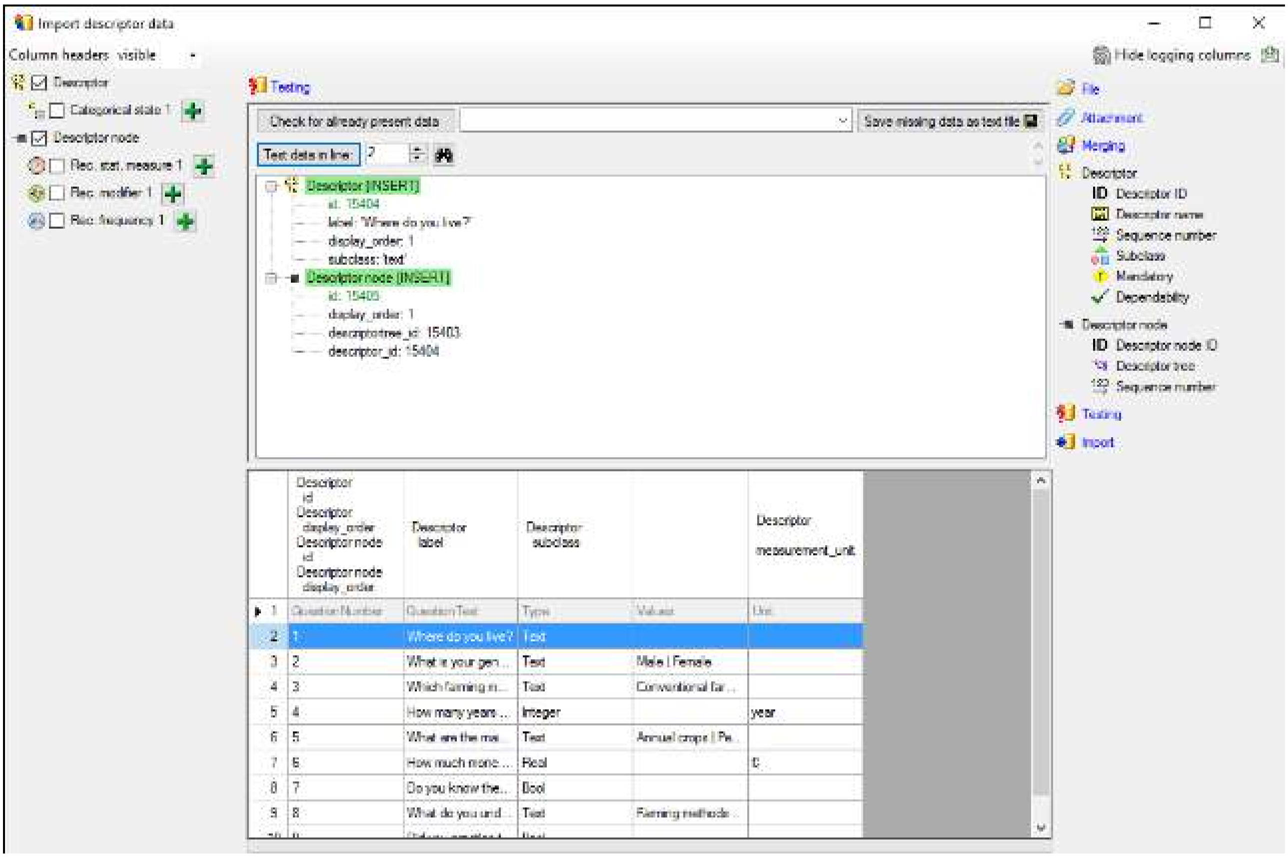
Finally select import step **Descriptor tree**, select data column "descriptortree_id", choose ● **For all:** and select entry "Main tree for Agricultural survey" from the drop down (see below). With this adjustment every imported descriptor will automatically be assigned to that descriptor tree.

	Data column				
☑	descriptortree_id	○ From file	Pre.:	Post.:	● For all: or Agricultural survey

Remark: Although descriptortree_id is a numeric value in the database, the externally visible descriptor tree name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. In our example no error occured and the test for the first data line is shown below.



Descriptor [INSERT]
- id: 15404
- label: 'Where do you live?'
- display_order: 1
- subclass: 'text'

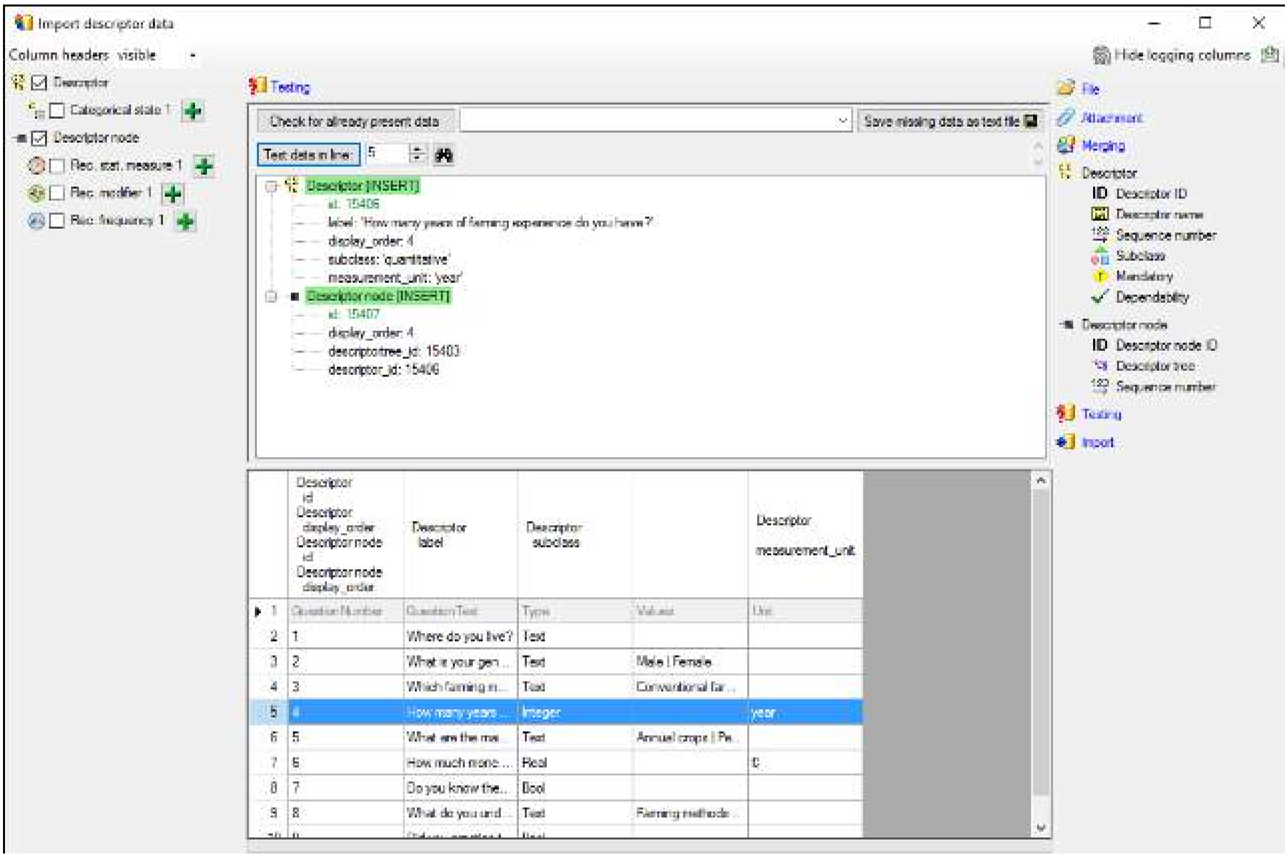
Descriptor node [INSERT]
- id: 15405
- display_order: 1
- descriptortree_id: 15403
- descriptor_id: 15404

	Descriptor id Descriptor display_order Descriptor node id Descriptor node display_order	Descriptor label	Descriptor subclass		Descriptor measurement_unit
1	Question Number	Question Text	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the ma...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods...	

You can see that in table "Descriptor" for data column "id" a new value 325050 is generated - remember that from file column "ParamID" the value 1 was selected. The mapping of the external value (1) to the internal value (325050) in table "Descriptor" will be stored in the "ImportMapping" table of the actual import session. I.e. if in a subsequent import step for the same session a "Descriptor.id=1" is specified in the import schema, it will automatically be translated to the internal "Descriptor.id=325050". Anyway, usually you do not have to take care about this automatic translation. This example shall only demonstrate the meaning of the import sessions.

Remark: Since testing works with transaction rollback, the "id" values shown in the test window are different from the values resulting from a real import.

As a second example data line 4 with "DataType=Integer" was selected to demonstrate that the descriptor subtype is correctly set to "quantitative" (see below).



Test data in line: 5

- Descriptor [INSERT]
  - id: 15406
  - label: 'How many years of farming experience do you have?'
  - display_order: 4
  - subclass: 'quantitative'
  - measurement_unit: 'year'
- Descriptor node [INSERT]
  - id: 15407
  - display_order: 4
  - descriptortree_id: 15403
  - descriptor_id: 15406

	Descriptor id Descriptor display_order Descriptor node id Descriptor node display_order	Descriptor label	Descriptor subclass		Descriptor measurement_unit
1	Question Number	Question Text	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the ma...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).

Schedule for import of tab-separated text files into DiversityDescriptions

Target within DiversityDescriptions: **Descriptor**

Schedule version: **1**
Database version: **03.00.17**
Lines: **2 - 10**
First line contains column definition: **✓**
Encoding: **ANSI**
Language: **US**

Tables **Descriptor** (Descriptor) Merge handling: **Insert** **Column in table**	?	Ke y	Co py	Pr e	P st
id	?				
label					
display_order					
subclass					

measurement_unit					

DescriptorTreeNode (DescriptorTreeNode)
Parent: Descriptor
Merge handling: **Insert**

Column in table	?	Key	Copy	Pre	Post	File pos.	Transformations	Value	Source	Table
id	**?**					0			File	
display_order						0			File	
descriptortree_id								Main tree for Agricultural survey	Interface	
descriptor_id									ParentTable	

Lines that could not be imported will be marked with a red background while imported lines are marked green.

If you want to save lines that produce errors during the import in a separate file, use the "Save failed lines" option. The protocol of the import will contain all settings acording to the used schema and an overview containing the number of inserted, updated, unchanged and failed lines (see below).

Protocol

Responsible: **Link**
Date: **Dienstag, 11. April 2017, 12:56:46**
Server: **training.diversityworkbench.de**
Database: **DiversityDescriptions_Workshop**
Lines total: 9
Lines imported: 9

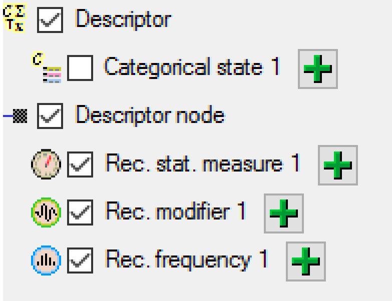
Next: Step 3 - Insert recommended values of descriptors

Step 3 - Insert recommended values of descriptors

Now we have imported the descriptors and assigned them to a descriptor tree. Since we have several quantitative descriptors, we should at least assign one recommended statistical measure to these descriptors. In this step we will additionally insert recommended modifier and frequency vales. If your database does not yet include modifier and frequency values, you might like to interrupt here and insert them according chapter Edit projects - Modifier/Frequency tab of this manual.

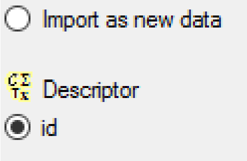
Finally we want to set the "values_are_integer" flag for the descriptor, that is specified as "Integer" in the file column "Type". We could have done this during the previous import step, but here we can demonstrate the update existing data sets with the import wizard.

In the selection list on the left side of the window select **Rec. stat. measure 1**, **Rec. modifier 1** and **Rec. frequency 1** (see below).



☑ Descriptor
☐ Categorical state 1
☑ Descriptor node
☑ Rec. stat. measure 1
☑ Rec. modifier 1
☑ Rec. frequency 1

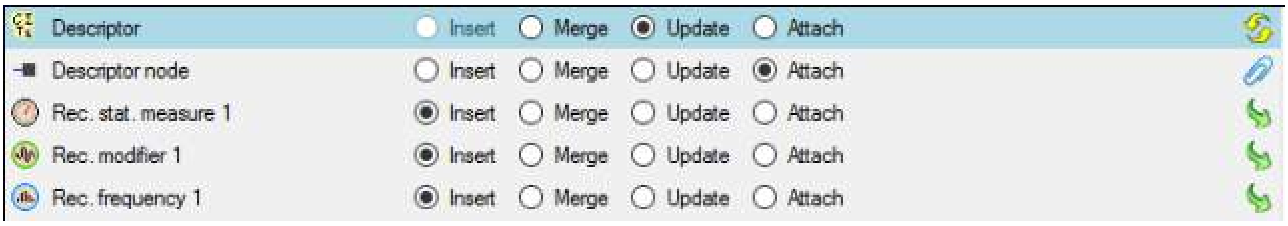
In this step we attach the recommended values to all descriptor nodes, therefore we will not change anything in the descriptor or descriptor node but will attach data. In import step **Attachment** at the right side select **id** (see below).



○ Import as new data

Descriptor
● id

Select the import step **Merge** from the list. For **Descriptor** we select the **Update** option because the "values_are_integer" column shall be updated. For **Descriptor node** we select the **Attach** option because this tables shall not be changed. For all other steps **Insert** should already be selected, because new entries have to be inserted (see below).



Descriptor ○ Insert ○ Merge ● Update ○ Attach
Descriptor node ○ Insert ○ Merge ○ Update ● Attach
Rec. stat. measure 1 ● Insert ○ Merge ○ Update ○ Attach
Rec. modifier 1 ● Insert ○ Merge ○ Update ○ Attach
Rec. frequency 1 ● Insert ○ Merge ○ Update ○ Attach

Deselect every column from import steps **Descriptor** and **Descriptor node** except "id". Mark the "id" columns as **Key column** for comparison during attachment. The "id" column of import step **Descriptor** now looks as shown below.

☑ id Pre.: Post.: 0

The "id" column of import step **Descriptor node** now looks as shown below.

☑ id ● From file Pre.: Post.: 0 ○ For all:

Selecting the values

In the step table at the right side click on the import step **Rec. stat. measure 1** and in the center window the assignemt data for the statistical measure ("measure_id") are displayed. Click on to make this the decisive column, further click on **For all:** and select entry "Central or typical value (human estimate)" from the drop down (see below).

☑ measure_id ○ From file Pre.: Post.: ● For all: Central or typical val

Select values for **Rec. modifier 1** and **Rec. frequency 1** in the same way, the actually selected modifier and frequency values do not matter for this tutorial (see below).

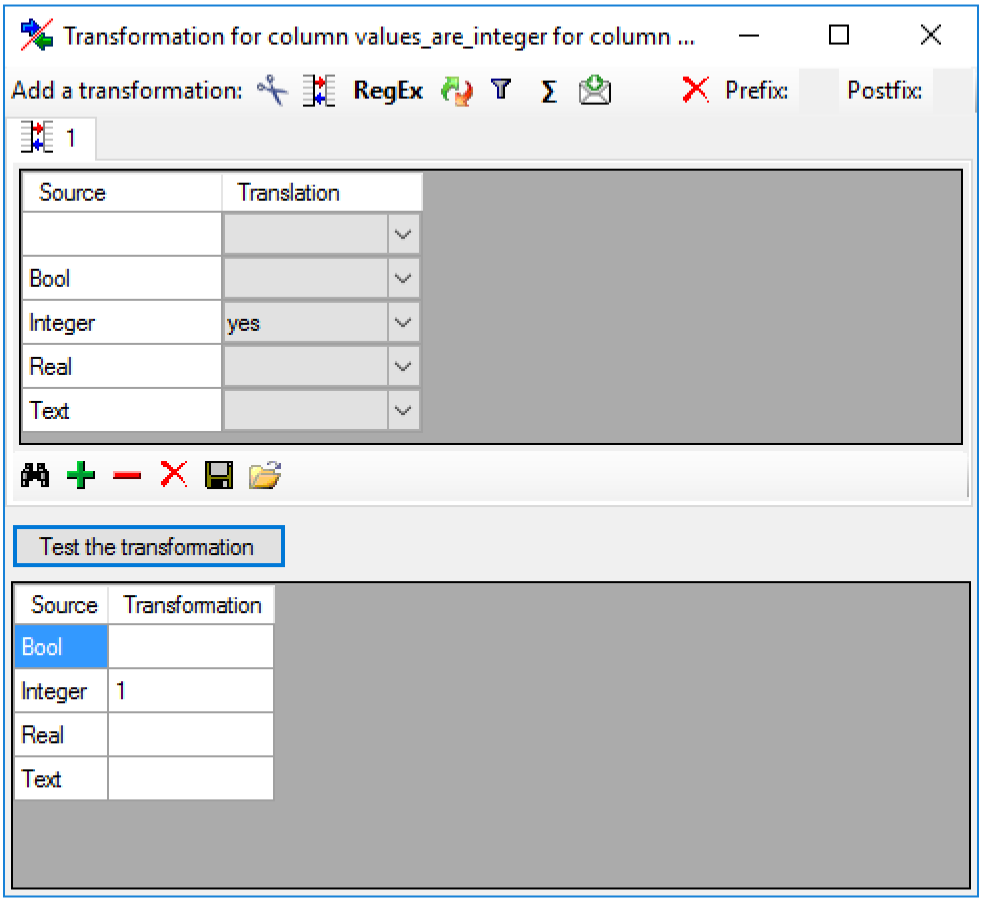
☑ modifier_id ○ From file Pre.: Post.: ● For all: almost

☑ frequency_id ○ From file Pre.: Post.: ● For all: often

Remark: Although measure_id, modifier_id and frequency_id are numeric values in the database, the externally visible names are expected here. Since this names are unambigious, the corresponding ids will be determined during import.

If you want to insert more than one recommended value of a type, click on button of the import step at the left side of the window. Select the new inserted step and supply the "measure_id", "modifier_id" or "frequency_id" as described above.

Now we will enter the update of the "values_are_integer" data column. Select the import step **Descriptor** and select the "values_are_integer" line. Click on **From file** and select the file column "Type". Now click on button to open the transformation window. As only transformation step select to insert a translation table and to insert the values contained in the file column. For "Integer" the data column value shall be set to "yes" as shown below.



Source	Translation
Bool	
Integer	yes
Real	
Text	

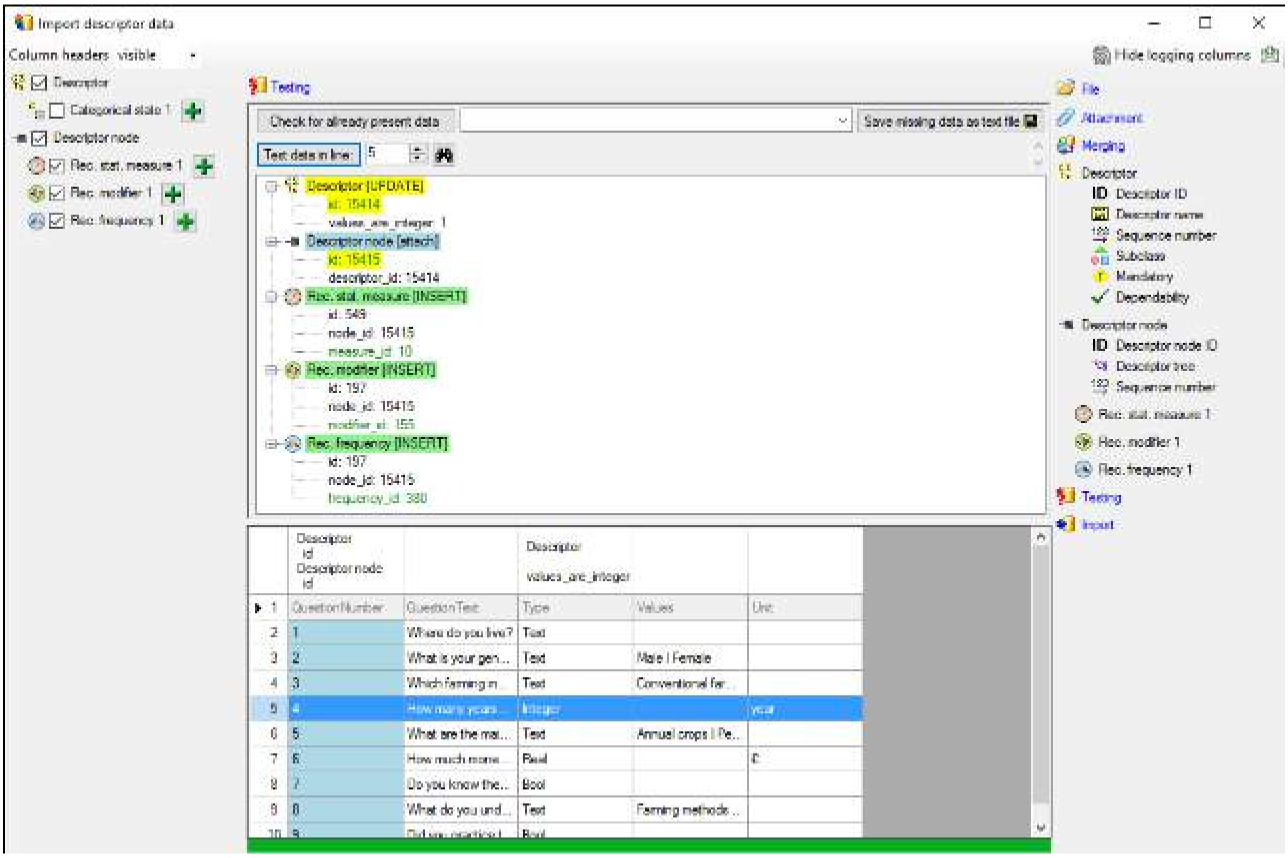
Source	Transformation
Bool	
Integer	1
Real	
Text	

The "values_are_integer" column of import step **Descriptor** now looks as show below.


☑ values_are_integer ● From file Pre.: Post.: 2 ○ For all: yes

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. In our example no error occured and the test for the fifth data line is shown below.



Descriptor [UPDATE]
- id: 15414
- values_are_integer: 1

Descriptor node [attach]
- id: 15415
- descriptor_id: 15414

Rec. stat. measure [INSERT]
- id: 549
- node_id: 15415
- measure_id: 10

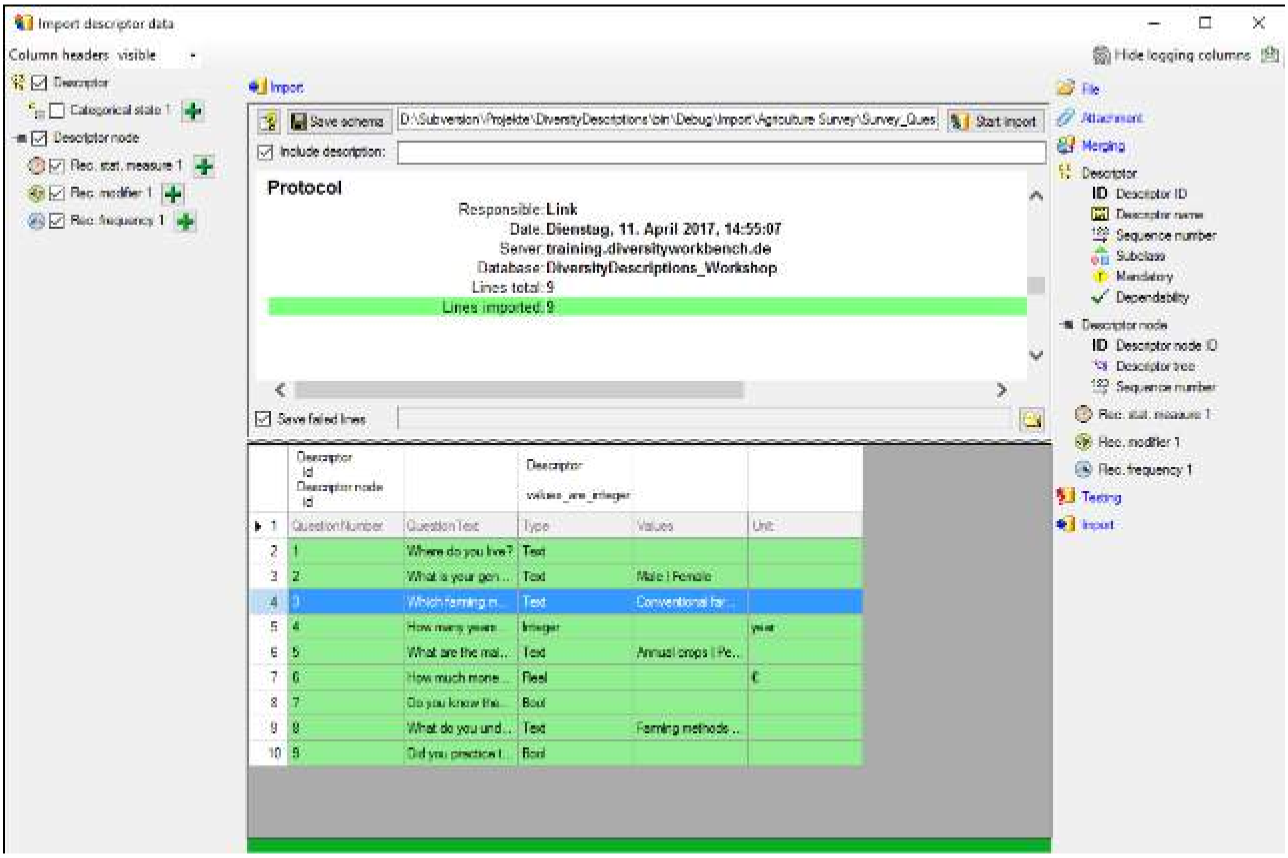
Rec. modifier [INSERT]
- id: 197
- node_id: 15415
- modifier_id: 155

Rec. frequency [INSERT]
- id: 197
- node_id: 15415
- frequency_id: 380

	Descriptor id Descriptor node id		Descriptor values_are_integer		
1	Question Number	Question Text	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming in...	Text	Conventional far...	
5	4	How many years...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. The imported data lines are marked green (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Ques

☑ Include description:

Protocol

Responsible: **Link**
Date: **Dienstag, 11. April 2017, 14:55:07**
Server: **training.diversityworkbench.de**
Database: **DiversityDescriptions_Workshop**
Lines total: 9
Lines imported: 9

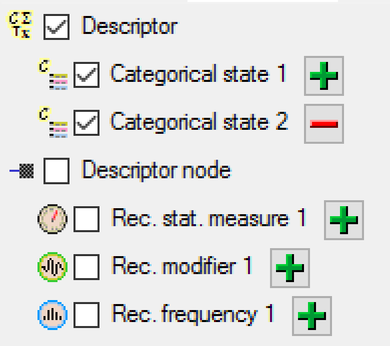
☑ Save failed lines

	Descriptor Id Descriptor node Id		Descriptor values_are_integer		
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

Next: Step 4 - Import of categorical states for boolean data

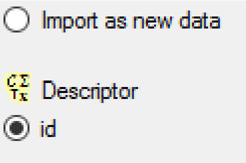
Step 4 - Import of categorical states for boolean data

Now we want to import categorical states for the descriptors specified as "Bool" in the table. In the selection list on the left side of the window deselect **Descriptor node**, **Rec. stat. measure 1**, **Rec. modifier 1** and **Rec. frequency 1**. Select **Categorical state 1**, click on the + button to insert a second categorical state and select it, too (see below).



☑ Descriptor
☑ Categorical state 1 +
☑ Categorical state 2 −
☐ Descriptor node
☐ Rec. stat. measure 1 +
☐ Rec. modifier 1 +
☐ Rec. frequency 1 +

In this step we attach two categorical states named "Yes" and "No" at those descriptors that are marked as "Bool" in file column "Type". The state values are not present in the "Survey_Questions.txt" file, but in the "Survey_answers.txt" files we can see the values. In import step **Attach** at the right side we select **id** (see below). It indicates that we do not want to insert new descriptors but attach data to an existing descriptor.



○ Import as new data

Descriptor
● id

Select the import step **Merge** from the list. For **Descriptor** we select the **Attach** option because this table shall not be changed, for **Categorical state 1** we select **Insert**, because a new entry shall be inserted (see below).

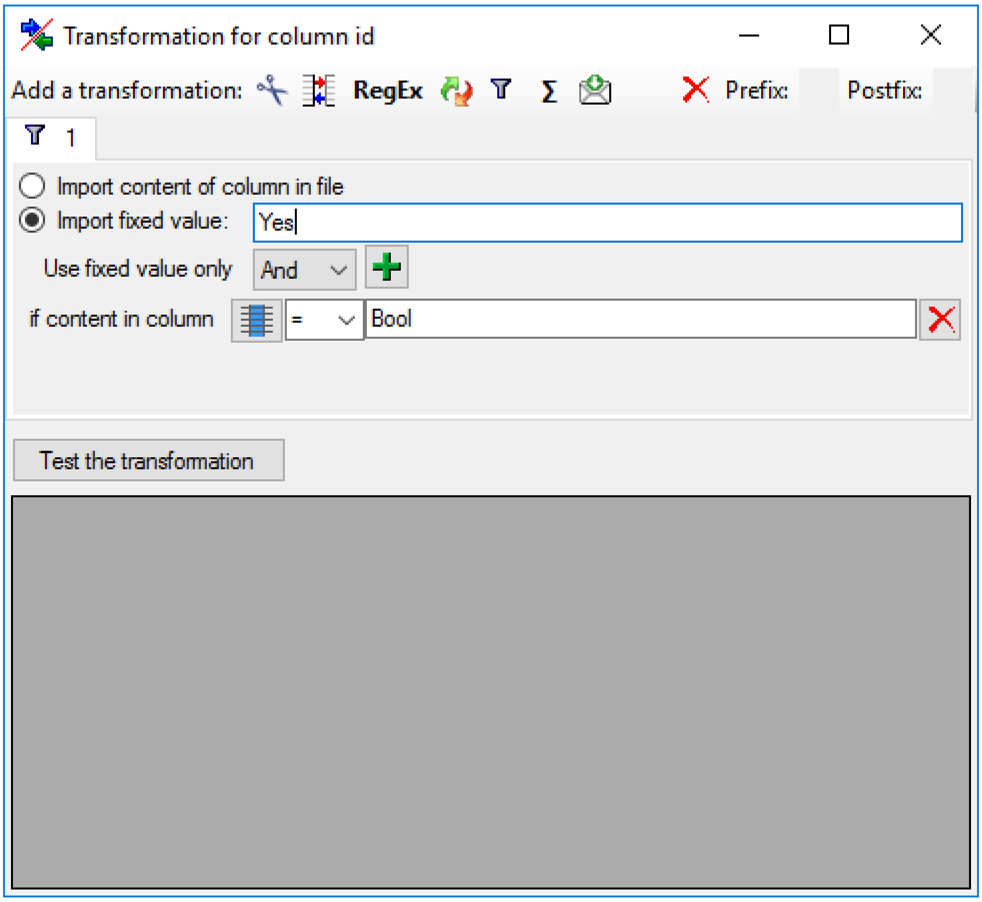
Descriptor	○ Insert	○ Merge	○ Update	● Attach
Categorical state 1	● Insert	○ Merge	○ Update	○ Attach
Categorical state 2	● Insert	○ Merge	○ Update	○ Attach

Deselect every column from import step **Descriptor** except "id". Mark the "id" column as **Key column** for comparison during attachment (see below).

☑ id Pre.: Post.: 0

Inserting the categorical states

In the import step **Categorical state 1** click on **Categorical state ID** and in the center window the assignemt data for the categorical state id ("id") are displayed. Click on ? to make this the decisive column, further click on **From file** to select the column "Type" as data source. Now click on button to define a transformation. In the tranformation window click on to select a filter, then select ● **Import fixed value** and enter the value **Yes**. Now click on the button choose column "Type" from the file and enter compare value **Bool** (see below).



○ Import content of column in file

● Import fixed value: Yes

Use fixed value only: And

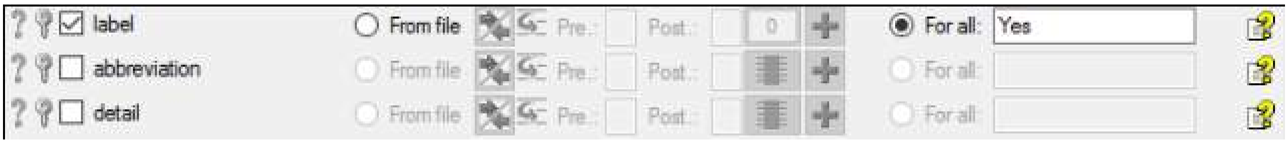
if content in column = Bool

This filter has the following effect: If file column "Type" contains value **"Bool"**, the value **Yes** is provided for import, otherwise the file row will be ignored. The column now looks as shown below.

Remark: The **Categorical state ID** is a number that is generated automatically from the database when a new categorical state is created. At first sight it seems confusing that we select a string for this numeric key. The point is that in the file with the description data the corresponding catogorical state is idenified by exactly this categorical state name. Since we select this categorical state name for the **Categorical state ID**, the mapping between these two values will be stored in a separate import mapping table for the actual import session. In the later import steps this mapping table will allow to find the correct categorical state.

☑ id ● From file Pre.: Post.: 2 ○ For all:

In the import step **Categorical state 1** click on **Categorical state name** and in the center window the assignemt data for the categorical state name ("label"), its abbreviation and detailled description ("abbreviation" and "details") are displayed. Select "label" and click on ● **For all:** and enter the value **Yes**. The column now looks as shown below.

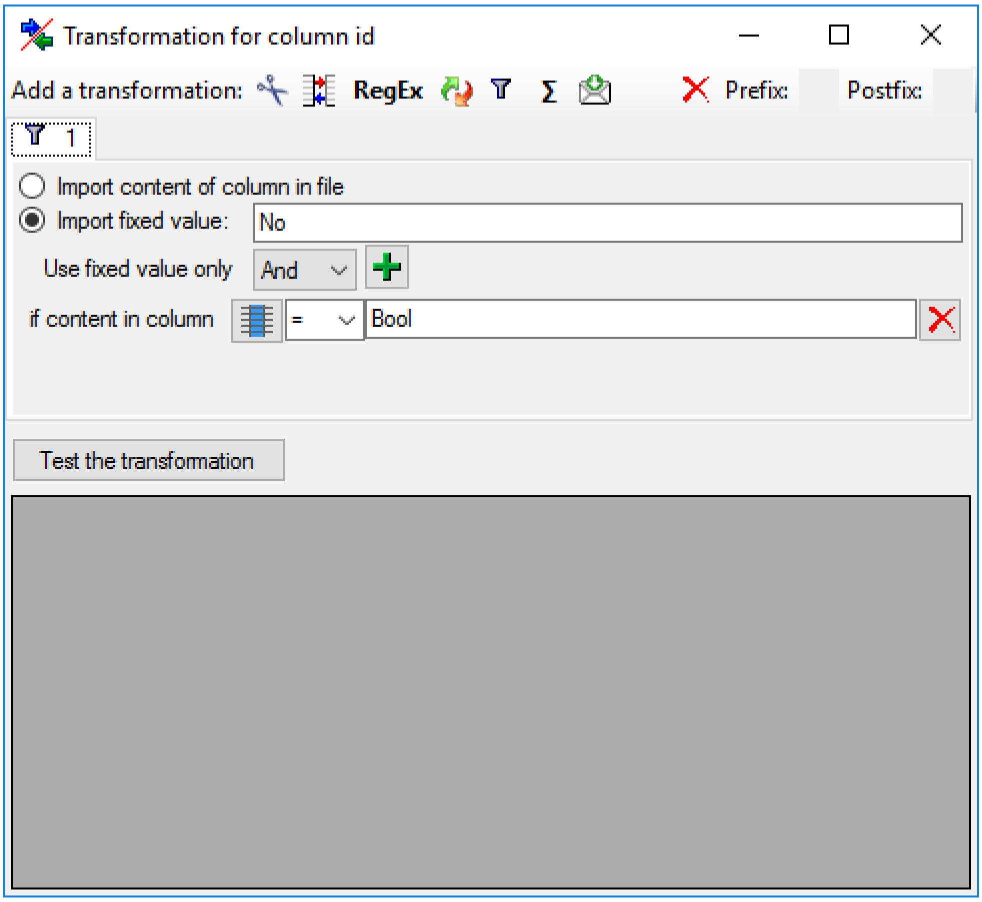


☑ label ○ From file Pre.: Post.: 0 ● For all: Yes
☐ abbreviation ○ From file Pre.: Post.: ○ For all:
☐ detail ○ From file Pre.: Post.: ○ For all:

Finally we supply the **Sequence number**. Select **For all:** with **1** (see below).


☑ display_order ○ From file Pre.: Post.: 0 ● For all: 1

In the import step **Categorical state 2** click on **Categorical state ID** and in the center window the assignemt data for the categorical state id ("id") are displayed. Click on to make this the decisive column, further click on **From file** to select the column "Type" as data source. Now click on button to define a transformation. In the tranformation window click on to select a filter, then select **Import fixed value** and enter the value **No**. Now click on the button choose column "Type" from the file and enter compare value **Bool** (see below).


Transformation for column id

○ Import content of column in file
● Import fixed value: No
Use fixed value only And
if content in column = Bool

This filter has the following effect: If file column "DataType" contains value **"Bool"**, the value **No** is provided for import, otherwise the file row will be ignored. The column now looks as shown below.


☑ id ● From file Pre.: Post.: 2 ○ For all:

In the import step **Categorical state 1** click on **Categorical state name** and in the center window the assignemt data for the categorical state name ("label"), its abbreviation and detailled description ("abbreviation" and "details") are displayed. Select "label" and click on **For all:** and enter the value **Yes**. The column now looks as shown below.

☑ label ○ From file ● For all: No

☐ abbreviation ○ From file ○ For all:

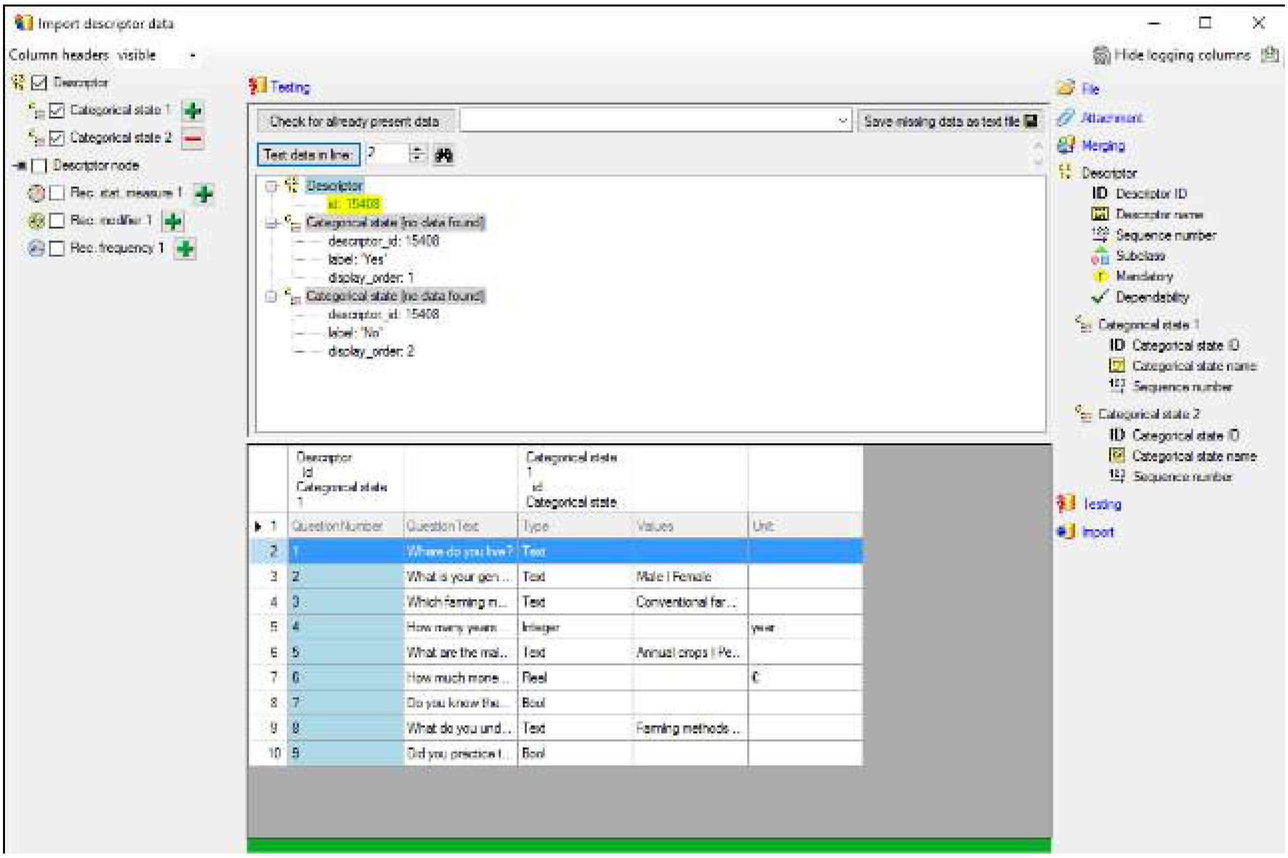
☐ detail ○ From file ○ For all:

Finally we supply the 123 **Sequence number**. Select ● **For all:** with "2" (see below).

☑ display_order ○ From file ● For all: 2

Testing

To test if all requirements for the import are met use the **Testing** step. First the test for data line 2 is shown below, which is an example for a non "Bool" descriptor.

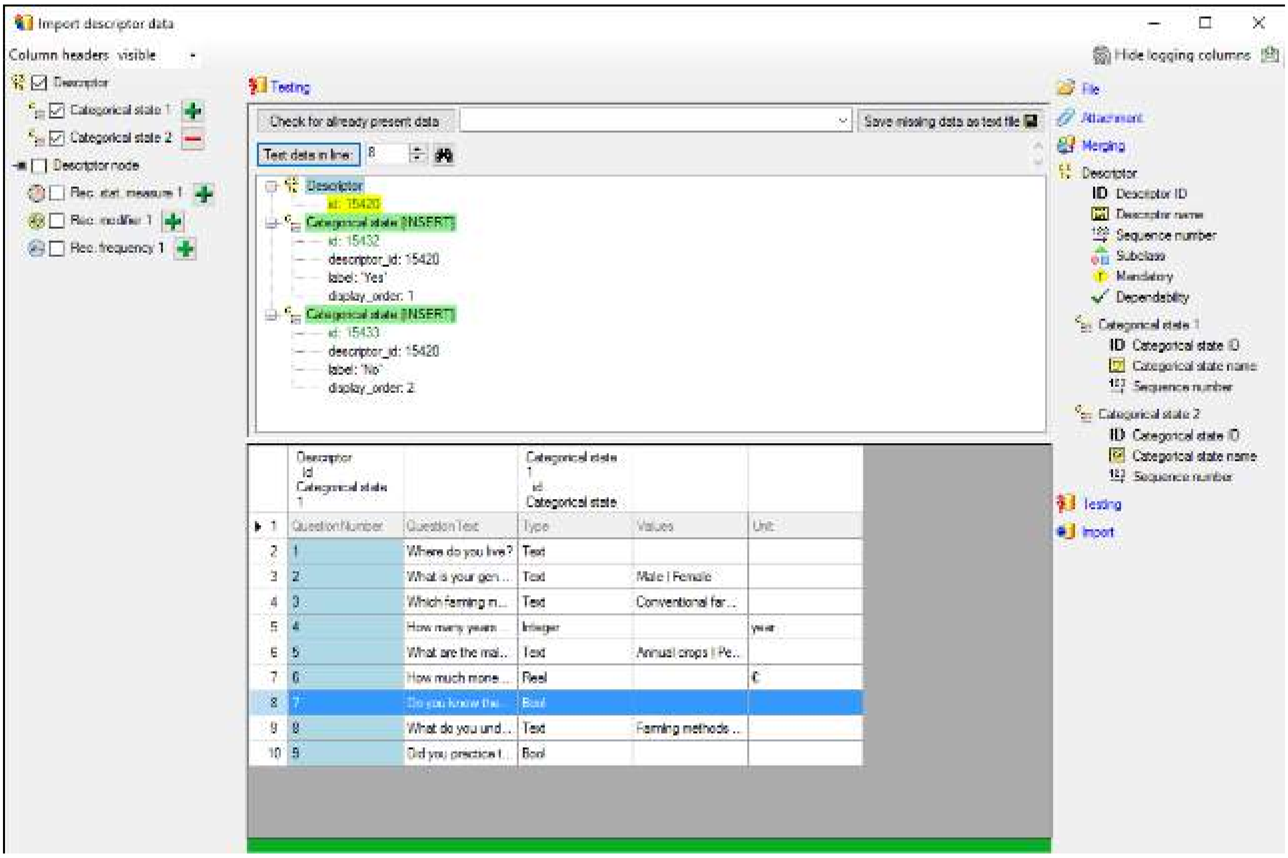


Test data in line: 2

```
Descriptor
    id: 15408
Categorical state [no data found]
    descriptor_id: 15408
    label: 'Yes'
    display_order: 1
Categorical state [no data found]
    descriptor_id: 15408
    label: 'No'
    display_order: 2
```

	Descriptor Id Categorical state 1		Categorical state 1 Id Categorical state		
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen ...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone ...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

No data shall be inserted. Below the test result for data line 8, a "Bool" descriptor, is shown.



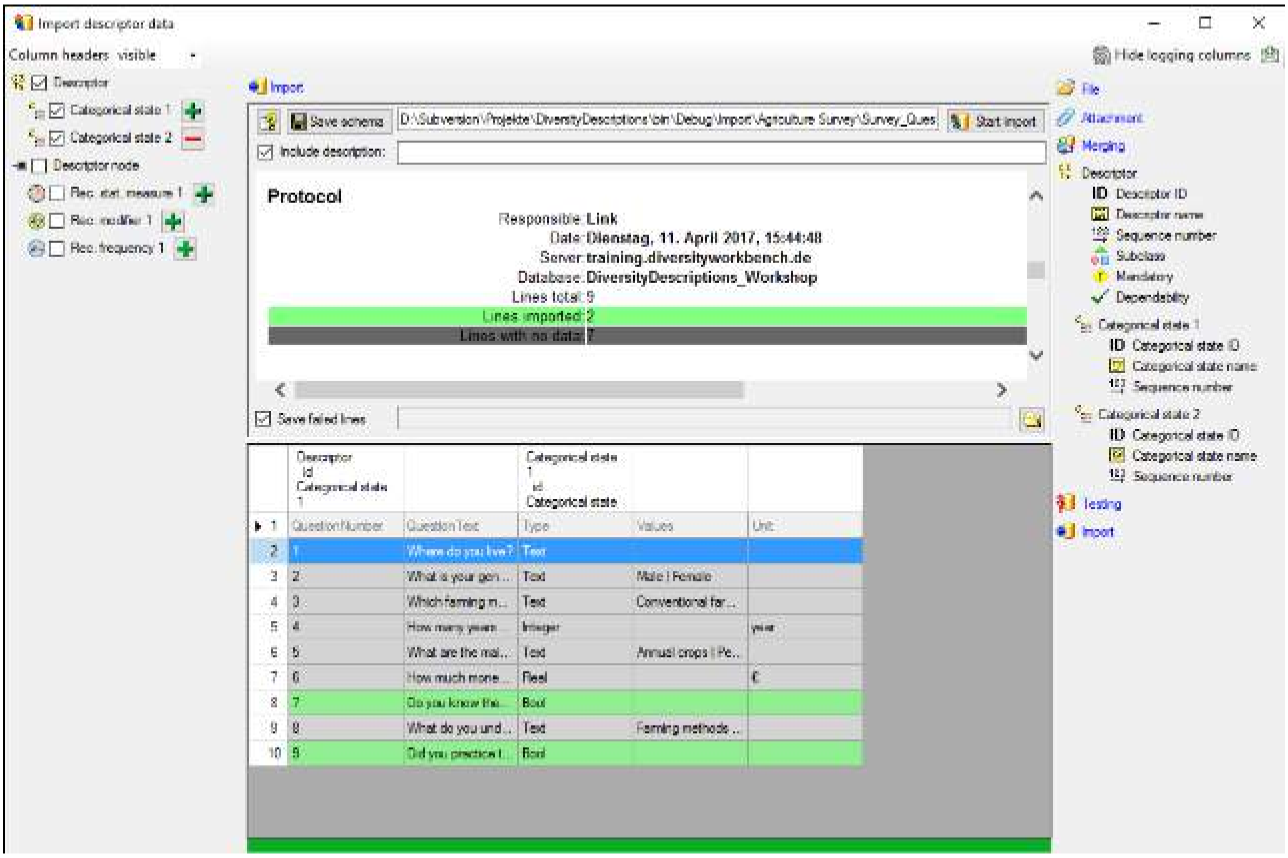
Test data in line: 8

```
Descriptor
    id: 15420
Categorical state [INSERT]
    id: 15432
    descriptor_id: 15420
    label: 'Yes'
    display_order: 1
Categorical state [INSERT]
    id: 15433
    descriptor_id: 15420
    label: 'No'
    display_order: 2
```

	Descriptor id Categorical state 1		Categorical state 1 id Categorical state		
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen…	Text	Male | Female	
4	3	Which farming m…	Text	Conventional far…	
5	4	How many years …	Integer		year
6	5	What are the mai…	Text	Annual crops | Pe…	
7	6	How much mone…	Real		€
8	7	Do you know the…	Bool		
9	8	What do you und…	Text	Farming methods …	
10	9	Did you practice t…	Bool		

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. The imported data lines are marked green, the ignored data lines grey (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Ques

☑ Include description:

Protocol

Responsible: **Link**
Date: **Dienstag, 11. April 2017, 15:44:48**
Server: **training.diversityworkbench.de**
Database: **DiversityDescriptions_Workshop**
Lines total: 9
Lines imported: 2
Lines with no data: 7

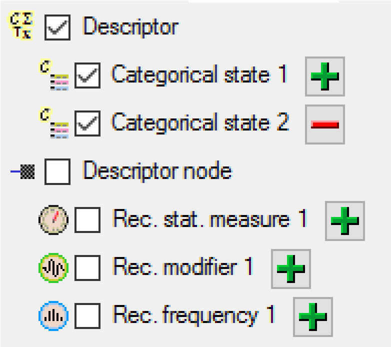
☑ Save failed lines

	Descriptor Id Categorical state 1		Categorical state 1 id Categorical state		
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	
10	9	Did you practice t...	Bool		

Next: Step 5 - Import of categorical states and update of descriptor

Step 5 - Import of categorical states and update of descriptor data

Now we want to import the categorical states that are specified in file column "Values" and set the subclass for those descriptors from "text" to "categorical". In the selection list on the left side of the window **Descriptor**, **Categorical state 1** and **Categorical state 2** are still selected and **Descriptor node 1** is deselected (see below). Furthermore the descriptor id is selected for attachment.

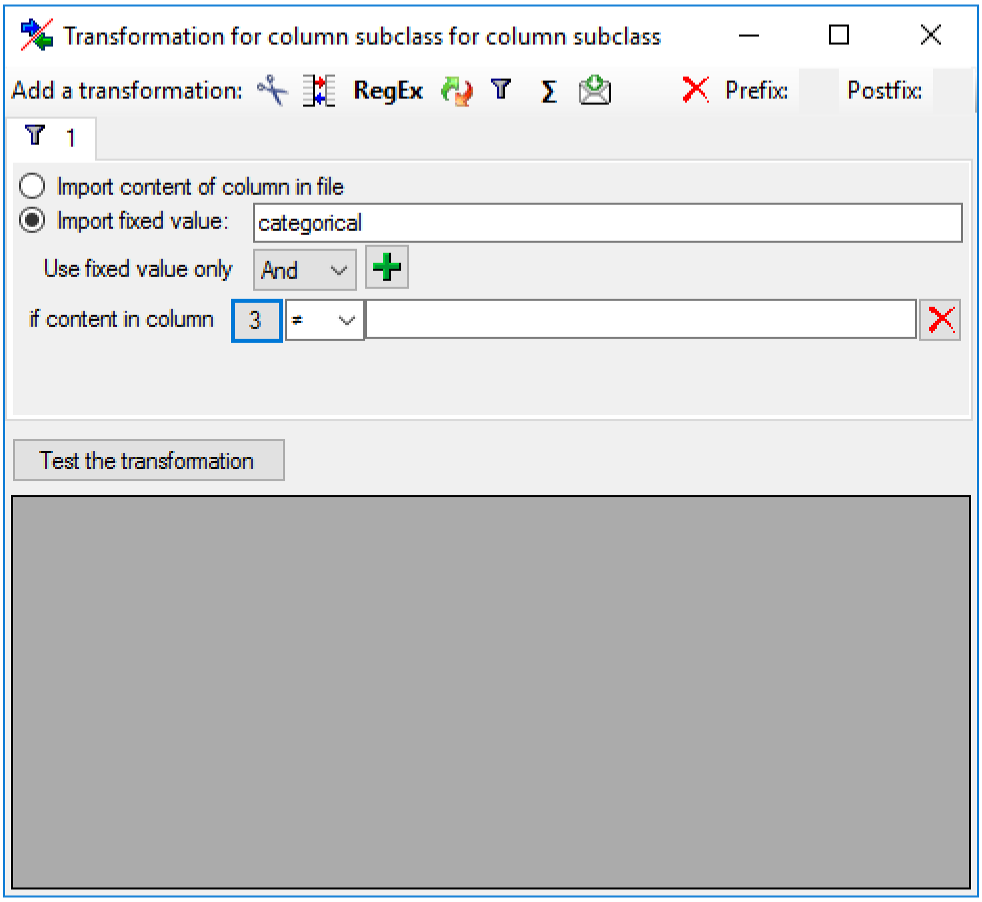


☑ Descriptor
☑ Categorical state 1
☑ Categorical state 2
☐ Descriptor node
☐ Rec. stat. measure 1
☐ Rec. modifier 1
☐ Rec. frequency 1

Since we want to change the descriptor data, we have to change the import step **Merge** from the list. For **Descriptor** we select the **Update** option (see below).

Descriptor ○ Insert ○ Merge ● Update ○ Attach
Categorical state 1 ● Insert ○ Merge ○ Update ○ Attach
Categorical state 2 ● Insert ○ Merge ○ Update ○ Attach

In the import step **Descriptor** click on **Subclass**, select file column "Values" and click on button to open the transformations. By clicking the button the transformations of previous steps are removed. In the tranformation window click on to select a filter, then select **Import a fixed value** and enter the value **categorical**. Now click on the button choose column "Values" from the file and select <not equal> blank (see below).


Transformation for column subclass for column subclass

Add a transformation: RegEx Prefix: Postfix:

1

○ Import content of column in file

● Import fixed value: categorical

Use fixed value only: And

if content in column 3 ≠

This filter will provide the value "categorical" for database column "subclass" if file column "Values" is not empty. If "Value" is empty, no value is provided and the "subclass" stays unchanged. The column now looks as shown below.

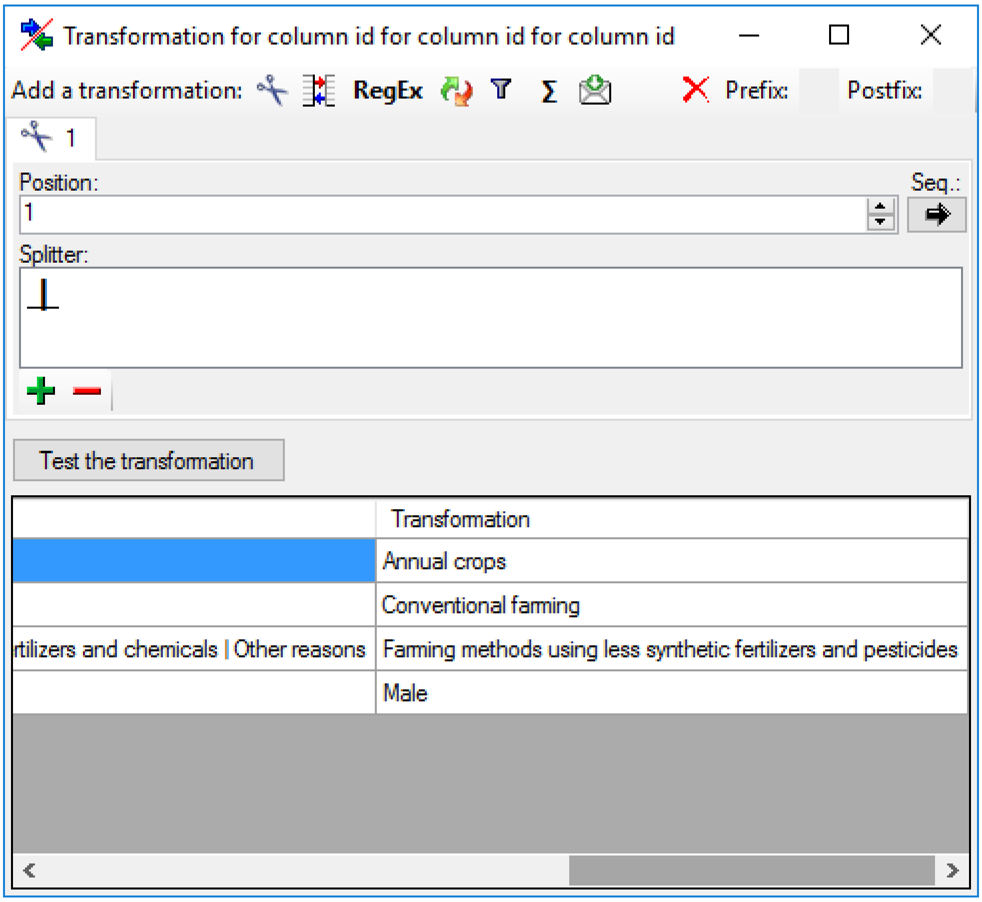

☑ subclass ● From file Pre.: Post.: 2 ○ For all: Categorical descripto

Inserting the categorical states

A closer look on the "Values" file column shows that the states are provided as a list of values separated by the pipe symbol and blanks (" | "). To get the single state values, we have to split off a value at the string " | ". This value will then be used for the **Categorical state ID** and the **Categorical state name**.

In the import step **Categorical state 1** click on **Categorical state ID** and in the center window the assignemt data for the categorical state id ("id") are displayed. Click on to make this the decisive column, further click on **From file** to select the column "Values" as data source. Now click on button to define a transformation.

In the tranformation window click on the cut transformation, enter **Position:** **1**, click on to enter splitter character **|** (blank, pipe, blank). By clicking on button **[Test the tranformation]** you can check the transformation results (see below).


Transformation for column id for column id for column id

Position: 1

Seq.:

Splitter:

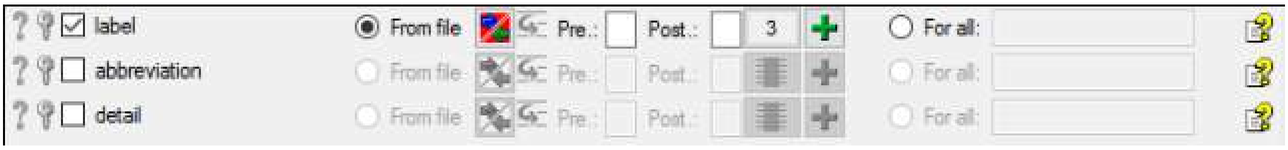
	Transformation
	Annual crops
	Conventional farming
rtilizers and chemicals | Other reasons	Farming methods using less synthetic fertilizers and pesticides
	Male

The column now looks as shown below.


☑ id ● From file Pre.: Post.: 4

Remark: The ID **Categorical state ID** is a number that is generated automatically from the database when a new categorical state is created. At first sight it seems confusing that we select a string - the catigorical state name - for this numeric key. The point is that in the file with the description data the corresponding catogorical state is idenified by exactly this categorical state name. Since we select this categorical state name for the ID **Categorical state ID**, the mapping between these two values will be stored in a separate import mapping table for the actual import session. In the later import steps this mapping table will allow to find the correct categorical state.

Now supply exactly the same filter settings for **Categorical state name** but do not mark it as decisive column (see below).


☑ label ● From file Pre.: Post.: 3 ○ For all:

☐ abbreviation ○ From file Pre.: Post.: ○ For all:

☐ detail ○ From file Pre.: Post.: ○ For all:

Finally we supply the 123 **Sequence number**. Select ● **For all:** with **1** (see below).


☑ display_order ○ From file Pre.: Post.: 0 ● For all: 1

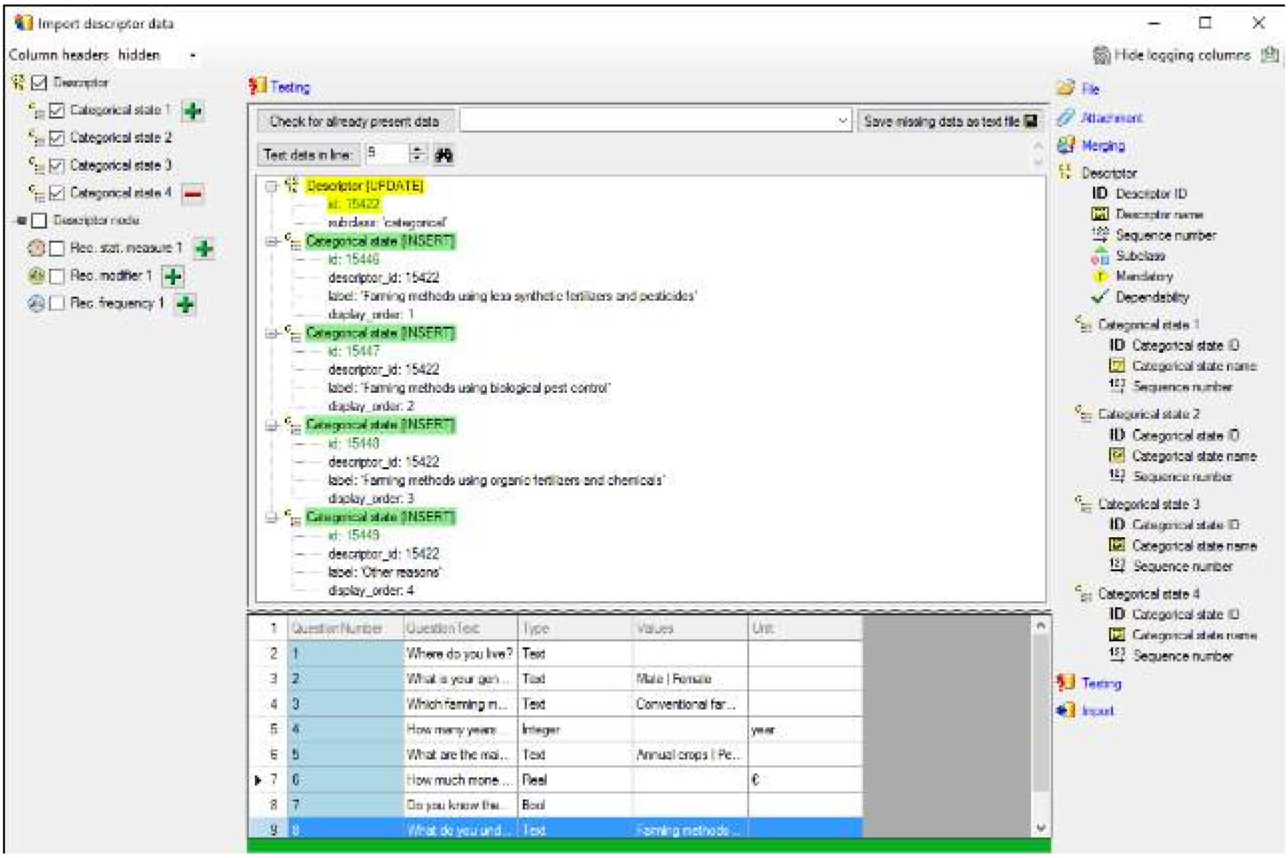
And now there is some "fun":

The longest entry in column "Values" contains four entries separated by pipes and blanks.

Therefore click two more times on the ✚ button of step **Categorical state 1** on the left side and select the new steps **Categorical state 3** and **Categorical state 4**. For each of the remaining steps supply the columns in the same way as for **Categorical state 1**, but increase the **Position:** value in the cut transformations and the **For all:** value in **Sequence number**.

Testing

To test if all requirements for the import are met use the **Testing** step. The test for data line 9, where all eleven descriptor states are present, is shown below.

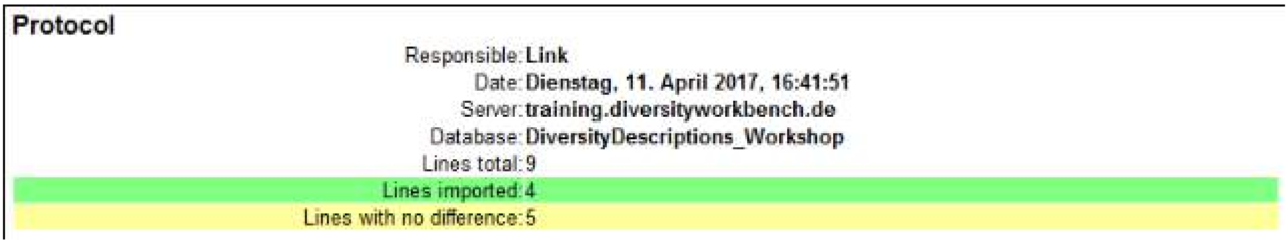


Descriptor [UPDATE]
id: 15422
subclass: 'categorical'
Categorical state [INSERT]
id: 15446
descriptor_id: 15422
label: 'Farming methods using less synthetic fertilizers and pesticides'
display_order: 1
Categorical state [INSERT]
id: 15447
descriptor_id: 15422
label: 'Farming methods using biological pest control'
display_order: 2
Categorical state [INSERT]
id: 15448
descriptor_id: 15422
label: 'Farming methods using organic fertilizers and chemicals'
display_order: 3
Categorical state [INSERT]
id: 15449
descriptor_id: 15422
label: 'Other reasons'
display_order: 4

1	Question Number	Question Text	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gen...	Text	Male | Female	
4	3	Which farming m...	Text	Conventional far...	
5	4	How many years ...	Integer		year
6	5	What are the mai...	Text	Annual crops | Pe...	
7	6	How much mone...	Real		€
8	7	Do you know the...	Bool		
9	8	What do you und...	Text	Farming methods ...	

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There were 4 lines that contained descriptors (see below).



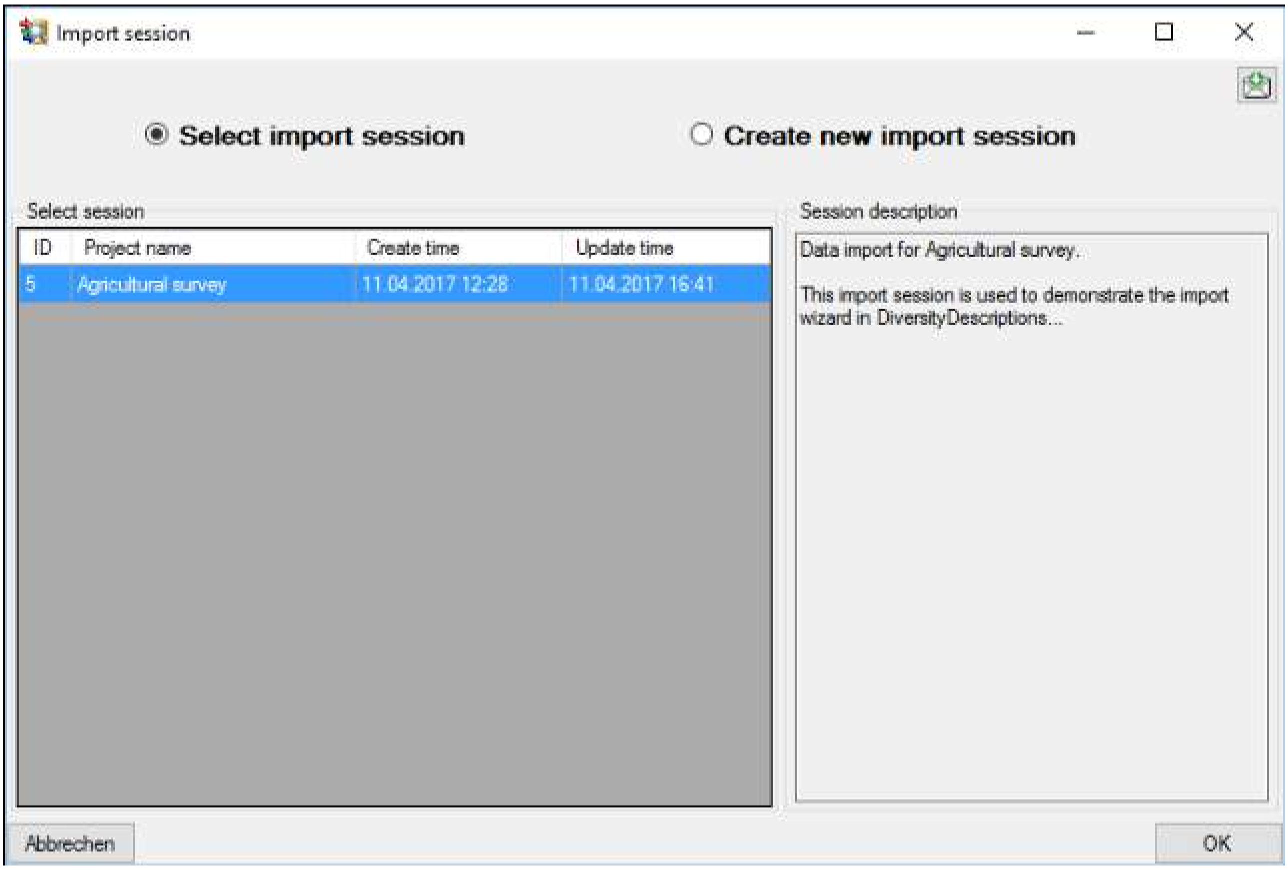
Protocol

Responsible: Link
Date: Dienstag, 11. April 2017, 16:41:51
Server: training.diversityworkbench.de
Database: DiversityDescriptions_Workshop
Lines total: 9
Lines imported: 4
Lines with no difference: 5

Next: Step 6 - Import of descriptions

Step 6 - Import of descriptions

Choose **Data -> Import -> Wizard -> Import descriptions ...** from the menu. A window as shown below will open to select an import session. Select session for project "MycoPhylogenyNet".

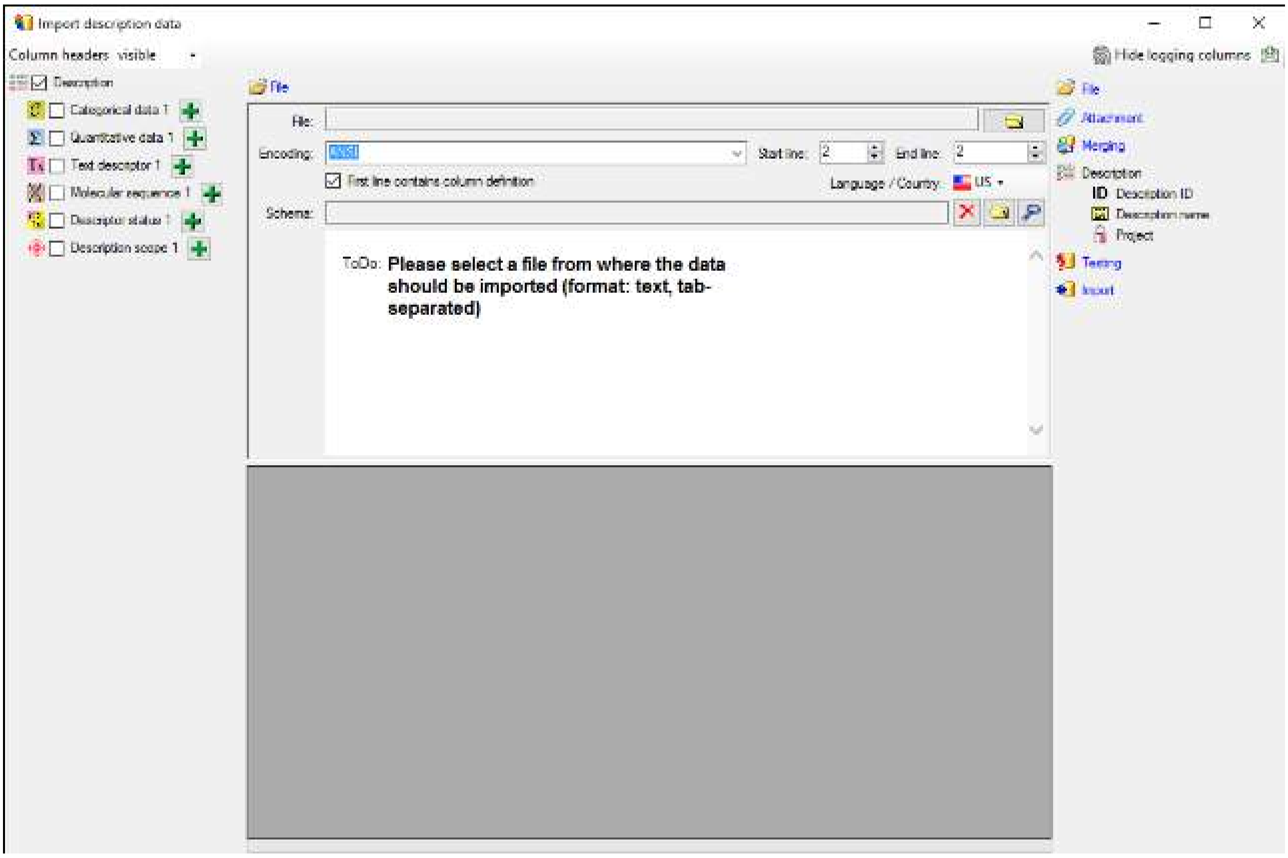


ID	Project name	Create time	Update time
5	Agricultural survey	11.04.2017 12:28	11.04.2017 16:41

Data import for Agricultural survey.

This import session is used to demonstrate the import wizard in DiversityDescriptions...

After clicking **[OK]** the following window opens that will lead you through the import of the description data.



File:

Encoding: ANSI

Start line: 2

End line: 2

☑ First line contains column definition

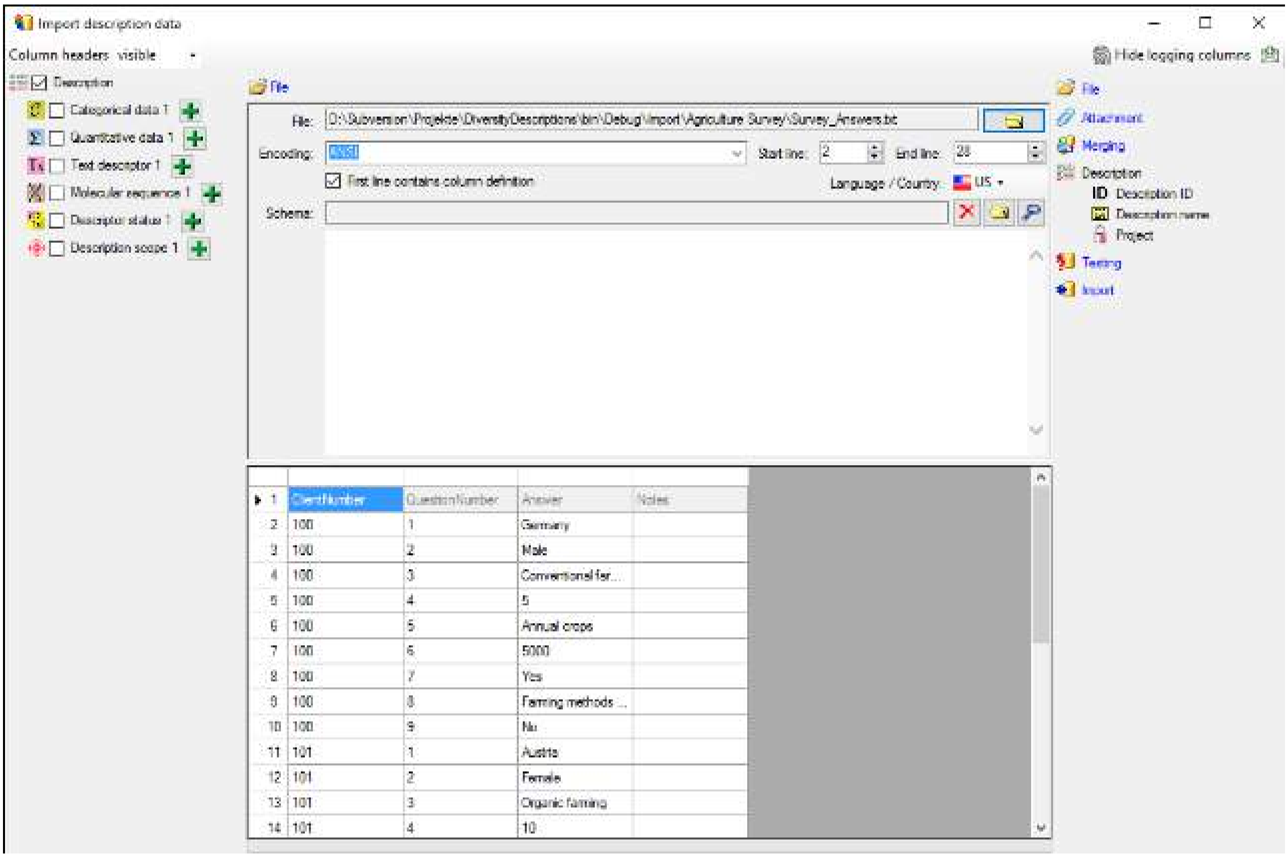
Language / Country: US

Schema:

ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

Choosing the File

Choose step **File** an open file "Survey_Answers.txt". The chosen encoding **ANSI** of the file should be sufficiend. The file column "ClientNumber" contains the description names that shall be imported. Since there are no other description specific data, the same column will be used for the as unique ID to identify each description.



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Answers.txt

Encoding: ANSI   Start line: 2   End line: 28

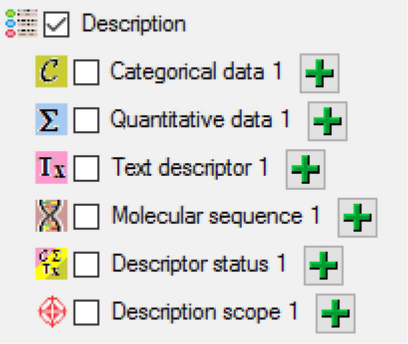
☑ First line contains column definition   Language / Country: US

Schema:

1	ClientNumber	QuestionNumber	Answer	Notes
2	100	1	Germany	
3	100	2	Male	
4	100	3	Conventional far...	
5	100	4	5	
6	100	5	Annual crops	
7	100	6	5000	
8	100	7	Yes	
9	100	8	Farming methods ...	
10	100	9	No	
11	101	1	Austria	
12	101	2	Female	
13	101	3	Organic farming	
14	101	4	10	

Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import.



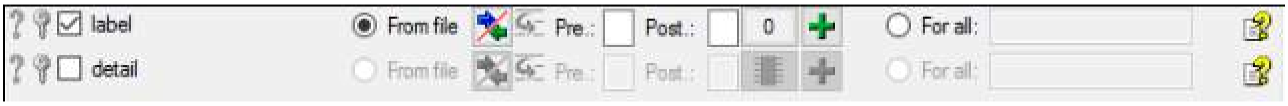
Since each description name rsp. ID occurs in several lines of the file, subsequent tries to import the same description would cause errors, if the standard merge handling **Insert** was used. We have to change the import step **Merge** from the list. For **Description** we select the **Merge** option (see below).

Description ○ Insert ● Merge ○ Update ○ Attach

The step **Description** is already selected and cannot be de-selected (see above). In the step table at the right side you find the import step **Descriptor** and below the data groups of the import step. Click on ID **Description ID** and in the center window the assignemt data for the description id ("id") are displayed. Click on ? to make this the decisive column and on to allow the merge comparison, further click on **From file** to select the column "ClientNumber" as data source. After that the column should look as shown below.


☑ id ● From file Pre.: Post.: 0 ○ For all:

Now the description name must be selected, therefore click on **Description name**. The center window shows two data columns: "label" and "detail". Click on **From file** in the "label" line to select file column "ClientNumber". After that the columns should look as shown below.


☑ label ● From file Pre.: Post.: 0 ○ For all:

☐ detail ○ From file Pre.: Post.: ○ For all:

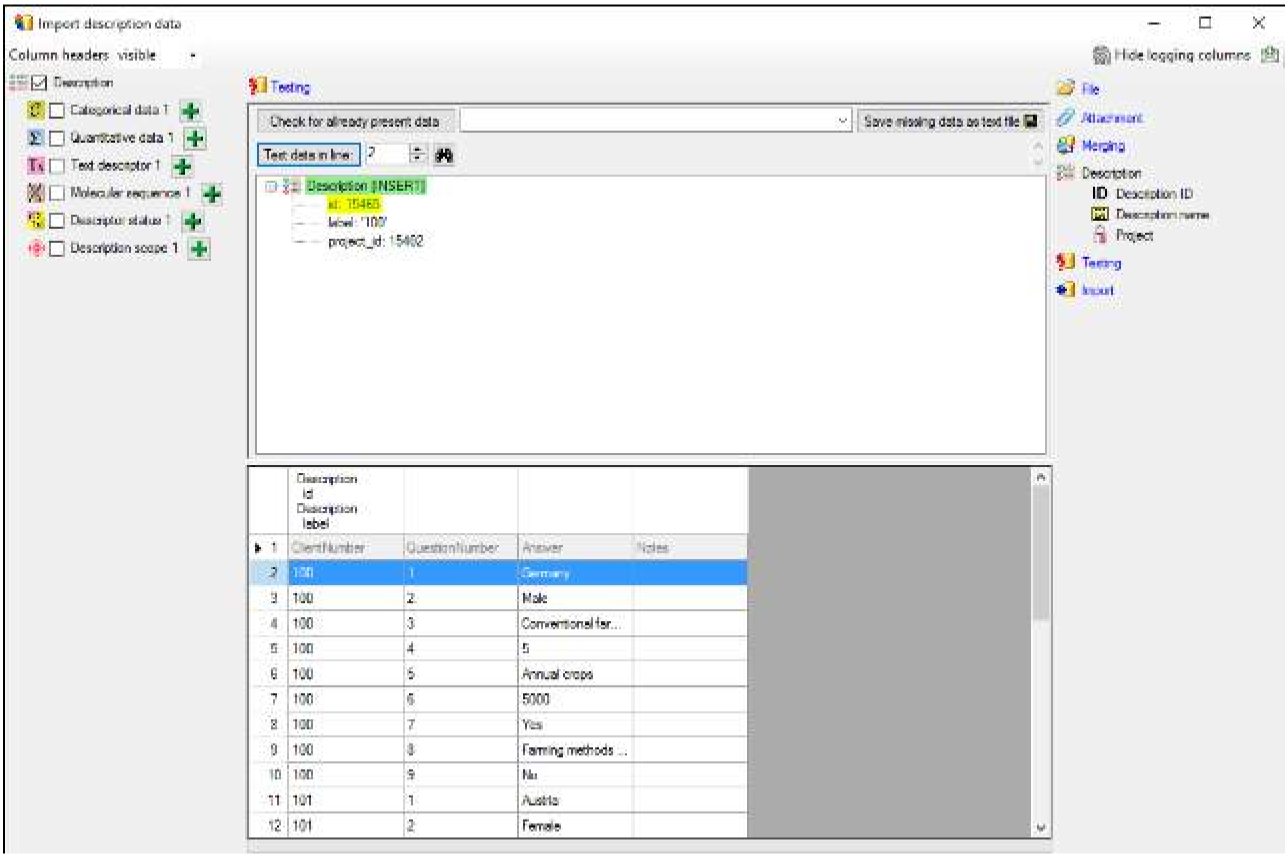
Finally select import step **Project**, select data column "project_id", choose **For all:** and select entry "Agricultural survey" from the drop down (see below). With this adjustment every imported description will automatically be assigned to that project.


☑ project_id ○ From file Pre.: Post.: ● For all: Agricultural survey

Remark: Although project_id is a numeric value in the database, the externally visible project name is expected here. Since this name is unambigious, the corresponding id will be determined during import.

Testing

To test if all requirements for the import are met use the **Testing** step. The test for the first data line is shown below.



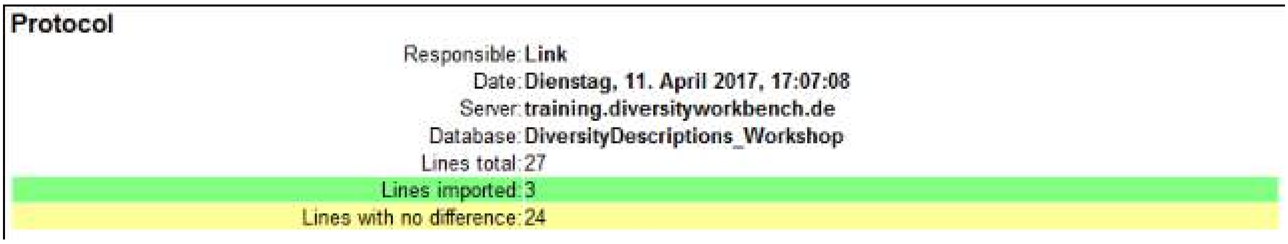
Test data in line: 2

Description [INSERT]
id: 15465
label: '100'
project_id: 15402

	Description id Description label			
1	ClientNumber	QuestionNumber	Answer	Notes
2	100	1	Germany	
3	100	2	Male	
4	100	3	Conventional far...	
5	100	4	5	
6	100	5	Annual crops	
7	100	6	5000	
8	100	7	Yes	
9	100	8	Farming methods ...	
10	100	9	No	
11	101	1	Austria	
12	101	2	Female	

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There were three different descriptions (see below).



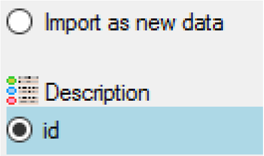
Protocol

Responsible: **Link**
Date: **Dienstag, 11. April 2017, 17:07:08**
Server: **training.diversityworkbench.de**
Database: **DiversityDescriptions_Workshop**
Lines total: 27
Lines imported: 3
Lines with no difference: 24

[Next: Step 7 - Import of description data]

Step 7 - Import of description data

In this step we attach categorical, quantitative and text data to the descriptions. In import step **Attach** at the right side we select ●**id** (see below). It indicates that we do not want to attach data to an existing description.

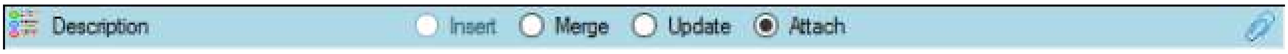


○ Import as new data

Description

● id

Select the import step **Merging** from the list. For **Description** we select the **Attach** option because this table shall not be changed (see below).



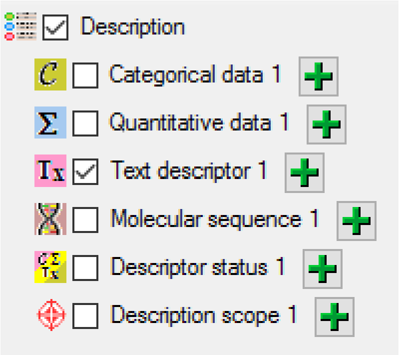
Description ○ Insert ○ Merge ○ Update ● Attach

Deselect every column from import step **Description** except "id". The "id" column was already marked as **Key column** for comparison in the previous step. Now the column looks as shown below.

☑ id Pre.: ☐ Post.: ☐ 0

Inserting text descriptor data

We will now include the text, quantitative, categorical and status data step by step. First we will attach the text descriptor data. Select the **Text descriptor 1** step at the left (see below).



- ☑ Description
  - ☐ Categorical data 1
  - ☐ Quantitative data 1
  - ☑ Text descriptor 1
  - ☐ Molecular sequence 1
  - ☐ Descriptor status 1
  - ☐ Description scope 1

At the right side you find the import step **Text descriptor 1** and below the data groups of the import step. Click on **Descriptor ID** and in the center window the assignemt data for the referenced descriptor's id ("descriptor_id") are displayed. Click on ●**From file** to select the file column "QuestionNumber" as data source. After that the column should look as shown below.

☑ descriptor_id ● From file Pre.: ☐ Post.: ☐ 1 ○ For all: Where do you live?

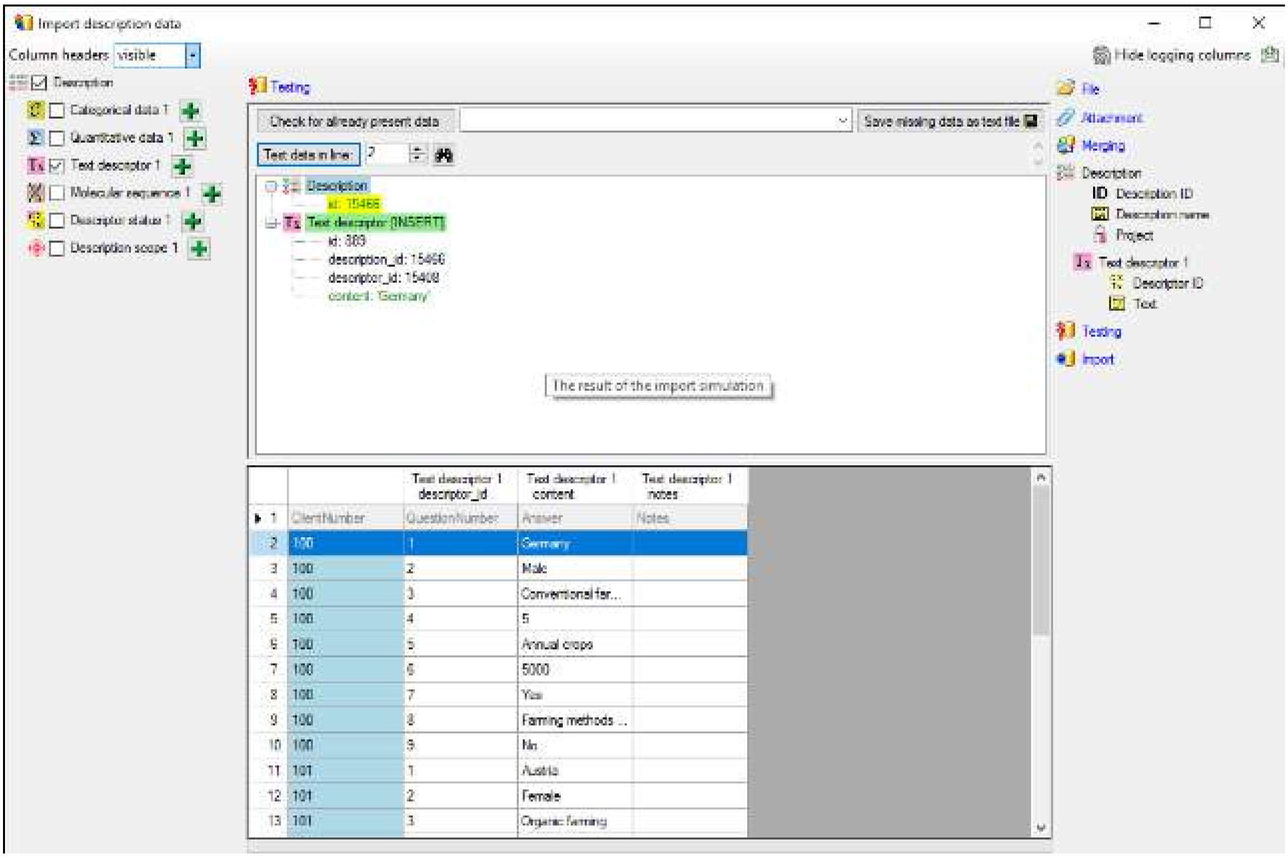
Now the description text must be selected, therefore click on **Text**. The center window shows two data columns: "content" and "notes". In line "content" click on ? to make it the decisive column, further on ●**From file** to select file column "Answer". In line "notes" click on ●**From file** to select file column "Notes". After that the columns should look as shown below.

☑ content ● From file Pre.: ☐ Post.: ☐ 2 ○ For all:

☑ notes ● From file Pre.: ☐ Post.: ☐ 3 ○ For all:

Testing the text descriptor data import

To test if all requirements for the import are met use the **Testing** step. The test for the first data line is shown below.



Column headers: visible

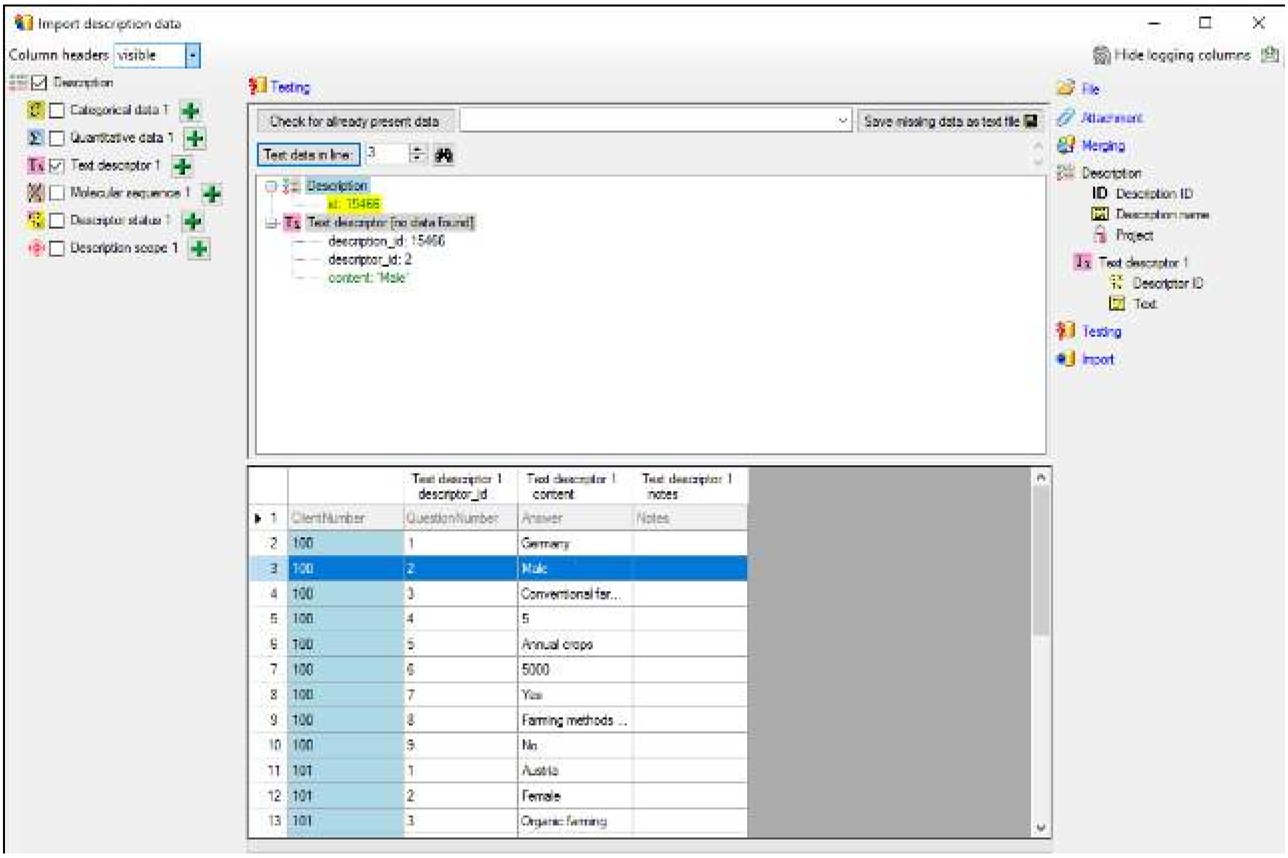
☐ Categorical data 1
☐ Quantitative data 1
☑ Text descriptor 1
☐ Molecular sequence 1
☐ Descriptor status 1
☐ Description scope 1

Test data in line: 2

- Description
  - id: 15466
- Text descriptor [INSERT]
  - id: 389
  - description_id: 15466
  - descriptor_id: 15408
  - content: 'Germany'

		Text descriptor 1 descriptor_id	Text descriptor 1 content	Text descriptor 1 notes
1	ClientNumber	QuestionNumber	Answer	Notes
2	100	1	Germany	
3	100	2	Male	
4	100	3	Conventional far...	
5	100	4	5	
6	100	5	Annual crops	
7	100	6	5000	
8	100	7	Yes	
9	100	8	Farming methods ...	
10	100	9	No	
11	101	1	Austria	
12	101	2	Female	
13	101	3	Organic farming	

An additional test is done for the next data line. This line contains no text data but a categorical state. You can see below that this line will not be imported as text descriptor data, because the descriptor (given by **Descriptor ID**) is automatically checked for the correct type.

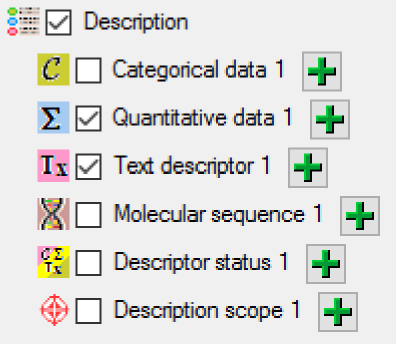


Description
id: 15466
Text descriptor [no data found]
description_id: 15466
descriptor_id: 2
content: 'Male'

		Text descriptor 1 descriptor_id	Text descriptor 1 content	Text descriptor 1 notes
1	ClientNumber	QuestionNumber	Answer	Notes
2	100	1	Germany	
3	100	2	Male	
4	100	3	Conventional far...	
5	100	4	5	
6	100	5	Annual crops	
7	100	6	5000	
8	100	7	Yes	
9	100	8	Farming methods ...	
10	100	9	No	
11	101	1	Austria	
12	101	2	Female	
13	101	3	Organic farming	

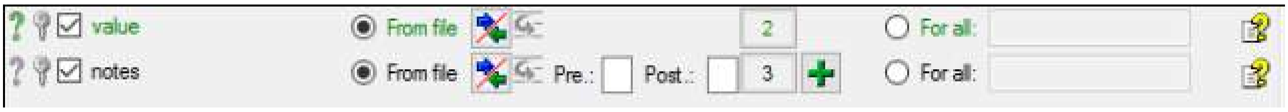
Inserting quantitative summary data

We will now include the quantitative summary data. Select the Σ **Quantitative data 1** step (see below).


☑ Description
☐ Categorical data 1
☑ Quantitative data 1
☑ Text descriptor 1
☐ Molecular sequence 1
☐ Descriptor status 1
☐ Description scope 1

At the right side you find the import step Σ **Quantitative data 1** and below the data groups of the import step. Click on **Descriptor ID** and select the file column "QuestionNumber" as data source.

Now the value must be selected, therefore click on **Value**. The center window shows two data columns: "value" and "notes". In line "value" click on ? to make it the decisive column, further on ● **From file** to select file column "Answer". In line "notes" click on ● **From file** to select file column "Notes". After that the columns should look as shown below.

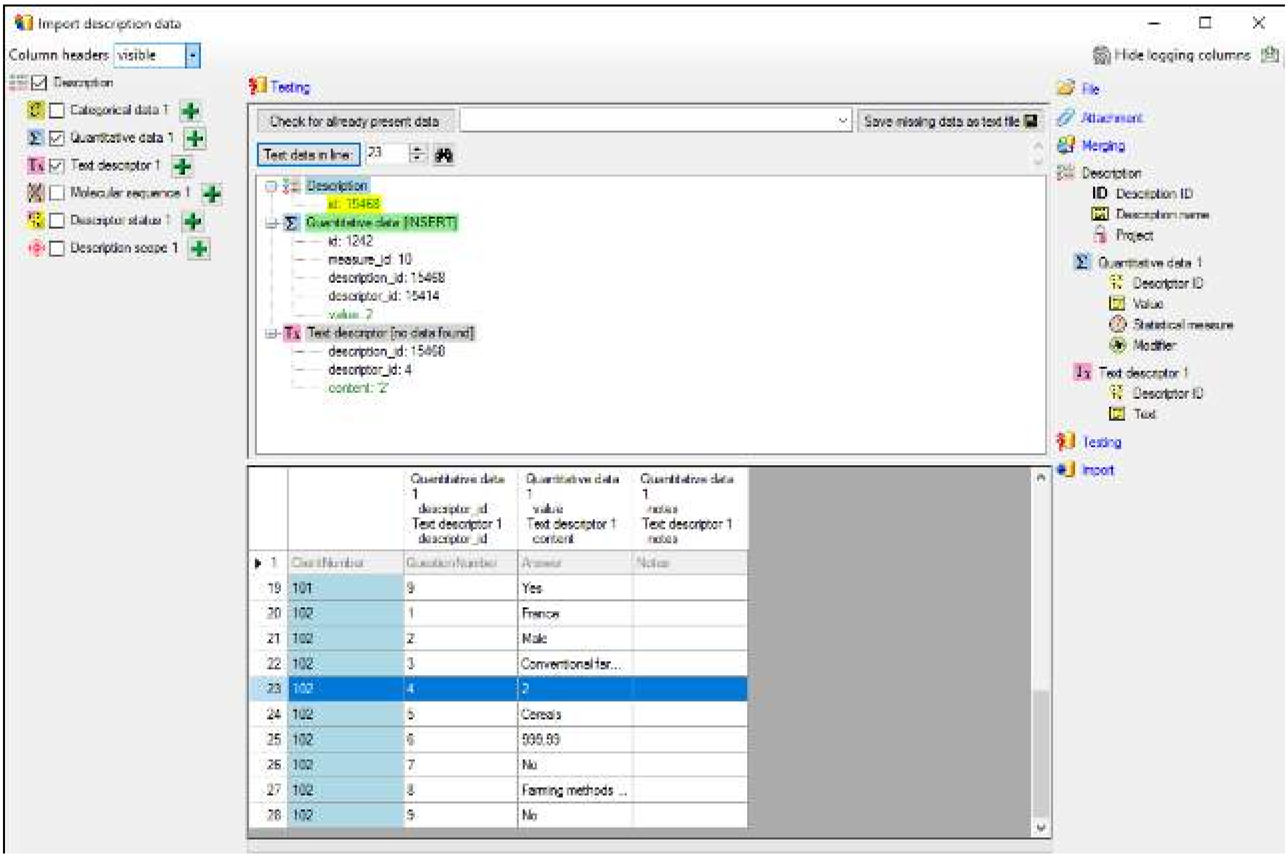

? ☑ value ● From file 2 ○ For all:
? ☑ notes ● From file Pre.: Post.: 3 ○ For all:

For quantitavie measures you must specify which statistical measure is given by the value. We assume all imported values are mean values, therefore click on the import step **Statistical measure** and in the center window the assignemt data for the statistical measure ("measure_id") are displayed. Click on ● **For all:** and select entry "Central or typical value (human estimate)" from the drop down (see below).

☑ measure_id — ● For all: Central or typical valu

Testing the quantitative summary data import

To test if all requirements for the import are met use the **Testing** step. The test for data line 25 with integer data is shown below.

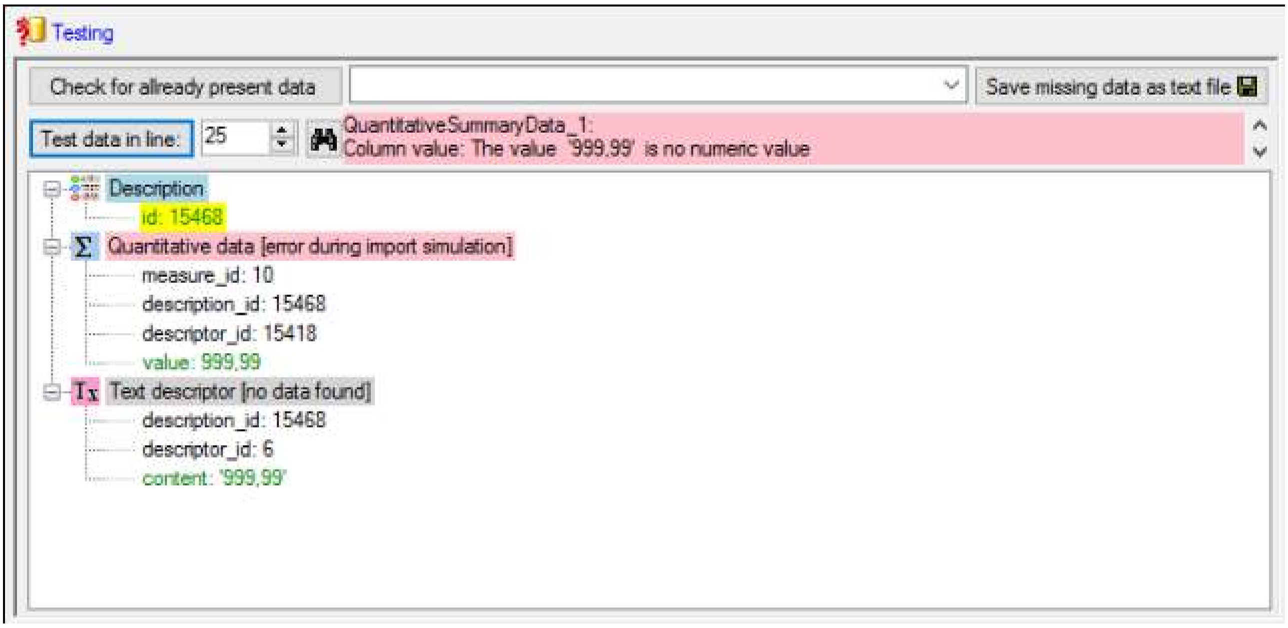


Test data in line: 23

```
Description
    id: 15468
Quantitative data [INSERT]
    id: 1242
    measure_id: 10
    description_id: 15468
    descriptor_id: 15414
    value: 2
Text descriptor [no data found]
    description_id: 15468
    descriptor_id: 4
    content: '2'
```

		Quantitative data 1 descriptor_id Text descriptor 1 descriptor_id	Quantitative data 1 value Text descriptor 1 content	Quantitative data 1 notes Text descriptor 1 notes
1	ClientNumber	QuestionNumber	Answer	Notes
19	101	9	Yes	
20	102	1	France	
21	102	2	Male	
22	102	3	Conventional far...	
23	102	4	2	
24	102	5	Cereals	
25	102	6	999.99	
26	102	7	No	
27	102	8	Farming methods ...	
28	102	9	No	

The test for data line 25, which contains real number **fails** (see below).

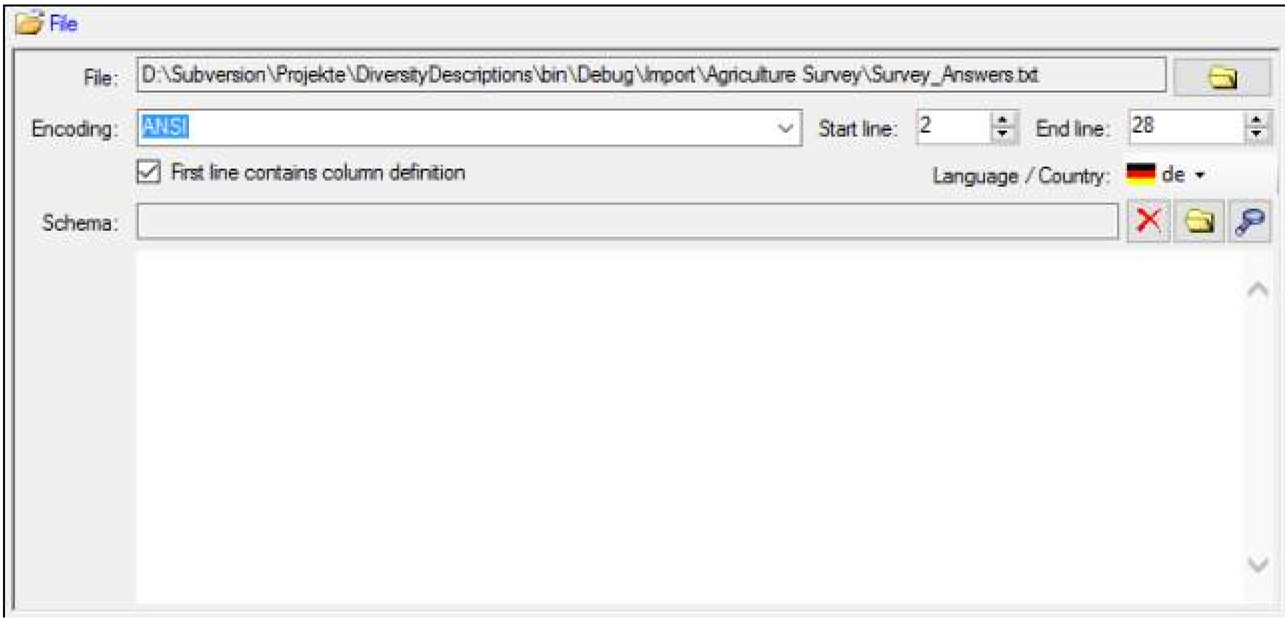


Test data in line: 25

QuantitativeSummaryData_1:
Column value: The value '999,99' is no numeric value

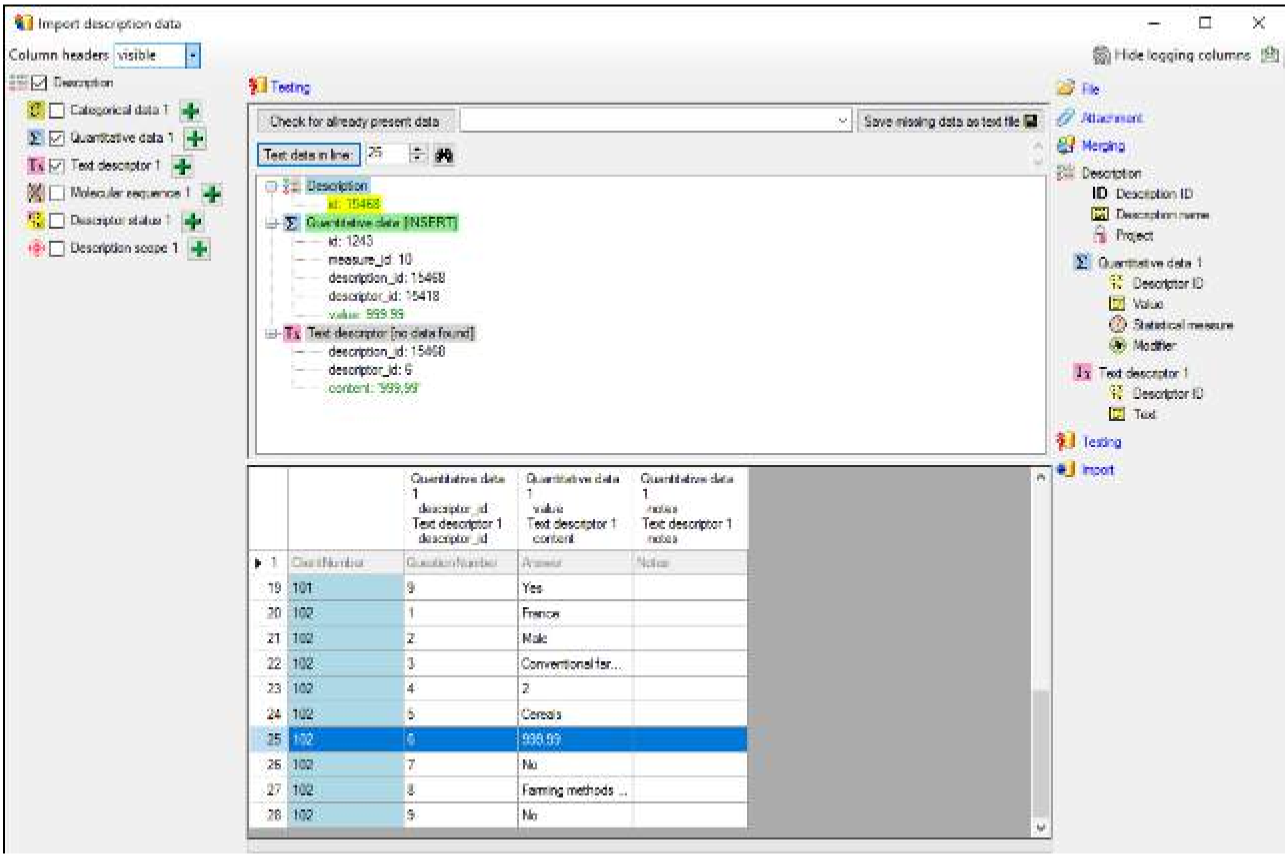
- Description
  - id: 15468
- Quantitative data [error during import simulation]
  - measure_id: 10
  - description_id: 15468
  - descriptor_id: 15418
  - value: 999,99
- Text descriptor [no data found]
  - description_id: 15468
  - descriptor_id: 6
  - content: '999,99'

A closer look on the data in column "Answer" shows that the decimal separator is a comma, because the table has been generated by a progam using the German localization. The database expects a decimal point as separator. To interpret the localized file values correctly, select the step **File** and choose **Language / Country: de** (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Agriculture Survey\Survey_Answers.txt
Encoding: ANSI
Start line: 2
End line: 28
☑ First line contains column definition
Language / Country: de
Schema:

With this settings the test now works fine (see below).



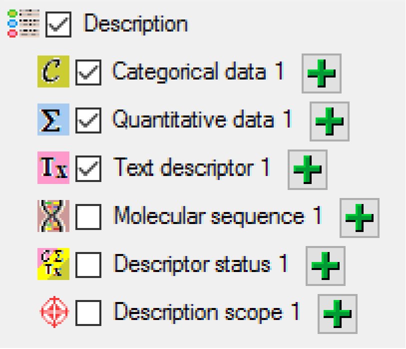
Test data in line: 25

```
Description
    id: 15468
Quantitative data [INSERT]
    id: 1243
    measure_id: 10
    description_id: 15468
    descriptor_id: 15418
    value: 999.99
Text descriptor [no data found]
    description_id: 15468
    descriptor_id: 5
    content: '999,99'
```

		Quantitative data 1 descriptor_id Text descriptor 1 descriptor_id	Quantitative data 1 value Text descriptor 1 content	Quantitative data 1 notes Text descriptor 1 notes
▶ 1	ClientNumber	QuestionNumber	Answer	Notes
19	101	9	Yes	
20	102	1	France	
21	102	2	Male	
22	102	3	Conventional far...	
23	102	4	2	
24	102	5	Cereals	
25	102	6	999.99	
26	102	7	No	
27	102	8	Farming methods ...	
28	102	9	No	

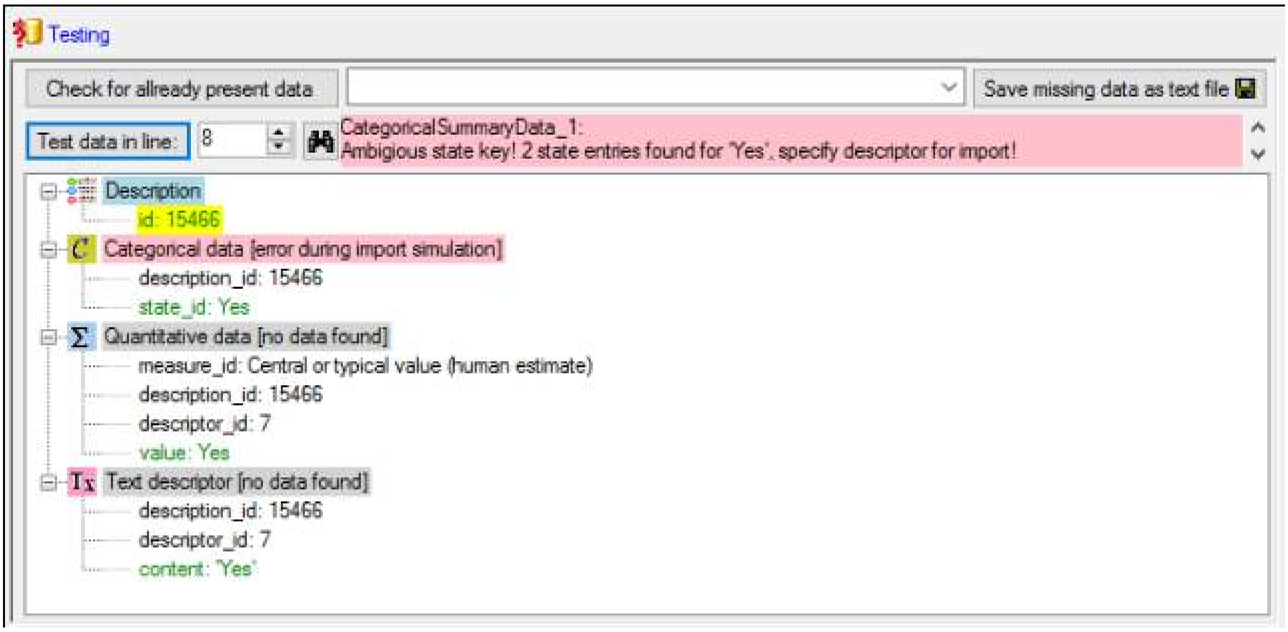
Inserting categorical summary data

Now we will include the categorical summary data. Select the **Categorical data 1** step at the left (see below).



☑ Description
☑ Categorical data 1
☑ Quantitative data 1
☑ Text descriptor 1
☐ Molecular sequence 1
☐ Descriptor status 1
☐ Description scope 1

At the right side you find the import step **Categorical data 1** and below the data groups of the import step. Click on **Categorical state ID**. The center window shows the data column "state_id". Click on ? to make it the decisive column, further on ● **From file** to select file column "Answer". If you perform a quick import test you will see that this setting works perfectly for data file lines 3, 4 and 6, but fails for line 8 (see below).



CategoricalSummaryData_1:
Ambigious state key! 2 state entries found for 'Yes', specify descriptor for import!

- Description
  - id: 15466
- Categorical data [error during import simulation]
  - description_id: 15466
  - state_id: Yes
- Quantitative data [no data found]
  - measure_id: Central or typical value (human estimate)
  - description_id: 15466
  - descriptor_id: 7
  - value: Yes
- Text descriptor [no data found]
  - description_id: 15466
  - descriptor_id: 7
  - content: 'Yes'

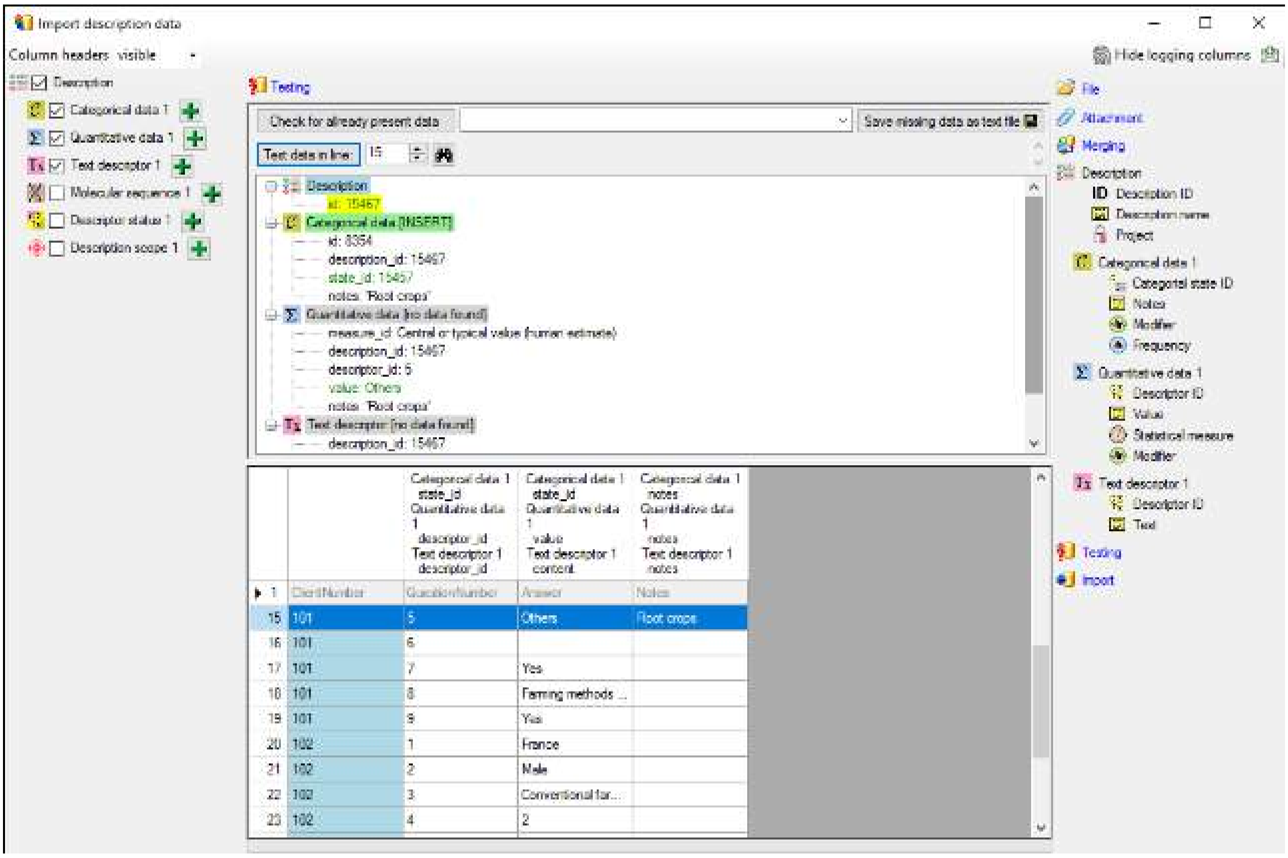
The reason is that we used the state name as external key for the categorical state. For the descriptors 6 and 8, which both represent boolean values, the states names are ambigious ("Yes" and "No" for both descriptors), therefore the import wizard does not know which descriptor shall be used. To overcome this ambiguity the **Categorical state ID** step allows the additional specification of the descriptor id. Select import step **Categorical state ID**. In the center click on the button at the end of line "state_id". Select file column "QuestionNumber", which contains the reference to the descriptor and enter the separator character **|** (pipe symbol) in field **Pre.:** of the new line. After that the column should look as shown below.

If you repeat the quick import test for line 8, it will now work.

Now click on **Notes**. The center window shows the data column "notes". Click on **From file** to select file column "Notes". After that the columns should look as shown below.

Testing the categorical summary data import

To test if all requirements for the import are met use the **Testing** step. The test for data line 15 with categorical data and notes is shown below.

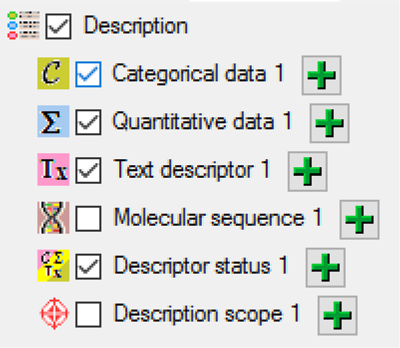


```
Description
    id: 15467
Categorical data [INSERT]
    id: 8354
    description_id: 15467
    state_id: 15457
    notes: 'Root crops'
Quantitative data [no data found]
    measure_id: Central or typical value (human estimate)
    description_id: 15467
    descriptor_id: 5
    value: Others
    notes: 'Root crops'
Text descriptor [no data found]
    description_id: 15467
```

		Categorical data 1 state_id Quantitative data 1 descriptor_id Text descriptor 1 descriptor_id	Categorical data 1 state_id Quantitative data 1 value Text descriptor 1 content	Categorical data 1 notes Quantitative data 1 notes Text descriptor 1 notes
1	ClientNumber	QuestionNumber	Answer	Notes
15	101	5	Others	Root crops
16	101	6		
17	101	7	Yes	
18	101	8	Farming methods ...	
19	101	9	Yes	
20	102	1	France	
21	102	2	Male	
22	102	3	Conventional far...	
23	102	4	2	

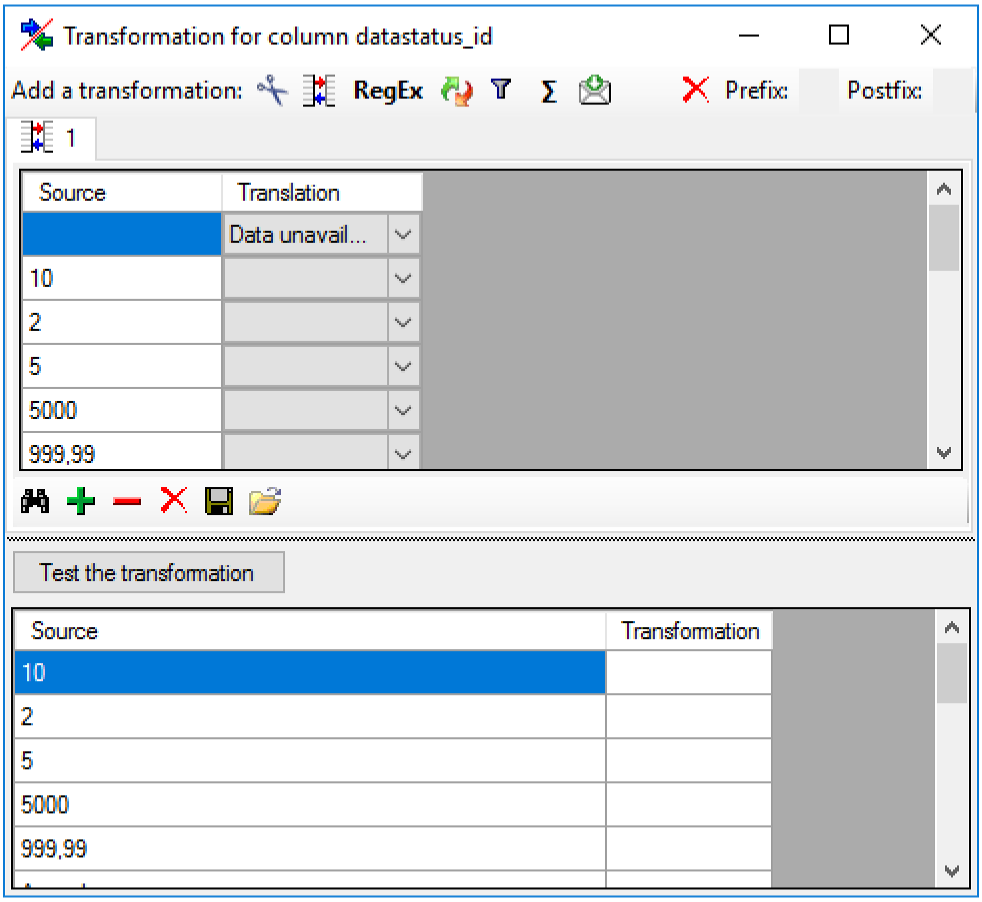
Inserting the descriptor status dataata

There is an empty lines in the file. For this line we want to set the descriptor status "Data unavailable" to indicate that the descriptor should be present in the description. Select the **Descriptor status 1** step at the left (see below).



At the right side you find the import step **Descriptor status 1** and below the data groups of the import step. Click on **Descriptor ID** and select the file column "QuestionNumber" as data source. Furthermore click on **Notes** and select the file column "Notes".

Now click on **Data status**. The center window shows the data column "statusdata_id". Click on to make it the decisive column, further on **From file** to select file column "Answer". Now click on button to define a transformation. In the tranformation window click on to select translation. In the translation window click the button to list the values contained in the file column. For the empty entry in the first line select the translation value "Data unavailable" (see below). All data entries will therefore be mapped to "empty", i.e. no data status will be set. Only if the data file line ist empty, the selected data status will be inserted.

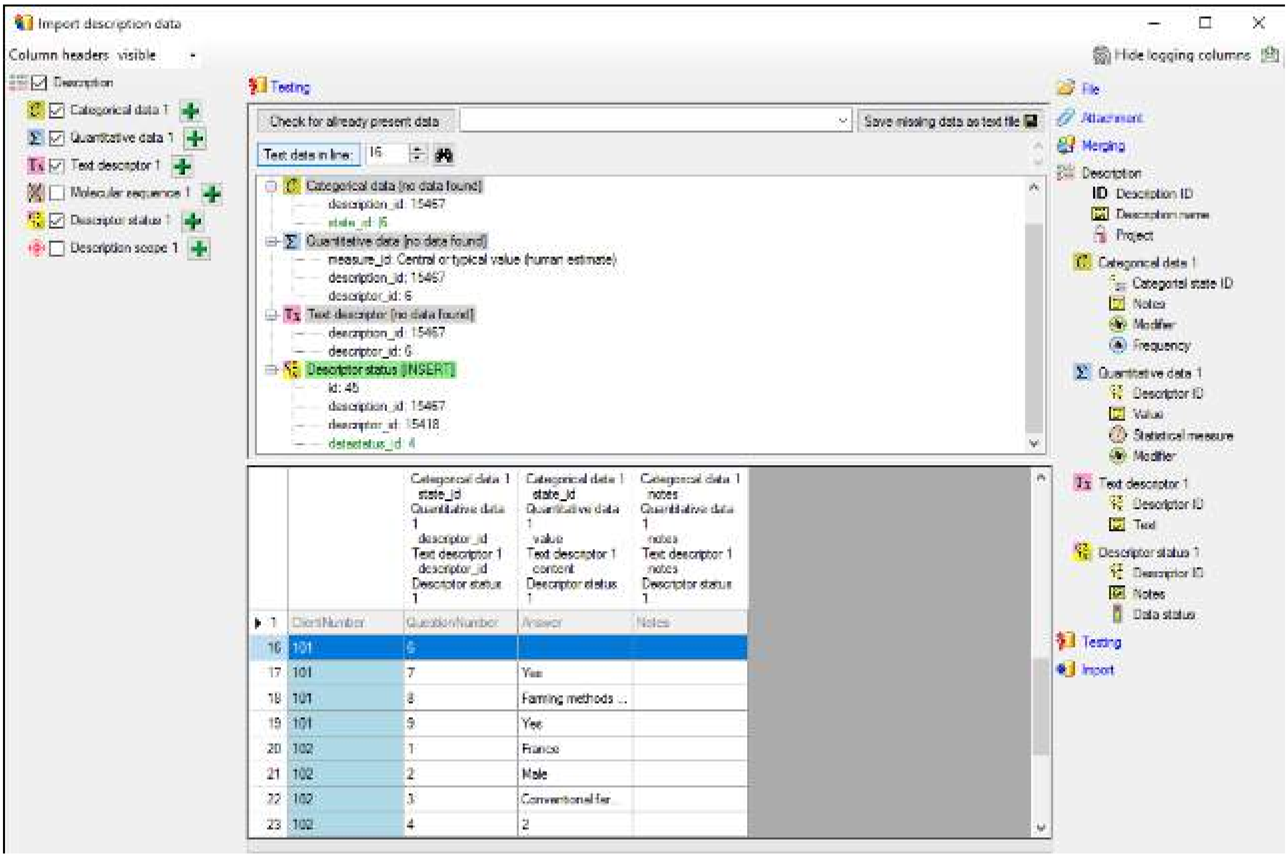


Source	Translation
	Data unavail...
10	
2	
5	
5000	
999,99	

Source	Transformation
10	
2	
5	
5000	
999,99	

Testing the descriptor status data import

To test if all requirements for the import are met use the **Testing** step. The test for data line 16 is shown below.



Column headers: visible

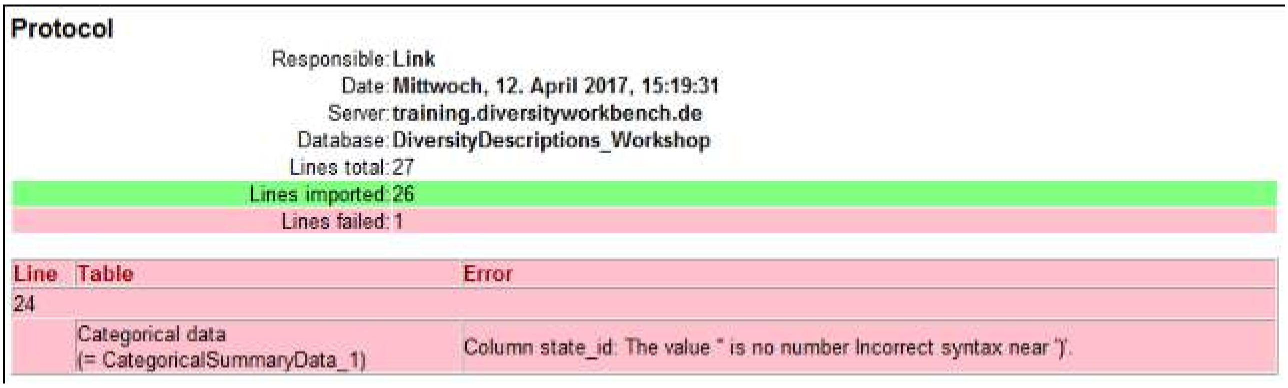
Test data in line: 16

```
Categorical data [no data found]
    description_id: 15467
    state_id: 6
Quantitative data [no data found]
    measure_id: Central or typical value (human estimate)
    description_id: 15467
    descriptor_id: 6
Text descriptor [no data found]
    description_id: 15467
    descriptor_id: 6
Descriptor status [INSERT]
    id: 45
    description_id: 15467
    descriptor_id: 15418
    datastatus_id: 4
```

		Categorical data 1 state_id Quantitative data 1 descriptor_id Text descriptor 1 descriptor_id Descriptor status 1	Categorical data 1 state_id Quantitative data 1 value Text descriptor 1 content Descriptor status 1	Categorical data 1 notes Quantitative data 1 notes Text descriptor 1 notes Descriptor status 1
1	ClientNumber	QuestionNumber	Answer	Notes
16	101	6		
17	101	7	Yes	
18	101	8	Farming methods ...	
19	101	9	Yes	
20	102	1	France	
21	102	2	Male	
22	102	3	Conventional far...	
23	102	4	2	

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There were 26 lines imported and one failed line (see below).



Protocol

Responsible: **Link**
Date: **Mittwoch, 12. April 2017, 15:19:31**
Server: **training.diversityworkbench.de**
Database: **DiversityDescriptions_Workshop**
Lines total: 27
Lines imported: 26
Lines failed: 1

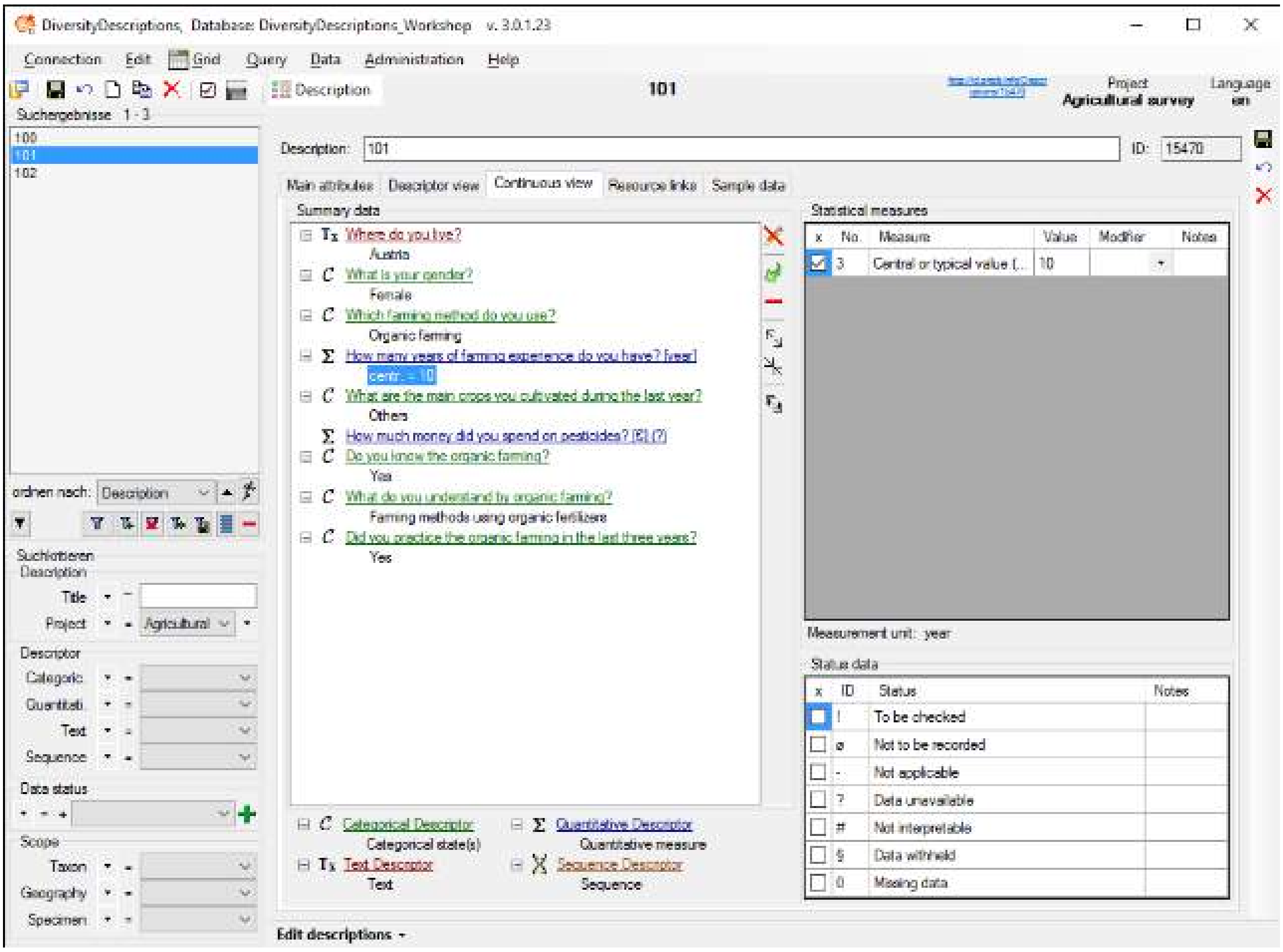
Line	Table	Error
24		
	Categorical data (= CategoricalSummaryData_1)	Column state_id: The value '' is no number Incorrect syntax near ')'.

The erroneous lines may be stored into separate text files for a detailled analysis and a separate import after error corrections. In out example the error is caused by the undefined value "Cereals" in the "Answer" column of file line 24.

Next: Epilogue

Epilogue

When you close the import wizard and start a query for descriptions of project "Agricultural survey" you will find the three datasets and the imported descriptor data (see image below).



101

Project: Agricultural survey

Language: en

Search results:
- 100
- 101
- 102

ordnen nach: Description

Project: Agricultural

Description: 101

ID: 15470

Summary data:

- Where do you live?
  - Austria
- What is your gender?
  - Female
- Which farming method do you use?
  - Organic farming
- How many years of farming experience do you have? [year]
  - centr. = 10
- What are the main crops you cultivated during the last year?
  - Others
- How much money did you spend on pesticides? [€] (?)
- Do you know the organic farming?
  - Yes
- What do you understand by organic farming?
  - Farming methods using organic fertilizers
- Did you practice the organic farming in the last three years?
  - Yes

Statistical measures:

x	No.	Measure	Value	Modifier	Notes
☑	3	Central or typical value (...	10		

Measurement unit: year

Status data:

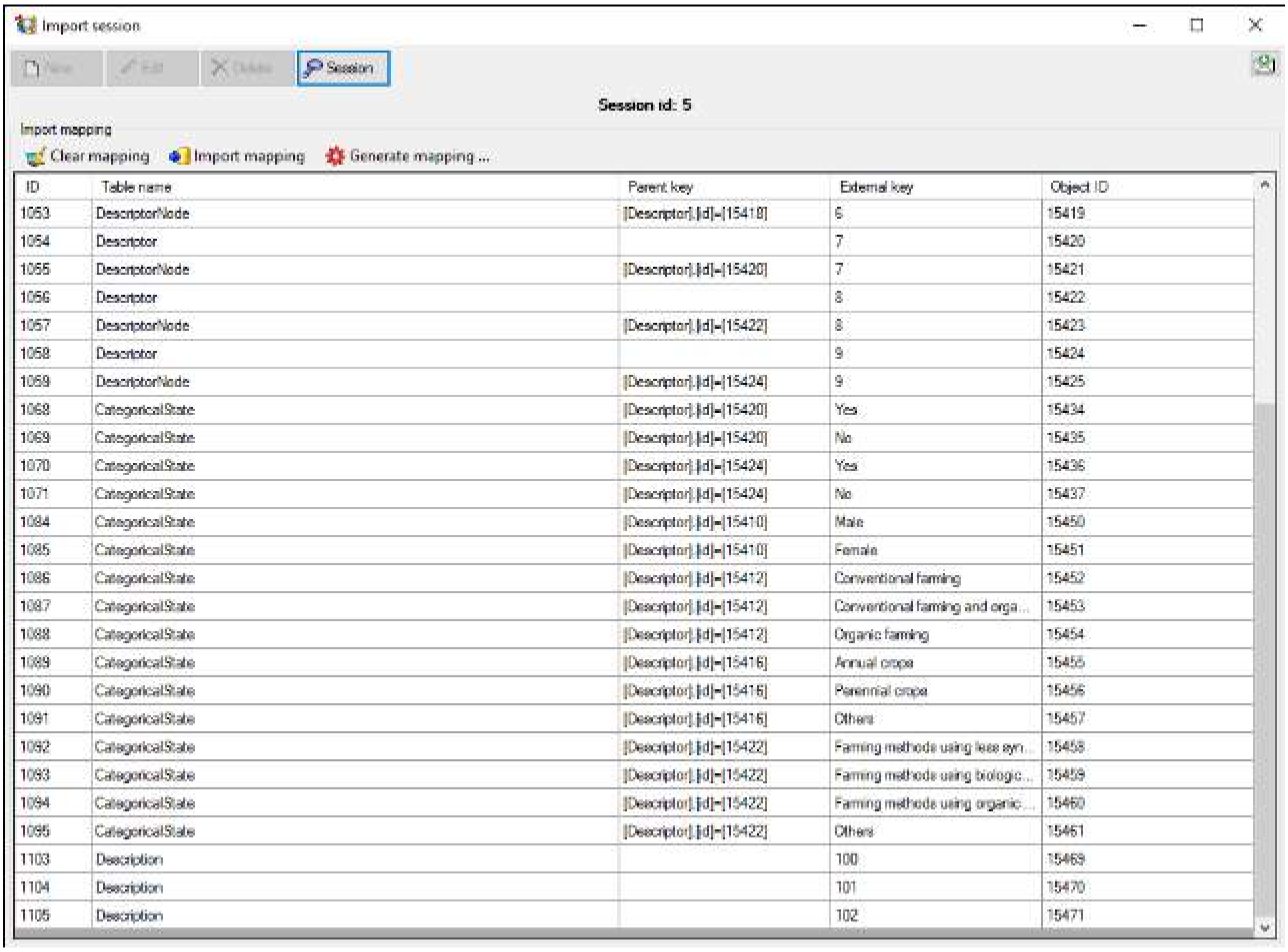
x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☐	$	Data withheld	
☐	0	Missing data	

Finnally two more aspects of the imports wizard shall be discussed from a retrospective view. The first one concerns the mapping of external and internal keys and the role of the import session. The second one takes a closer look on the role of the "ID" columns during import.

Mapping of external and internal keys

When opening the import wizard you have to select rsp. create an import session. Imports into Diversity Descriptions usually require at least two import operations, e.g. for descriptors and descriptions. The description data reference descriptors or categorical states. Within the database those relations are built based on numeric values that are provided by the database during creation of the corresponding objects. In the external data files the relations are usually built by numbers coordinated by the user ("QuestionNumber") or by the entity names.

The import session stores the external and internal key values in separate database tables and therefore builds a bracket around the different import operations. Each import session is assigned to one local project, but for each project several import sessions may be created. The mapping data may be viewed by opening the menu item **Data -> Import -> Wizard -> Organize sessions ...**, selecting the session and clicking the button **Mapping** (see image below).



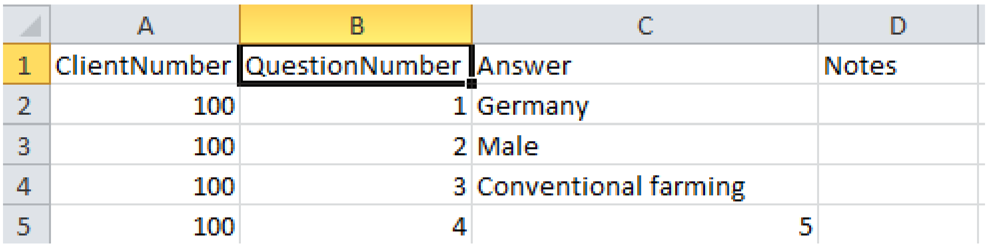
Session id: 5

Import mapping

ID	Table name	Parent key	External key	Object ID
1053	DescriptorNode	[Descriptor].[id]=[15418]	6	15419
1054	Descriptor		7	15420
1055	DescriptorNode	[Descriptor].[id]=[15420]	7	15421
1056	Descriptor		8	15422
1057	DescriptorNode	[Descriptor].[id]=[15422]	8	15423
1058	Descriptor		9	15424
1059	DescriptorNode	[Descriptor].[id]=[15424]	9	15425
1068	CategoricalState	[Descriptor].[id]=[15420]	Yes	15434
1069	CategoricalState	[Descriptor].[id]=[15420]	No	15435
1070	CategoricalState	[Descriptor].[id]=[15424]	Yes	15436
1071	CategoricalState	[Descriptor].[id]=[15424]	No	15437
1084	CategoricalState	[Descriptor].[id]=[15410]	Male	15450
1085	CategoricalState	[Descriptor].[id]=[15410]	Female	15451
1086	CategoricalState	[Descriptor].[id]=[15412]	Conventional farming	15452
1087	CategoricalState	[Descriptor].[id]=[15412]	Conventional farming and orga...	15453
1088	CategoricalState	[Descriptor].[id]=[15412]	Organic farming	15454
1089	CategoricalState	[Descriptor].[id]=[15416]	Annual crops	15455
1090	CategoricalState	[Descriptor].[id]=[15416]	Perennial crops	15456
1091	CategoricalState	[Descriptor].[id]=[15416]	Others	15457
1092	CategoricalState	[Descriptor].[id]=[15422]	Farming methods using less syn...	15458
1093	CategoricalState	[Descriptor].[id]=[15422]	Farming methods using biologic...	15459
1094	CategoricalState	[Descriptor].[id]=[15422]	Farming methods using organic...	15460
1095	CategoricalState	[Descriptor].[id]=[15422]	Others	15461
1103	Description		100	15469
1104	Description		101	15470
1105	Description		102	15471

Selecting import columns for the "ID" fields

As an addition to the tutorial steps a closer look on the role of the "ID" fields shall be taken. In principle the most important IDs during import concern the ID **Descriptor ID** and the ID **Categorical state ID** during descriptor import. To decide which file column shall be used for that values during import, it is important to know how these elements are referenced in the other files.



	A	B	C	D
1	ClientNumber	QuestionNumber	Answer	Notes
2	100	1	Germany	
3	100	2	Male	
4	100	3	Conventional farming	
5	100	4	5	

For the descriptor import, you should take a look at the description data table (see above), which is part of the tutorial example. The descriptor is referenced by column "QestionNumber", which matches homonymous column of the descriptor data table (see below). Therefore the natural approach is to use this column as input for the ID **Descriptor ID** during the descriptor import. Since in most practical cases the descriptors will have a numbering column, which is used in the referencing table. Surely more variety exists in the way the categorical states are listed in the descriptor data file and the way they are referenced by the description data file.

	A	B	C	D	
1	QuestionNumber	QuestionText	Type	Values	Unit
2	1	Where do you live?	Text		
3	2	What is your gender?	Text	Male | Female	
4	3	Which farming method do you use?	Text	Conventional farming | Conventional farmi	
5	4	How many years of farming experience do you have?	Integer		year

In the tutorial the first complication is that the possible states are all concatenated, separated by a semicolon, into a single column of the descriptor data file. This causes some effort in the transformation, because the states have to be splitted into the single values. The question is, what is the ID**Categorical state ID**? The answer can be found in the upper table, because the state name is explicitely mentioned in the description data file as reference. I.e. for the descriptor import the state name must be used for the ID**Categorical state ID**, too.

In Diversity Descriptions the categorical state names must be unique in relation to their descriptor. But different descriptors may have states with the same names. In our example this situation occures with the two boolean descriptors (states "Yes" and "No") and the state value "Others", wich is used by two descriptors. Therefore it is generally recommended to specify the descriptor for the import of categorical summary data as demonstrated in the tutorial.

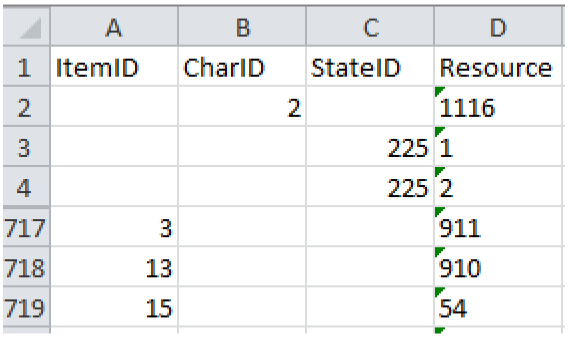
Import wizard - tutorial for advanced functions

The second part of the import wizard tutorial is dedicated to some advanced functions of the import wizard. When data are imported from the file formats DELTA or SDD, no import mapping information is stored, because all logical references are completely satisfied within the data files. The starting point of this tutorial, which was taken from a real life example, is a database imported from a DELTA file. For the datasets a lot of pictures are available on a web server. A web application reads the data from the original database (where the DELTA file was generated) and gets the information about available pictures from a second database to display both in a browser. From the original databases several tables were extracted and now the pictures shall be appended to the imported data.

Overview of the data tables and necessary import steps

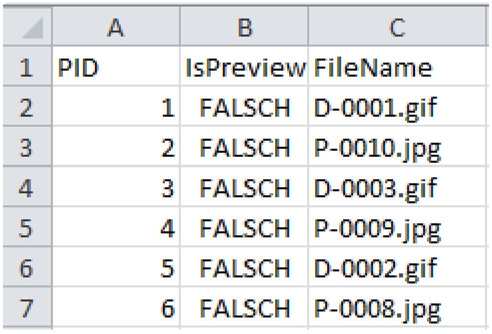
From the original database several tables have been extracted that contain the descriptor names, categorical state names and description names, together with their internal IDs in the foreign database. Additionally there is a table that assigns picture IDs to the IDs of descriptors, categorical states and descriptions. The last table connects the picture IDs to file names. In DiversityDescriptions resources are represented by the tablese "Resource", which holds some general information and is linked to descriptors, categorical states or descriptions. Table "Resource variant" holds the URL of the resources and each table row is assigned to one entry in table "Resource".

Find below a part of the table "Deemy_RSC.txt", which corresponds quite well to the table "Resource" in DiversityDescriptions. It references either to a description ("ItemID"), a descriptor ("CharID") or a categorical state ("StateID").



	A	B	C	D
1	ItemID	CharID	StateID	Resource
2		2		1116
3			225	1
4			225	2
717	3			911
718	13			910
719	15			54

The value in column "Resource" corresponds to column "PID" of the table "Deemy_IMG.txt" (see below), where the picture file name is specified. Since all pictures are accessible over a URL containing that file name, this table can be used for import to data table "Resource variant" in DiversityDescriptions.

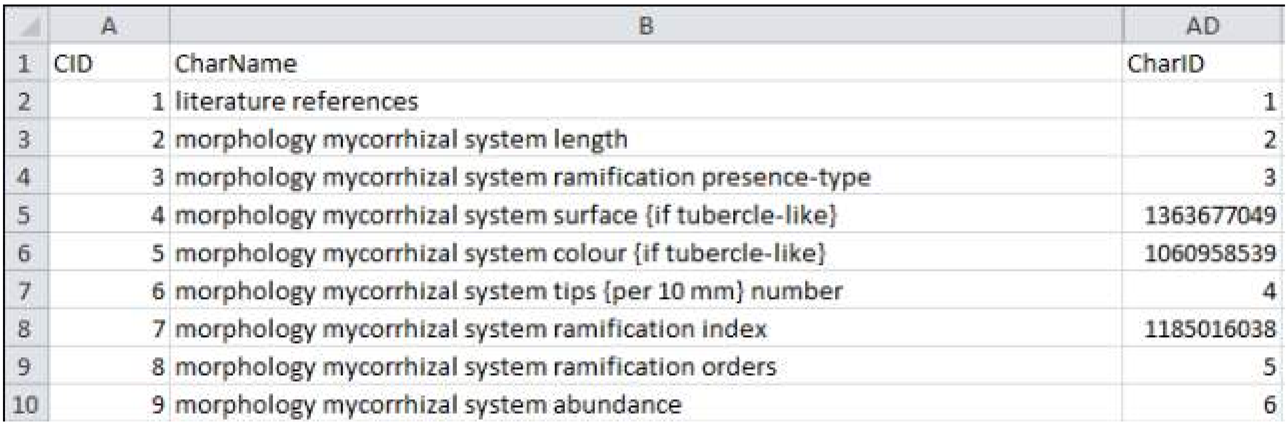


	A	B	C
1	PID	IsPreview	FileName
2	1	FALSCH	D-0001.gif
3	2	FALSCH	P-0010.jpg
4	3	FALSCH	D-0003.gif
5	4	FALSCH	P-0009.jpg
6	5	FALSCH	D-0002.gif
7	6	FALSCH	P-0008.jpg

To import the picture data, first the data in table "Deemy_RSC.txt" must be appended to the existing descriptors, categorical states and descriptions. Then the data from table "Deemy_IMG.txt" must be appended to the resource entries. Since the basic data are imported from a DELTA file, no mapping information have been stored, which are needed to append the resource data. Therefore at first the mapping information must be imported from three additional tables.

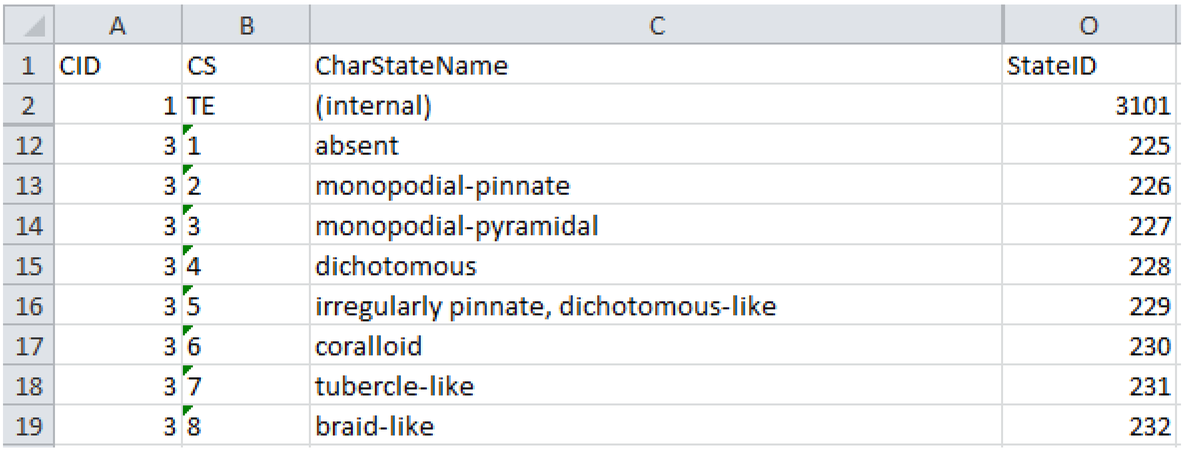
Mapping data

To allow appending of resource data to the existing database objects, we first must create the mapping information of the external IDs of the foreign database to the actual IDs in DiversityDescriptions. Find below the table "Deemy_Char.txt", which contains the descriptor name ("CharName"), the internal "CharID" and an external "CID".



	A	B	AD
1	CID	CharName	CharID
2	1	literature references	1
3	2	morphology mycorrhizal system length	2
4	3	morphology mycorrhizal system ramification presence-type	3
5	4	morphology mycorrhizal system surface {if tubercle-like}	1363677049
6	5	morphology mycorrhizal system colour {if tubercle-like}	1060958539
7	6	morphology mycorrhizal system tips {per 10 mm} number	4
8	7	morphology mycorrhizal system ramification index	1185016038
9	8	morphology mycorrhizal system ramification orders	5
10	9	morphology mycorrhizal system abundance	6

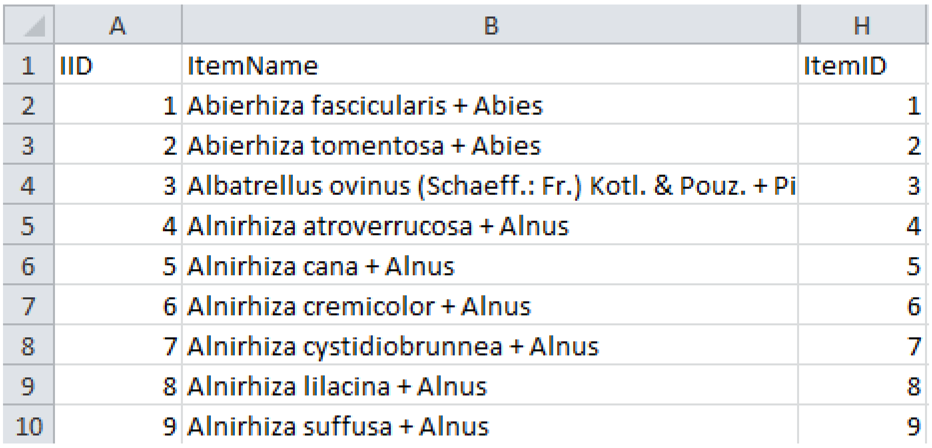
For the picture import each descriptor must be mapped to its "CharID", which can be done by a special mapping import available in the **Import session** form. When we now take a look at the "Deemy_CS.txt" (see below), which contains the categorical state data, we discover a problem: The categorical states contain the required "StateID", but they are connected to their descriptors by the value "CID", not "CharID".



	A	B	C	O
1	CID	CS	CharStateName	StateID
2	1	TE	(internal)	3101
12	3	1	absent	225
13	3	2	monopodial-pinnate	226
14	3	3	monopodial-pyramidal	227
15	3	4	dichotomous	228
16	3	5	irregularly pinnate, dichotomous-like	229
17	3	6	coralloid	230
18	3	7	tubercle-like	231
19	3	8	braid-like	232

This problem can be solved by importing the descriptor mapping twice: First the descriptor mapping is imported by using the "CID" and the categorical states are appended to the descriptors. Then the descriptor mapping is cleared and imported again, this time using the final value from column "CharID".

The last table is "Deemy_Item.txt", which contains the mapping information for the descriptions. Here the data column "ItemID" must be mapped to the descriptions (see below).

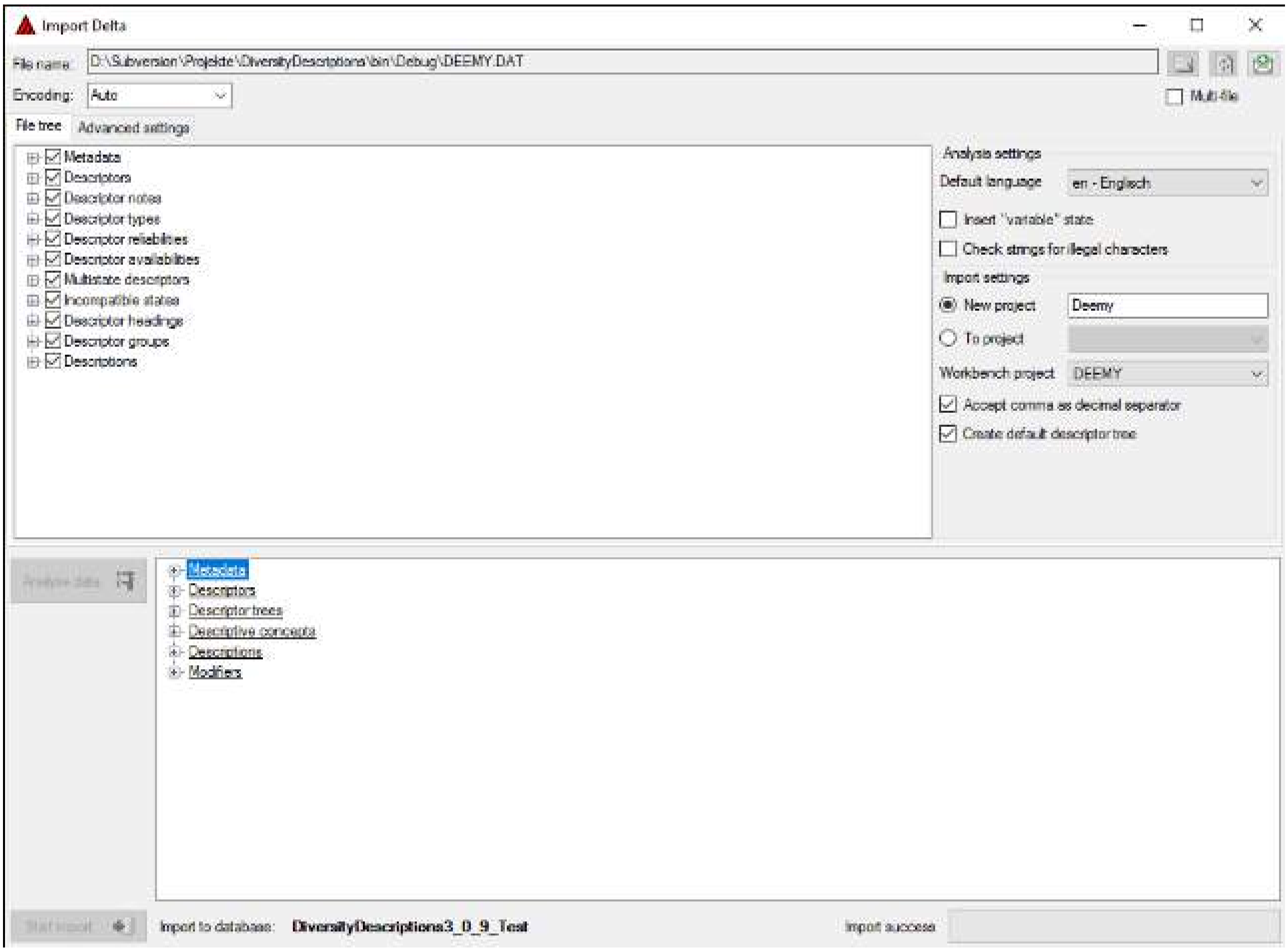


	A	B	H
1	IID	ItemName	ItemID
2	1	Abierhiza fascicularis + Abies	1
3	2	Abierhiza tomentosa + Abies	2
4	3	Albatrellus ovinus (Schaeff.: Fr.) Kotl. & Pouz. + Pi	3
5	4	Alnirhiza atroverrucosa + Alnus	4
6	5	Alnirhiza cana + Alnus	5
7	6	Alnirhiza cremicolor + Alnus	6
8	7	Alnirhiza cystidiobrunnea + Alnus	7
9	8	Alnirhiza lilacina + Alnus	8
10	9	Alnirhiza suffusa + Alnus	9

Next: Step 1 - Preparations: Data import from DELTA file and new import session

Step 1 - Preparations: Data import from DELTA file and new import session

Choose **Data -> Import -> Import DELTA ...** (see Import DELTA file) from the menu and import the DELTA file to project "Deemy" (see below). If the original database contains special characters, e.g. the German letters "ä", "ö" or "ü", it is recommended to specify the export character set "Unicode" or "UTF" if the application allows that. If the character set "ANSI" or "ASCII" was used, you may try the corresponding encoding setting to get a satifactory import result. The option "Accept comma as decimal separator" was checked, because the export has been done on a German computer system, where a value like "3.14" is exported as "3,14".


Import Delta

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\DEEMY.DAT

Encoding: Auto

☐ Multi-file

Analysis settings

Default language: en - Englisch

☐ Insert "variable" state

☐ Check strings for illegal characters

Import settings

● New project: Deemy

○ To project

Workbench project: DEEMY

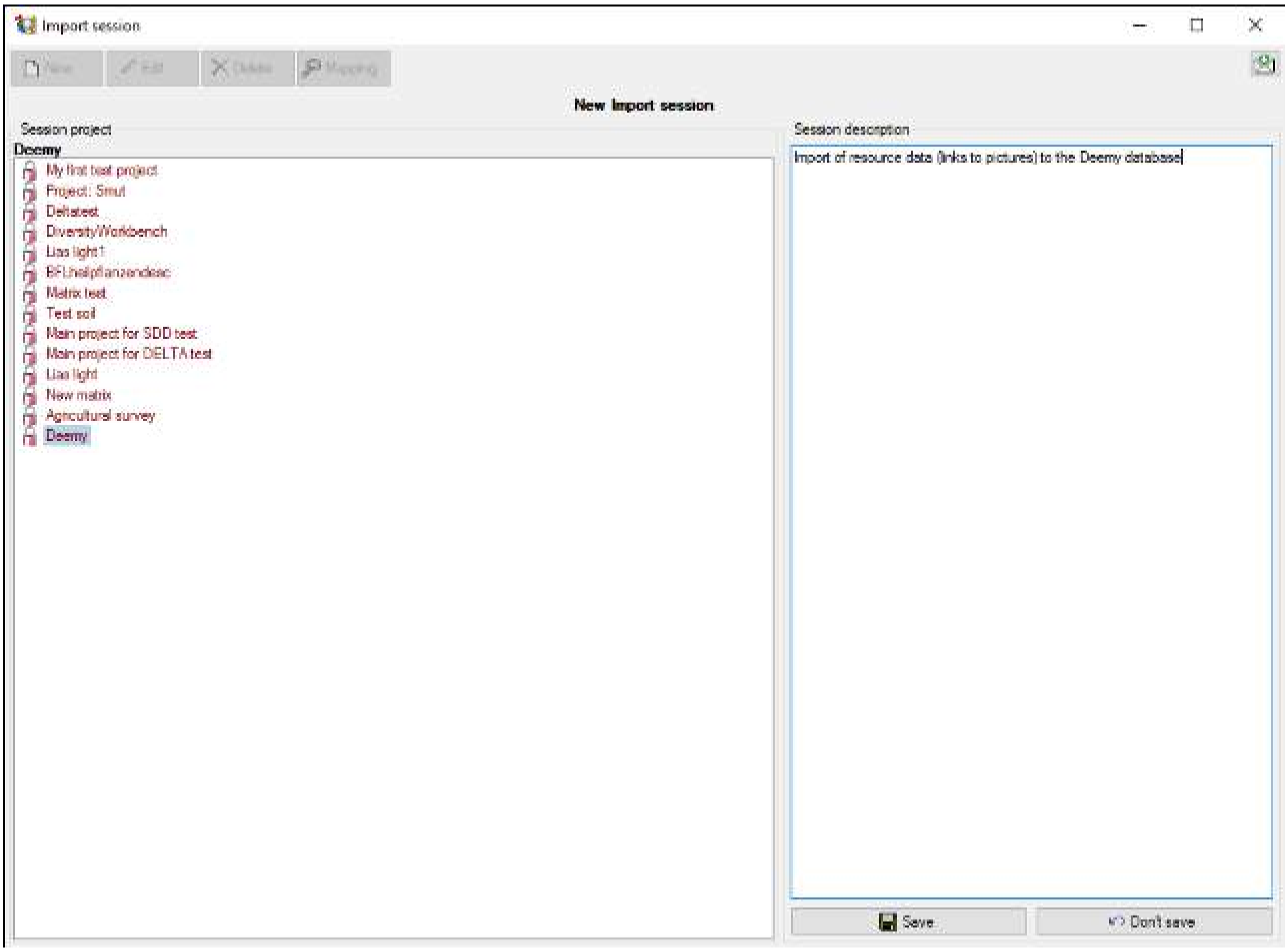
☑ Accept comma as decimal separator

☑ Create default descriptor tree

Import to database: **DiversityDescriptions3_0_9_Test**

Import success

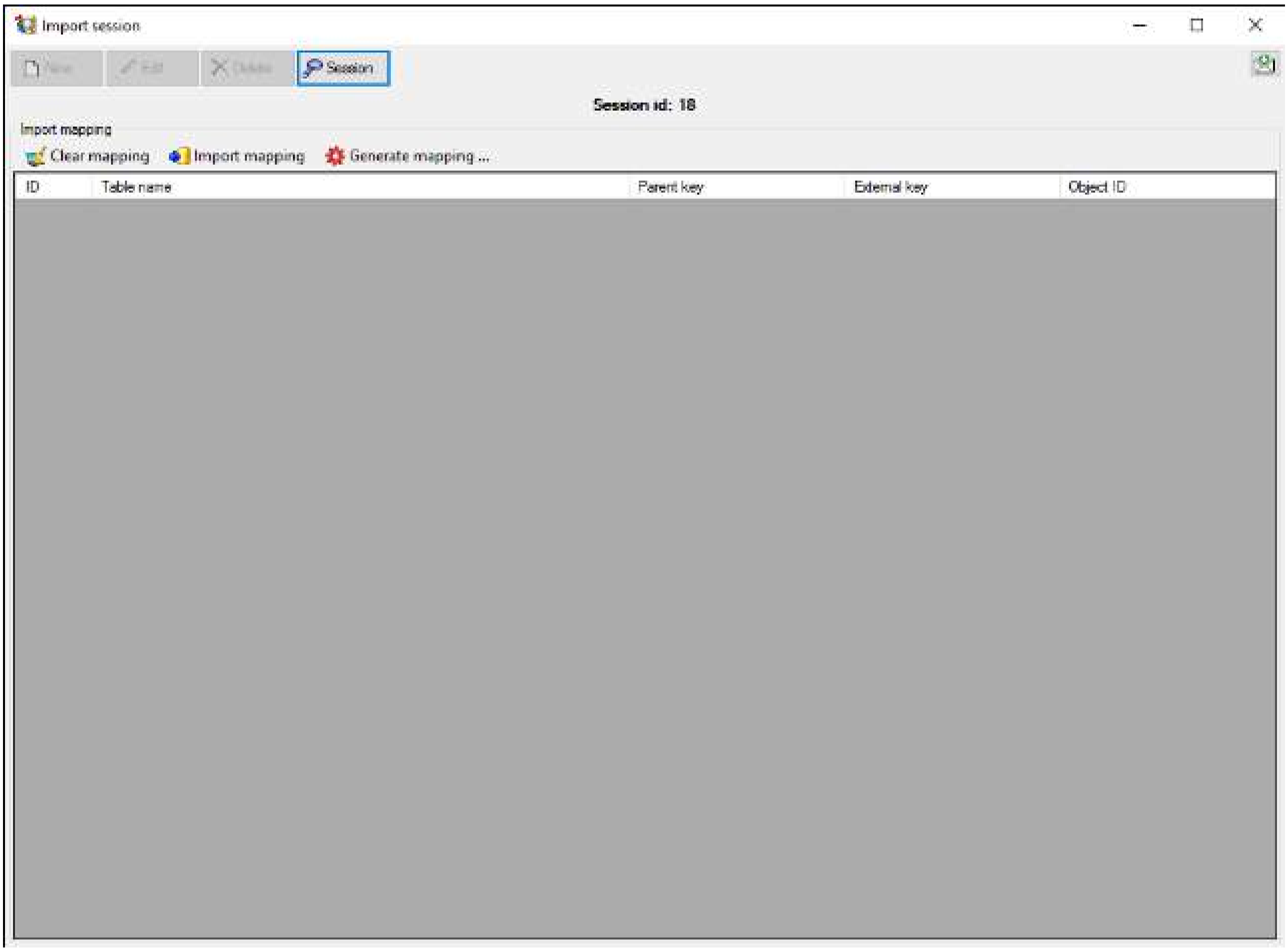
Close the window above and choose **Data -> Import -> Wizard -> Organize session ...** from the menu. A window as shown below will open, click the **New** button to create a new import session. Select project "Deemy" and enter a session description. Finally click button **Save** to store the data (see below).



Session project
Deemy

Session description
Import of resource data (links to pictures) to the Deemy database

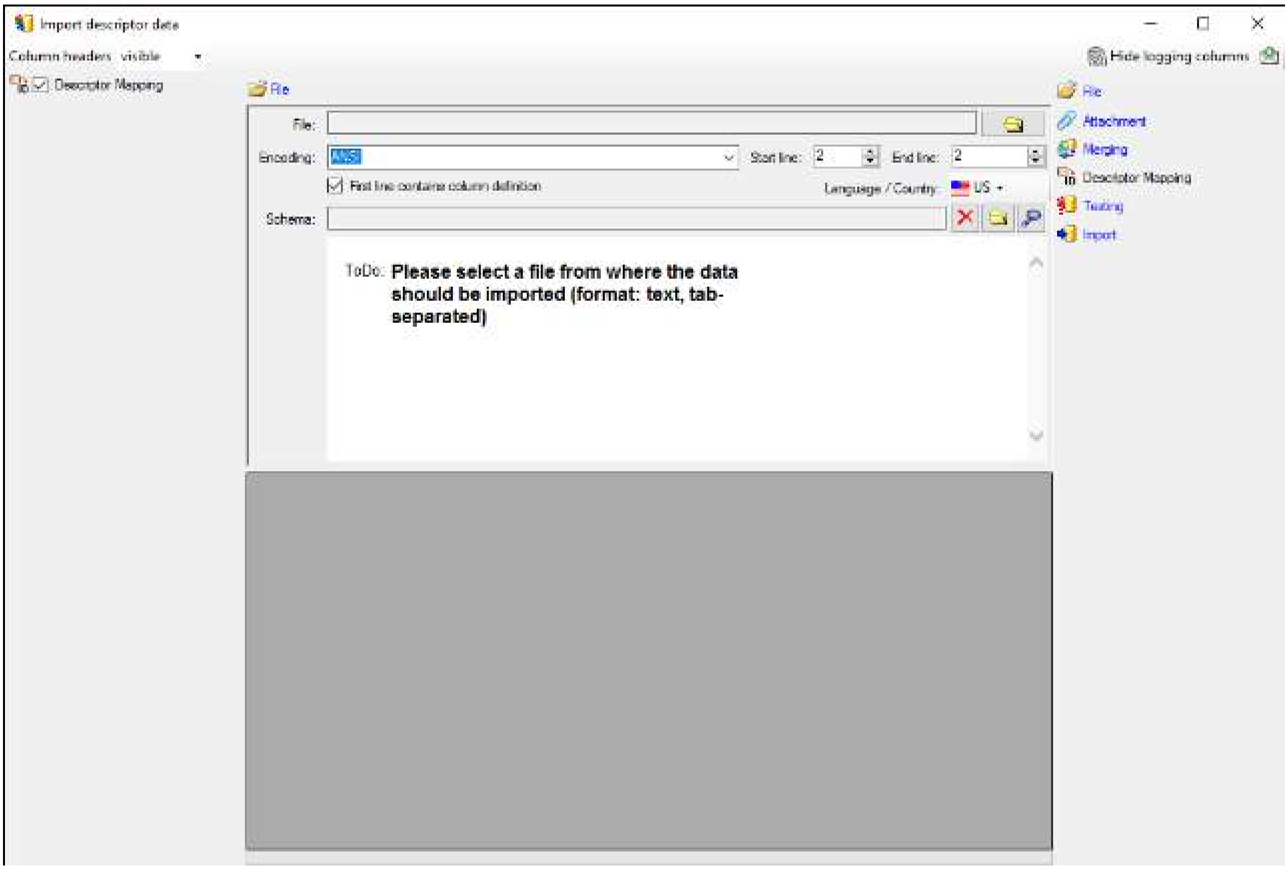
When you now click on button **Mapping** you can see that no mapping data are available (see below).



Next: Step 2 - Import of categorical state mapping

Step 2 - Import categorical state mapping

In the **Import session** form choose **Import mapping ->** **Descriptor ...** from the menu. A window as shown below opens that will lead you through the import of the descriptor mapping data.



Column headers: visible

Encoding: ANSI

Start line: 2

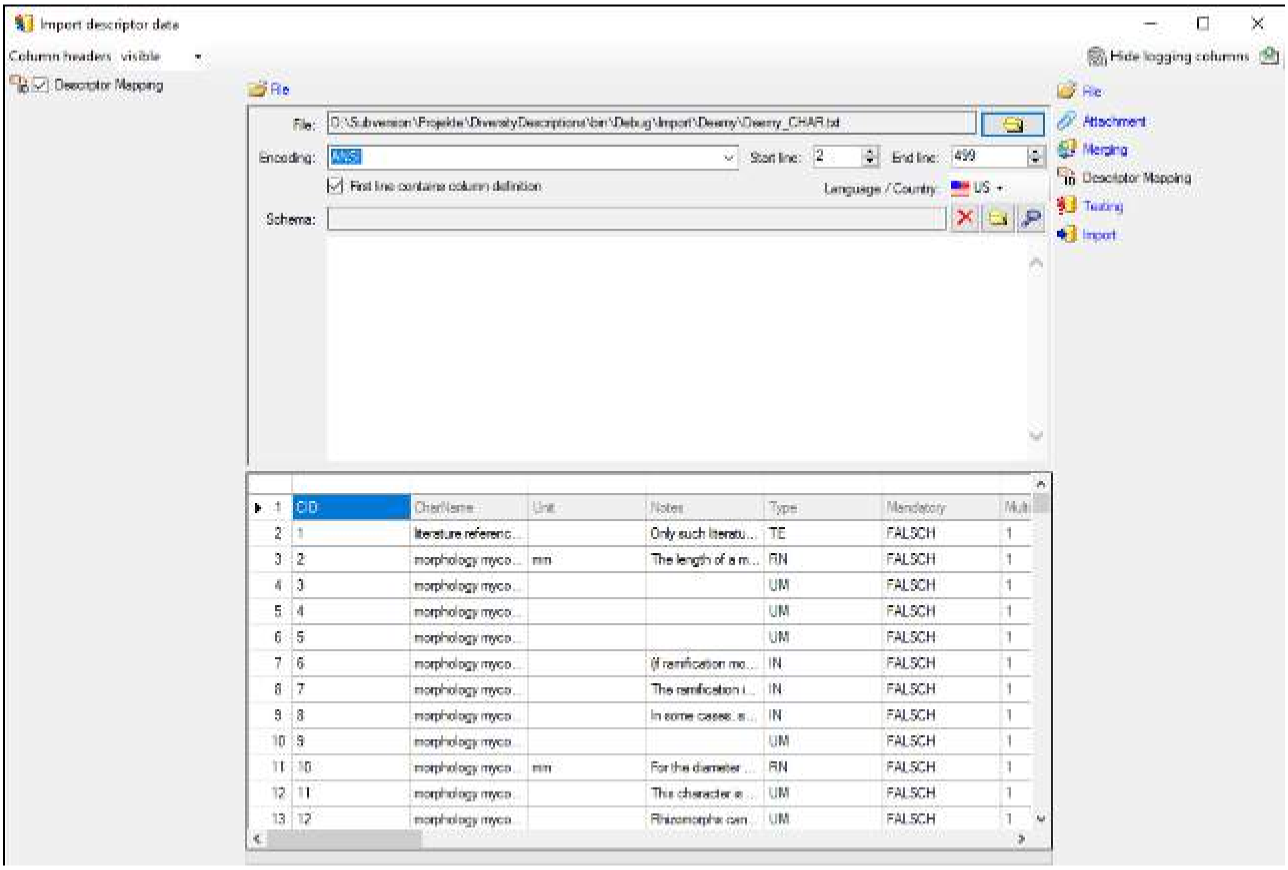
End line: 2

☑ First line contains column definition

Language / Country: US

ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

The only available import step **Descriptor Mapping** is already selected at the left side of the window. Now choose the **File** from where the data should be imported. Open file "Deemy_CHAR.txt". The chosen encoding **ANSI** of the file is sufficient. The file column "CharName" contains the descriptor names and file column "CID" the external ID needed for the import of the categorical state mapping import (see below).



☑ Descriptor Mapping

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_CHAR.txt

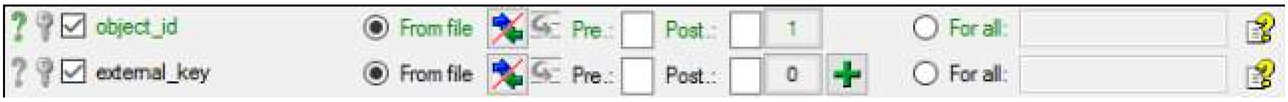
Encoding: ANSI Start line: 2 End line: 499

☑ First line contains column definition Language / Country: US

Schema:

1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		(if ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases, a...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter ...	RN	FALSCH	1
12	11	morphology myco...		This character a...	UM	FALSCH	1
13	12	morphology myco...		Rhizomorphs can...	UM	FALSCH	1

In the step table at the right side you find the import step **Descriptor Mapping**. Click on it and in the center window the assignemt data for the internal "object_id" and the "external_key" are displayed. In column "object_id" click on ? to make this the decisive column, further click on ● **From file** to select the column "CharName" as data source. Now click on the In column "external_key" click on ● **From file** to select the column "CID" as data source. After that the columns should look as shown below.



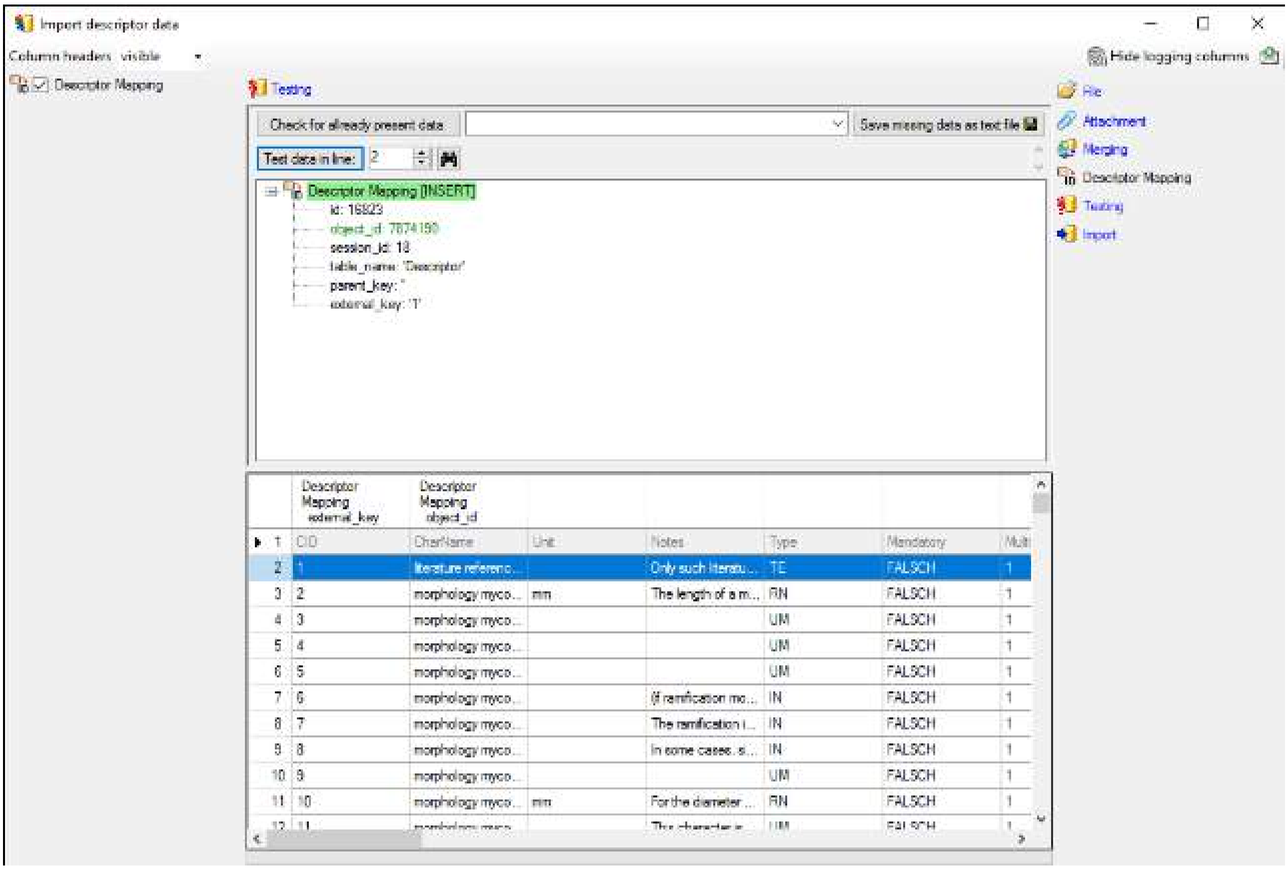
☑ object_id ● From file Pre.: Post.: 1 ○ For all:

☑ external_key ● From file Pre.: Post.: 0 ○ For all:

Remark: In the import wizards for the import mapping "object_id" allways represents the internal ID of the database. The matching database entry is searched by comparing the label of the database entry to the selected file column. If there are several descriptors (or descriptions) with identical names, the import will generate errors. For categorical states a special handling is available if the state names are not unique.

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. In our example no error occured and the test for the first data line is shown below.



Column headers visible

☑ Descriptor Mapping

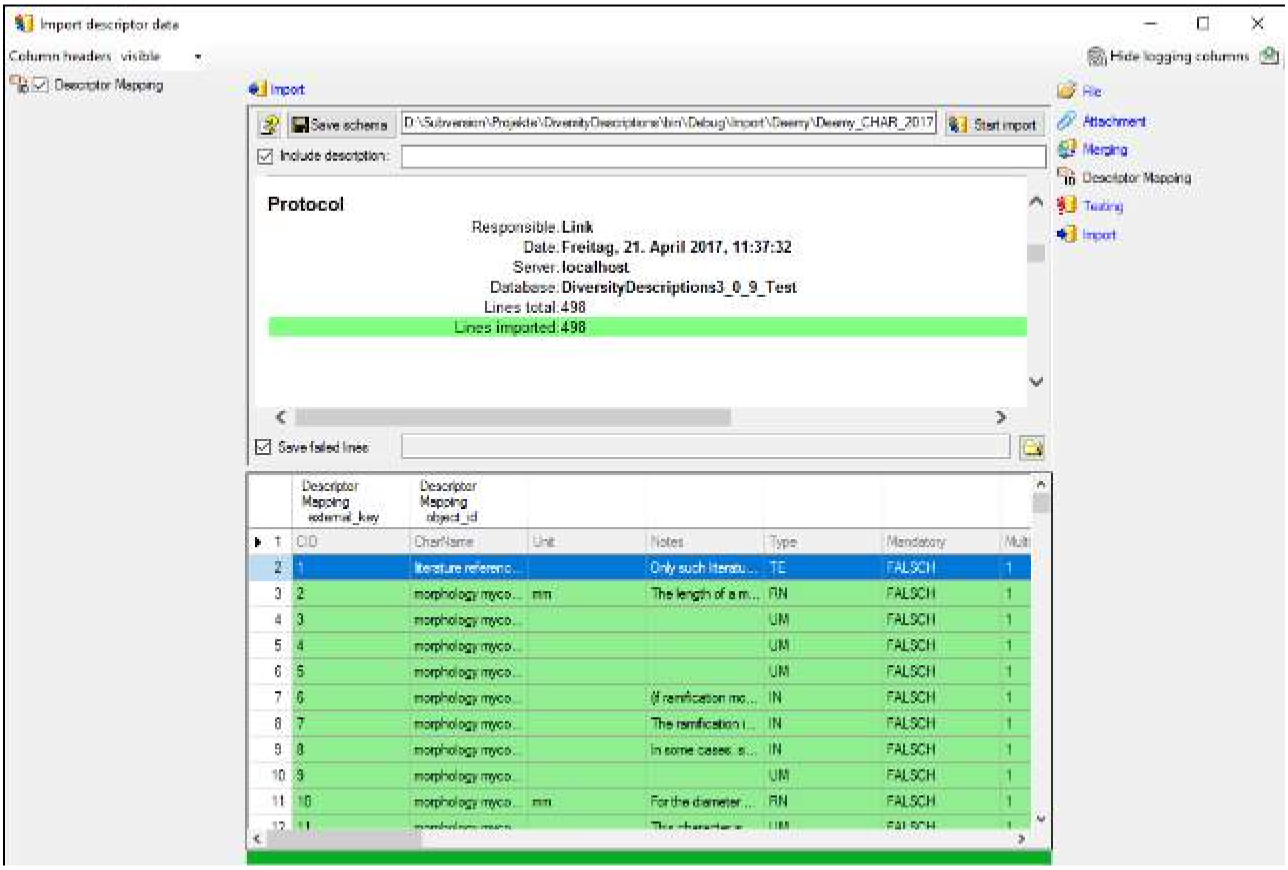
Test data in line: 2

```
Descriptor Mapping [INSERT]
    id: 16823
    object_id: 7874190
    session_id: 18
    table_name: 'Descriptor'
    parent_key: ''
    external_key: '1'
```

	Descriptor Mapping external_key	Descriptor Mapping object_id					
1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		(if ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases, s...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter ...	RN	FALSCH	1

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_CHAR_2017

☑ Include description:

Protocol

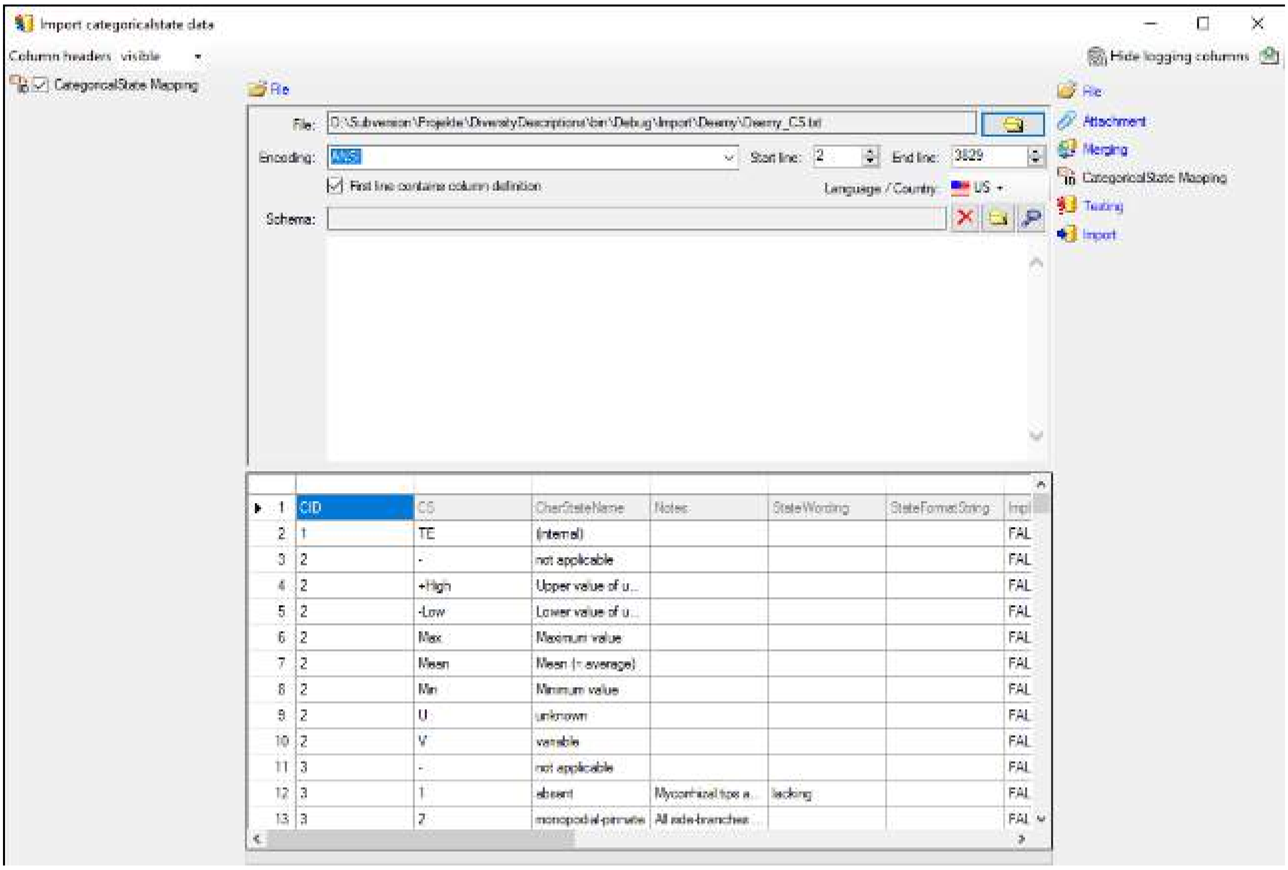
Responsible: **Link**
Date: **Freitag, 21. April 2017, 11:37:32**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 498
Lines imported: 498

☑ Save failed lines

	Descriptor Mapping external_key	Descriptor Mapping object_id					
1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		If ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases: s...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter ...	RN	FALSCH	1

Append categorical state mapping

Close the import form for descriptors. In the **Import session** form choose **Import mapping ->** **Categorical state ...** from the menu and open file "Deemy_CS.txt" (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_CS.txt

Encoding: ANSI Start line: 2 End line: 3829

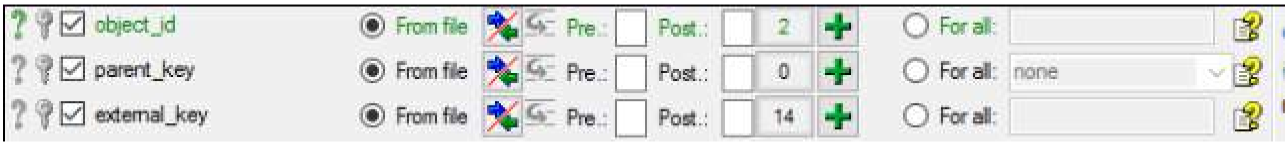
☑ First line contains column definition

Language / Country: US

Schema:

1	CID	CS	CharStateName	Notes	StateWording	StateFormatString	Impl
2	1	TE	(internal)				FAL
3	2	-	not applicable				FAL
4	2	+High	Upper value of u...				FAL
5	2	-Low	Lower value of u...				FAL
6	2	Max	Maximum value				FAL
7	2	Mean	Mean (= average)				FAL
8	2	Min	Minimum value				FAL
9	2	U	unknown				FAL
10	2	V	variable				FAL
11	3	-	not applicable				FAL
12	3	1	absent	Mycorrhizal tips a...	lacking		FAL
13	3	2	monopodial-pinnate	All side-branches ...			FAL

The only available import step **CategoricalState Mapping** is already selected at the left side of the window. In the step table at the right side you find the import step **CategoricalState Mapping**, too. Click on it and in the center window the assignemt data for the internal "object_id", the "parent_key" and the "external_key" are displayed. In column "object_id" click on ? to make this the decisive column, further click on ● **From file** to select the column "CharStateName" as data source. In column "parent_key" you have to specify the parent of the categorical state, i.e. the external descriptor ID. Therefore click on ● **From file** to select the column "CID" as data source. In column "external_key" click on ● **From file** to select the column "StateID" as data source. After that the columns should look as shown below.



☑ object_id ● From file Pre.: Post.: 2 ○ For all:

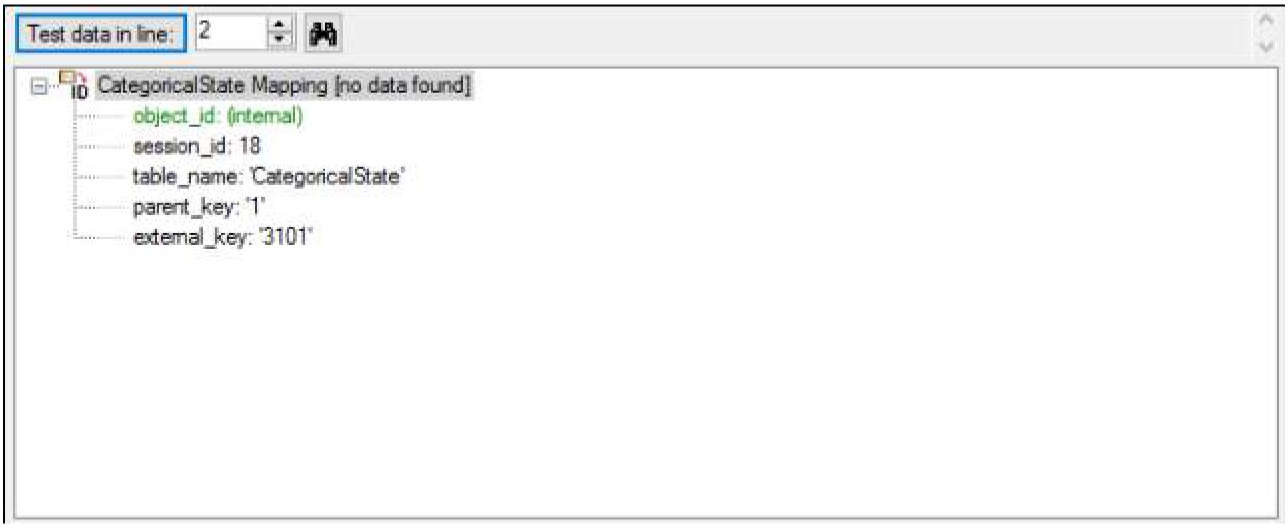
☑ parent_key ● From file Pre.: Post.: 0 ○ For all: none

☑ external_key ● From file Pre.: Post.: 14 ○ For all:

In the source database of this example not only the categorical states as known in DiversityDescriptions are present, but also some "pseudo states" that represent statistical measures of quantitative descriptors or the data status value "not applicable". The real categorical states can be recognized by a numeric value in file column "CS". In any case the import wizard check if a categorical state with the label specified in file column "CharStateName" exists in the database. Therefore let's do a first test for some selected file lines.

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. Perform the import test for file lines 2, 13 and 12 (see below).

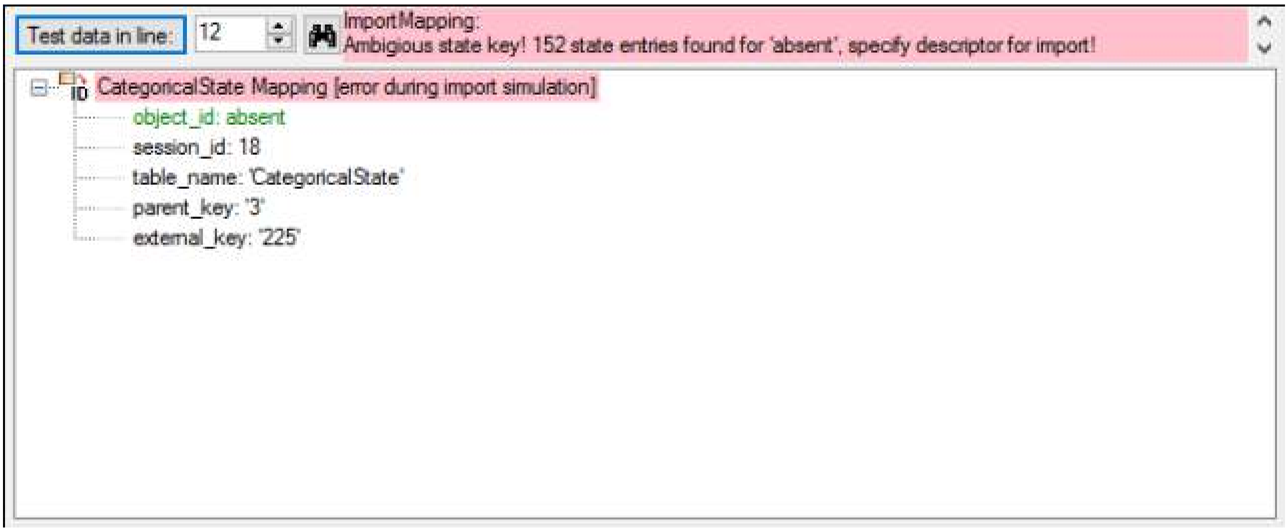


```
CategoricalState Mapping [no data found]
    object_id: (internal)
    session_id: 18
    table_name: 'CategoricalState'
    parent_key: '1'
    external_key: '3101'
```

The file line 2 refers to parent "CID=1", which belongs to a text descriptor. The pseudo state "(internal)" was not found as a categorical state in the database, therefore not import is performend for the file line.

```
CategoricalState Mapping [INSERT]
    id: 17322
    object_id: 7874194
    session_id: 18
    table_name: 'CategoricalState'
    parent_key: '[Descriptor].[id]=[7874192]'
    external_key: '226'
```

The file line 13 refers to parent "CID=3", which belongs to a categorical descriptor. The categorical state "monopodial-pinnate" was found exactly once in the database, therefore the import test was successful.



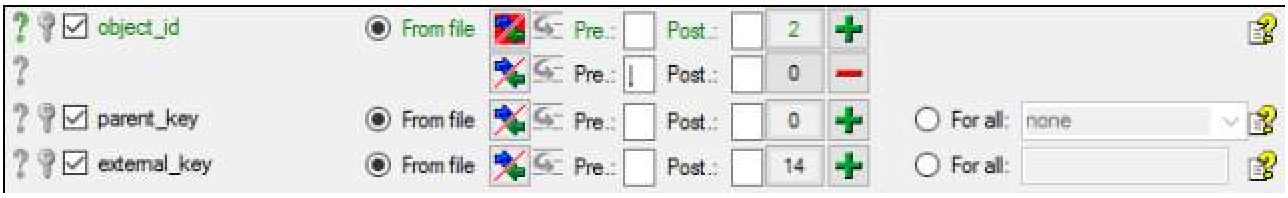
12

ImportMapping:
Ambigious state key! 152 state entries found for 'absent', specify descriptor for import!

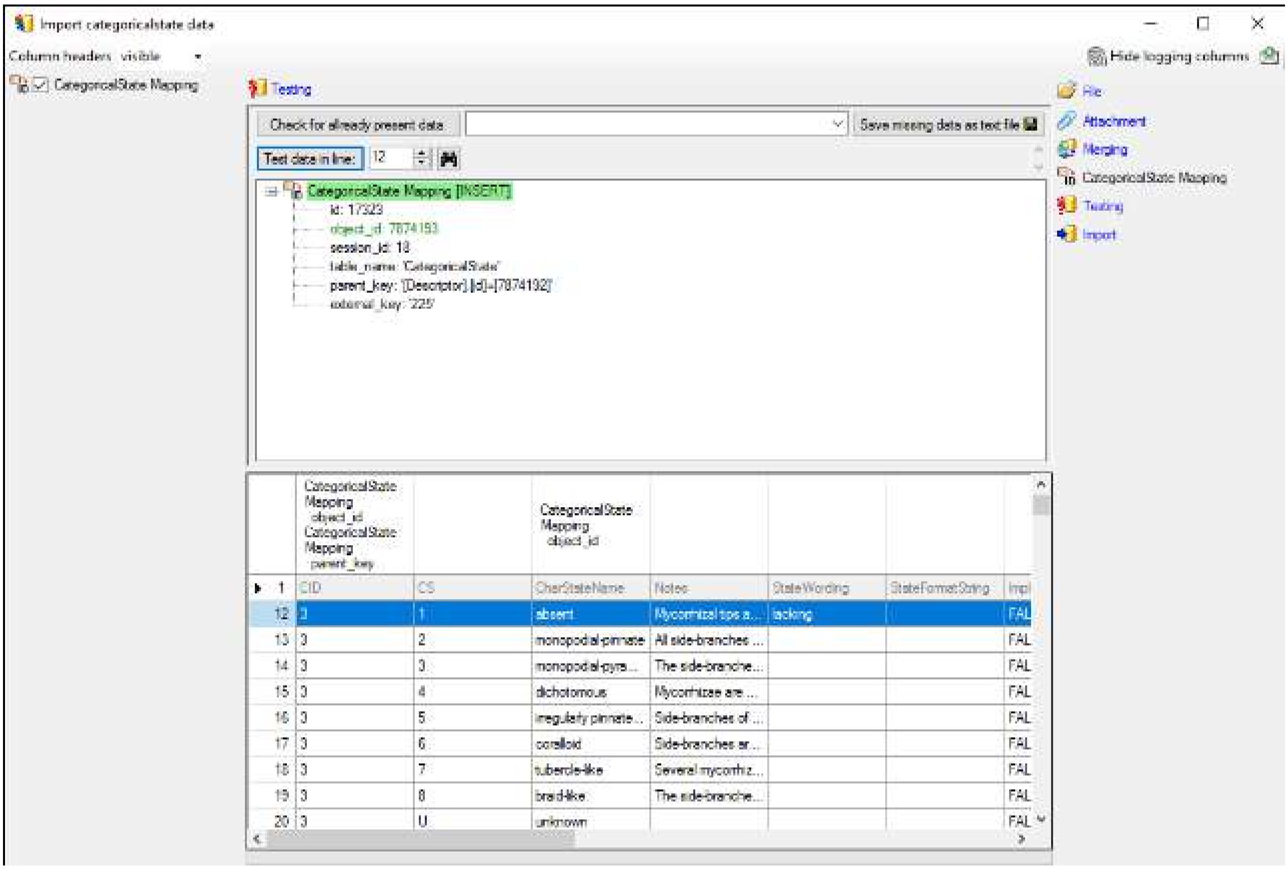
CategoricalState Mapping [error during import simulation]
- object_id: absent
- session_id: 18
- table_name: 'CategoricalState'
- parent_key: '3'
- external_key: '225'

The file line 12 refers to parent "CID=3", which belongs to a categorical descriptor. But the categorical state "absent" was found 152 time in the database. Therefore it was not possible to find the correct categorical state. But the error message already gives a hint how to solve the problem: To get an unambigious match, additionally the (external) descriptor ID must be specified.

Select the import step **CategoricalState Mapping** and click on the button at the end of line "object_id". Select file column "CID", which contains the reference to the descriptor and enter the separator character **|** (pipe symbol) in field **Pre.:** of the new line. Additionally click on button in the first line of "object_id". In the transformation window insert one replacement (button): Replace **
** by **
** . This transformation is neccessary, because the formatting tag "<br>" will be converted to the standardized format "
 during export from the original database and import from DELTA. You can check that transformation by the test functions for lines 1860 and 3555. After that the column should look as shown below.


☑ object_id ● From file Pre.: Post.: 2
Pre.: | Post.: 0
☑ parent_key ● From file Pre.: Post.: 0 ○ For all: none
☑ external_key ● From file Pre.: Post.: 14 ○ For all:

The import test with file line 12 now gives a positive result as shown below..

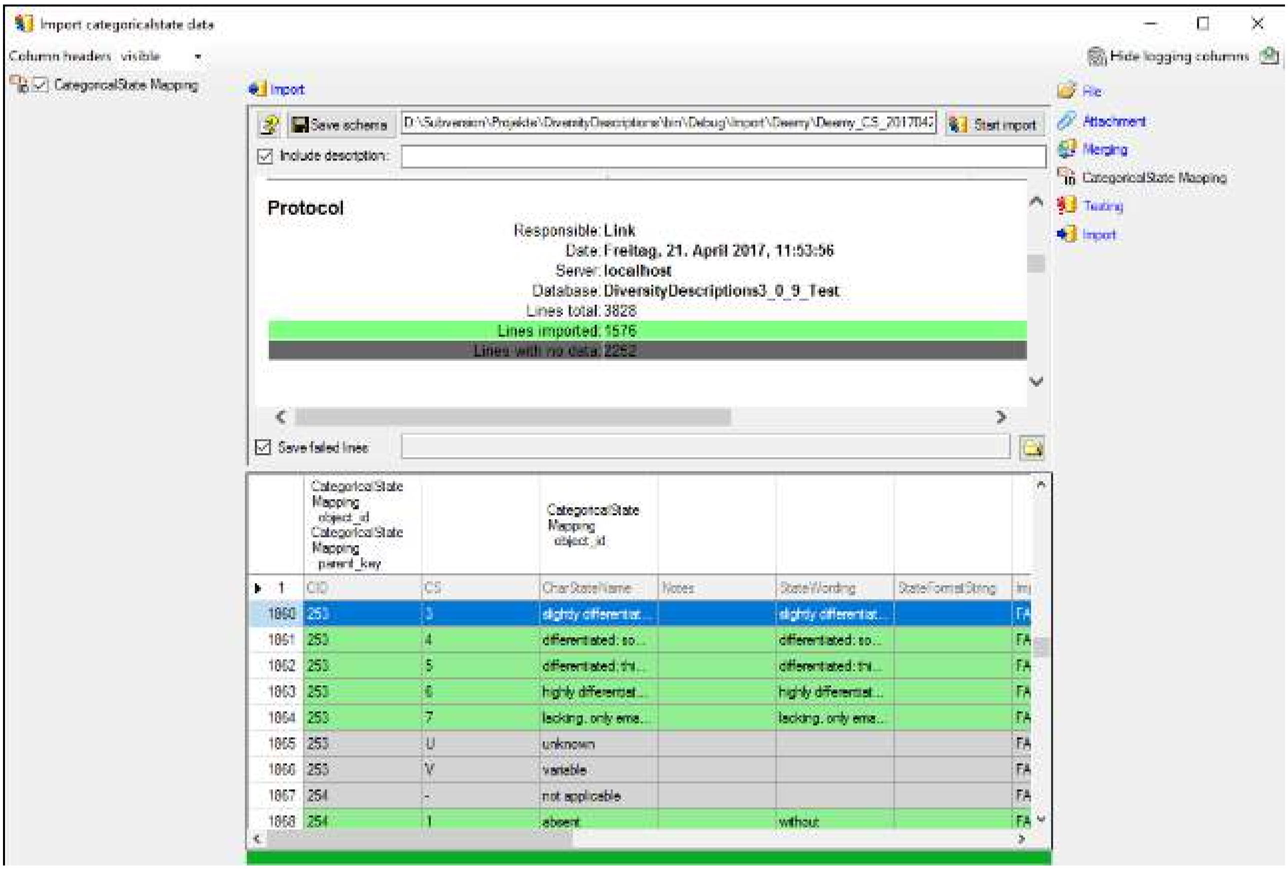


```
CategoricalState Mapping [INSERT]
    id: 17323
    object_id: 7874193
    session_id: 18
    table_name: 'CategoricalState'
    parent_key: '[Descriptor].[id]=[7874192]'
    external_key: '225'
```

	CategoricalState Mapping object_id CategoricalState Mapping parent_key		CategoricalState Mapping object_id				
1	CID	CS	CharStateName	Notes	StateWording	StateFormatString	Impl
12	3	1	absent	Mycorrhizal tips a...	lacking		FAL
13	3	2	monopodial-pinnate	All side-branches ...			FAL
14	3	3	monopodial-pyra...	The side-branche...			FAL
15	3	4	dichotomous	Mycorrhizae are ...			FAL
16	3	5	irregularly pinnate...	Side-branches of ...			FAL
17	3	6	coralloid	Side-branches ar...			FAL
18	3	7	tubercle-like	Several mycorrhiz...			FAL
19	3	8	braid-like	The side-branche...			FAL
20	3	U	unknown				FAL

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. The imported data lines are marked green (see below).



Protocol

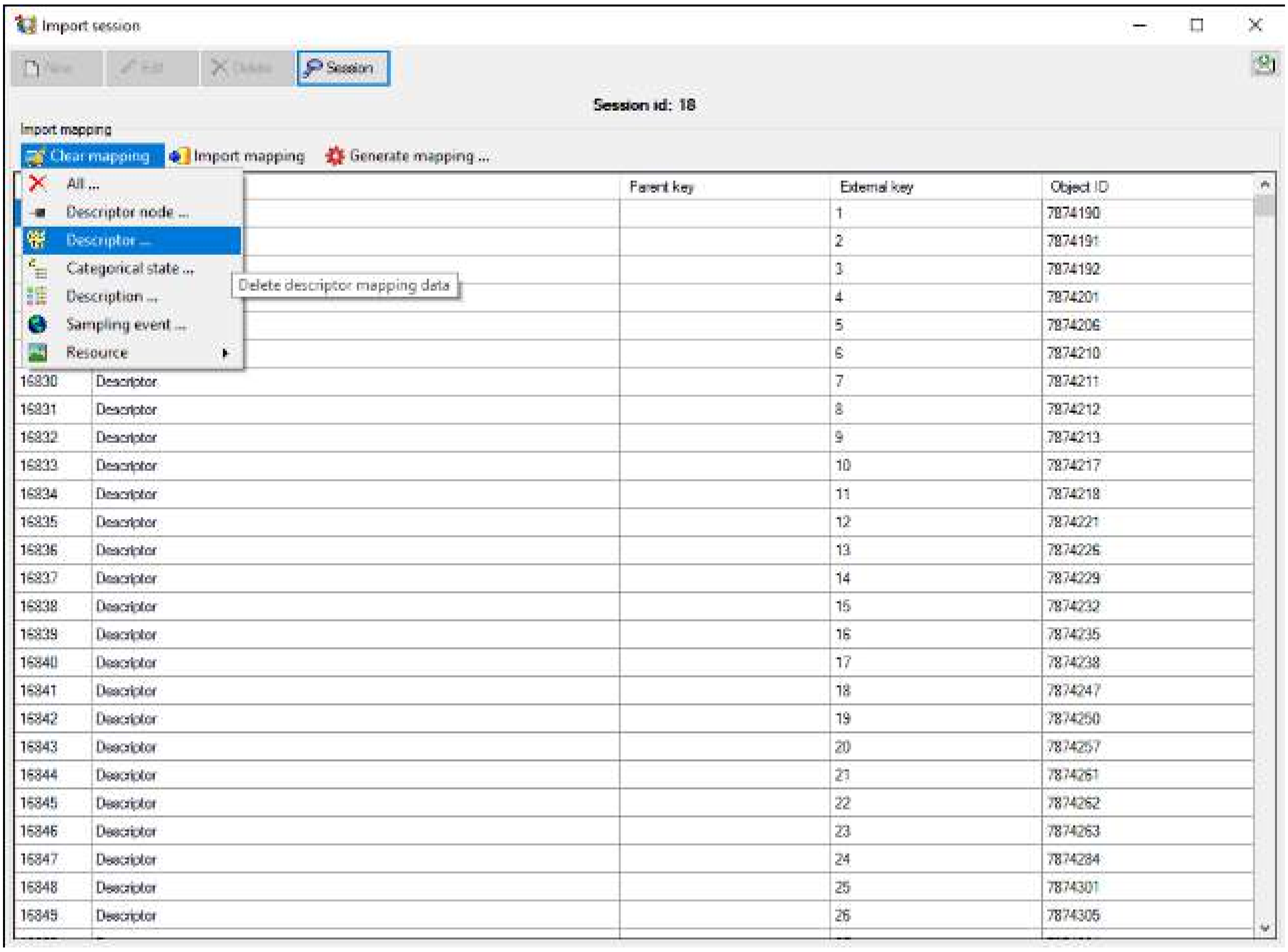
Responsible: Link
Date: Freitag, 21. April 2017, 11:53:56
Server: localhost
Database: DiversityDescriptions3_0_9_Test
Lines total: 3828
Lines imported: 1576
Lines with no data: 2252

	CategoricalState Mapping object_id CategoricalState Mapping parent_key		CategoricalState Mapping object_id				
1	CID	CS	CharStateName	Notes	StateWording	StateFormatString	Im
1860	253	3	slightly differentiat...		slightly differentiat...		FA
1861	253	4	differentiated: so...		differentiated: so...		FA
1862	253	5	differentiated: thi...		differentiated: thi...		FA
1863	253	6	highly differentiat...		highly differentiat...		FA
1864	253	7	lacking, only ema...		lacking, only ema...		FA
1865	253	U	unknown				FA
1866	253	V	variable				FA
1867	254	-	not applicable				FA
1868	254	1	absent		without		FA

Next: Step 3 - Import of descriptor mapping

Step 3 - Import of descriptor mapping

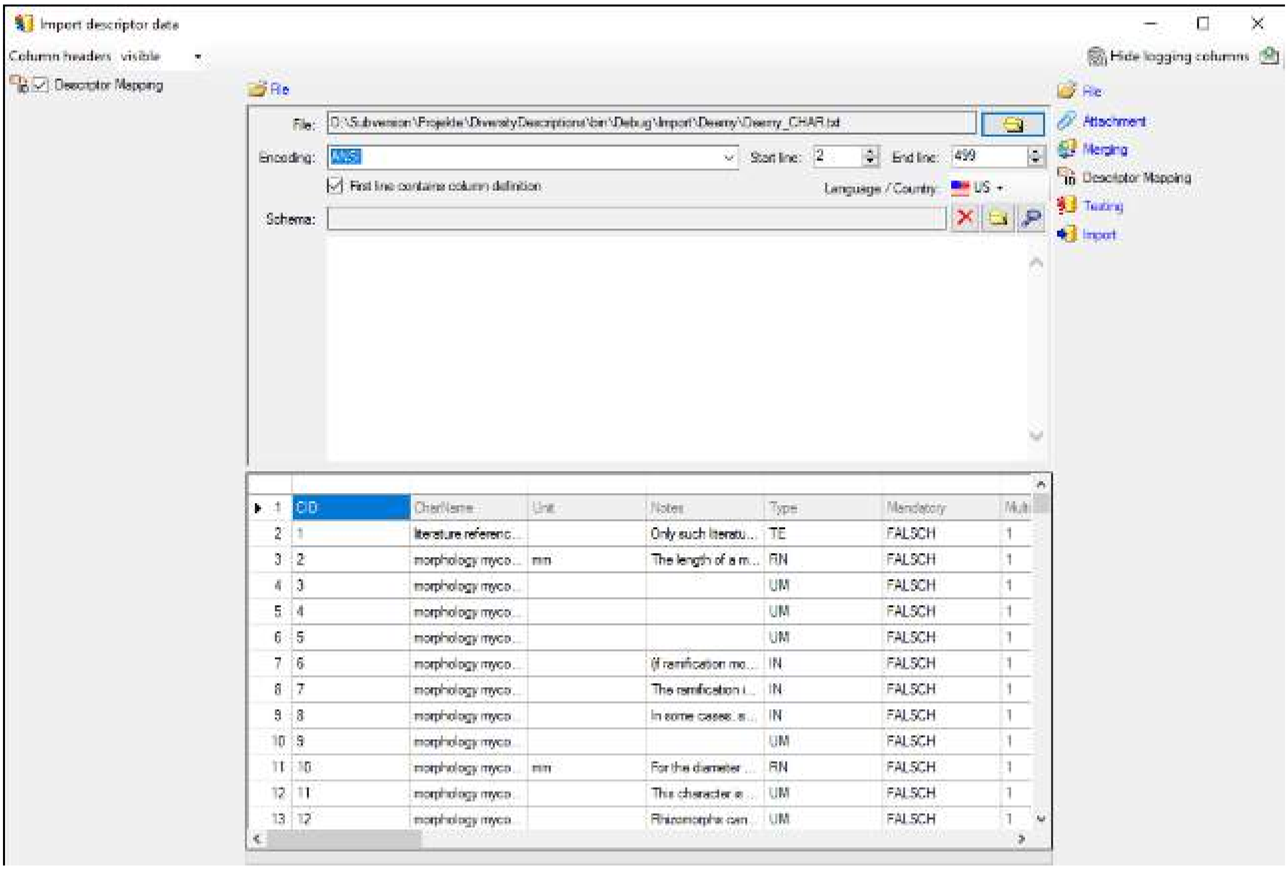
Close the import form for the categorical state mapping. In the **Import session** form choose **Clear mapping ->** **Descriptor** from the menu (see below) and answer the followind question with "Yes". This mapping is based on data column "CID" and was needed in the previous step to append the categorical state mapping data. For the picture import the descriptor mapping based on data column "CharID" is required.



Session id: 18

		Parent key	External key	Object ID
			1	7874190
			2	7874191
			3	7874192
			4	7874201
			5	7874206
			6	7874210
16830	Descriptor		7	7874211
16831	Descriptor		8	7874212
16832	Descriptor		9	7874213
16833	Descriptor		10	7874217
16834	Descriptor		11	7874218
16835	Descriptor		12	7874221
16836	Descriptor		13	7874226
16837	Descriptor		14	7874229
16838	Descriptor		15	7874232
16839	Descriptor		16	7874235
16840	Descriptor		17	7874238
16841	Descriptor		18	7874247
16842	Descriptor		19	7874250
16843	Descriptor		20	7874257
16844	Descriptor		21	7874261
16845	Descriptor		22	7874262
16846	Descriptor		23	7874263
16847	Descriptor		24	7874284
16848	Descriptor		25	7874301
16849	Descriptor		26	7874305

In the **Import session** form choose **Import mapping ->** **Descriptor ...** from the menu and open file "Deemy_CHAR.txt". The file column "CharName" contains the descriptor names and file column "CharID" the foreign ID (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_CHAR.txt

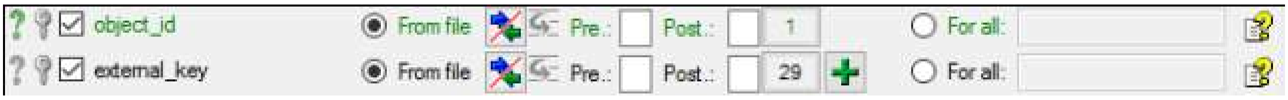
Encoding: ANSI Start line: 2 End line: 499

☑ First line contains column definition Language / Country: US

Schema:

1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		(if ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases: a...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter ...	RN	FALSCH	1
12	11	morphology myco...		This character is ...	UM	FALSCH	1
13	12	morphology myco...		Rhizomorphs can ...	UM	FALSCH	1

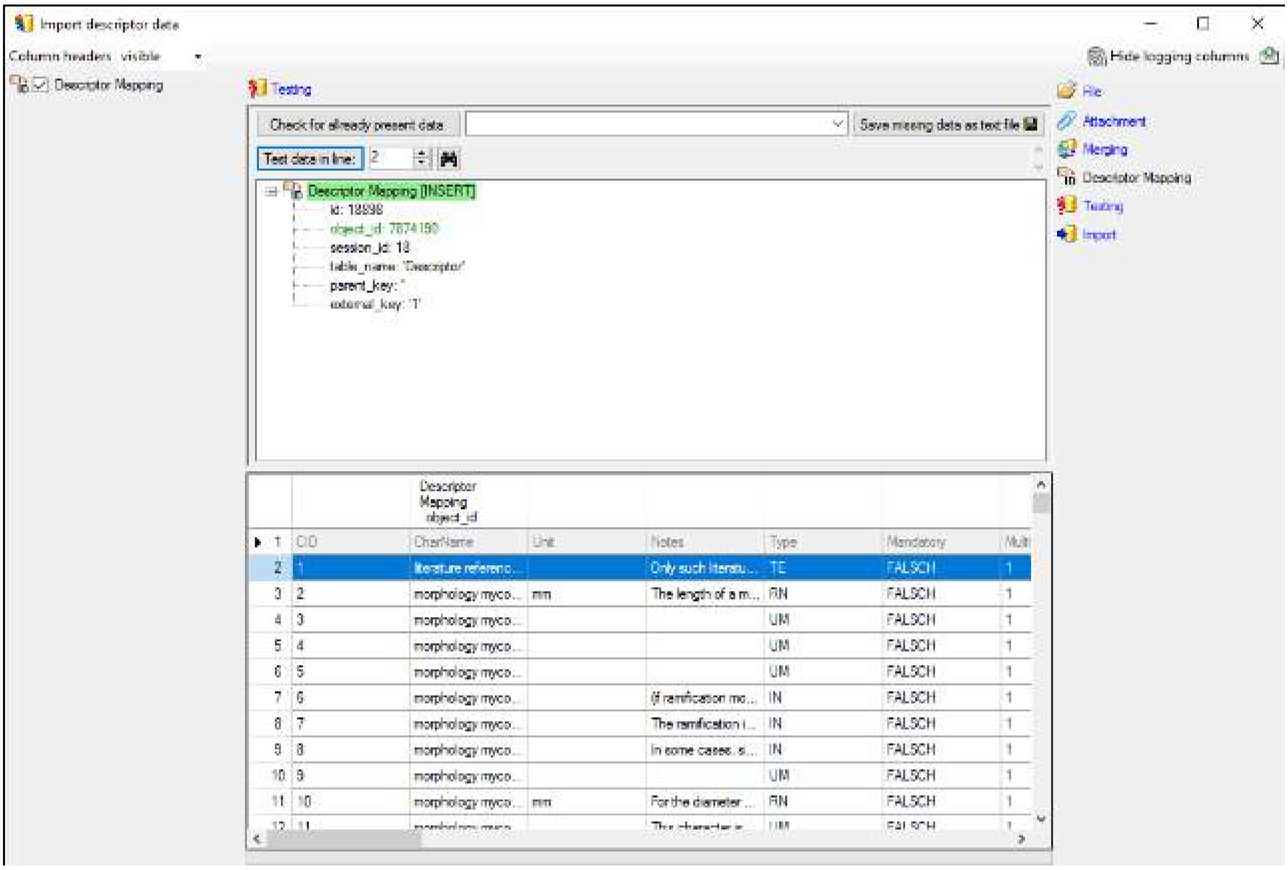
In the step table at the right side you find the import step **Descriptor Mapping**. Click on it and in the center window the assignemt data for the internal "object_id" and the "external_key" are displayed. In column "object_id" click on ?to make this the decisive column, further click on ● **From file** to select the column "CharName" as data source. Now click on the In column "external_key" click on ● **From file** to select the column "CharID" as data source. After that the columns should look as shown below.


? ☑ object_id ● From file Pre.: ☐ Post.: ☐ 1 ○ For all:

? ☑ external_key ● From file Pre.: ☐ Post.: ☐ 29 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and than click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. In our example no error occured and the test for the first data line is shown below.



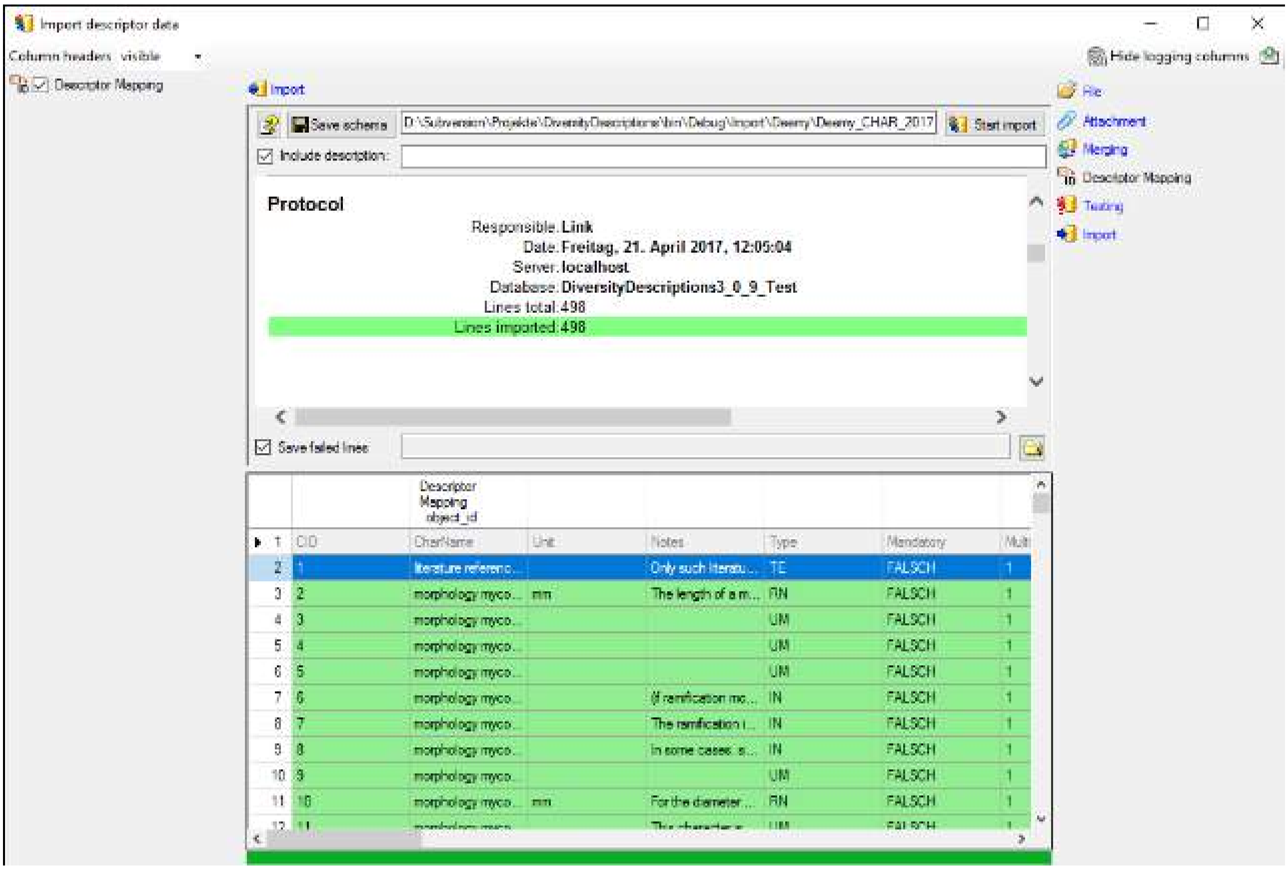
Test data in line: 2

Descriptor Mapping [INSERT]
- id: 18898
- object_id: 7874190
- session_id: 18
- table_name: 'Descriptor'
- parent_key: ''
- external_key: '1'

		Descriptor Mapping object_id					
1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		(if ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases, s...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter ...	RN	FALSCH	1

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_CHAR_2017

☑ Include description:

Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 12:05:04**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 498
Lines imported: 498

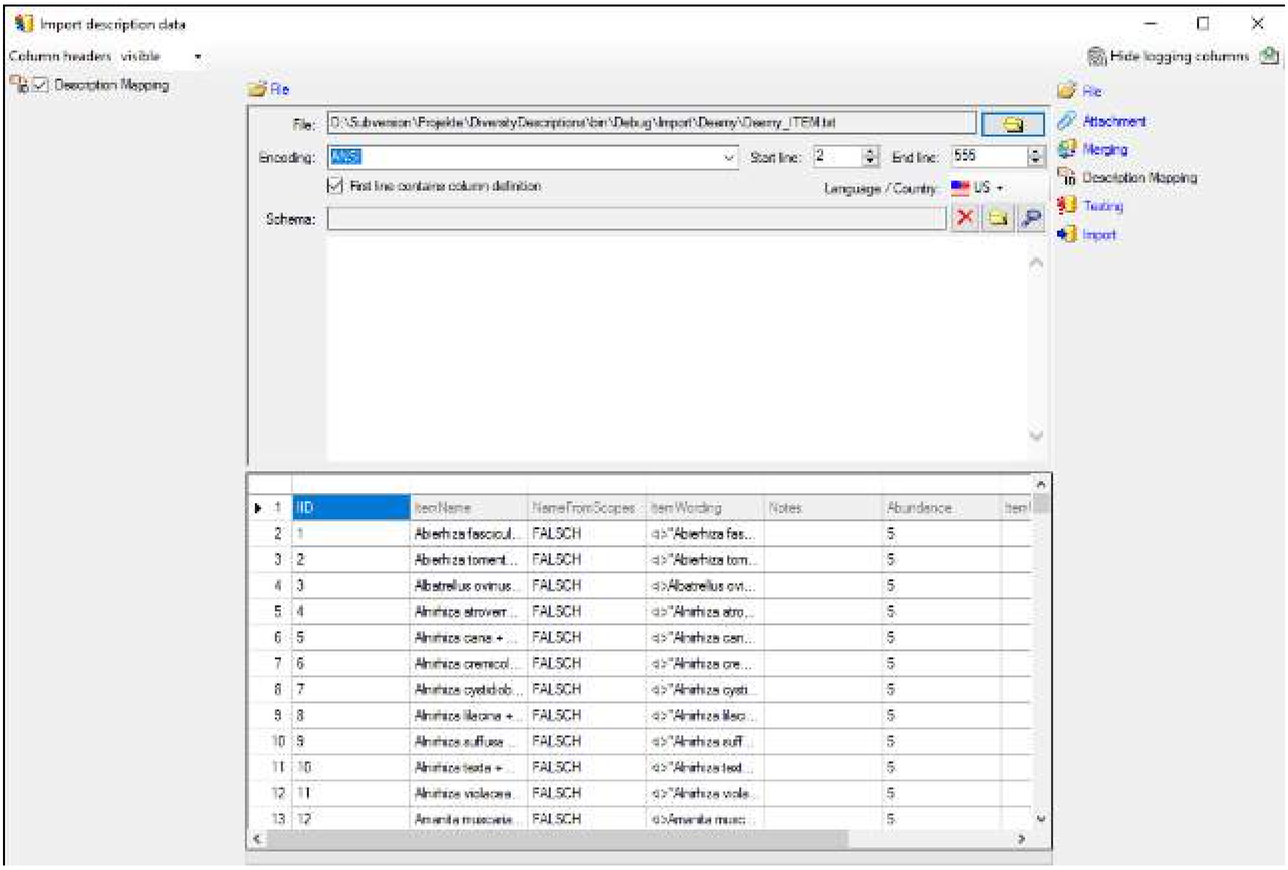
☑ Save failed lines

		Descriptor Mapping object_id					
1	CID	CharName	Unit	Notes	Type	Mandatory	Mult
2	1	literature referenc...		Only such literatu...	TE	FALSCH	1
3	2	morphology myco...	mm	The length of a m...	RN	FALSCH	1
4	3	morphology myco...			UM	FALSCH	1
5	4	morphology myco...			UM	FALSCH	1
6	5	morphology myco...			UM	FALSCH	1
7	6	morphology myco...		if ramification mo...	IN	FALSCH	1
8	7	morphology myco...		The ramification i...	IN	FALSCH	1
9	8	morphology myco...		In some cases: s...	IN	FALSCH	1
10	9	morphology myco...			UM	FALSCH	1
11	10	morphology myco...	mm	For the diameter...	RN	FALSCH	1

Next: Step 4 - Import of description mapping

Step 4 - Import description mapping

Close the import form for descriptors. In the **Import session** form choose **Import mapping -> Description ...** from the menu and open file "Deemy_ITEM.txt" (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_ITEM.txt

Encoding: ANSI

Start line: 2

End line: 556

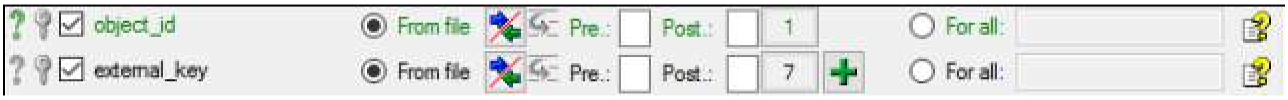
☑ First line contains column definition

Language / Country: US

Schema:

1	IID	ItemName	NameFromScopes	ItemWording	Notes	Abundance	Item
2	1	Abierhiza fascicul...	FALSCH	<i>"Abierhiza fas...		5	
3	2	Abierhiza toment...	FALSCH	<i>"Abierhiza tom...		5	
4	3	Albatrellus ovinus...	FALSCH	<i>Albatrellus ovi...		5	
5	4	Alnirhiza atrovirr...	FALSCH	<i>"Alnirhiza atro...		5	
6	5	Alnirhiza cana + ...	FALSCH	<i>"Alnirhiza can...		5	
7	6	Alnirhiza cremicol...	FALSCH	<i>"Alnirhiza cre...		5	
8	7	Alnirhiza cystidiob...	FALSCH	<i>"Alnirhiza cysti...		5	
9	8	Alnirhiza lilacina + ...	FALSCH	<i>"Alnirhiza lilac...		5	
10	9	Alnirhiza suffusa ...	FALSCH	<i>"Alnirhiza suff...		5	
11	10	Alnirhiza texta + ...	FALSCH	<i>"Alnirhiza text...		5	
12	11	Alnirhiza violacea...	FALSCH	<i>"Alnirhiza viola...		5	
13	12	Amanita muscaria...	FALSCH	<i>Amanita musc...		5	

The only available import step **Description Mapping** is already selected at the left side of the window. In the step table at the right side you find the import step **Description Mapping**, too. Click on it and in the center window the assignemt data for the internal "object_id" and the "external_key" are displayed. In column "object_id" click on to make this the decisive column, further click on ● **From file** to select the column "ItemName" as data source. In column "external_key" click on ● **From file** to select the column "ItemID" as data source. After that the columns should look as shown below.

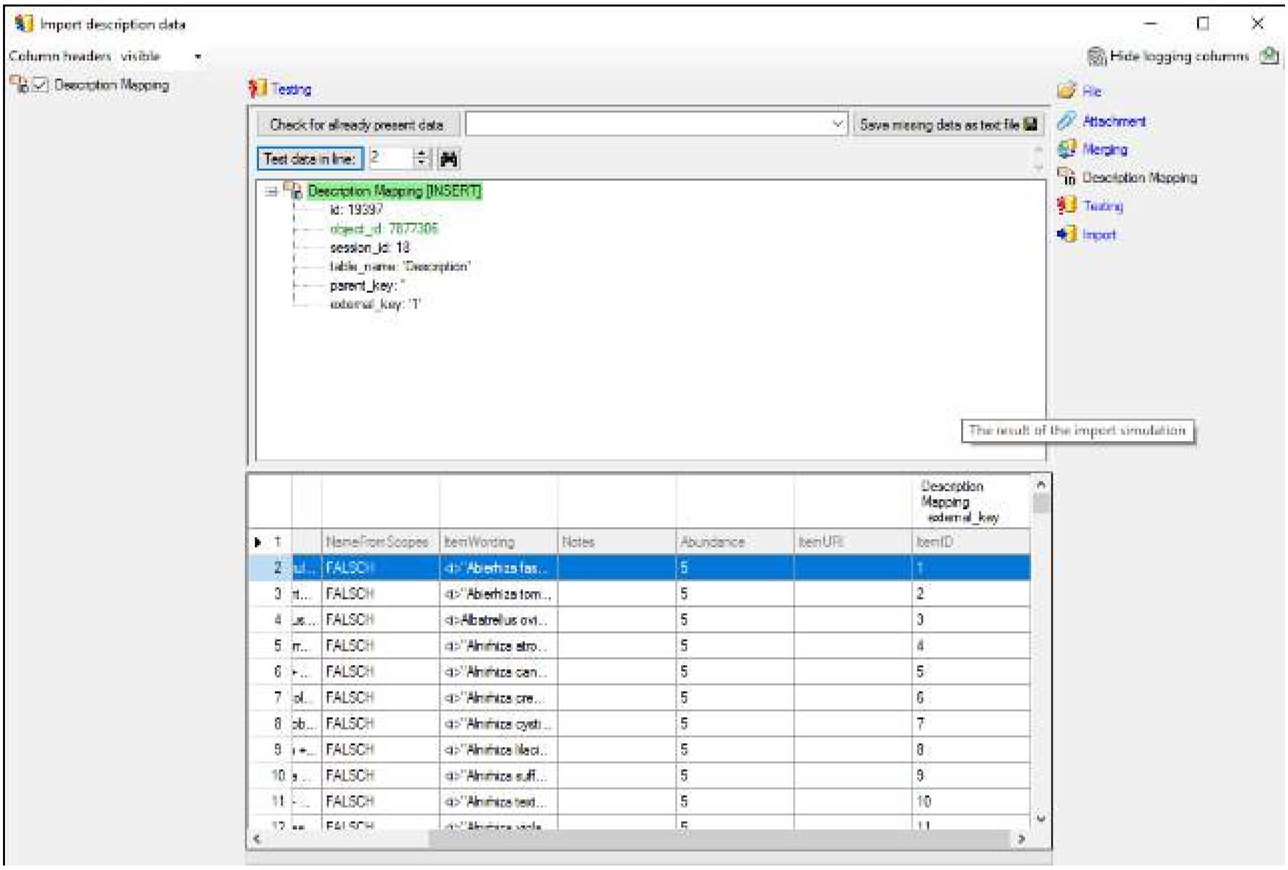


☑ object_id ● From file Pre.: ☐ Post.: ☐ 1 ○ For all:

☑ external_key ● From file Pre.: ☐ Post.: ☐ 7 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. You can use a certain line in the file for your test and then click on the **Test data in line:** button. If there are still unmet requirements, these will be listed in a window. In our example no error occured and the test for the first data line is shown below.



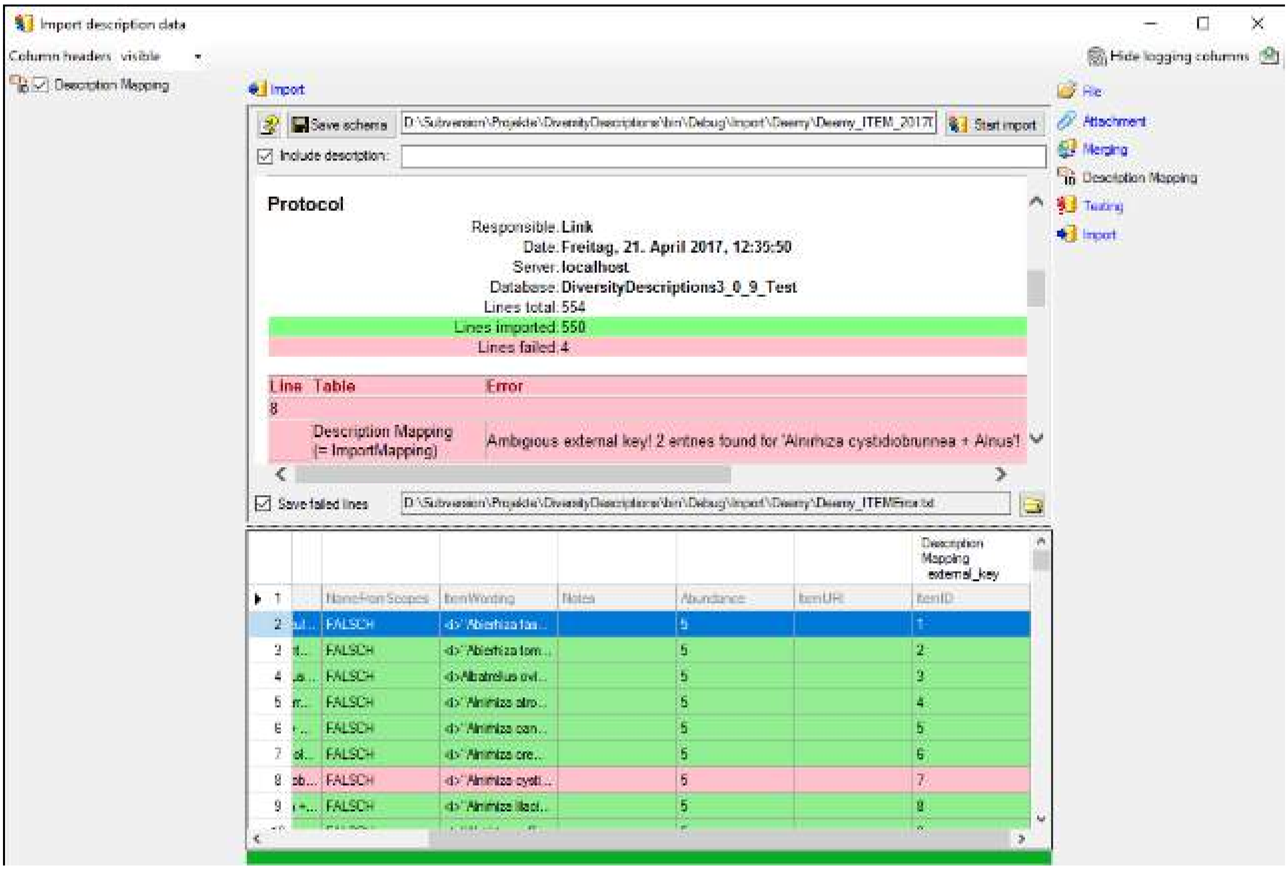
Test data in line: 2

```
Description Mapping [INSERT]
    id: 19397
    object_id: 7877306
    session_id: 18
    table_name: 'Description'
    parent_key: ''
    external_key: '1'
```

							Description Mapping external_key
1		NameFromScopes	ItemWording	Notes	Abundance	ItemURI	ItemID
2	ul...	FALSCH	d>''Abierhiza fas...		5		1
3	ri...	FALSCH	d>''Abierhiza tom...		5		2
4	us...	FALSCH	d>Albatrellus ovi...		5		3
5	m...	FALSCH	d>''Alnihiza atro...		5		4
6	+...	FALSCH	d>''Alnihiza can...		5		5
7	ol...	FALSCH	d>''Alnihiza cre...		5		6
8	ob...	FALSCH	d>''Alnihiza cyst...		5		7
9	+...	FALSCH	d>''Alnihiza lleci...		5		8
10	s...	FALSCH	d>''Alnihiza suff...		5		9
11	-...	FALSCH	d>''Alnihiza test...		5		10
12		FALSCH			5		11

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. The imported data lines are marked green (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_ITEM_2017

☑ Include description:

Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 12:35:50**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 554
Lines imported: 550
Lines failed: 4

Line	Table	Error
8		
	Description Mapping (= ImportMapping)	Ambigious external key! 2 entries found for 'Alnirhiza cystidiobrunnea + Alnus'!

☑ Save failed lines D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_ITEMError.txt

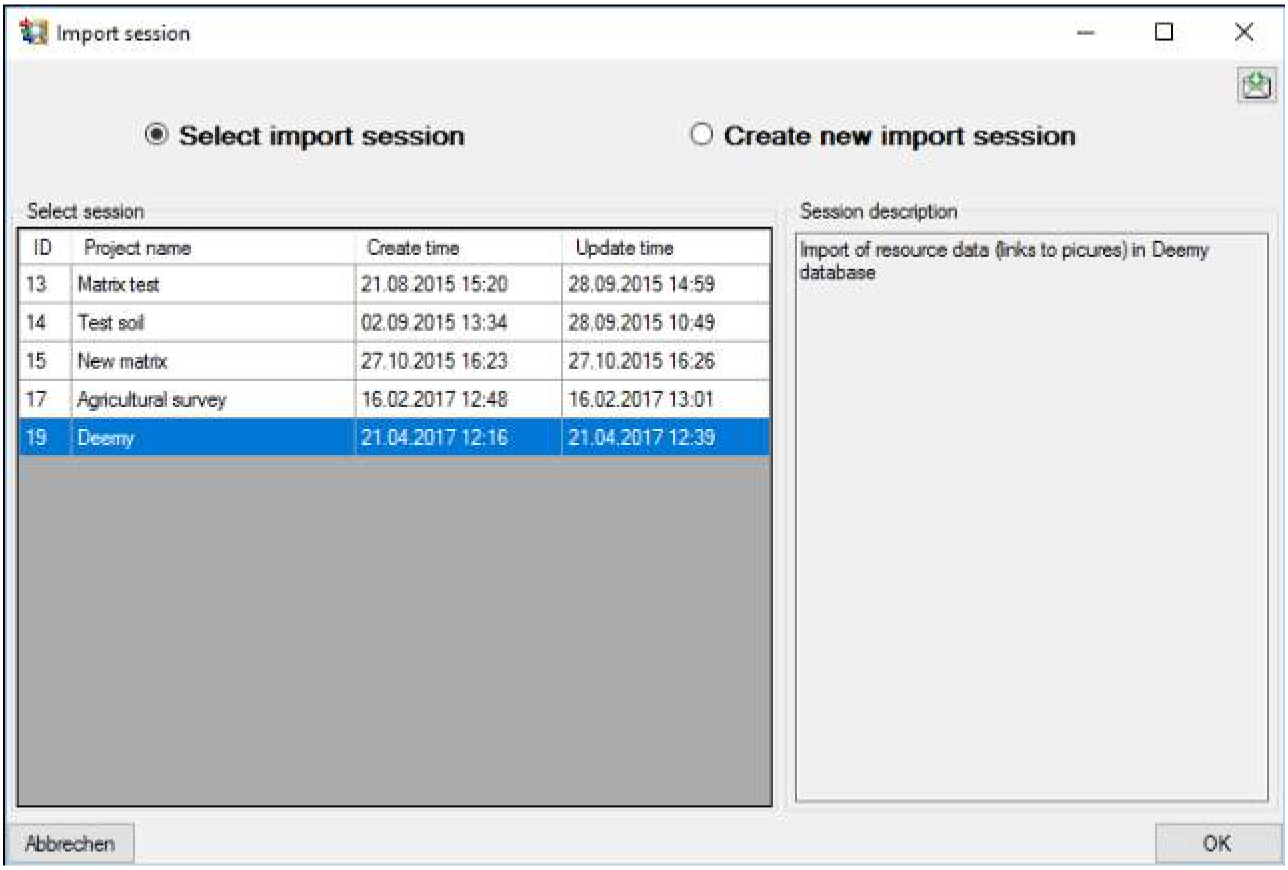
							Description Mapping external_key
1		NameFromScopes	ItemWording	Notes	Abundance	ItemURI	ItemID
2	ul...	FALSCH	<d>`Abierhiza fas...		5		1
3	t...	FALSCH	<d>`Abierhiza tom...		5		2
4	us...	FALSCH	<d>Albatrellus ovi...		5		3
5	r...	FALSCH	<d>`Alnirhiza atro...		5		4
6	+...	FALSCH	<d>`Alnirhiza can...		5		5
7	ol...	FALSCH	<d>`Alnirhiza cre...		5		6
8	ob...	FALSCH	<d>`Alnirhiza cysti...		5		7
9	+...	FALSCH	<d>`Alnirhiza lilaci...		5		8

The failed lines are in this example caused by duplicate item names twice in the database. This problem can be fixed by renaming the ambigious entries in the database and the import file, e.g. to "Alnirhiza cystidiobrunnea + Alnus 1" and "Alnirhiza cystidiobrunnea + Alnus 2" rsp. "Lactarius omphaliformis Romagn. + Alnus 1" and "Lactarius omphaliformis Romagn. + Alnus 2".

Next: Step 5 - Import of resources for descriptors

Step 5 - Import of resources for descriptors

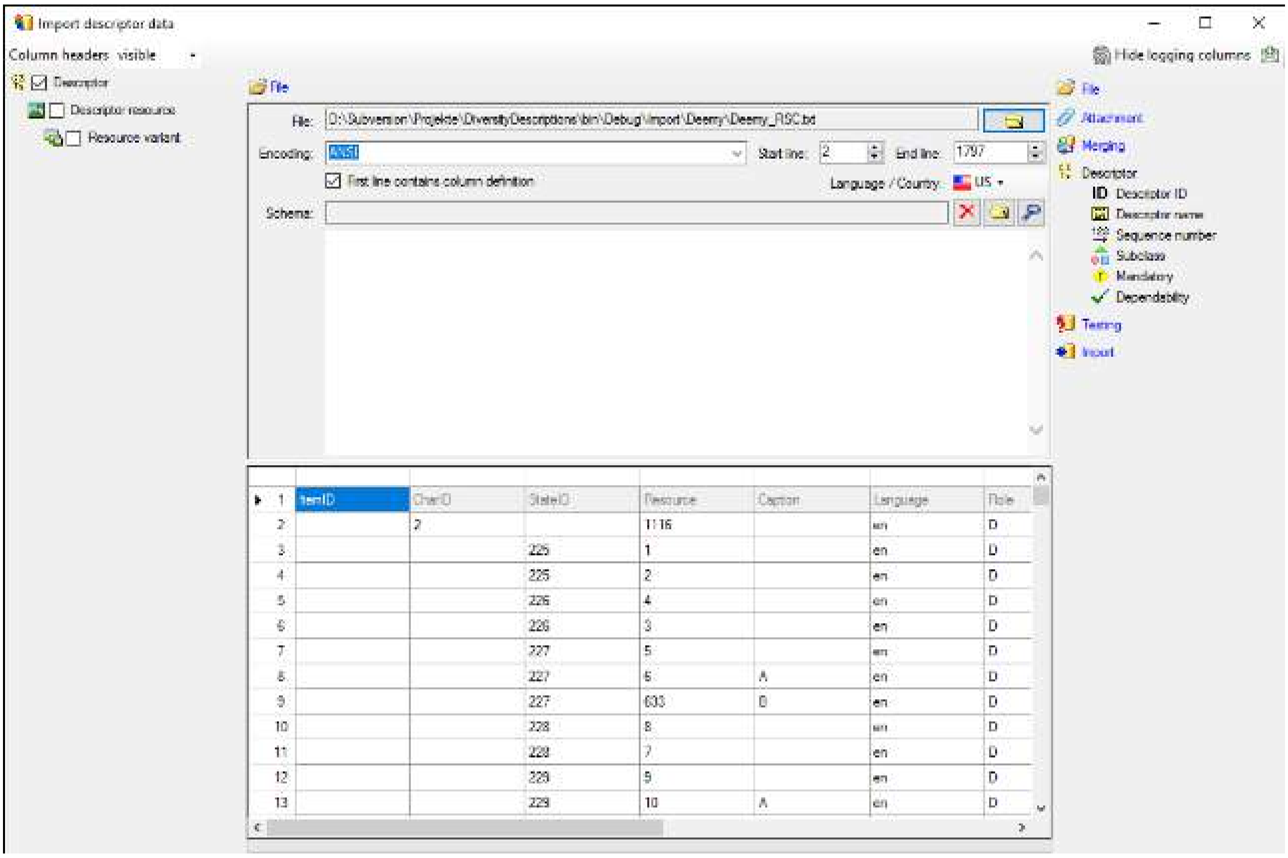
Close the import wizard for the mapping data and the import session window. Now choose **Data -> Import -> Wizard -> Import resources -> Descriptor resources ...** from the menu. A window as shown below will open to select an import session. Select the session for project "Deemy".



ID	Project name	Create time	Update time
13	Matrix test	21.08.2015 15:20	28.09.2015 14:59
14	Test soil	02.09.2015 13:34	28.09.2015 10:49
15	New matrix	27.10.2015 16:23	27.10.2015 16:26
17	Agricultural survey	16.02.2017 12:48	16.02.2017 13:01
19	Deemy	21.04.2017 12:16	21.04.2017 12:39

Session description: Import of resource data (links to picures) in Deemy database

After clicking **[OK]** the following window opens that will lead you through the import of the descriptor resource data. Open file "Deemy_RSC.txt" (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSC.txt

Encoding: ANSI

Start line: 2

End line: 1797

☑ First line contains column definition

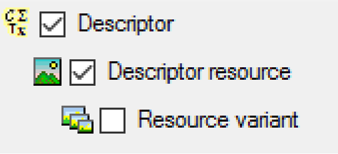
Language / Country: US

Schema:

1	ItemID	CharID	StateID	Resource	Caption	Language	Role
2		2		1116		en	D
3			225	1		en	D
4			225	2		en	D
5			226	4		en	D
6			226	3		en	D
7			227	5		en	D
8			227	6	A	en	D
9			227	633	B	en	D
10			228	8		en	D
11			228	7		en	D
12			229	9		en	D
13			229	10	A	en	D

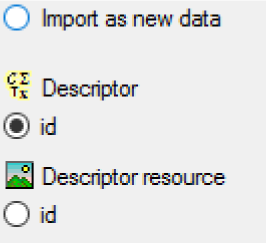
Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import. The step **Descriptor** is already selected, additionally check the step **Descriptor resource** (see below).



☑ Descriptor
☑ Descriptor resource
☐ Resource variant

We attach the descriptor resource values to the descriptors, therefore we will not change anything in the descriptor but will attach data. In import step **Attachment** at the right side select **Descriptor** **id** (see below).

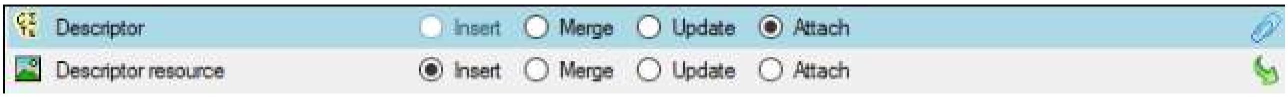


○ Import as new data

Descriptor
● id

Descriptor resource
○ id

Select the import step **Merge** from the list. For **Descriptor** we select the **Attach** option because this tables shall not be changed, for the other step **Insert** should already be selected, because a new entry has to be inserted (see below).



Descriptor ○ Insert ○ Merge ○ Update ● Attach

Descriptor resource ● Insert ○ Merge ○ Update ○ Attach

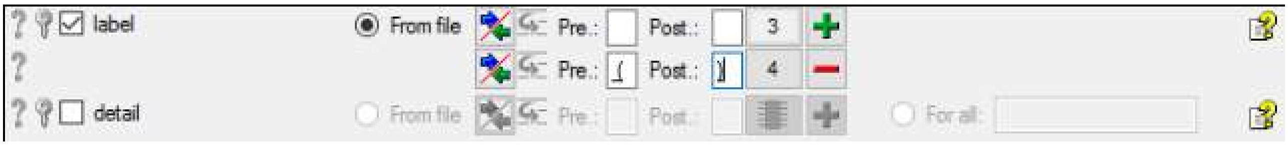
In the step table at the right side you find the import steps **Descriptor** and **Descriptor resource** and below them the data groups of the import steps. Deselect every column from import step **Descriptor** except "id". Mark the "id" column as **Key column** for comparison during attachment and click on **From file** to select the column "CharID" as data source. The "id" column of import step **Descriptor** now looks as shown below.

☑ id Pre.: Post.: 1

In the import step **Descriptor resource** click on **Resource ID** and in the center window the assignemt data for the resource id ("id") are displayed. Click on ?to make this the decisive column, further click on **From file** to select the column "Resource" as data source. After that the column should look as shown below.

☑ id ● From file Pre.: Post.: 3 ○ For all:

Click on **Resource name**. The center window shows the data column "label". Click on **From file** in the "label" line to select file column "Resource". After the resource number the value in data column "Caption" shall be inserted, included in brackets, if it is present. Click on the +button at the end of line "label" and select column "Caption". Enter **(** (blank and opening bracket) in field **Pre.:** and **)** in field **Post.:** of the new line. After that the column should look as shown below.



☑ label ● From file Pre.: Post.: 3

Pre.: (Post.:) 4

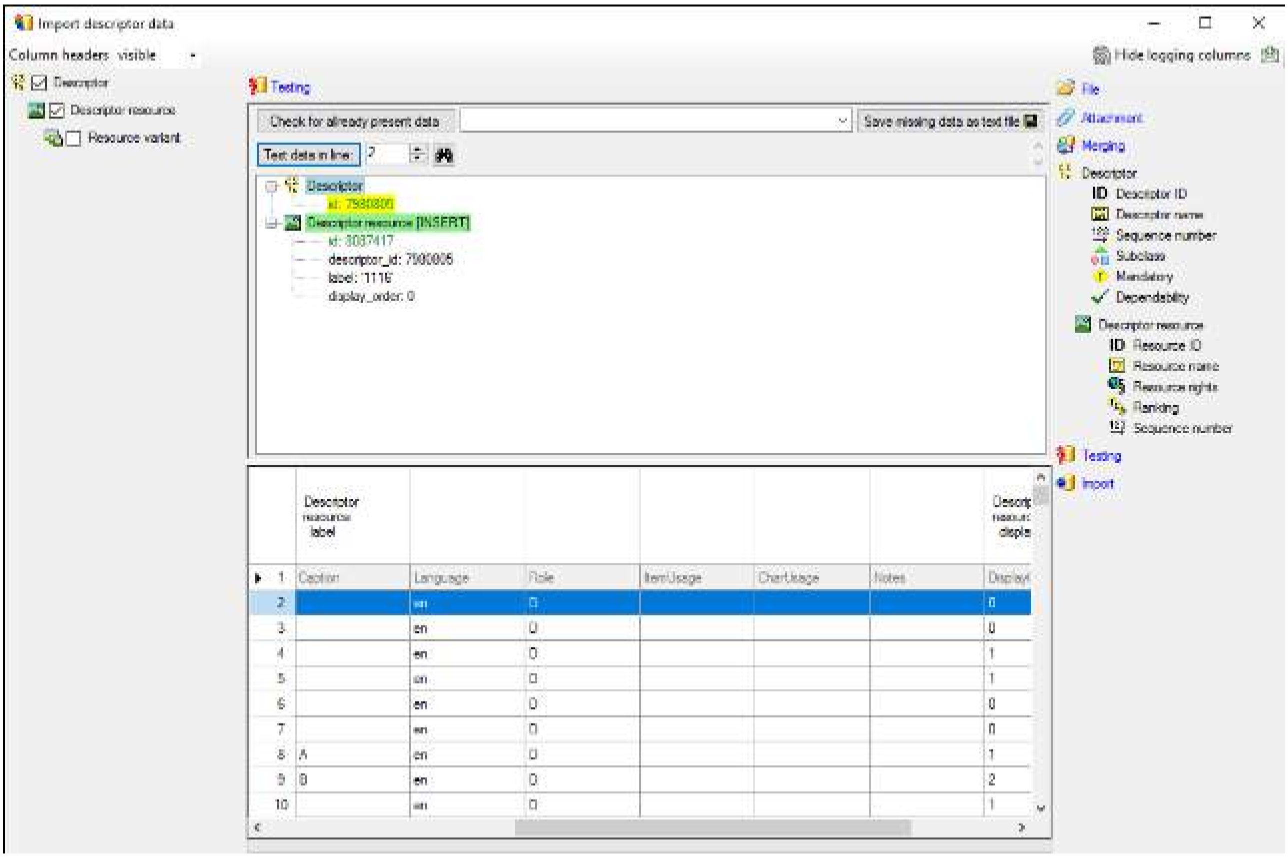
☐ detail ○ From file Pre.: Post.: ○ For all:

Finally click on **Sequence number**. In the center window select the data column "display_order", click on **From file** and select file column "DisplayOrder" (see below).

☑ display_order ● From file Pre.: Post.: 10 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. The test for the first data line is shown below.



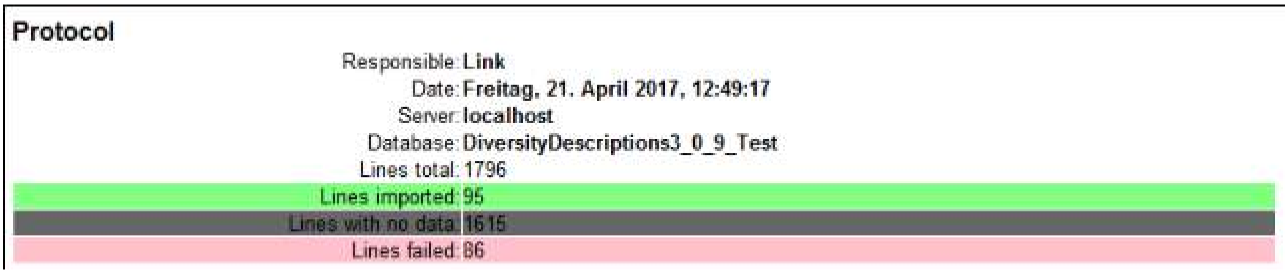
Test data in line: 2

Descriptor
id: 7980806
Descriptor resource [INSERT]
id: 3037417
descriptor_id: 7980806
label: '1116'
display_order: 0

	Descriptor resource label						Descriptor resource display
1	Caption	Language	Role	ItemUsage	ChartUsage	Notes	Display
2		en	0				0
3		en	0				0
4		en	0				1
5		en	0				1
6		en	0				0
7		en	0				0
8	A	en	0				1
9	B	en	0				2
10		en	0				1

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There are 86 lines that were not imported due to duplicate entries (see below).



Protocol

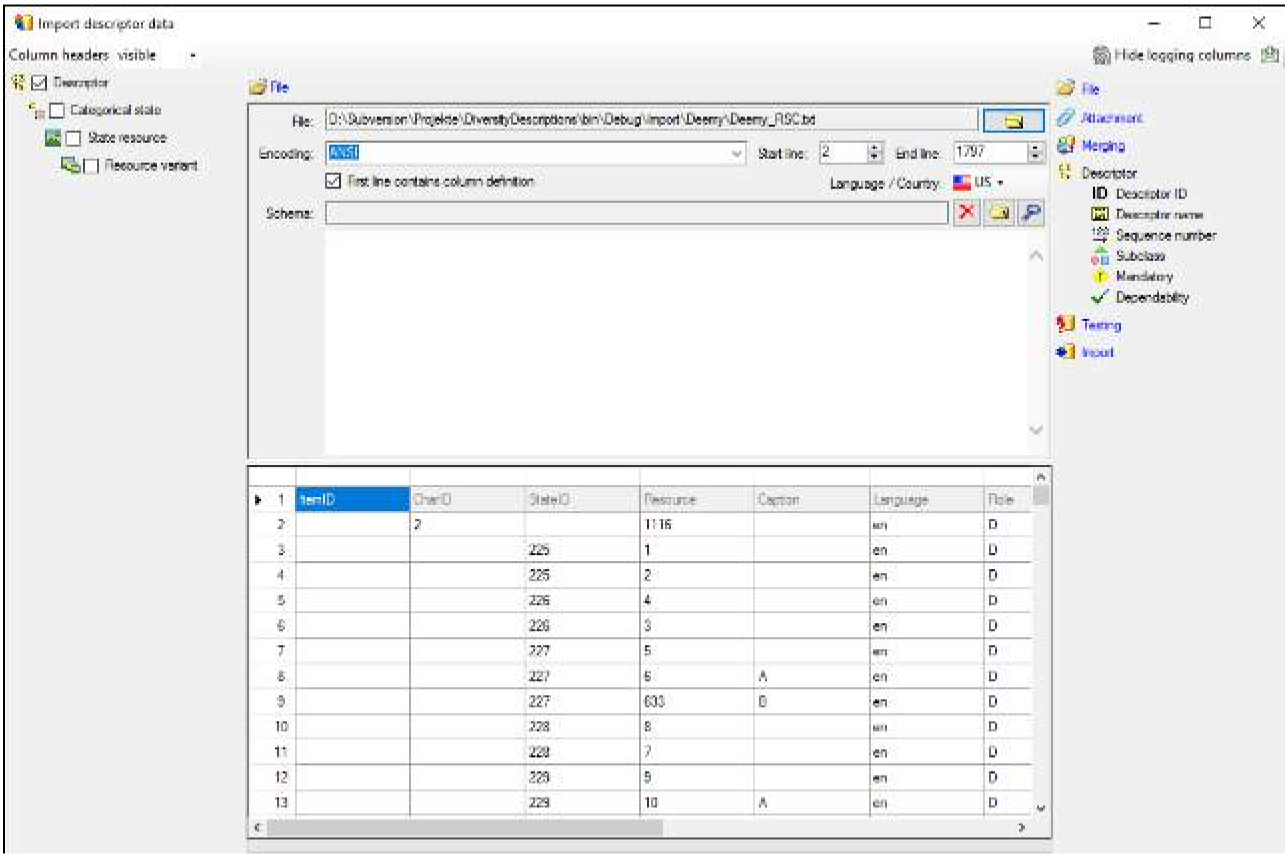
Responsible: **Link**
Date: **Freitag, 21. April 2017, 12:49:17**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 1796
Lines imported: 95
Lines with no data: 1615
Lines failed: 86

The failed lines are caused by duplicate entries, i.e. the resource was already imported for the descriptor.

Next: Step 6 - Import of resources for categorical states

Step 6 - Import of resources for categorical states

Close the import wizard for the descriptor resources. Now choose **Data -> Import -> Wizard -> Import resources -> State resources ...** from the menu, select the session for project "Deemy". The following window opens that will lead you through the import of the categorical state resource data. Open file "Deemy_RSC.txt" (see below).



☑ Descriptor
☐ Categorical state
☐ State resource
☐ Resource variant

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSC.txt

Encoding: ANSI

Start line: 2

End line: 1797

☑ First line contains column definition

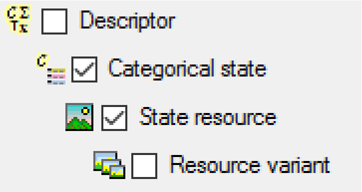
Language / Country: US

Schema:

1	ItemID	CharID	StateID	Resource	Caption	Language	Role
2		2		1116		en	D
3			225	1		en	D
4			225	2		en	D
5			226	4		en	D
6			226	3		en	D
7			227	5		en	D
8			227	6	A	en	D
9			227	633	B	en	D
10			228	8		en	D
11			228	7		en	D
12			229	9		en	D
13			229	10	A	en	D

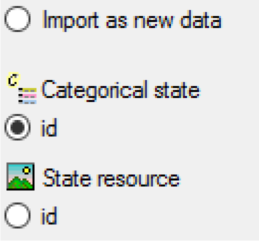
Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import. Deselect the step **Descriptor**, it is not needed since the categorical states have been assigned unambiguous external IDs in step 3. Check the steps **Categorical state** and **State resource** (see below).



☐ Descriptor
☑ Categorical state
☑ State resource
☐ Resource variant

We attach the state resource values to the categorical states, therefore we will not change anything in the categorical state but will attach data. In import step **Attachment** at the right side select **Categorial state** ● **id** (see below).

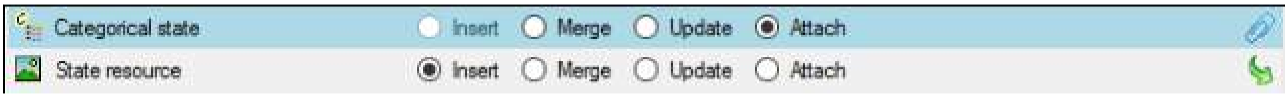


○ Import as new data

Categorical state
● id

State resource
○ id

Select the import step **Merge** from the list. For **Categorical state** we select the **Attach** option because this tables shall not be changed, for the other step **Insert** should already be selected, because a new entry has to be inserted (see below).



Categorical state ○ Insert ○ Merge ○ Update ● Attach
State resource ● Insert ○ Merge ○ Update ○ Attach

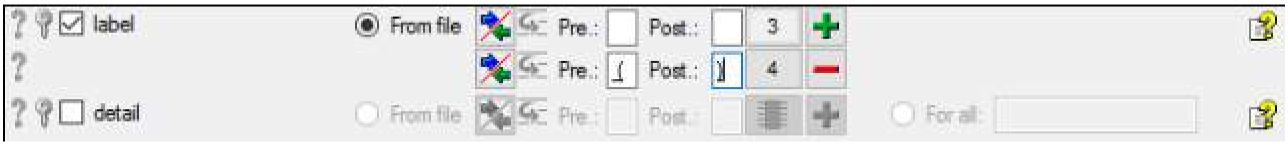
In the step table at the right side you find the import steps **Categorical state** and **State resource** and below them the data groups of the import steps. Deselect every column from import step **Categorical state** except "id". Mark the "id" column as **Key column** for comparison during attachment and click on ◉ **From file** to select the column "StateID" as data source. The "id" column of import step **Categorical state** now looks as shown below.

☑ id Pre.: Post.: 2

In the import step **State resource** click on **Resource ID** and in the center window the assignemt data for the resource id ("id") are displayed. Click on ? to make this the decisive column, further click on ◉ **From file** to select the column "Resource" as data source. After that the column should look as shown below.

☑ id ● From file Pre.: Post.: 3 ○ For all:

Click on **Resource name**. The center window shows the data column "label". Click on ◉ **From file** in the "label" line to select file column "Resource". After the resource number the value in data column "Caption" shall be inserted, included in brackets, if it is present. Click on the + button at the end of line "label" and select column "Caption". Enter **(** (blank and opening bracket) in field **Pre.:** and **)** in field **Post.:** of the new line. After that the column should look as shown below.



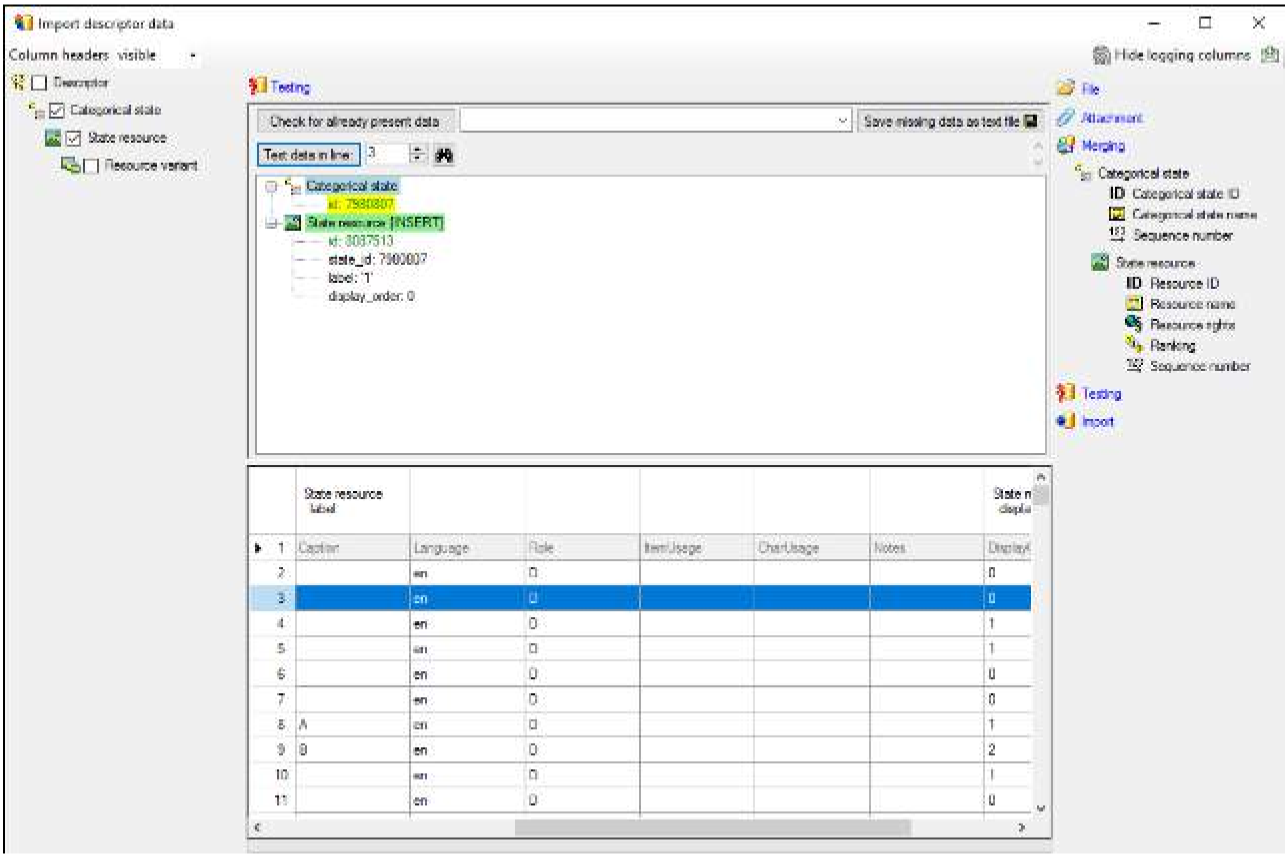
☑ label ● From file Pre.: Post.: 3
Pre.: (Post.:) 4
☐ detail ○ From file Pre.: Post.: ○ For all:

Finally click on **Sequence number**. In the center window select the data column "display_order", click on ◉ **From file** and select file column "DisplayOrder" (see below).

☑ display_order ● From file Pre.: Post.: 10 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. The test for the second data line is shown below.



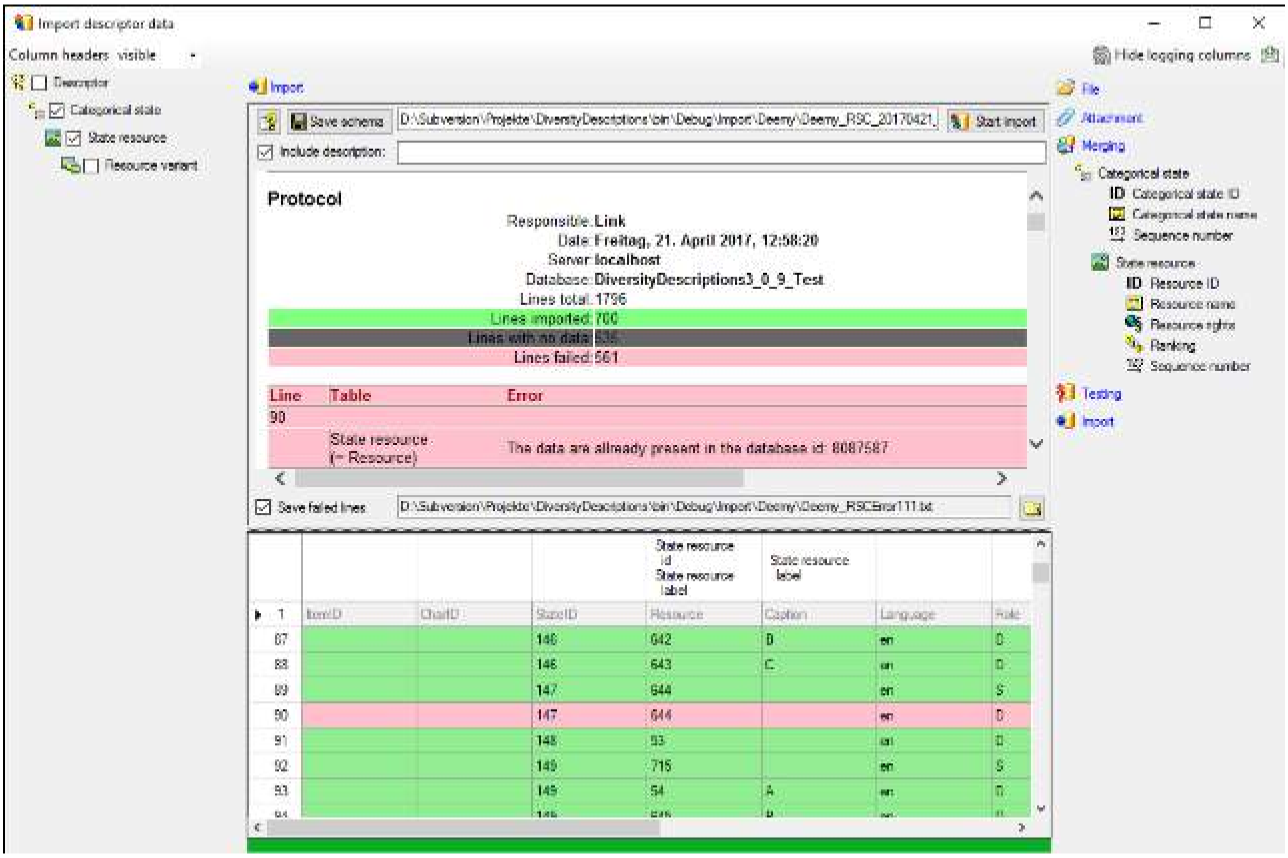
Test data in line: 3

```
Categorical state
    id: 7980807
State resource [INSERT]
    id: 3037513
    state_id: 7980807
    label: '1'
    display_order: 0
```

	State resource label						State n displa
1	Caption	Language	Role	ItemUsage	CharUsage	Notes	Display
2		en	0				0
3		en	0				0
4		en	0				1
5		en	0				1
6		en	0				0
7		en	0				0
8	A	en	0				1
9	B	en	0				2
10		en	0				1
11		en	0				0

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There are 561 lines that were not imported due to duplicate entries (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSC_20170421_

☑ Include description:

Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 12:58:20**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 1796
Lines imported: 700
Lines with no data: 535
Lines failed: 561

Line	Table	Error
90		
	State resource (= Resource)	The data are allready present in the database id: 8087587

☑ Save failed lines D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSCError111.txt

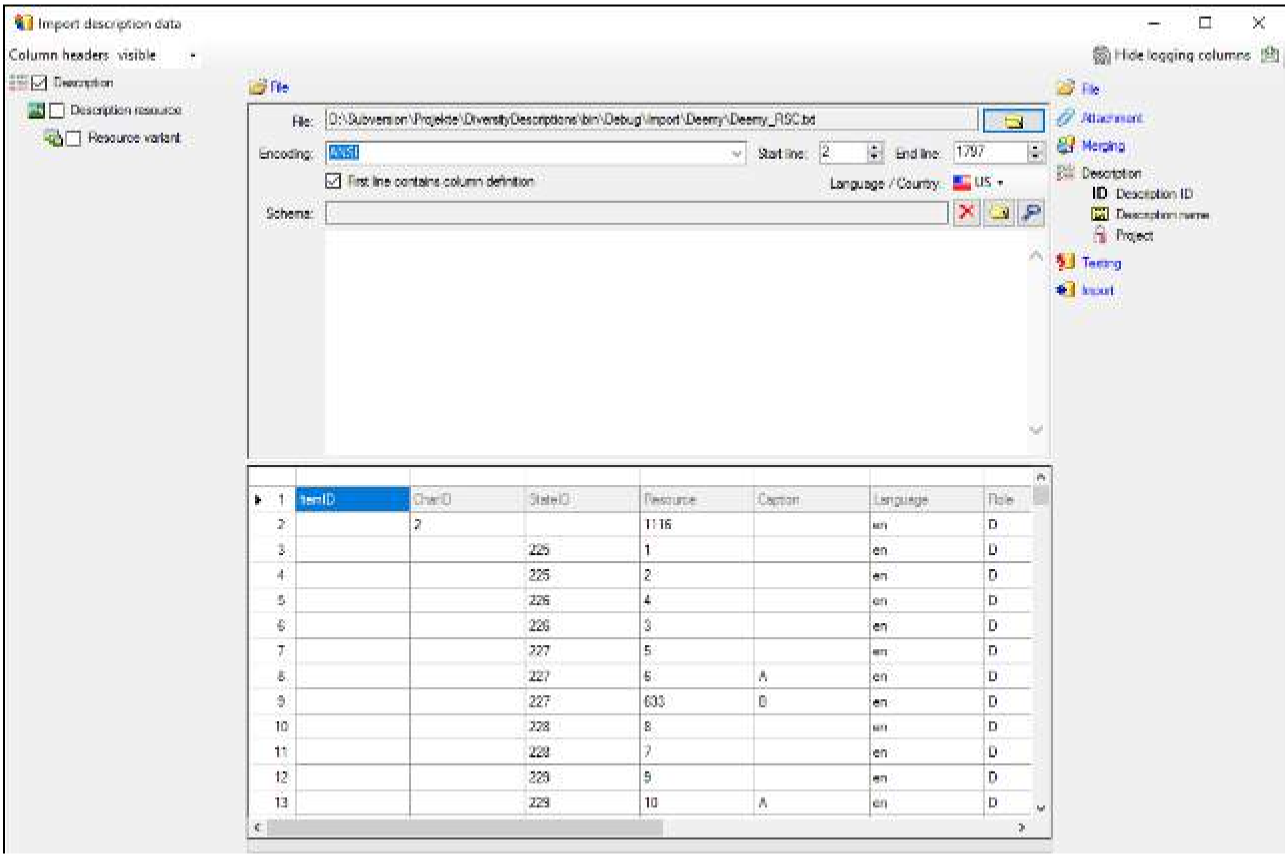
				State resource id State resource label	State resource label		
1	ItemID	CharID	StateID	Resource	Caption	Language	Role
87			146	642	B	en	D
88			146	643	C	en	D
89			147	644		en	S
90			147	644		en	D
91			148	53		en	D
92			149	715		en	S
93			149	54	A	en	D

The failed lines are caused by duplicate entries, i.e. the resource was already imported for the categorical state.

Next: Step 7 - Import of resources for descriptions

Step 7 - Import of resources for descriptions

Close the import wizard for the state resources. Now choose **Data -> Import -> Wizard -> Import resources -> Description resources ...** from the menu, select the session for project "Deemy". The following window opens that will lead you through the import of the categorical state resource data. Open file "Deemy_RSC.txt" (see below).



☑ Description
☐ Description resource
☐ Resource variant

File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSC.txt

Encoding: ANSI

Start line: 2

End line: 1797

☑ First line contains column definition

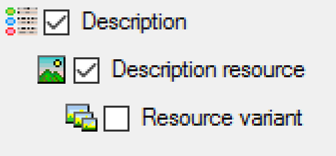
Language / Country: US

Schema:

1	ItemID	CharID	StateID	Resource	Caption	Language	Role
2		2		1116		en	D
3			225	1		en	D
4			225	2		en	D
5			226	4		en	D
6			226	3		en	D
7			227	5		en	D
8			227	6	A	en	D
9			227	633	B	en	D
10			228	8		en	D
11			228	7		en	D
12			229	9		en	D
13			229	10	A	en	D

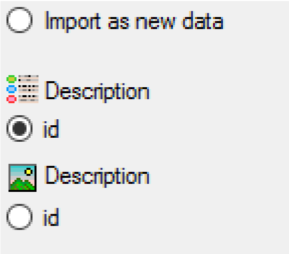
Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import. Step **Description** is already selected. Aditionally check step **Description resource** (see below).



☑ Description
☑ Description resource
☐ Resource variant

We attach the description resource values to the descriptions, therefore we will not change anything in the description but will attach data. In import step **Attachment** at the right side select **Description** **id** (see below).



○ Import as new data

Description

● id

Description

○ id

Select the import step **Merge** from the list. For **Description** we select the **Attach** option because this tables shall not be changed, for the other step **Insert** should already be selected, because a new entry has to be inserted (see below).

Description ○ Insert ○ Merge ○ Update ● Attach

Description resource ● Insert ○ Merge ○ Update ○ Attach

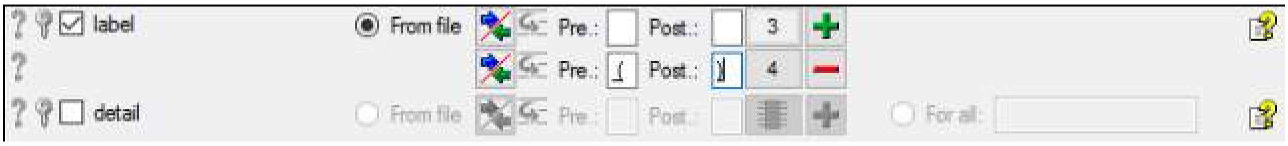
In the step table at the right side you find the import steps **Description** and **Description resource** and below them the data groups of the import steps. Deselect every column from import step **Description** except "id". Mark the "id" column as **Key column** for comparison during attachment and click on **From file** to select the column "ItemID" as data source. The "id" column of import step **Description** now looks as shown below.

id Pre.: Post.: 0

In the import step **Description resource** clickon **Resource ID** and in the center window the assignment data for the resource id ("id") are displayed. Click on to make this the decisive column, further click on **From file** to select the column "Resource" as data source. After that the column should look as shown below.

☑ id ● From file Pre.: Post.: 3 ○ For all:

Click on **Resource name**. The center window shows the data column "label". Click on **From file** in the "label" line to select file column "Resource". After the resource number the value in data column "Caption" shall be inserted, included in brackets, if it is present. Click on the button at the end of line "label" and select column "Caption". Enter **(** (blank and opening bracket) in field **Pre.:** and **)** in field **Post.:** of the new line. After that the column should look as shown below.



☑ label ● From file Pre.: Post.: 3

Pre.: (Post.:) 4

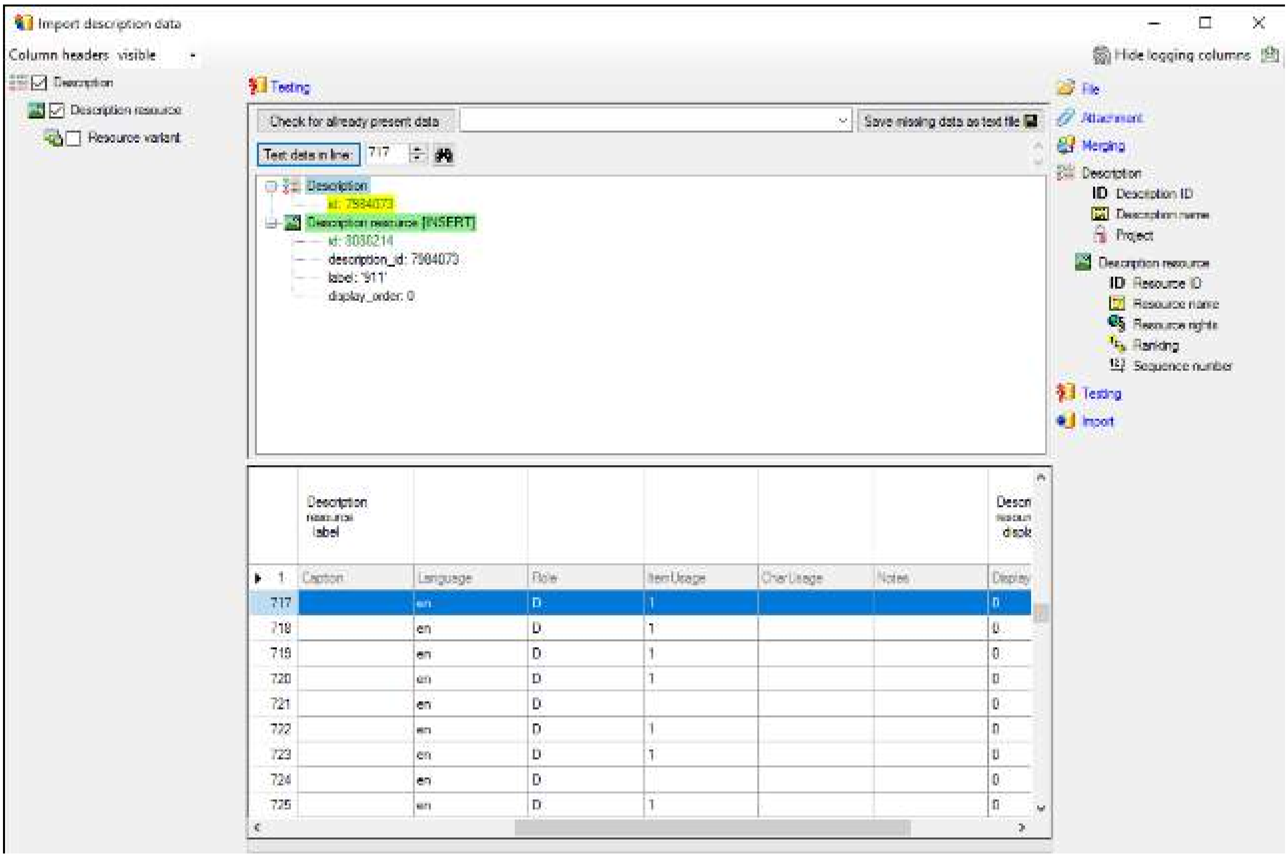
☐ detail ○ From file Pre.: Post.: ○ For all:

Finally click on **Sequence number**. In the center window select the data column "display_order", click on **From file** and select file column "DisplayOrder" (see below).

☑ display_order ● From file Pre.: Post.: 10 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. The test for the data line 717 is shown below.



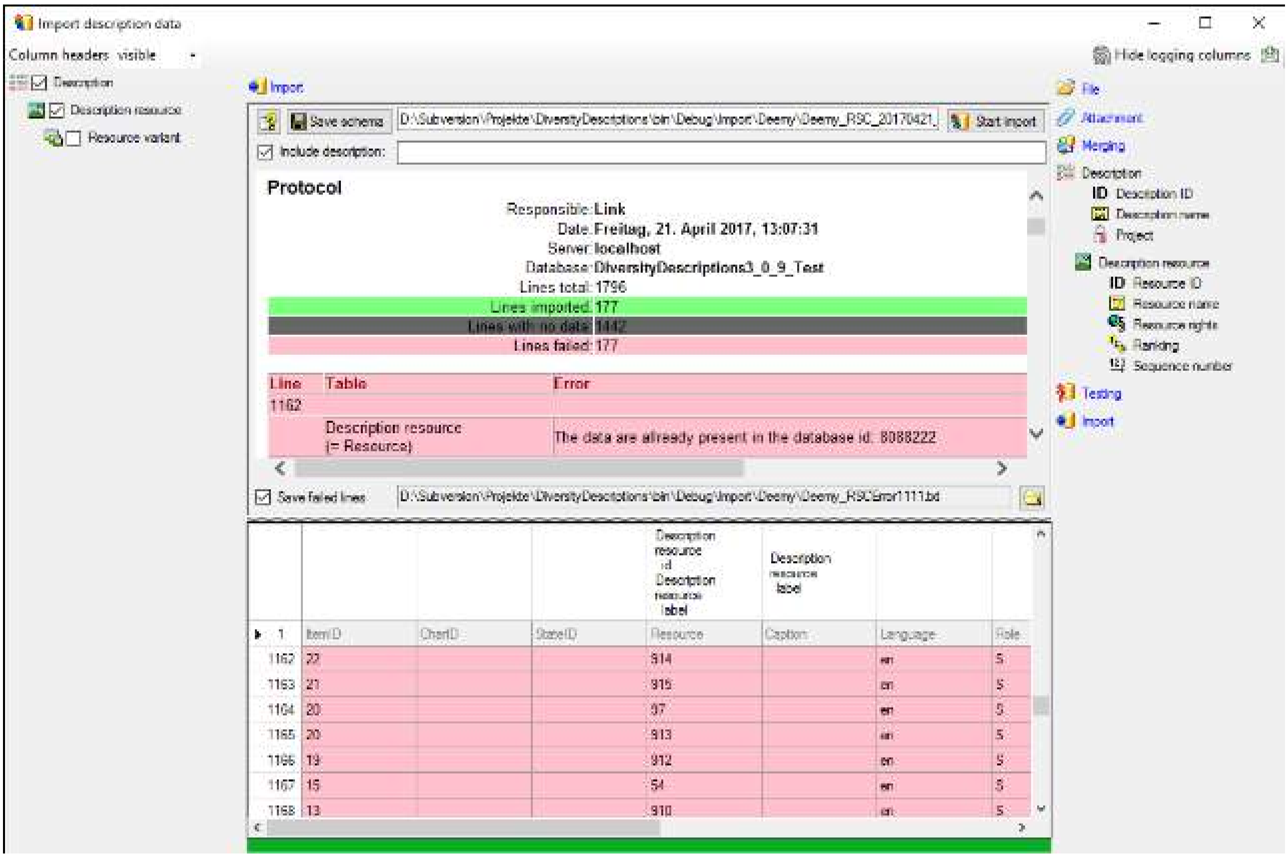
Test data in line: 717

- Description
  - id: 7984073
- Description resource [INSERT]
  - id: 3030214
  - description_id: 7984073
  - label: '911'
  - display_order: 0

	Description resource label						Descr resour displ
1	Caption	Language	Role	Item Usage	Char Usage	Notes	Display
717		en	D	1			0
718		en	D	1			0
719		en	D	1			0
720		en	D	1			0
721		en	D				0
722		en	D	1			0
723		en	D	1			0
724		en	D				0
725		en	D	1			0

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. There are 177 lines that were not imported due to duplicate entries (see below).



D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSC_20170421_

Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 13:07:31**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 1796
Lines imported: 177
Lines with no data: 1442
Lines failed: 177

Line	Table	Error
1162		
	Description resource (= Resource)	The data are already present in the database id: 8088222

D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_RSCError1111.txt

				Description resource id Description resource label	Description resource label		
1	ItemID	CharID	StateID	Resource	Caption	Language	Role
1162	22			914		en	5
1163	21			915		en	5
1104	20			97		en	5
1165	20			913		en	5
1166	19			912		en	5
1167	15			54		en	5
1168	13			910		en	5

The failed lines are caused by duplicate entries, i.e. the resource was already imported for the description.

Next: Step 8 - Import of resource variants

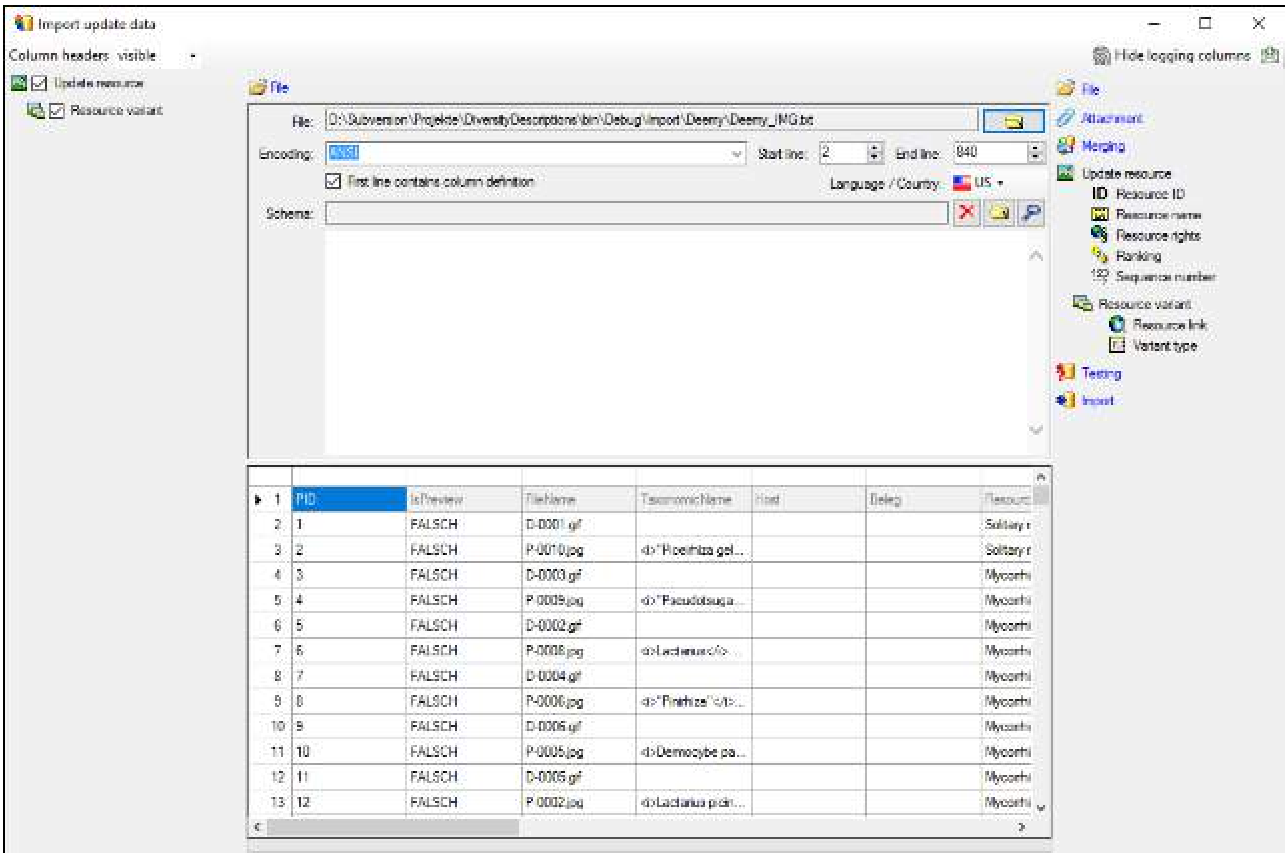
Step 8 - Import of resource variants

The import wizards used in step 5 up to step 7 allow appending a resource variant to one resource. Those wizards can be used most efficiently if the data that are needed for the resource table and the resource variant are located at the same file. In our example there is the complication that the direction of the resource reference is in the opposite direction than in the original database. In DiversityDescription a resource references e.g. a descriptor and one or more resource variants reference the resource. In the original database several entities, e.g. descriptors or states, may reference the same picture.

During the import of the resources we used the picture number as the external key of the resources. Together with their parent key, e.g. a descriptor ID, this gives unambiguous entries although the external resource ID alone is ambiguous. Now we want to create a resource variant, containing the URL of the picture, for each resource entry with the same external resource ID.

Since this "multiple" import is no standard feature of the import wizard, the following description shows a work-around: During the import the first resource entry with a matching "Resource ID" that is not referenced by any Resource variant will be available for data update and appending of a new resource variant. A repeated import with the same setting will find the next resource entry and so on until all ambigious resource entries are processed.

Close the import wizard for the description resources. Now choose **Data -> Import -> Wizard -> Import resources -> Resource variants ...** from the menu, select the session for project "Deemy". The following window opens that will lead you through the import of the categorical state resource data. Open file "Deemy_IMG.txt" (see below).



File: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\Deemy\Deemy_IMG.txt

Encoding: ANSI

Start line: 2

End line: 840

☑ First line contains column definition

Language / Country: US

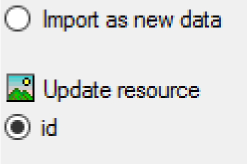
Schema:

1	PID	IsPreview	FileName	TaxonomicName	Host	Beleg	Resourc
2	1	FALSCH	D-0001.gif				Solitary r
3	2	FALSCH	P-0010.jpg	<i>"Piceirhiza gel...			Solitary r
4	3	FALSCH	D-0003.gif				Mycorrhi
5	4	FALSCH	P-0009.jpg	<i>"Pseudotsuga...			Mycorrhi
6	5	FALSCH	D-0002.gif				Mycorrhi
7	6	FALSCH	P-0008.jpg	<i>Lactarius</i>...			Mycorrhi
8	7	FALSCH	D-0004.gif				Mycorrhi
9	8	FALSCH	P-0006.jpg	<i>"Pinirhiza"</i>...			Mycorrhi
10	9	FALSCH	D-0006.gif				Mycorrhi
11	10	FALSCH	P-0005.jpg	<i>Dermocybe pa...			Mycorrhi
12	11	FALSCH	D-0005.gif				Mycorrhi
13	12	FALSCH	P-0002.jpg	<i>Lactarius picin...			Mycorrhi

Selecting the data ranges

In the selection list on the left side of the window all possible import steps for the data are listed according to the type of data you want to import. The available steps **Update resource** and **Resource variant** are already selected.

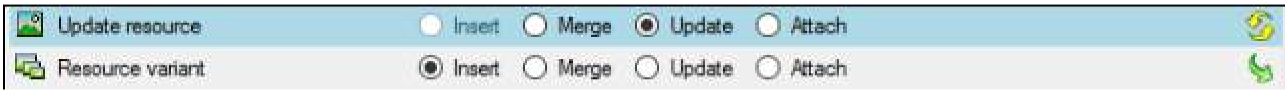
We want to update some fields of the resource table with values form the data file attach the resource variant to the resource. In import step **Attachment** at the right side select **Update resource** **id** (see below). Note: With this import wizard only update of resources is supported.


○ Import as new data

Update resource

● id

Select the import step **Merge** from the list. For **Update resource** we keep the **Merge** option because this table shall be updated, for the other step **Insert** should already be selected, because a new entry has to be inserted (see below).

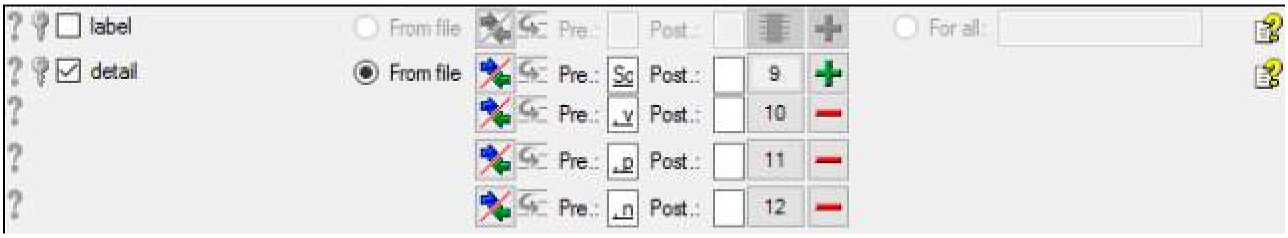

Update resource ○ Insert ○ Merge ● Update ○ Attach

Resource variant ● Insert ○ Merge ○ Update ○ Attach

In the import step **Update resource** click on **Resource ID** and in the center window the assignment data for the resource id ("id") are displayed. Click on to make this the decisive column. Mark the "id" column as **Key column** for comparison during attachment and click on **From file** to select the column "PID" as data source. After that the column should look as shown below.


☑ id Pre.: Post.: 0

Click on **Resource name**. The center window shows the data column "label" and "detail". Deselect the "label" entry and select "detail". Click on **From file** to select the column "SourceTitle" as data source and enter **Source:** in field **Pre.:** (double-click in the field to open a separate edit window). Now click on the button at the end of line "detail", select file column "Volume" and enter **, vol.** in field **Pre.:**. Repeat the last step for file columns "Pages" (**, p.**) and "ReferenceNotes" (**, notes:**). After that the column should look as shown below.


☐ label ○ From file Pre.: Post.: ○ For all:

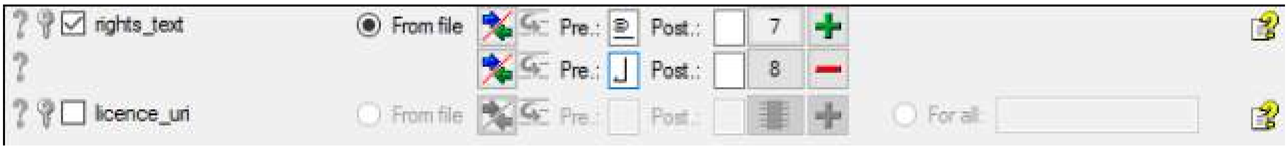
☑ detail ● From file Pre.: So Post.: 9

Pre.: , v Post.: 10

Pre.: , p Post.: 11

Pre.: , n Post.: 12

Click on **Resource rights** and in the center window the assignment data for the resource rights are displayed. Select "rights_text". Click on **From file** to select the column "Author" as data source and enter **©** (Alt+0169 and a blank) in field **Pre.:**. Now click on the button at the end of line "rights_text", select file column "DateYear" and enter **,** in field **Pre.:**. After that the column should look as shown below.


☑ rights_text ● From file Pre.: © Post.: 7

Pre.: , Post.: 8

☐ licence_uri ○ From file Pre.: Post.: ○ For all:

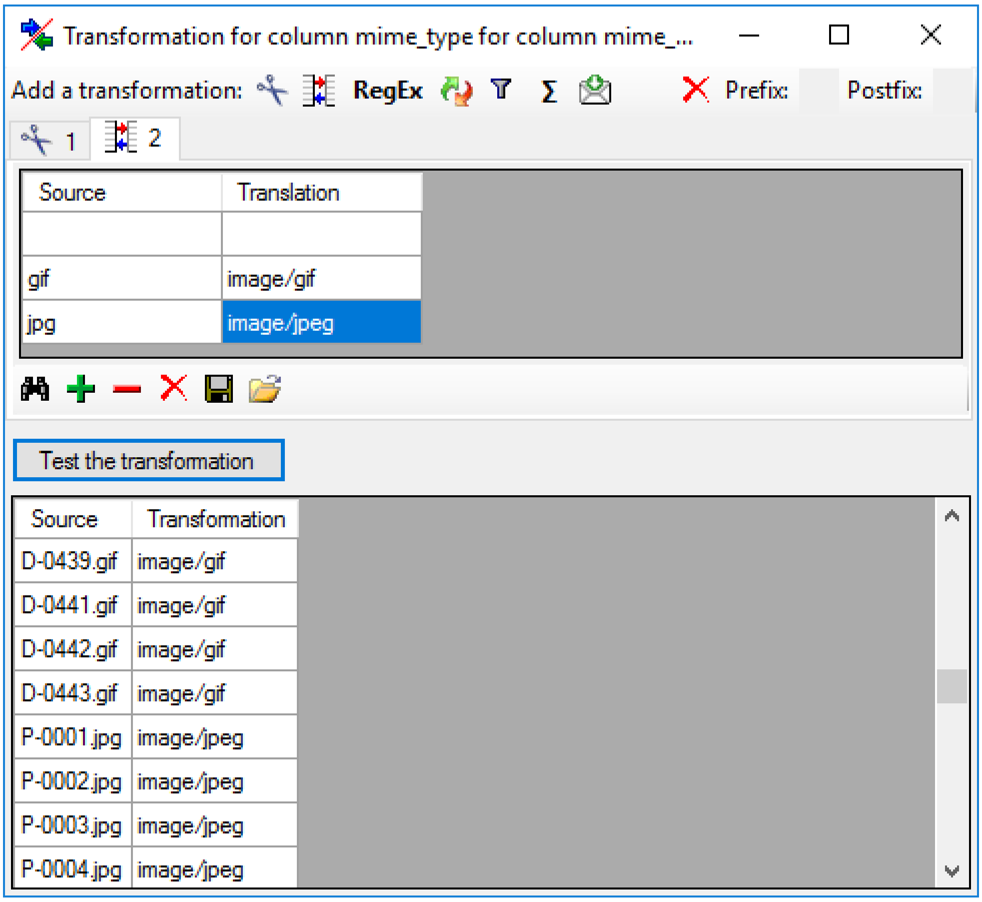
In the import step **Resource variant** click on **Resource link**. The center window shows the data column "url". Click on ? to make this the decisive column and on ● **From file** in the "url" line to select file column "FileName". Double-click on the text box after **Pre.:** to open a separate edit window. Here enter the web address of the picture server where the files are located and confirm with **"OK"**. After that the column should look as shown below.

☑ url ● From file Pre.: Post.: 2 ○ For all:

Click on **Variant type**. In the center window select the data column "variant_id", click on ● **For all:** and select the value "good quality" (see below).

☑ variant_id ○ From file Pre.: Post.: ● For all: good quality

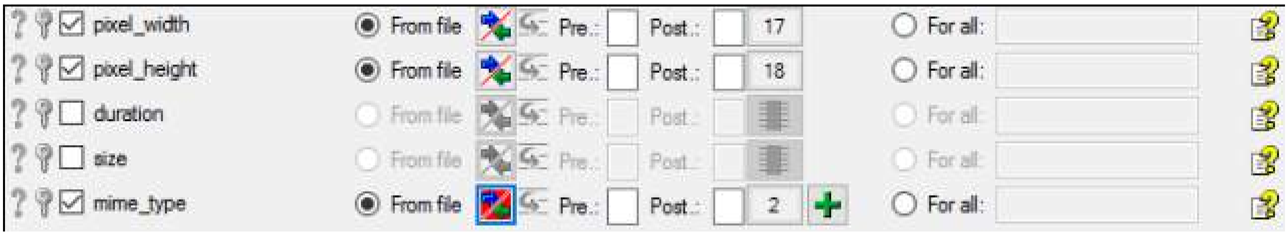
Click on the import step **Resource variant** to find some ungrouped fields. In the center window select the data column "pixel_width", click on ● **From file** and select the value "WidthD". Now select the data column "pixel_height", click on ● **From file** and select the value "HeightD". Finally select the data column "mime_type", click on ● **From file** and select the value "FileName". Click on button to define a transformation. In the transformation window click on the cut transformation, enter **Position: 2**, click on **+** to enter splitter character **.** (period) to extract the file extension. Now click on to insert a translation table and to insert the values contained in the file column. "gif" shall be converted to **image/gif**, "jpg" will become **image/jpeg** (see below).



Source	Translation
gif	image/gif
jpg	image/jpeg

Source	Transformation
D-0439.gif	image/gif
D-0441.gif	image/gif
D-0442.gif	image/gif
D-0443.gif	image/gif
P-0001.jpg	image/jpeg
P-0002.jpg	image/jpeg
P-0003.jpg	image/jpeg
P-0004.jpg	image/jpeg

After that the columns should look as shown below.



☑ pixel_width ● From file Pre.: Post.: 17 ○ For all:

☑ pixel_height ● From file Pre.: Post.: 18 ○ For all:

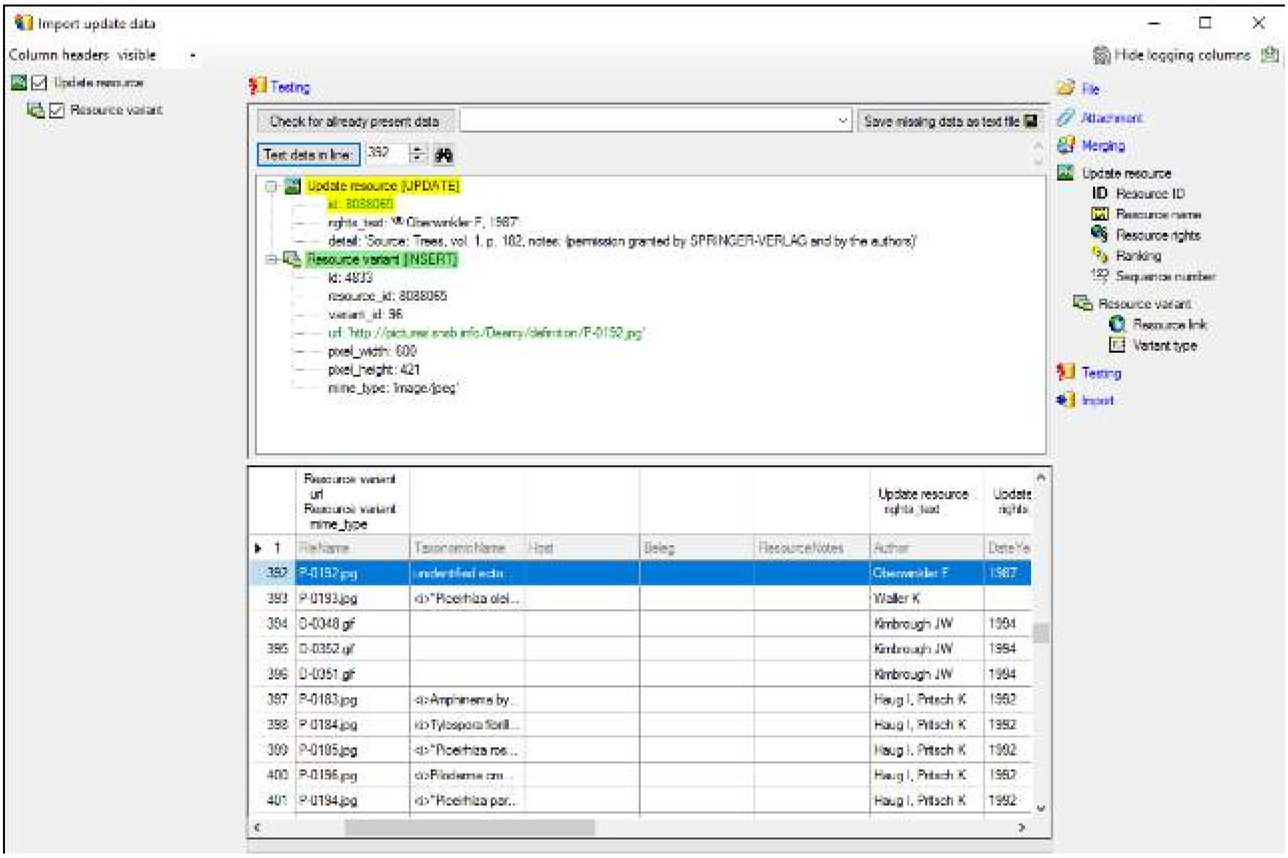
☐ duration ○ From file Pre.: Post.: ○ For all:

☐ size ○ From file Pre.: Post.: ○ For all:

☑ mime_type ● From file Pre.: Post.: 2 ○ For all:

Testing

To test if all requirements for the import are met use the **Testing** step. The test for the first data line is shown below.



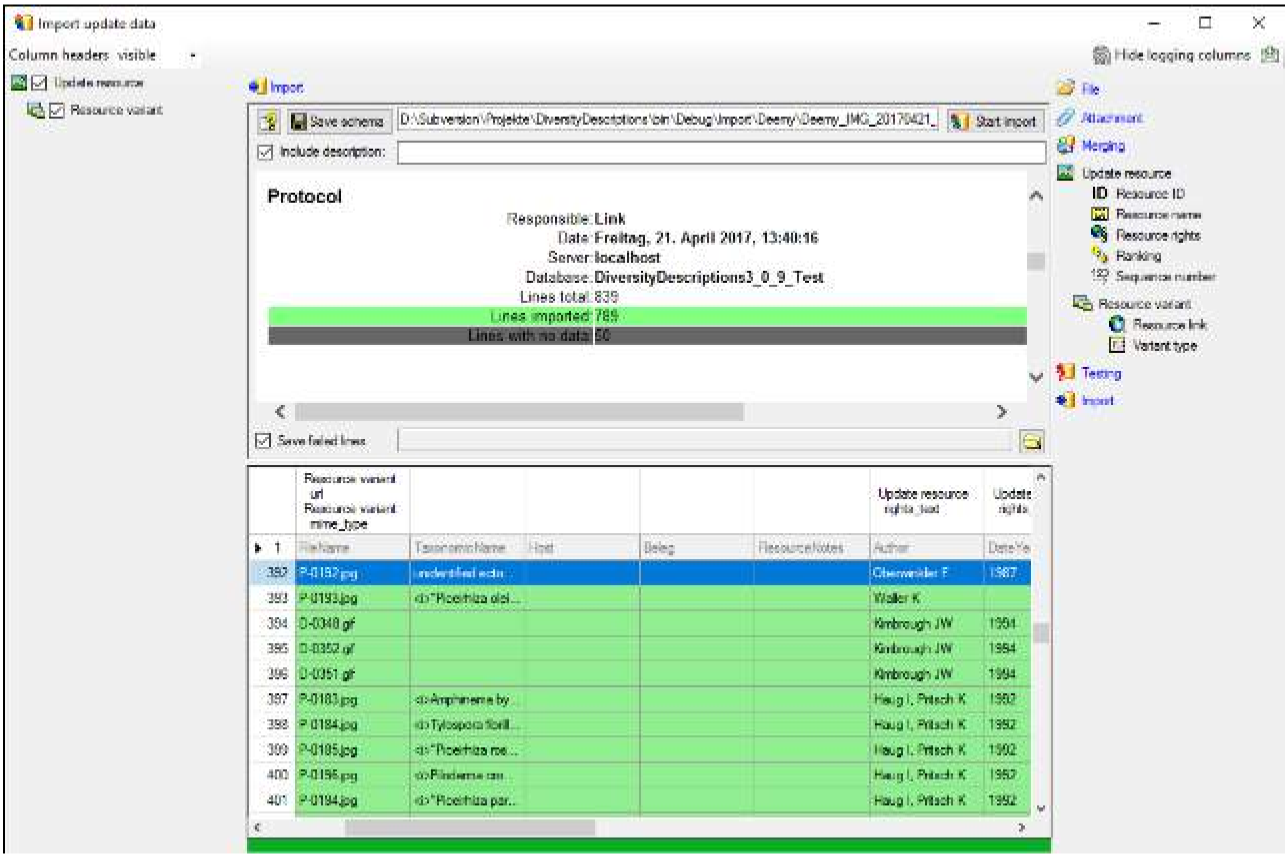
Test data in line: 392

```
Update resource [UPDATE]
    id: 8088065
    rights_text: '© Oberwinkler F, 1987'
    detail: 'Source: Trees, vol. 1, p. 182, notes: (permission granted by SPRINGER-VERLAG and by the authors)'
Resource variant [INSERT]
    id: 4833
    resource_id: 8088065
    variant_id: 96
    url: 'http://pictures.snsb.info/Deemy/definition/P-0192.jpg'
    pixel_width: 600
    pixel_height: 421
    mime_type: 'image/jpeg'
```

	Resource variant url Resource variant mime_type					Update resource rights_text	Update rights
1	FileName	TaxonomicName	Host	Beleg	ResourceNotes	Author	DateYe
392	P-0192.jpg	unidentified ecto...				Oberwinkler F	1987
393	P-0193.jpg	<i>"Piceirhiza olei...				Waller K	
394	D-0348.gif					Kimbrough JW	1994
395	D-0352.gif					Kimbrough JW	1994
396	D-0351.gif					Kimbrough JW	1994
397	P-0183.jpg	<i>Amphinema by...				Haug I, Pritsch K	1992
398	P-0184.jpg	<i>Tylospora fibril...				Haug I, Pritsch K	1992
399	P-0185.jpg	<i>"Piceirhiza ros...				Haug I, Pritsch K	1992
400	P-0196.jpg	<i>Piloderma cro...				Haug I, Pritsch K	1992
401	P-0194.jpg	<i>"Piceirhiza par...				Haug I, Pritsch K	1992

Import

With the last step you can start to import the data into the database. If you want to repeat the import with the same settings and data of the same structure, you can save a schema of the current settings. As mentioned in the introduction, the import step has to be repeated until no more resource variant is imported. At the first run 789 lines were imported (see below).

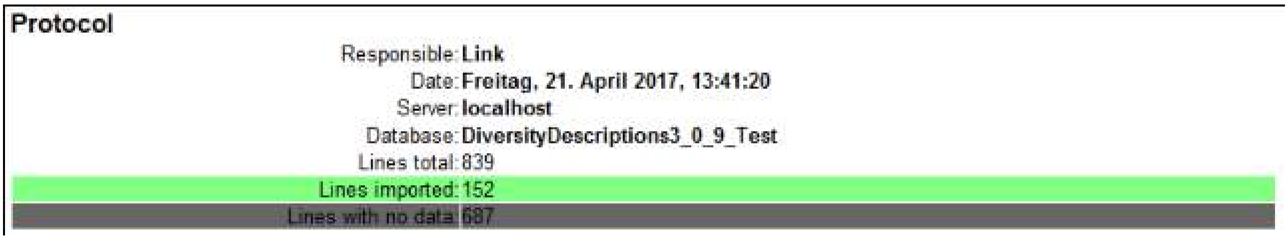


Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 13:40:16**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 839
Lines imported: 789
Lines with no data: 50

	Resource variant url Resource variant mime_type					Update resource rights_text	Update rights
1	FileName	TaxonomicName	Host	Beleg	ResourceNotes	Author	DateYe
392	P-0192.jpg	unidentified ecto...				Oberwinkler F	1987
393	P-0193.jpg	<i>"Piceirhiza albi...				Waller K	
394	D-0348.gif					Kimbrough JW	1994
395	D-0352.gif					Kimbrough JW	1994
396	D-0351.gif					Kimbrough JW	1994
397	P-0183.jpg	<i>Amphinema by...				Haug I, Pritsch K	1992
398	P-0184.jpg	<i>Tylospora fibril...				Haug I, Pritsch K	1992
399	P-0185.jpg	<i>"Piceirhiza ne...				Haug I, Pritsch K	1992
400	P-0186.jpg	<i>Piloderma cro...				Haug I, Pritsch K	1992
401	P-0194.jpg	<i>"Piceirhiza par...				Haug I, Pritsch K	1992

At the second run, started by another click on **Start import**, 152 lines were imported (see below).



Protocol

Responsible: **Link**
Date: **Freitag, 21. April 2017, 13:41:20**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 839
Lines imported: 152
Lines with no data: 687

Finally, at the seventh run no further line is imported (see below).

Protocol

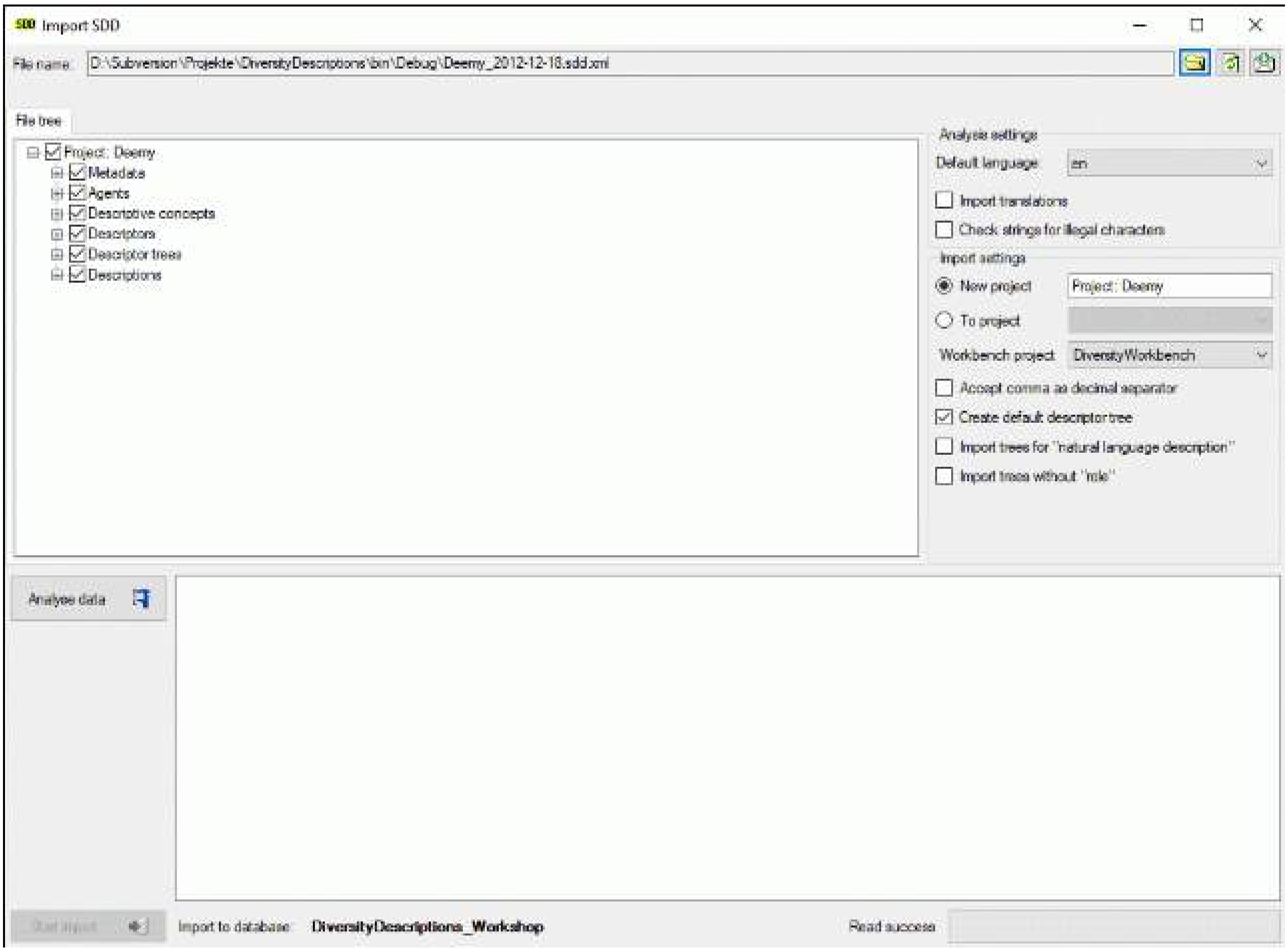
Responsible: **Link**
Date: **Freitag, 21. April 2017, 13:43:17**
Server: **localhost**
Database: **DiversityDescriptions3_0_9_Test**
Lines total: 839
Lines with no data: 839

Import SDD file

Remarks:

- To import data from an SDD file at least TerminologyEditor rights are neccessary.
- Currently SDD statements concerning natural laguage descriptions and identification keys are not evaluated.

With this form you can import data from an XML file according schema SDD 1.1 rev 5 into the database. You may download an example SDD file with from the Diversity Descriptions example file repository. Choose **Data -> Import -> Import SDD ...** from the menu to open the window for the import. In the window click on the button to select the file with the data you want to import. If during analysis or import any problems occur, you may click on the button to reload the file and re-initialize the window.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy_2012-12-18.sdd.xml

☑ Project: Deemy
  ☑ Metadata
  ☑ Agents
  ☑ Descriptive concepts
  ☑ Descriptors
  ☑ Descriptor trees
  ☑ Descriptions

Default language: en
☐ Import translations
☐ Check strings for illegal characters
● New project: Project: Deemy
○ To project
Workbench project: DiversityWorkbench
☐ Accept comma as decimal separator
☑ Create default descriptor tree
☐ Import trees for "natural language description"
☐ Import trees without "role"

Import to database: **DiversityDescriptions_Workshop**

Read success

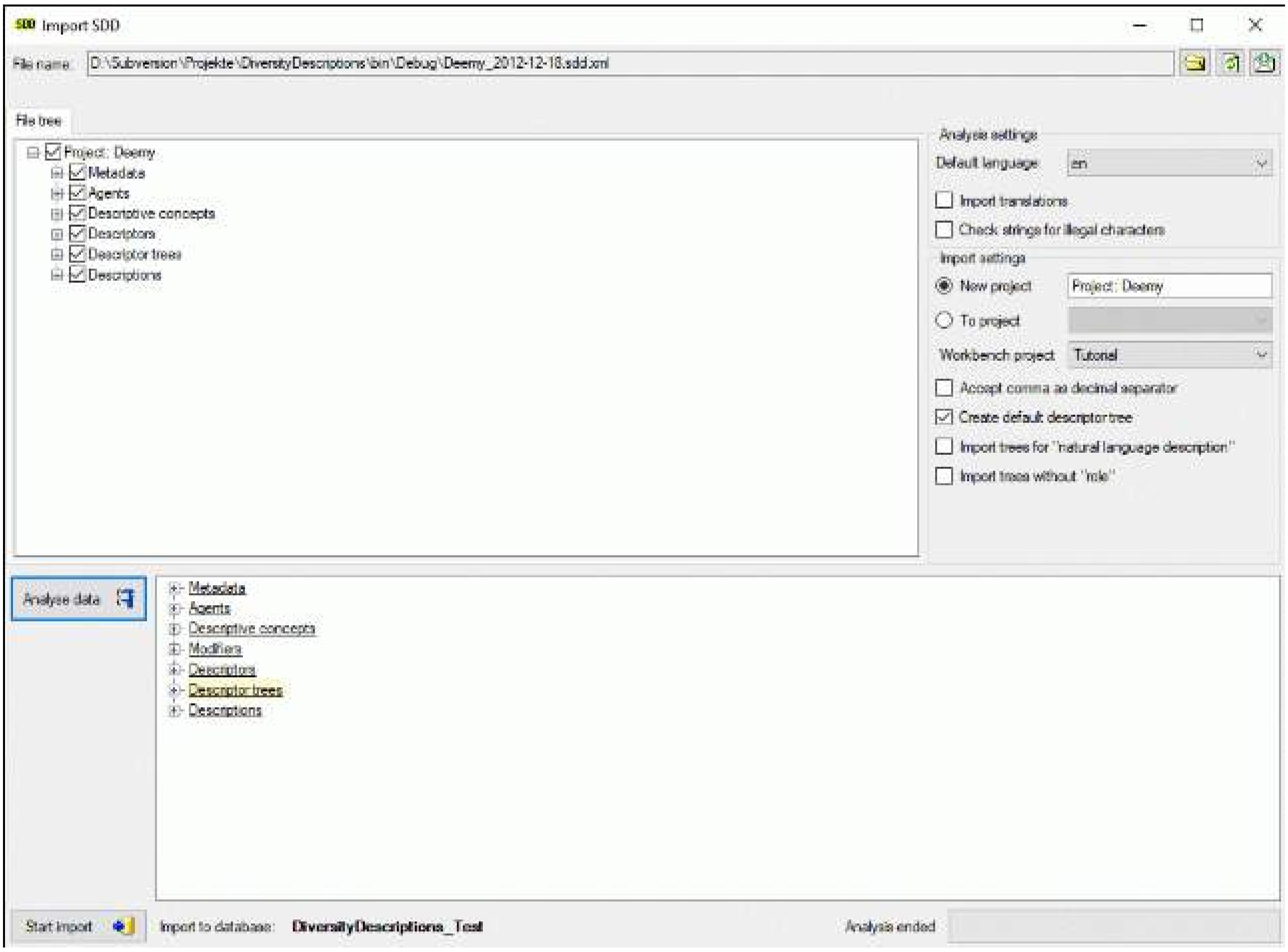
The contents of the file will be shown in the upper part of the **File tree** tab page. In the **Analysis settings** part you find the document's **Default language**. If additional laguages are contained in the document, you may select one of them as the new default language of the database. By checking **Import translations** you select all additional document languages for the import. This option is automatically pre-selected if more than one language has been found in the file. In the bottom part of the window you find the import database and the actual processing state.

If the **Check strings for illegal characters** option is checked, all string literals that shall be exported from database are scanned for illegal non-printable characters and matches are replaced by a double exclamation mark ("‼"). Activating this option may increase the analysis processing time.

In the file tree you may deselect entries that shall not be imported into the database. Use that option very carefully, because if you deselect entries that are being referenced by other parts of the input tree, e.g. descriptors referenced by descriptions, the analysis or import step might become erronous!

Analysis

To analyse the data in the file click on the **Analyse data** button. During the analysis the program checks the dependencies between the different parts of the data and builds up an analysis tree in the lower part of the window. The analysis tree contains all data in a suitable format for the final import step. During data analysis the icon of the button changes to and you may abort processing by clicking the button.


Import SDD

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy_2012-12-18.sdd.xml

Analysis settings

Default language: en

☐ Import translations

☐ Check strings for illegal characters

Import settings

● New project: Project: Deemy

○ To project

Workbench project: Tutorial

☐ Accept comma as decimal separator

☑ Create default descriptor tree

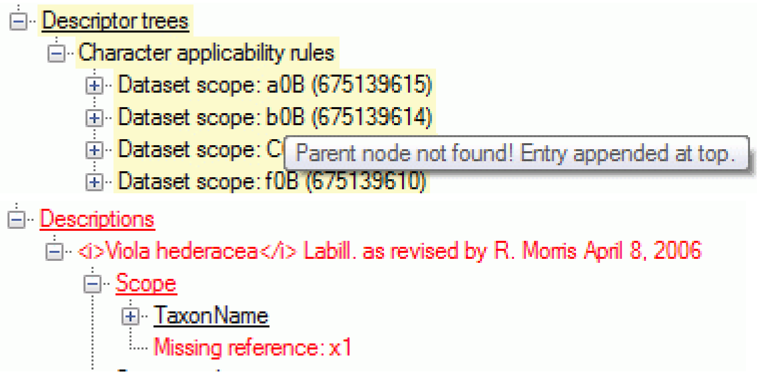
☐ Import trees for "natural language description"

☐ Import trees without "role"

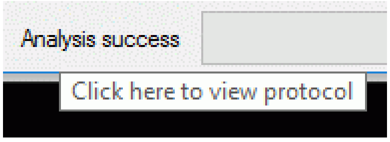
Import to database: DiversityDescriptions_Test

Analysis ended

After analysis a message window informs you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as tool tip or the tree node text itself tells the problem (see examples below). By clicking on the status text besides the progress bar, you can open an analysis protocol (see below, right).



Descriptor trees
Character applicability rules
Dataset scope: a0B (675139615)
Dataset scope: b0B (675139614)
Dataset scope: C
Parent node not found! Entry appended at top.
Dataset scope: f0B (675139610)
Descriptions
<i>Viola hederacea</i> Labill. as revised by R. Morris April 8, 2006
Scope
TaxonName
Missing reference: x1



Analysis success

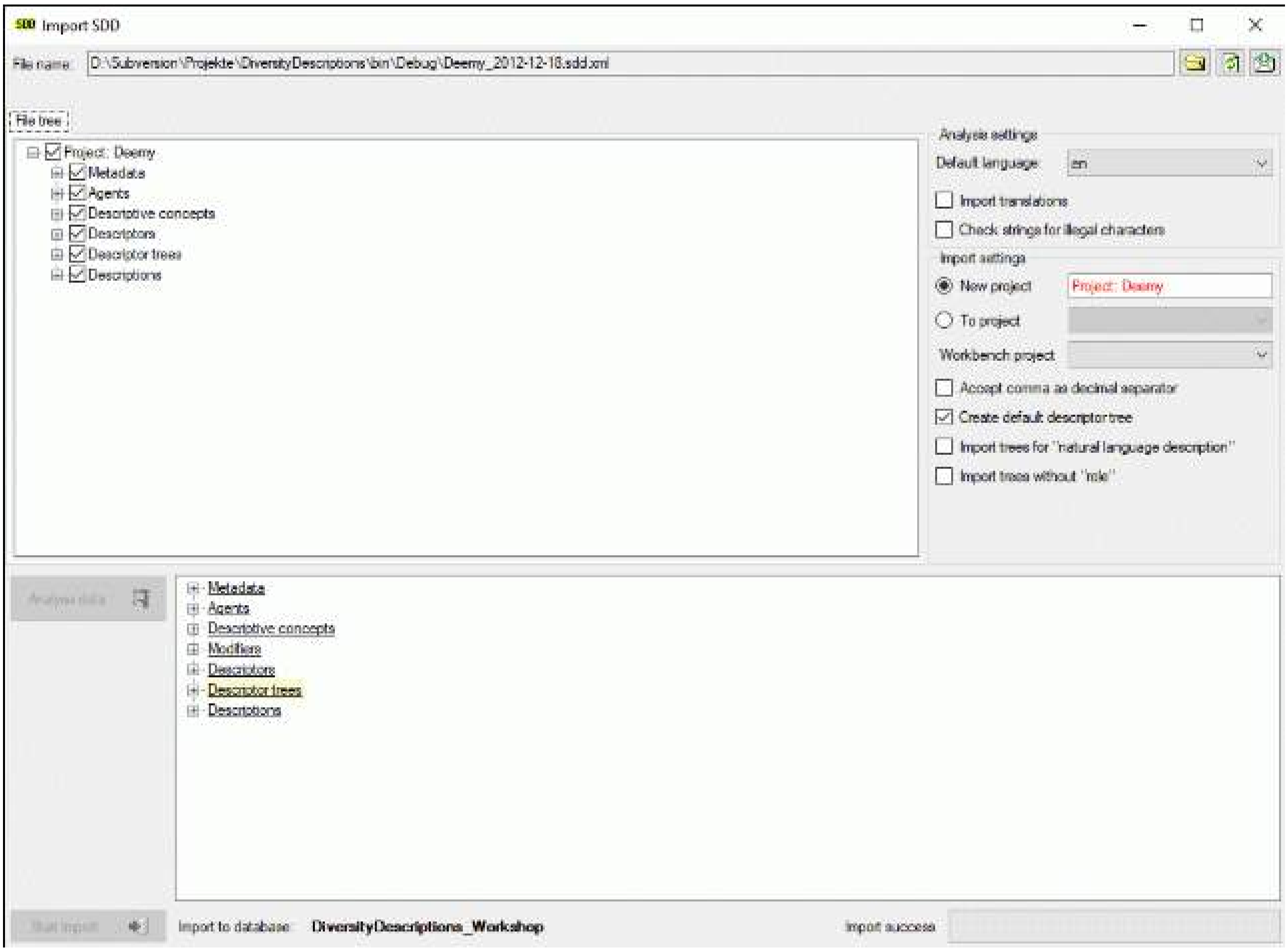
If an analysis error occured, you are not able to proceed. You will first have to correct the problem, e.g. by excluding the erronous descriptor in the example above (after reloading the file). If a warning occured, it might not cause problems during import, but you should take a closer look if the imported data will be correct.

Import

Before starting the import, you should take a look at the import options:

- **New project** - import data to a new project.
  The project name is specified in the text box right from this radio button.
  This option is only available if at least ProjectManager rights are available.
- **To project** - import data to an existing project.
  The combo box at the right shows all projects where write access is possible.
  If only TerminologyEditor rights are availabe, no changes in the existing project (e.g. detail or copyright) will be done.
- **Worlbench project** specifies the assigned workbench project if "New project" is selected for import.
- **Accept comma as decimal separator** shall help to overcome problems with localization of some programs that create SDD files.
  If this option is checked, a floating point value like "1,0" (e.g. used in german localizations) instead of "1.0" will be accepted as "1".
- **Create default descriptor tree** creates a default descriptor tree and assigns all imported descriptors to that tree.
  Additionally the statistical measures "Minimum", "Lower limit", "Mean", "Upper limit" and "Maximum" are set as recommended for all quantitative descriptors.
  This option is useful to avoid unassigned descriptors if the import file does not specify any descriptor tree assignments.
- **Import trees for natural language descriptions** - currently natural language descriptions are ignored.
- **Import trees without "role"** - usually those trees only contain descriptor dependency information.

To start the import click on the **Start import** button. Now the data from the analysis tree are written into a local database cache and finally stored into the database.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy_2012-12-18.sdd.xml

- ☑ Project: Deemy
  - ☑ Metadata
  - ☑ Agents
  - ☑ Descriptive concepts
  - ☑ Descriptors
  - ☑ Descriptor trees
  - ☑ Descriptions

Analysis settings

Default language: en

☐ Import translations

☐ Check strings for illegal characters

Import settings

● New project: Project: Deemy

○ To project

Workbench project

☐ Accept comma as decimal separator

☑ Create default descriptor tree

☐ Import trees for "natural language description"

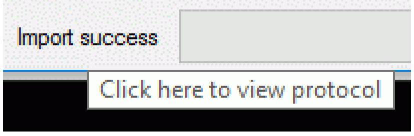
☐ Import trees without "role"

- Metadata
- Agents
- Descriptive concepts
- Modifiers
- Descriptors
- Descriptor trees
- Descriptions

Import to database: **DiversityDescriptions_Workshop**

Import success

After import a message window inform you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as bubble help or the tree node text itself tells the problem. By clicking on the status text besides the progress bar, you can open an import protocol (see below).


Import success

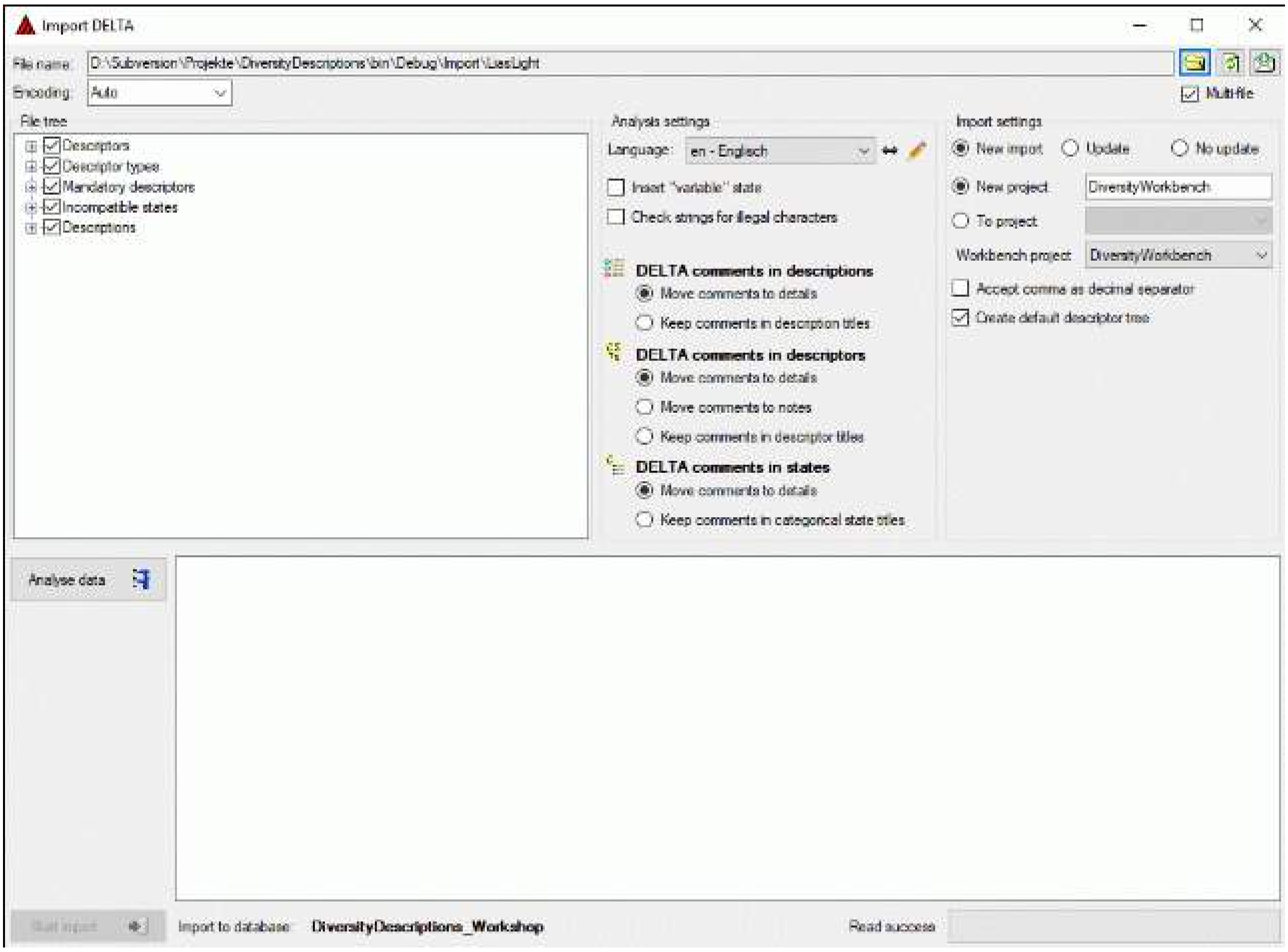
Click here to view protocol

Import DELTA file

Remark:

- To import data from a DELTA file at least TerminologyEditor rights are neccessary.

With this form you can import data from a file in DELTA format into the database. Choose **Data -> Import -> Import DELTA ...** from the menu to open the window for the import. In the window click on the button to select the file with the data you want to import. If the **Multi-file** option is selected before pressing the button, a folder selection window opens to select the folder where the DELTA files are located. For muti-file processing currently the files "chars", "items", "specs" and "extra" are evaluated. If during analysis or import any problems occur, you may click on the button to reload the file and re-initialize the window.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\LiasLight
Encoding: Auto
☑ Multi-file

File tree:
- ☑ Descriptors
- ☑ Descriptor types
- ☑ Mandatory descriptors
- ☑ Incompatible states
- ☑ Descriptions

Analysis settings
Language: en - Englisch
☐ Insert "variable" state
☐ Check strings for illegal characters

DELTA comments in descriptions
● Move comments to details
○ Keep comments in description titles

DELTA comments in descriptors
● Move comments to details
○ Move comments to notes
○ Keep comments in descriptor titles

DELTA comments in states
● Move comments to details
○ Keep comments in categorical state titles

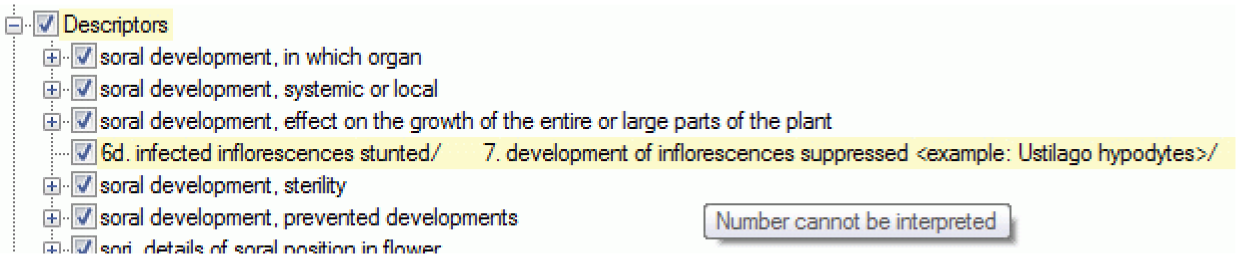
Import settings
● New import ○ Update ○ No update
● New project: DiversityWorkbench
○ To project:
Workbench project: DiversityWorkbench
☐ Accept comma as decimal separator
☑ Create default descriptor tree

Import to database: **DiversityDescriptions_Workshop**
Read success

The contents of the file will be shown in the upper part of the **File tree** section. If special characters are not displayed corretly, try a different **Encoding** setting, e.g. "ANSI", and reload the document using the button. In the bottom part of the window you find the import database and the actual processing state.

In the file tree you may deselect entries that shall not be imported into the database. Use that option very carefully, because if you deselect entries that are being referenced by other parts of the input tree, e.g. descriptors referenced by descriptions, the analysis or import step might become erronous!

If during reading of the files expressions cannot be interpreted, suspicious entries are maked with yellow background (warning) in the file tree. When you move the mouse curser over the marked entries, you get additional information as tool tip or the tree node text itself tells the problem (see example below).



☑ Descriptors
☑ soral development, in which organ
☑ soral development, systemic or local
☑ soral development, effect on the growth of the entire or large parts of the plant
☑ 6d. infected inflorescences stunted/ 7. development of inflorescences suppressed <example: Ustilago hypodytes>/
☑ soral development, sterility
☑ soral development, prevented developments
☑ sori, details of soral position in flower

Number cannot be interpreted

Analysis

To analyse the data in the file click on the **Analyse data** button. During the analysis the program checks the dependencies between the different parts of the data and builds up an analysis tree in the lower part of the window. The analysis tree contains all data in a suitable format for the final import step. During data analysis the icon of the button changes to STOP and you may abort processing by clicking the button.

In the **Analysis settings** section (see image below) you set the document's **Language**. You man change the display and sorting of the entries in the **Language** combo box from "<code> - <description>" to "<description> - <code>" (and back) by clicking the button ⇔. If you need language codes that are not included in the list, click the ✏ button. For more details see Edit language codes.

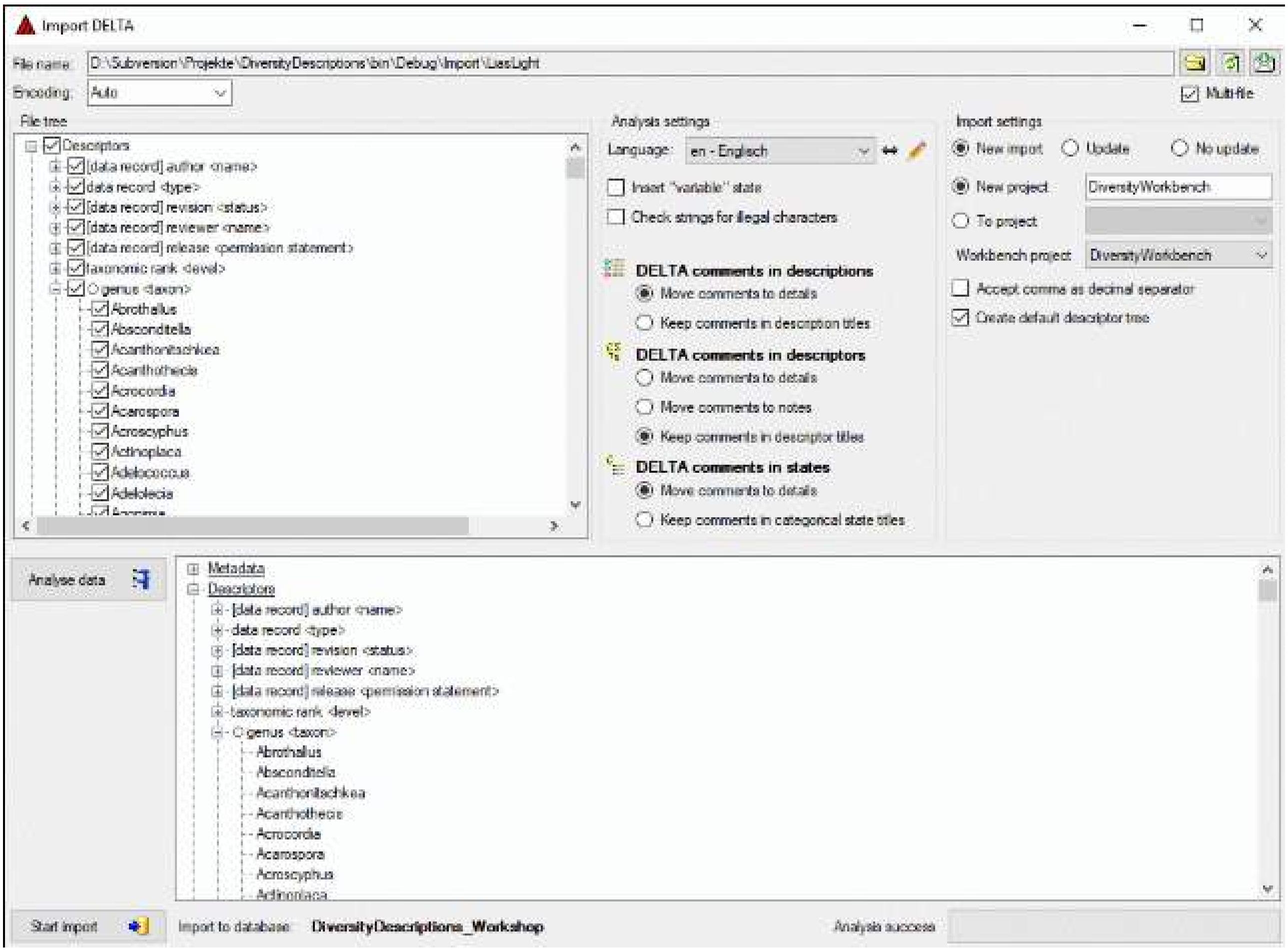
The **Insert "variable" state** controls the handling of the DELTA state "V" for categorical summary data. If possible, a categorical state "variable" is inserted to the descriptor data and set in the summary data, when the state "V" is present in the description data.

If the **Check strings for illegal characters** option is checked, all string literals that shall be exported from database are scanned for illegal non-printable characters and matches are replaced by a double exclamation mark ("‼"). Activating this option may increase the analysis processing time.

In DELTA text in angle bracket (<text>) usually denotes comments, which are by default imported into the "Details" fields of the database. In the lower parts of the **Analysis settings** you may adjust a different handling for description, descriptor and categorical state items.

- For **DELTA comments in descriptions** you may **Move comments to details** (default) or **Keep comments in description titles**.
- For **DELTA comments in descriptors** you may **Move comments to details** (default), **Move comments to notes** or **Keep comments in descriptor titles**.
- For **DELTA comments in categorical states** you may **Move comments to details** (default) or **Keep comments in categorical state titles**.

After changing one of these settings click on the **Analyse data** button to make the changes effective.



Language: en - Englisch

☐ Insert "variable" state

☐ Check strings for illegal characters

DELTA comments in descriptions

● Move comments to details

○ Keep comments in description titles

DELTA comments in descriptors

○ Move comments to details

○ Move comments to notes

● Keep comments in descriptor titles

DELTA comments in states

● Move comments to details

○ Keep comments in categorical state titles

● New import ○ Update ○ No update

● New project: DiversityWorkbench

○ To project

Workbench project: DiversityWorkbench

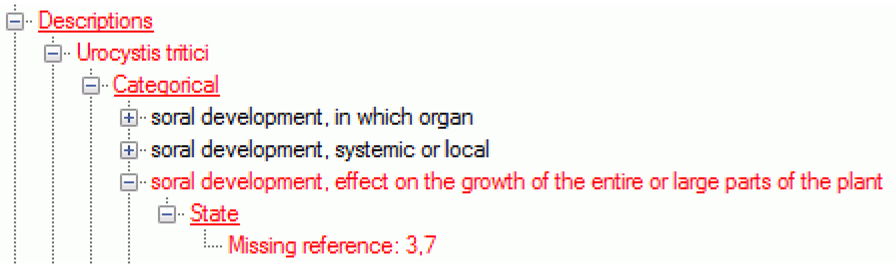
☐ Accept comma as decimal separator

☑ Create default descriptor tree

Import to database: **DiversityDescriptions_Workshop**

Analysis success

After analysis a message window informs you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as bubble help or the tree node text itself tells the problem (see example below). By clicking on the status text besides the progress bar, you can open an analysis protocol (see below, right).


Descriptions

Urocystis tritici

Categorical

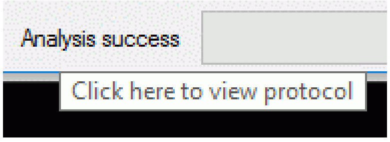
soral development, in which organ

soral development, systemic or local

soral development, effect on the growth of the entire or large parts of the plant

State

Missing reference: 3,7



If an analysis error occured, you are not able to proceed. You will first have to correct the problem, e.g. by excluding the erronous descriptor in the example above (after reloading the file). If a warning occured, it might not cause problems during import, but you should take a closer look if the imported data will be correct.

Import

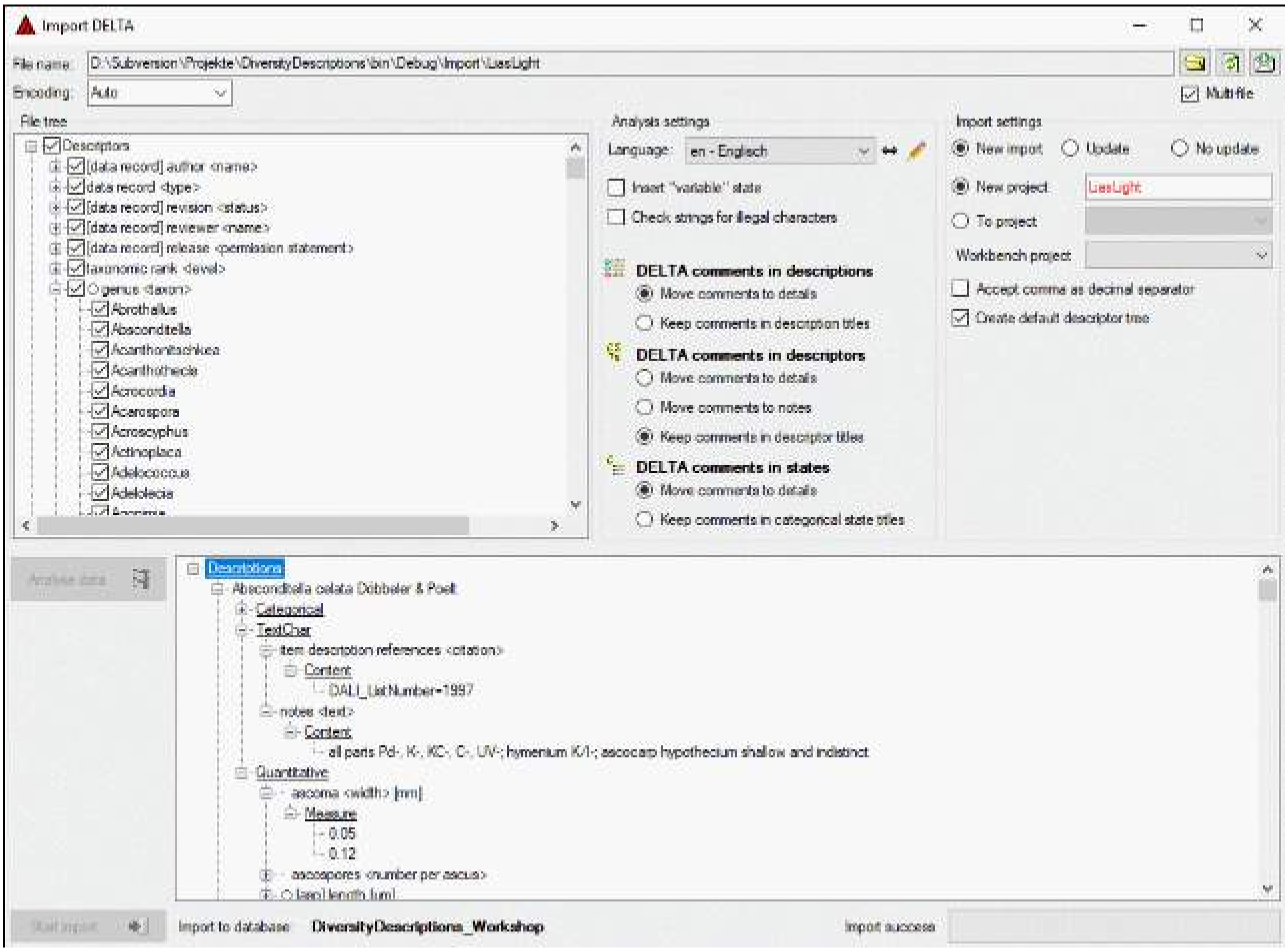
If you want to import new data to a project you have two import options:

- **New import** - import new data and save mapping information to an import session.
  For descriptors, categorical states and descriptions the mapping information from the DELTA import will be storen in an import session. Therefore by a subsequent import run updated information, e.g. a modified label or detail information can be done (see section "Update" below).
- **No update** - import new data without saving of mapping information.
  This option might be faster, but you will not be able to update the titles or to import additional translations from a DELTA file.

Before starting the import, you should take a look at the import settings:

- **New project** - import data to a new project.
  The project name is specified in the text box right from this radio button.
  This option is only available if at least ProjectManager rights are available.
- **To project** - import data to an existing project.
  The combo box at the right shows all projects where write access is possible.
  If only TerminologyEditor rights are availabe, no changes in the existing project (e.g. detail or copyright) will be done.
- **Worlbench project** specifies the assigned workbench project if "New project" is selected for import.
- **Accept comma as decimal separator** shall help to overcome problems with localization of some programs that create DELTA files.
  If this option is checked, a floating point value like "1,0" (e.g. used in german localizations) instead of "1.0" will be accepted as "1".
- **Create default descriptor tree** creates a default descriptor tree and assigns all imported descriptors to that tree.
  Additionally the statistical measures "Minimum", "Lower limit", "Mean", "Upper limit" and "Maximum" are set as recommended for all quantitative descriptors.
  This option is useful to avoid unassigned descriptors if the import file does not specify any descriptor tree assignments.

To start the import click on the **Start import** button. Now the data from the analysis tree are written into a local database cache and finally stored into the database.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\LiasLight

Encoding: Auto

☑ Multi file

Language: en - Englisch

☐ Insert "variable" state

☐ Check strings for illegal characters

DELTA comments in descriptions

● Move comments to details

○ Keep comments in description titles

DELTA comments in descriptors

○ Move comments to details

○ Move comments to notes

● Keep comments in descriptor titles

DELTA comments in states

● Move comments to details

○ Keep comments in categorical state titles

● New import ○ Update ○ No update

● New project: LiasLight

○ To project

Workbench project:

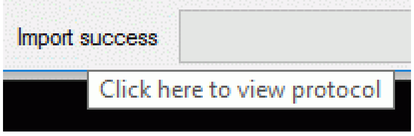
☐ Accept comma as decimal separator

☑ Create default descriptor tree

Import to database: **DiversityDescriptions_Workshop**

Import success

After import a message window inform you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as bubble help or the tree node text itself tells the problem. By clicking on the status text besides the progress bar, you can open an import protocol (see below).


Import success

Click here to view protocol

Handling of special DELTA states

In the DELTA format the special states "**-**" (not applicable), "**U**" (unknown) and "**V**" (variable) are available for categorical and quantitative characters. These states are treated in the folloging manner during import:

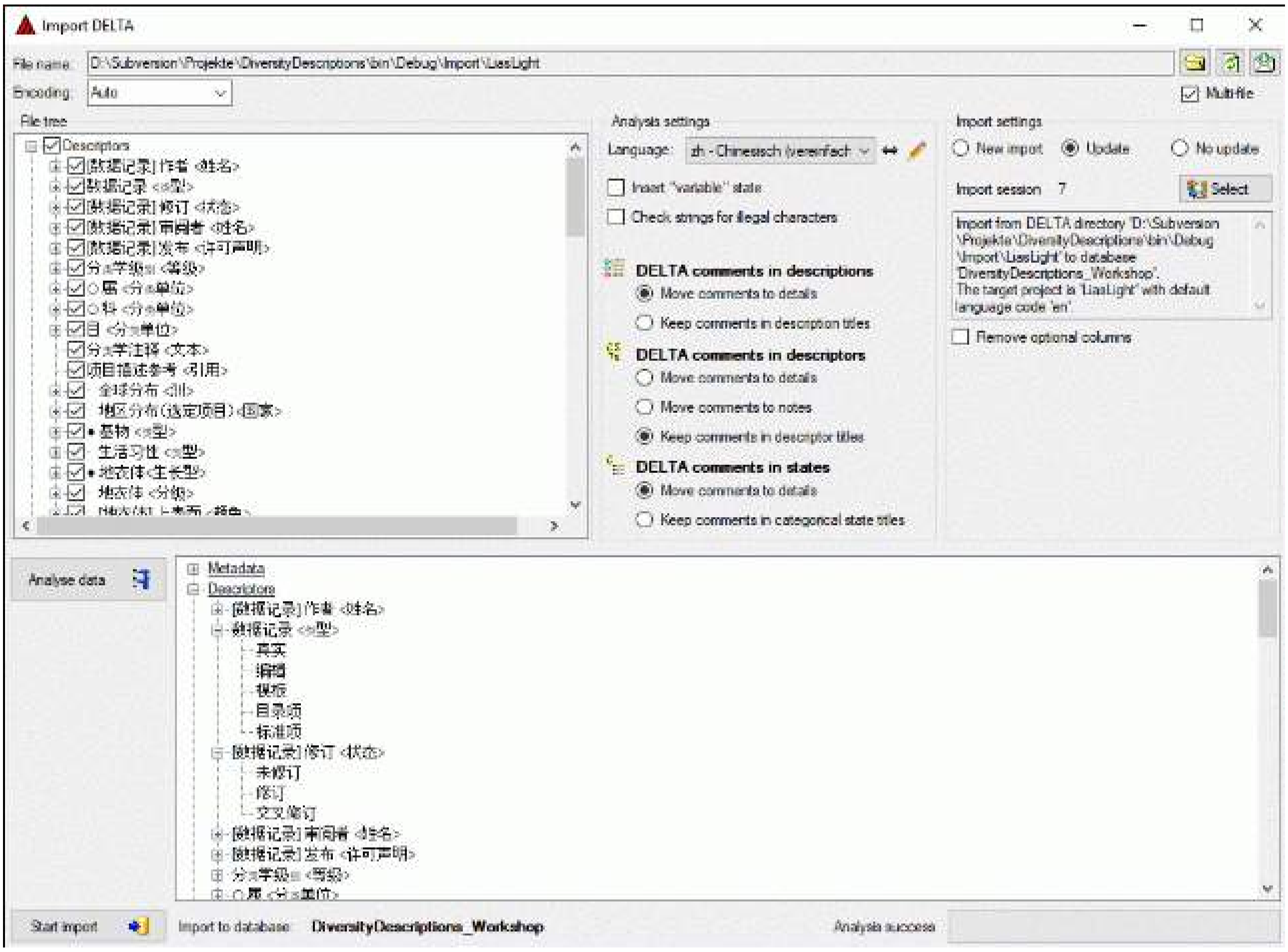
- "**-**" (not applicable)
  The data status "**Not applicable**" is set.
- "**U**" (unknown)
  The data status "**Data unavailable**" is set.
- "**V**" (variable)
  The data status "**Not interpreterable**" is set.

Update

If you imported new data using option **New import**, a new import session with the following data will be created:

- **Descriptor keys** - the "character number" that is used in DELTA to identify a dedicated character.
- **Categorical state keys** - the "state number" that is used in DELTA, together with the "character number", to identify a dedicated chategorical state.
- **Description keys** - the item position in the item list. Since in DELTA there are no explicit item numbers, the position within the item list is taken for this key. If you want to update the items using the DELTA import, you must be sure that the item list has **exactly the same sequence** as for the first import!

For those entities you may update the columns "label", "detail" and "data_entry_notes" (only for descriptors). To achive this, you must specify the same **Language** in the **Analysis settings** as adjusted as project language. If you specify a different **Default language**, the data will be imported as translations for the columns "label" rsp. "detail" (see image below). For descriptor column "data_entry_notes" translations are not supported.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\LiasLight

Encoding: Auto

☑ Multifile

Analysis settings

Language: zh - Chinesisch (vereinfacht

☐ Insert "variable" state

☐ Check strings for illegal characters

DELTA comments in descriptions

● Move comments to details

○ Keep comments in description titles

DELTA comments in descriptors

○ Move comments to details

○ Move comments to notes

● Keep comments in descriptor titles

DELTA comments in states

● Move comments to details

○ Keep comments in categorical state titles

Import settings

○ New import ● Update ○ No update

Import session 7

Import from DELTA directory 'D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\LiasLight' to database 'DiversityDescriptions_Workshop'. The target project is 'LiasLight' with default language code 'en'.

☐ Remove optional columns

Import to database DiversityDescriptions_Workshop

Analysis success

Preparation

By changing the **Analysis settings** and a clicking the **Analyse data** button you may modify the handling of DELTA comments. E.g. if you used the default settings during a past import, a DELTA character "data record <type>" was imported as descriptor "data record" and "type" was written into the columns "detail". In the **Analysis settings** you may now select option **Keep comments in descriptor titles** to update the descriptor title to "data record <type>".

Import settings

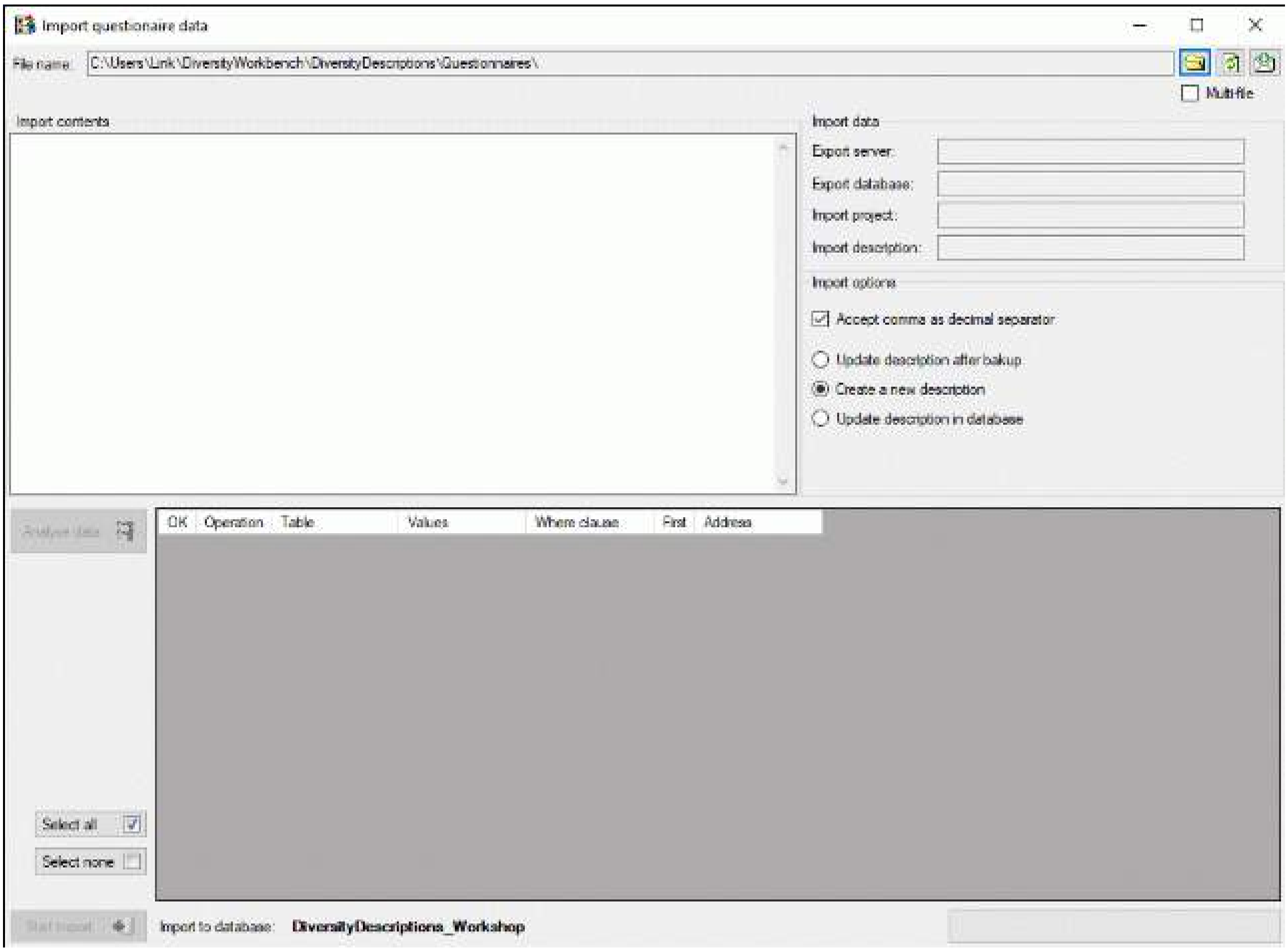
Before starting the import, you should take a look at the import options:

- **Update** - perform an update import.
- **Import session** - click on button **Select** to select the correct import session.
  In the text box below that option the automatically generated descriptive text of the import session is displayed.
- **Remove optional columns** - clear optional columns if no contents is present.
  If during update import for an optional column ("detail" rsp. "data_entry_note") no data are present, by default an existing entry in the database will not be removed. Check this option to clear the data.

Start the import click on the **Start import** button. Now the data from the analysis tree are written into a local database cache and finally stored into the database.

Import questionnaire data

With this form you can import response data generated by an HTML questionnaire (see Export questionnaires). Choose **Data -> Import -> Import questionnaire data ...** from the menu to open the window for the import. In the window click on the button to select the text file with the data you want to import. If during analysis or import any problem occurs, you may click on the button to reload the file and re-initialize the window.



Import questionaire data

File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\

☐ Multi file

Import options

☑ Accept comma as decimal separator

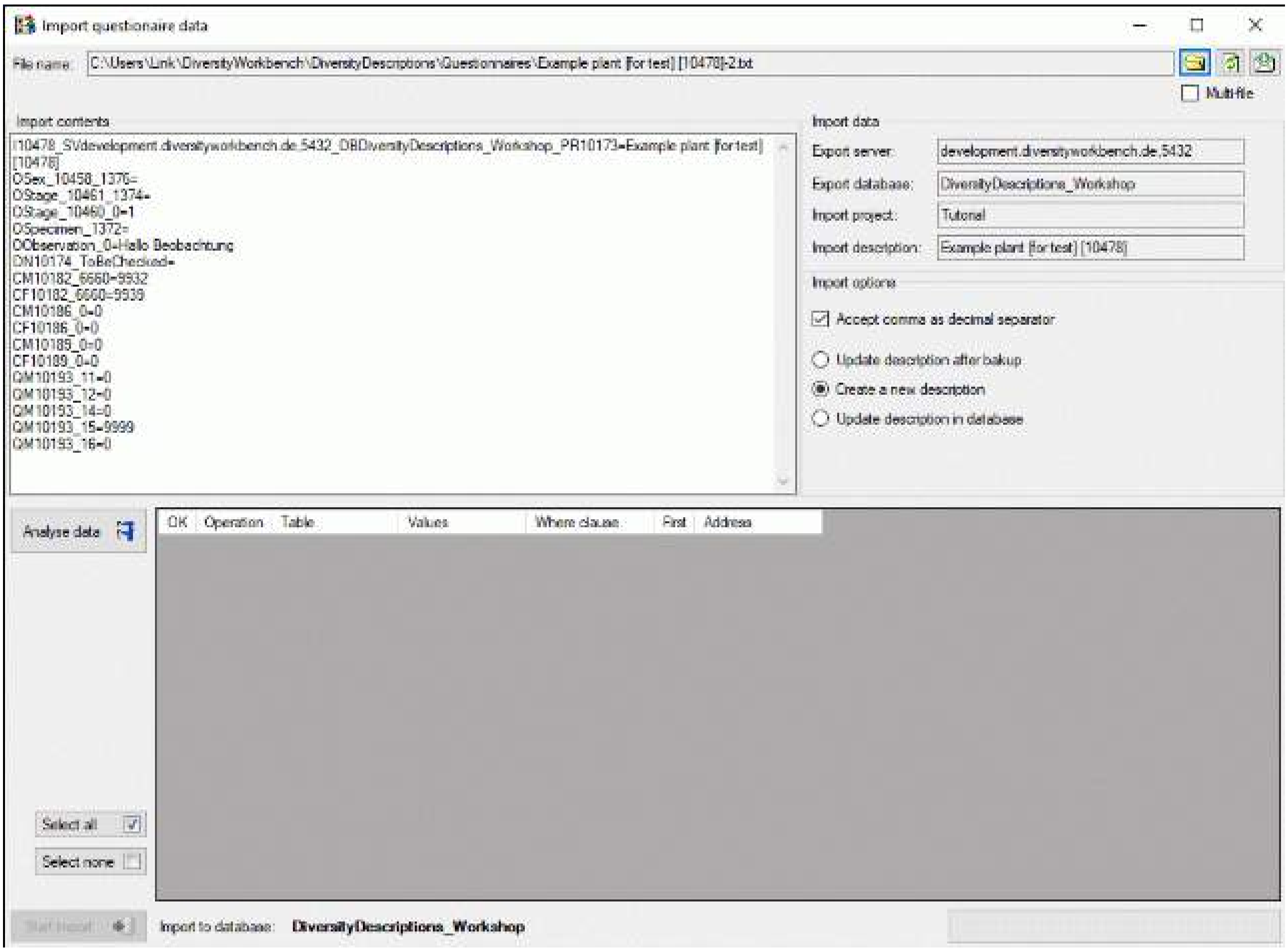
○ Update description after bakup

● Create a new description

○ Update description in database

Import to database: **DiversityDescriptions_Workshop**

The contents of the file will be shown in the upper part of the **Import contents** section. You may edit the contents or even enter the whole data by copy - paste. In the **Import data** part you find the basic dataset parameters **Export server**, **Export database**, **Import project** and **Import description** (see image below). If there is a mismatch, e.g. because the questionnaire was generated from a different database than your import database, an appropriate error will be reported.



File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\Example plant [for test] [10478]-2.txt

☐ Multi-file

Import contents

```
I10478_SVdevelopment.diversityworkbench.de.5432_DBDiversityDescriptions_Workshop_PR10173=Example plant [for test]
[10478]
OSex_10458_1376=
OStage_10461_1374=
OStage_10460_0=1
OSpecimen_1372=
OObservation_0=Hallo Beobachtung
DN10174_ToBeChecked=
CM10182_6660=9932
CF10182_6660=9939
CM10186_0=0
CF10186_0=0
CM10189_0=0
CF10189_0=0
QM10193_11=0
QM10193_12=0
QM10193_14=0
QM10193_15=9999
QM10193_16=0
```

Import data

Export server: development.diversityworkbench.de,5432
Export database: DiversityDescriptions_Workshop
Import project: Tutorial
Import description: Example plant [for test] [10478]

Import options

☑ Accept comma as decimal separator

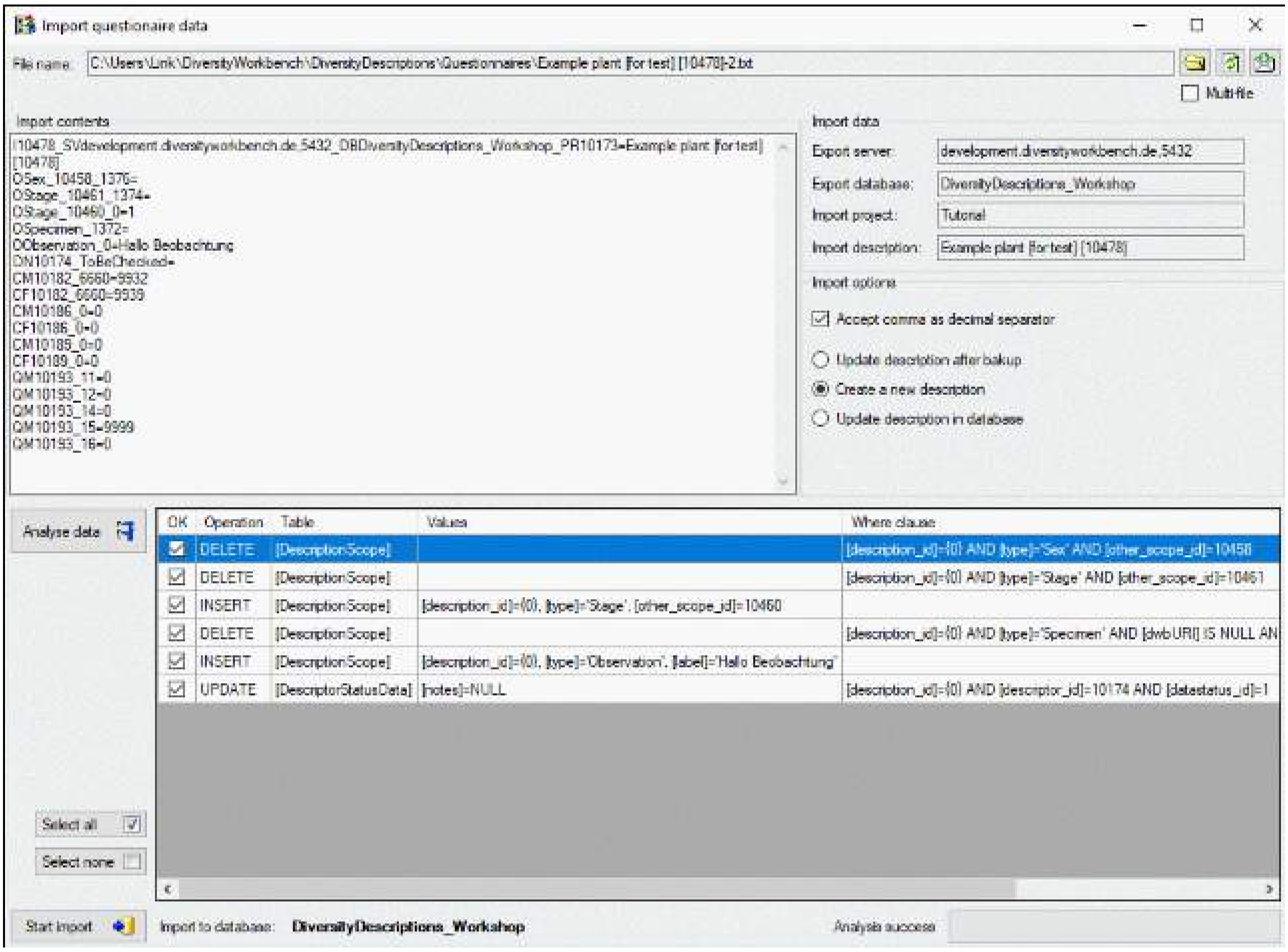
○ Update description after bakup
● Create a new description
○ Update description in database

Select all ☑
Select none ☐

Import to database: **DiversityDescriptions_Workshop**

Analysis

To analyse the data in the file click on the **Analyse data** button. During the analysis the program compares the reported data to the entries in the database and presents the planned database operations in the lower part of the window (see image below). By checking **Accept comma as decimal separator** in the **Import options** section you can overcome problems with localization of the computer where the questionnaire was filled in. If this option is checked, a floating point value like "1,0" (e.g. used in german localizations) instead of "1.0" will be accepted as "1".



File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\Example plant [for test] [10478]-2.txt

```
[10478_SVdevelopment.diversityworkbench.de,5432_DBDiversityDescriptions_Workshop_PR10173=Example plant [for test]
[10478]
OSex_10458_1376=
OStage_10461_1374=
OStage_10460_0=1
OSpecimen_1372=
OObservation_0=Hallo Beobachtung
DN10174_ToBeChecked=
CM10182_6660=9932
CF10182_6660=9939
CM10186_0=0
CF10186_0=0
CM10189_0=0
CF10189_0=0
QM10193_11=0
QM10193_12=0
QM10193_14=0
QM10193_15=9999
QM10193_16=0
```

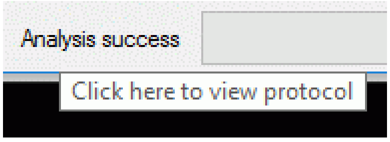
Export server: development.diversityworkbench.de,5432
Export database: DiversityDescriptions_Workshop
Import project: Tutorial
Import description: Example plant [for test] [10478]

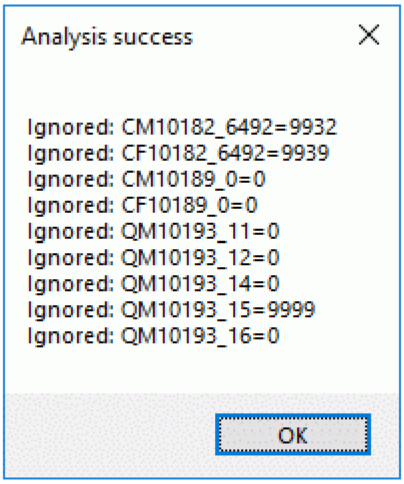
☑ Accept comma as decimal separator
○ Update description after bakup
● Create a new description
○ Update description in database

OK	Operation	Table	Values	Where clause
☑	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Sex' AND [other_scope_id]=10458
☑	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Stage' AND [other_scope_id]=10461
☑	INSERT	[DescriptionScope]	[description_id]={0}, [type]='Stage', [other_scope_id]=10460	
☑	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Specimen' AND [dwbURI] IS NULL AN
☑	INSERT	[DescriptionScope]	[description_id]={0}, [type]='Observation', [label]='Hallo Beobachtung'	
☑	UPDATE	[DescriptorStatusData]	[notes]=NULL	[description_id]={0} AND [descriptor_id]=10174 AND [datastatus_id]=1

Import to database: **DiversityDescriptions_Workshop**

After analysis a message window informs you about errors or ignored input lines. By clicking on the status text besides the progress bar, you can open an analysis protocol (see below).





Ignored: CM10182_6492=9932
Ignored: CF10182_6492=9939
Ignored: CM10189_0=0
Ignored: CF10189_0=0
Ignored: QM10193_11=0
Ignored: QM10193_12=0
Ignored: QM10193_14=0
Ignored: QM10193_15=9999
Ignored: QM10193_16=0

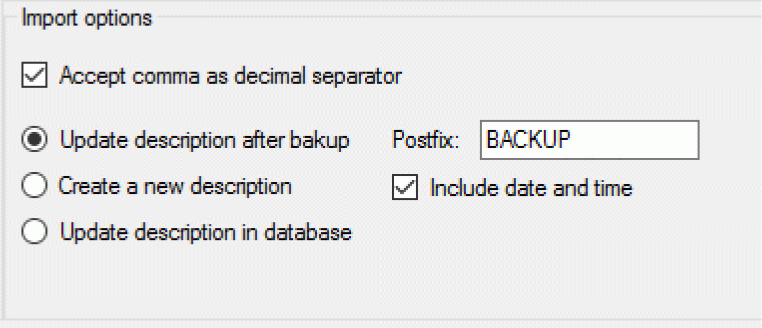
If an analysis error occured, you are not able to proceed. If ignored lines are reported, this fact is usually uncritical. Most of them concern "modifier" or "frequency" values (prefix CM, CF or QM) where the questionnaire reports the actual values, not only the differences.

Import

Before starting the import, you should take a look at the remaining **Import options**:

- **Update description after backup**
  Create a backup of the original description data and then update the original description in the database. If this option is chosen, you may enter a **Postfix** that will be appended at the backup description name. Additionally you may select the option **Include data and time** to append these data at the backup name, too (see image below).
- **Create a new description** (only option for new descritpions)
  Make a copy of the original description data and then updatde the copy in the database.
- **Update description in database**
  The original description in the database will be updated.

If the description entries in your database are referenced by other applications, you should update the original database entry, i.e. use the first or third option. The reason is that references from other databases usually use the description id, which will be different for the copied description. To ensure that the questionnaire data are correct, you can import them useing the option **Create a new description**, verify the imported data and finally import them to the original description using option **Update description in database**.


Import options

☑ Accept comma as decimal separator

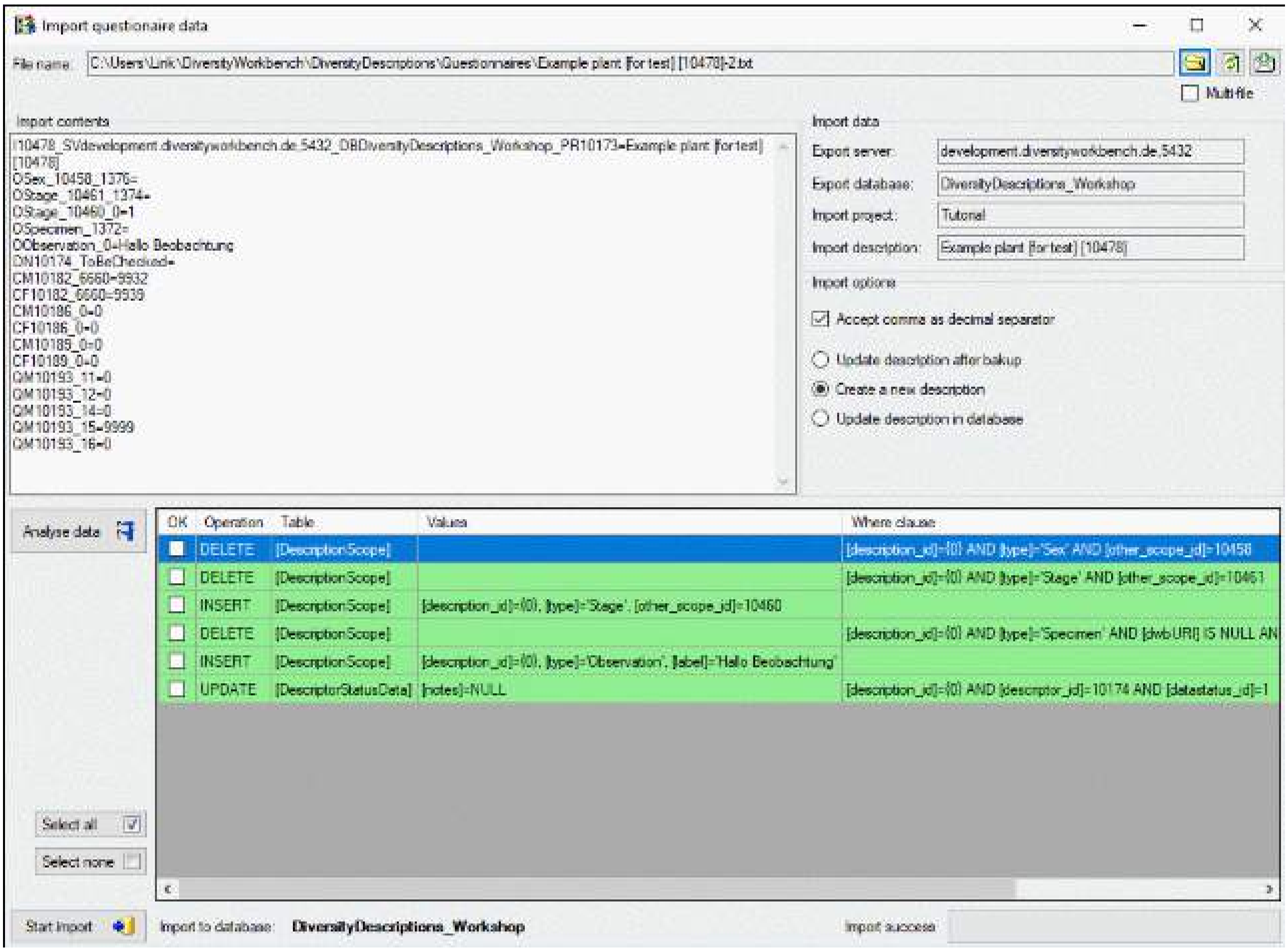
● Update description after bakup
○ Create a new description
○ Update description in database

Postfix: BACKUP

☑ Include date and time

Before performing the import you may include or exclude single database operations by setting or removing the check mark in column "OK". You may select or deselect all operations by clicking the buttons **Select all** rsp. **Select none**. Please be aware that deselecting single operation might lead to unexpected results.

To start the import click on the **Start import** button (see image below).



File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\Example plant [for test] [10478]-2.txt

☐ Multi file

Import contents

```
I10478_SVdevelopment.diversityworkbench.de.5432_DBDiversityDescriptions_Workshop_PR10173=Example plant [for test]
[10478]
OSex_10458_1376=
OStage_10461_1374=
OStage_10460_0=1
OSpecimen_1372=
OObservation_0=Hallo Beobachtung
DN10174_ToBeChecked=
CM10182_6660=9932
CF10182_6660=9939
CM10186_0=0
CF10186_0=0
CM10189_0=0
CF10189_0=0
QM10193_11=0
QM10193_12=0
QM10193_14=0
QM10193_15=9999
QM10193_16=0
```

Import data

Export server: development.diversityworkbench.de,5432

Export database: DiversityDescriptions_Workshop

Import project: Tutorial

Import description: Example plant [for test] [10478]

Import options

☑ Accept comma as decimal separator

○ Update description after bakup

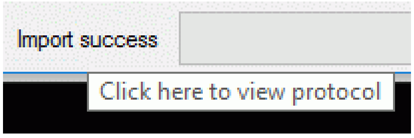
● Create a new description

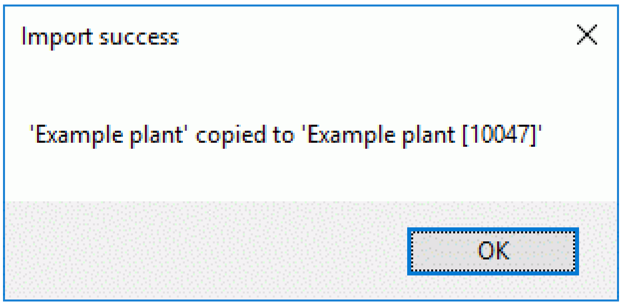
○ Update description in database

OK	Operation	Table	Values	Where clause
☐	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Sex' AND [other_scope_id]=10458
☐	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Stage' AND [other_scope_id]=10461
☐	INSERT	[DescriptionScope]	[description_id]={0}, [type]='Stage', [other_scope_id]=10460	
☐	DELETE	[DescriptionScope]		[description_id]={0} AND [type]='Specimen' AND [dwbURI] IS NULL AN
☐	INSERT	[DescriptionScope]	[description_id]={0}, [type]='Observation', [label]='Hallo Beobachtung'	
☐	UPDATE	[DescriptorStatusData]	[notes]=NULL	[description_id]={0} AND [descriptor_id]=10174 AND [datastatus_id]=1

Import to database: **DiversityDescriptions_Workshop**

After import a message window inform you if any occured. Sucessful database operations are shown with green background, unsuccessful operations with red background. When you move the mouse curser over the red entries, you get additional information as bubble help. By clicking on the status text besides the progress bar, you can open an import protocol (see below).

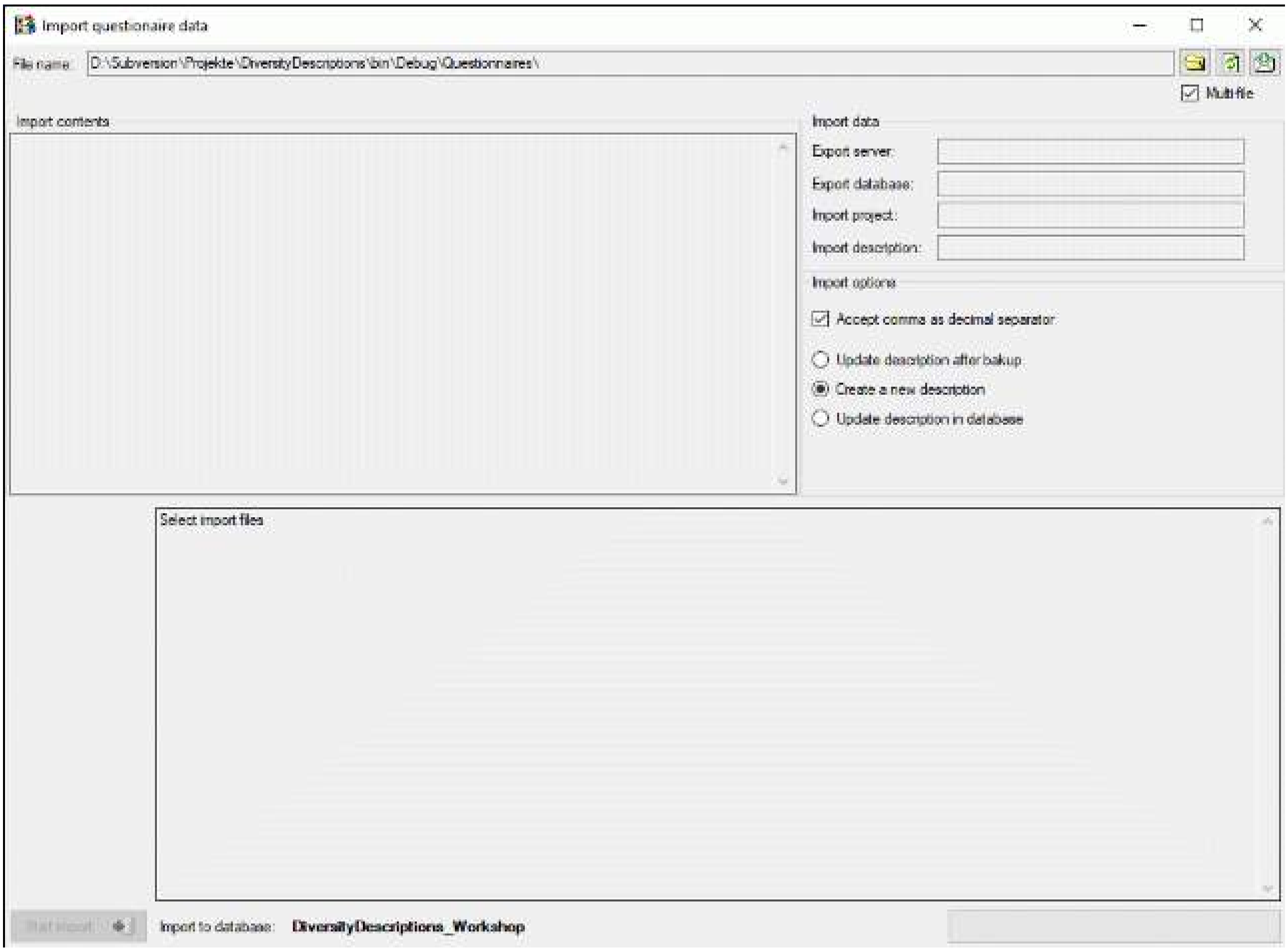




'Example plant' copied to 'Example plant [10047]'

Batch import

If you want to import several qustionaire result files, there is the comfortable option to do a batch import. When you select the option Multi-file, the window changes as shown below.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\

☑ Multi-file

☑ Accept comma as decimal separator

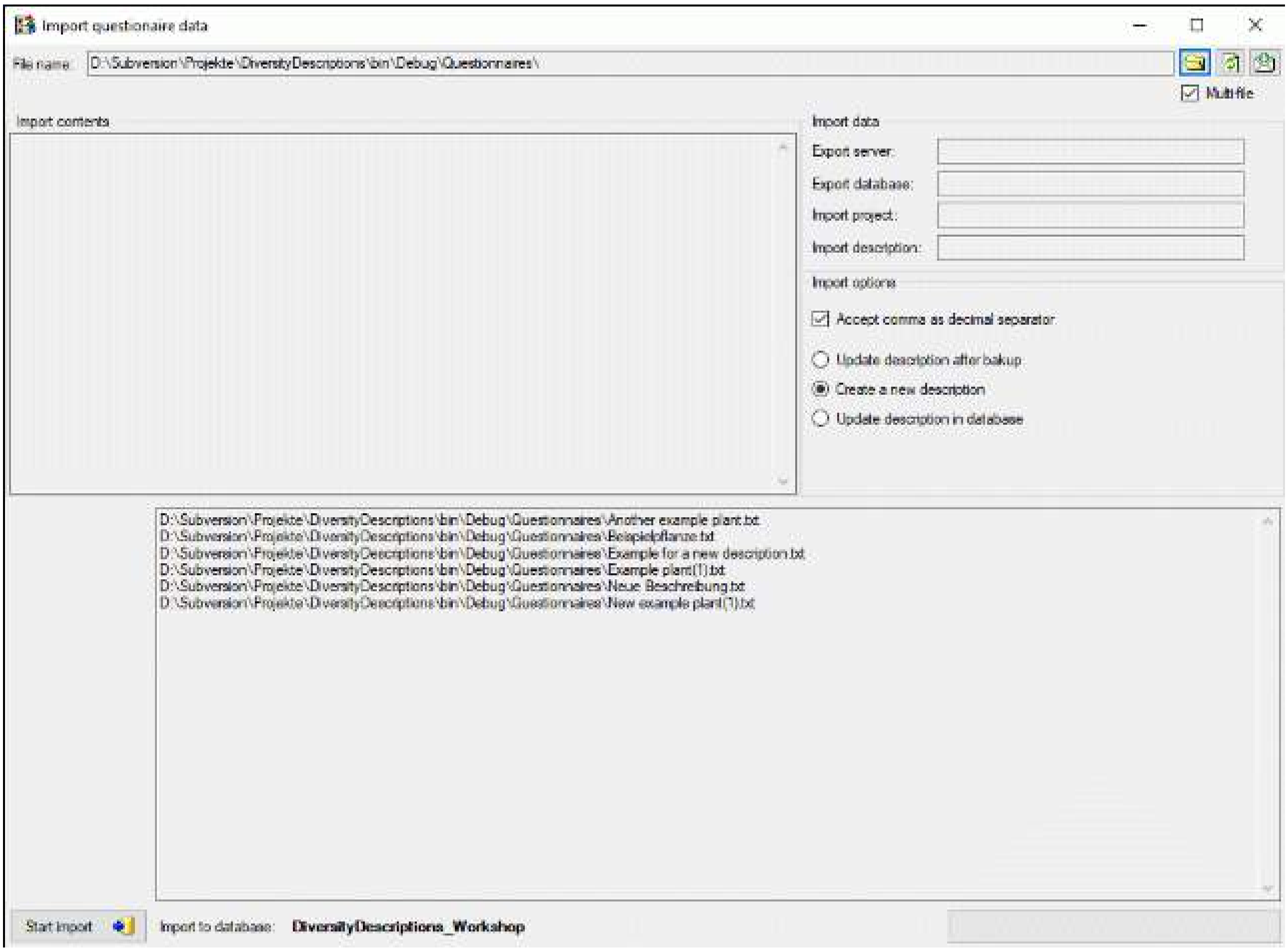
○ Update description after bakup

● Create a new description

○ Update description in database

Import to database: **DiversityDescriptions_Workshop**

Click on the 📁button and select all text files you want to import. In the lower part of the window the selected files will belisted (see image below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\

☑ Multi file

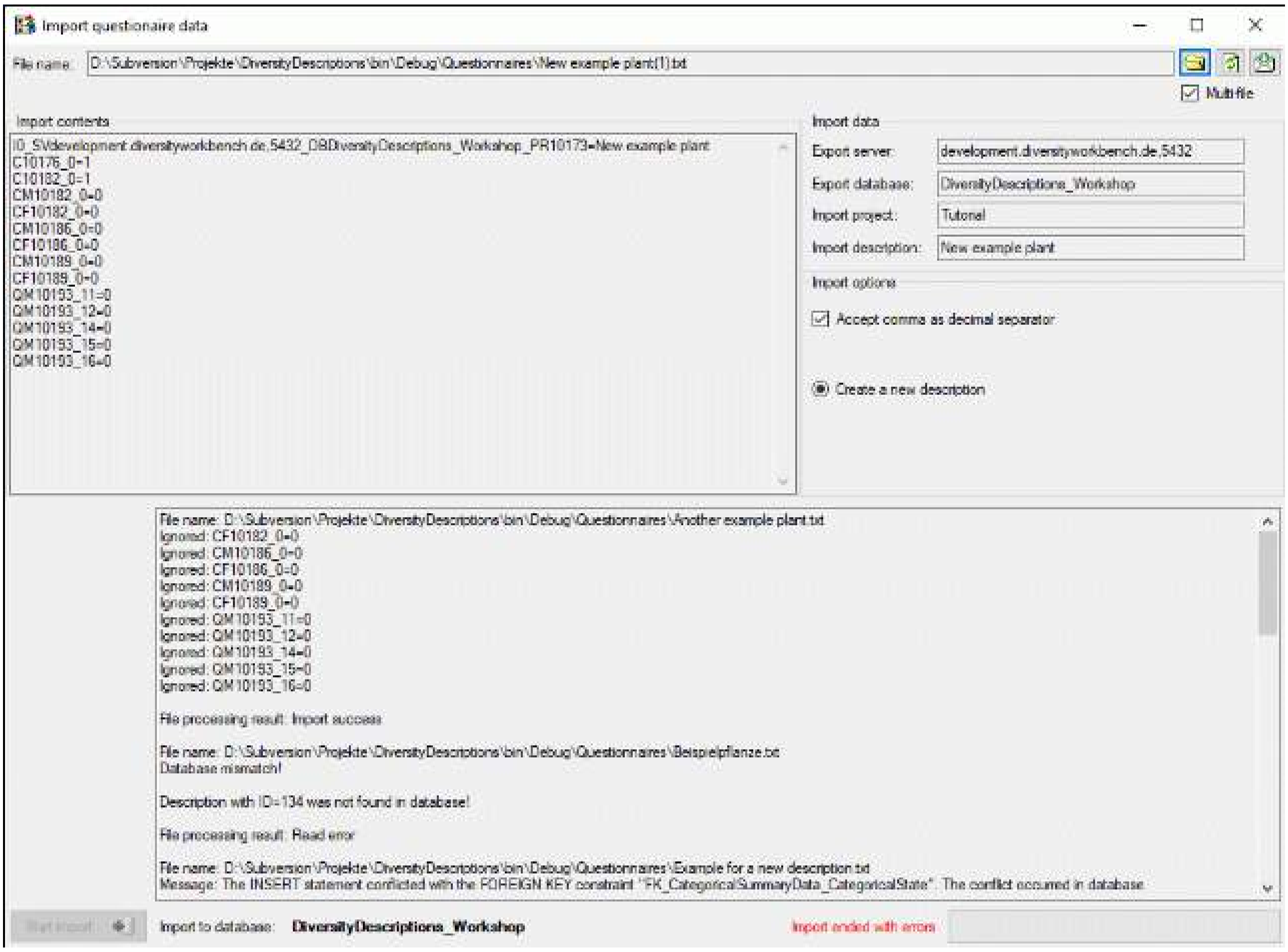
☑ Accept comma as decimal separator

○ Update description after bakup
● Create a new description
○ Update description in database

```
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Another example plant.txt
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Beispielpflanze.txt
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Example for a new description.txt
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Example plant(1).txt
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Neue Beschreibung.txt
D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\New example plant(1).txt
```

Import to database: **DiversityDescriptions_Workshop**

After checking the **Import options** click on the **Start import** button to start the import. In the lower part of the window you find the processing result for each selected file (see image below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\New example plant(1).txt

☑ Multi-file

Import contents

```
ID_SVdevelopment.diversityworkbench.de,5432_DBDiversityDescriptions_Workshop_PR10173=New example plant
C10176_0=1
C10182_0=1
CM10182_0=0
CF10182_0=0
CM10186_0=0
CF10186_0=0
CM10189_0=0
CF10189_0=0
QM10193_11=0
QM10193_12=0
QM10193_14=0
QM10193_15=0
QM10193_16=0
```

Import data

Export server: development.diversityworkbench.de,5432
Export database: DiversityDescriptions_Workshop
Import project: Tutorial
Import description: New example plant

Import options

☑ Accept comma as decimal separator

● Create a new description

```
File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Another example plant.txt
Ignored: CF10182_0=0
Ignored: CM10186_0=0
Ignored: CF10186_0=0
Ignored: CM10189_0=0
Ignored: CF10189_0=0
Ignored: QM10193_11=0
Ignored: QM10193_12=0
Ignored: QM10193_14=0
Ignored: QM10193_15=0
Ignored: QM10193_16=0

File processing result: Import success

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Beispielpflanze.txt
Database mismatch!

Description with ID=134 was not found in database!

File processing result: Read error

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Questionnaires\Example for a new description.txt
Message: The INSERT statement conflicted with the FOREIGN KEY constraint "FK_CategoricalSummaryData_CategoricalState". The conflict occurred in database
```

Import to database: **DiversityDescriptions_Workshop**

Import ended with errors

Export

There are several export mechanisms:

Matrix wizard: Export descriptor and description data as tabulator separated text file generate an import schema for the matrix import wizard.

List export: Export data as tabulator-separated text file.

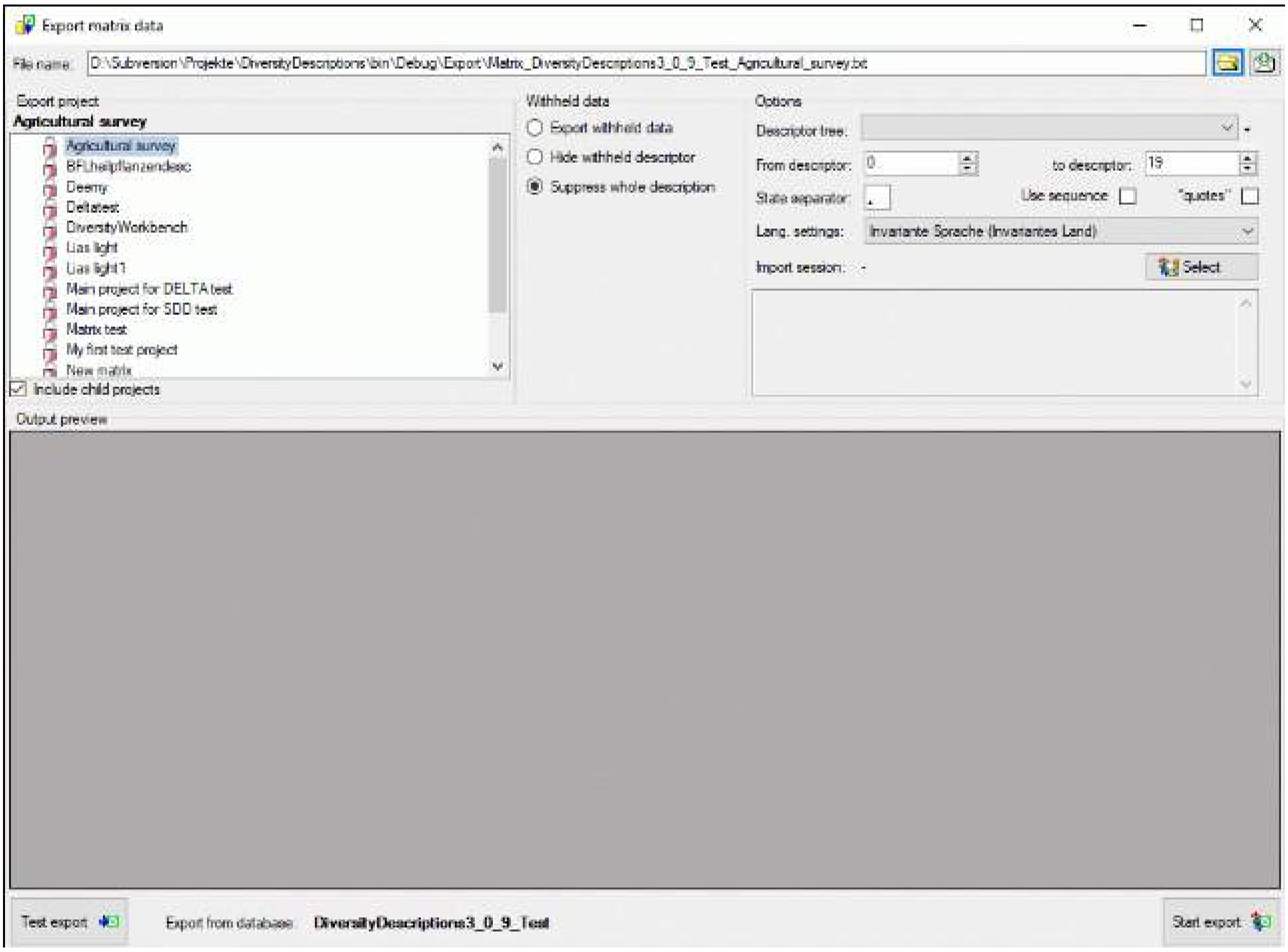
Structured export: Export data as structued data file, e.g. XML according to the SDD schema 1.1 rev 5 or DELTA text file.

Export questionaires: Export description data of a project or from a quey list as HTML forms.

CSV export: Export data in a tab separated format for external analysis.

Matrix export wizard for tab separated lists

With this form you can export the descriptor and description data from the database to a tabulator separated text file. The output includes the database keys. Furthermore you have the option to create rsp. update import mapping data and generate an matrix import schema. Therefore you may correct the data, e.g. by using a spreadsheet program and re-import the changes by using the matrix import wizard. Choose **Data -> Export -> Matrix wizard ...** from the menu to open the window for the export.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\Matrix_DiversityDescriptions3_0_9_Test_Agricultural_survey.txt

Export project
Agricultural survey

- Agricultural survey
- BFLheilpflanzendesc
- Deemy
- Deltatest
- DiversityWorkbench
- Lias light
- Lias light1
- Main project for DELTA test
- Main project for SDD test
- Matrix test
- My first test project
- New matrix

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options
Descriptor tree:
From descriptor: 0
to descriptor: 19
State separator: ,
Use sequence ☐
"quotes" ☐
Lang. settings: Invariante Sprache (Invariantes Land)
Import session: -

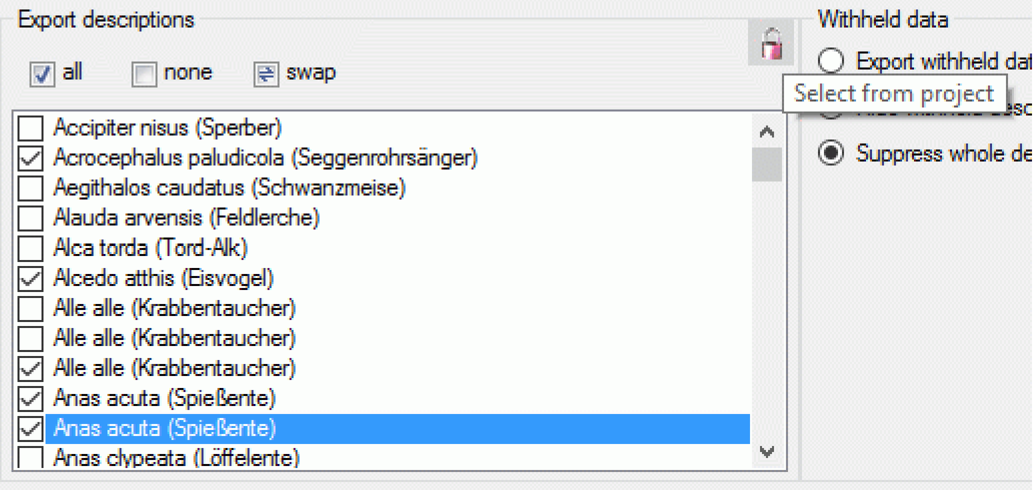
Export from database: **DiversityDescriptions3_0_9_Test**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked. You may pass a description list to the form by starting a query in mode "Edit descriptions". Now you have the option to select single descriptions for export. In this case the **Export project** section shows the button 📄 to switch to the list view (see below).

Libellen
Pflanzen
Pilze
Schmetterlinge
Vögel

☑ Include child projects

In the **Export descriptions** section you find all description titles that have been passed to the export form (see below). You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the ⇄ **swap** button. By clicking the button 🔒you will return to the **Export project** view.



☐ Accipiter nisus (Sperber)
☑ Acrocephalus paludicola (Seggenrohrsänger)
☐ Aegithalos caudatus (Schwanzmeise)
☐ Alauda arvensis (Feldlerche)
☐ Alca torda (Tord-Alk)
☑ Alcedo atthis (Eisvogel)
☐ Alle alle (Krabbentaucher)
☐ Alle alle (Krabbentaucher)
☑ Alle alle (Krabbentaucher)
☑ Anas acuta (Spießente)
☑ Anas acuta (Spießente)
☐ Anas clypeata (Löffelente)

The **Withheld data** section allows control over export of datasets that contain entries with data status "Data withheld". Option **Supress whole description** (default) excludes all descriptions form export where at least on descriptor is marked with "Data withheld". Option **Hide withheld descriptor** excludes only the corresponding descriptor data from the description. Option **Export withheld data** does not exclude any data from export.

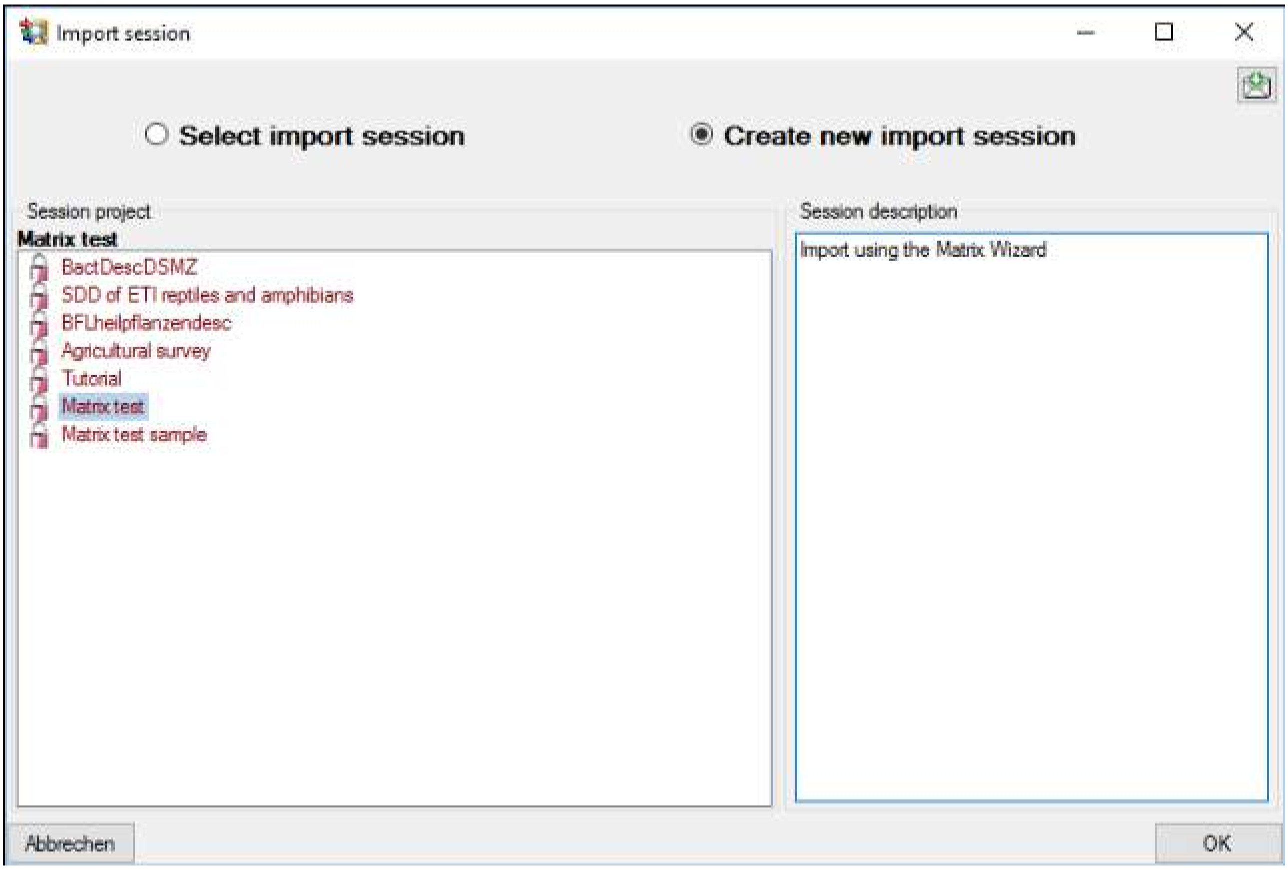
The **Options** section allows the selection of the **Descriptor tree:** and descriptor sequence number bounds (**From descriptor:** and **to descriptor:**) for restriction of output table columns.

If you select option **Use sequence**, the descriptor state sequence numbers will be inserted into the output table instead of the state names. These sequence numbers will be inserted into the selected import session (see below) for a later re-import of the data. If you export the descriptive data to edit them with a spreadsheet tool, e.g. Microsoft Excel, you have to identify the active categorical states by their sequence number.

To include all export data in quotes, check option **"quotes"**. By specifying the **State separator:** (default ,) you determine how multiple categorical state values will be concatenated in the table cells. By changing the selected **Lang. settings:** you may adapt the output of floating point numbers or date and time fields to your needs.

Import session

The section **Import session:** is relevant if you want to edit the description data in a separate spreadsheet programme and re-import the edited data using the Matrix Import Wizard. To select an import session cick on button **Select** and a window as shown below will be opened. You may either select an existing import session, which will be updated with the exported data, or create a new one.

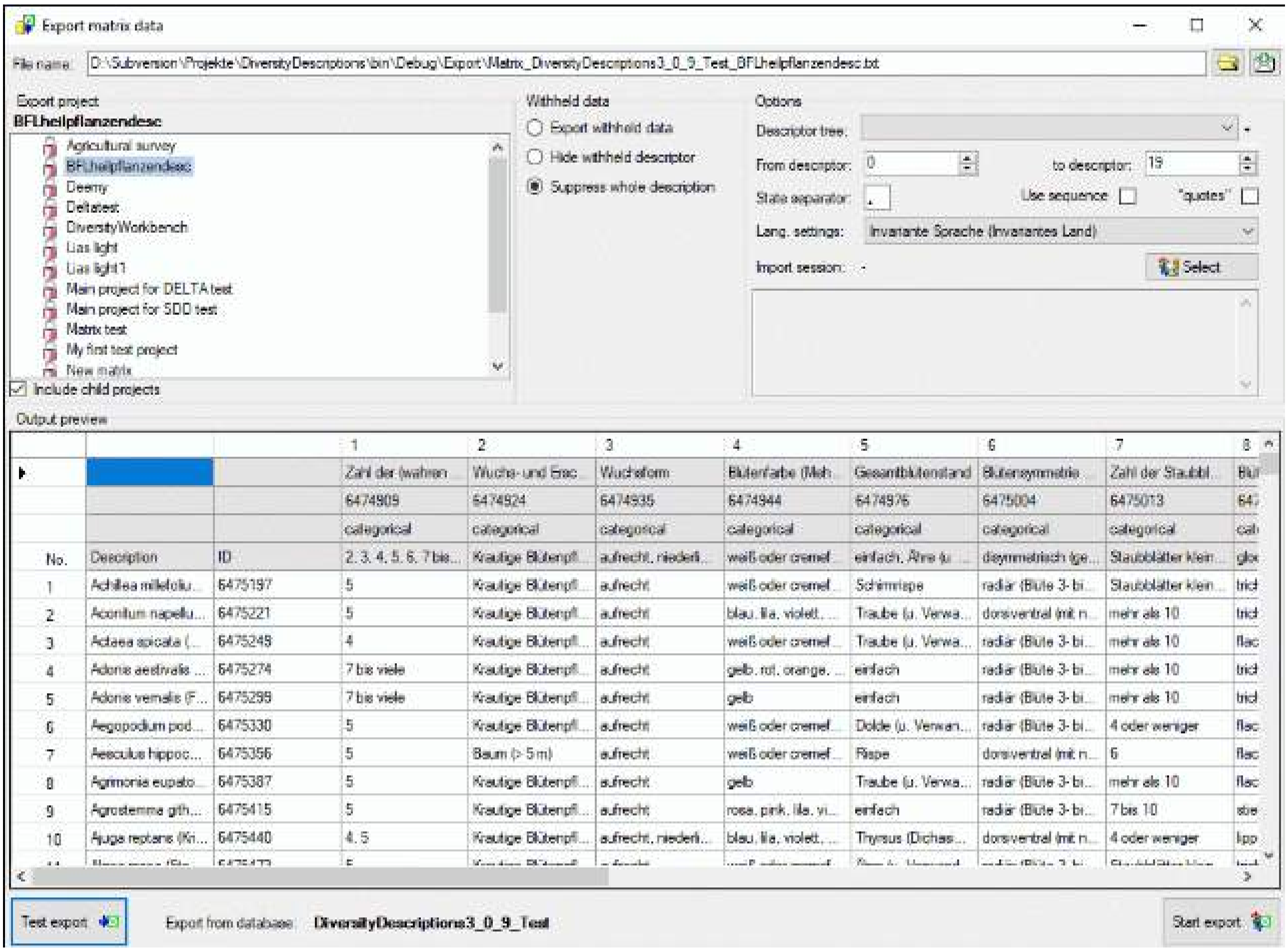


Import using the Matrix Wizard

During generation of the matrix data file the relevant data for re-import will be stored in the selected import session. Additionally an xml import schema file will be generated as **<resources directory>\Export\Matrix_<Database name>_<Project>_Schema.xml**. If you do not require the data for re-import, simply do not select an import session or click on button to cancel an existing selection.

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Export\Matrix_<Database name>_<Project>.txt**. This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\Matrix_DiversityDescriptions3_0_9_Test_BFLheilpflanzendesc.txt

Export project
BFLheilpflanzendesc

- Agricultural survey
- BFLheilpflanzendesc
- Deemy
- Deltatest
- DiversityWorkbench
- Lias light
- Lias light1
- Main project for DELTA test
- Main project for SDD test
- Matrix test
- My first test project
- New matrix

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options
Descriptor tree:
From descriptor: 0
to descriptor: 19
State separator: ,
Use sequence ☐
"quotes" ☐
Lang. settings: Invariante Sprache (Invariantes Land)
Import session: -

Output preview

			1	2	3	4	5	6	7	8
			Zahl der (wahren ...	Wuchs- und Ersc...	Wuchsform	Blütenfarbe (Meh...	Gesamtblütenstand	Blütensymmetrie ...	Zahl der Staubbl...	Blü
			6474909	6474924	6474935	6474944	6474976	6475004	6475013	64
			categorical	categorical	categorical	categorical	categorical	categorical	categorical	cat
No.	Description	ID	2, 3, 4, 5, 6, 7 bis...	Krautige Blütenpfl...	aufrecht, niederli...	weiß oder cremef...	einfach, Ähre (u. ...	disymmetrisch (ge...	Staubblätter klein...	glo
1	Achillea millefoliu...	6475197	5	Krautige Blütenpfl...	aufrecht	weiß oder cremef...	Schirmrispe	radiär (Blüte 3- bi...	Staubblätter klein...	trich
2	Aconitum napellu...	6475221	5	Krautige Blütenpfl...	aufrecht	blau, lila, violett, ...	Traube (u. Verwa...	dorsiventral (mit n...	mehr als 10	trich
3	Actaea spicata (...	6475248	4	Krautige Blütenpfl...	aufrecht	weiß oder cremef...	Traube (u. Verwa...	radiär (Blüte 3- bi...	mehr als 10	flac
4	Adonis aestivalis ...	6475274	7 bis viele	Krautige Blütenpfl...	aufrecht	gelb, rot, orange, ...	einfach	radiär (Blüte 3- bi...	mehr als 10	trich
5	Adonis vernalis (F...	6475299	7 bis viele	Krautige Blütenpfl...	aufrecht	gelb	einfach	radiär (Blüte 3- bi...	mehr als 10	trich
6	Aegopodium pod...	6475330	5	Krautige Blütenpfl...	aufrecht	weiß oder cremef...	Dolde (u. Verwan...	radiär (Blüte 3- bi...	4 oder weniger	flac
7	Aesculus hippoc...	6475356	5	Baum (> 5 m)	aufrecht	weiß oder cremef...	Rispe	dorsiventral (mit n...	6	flac
8	Agrimonia eupato...	6475387	5	Krautige Blütenpfl...	aufrecht	gelb	Traube (u. Verwa...	radiär (Blüte 3- bi...	mehr als 10	flac
9	Agrostemma gith...	6475415	5	Krautige Blütenpfl...	aufrecht	rosa, pink, lila, vi...	einfach	radiär (Blüte 3- bi...	7 bis 10	ste
10	Ajuga reptans (Kri...	6475440	4, 5	Krautige Blütenpfl...	aufrecht, niederli...	blau, lila, violett, ...	Thyrsus (Dichas...	dorsiventral (mit n...	4 oder weniger	lipp

Export from database: **DiversityDescriptions3_0_9_Test**

To check the export, click on the **Test export** button. In the **Output preview** data grid the first few lines will be displayed (see picture above). To generate the table file press the **Start export** button. During test and export the icon of the button changes to STOP and you may abort processing by clicking the button.

List export

There are several exports for tabulator-separated text files:

Export descriptors list: Export descriptor data as tabulator separated text file.

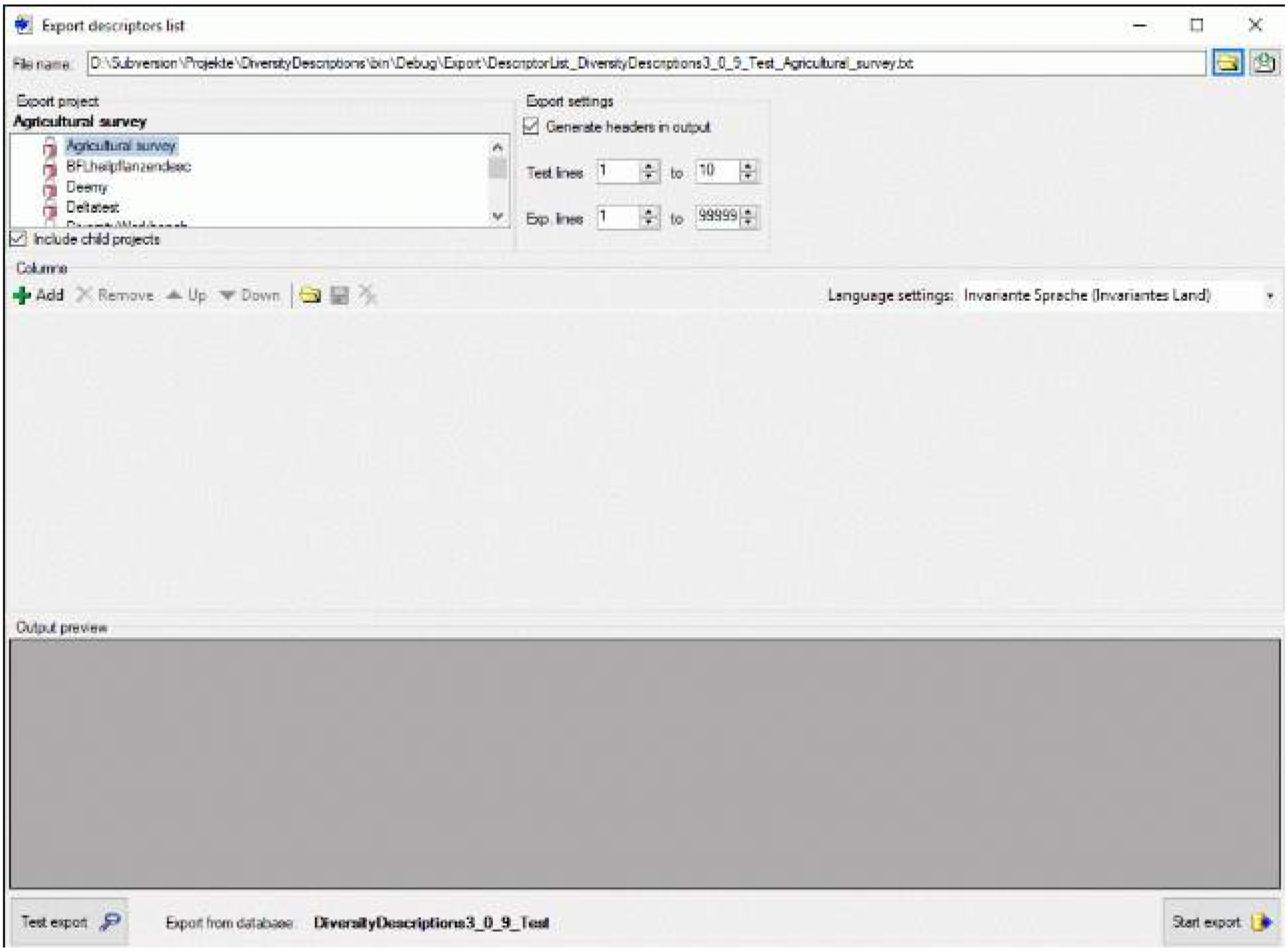
Export descriptions list: Export description data as tabulator separated text file.

Export sample data list: Export sample data as tabulator separated text file.

Export resource data list: Export resource data as tabulator separated text file for data review and possible re-import of modified data.

Export Descriptors List

With this form you can export descriptor data from the database to an tabulator separated text file. Choose **Data -> Export -> Export lists -> Descriptors list ...** from the menu to open the window for the export.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptorList_DiversityDescriptions3_0_9_Test_Agricultural_survey.txt

Export project: **Agricultural survey**
- Agricultural survey
- BFLheilpflanzendesc
- Deemy
- Deltatest

☑ Include child projects

Export settings
☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

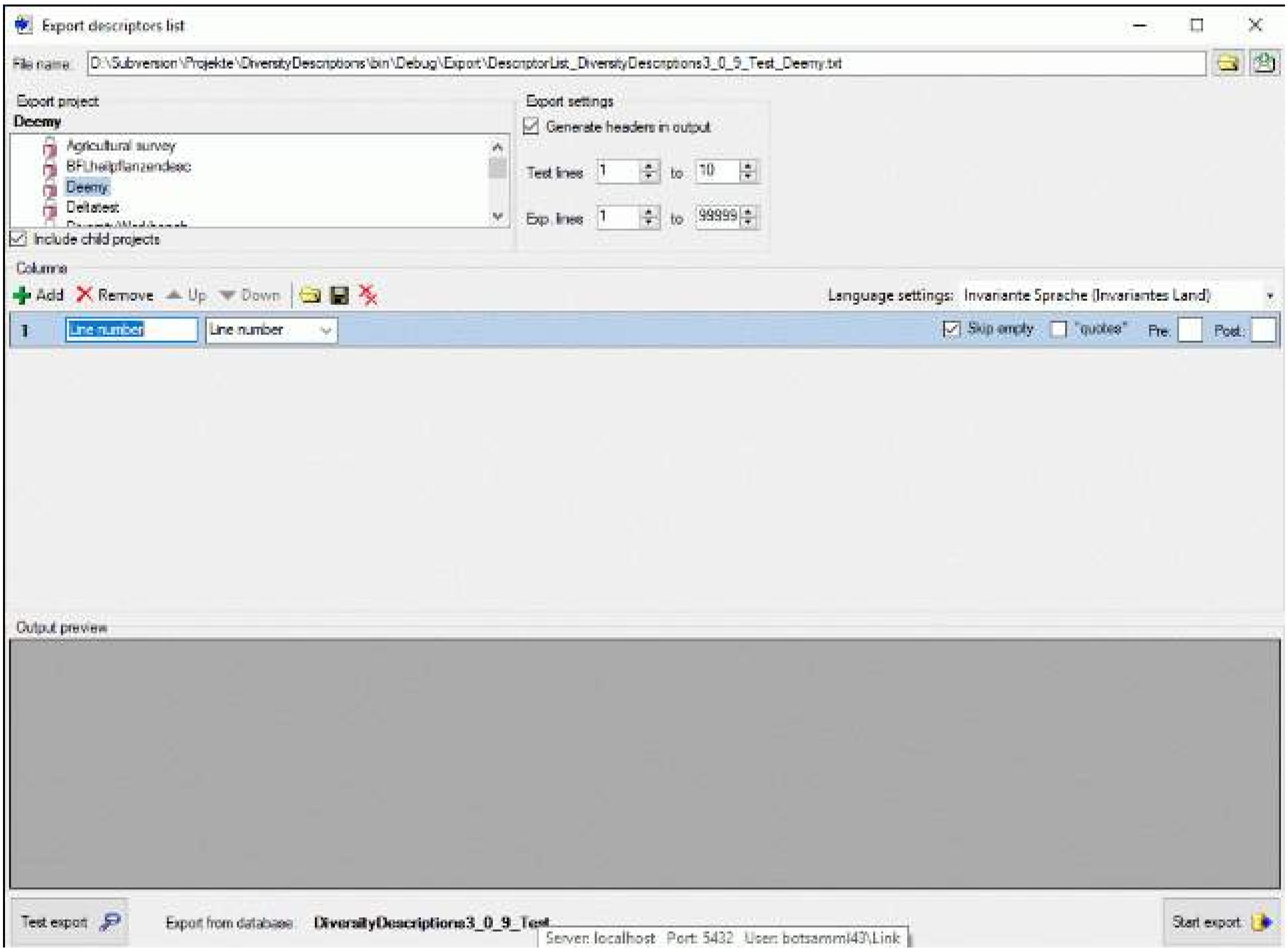
Export from database: **DiversityDescriptions3_0_9_Test**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked.

The **Export settings** allows the inclusion of a header line in the output by checking the option **Generate headers in output**. Additionally the lines displayed in the **Test output** section may be selected by specifying the first and last line number in **Test lines [start] to [end]**. For the generated output you may adjust the lines that shall be exported in **Exp. lines [start] to [end]**. For the end line a maximum value of **99999** may be entered, which means export of the whole data beginning from the start line.

Columns

To generate a list output, you have to determine the data columns that shall be present in the descriptors list. To include a new column press the **Add** button in the tool strip of the **Columns** section. A control representing a single output column will be added at the end of the column list (see picture below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptorList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project
Deemy
Agricultural survey
BFLheilpflanzendesc
Deemy
Deltatest
☑ Include child projects

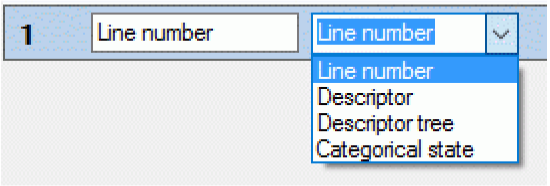
Export settings
☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Columns
Language settings: Invariante Sprache (Invariantes Land)
1 Line number Line number ☑ Skip empty ☐ "quotes" Pre: Post:

Output preview

Export from database: **DiversityDescriptions3_0_9_Test**
Server: localhost Port: 5432 User: botsamml43\Link

The **Columns** control shows the column number, a text box for the column header (title) and the source selector (see below).

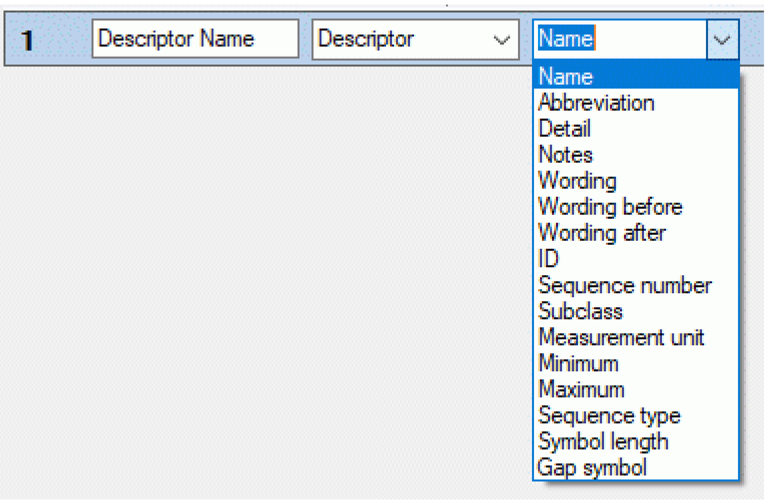


1 Line number Line number

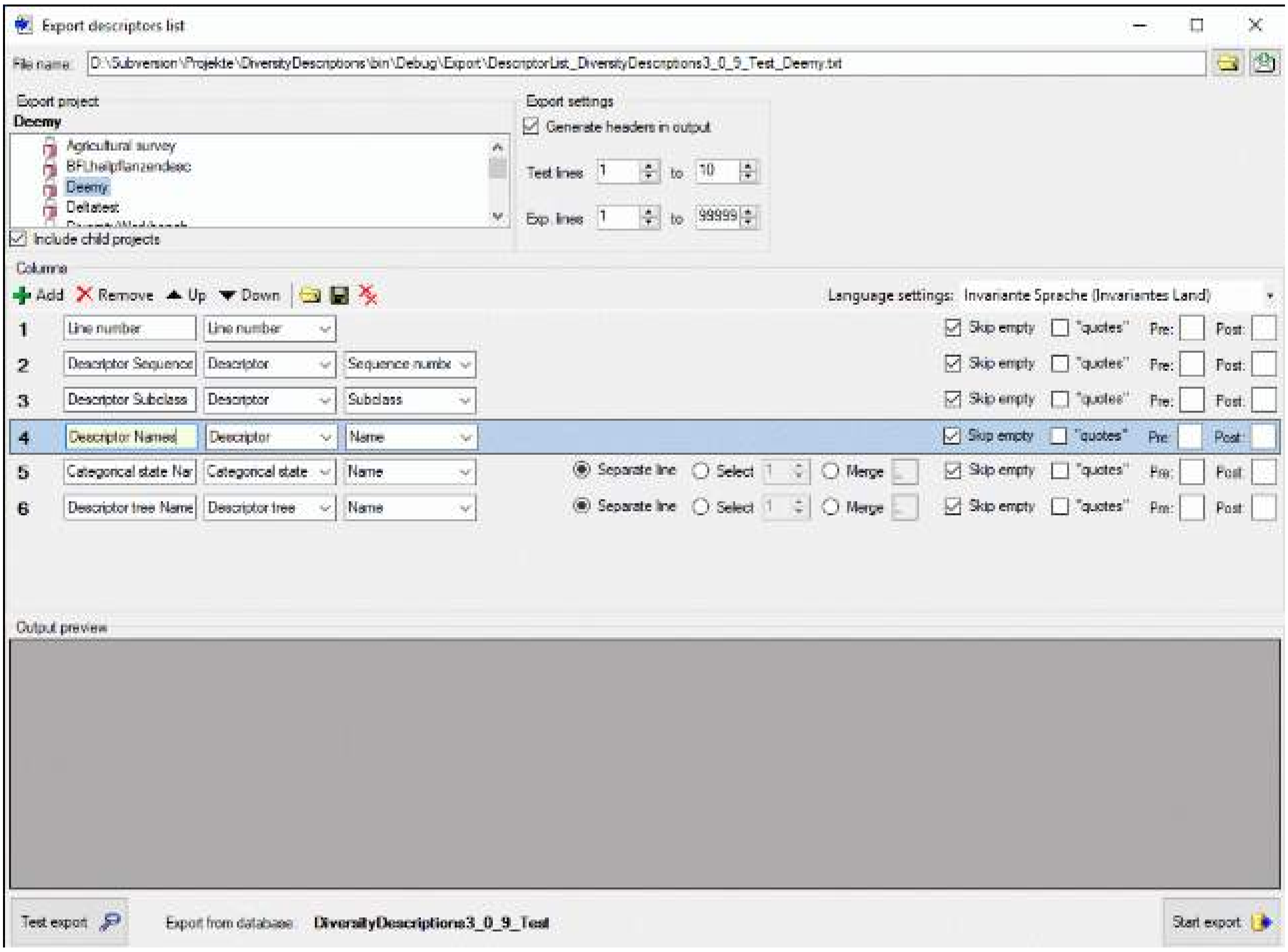
As source you may select one of the following values:

Line number	Number of the data line in the output file
Descriptor	Descriptor data, e.g. name of the descriptor
Descriptor tree	Assigned descriptor tree(s)
Categorical state	Categorical state(s) of a certain descriptor

Depending on the selected data source one or more additional selection boxes will appear in the descriptor column control. The target (see picture below) selects the filed from the database that shall be inserted.


1 Descriptor Name | Descriptor | Name

As long as you did not enter a value for the column header, a reasonable suggestion depending on the selected values will be inserted. You may enter a different column header, then the background color changes to light yellow to indicate that it will not be updated automatically anymore (see picture below, column 4). Double-click on the header to open a separate edit window.


Export descriptors list

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptorList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project: Deemy

Export settings: ☑ Generate headers in output; Test lines 1 to 10; Exp. lines 1 to 99999

☑ Include child projects

Language settings: Invariante Sprache (Invariantes Land)

1 Line number | Line number | ☑ Skip empty ☐ "quotes" Pre: Post:
2 Descriptor Sequence | Descriptor | Sequence numbe | ☑ Skip empty ☐ "quotes" Pre: Post:
3 Descriptor Subclass | Descriptor | Subclass | ☑ Skip empty ☐ "quotes" Pre: Post:
4 Descriptor Names | Descriptor | Name | ☑ Skip empty ☐ "quotes" Pre: Post:
5 Categorical state Nar | Categorical state | Name | ● Separate line ○ Select 1 ○ Merge | ☑ Skip empty ☐ "quotes" Pre: Post:
6 Descriptor tree Name | Descriptor tree | Name | ● Separate line ○ Select 1 ○ Merge | ☑ Skip empty ☐ "quotes" Pre: Post:

Export from database: DiversityDescriptions3_0_9_Test

Output formatting is controlled with check box **"quotes"** that includes the whole output text in quotes and text boxes **Pre:** and **Post:**, which allow inclusion of the values in prefix and postfix strings. By selecting the check box **Skip empty** a blank output will be inserted instead of the specified prefix and postfix strings or quotes, if no value is present. If for a column multiple values may be present, e.g. in case of categorical descriptors where several categorical states might be present, there is the choice of inserting additional lines for multiple values (**Separate line**), selecting a single value (**Select**) or merging the values to a single output string (**Merge**). For option **Select** you have specify if the first, second or other values shall be selected. For option Merge you may specify a separator string that shall be inserted between two values (default is **;**). To open a separate edit window for the **Pre**, **Post** or **Merge values** strings, e.g. because a longer value shall be entered, double-click on the correspondent text box.

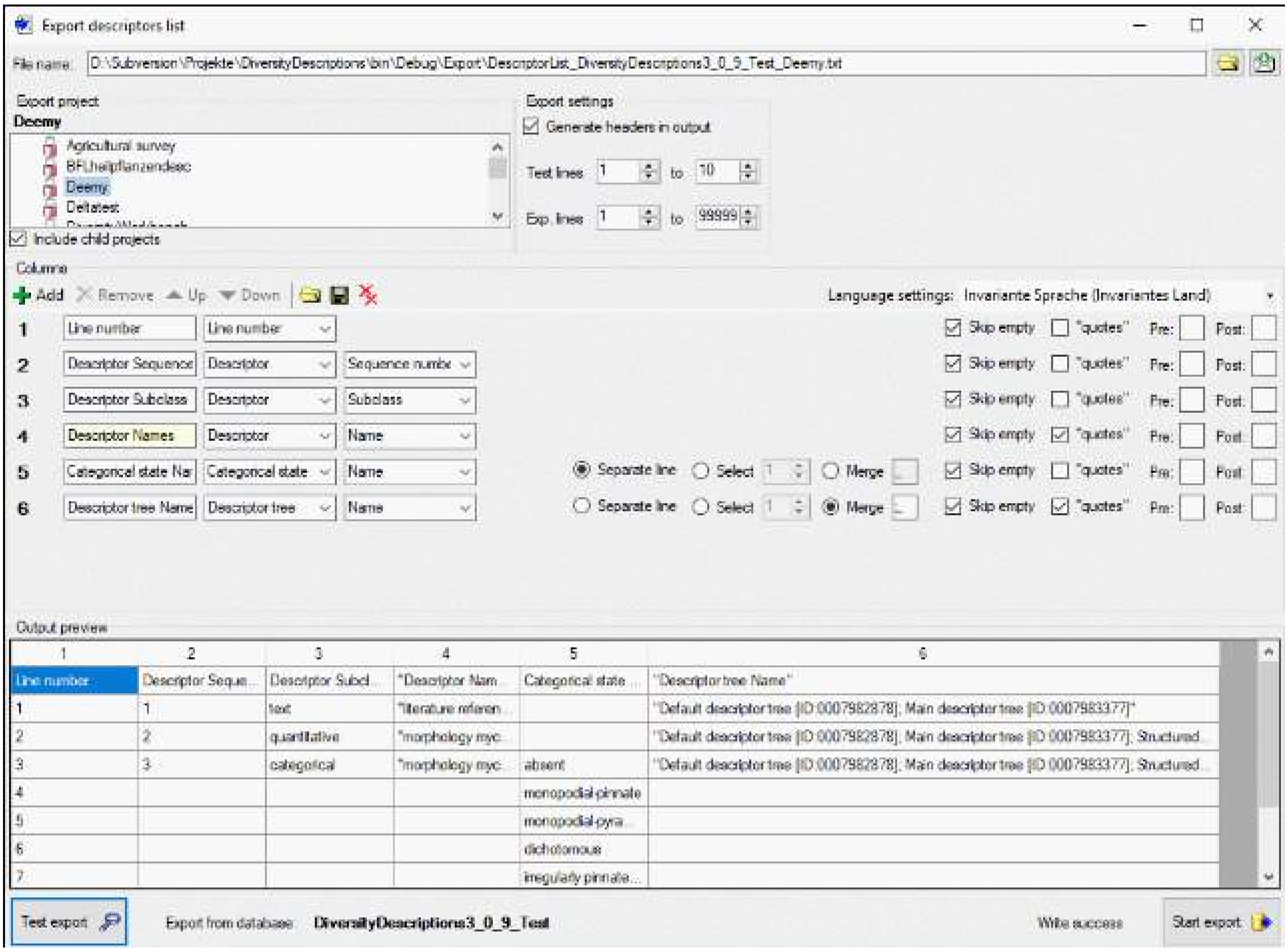
Any selected column may be shifted to another position using the ▲**Up** and ▼**Down** buttons or deleted with the ✕**Remove** button of the tool strip. With button ✕you may delete all columns. The complete export schema may be saved into an XML file using the button , which opens a dialog window to enter the file name and location. By default the schema file name is generated as:

<resources directory>\ExportSchema\DescriptiorList_<Database name>_<Project>.xml

The XML schema file includes information concerning the database, the project and the output columns. By pressing the button in the **Columns** section, a schema file can be opened.

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Export\DescriptorList_<Database name>_<Project>.txt**. This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name.



Export descriptors list

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptorList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project
Deemy
Agricultural survey
BFLheilpflanzendesc
Deemy
Deltatest

☑ Include child projects

Export settings
☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Columns

Language settings: Invariante Sprache (Invariantes Land)

1 Line number | Line number | ☑ Skip empty ☐ "quotes" Pre: Post:
2 Descriptor Sequence | Descriptor | Sequence numbe | ☑ Skip empty ☐ "quotes" Pre: Post:
3 Descriptor Subclass | Descriptor | Subclass | ☑ Skip empty ☐ "quotes" Pre: Post:
4 Descriptor Names | Descriptor | Name | ☑ Skip empty ☑ "quotes" Pre: Post:
5 Categorical state Nar | Categorical state | Name | ● Separate line ○ Select 1 ○ Merge | ☑ Skip empty ☐ "quotes" Pre: Post:
6 Descriptor tree Name | Descriptor tree | Name | ○ Separate line ○ Select 1 ● Merge | ☑ Skip empty ☑ "quotes" Pre: Post:

Output preview

1	2	3	4	5	6
Line number	Descriptor Seque...	Descriptor Subcl...	"Descriptor Nam...	Categorical state ...	"Descriptor tree Name"
1	1	text	"literature referen...		"Default descriptor tree [ID:0007982878]; Main descriptor tree [ID:0007983377]"
2	2	quantitative	"morphology myc...		"Default descriptor tree [ID:0007982878]; Main descriptor tree [ID:0007983377]; Structured...
3	3	categorical	"morphology myc...	absent	"Default descriptor tree [ID:0007982878]; Main descriptor tree [ID:0007983377]; Structured...
4				monopodial-pinnate	
5				monopodial-pyra...	
6				dichotomous	
7				irregularly pinnate...	

Export from database **DiversityDescriptions3_0_9_Test**

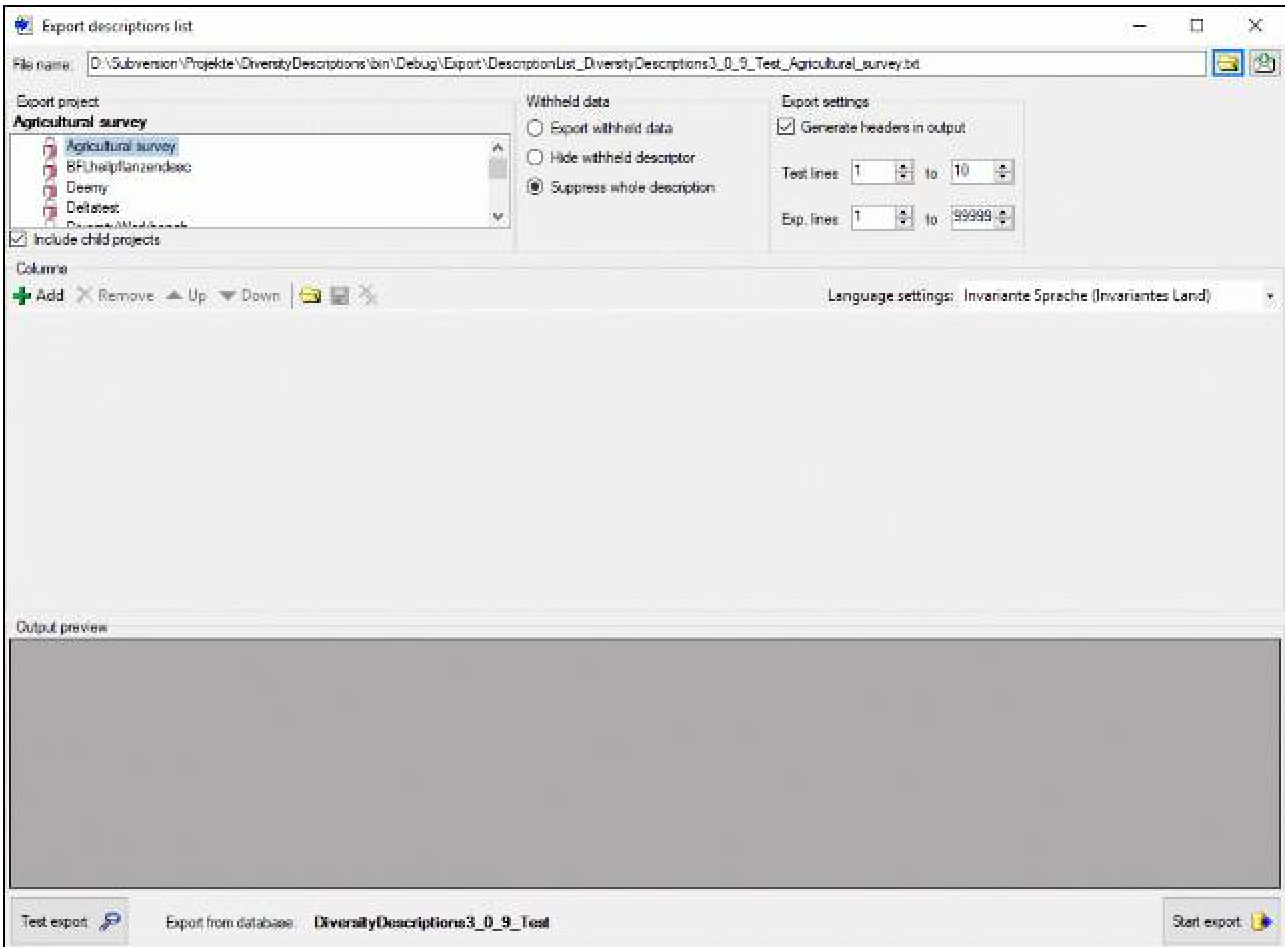
Write success

To check the export, click on the **Test export** button. By changing the selected **Language**

settings: you may adapt the output of floating point numbers or date and time fields to your needs. In the **Output preview** grid view the lines specified in the **Export settings** (**Test lines [start] to [end]**) will be displayed (see picture above). To generate the table file press the **Start export** button. During test and export the icon of the button changes to STOP and you may abort processing by clicking the button.

Export Descriptions List

With this form you can export description data from the database to a tabulator separated text file. Choose **Data -> Export -> Export lists -> Descriptions list ...** from the menu to open the window for the export.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptionList_DiversityDescriptions3_0_9_Test_Agricultural_survey.txt

Export project
Agricultural survey
- Agricultural survey
- BFLheilpflanzendesc
- Deemy
- Deltatest

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Export settings
☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

Export from database: **DiversityDescriptions3_0_9_Test**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked. You may pass a description list to the form by starting a query in mode "Edit descriptions". If all descriptions in the list belong to the same project, you have the option to select single descriptions for export. In this case the **Export project** section shows the button to switch to the list view (see below).

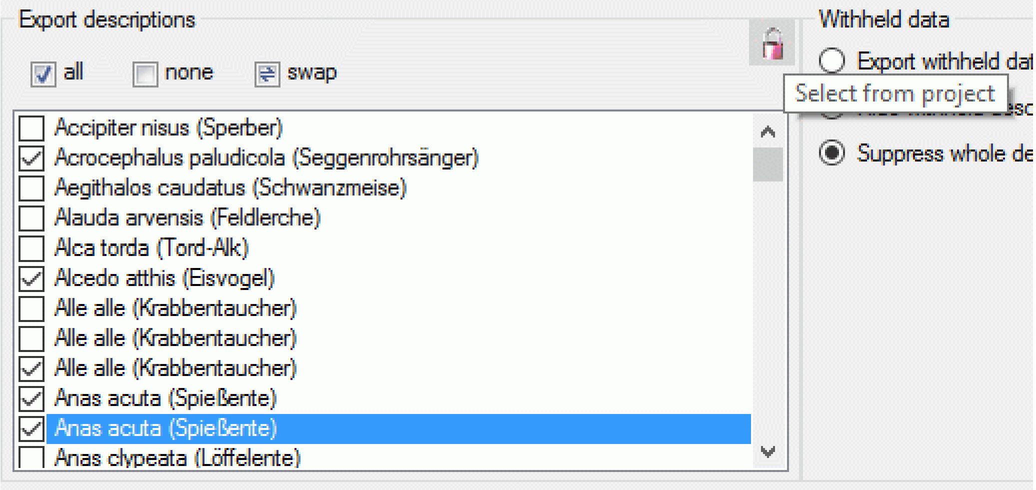
- Libellen
- Pflanzen
- Pilze
- Schmetterlinge
- Vögel

○ Export withhe

● Suppress wh

☑ Include child projects

In the **Export descriptions** section you find all description titles that have been passed to the export form (see below). You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. By clicking the button you will return to the **Export project** view.



☑ all ☐ none swap

- ☐ Accipiter nisus (Sperber)
- ☑ Acrocephalus paludicola (Seggenrohrsänger)
- ☐ Aegithalos caudatus (Schwanzmeise)
- ☐ Alauda arvensis (Feldlerche)
- ☐ Alca torda (Tord-Alk)
- ☑ Alcedo atthis (Eisvogel)
- ☐ Alle alle (Krabbentaucher)
- ☐ Alle alle (Krabbentaucher)
- ☑ Alle alle (Krabbentaucher)
- ☑ Anas acuta (Spießente)
- ☑ Anas acuta (Spießente)
- ☐ Anas clypeata (Löffelente)

○ Export withheld dat

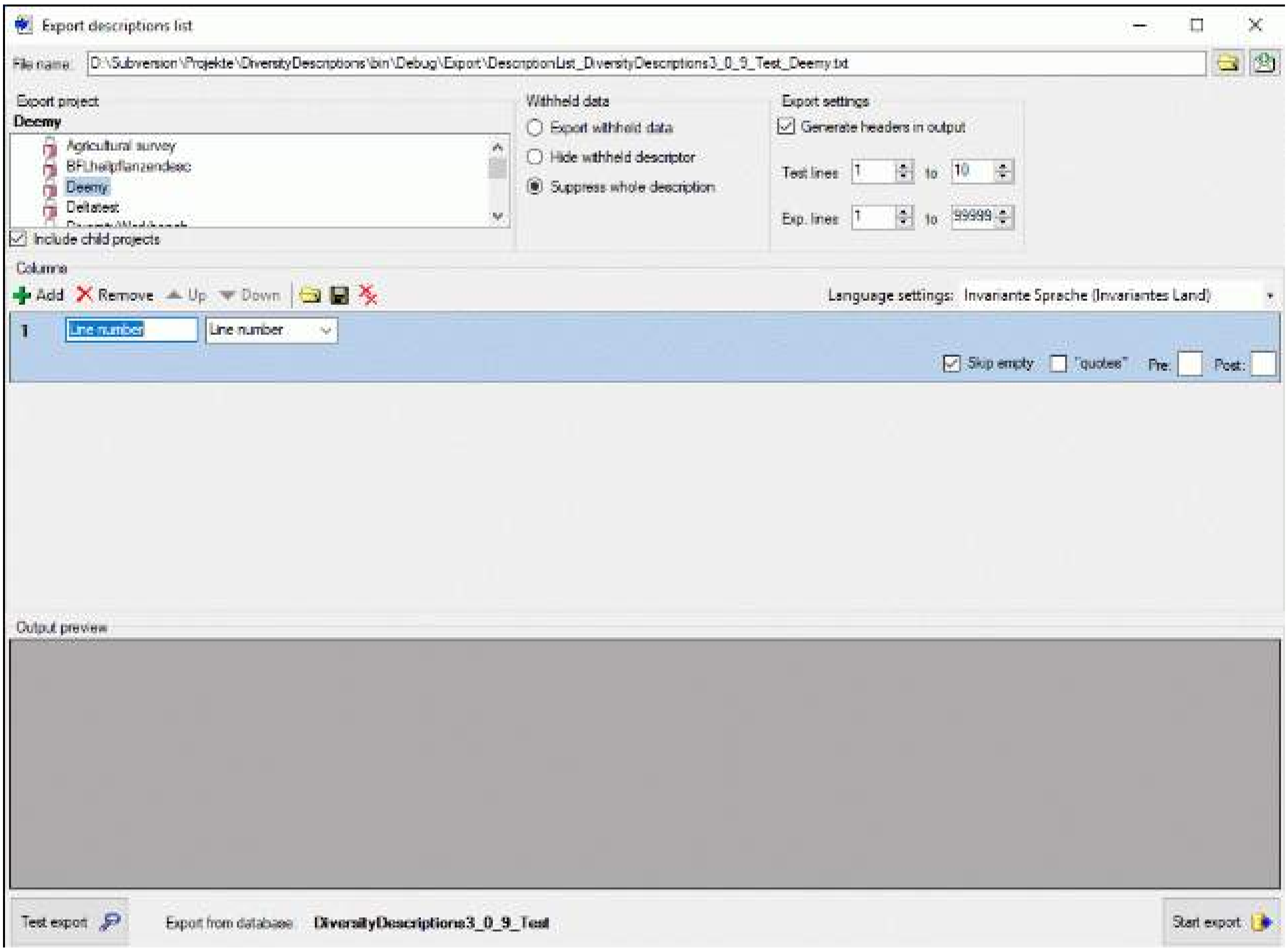
● Suppress whole de

The **Withheld data** section allows control over export of datasets that contain entries with data status "Data withheld". Option **Supress whole description** (default) excludes all descriptions form export where at least on descriptor is marked with "Data withheld". Option **Hide withheld descriptor** excludes only the corresponding descriptor data from the description. Option **Export withheld data** does not exclude any data from export.

The **Export settings** allows the inclusion of a header line in the output by checking the option **Generate headers in output**. Additionally the lines displayed in the **Test output** section may be selected by specifying the first and last line number in **Test lines [start] to [end]**. For the generated output you may adjust the lines that shall be exported in **Exp. lines [start] to [end]**. For the end line a maximum value of **99999** may be entered, which means export of the whole data beginning from the start line.

Columns

To generate a list output, you have to determine the data columns that shall be present in the descriptions list. To include a new column press the **Add** button in the tool strip of the **Columns** section. A control representing a single output column will be added at the end of the column list (see picture below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptionList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project: Deemy

☑ Include child projects

○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

☑ Generate headers in output

Test lines: 1 to 10

Exp. lines: 1 to 99999

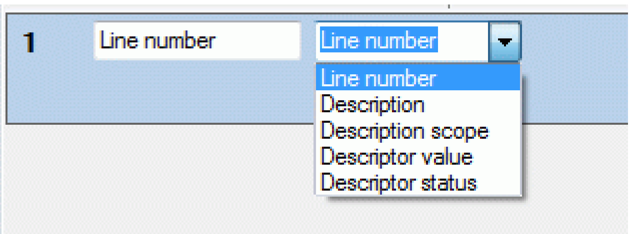
Language settings: Invariante Sprache (Invariantes Land)

1 Line number Line number

☑ Skip empty ☐ "quotes" Pre: Post:

Export from database: DiversityDescriptions3_0_9_Test

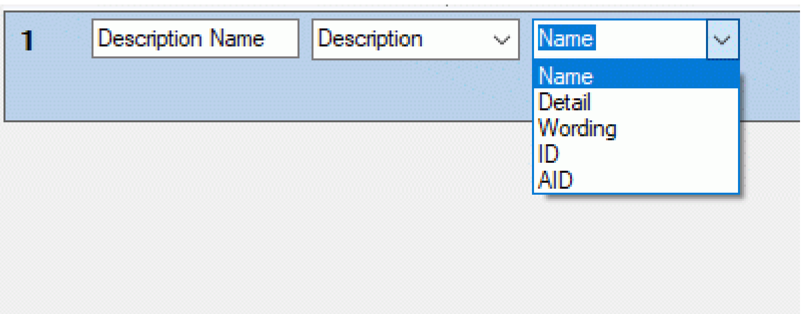
The **Columns** control shows the column number, a text box for the column header (title) and the source selector (see below).



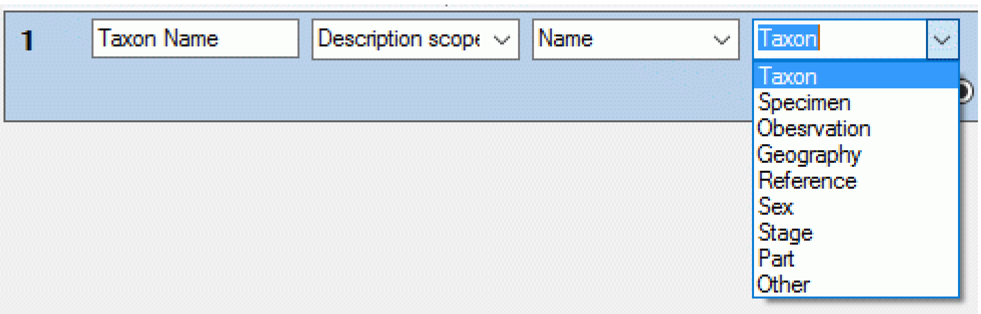
As source you may select one of the following values:

Line number	Number of the data line in the output file
Description	Description data, e.g. name of the description entry
Description scope	Description scope data, e.g. taxon, specimen or sex
Descriptor value	Value(s) of a certain descriptor
Descriptor status	Data status of a certain descriptor

Depending on the selected data source one or more additional selection boxes will appear in the description column control. The target (see picture below left) selects the field from the database that shall be inserted. If you select "Description scope" as data source, a selection box for filtering will be inserted to determine the scope category (see picture below right).

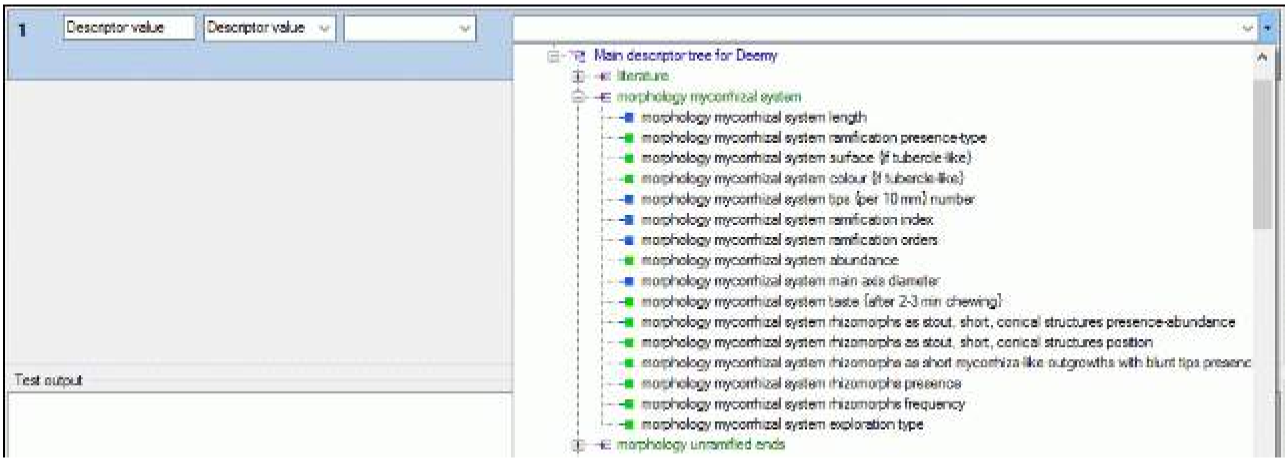


1 Description Name | Description | Name



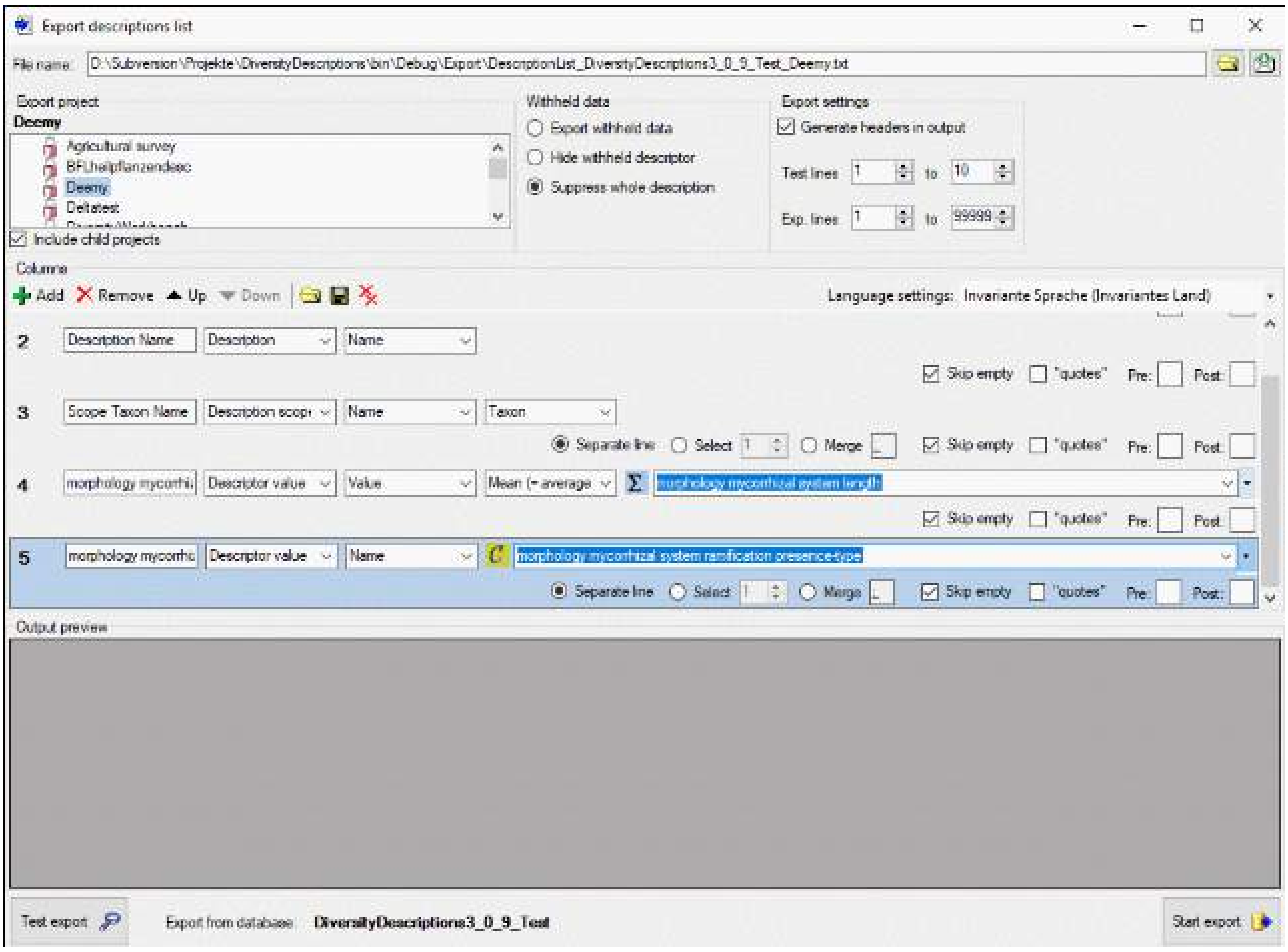
1 Taxon Name | Description scope | Name | Taxon

If you select "Descriptor value" or "Descriptor status" as data source, a selection box for the descriptor will be inserted (see picture below). The descriptor can be selected from an alphabetical list or from the descriptor tree by clicking ▾ . In case of "Descriptor value" the target selection box entries depend on the descriptor type. For categorical descriptors you may select name, abbreviation, detail, wording, ID or notes of the categorical states. For quantitative descriptors you may select the value or notes of a specific statistical measure (separate selection box). For text and sequence descriptors you may select the text or notes.



1 Descriptor value | Descriptor value

As long as you did not enter a value for the column header, a reasonable suggestion depending on the selected values will be inserted. You may enter a different column header, then the background color changes to light yellow to indicate that it will not be updated automatically anymore (see picture below, columns 4 and 5). Double-click on the header to open a separate edit window.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptionList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project: **Deemy**

☑ Include child projects

○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

2 Description Name | Description | Name — ☑ Skip empty ☐ "quotes" Pre: Post:

3 Scope Taxon Name | Description scope | Name | Taxon — ● Separate line ○ Select 1 ○ Merge ☑ Skip empty ☐ "quotes" Pre: Post:

4 morphology mycorrhi | Descriptor value | Value | Mean (= average | morphology mycorrhizal system length — ☑ Skip empty ☐ "quotes" Pre: Post:

5 morphology mycorrhi | Descriptor value | Name | morphology mycorrhizal system ramification presence-type — ● Separate line ○ Select 1 ○ Merge ☑ Skip empty ☐ "quotes" Pre: Post:

Export from database: **DiversityDescriptions3_0_9_Test**

Output formatting is controlled with check box **"quotes"** that includes the whole output text in quotes and text boxes **Pre:** and **Post:**, which allow inclusion of the values in prefix and postfix strings (default is "). By selecting the check box **Skip empty** a blank output will be inserted instead of the specified prefix and postfix strings, if no value is present. If for a column multiple values may be present, e.g. in case of categorical descriptors several categorical states might be present, there is the choice of insterting additional lines for multiple values (**Separate line**), selecting a single value (**Select**) or merging the values to a single output string (**Merge**). For option **Select** you have specify if the first, second or other values shall be selected. For option Merge you may specify a separator string that shall be inserted between two values (default is **;**). To open a separate edit window for the **Pre:**, **Post:** or **Merge** strings, e.g. because a longer value shall be entered, double-click on the correspondent text box.

Any selected column may be shifted to another position using the ▲**Up** and ▼**Down** buttons or deleted with the ✕**Remove** button of the tool strip. With button ✕you may delete all columns. The complete export schema may be saved into an XML file using the button 💾, which opens a dialog window to enter the file name and location. By default the schema file name is generated as:

<resources directory>\ExportSchema\DescriptionList_<Database name>_<Project>.xml

The XML schema file includes information concerning the database, the project, handling of withheld data and the output columns. By pressing the 📂button in the **Columns** section, a schema file can be opened. If the schema does not meet the active database, especially descriptor dependent columns might be erroneous because of unknown values. This is indicated by a red background color (see picture below).

1 Line number | Line number

☑ Skip empty ☐ "quotes" Pre: Post:

2 Description | Description | Name

☑ Skip empty ☐ "quotes" Pre: Post:

3 Taxon | Description scope | Name | Taxon

● Select value 1 ○ Merge values ☑ Skip empty ☐ "quotes" Pre: Post:

4 Body shape | Descriptor value | anatomy chlamydospores colour

☑ Skip empty ☐ "quotes" Pre: Post:

5 Flattening of body | Descriptor value | anatomy chlamydospores colour

☑ Skip empty ☐ "quotes" Pre: Post:

6 Crown shape | Descriptor value | anatomy chlamydospores colour

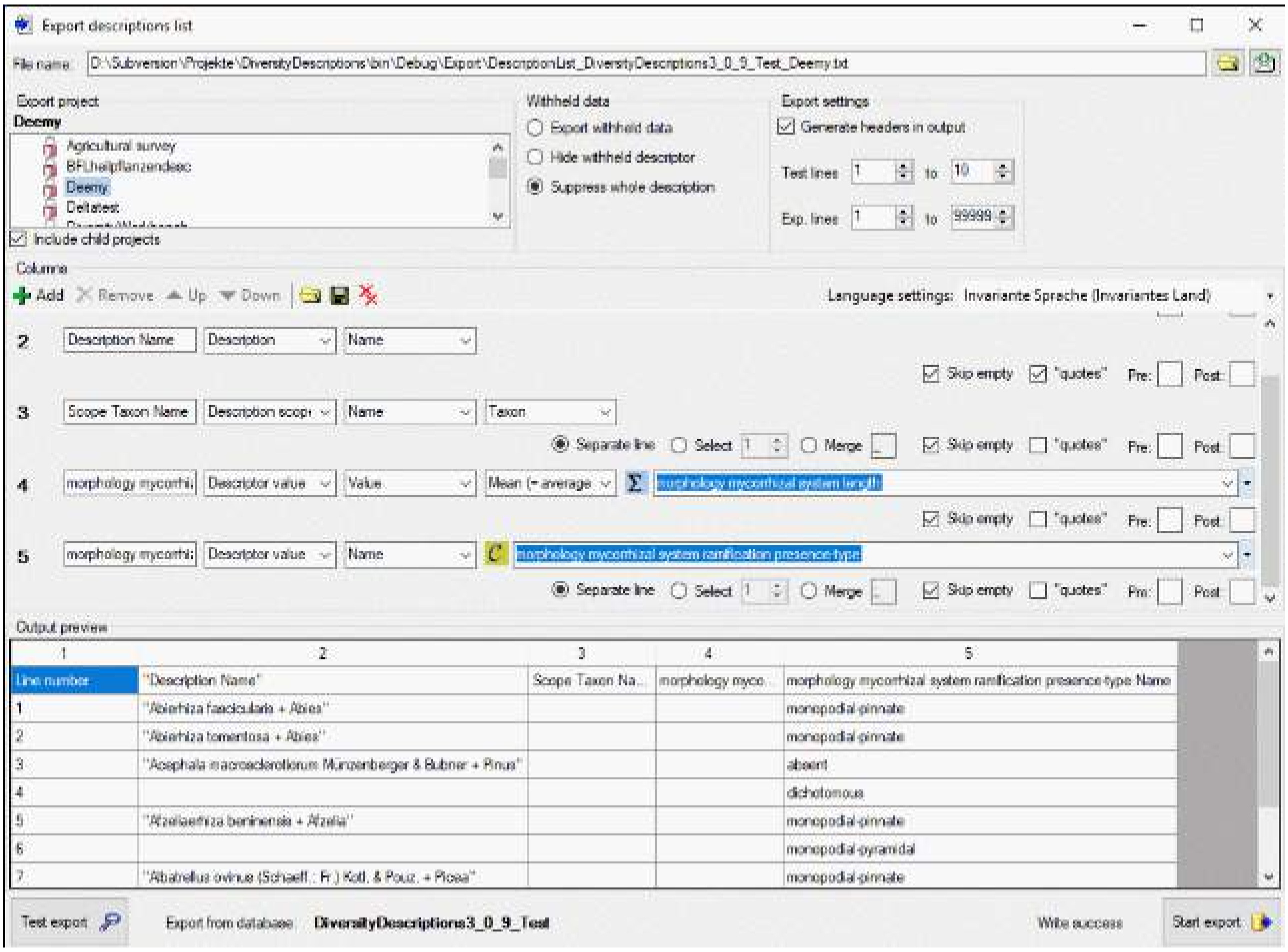
☑ Skip empty ☐ "quotes" Pre: Post:

7 Status of Body shape | Descriptor status | Name | anatomy chlamydospores colour

○ Select value 1 ● Merge values & ☑ Skip empty ☐ "quotes" Pre: Post:

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Export\DescriptionList_<Database name>_<Project>.txt**. This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DescriptionList_DiversityDescriptions3_0_9_Test_Deemy.txt

Export project: Deemy

Agricultural survey
BFLheilpflanzendesc
Deemy
Deltatest

☑ Include child projects

Withheld data:
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Export settings:
☑ Generate headers in output
Test lines 1 to 10
Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

2 Description Name | Description | Name

☑ Skip empty ☑ "quotes" Pre: Post:

3 Scope Taxon Name | Description scope | Name | Taxon

● Separate line ○ Select 1 ○ Merge ☑ Skip empty ☐ "quotes" Pre: Post:

4 morphology mycorrhi | Descriptor value | Value | Mean (= average | Σ morphology mycorrhizal system length

☑ Skip empty ☐ "quotes" Pre: Post:

5 morphology mycorrhi | Descriptor value | Name | C morphology mycorrhizal system ramification presence-type

● Separate line ○ Select 1 ○ Merge ☑ Skip empty ☐ "quotes" Pre: Post:

Output preview

1	2	3	4	5
Line number	"Description Name"	Scope Taxon Na...	morphology myco...	morphology mycorrhizal system ramification presence-type Name
1	"Abierhiza fascicularis + Abies"			monopodial-pinnate
2	"Abierhiza tomentosa + Abies"			monopodial-pinnate
3	"Acephala macrosclerotiorum Münzenberger & Bubner + Pinus"			absent
4				dichotomous
5	"Afzeliaerhiza beninensis + Afzelia"			monopodial-pinnate
6				monopodial-pyramidal
7	"Albatrellus ovinus (Schaeff. : Fr.) Kotl. & Pouz. + Picea"			monopodial-pinnate

Export from database: DiversityDescriptions3_0_9_Test

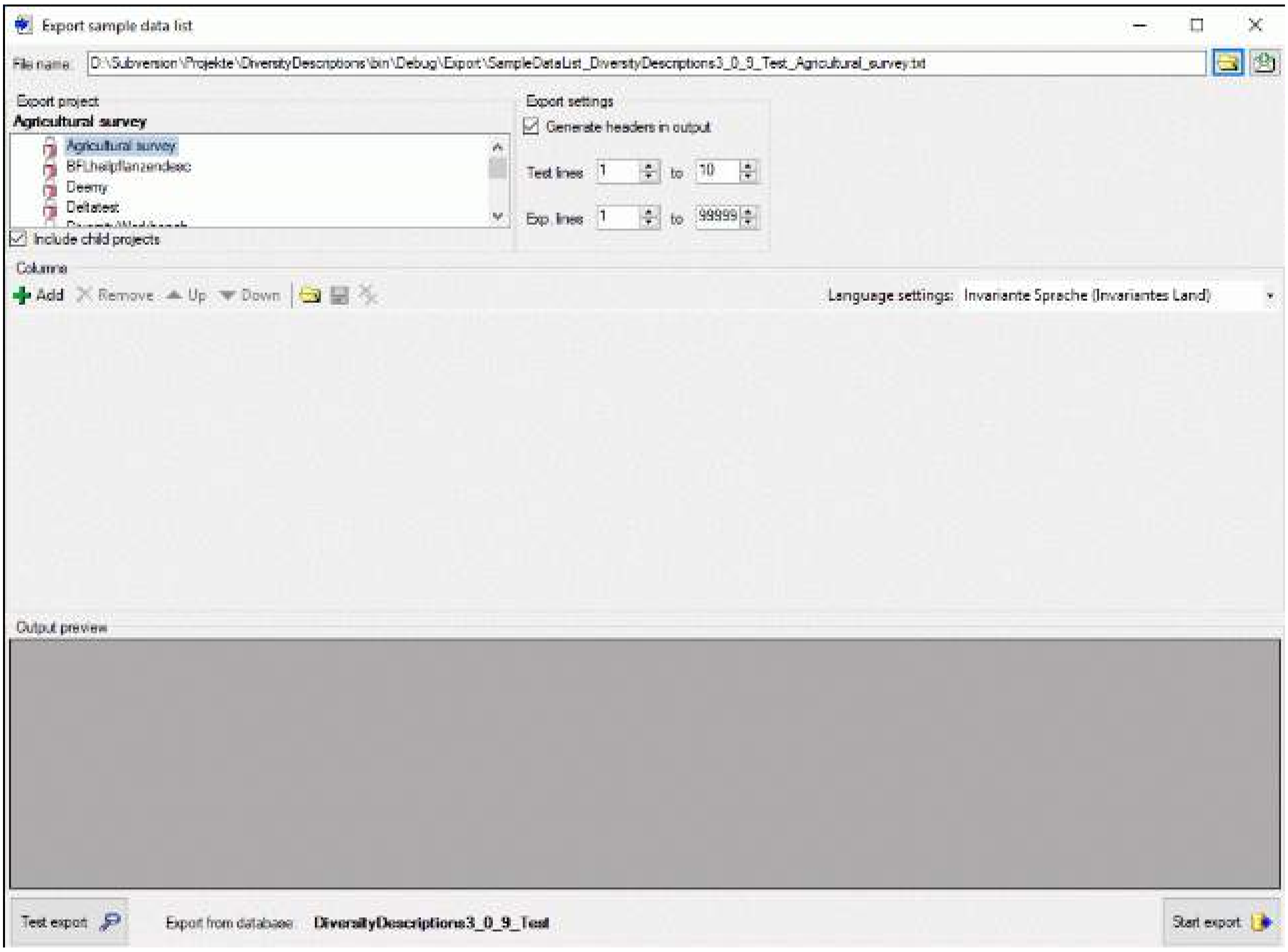
Write success

To check the export, click on the **Test export** button. By changing the selected **Language settings:** you may adapt the output of floating point numbers or date and time fields to your needs. In the **Output preview** grid view the lines specified in the **Export settings** (**Test**

lines [start] to [end]) will be displayed (see picture above). To generate the table file press the **Start export** button. During test and export the icon of the button changes to STOP and you may abort processing by clicking the button.

Export Sample Data List

With this form you can export sample data from the database to a tabulator separated text file. Choose **Data -> Export -> Export lists -> Sample data list ...** from the menu to open the window for the export.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\SampleDataList_DiversityDescriptions3_0_9_Test_Agricultural_survey.txt

Agricultural survey

- Agricultural survey
- BFLheilpflanzendesc
- Deemy
- Deltatest

☑ Include child projects

☑ Generate headers in output

Test lines 1 to 10

Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

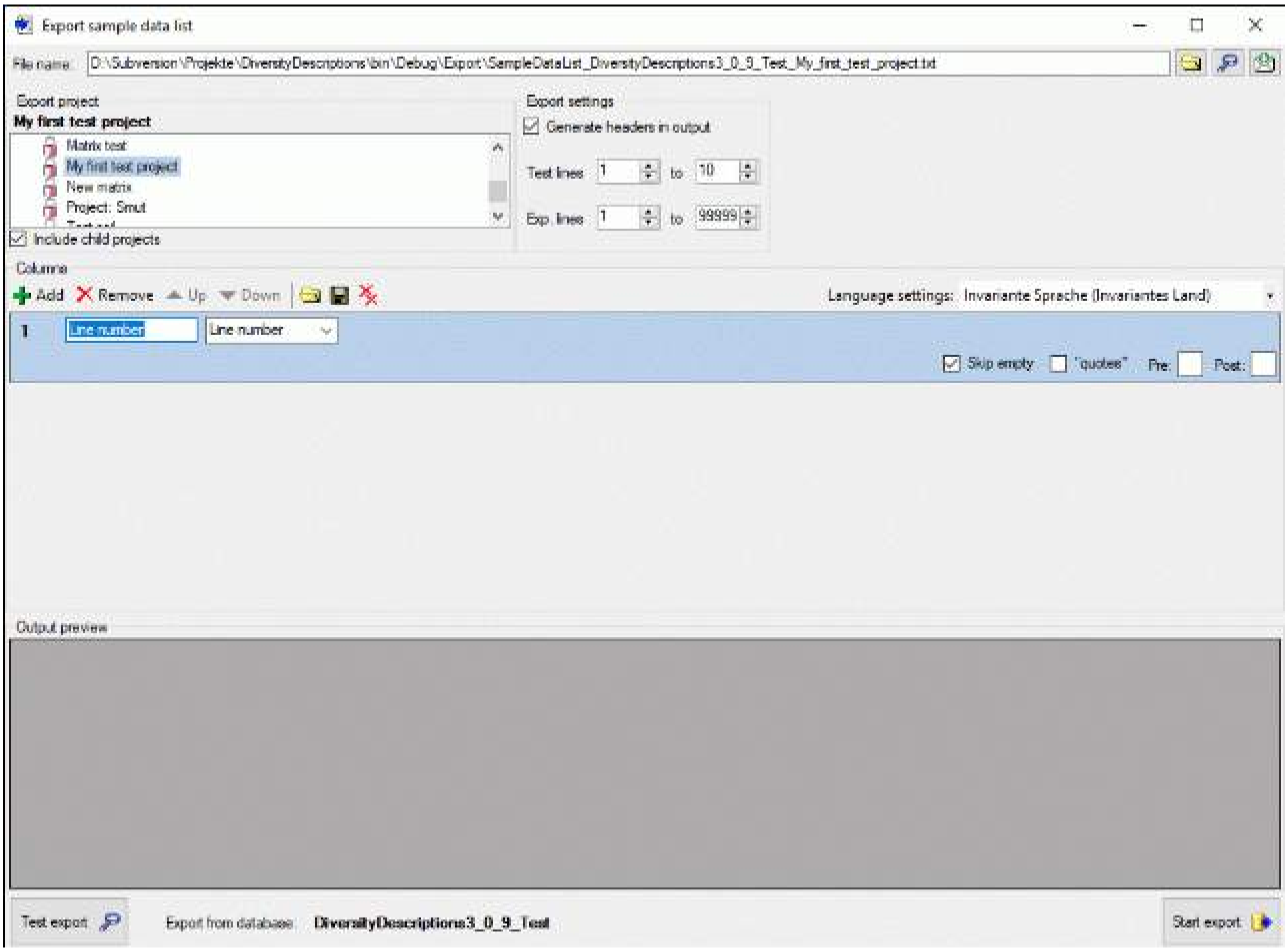
Export from database: **DiversityDescriptions3_0_9_Test**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked.

The **Export settings** allows the inclusion of a header line in the output by checking the option **Generate headers in output**. Additionally the lines displayed in the **Test output** section may be selected by specifying the first and last line number in **Test lines [start] to [end]**. For the generated output you may adjust the lines that shall be exported in **Exp. lines [start] to [end]**. For the end line a maximum value of **99999** may be entered, which means export of the whole data beginning from the start line.

Columns

To generate a list output, you have to determine the data columns that shall be present in the descriptions list. To include a new column press the **Add** button in the tool strip of the **Columns** section. A control representing a single output column will be added at the end of the column list (see picture below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\SampleDataList_DiversityDescriptions3_0_9_Test_My_first_test_project.txt

My first test project

☑ Include child projects

☑ Generate headers in output

Test lines 1 to 10

Exp. lines 1 to 99999

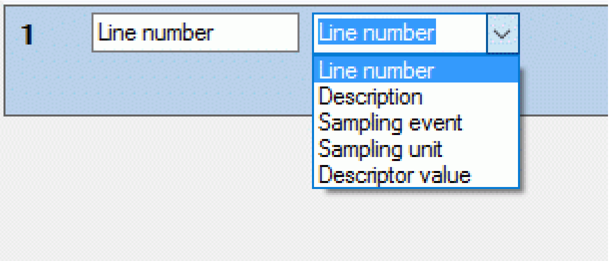
Language settings: Invariante Sprache (Invariantes Land)

1 Line number Line number

☑ Skip empty ☐ "quotes" Pre: Post:

Export from database: **DiversityDescriptions3_0_9_Test**

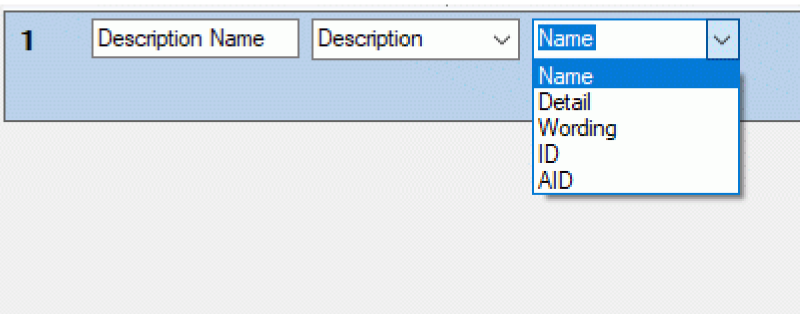
The **Columns** control shows the column number, a text box for the column header (title) and the source selector (see below).



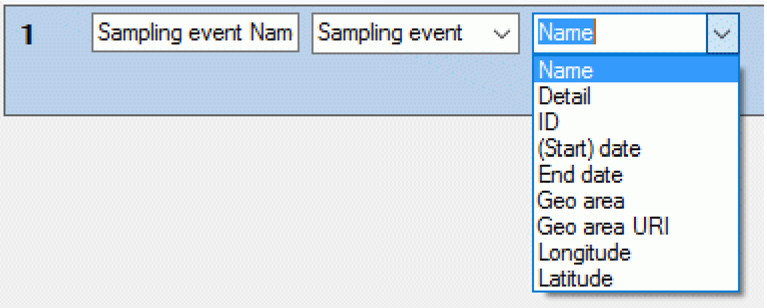
As source you may select one of the following values:

Line number	Number of the data line in the output file
Description	Description data, e.g. name of the description entry
Sampling event	Sampling event data, e.g. name, detail or start date
Sampling unit	Sampling unit data, e.g. ID, specimen or specimen URI
Descriptor value	Sample value(s) of a certain descriptor

Depending on the selected data source one or more additional selection boxes will appear in the description column control. The target (see pictures below) selects the field from the database that shall be inserted..

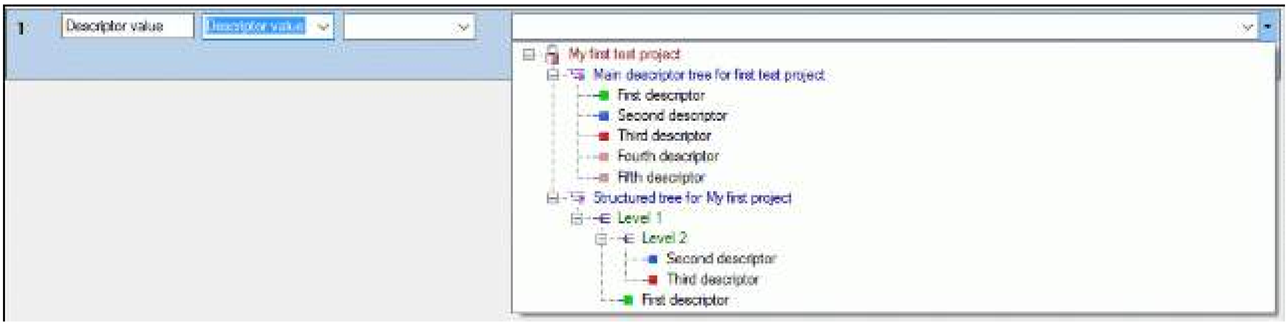


1 Description Name | Description | Name



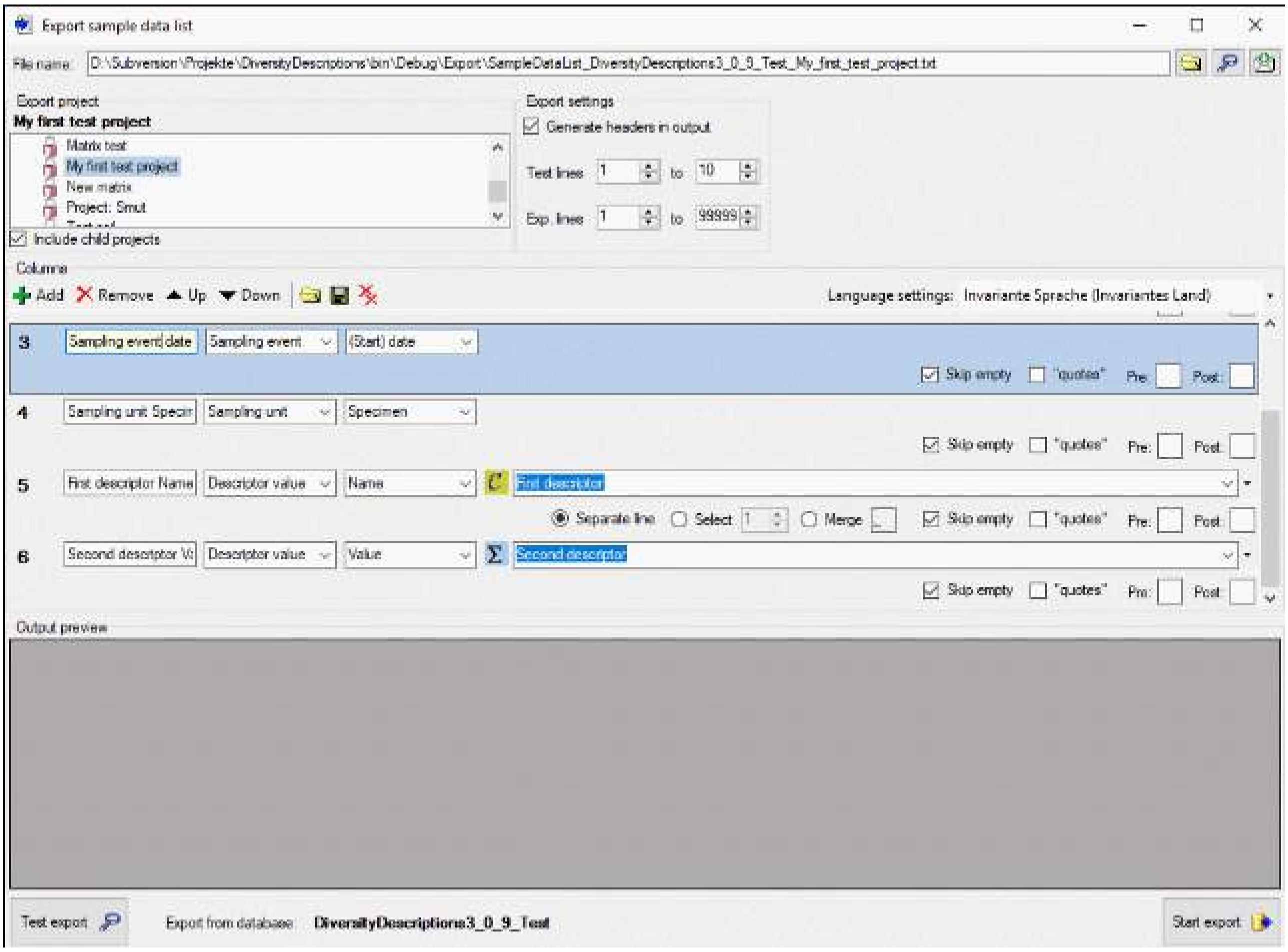
1 Sampling event Nam | Sampling event | Name

If you select "Descriptor value" as data source, a selection box for the descriptor will be inserted (see picture below). The descriptor can be selected from an alphabetical list or from the descriptor tree by clicking ▾ . The target selection box entries depend on the descriptor type. For categroica descriptors you may select name, abbreviation, detail or ID of the categorical states, for quantitative descriptors you may select the value or notes, for text and sequence descriptors you may select the text or notes.



1 Descriptor value | Descriptor value

As long as you did not enter a value for the column header, a reasonable suggestion depending on the selected values will be inserted. You may enter a different column header, then the background color changes to light yellow to indicate that it will not be updated automatically anymore (see picture below, column 3). Double-click on the header to open a separate edit window.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\SampleDataList_DiversityDescriptions3_0_9_Test_My_first_test_project.txt

Export project: **My first test project**
- Matrix test
- My first test project
- New matrix
- Project: Smut

☑ Include child projects

☑ Generate headers in output

Test lines 1 to 10

Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

3 Sampling event date | Sampling event | (Start) date — ☑ Skip empty ☐ "quotes" Pre: Post:

4 Sampling unit Specim | Sampling unit | Specimen — ☑ Skip empty ☐ "quotes" Pre: Post:

5 First descriptor Name | Descriptor value | Name | First descriptor — ● Separate line ○ Select 1 ○ Merge — ☑ Skip empty ☐ "quotes" Pre: Post:

6 Second descriptor V: | Descriptor value | Value | Second descriptor — ☑ Skip empty ☐ "quotes" Pre: Post:

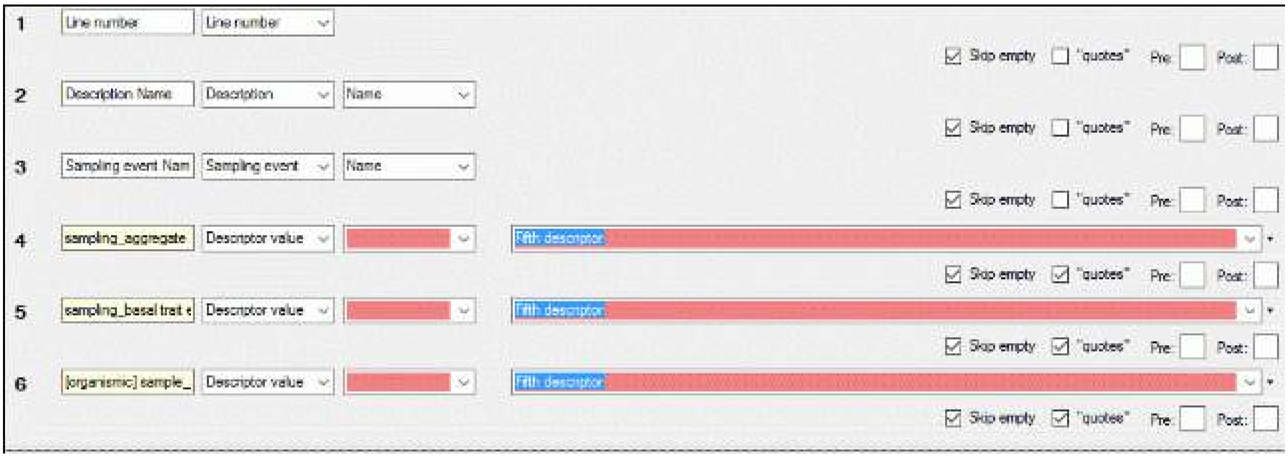
Export from database: **DiversityDescriptions3_0_9_Test**

Output formatting is controlled with check box **"quotes"** that includes the whole output text in quotes and text boxes **Pre:** and **Post:**, which allow inclusion of the values in prefix and postfix strings (default is "). By selecting the check box **Skip empty** a blank output will be inserted instead of the specified prefix and postfix strings, if no value is present. If for a column multiple values may be present, e.g. in case of categorical descriptors several categorical states might be present, there is the choice of inserting additional lines for multiple values (**Separate line**), selecting a single value (**Select**) or merging the values to a single output string (**Merge**). For option **Select** you have specify if the first, second or other values shall be selected. For option Merge you may specify a separator string that shall be inserted between two values (default is **;**). To open a separate edit window for the **Pre:**, **Post:** or **Merge** strings, e.g. because a longer value shall be entered, double-click on the correspondent text box.

Any selected column may be shifted to another position using the ▲**Up** and ▼**Down** buttons or deleted with the ✕**Remove** button of the tool strip. With button ✕you may delete all columns. The complete export schema may be saved into an XML file using the button 💾and a dialog window will be opened. By default the schema file name is generated as:

<resources directory>\ExportSchema\SampleDataList_<Database name>_<Project>.xml

The XML schema file includes information concerning the database, the project, handling of withheld data and the output columns. By pressing the 📂button in the **Columns** section, a schema file can be opened. If the schema does not meet the active database, especially descriptor dependent columns might be erroneous because of unknown values. This is indicated by a red background color (see picture below).



1 Line number | Line number
☑ Skip empty ☐ "quotes" Pre: Post:

2 Description Name | Description | Name
☑ Skip empty ☐ "quotes" Pre: Post:

3 Sampling event Nam | Sampling event | Name
☑ Skip empty ☐ "quotes" Pre: Post:

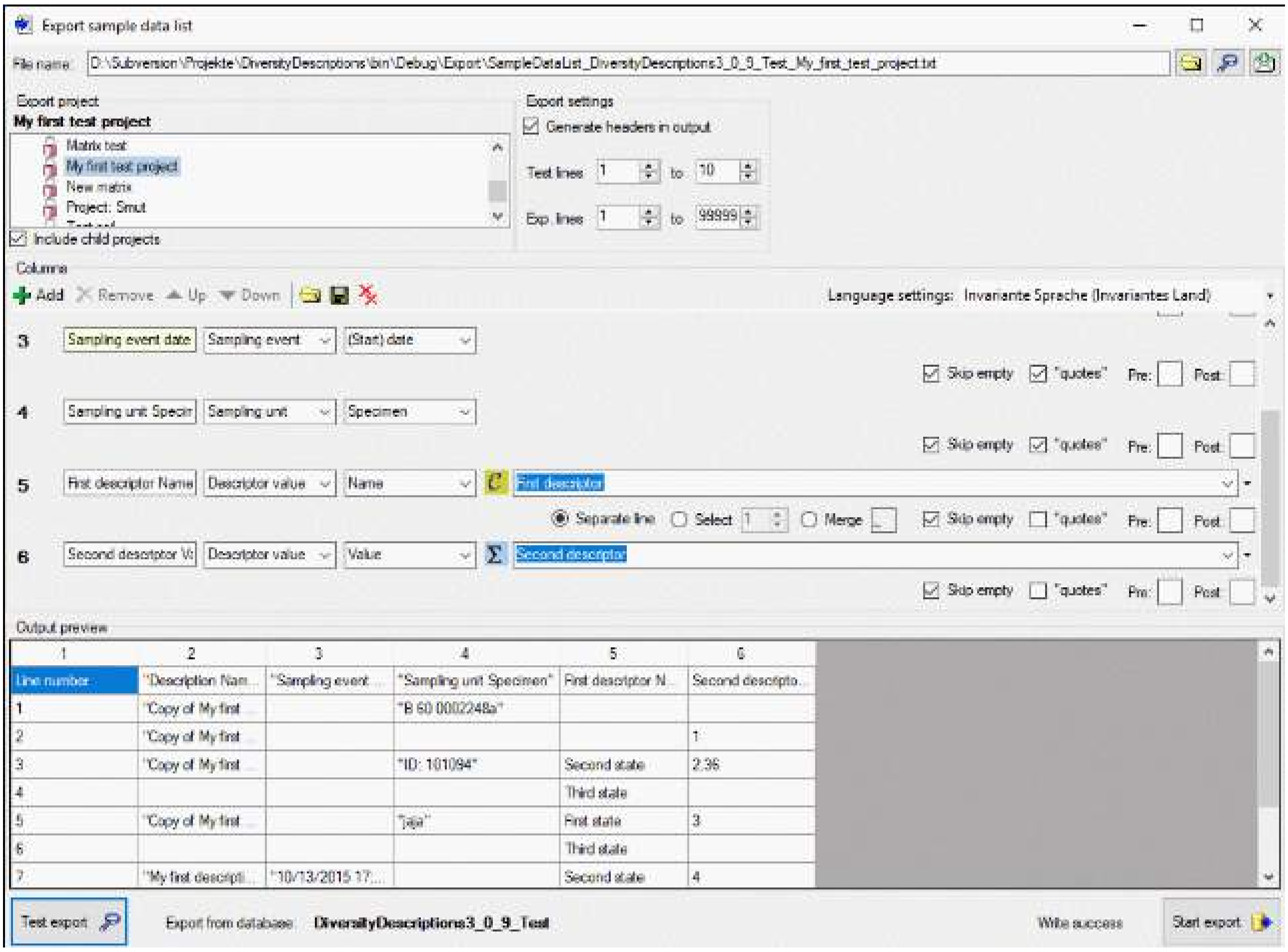
4 sampling_aggregate | Descriptor value | Fifth descriptor
☑ Skip empty ☑ "quotes" Pre: Post:

5 sampling_basal trait e | Descriptor value | Fifth descriptor
☑ Skip empty ☑ "quotes" Pre: Post:

6 [organismic] sample_ | Descriptor value | Fifth descriptor
☑ Skip empty ☑ "quotes" Pre: Post:

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Export\SampleDataList_<Database name>_<Project>.txt**. This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\SampleDataList_DiversityDescriptions3_0_9_Test_My_first_test_project.txt

Export project: **My first test project**

☑ Include child projects

Export settings: ☑ Generate headers in output

Test lines 1 to 10

Exp. lines 1 to 99999

Language settings: Invariante Sprache (Invariantes Land)

3 Sampling event date | Sampling event | (Start) date
☑ Skip empty ☑ "quotes" Pre: Post:

4 Sampling unit Specim | Sampling unit | Specimen
☑ Skip empty ☑ "quotes" Pre: Post:

5 First descriptor Name | Descriptor value | Name | First descriptor
● Separate line ○ Select 1 ○ Merge ☑ Skip empty ☐ "quotes" Pre: Post:

6 Second descriptor Va | Descriptor value | Value | Second descriptor
☑ Skip empty ☐ "quotes" Pre: Post:

Output preview

1	2	3	4	5	6
Line number	"Description Nam...	"Sampling event ...	"Sampling unit Specimen"	First descriptor N...	Second descripto...
1	"Copy of My first ...		"B 60 0002248a"		
2	"Copy of My first ...				1
3	"Copy of My first ...		"ID: 101094"	Second state	2.36
4				Third state	
5	"Copy of My first ...		"jaja"	First state	3
6				Third state	
7	"My first descripti...	"10/13/2015 17:...		Second state	4

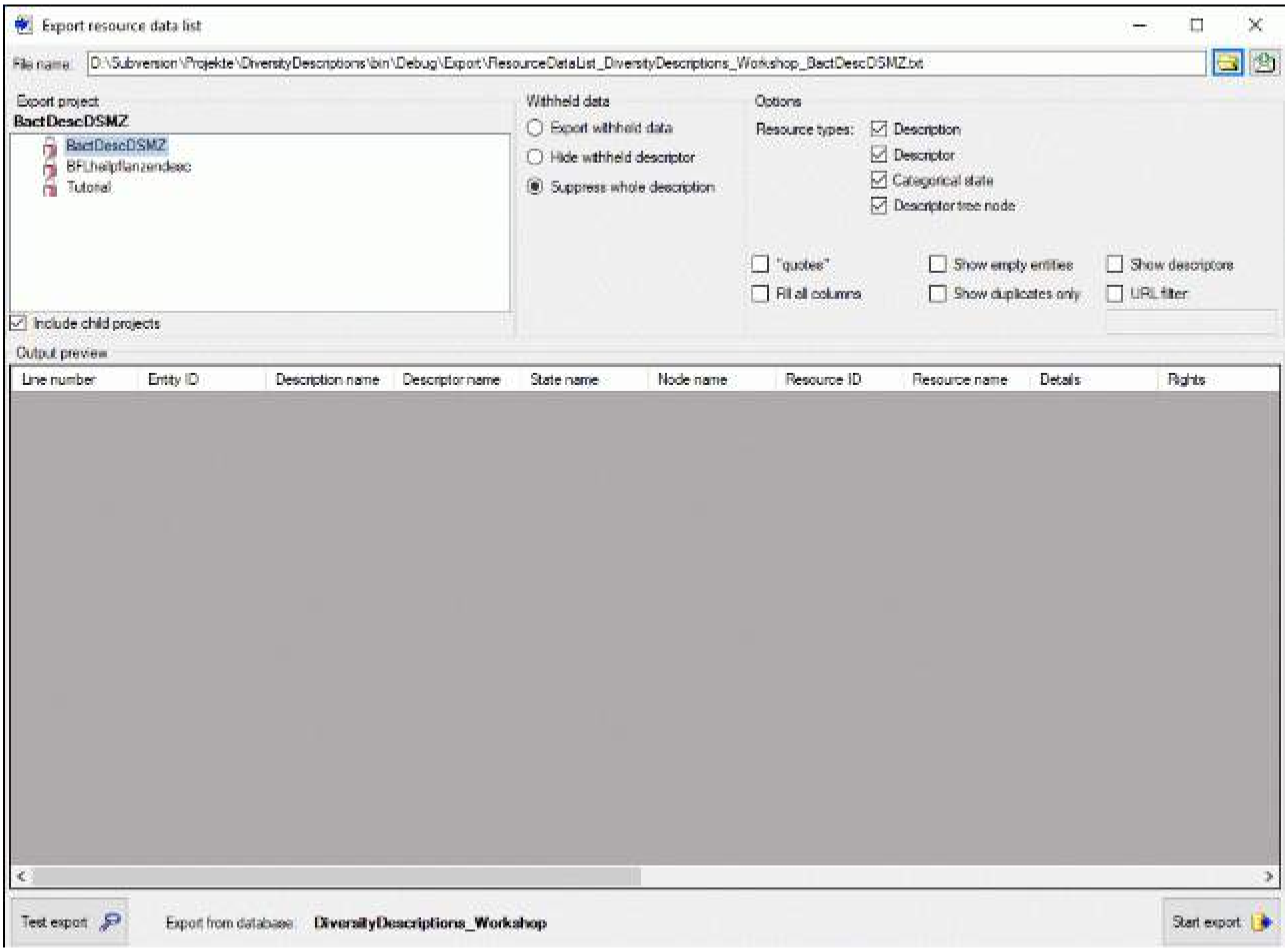
Export from database: **DiversityDescriptions3_0_9_Test**

Write success

To check the export, click on the **Test export** button. By changing the selected **Language settings:** you may adapt the output of floating point numbers or date and time fields to your needs. In the **Output preview** grid view the lines specified in the **Export settings** (**Test lines [start] to [end]**) will be displayed (see picture above). To generate the table file press the **Start export** button. During test and export the icon of the button changes to STOP and you may abort processing by clicking the button.

Export resource data list

With this form you can export the resource data (see tables Resource and ResourceVariant) from the database to a tabulator separated text file. Since the output includes the database keys, you may correct the data, e.g. by using a spreadsheet program and re-import the changes by using the import wizard. Choose **Data ->** **Export ->** **Export lists ->** **Resource list ...** from the menu to open the window for the export.



Export resource data list

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\ResourceDataList_DiversityDescriptions_Workshop_BactDescDSMZ.txt

Export project: **BactDescDSMZ**

- BactDescDSMZ
- BFLheilpflanzendesc
- Tutorial

☑ Include child projects

Withheld data

○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options

Resource types: ☑ Description ☑ Descriptor ☑ Categorical state ☑ Descriptor tree node

☐ "quotes" ☐ Fill all columns ☐ Show empty entities ☐ Show duplicates only ☐ Show descriptors ☐ URL filter

Output preview

Line number	Entity ID	Description name	Descriptor name	State name	Node name	Resource ID	Resource name	Details	Rights

Export from database: **DiversityDescriptions_Workshop**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked.

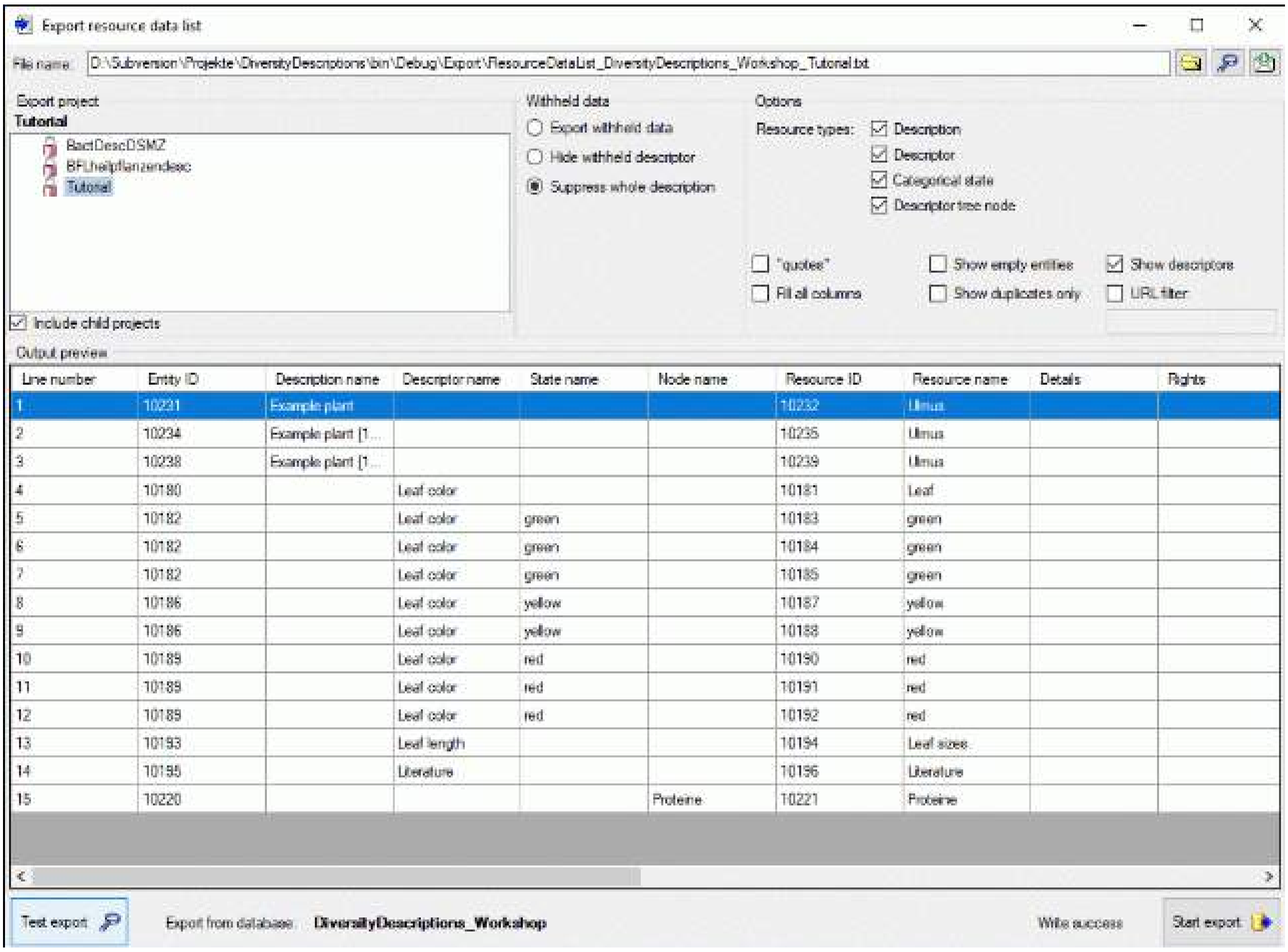
The **Withheld data** section allows control over export of datasets that contain entries with data status "Data withheld". Option **Supress whole description** (default) excludes all descriptions form export where at least on descriptor is marked with "Data withheld". Option **Hide withheld descriptor** excludes only the corresponding descriptor data from the description. Option **Export withheld data** does not exclude any data from export.

The **Options** section allows the selection of the **Resource types** for output ("Description", "Descriptor", "Categorical state" and "Descriptor tree node"). To include all export data in quotes, check option **"quotes"**. If option **Fill all columns** is checked, resource variant data that are inherited from the row above will be explicitely repeated in the actual row. To include all data rows that do not have resources select option **Show empty entities**. If you select **Show descriptors**, the descriptor titles will be inserted for categorical states. By checking option **Show duplicates only** you may list resource links that are referenced by more than one entity of the same type.

You may restrict the resource data list to resource links that include a specified substring by selecting the **URL filter** option and entering the required string in the text field below.

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Export\ResourceDataList_<Database name>_<Project>.txt** . This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\ResourceDataList_DiversityDescriptions_Workshop_Tutorial.txt

Export project
Tutorial
- BactDescDSMZ
- BFLheilpflanzendesc
- Tutorial

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options
Resource types: ☑ Description
☑ Descriptor
☑ Categorical state
☑ Descriptor tree node

☐ "quotes"
☐ Fill all columns
☐ Show empty entities
☐ Show duplicates only
☑ Show descriptors
☐ URL filter

Output preview

Line number	Entity ID	Description name	Descriptor name	State name	Node name	Resource ID	Resource name	Details	Rights
1	10231	Example plant				10232	Ulmus		
2	10234	Example plant [1...				10235	Ulmus		
3	10238	Example plant [1...				10239	Ulmus		
4	10180		Leaf color			10181	Leaf		
5	10182		Leaf color	green		10183	green		
6	10182		Leaf color	green		10184	green		
7	10182		Leaf color	green		10185	green		
8	10186		Leaf color	yellow		10187	yellow		
9	10186		Leaf color	yellow		10188	yellow		
10	10189		Leaf color	red		10190	red		
11	10189		Leaf color	red		10191	red		
12	10189		Leaf color	red		10192	red		
13	10193		Leaf length			10194	Leaf sizes		
14	10195		Literature			10196	Literature		
15	10220				Proteine	10221	Proteine		

Export from database: **DiversityDescriptions_Workshop**
Write success

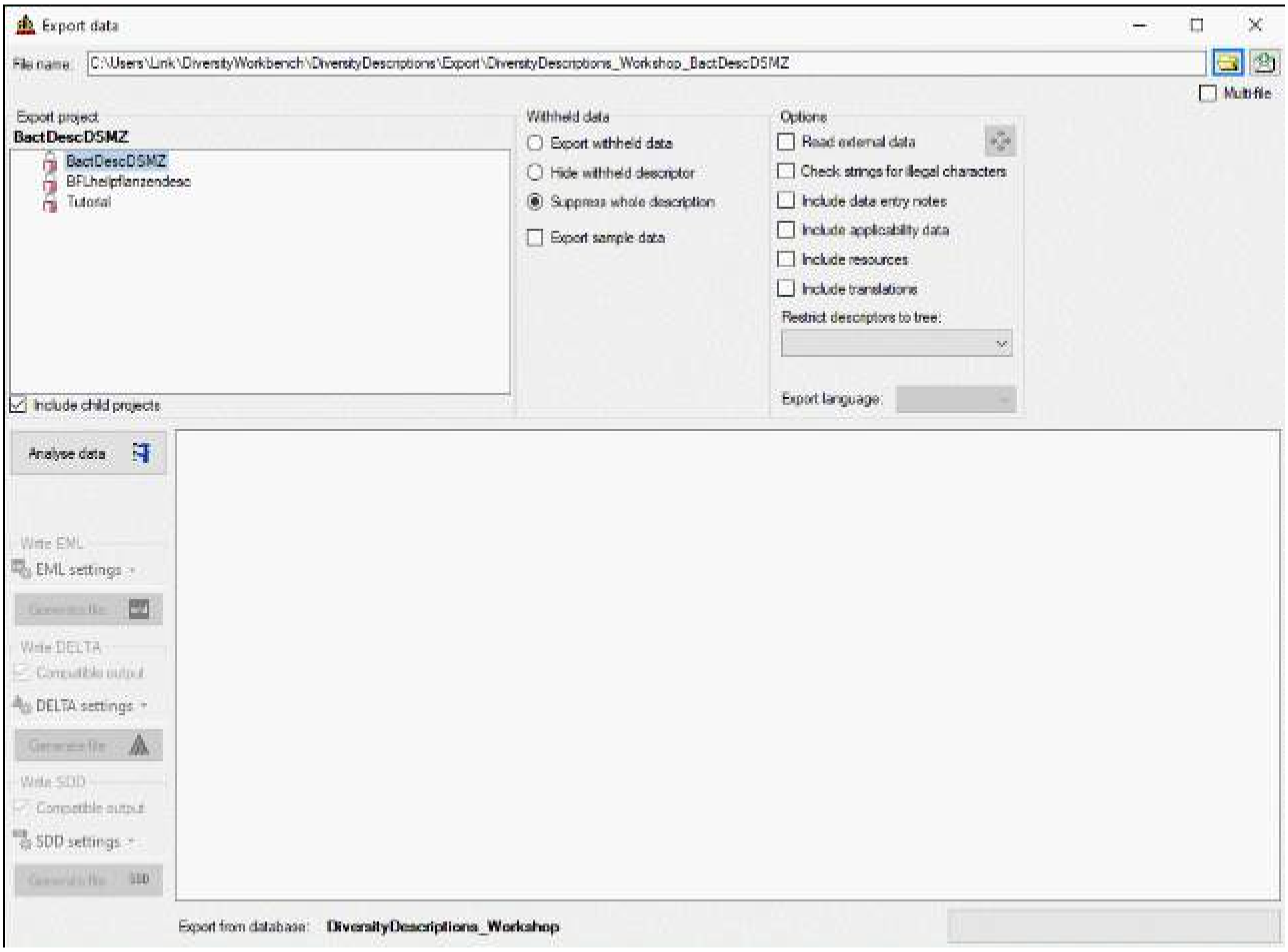
To check the export, click on the **Test export** button. In the **Output preview** data grid the first few lines will be displayed (see picture above). To generate the table file press the **Start export** button. During test and export the icon of the button changes to STOP and you may abort processing by clicking the button.

Re-import

The review output includes all database keys that can be sufficiently used to identify the affected data row. When the modified data shall be re-imported, the internal keys must be available to the import wizard. This can easily be done by creating a new import session and using the option **Generate mapping ...** in form Import sessions.

Export data as SDD, DELTA or EML

With this form you can export data from the database to an DELTA file. Choose **Data -> Export -> Export SDD/DELTA ...** from the menu to open the window for the export.


Export data

File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Export\DiversityDescriptions_Workshop_BactDescDSMZ

☐ Multifile

Export project: **BactDescDSMZ**

- BactDescDSMZ
- BFLhelpflanzendesc
- Tutorial

☑ Include child projects

Withheld data

○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description
☐ Export sample data

Options

☐ Read external data
☐ Check strings for illegal characters
☐ Include data entry notes
☐ Include applicability data
☐ Include resources
☐ Include translations

Restrict descriptors to tree:

Export language:

Export from database: **DiversityDescriptions_Workshop**

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exportes. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked. You may pass a description list to the form by starting a query in mode "Edit descriptions". Now you have the option to select single descriptions for export. In this case the **Export project** section shows the button to switch to the list view (see below).


Export project: **Libellen**

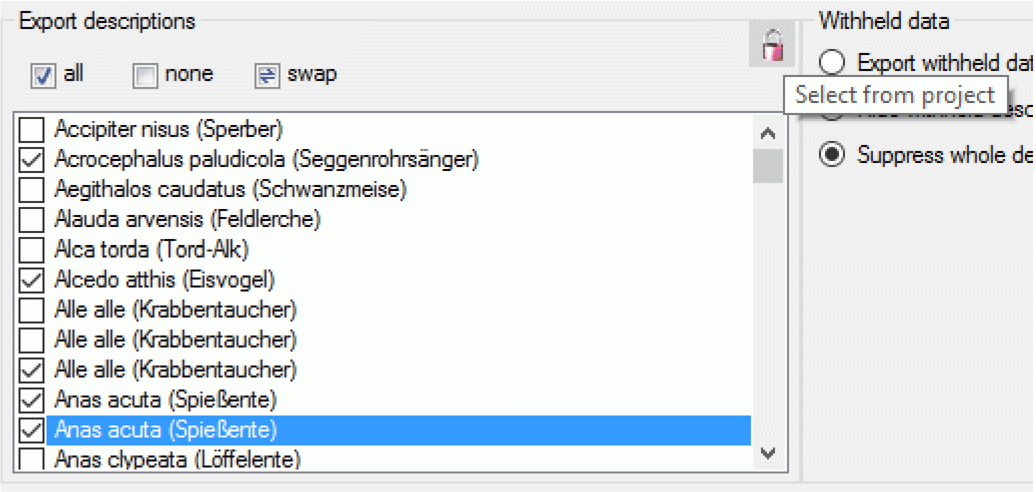
- Libellen
- Pflanzen
- Pilze
- Schmetterlinge
- Vögel

☑ Include child projects

Withheld data

○ Export withhe
● Suppress wh

In the **Export descriptions** section you find all description titles that have been passed to the export form (see below). You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. By clicking the button you will return to the **Export project** view.



Export descriptions

☑ all ☐ none swap

☐ Accipiter nisus (Sperber)
☑ Acrocephalus paludicola (Seggenrohrsänger)
☐ Aegithalos caudatus (Schwanzmeise)
☐ Alauda arvensis (Feldlerche)
☐ Alca torda (Tord-Alk)
☑ Alcedo atthis (Eisvogel)
☐ Alle alle (Krabbentaucher)
☐ Alle alle (Krabbentaucher)
☑ Alle alle (Krabbentaucher)
☑ Anas acuta (Spießente)
☑ Anas acuta (Spießente)
☐ Anas clypeata (Löffelente)

Withheld data

○ Export withheld dat

Select from project

● Suppress whole de

The **Withheld data** section allows control over export of datasets that contain entries with data status "Data withheld". Option **Supress whole description** (default) excludes all descriptions form export where at least on descriptor is marked with "Data withheld". Option **Hide withheld descriptor** excludes only the corresponding descriptor data from the description. Option **Export withheld data** does not exclude any data from export. Check option **Export sample data** to include sampling events and units in the analysis output.

In the **Options** section you find the items **Read external data**. By selecting this item you enable access to external databases linked by description scopes or the related workbench project. The foreign data are included in the analysis tree and may be exported, e.g. to a SDD file. You may check the external data connections by clicking the button.

If **Check strings for illegal characters** in the **Options** section is selected, all string literals that shall be exported from database are scanned for illegal non-printable characters and matches are replaced by a double exclamation mark ("‼") in the output file. Although DiversityDescriptions can handle non-printable characters, especially in case of SDD XML files some applications may have problems opening files with illegal characters.

With option **Include data entry notes** you allow the analysis step to store descriptor's data entry notes in the analysis tree. Depending on the export format, these data may be exported e.g. as "internal notes" (SDD).

With option **Include applicability data** you allow the analysis step to write available descriptor applicability data to the analysis tree as a dedicated "Dependency tree".

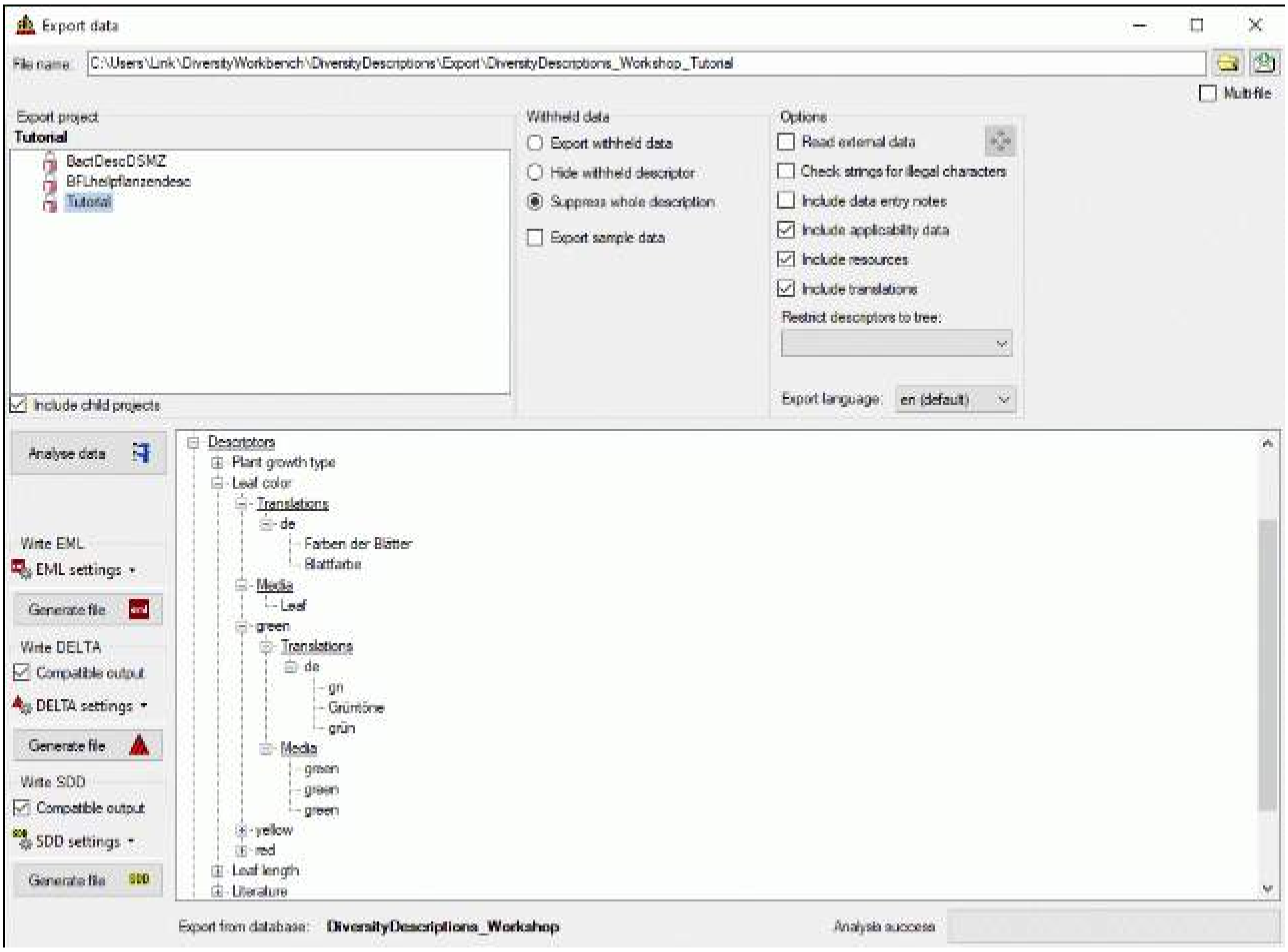
With option **Include resources** you allow the analysis step to write availble resource data to the analysis tree. This option is not relevant if you only want to export to a DELTA file.

If you select a descriptor tree in combo box **Restrict descriptors to tree:** only that descriptor tree and its descriptors will be included in the analysis tree (see next section). Be aware that you might get warnings during the analysis step when the respective descriptor data are omitted.

With option **Include translations** you allow the analysis step to write availble translations to the analysis tree. If you check this option and translations are available, you will see the available languages in the **Export language:** combo box after the analysis step.

Analysis

After clicking the **Analyse data** button the data for export are collected in the database an included into an analysis tree in the lower part of the window. The analysis tree contains all data in a suitable format for the final export step. During data analysis the icon of the button changes to STOP and you may abort processing by clicking the button.



File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Export\DiversityDescriptions_Workshop_Tutorial

☐ Multi-file

Export project
Tutorial
BactDescDSMZ
BFLhelpflanzendesc
Tutorial

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description
☐ Export sample data

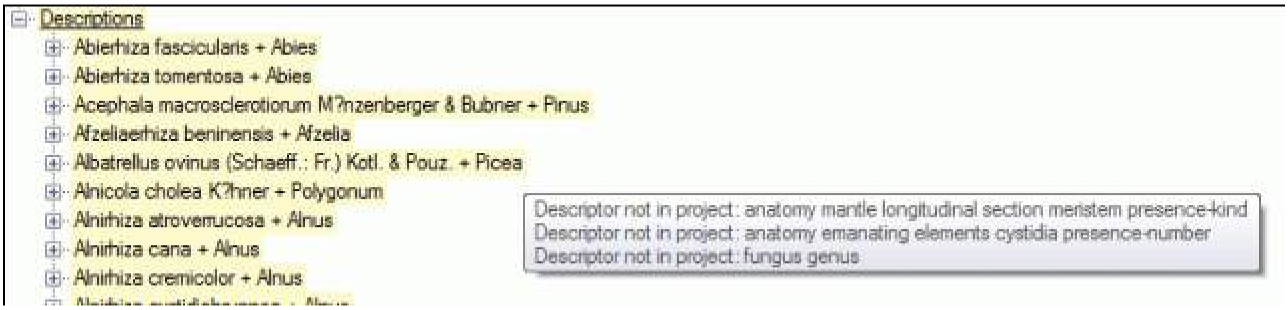
Options
☐ Read external data
☐ Check strings for illegal characters
☐ Include data entry notes
☑ Include applicability data
☑ Include resources
☑ Include translations
Restrict descriptors to tree:
Export language: en (default)

☑ Compatible output (DELTA)
☑ Compatible output (SDD)

```
Descriptors
  Plant growth type
  Leaf color
    Translations
      de
        Farben der Blätter
        Blattfarbe
    Media
      Leaf
    green
      Translations
        de
          grn
          Grüntöne
          grün
      Media
        green
        green
        green
    yellow
    red
  Leaf length
  Literature
```

Export from database: **DiversityDescriptions_Workshop**

After analysis a message window inform you if any warnings or errors occured. If there are descriptions that reference descriptors that are not part of the export project, these descriptor data wil be omitted and the descriptions will be marked with yellow background (warning). When you move the mouse curser over the marked entries, you get information about the omitted descriptors as tool tip (see examples below). Anyway you may continue export or fix the problem by including the missing descriptors in the descriptor tree (see section "Editing the descriptor"). If errors are indicated, please save the error log file and send a feedback by pressing the button.



```
Descriptions
  Abierhiza fascicularis + Abies
  Abierhiza tomentosa + Abies
  Acephala macrosclerotiorum M?nzenberger & Bubner + Pinus
  Afzeliaerhiza beninensis + Afzelia
  Albatrellus ovinus (Schaeff.: Fr.) Kotl. & Pouz. + Picea
  Alnicola cholea K?hner + Polygonum
  Alnirhiza atroverrucosa + Alnus
  Alnirhiza cana + Alnus
  Alnirhiza cremicolor + Alnus
```

Descriptor not in project: anatomy mantle longitudinal section meristem presence-kind
Descriptor not in project: anatomy emanating elements cystidia presence-number
Descriptor not in project: fungus genus

Export

Before starting the export, the export file name should be checked. Either a single SDD rsp. DELTA file can be generated or output to several files may be chosen by selecting the **Multi-file** option. In case of SDD export currently the data will always be stored in a single file ("SDD1.xml") located in the directory specified in the "File name" text box.

If the "Multi-file" option for DELTA export is activated, the "File name" text box shows the output path, which is by default generated as **<resources directory>\Export\<Database name>_<Project>**. This default setting may be modified by editing the "File name" or by navigating at the target location by pressing the button. For DELTA export in the target directory the files "specs", "chars", "items" and "extra" will be generated. For SDD export you will get the file "SDD1.XML". For EML export you will get the files "EML_MetaData.xml" and "EML_DataTable.txt".

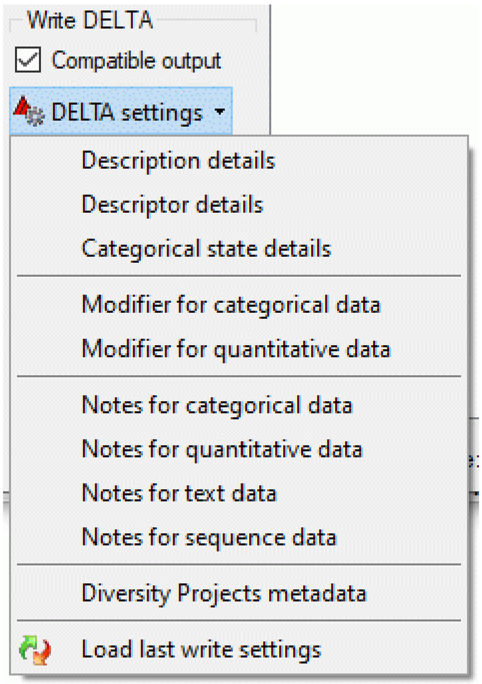
If output to a single file is selected, by default the file name is generated as **<resources directory>\Export\<Database name>_<Project>_<Type>** and additionally the exension ".xml" (SDD export) or ".dat" (DELTA export) will be appended. <Type> is "SDD1" for SDD and "DELTA" for the DELTA format. This default setting may be changed by editing the "File name" or by navigating at the target location by pressing the button.

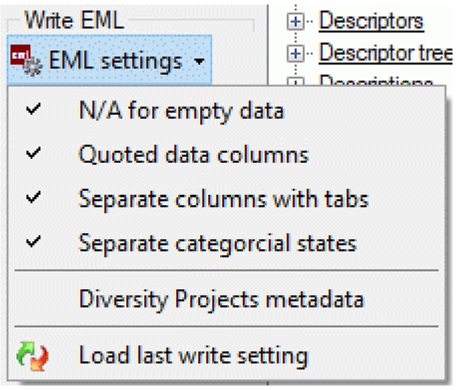
To start the export click on the **Generate file** button in the **Write SDD** group box to generate an SDD file or the **Generate file** button in the **Write Delta** group box to generate a DELTA file. Now the data from the analysis tree are written into the selected export file. The **Comptible** option controls generation of files with most possible compatibility to the DELTA rsp. SDD standard. On the other hand some data might not be present in the generated file, if this option is activated.

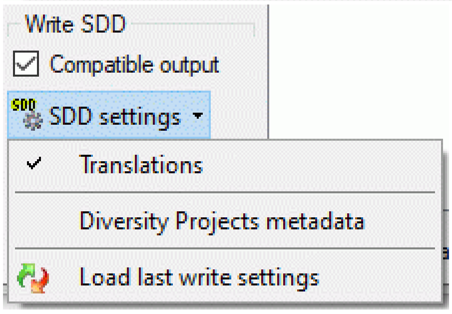
As an additional option you may generate file according the EML schema, which consists of a data table (tabulator separated text file) and an XML file that contains the metadata including column descriptions. Click on the **Generate file** button in the **Write EML** group box. The generated file names will have the endings **"_EML_DataTable.txt"** and **"_EML_Metadata.xml"**.

Pressing the drop down button **DELTA settings** in the **Write DELTA** group box opens the DELTA writer options. You can chose to include some detail text and notes in the DELTA output (see left image below). For descriptions, descriptors or categorical states the details will be appended as DELTA comments (included in angle brackets "< ... >") to the respective titles. The notes will be appended as DELTA comments of the corresponding summary data. If you already generated DELTA files, the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **DELTA settings** to close the option panel.

Pressing the drop down button **EML settings** in the **Write EML** group box opens the EML writer options. You can chose to include a special sign for empty column values or set the columns values in quotes (see center image below). Furthermore you may shose the column separator (tab stop rsp. comma) an decide if multiple categorical states shall be inserted as separate data columns. If you already generated EML files, the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **EML settings** to close the option panel.







Pressing the drop down button **SDD settings** in the **Write SDD** group box opens the SDD writer options. You can chose to include translations in the SDD output (see right image above). If you already generated SDD files ,the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **SDD settings** to close the option panel.

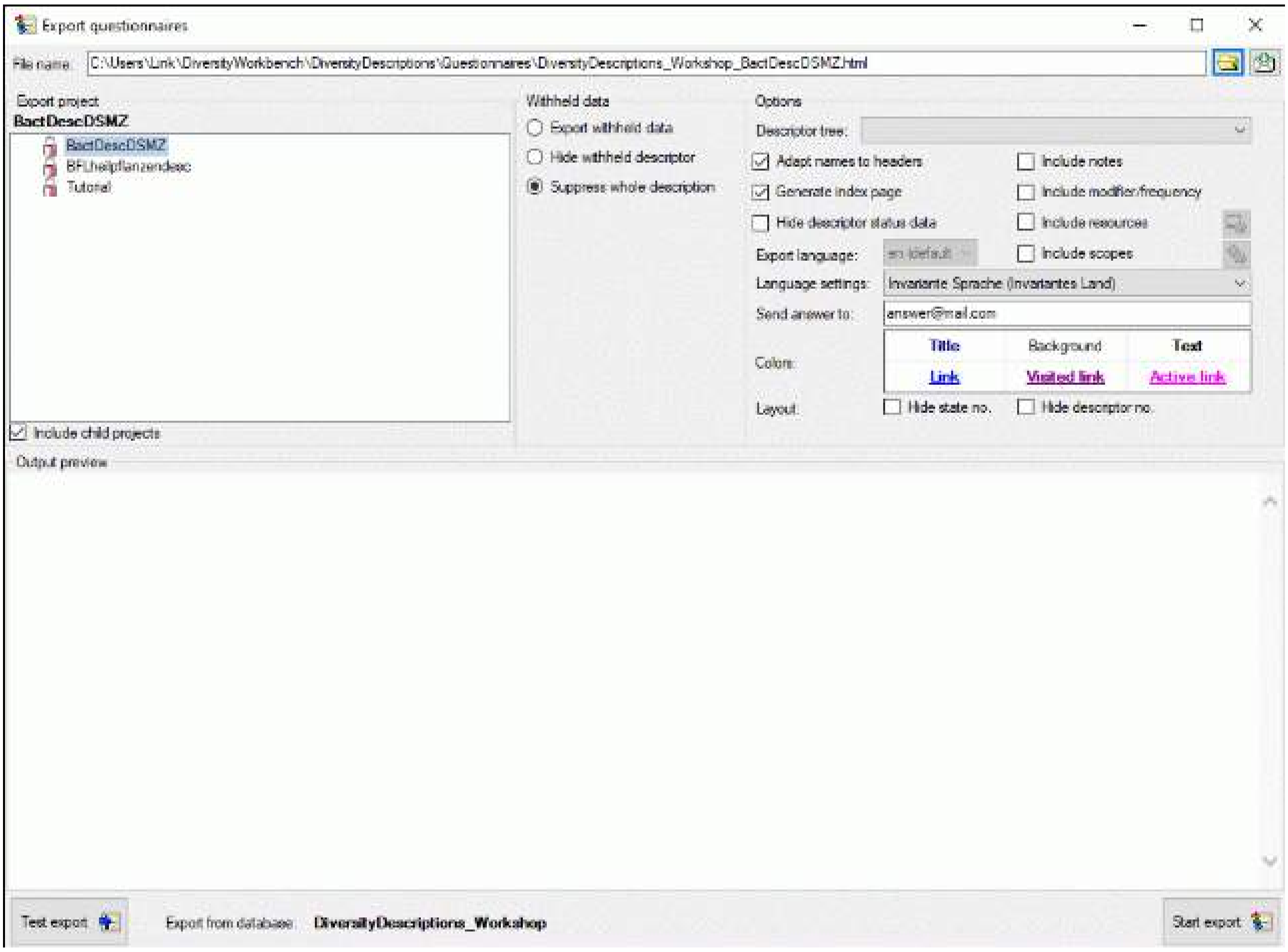
For all three output formats you have the option **Diversity Projects metadata**. If this option is selected, additional information from the corresponding project in the linked projects and agents databases will be retrieved. An EML metadata file (XML) will be generated that includes the retrieved metadata and references the generated data file(s).

While SDD can handle molecular sequence data, for DELTA export these data will be exported as text data. To preserve the sequence specific descriptor data, they will be inserted into the text character as a special comment with the format, e.g. "#6. Sequence descriptor <**[SequenceCharacter][ST:N][SL:1][GS:-][/SequenceCharacter]**>/". If during DELTA import this special comment is detected, it will be removed and the descriptor will be imported as a sequence descriptor using the given settings.

If the analysis tree includes sample data (see option **Export sample data**), they will be included as items at the end of the DELTA file. The naming of those spetial items will be **<description name> - <event name> - Unit <number>**. Sampling event data will not be included in the DELTA file.

Export questionnaires

With this form you can export description data from the database to HTML forms. You can open the generated HTML files, edit the data in the form and re-import the changes by using the import questionaire data function. Choose **Data -> Export -> Export questionnaires ...** from the menu to open the window for the export.



Export questionnaires

File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\DiversityDescriptions_Workshop_BactDescDSMZ.html

Export project
BactDescDSMZ
- BactDescDSMZ
- BFLheilpflanzendesc
- Tutorial

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

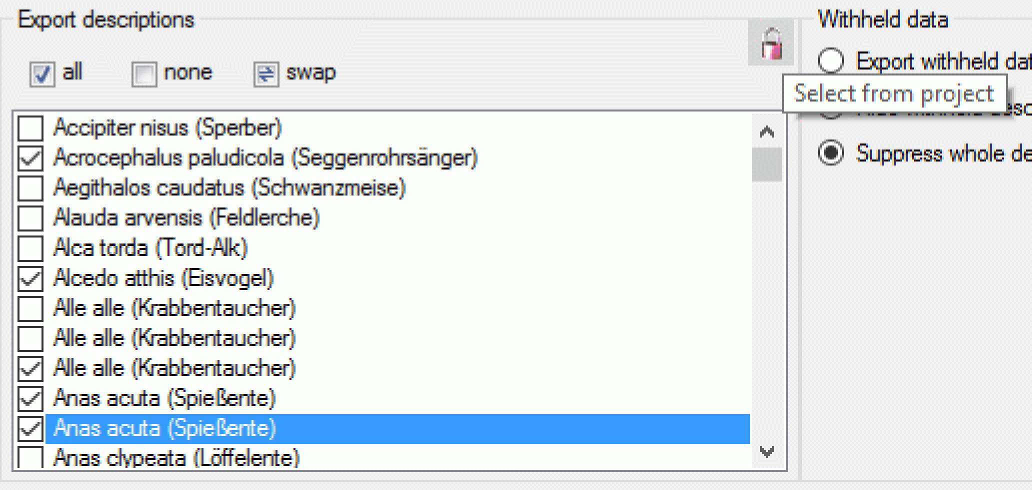
Options
Descriptor tree:
☑ Adapt names to headers
☐ Include notes
☑ Generate index page
☐ Include modifier/frequency
☐ Hide descriptor status data
☐ Include resources
Export language: en (default)
☐ Include scopes
Language settings: Invariante Sprache (Invariantes Land)
Send answer to: answer@mail.com
Colors: Title, Background, Text, Link, Visited link, Active link
Layout: ☐ Hide state no. ☐ Hide descriptor no.

Output preview

Test export
Export from database: **DiversityDescriptions_Workshop**
Start export

In the **Export project** section all projects of the database are shown as a tree. Select here the project that shall be exported. In case of hierarchically organized projects the subordinated projects will be included for export, if the **Include child projects** option is checked. You may pass a description list to the form by starting a query in mode "Edit descriptions". If all descriptions in the list belong to the same project, you have the option to select single descriptions for export. In this case the **Export project** section shows the button to switch to the list view (see below).

In the **Expot descriptions** section you find all description titles that have been passed to the export form (see below). You may select all entries by clicking the ☑ **all** button, deselect all entries by clicking the ☐ **none** button or toggle your selection by clicking the **swap** button. By clicking the button 🔒you will return to the **Export project** view.

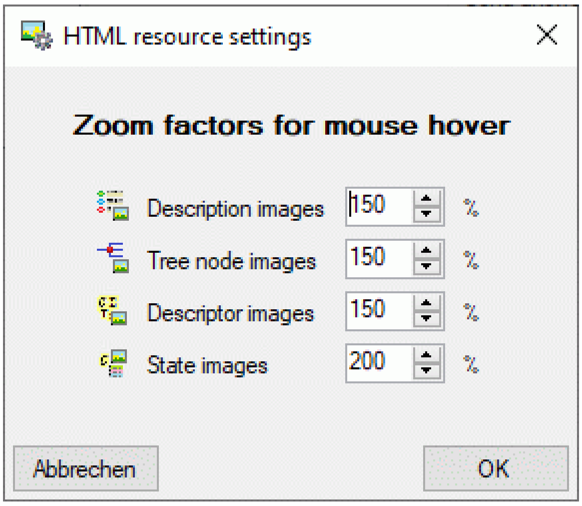


☐ Accipiter nisus (Sperber)
☑ Acrocephalus paludicola (Seggenrohrsänger)
☐ Aegithalos caudatus (Schwanzmeise)
☐ Alauda arvensis (Feldlerche)
☐ Alca torda (Tord-Alk)
☑ Alcedo atthis (Eisvogel)
☐ Alle alle (Krabbentaucher)
☐ Alle alle (Krabbentaucher)
☑ Alle alle (Krabbentaucher)
☑ Anas acuta (Spießente)
☑ Anas acuta (Spießente)
☐ Anas clypeata (Löffelente)

The **Withheld data** section allows control over export of datasets that contain entries with data status "Data withheld". Option **Supress whole description** (default) excludes all descriptions form export where at least on descriptor is marked with "Data withheld". Option **Hide withheld descriptor** excludes only the corresponding descriptor data from the description. Option **Export withheld data** does not exclude any data from export.

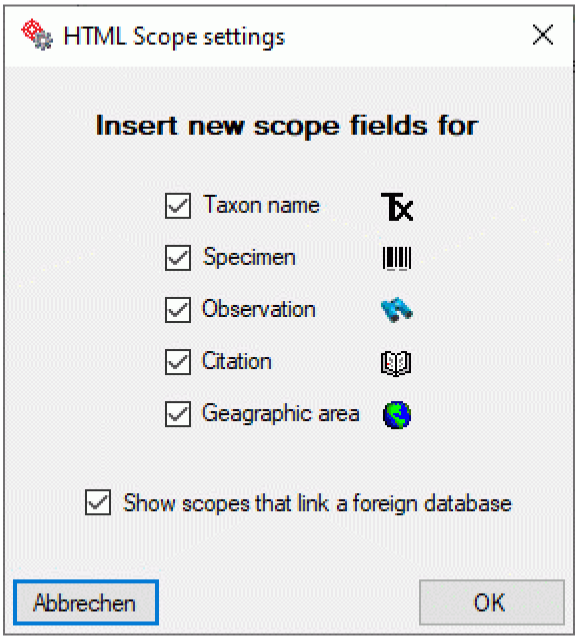
The **Options** section allows the selection of a **Descriptor tree** to determine the sequence and selection of descriptors for output. If a structured descriptor tree is selected, the first level descriptor tree nodes will be inserted as headers to structure the document. If option **Adapt names to headers** is checked, the descriptor names will be prefixed with the headers from the derscriptor tree. If **Generate index page** is checked, an alphabetically sorted index with links to the individual description pages will be generated. You may **Hide descriptor status data** in the generated forms (only visible in Web browser, not in the preview). With options **Include notes** and **Include modifier/frequency** you can control if notes and modifier or frequency values shall be included in the generated questionaires.

Check **Include resources** to include images for descriptions, descriptors, categorical states and descriptor tree nodes in the questionnaire. In the generated HTML questionnaire the images will be zoomed by a dedicated factor, when the mouse cursor is moved over it. The zoom factors may be adjusted by clicking on button (see image below on the left).


HTML resource settings

Zoom factors for mouse hover

Description images 150 %
Tree node images 150 %
Descriptor images 150 %
State images 200 %


HTML Scope settings

Insert new scope fields for

☑ Taxon name
☑ Specimen
☑ Observation
☑ Citation
☑ Geagraphic area

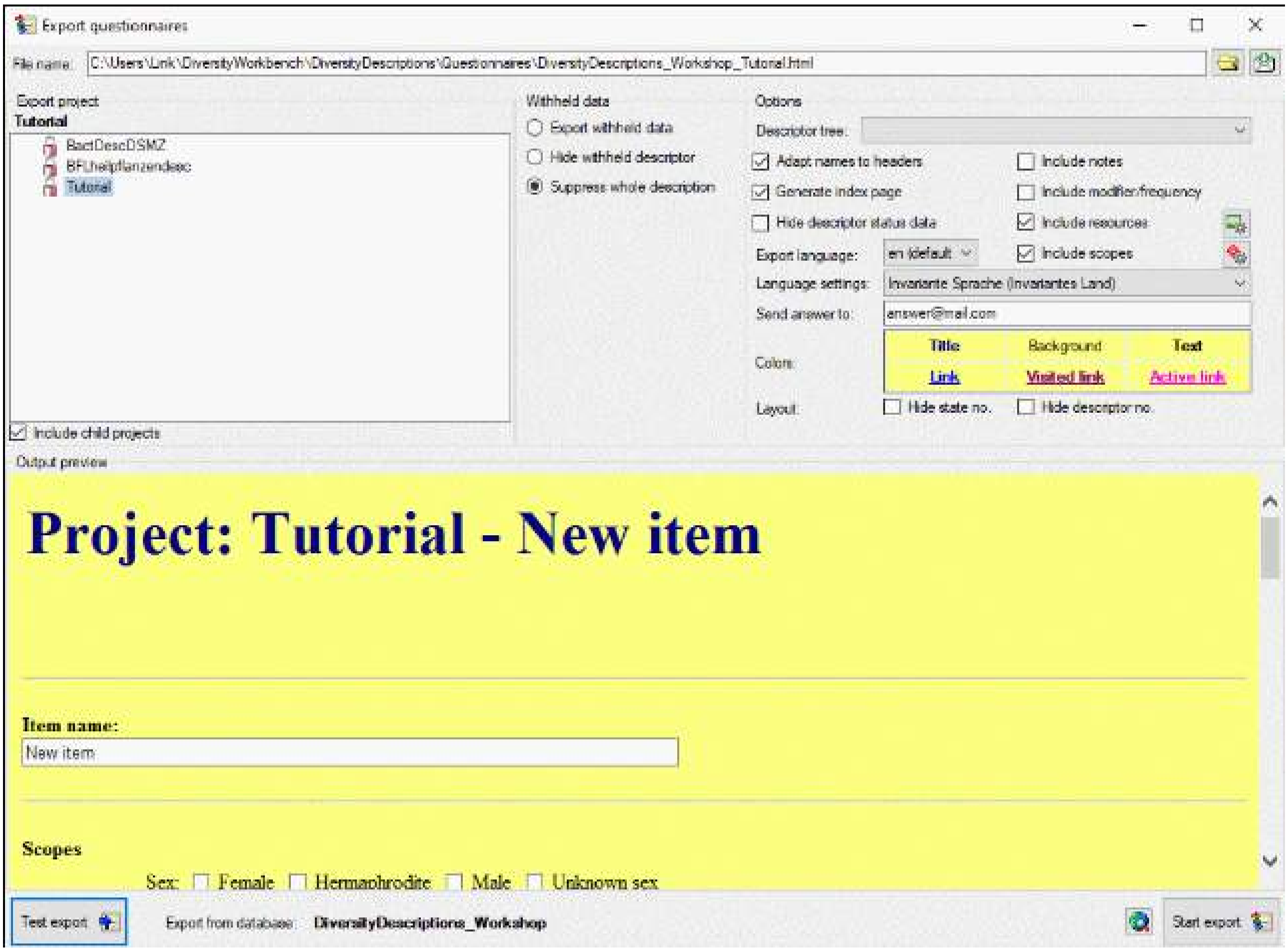
☑ Show scopes that link a foreign database

Check **Include scopes** to include a section for scope data in the questionnare. The scope values of the types "Sex", "Stage", "Part" and "Other scopes", which may be administered in the Edit project section, are included as check boxes. For the other scope types input boxes will be generated, where new values may be entered or existing values may be edited. If a scope value has been linked to a database entry, e.g. of a DiversityTaxonNames database, it cannot be modified. Therefore only a fixed text with the reference to the target database will be inserted in the questionnaire. By clicking on button you may decide for with scope types an input box for a new scope values shall be inserted or if scopes that cannot be modified shall be displayed (see image above on the right).

If for the selected projects translations are stored in the database, you may chose the **Export language**. If for any element no translation in the chosen export language is present, automatically the original text will be used. With field **Language settings** you can control the presentation of floating point values in the output, in field **Send answer to** you may enter the mail address to return the results. The **Colors** of several elements may be adapted to the personal preferences. Finally, the **Layout** options **Hide state no.** rsp. **Hide descriptor no.** my be checked to suppress the ordinal numbers before the desriptor titles and/or the state check boxes.

Test

To check the export, click on the **Test export** button. In the **Output preview** section an empty form for entering a new item will be displayed (see picture below). The file name is generated as **<resources directory>\Questionnaires\<Database name>_<Project>.txt** . This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the button besides the file name. Button opens the form in an external web browser.


Export questionnaires

File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\DiversityDescriptions_Workshop_Tutorial.html

Export project
Tutorial
- BactDescDSMZ
- BFLhelpflanzendesc
- Tutorial

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options
Descriptor tree:
☑ Adapt names to headers
☐ Include notes
☑ Generate index page
☐ Include modifier/frequency
☐ Hide descriptor status data
☑ Include resources
Export language: en (default)
☑ Include scopes
Language settings: Invariante Sprache (Invariantes Land)
Send answer to: answer@mail.com
Colors: Title, Background, Text, Link, Visited link, Active link
Layout: ☐ Hide state no. ☐ Hide descriptor no.

Output preview

Project: Tutorial - New item

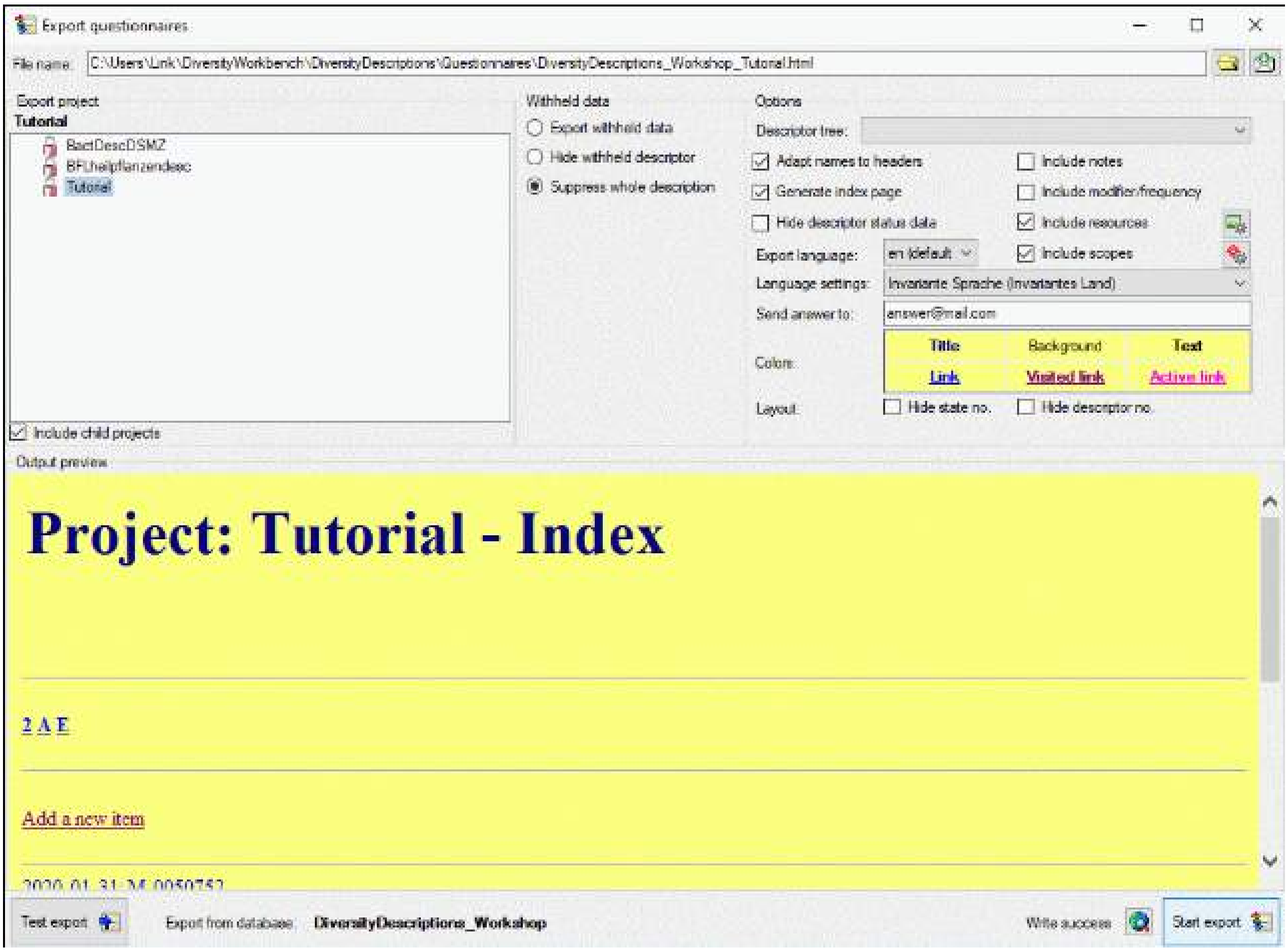
Item name:
New item

Scopes
Sex: ☐ Female ☐ Hermaphrodite ☐ Male ☐ Unknown sex

Export from database: **DiversityDescriptions_Workshop**

Export

Before starting the export, the export file name should be checked. The file name is generated as **<resources directory>\Questionaires\<Database name>_<Project>.txt**. This default setting may be changed by editing the **File name** or by navigating at the target location by pressing the 📂button besides the file name. To the selected name the description id rsp. "_Index" will be appended for the generated file.


Export questionnaires

File name: C:\Users\Link\DiversityWorkbench\DiversityDescriptions\Questionnaires\DiversityDescriptions_Workshop_Tutorial.html

Export project
Tutorial
- BactDescDSMZ
- BFLhelpflanzendesc
- Tutorial

☑ Include child projects

Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

Options
Descriptor tree:
☑ Adapt names to headers
☐ Include notes
☑ Generate index page
☐ Include modifier/frequency
☐ Hide descriptor status data
☑ Include resources
Export language: en (default)
☑ Include scopes
Language settings: Invariante Sprache (Invariantes Land)
Send answer to: answer@mail.com
Colors: Title, Background, Text, Link, Visited link, Active link
Layout: ☐ Hide state no. ☐ Hide descriptor no.

Output preview

Project: Tutorial - Index

2 A E

Add a new item

Test export
Export from database: **DiversityDescriptions_Workshop**
Write success
Start export

To generate the HTML files press the **Start export** button. During export the icon of the button changes to and you may abort processing by clicking the button. Button opens the form visible in the **Output preview** section in an external web browser (see image above).

Send reply

When you opened a HTML form in the web browser and modified data, you may download them as a text file for database import. At the bottom of the HTMS form click the button **Download revised description** (see image below). Since data collection is done using javascript, please take care that the script is not blocked by the web browser.


Send data to: *answer located at server mail.com*

Download revised description
Reset form

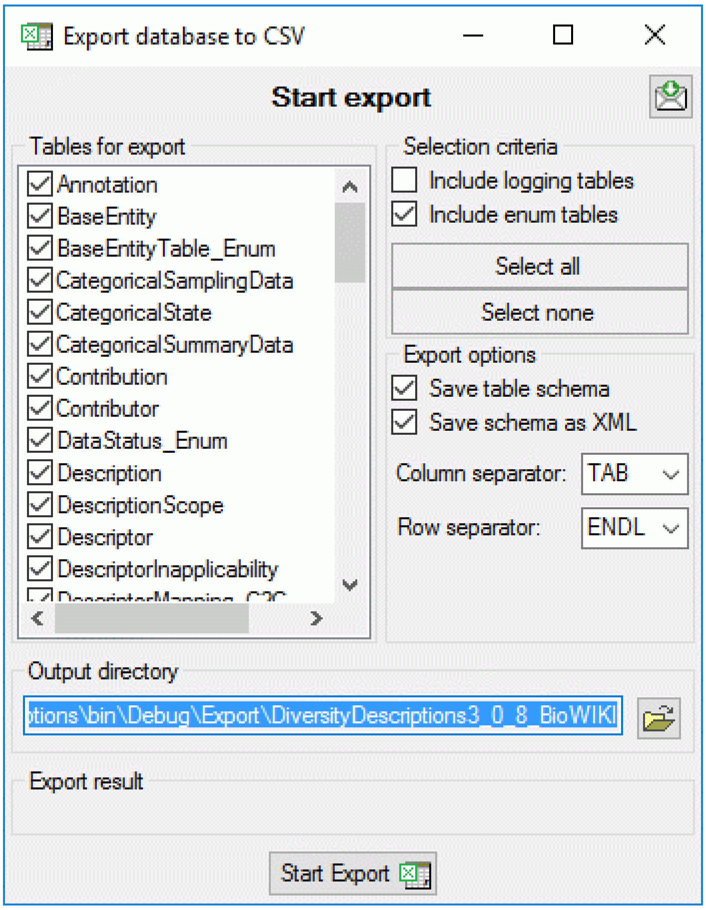
To download data please allow javascript in your browser!

Export CSV

Notes:

- The **Export CSV** function provides a direct copy of selected database table as tabulator separated text file. If you want to generate flles that give a strutured overview of descriptors or description data, you should prefer the **Export ... Lists** or the **Export Wizard** (coming soon).
- The **Export CSV** function requires the "Bulk Copy" tool, which is part of a local Microsoft SQL Server installation. If "Bulk Copy" is not available on your computer, you will get an error message after opening the window.

To export the tables of the database in the a tabulator, comma or semicolon separated format, choose **Data -> Export -> Export CSV ...** from the menu. A window as shown below will open where you can select the tables to be exported in sections **Selection criteria** and in the **Tables for export**.



Tables for export
☑ Annotation
☑ BaseEntity
☑ BaseEntityTable_Enum
☑ CategoricalSamplingData
☑ CategoricalState
☑ CategoricalSummaryData
☑ Contribution
☑ Contributor
☑ DataStatus_Enum
☑ Description
☑ DescriptionScope
☑ Descriptor
☑ DescriptorInapplicability

Selection criteria
☐ Include logging tables
☑ Include enum tables

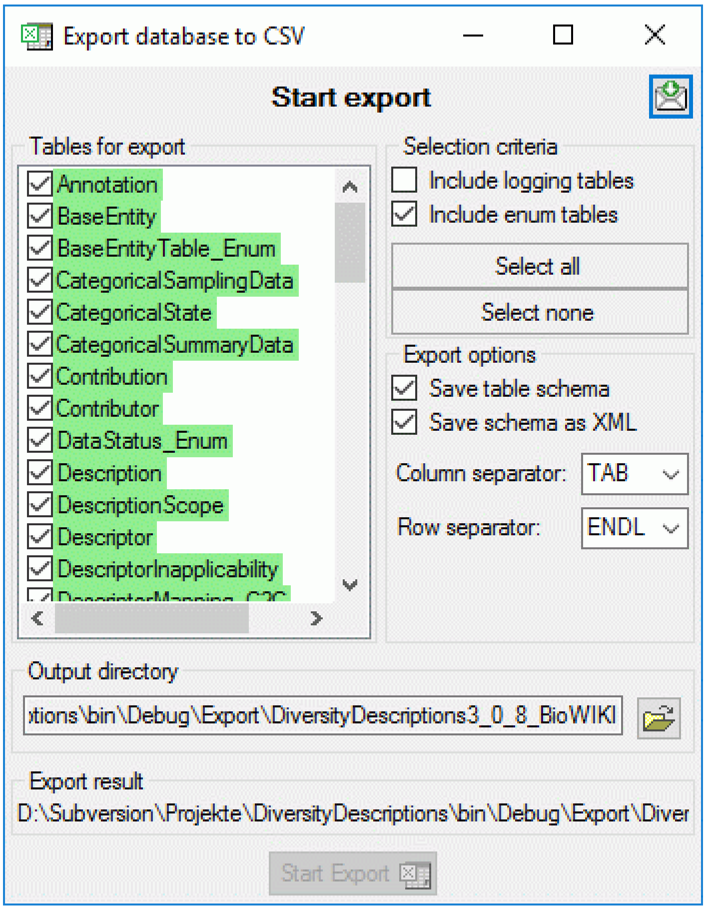
Export options
☑ Save table schema
☑ Save schema as XML

Column separator: TAB
Row separator: ENDL

Output directory
ptions\bin\Debug\Export\DiversityDescriptions3_0_8_BioWIKI

Export result

To start the export click on the **Start export** button. By default the data will be exported into a directory **<working directory>\Export\<database_name>**. Click on the button to select a different target directory before starting export.



Tables for export

☑ Annotation
☑ BaseEntity
☑ BaseEntityTable_Enum
☑ CategoricalSamplingData
☑ CategoricalState
☑ CategoricalSummaryData
☑ Contribution
☑ Contributor
☑ DataStatus_Enum
☑ Description
☑ DescriptionScope
☑ Descriptor
☑ DescriptorInapplicability
☑ DescriptorMapping_C2C

Selection criteria

☐ Include logging tables
☑ Include enum tables

Export options

☑ Save table schema
☑ Save schema as XML

Column separator: TAB
Row separator: ENDL

Output directory

tions\bin\Debug\Export\DiversityDescriptions3_0_8_BioWIKI

Export result

D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\Diver

After export the tables are marked with green backgound, if table schema and data were exported successfully. If only the data were exported, this is marked with yellow background, if nothing was exported, the background is red. A detailled export report can be viewd by a click on the export result file name.

File operations

Without any database access data files may be converted in the following directions:

Convert SDD file: Read an XML file according to the SDD schema 1.1 rev 5 and generate DELTA or EML files.

Convert DELTA file: Read DELTA text file(s) and generate SDD or EML files.

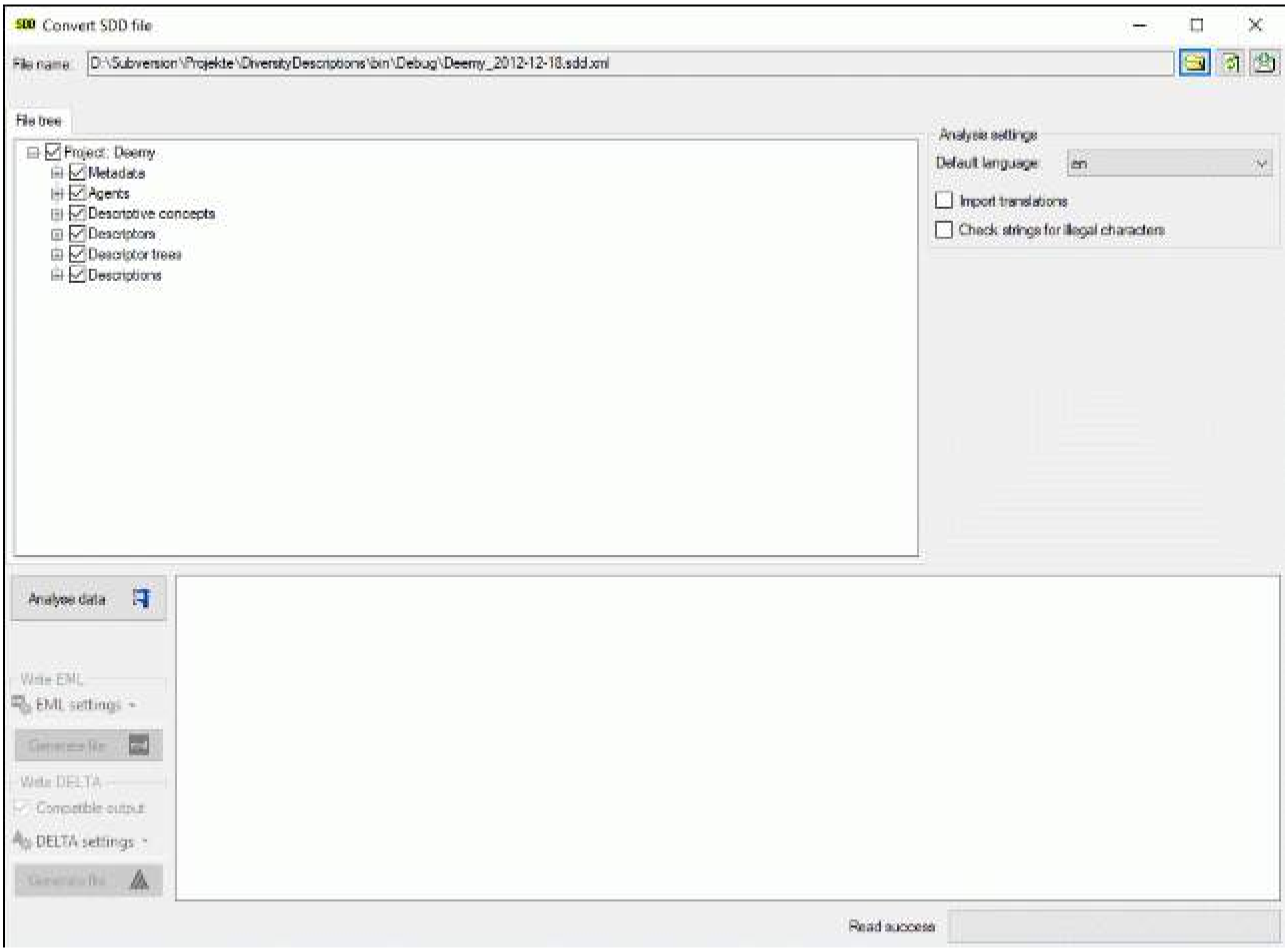
Additionally XML file check tools are available:

Check SDD file: Check if a text file is an XML file according to the SDD schema 1.1 rev 5.

Check EML file: Check if a text file is an XML file according to the EML schema 2.1.1.

Convert SDD file to DELTA or EML

With this form you can directly convert data from a file in XML file according schema SDD 1.1 rev 5 into a DELTA file. No connection to a database is needed for the conversion. Choose **Data -> File operations -> Convert data file -> SDD to DELTA ...** from the menu to open the window. In the window click on the button to select the file with the data you want to convert. If during analysis any problem occurs, you may click on the button to reload the file and re-initialize the window.


File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy_2012-12-18.sdd.xml

File tree
- ☑ Project: Deemy
  - ☑ Metadata
  - ☑ Agents
  - ☑ Descriptive concepts
  - ☑ Descriptors
  - ☑ Descriptor trees
  - ☑ Descriptions

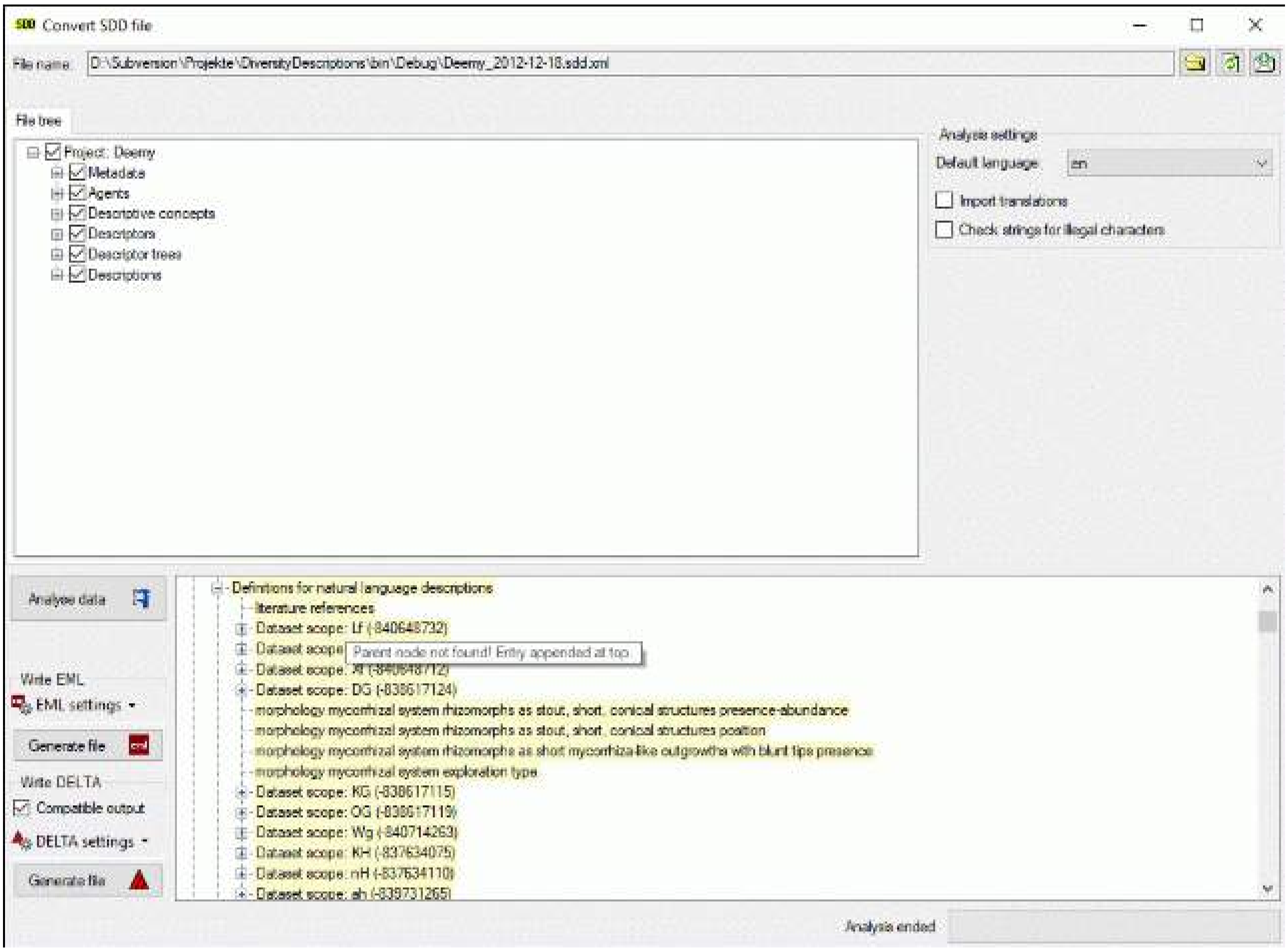
Analysis settings
Default language: en
☐ Import translations
☐ Check strings for illegal characters

The contents of the file will be shown in the upper part of the **File tree** tab page. In the **Analysis settings** part you find the documents' default language. If additional laguages are contained in the document, you may select one of them as the new language of the DELTA file. By checking **Import translations** you select all additional document languages for the analysis step. This option is automatically pre-selected if more than one language has been found in the file. In the bottom part of the window you find the actual processing state.

In the file tree you may deselect entries that shall not be imported into the database. Use that option very carefully, because if you deselect entries that are being referenced by other parts of the input tree, e.g. descriptors referenced by descriptions, the analysis step might become erronous!

Analysis

To analyse the data in the file click on the **Analyse data** button. During the analysis the program checks the dependencies between the different parts of the data and builds up an analysis tree in the lower part of the window. The analysis tree contains all data in a suitable format for the final step. During data analysis the icon of the button changes to STOP and you may abort processing by clicking the button.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy_2012-12-18.sdd.xml

- ☑ Project: Deemy
  - ☑ Metadata
  - ☑ Agents
  - ☑ Descriptive concepts
  - ☑ Descriptors
  - ☑ Descriptor trees
  - ☑ Descriptions

Default language: en

☐ Import translations

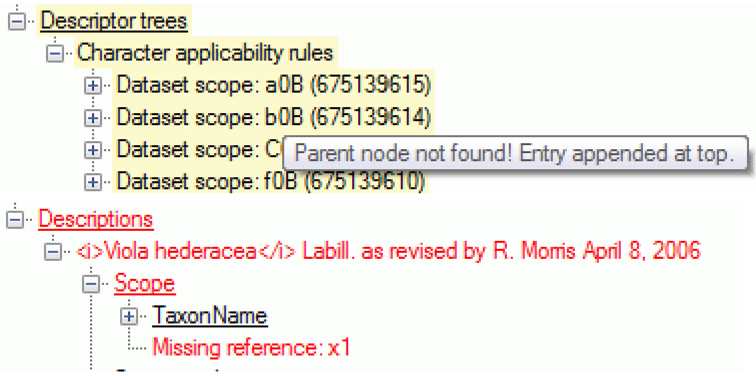
☐ Check strings for illegal characters

☑ Compatible output

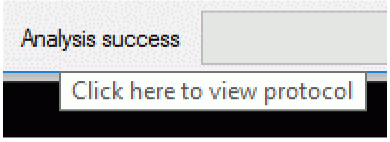
- Definitions for natural language descriptions
  - literature references
  - Dataset scope: Lf (-840648732)
  - Dataset scope Parent node not found! Entry appended at top.
  - Dataset scope: Al (-840648712)
  - Dataset scope: DG (-838617124)
  - morphology mycorrhizal system rhizomorphs as stout, short, conical structures presence-abundance
  - morphology mycorrhizal system rhizomorphs as stout, short, conical structures position
  - morphology mycorrhizal system rhizomorphs as short mycorrhiza-like outgrowths with blunt tips presence
  - morphology mycorrhizal system exploration type
  - Dataset scope: KG (-838617115)
  - Dataset scope: OG (-838617119)
  - Dataset scope: Wg (-840714263)
  - Dataset scope: KH (-837634075)
  - Dataset scope: nH (-837634110)
  - Dataset scope: ah (-839731265)

Analysis ended

After analysis a message window informs you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as tool tip or the tree node text itself tells the problem (see examples below). By clicking on the status text besides the progress bar, you can open an analysis protocol (see below, right).



- Descriptor trees
  - Character applicability rules
    - Dataset scope: a0B (675139615)
    - Dataset scope: b0B (675139614)
    - Dataset scope: C Parent node not found! Entry appended at top.
    - Dataset scope: f0B (675139610)
- Descriptions
  - <i>Viola hederacea</i> Labill. as revised by R. Morris April 8, 2006
    - Scope
      - TaxonName
      - Missing reference: x1



Analysis success

Click here to view protocol

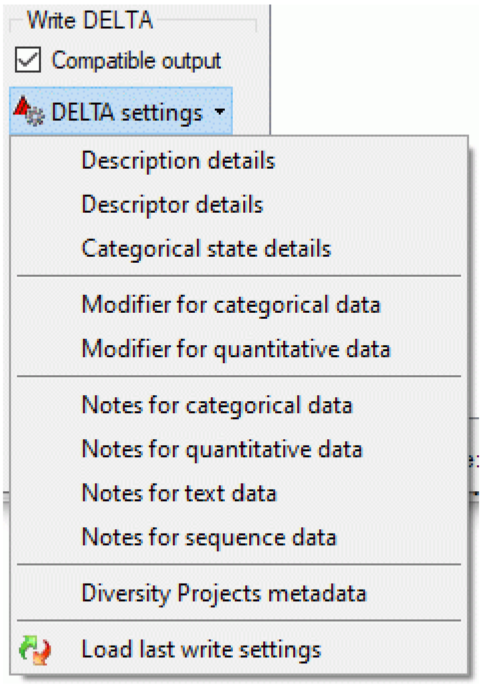
If an analysis error occured, you are not able to proceed. You will first have to correct the problem, e.g. by excluding the erronous descriptor in the example above (after reloading the file). If a warning occured, it might not cause further problems, but you should take a closer look if the converted data will be correct.

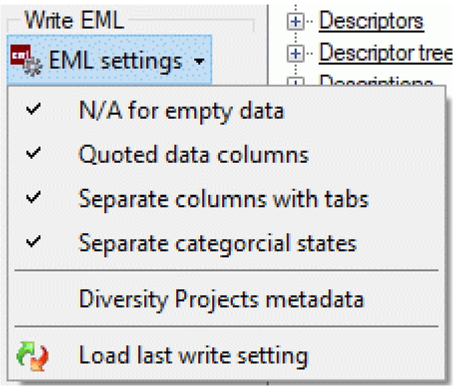
Write data

Pressing the **Generate file** button in the **Write Delta** group box opens a window to select the target delta file. By default the target file has the same name as the SDD file, followed by the extension ".dat". The **Comptible** option controls generation of files with most possible compatibility to the DELTA standard. On the other hand some data might not be present in the generated file, if this option is activated.

As an additional option you may generate file according the EML schema, which consists of a data table (tabulator separated text file) and an XML file that contains the metadata including column descriptions. Click on the **Generate file** button in the **Write EML** group box. The generated file names will have the endings **"_EML_DataTable.txt"** and **"_EML_Metadata.xml"**.

Pressing the drop down button **DELTA settings** in the **Write DELTA** group box opens the DELTA writer options. You can chose to include some detail text and notes in the DELTA output (see left image below). For descriptions, descriptors or categorical states the details will be appended as DELTA comments (included in angle brackets "< ... >") to the respective titles. The notes will be appended as DELTA comments of the corresponding summary data. If you already generated DELTA files, the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **DELTA settings** to close the option panel.





Pressing the drop down button **EML settings** in the **Write EML** group box opens the EML writer options. You can chose to include a special sign for empty column values or set the columns values in quotes (see right image above). Furthermore you may shose the column separator (tab stop rsp. comma) an decide if multiple categorical states shall be inserted as separate data columns. If you already generated EML files, the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **EML settings** to close the option panel.

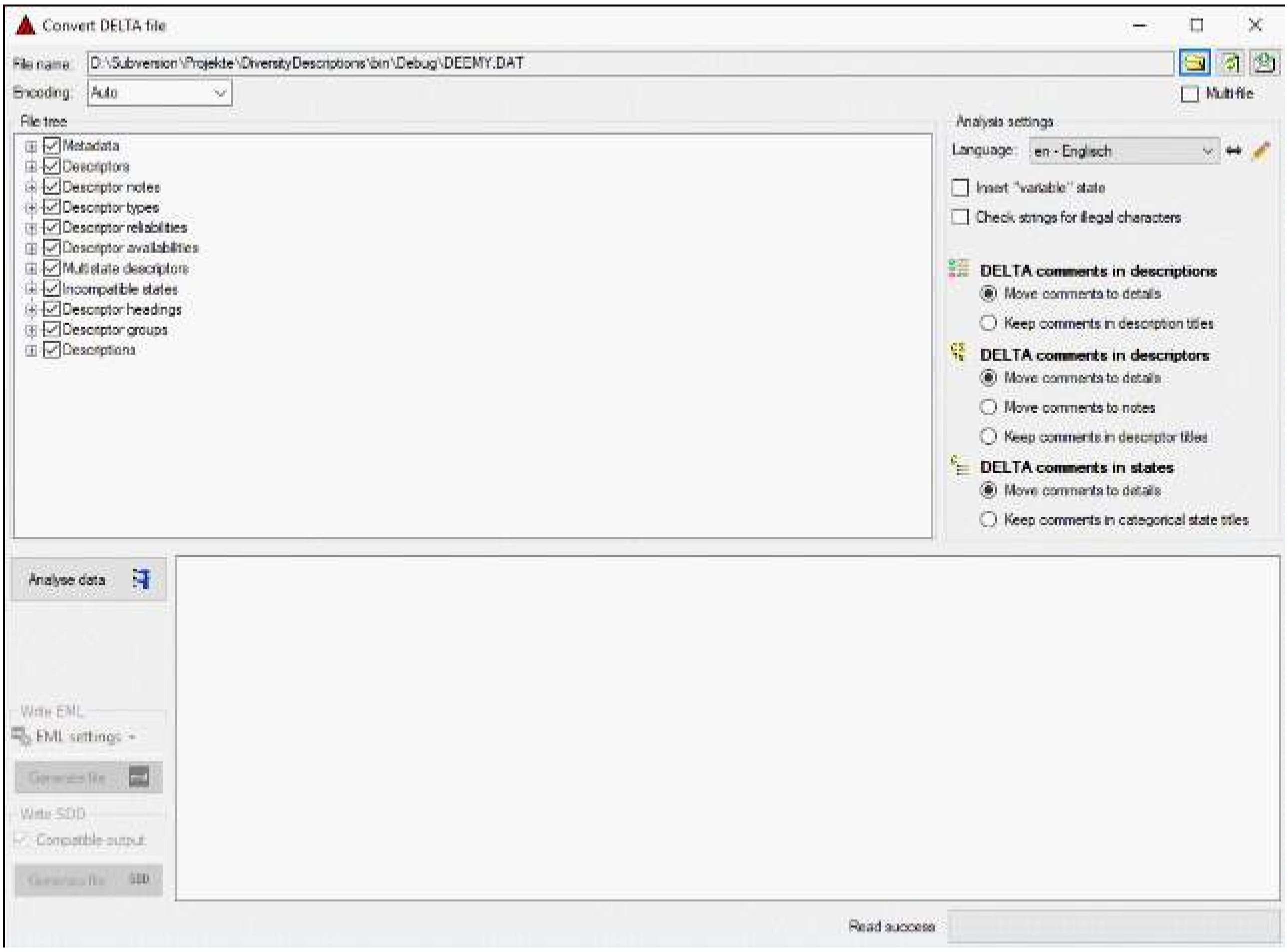
Handling of special sequence data

While SDD can handle molecular sequence data, for DELTA export these data will be exported as text data. To preserve the sequence specific descriptor data, they will be inserted into the text character as a special comment with the format, e.g. "#6. Sequence descriptor <**[SequenceCharacter][ST:N][SL:1][GS:-][/SequenceCharacter]**>/".

If the analysis tree includes sample data, they will be included as items at the end of the DELTA file. The naming of those spetial items will be **<description name> - <event name> - Unit <number>**. Sampling event data will not be included in the DELTA file.

Convert DELTA file to SDD or EML

With this form you can directly convert data from a file in DELTA format into an XML file according schema [SDD 1.1 rev 5](). No connection to a database is needed for the conversion. Choose **Data -> File operations -> Convert data file -> DELTA to SDD ...** from the menu to open the window. In the window click on the button to select the file with the data you want to convert. If the **Multi-file** option is selected before pressing the button, a folder selection window opens to select the folder where the DELTA files are located. For muti-file processing currently the files "chars", "items", "specs" and "extra" are evaluated. If during analysis any problem occurs, you may click on the button to reload the file and re-initialize the window.



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\DEEMY.DAT

Encoding: Auto

☐ Multi-file

File tree

- ☑ Metadata
- ☑ Descriptors
- ☑ Descriptor notes
- ☑ Descriptor types
- ☑ Descriptor reliabilities
- ☑ Descriptor availabilities
- ☑ Multistate descriptors
- ☑ Incompatible states
- ☑ Descriptor headings
- ☑ Descriptor groups
- ☑ Descriptions

Analysis settings

Language: en - Englisch

☐ Insert "variable" state

☐ Check strings for illegal characters

DELTA comments in descriptions

● Move comments to details

○ Keep comments in description titles

DELTA comments in descriptors

● Move comments to details

○ Move comments to notes

○ Keep comments in descriptor titles

DELTA comments in states

● Move comments to details

○ Keep comments in categorical state titles

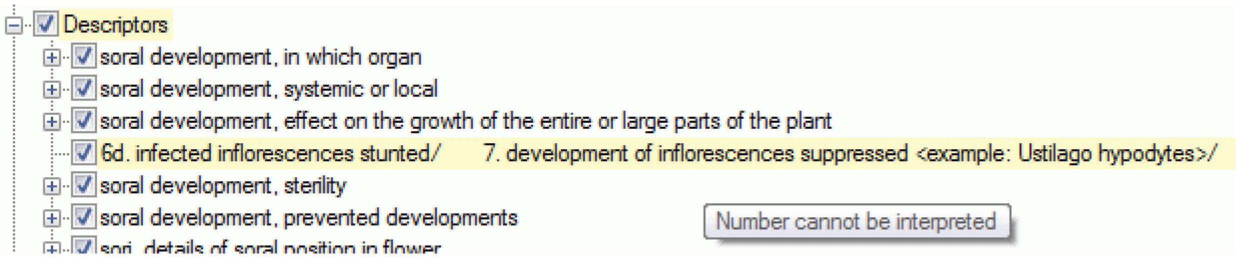
The contents of the file will be shown in the upper part of the **File tree** tab page. If special characters are not displayed corretly, try a different **Encoding** setting, e.g. "ANSI", and reload the document using the button.

The **Insert "variable" state** controls the handling of the DELTA state "V" for categorical summary data. If possible, a categorical state "variable" is inserted to the descriptor data and set in the summary data, when the state "V" is present in the description data.

If the **Check strings for illegal characters** option is checked, all string literals that shall be exported from database are scanned for illegal non-printable characters and matches are replaced by a double exclamation mark ("‼"). Activating this option may increase the analysis processing time.

In the file tree you may deselect entries that shall not be converted. Use that option very carefully, because if you deselect entries that are being referenced by other parts of the input tree, e.g. descriptors referenced by descriptions, the analysis step might become erronous!

If during reading of the files expressions cannot be interpreted, suspicious entries are maked with yellow background (warning) in the file tree. When you move the mouse curser over the marked entries, you get additional information as tool tip or the tree node text itself tells the problem (see example below).



☑ Descriptors
- ☑ soral development, in which organ
- ☑ soral development, systemic or local
- ☑ soral development, effect on the growth of the entire or large parts of the plant
- ☑ 6d. infected inflorescences stunted/ 7. development of inflorescences suppressed <example: Ustilago hypodytes>/
- ☑ soral development, sterility
- ☑ soral development, prevented developments
- ☑ sori, details of soral position in flower

Number cannot be interpreted

Analysis

To analyse the data in the file click on the **Analyse data** button. During the analysis the program checks the dependencies between the different parts of the data and builds up an analysis tree in the lower part of the window. The analysis tree contains all data in a suitable format for the final step. During data analysis the icon of the button changes to and you may abort processing by clicking the button.

In the **Analysis settings** section (see image below) you set the document's **Language**. You man change the display and sorting of the entries in the **Language** combo box from "<code> - <description>" to "<description> - <code>" (and back) by clicking the button ⇔. If you need language codes that are not included in the list, click the button. For more details see Edit language codes.

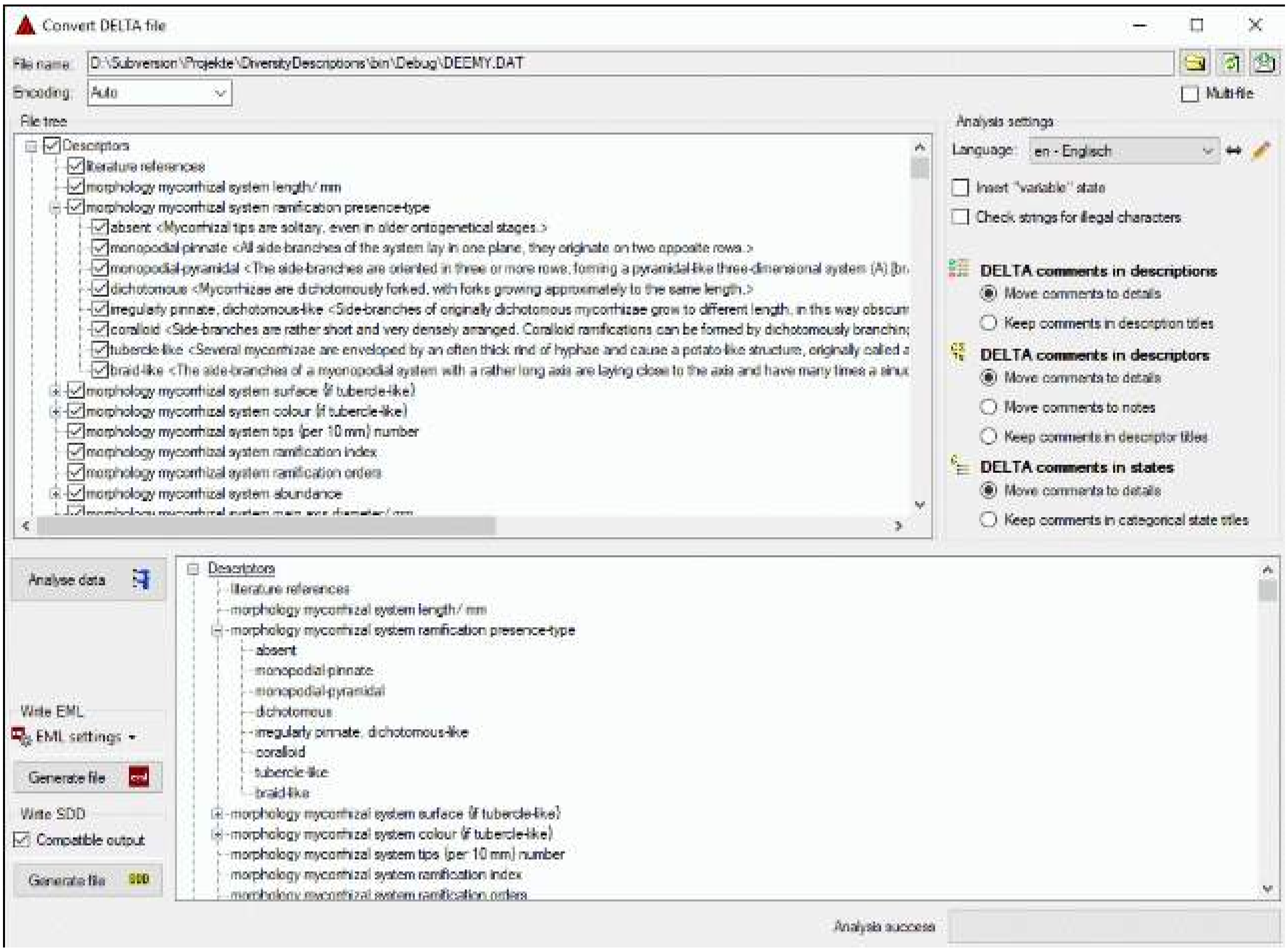
The **Insert "variable" state** controls the handling of the DELTA state "V" for categorical summary data. If possible, a categorical state "variable" is inserted to the descriptor data and set in the summary data, when the state "V" is present in the description data.

If the **Check strings for illegal characters** option is checked, all string literals that shall be exported from database are scanned for illegal non-printable characters and matches are replaced by a double exclamation mark ("‼"). Activating this option may increase the analysis processing time.

In DELTA text in angle bracket (<text>) usually denotes comments, which are by default imported into the "Details" fields of the database. In the lower parts of the **Analysis settings** you may adjust a different handling for description, descriptor and categorical state items.

- For **DELTA comments in descriptions** you may **Move comments to details** (default) or **Keep comments in description titles**.
- For **DELTA comments in descriptors** you may **Move comments to details** (default), **Move comments to notes** or **Keep comments in descriptor titles**.
- For **DELTA comments in categorical states** you may **Move comments to details** (default) or **Keep comments in categorical state titles**.

After changing one of these settings click on the **Analyse data** button to make the changes effective.



Convert DELTA file

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\DEEMY.DAT

Encoding: Auto

☐ Multi-file

File tree

- ☑ Descriptors
  - ☑ literature references
  - ☑ morphology mycorrhizal system length/ mm
  - ☑ morphology mycorrhizal system ramification presence-type
    - ☑ absent <Mycorrhizal tips are solitary, even in older ontogenetical stages.>
    - ☑ monopodial-pinnate <All side-branches of the system lay in one plane, they originate on two opposite rows.>
    - ☑ monopodial-pyramidal <The side-branches are oriented in three or more rows, forming a pyramidal-like three-dimensional system (A) [br
    - ☑ dichotomous <Mycorrhizae are dichotomously forked, with forks growing approximately to the same length.>
    - ☑ irregularly pinnate, dichotomous-like <Side-branches of originally dichotomous mycorrhizae grow to different length, in this way obscur
    - ☑ coralloid <Side-branches are rather short and very densely arranged. Coralloid ramifications can be formed by dichotomously branchin
    - ☑ tubercle-like <Several mycorrhizae are enveloped by an often thick rind of hyphae and cause a potato-like structure, originally called a
    - ☑ braid-like <The side-branches of a myonopodial system with a rather long axis are laying close to the axis and have many times a sinu
  - ☑ morphology mycorrhizal system surface (if tubercle-like)
  - ☑ morphology mycorrhizal system colour (if tubercle-like)
  - ☑ morphology mycorrhizal system tips (per 10 mm) number
  - ☑ morphology mycorrhizal system ramification index
  - ☑ morphology mycorrhizal system ramification orders
  - ☑ morphology mycorrhizal system abundance

Analysis settings

Language: en - Englisch

☐ Insert "variable" state

☐ Check strings for illegal characters

DELTA comments in descriptions

● Move comments to details

○ Keep comments in description titles

DELTA comments in descriptors

● Move comments to details

○ Move comments to notes

○ Keep comments in descriptor titles

DELTA comments in states

● Move comments to details

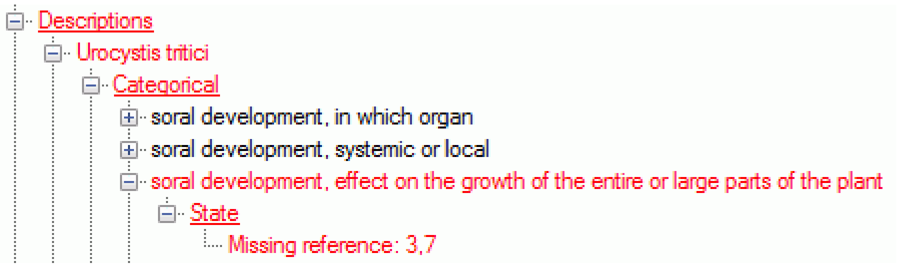
○ Keep comments in categorical state titles

☑ Compatible output

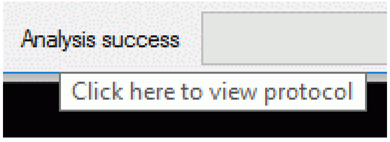
- Descriptors
  - literature references
  - morphology mycorrhizal system length/ mm
  - morphology mycorrhizal system ramification presence-type
    - absent
    - monopodial-pinnate
    - monopodial-pyramidal
    - dichotomous
    - irregularly pinnate, dichotomous-like
    - coralloid
    - tubercle-like
    - braid-like
  - morphology mycorrhizal system surface (if tubercle-like)
  - morphology mycorrhizal system colour (if tubercle-like)
  - morphology mycorrhizal system tips (per 10 mm) number
  - morphology mycorrhizal system ramification index
  - morphology mycorrhizal system ramification orders

Analysis success

After analysis a message window informs you if any warnings or errors occured. You can find detailled error and warning information at the file and/or analysis trees by entries with red text (error) or yellow background (warning). When you move the mouse curser over the marked entries, you get additional information as bubble help or the tree node text itself tells the problem (see example below). By clicking on the status text besides the progress bar, you can open an analysis protocol (see below, right).



- Descriptions
  - Urocystis tritici
    - Categorical
      - soral development, in which organ
      - soral development, systemic or local
      - soral development, effect on the growth of the entire or large parts of the plant
        - State
          - Missing reference: 3,7



Analysis success

Click here to view protocol

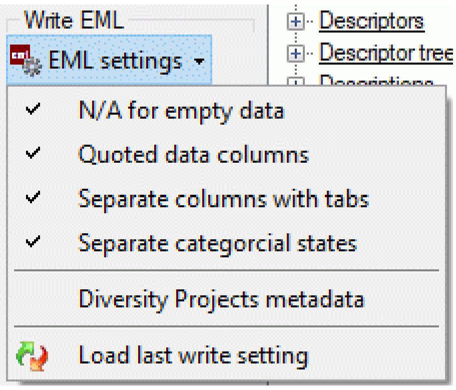
If an analysis error occured, you are not able to proceed. You will first have to correct the problem, e.g. by excluding the erronous descriptor in the example above (after reloading the file). If a warning occured, it might not cause further problems, but you should take a closer look if the converted data will be correct.

Write data

Pressing the **Generate file** SDD button in the **Write SDD** group box opens a window to select the target XML file. By default the target file has the same name as the DELTA file, followed by the extension ".xml". The **Comptible** option controls generation of files with most possible compatibility to the SDD standard. On the other hand some data might not be present in the generated file, if this option is activated.

As an additional option you may generate file according the EML schema, which consists of a data table (tabulator separated text file) and an XML file that contains the metadata including column descriptions. Click on the **Generate file** eml button in the **Write EML** group box. The generated file names will have the endings **"_EML_DataTable.txt"** and **"_EML_Metadata.xml"**.

Pressing the drop down button **EML settings** in the **Write EML** group box opens the EML writer options. You can chose to include a special sign for empty column values or set the columns values in quotes (see left image below). Furthermore you may shose the column separator (tab stop rsp. comma) an decide if multiple categorical states shall be inserted as separate data columns. If you already generated EML files, the used settings will be automatically saved and you may restore them using the option **Load last write settings**. Finally click button **EML settings** to close the option panel.



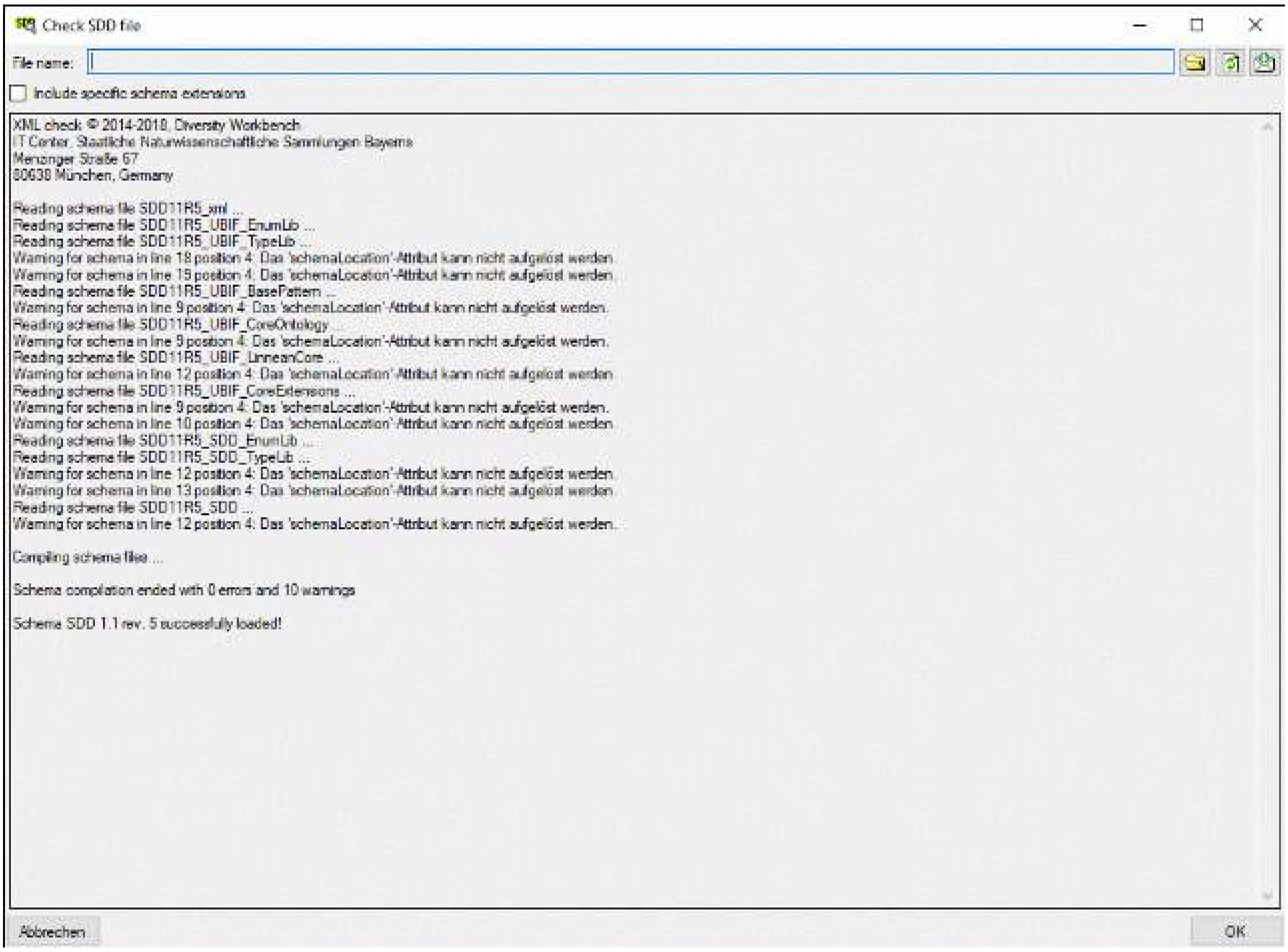
Handling of special DELTA states

In the DELTA format the special states "**-**" (not applicable), "**U**" (unknown) and "**V**" (variable) are available for categorical and quantitative characters. These states are treated in the folloging manner during import:

- "**-**" (not applicable)
  The data status "**Not applicable**" is set.
- "**U**" (unknown)
  The data status "**Data unavailable**" is set.
- "**V**" (variable)
  The data status "**Not interpreterable**" is set.

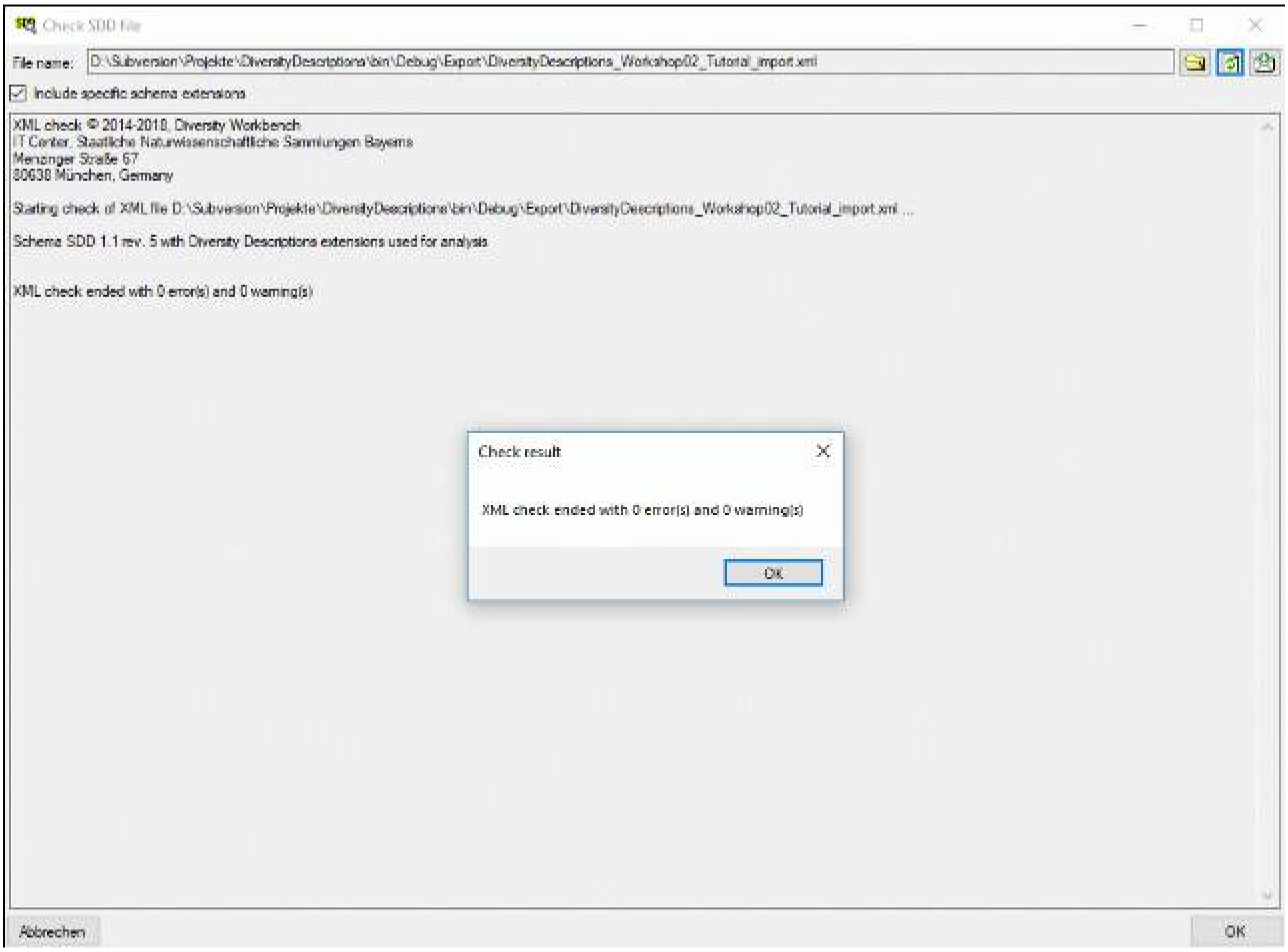
Check SDD file

With this form you can check if an XML file is compliant to the SDD 1.1 rev 5 schema. Choose **Data -> File operations -> Check SDD file ...** from the menu. After opening the window shown below the schema files will be automatically loaded.



```
XML check © 2014-2018, Diversity Workbench
IT Center, Staatliche Naturwissenschaftliche Sammlungen Bayerns
Menzinger Straße 67
80638 München, Germany

Reading schema file SDD11R5_xml ...
Reading schema file SDD11R5_UBIF_EnumLib ...
Reading schema file SDD11R5_UBIF_TypeLib ...
Warning for schema in line 18 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 19 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_UBIF_BasePattern ...
Warning for schema in line 9 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_UBIF_CoreOntology ...
Warning for schema in line 9 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_UBIF_LinneanCore ...
Warning for schema in line 12 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_UBIF_CoreExtensions ...
Warning for schema in line 9 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 10 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_SDD_EnumLib ...
Reading schema file SDD11R5_SDD_TypeLib ...
Warning for schema in line 12 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 13 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file SDD11R5_SDD ...
Warning for schema in line 12 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.

Compiling schema files ...

Schema compilation ended with 0 errors and 10 warnings

Schema SDD 1.1 rev. 5 successfully loaded!
```

In the window click on the button to select the file you want to check. The check results will be diplayed in the center part of the window. If you generated a SDD file using Diversity Descriptions with deactivated **Comptible** option, the check result may show warnings for elements with missing schema information. You may check the option **Include specific schema extensions**, then the Diversity Descriptions specific schema definitions will be included. By clicking the reload button or selecting another file you can start a new check (see image below).



File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DiversityDescriptions_Workshop02_Tutorial_import.xml

☑ Include specific schema extensions

```
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Starting check of XML file D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DiversityDescriptions_Workshop02_Tutorial_import.xml ...

Schema SDD 1.1 rev. 5 with Diversity Descriptions extensions used for analysis


XML check ended with 0 error(s) and 0 warning(s)
```
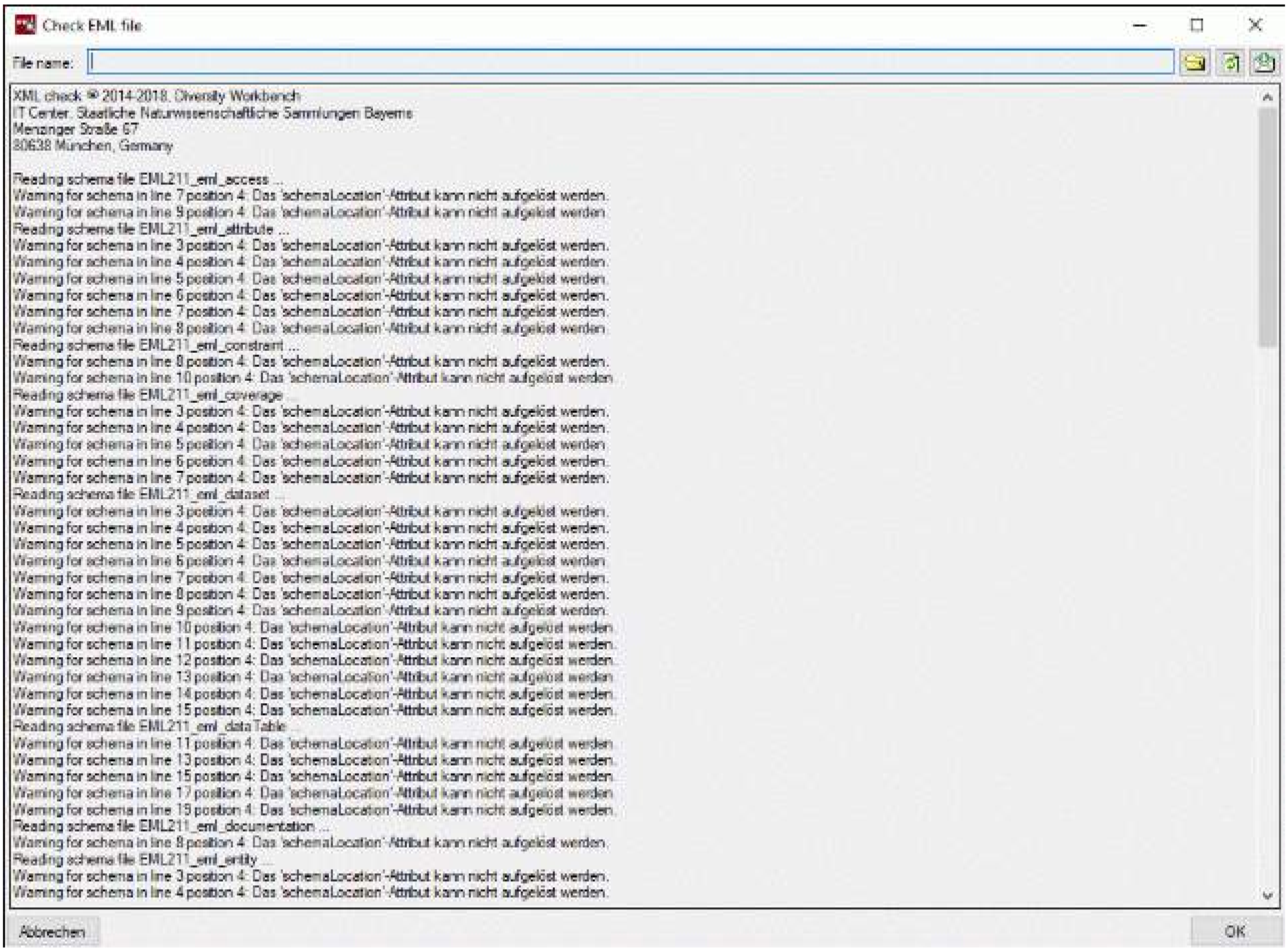

XML check ended with 0 error(s) and 0 warning(s)

Check EML file

With this form you can check if an XML file is compliant to the EML 2.1.1 schema. Choose **Data -> File operations -> Check EML file ...** from the menu. After opening the window shown below the schema files will be automatically loaded.



```
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80638 München, Germany

Reading schema file EML211_eml_access ...
Warning for schema in line 7 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 9 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_attribute ...
Warning for schema in line 3 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 4 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 5 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 6 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 7 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 8 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_constraint ...
Warning for schema in line 8 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 10 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_coverage ...
Warning for schema in line 3 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 4 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 5 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 6 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 7 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_dataset ...
Warning for schema in line 3 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 4 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 5 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 6 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 7 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 8 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 9 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 10 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 11 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 12 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 13 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 14 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 15 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_dataTable ...
Warning for schema in line 11 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 13 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 15 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 17 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 19 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_documentation ...
Warning for schema in line 8 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Reading schema file EML211_eml_entity ...
Warning for schema in line 3 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
Warning for schema in line 4 position 4: Das 'schemaLocation'-Attribut kann nicht aufgelöst werden.
```
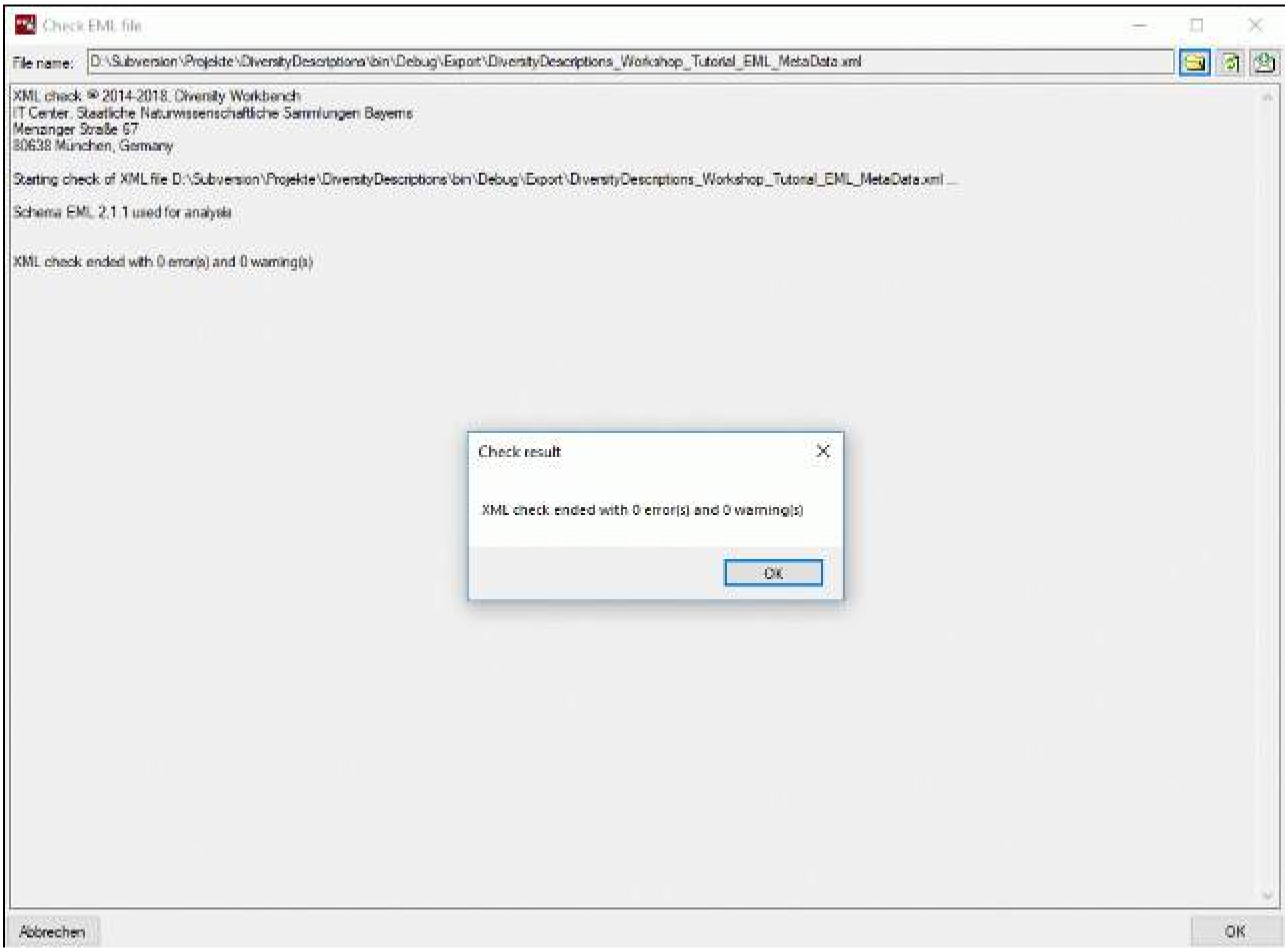

In the window click on the button to select the file you want to check. The check results will be diplayed in the center part of the window. By clicking the reload button you can start a new check (see image below).



```
XML check © 2014-2018, Diversity Workbench
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Starting check of XML file D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DiversityDescriptions_Workshop_Tutorial_EML_MetaData.xml ...

Schema EML 2.1.1 used for analysis


XML check ended with 0 error(s) and 0 warning(s)
```
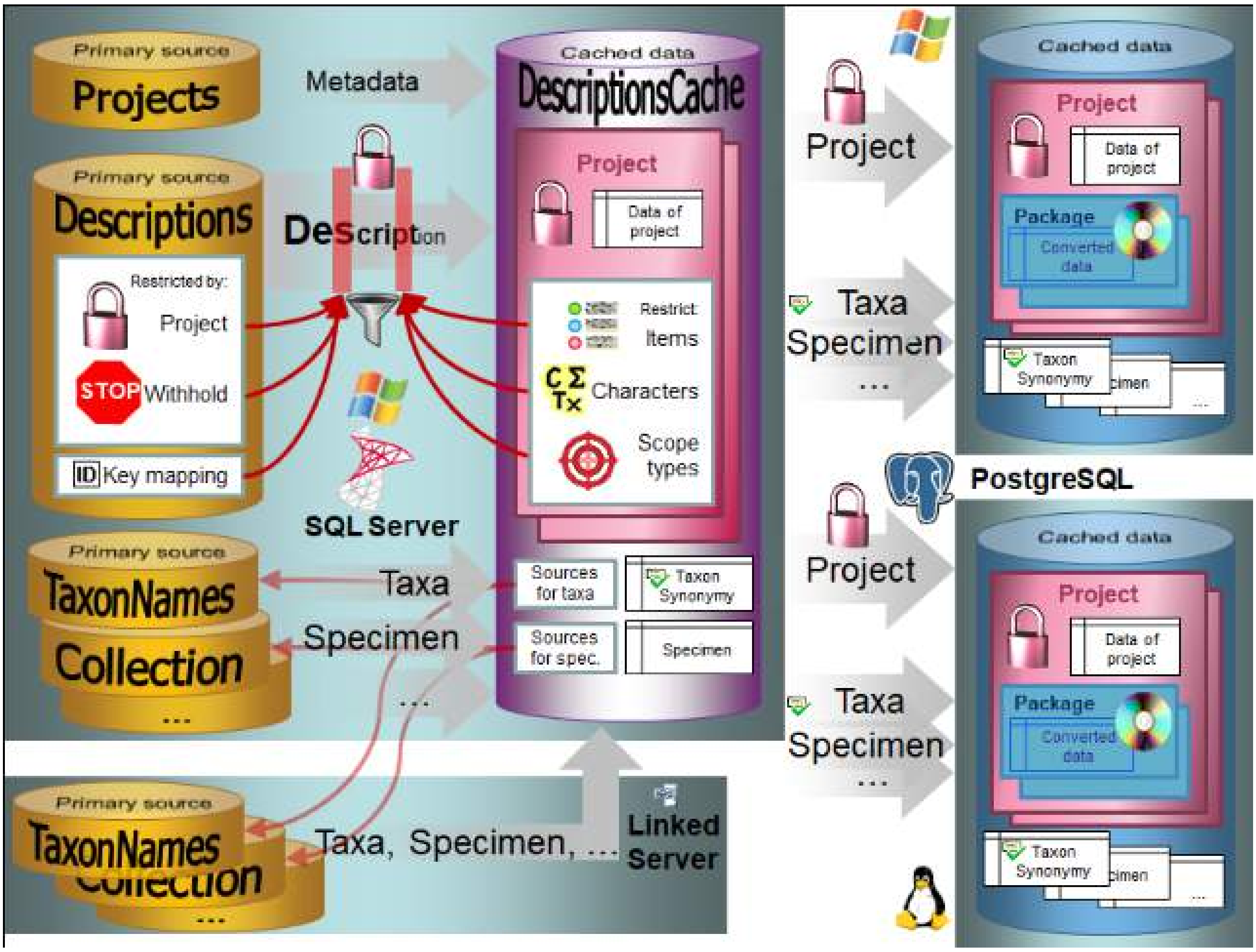

XML check ended with 0 error(s) and 0 warning(s)

Cache database

The cache databases for DiversityDescriptions are designed as sources for preformatted data for publication in e.g. public user portals like GBIF. The cache database by default has a name corresponding to the main source database, e.g. DiversityDescriptionsCache and is located on the same server. By itself it is the source for the data in Postgres (Version 10 or above) cache databases located on any Windows or Linux server (see image below). An overview for the basic steps is provided in chapter Basic steps for publication of data via the cache database.



Generating the cache database

To create a cache database you need to be a system administrator (s. Login administration). The creation of the cache database is described in the chapter Creation of the cache database.

Projects

The publication and transfer of the data is always related to a local project. Every local project has its own database schema containing the data tables etc. The metadata are defined via settings in a DiversityProjects database. The Projects module provides a stable identifier for each Project. The basic address has to be set in the Project module (choose

Administration - Stable identifier ... in the menu). Please turn to the module DiverisityProjects for further information. The metadata will be transferred into a table in the cache database. For further details see chapter Projects in the cache database.

Collections, references, taxonomy and other sources

As well as data from DiversityDescriptions, data from other modules like DiversityCollection containing specimen or observations, DiversityReferences containing citations and DiversityTaxonNames containing the taxonomy, including accepted names and synonyms are transferred into the cache database and may be retrieved from the local server or a linked server. The data of these sources are stored and transferred independent from the project data.

Basic steps for publication of data via the cache database

1 - Create the cache database

To create a cache database as shown in the chapter Creation of the cache databasee you need to be a system administrator (s. Login administration). After this step the cache database should be available and you can create a Postgres database as final target of your data.

2 - Create a Postgres database

The final formatting of the data e.g. for publication via webservice are performed in a Postgres database. If no server providing Postgres is available, you may install Postgres on your local machine (see https://www.postgresql.org/ for further information). The creation and administration of a Postgres database is described in chapter Administration of the Postgres cache databasess.

3 - Insert sources for taxonomic names, collection specimen, references etc.

This step is optional and depends upon the availability of a source for e.g. taxonomic names. You may either use sources from your local server or the public available sources provided by tnt.diversityworkbench.de (turn to http://www.snsb.info for further information). The needed settings are described in chapter Sources from other modules.

4 - Insert a project

The data published in the cache database are organized according to the (local) projects. Add a project as shown in chapter Projects in the cache database. Check the Mapping of IDs in the source database and make sure that the data within this project are not withheld from publication and that the ranges you want to publish are set properly (see chapter Restrictions for the datatransfer into the cache database).

5 - Transfer the data

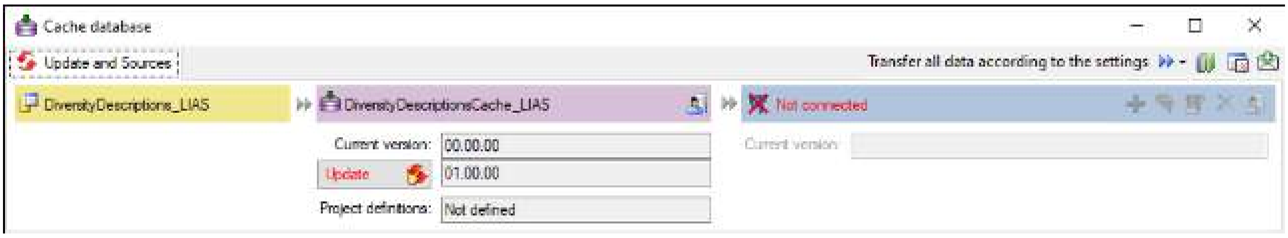
The final transfer of the data is described in chapter Sources for other modules and chapter Transfer of the data.

6 - Publish or export the data

To export the data or prepare them for publication according to the specifications of webservices etc. the data frequently need to be formatted. This is done with packages as described in chapter Administration of the Packages.

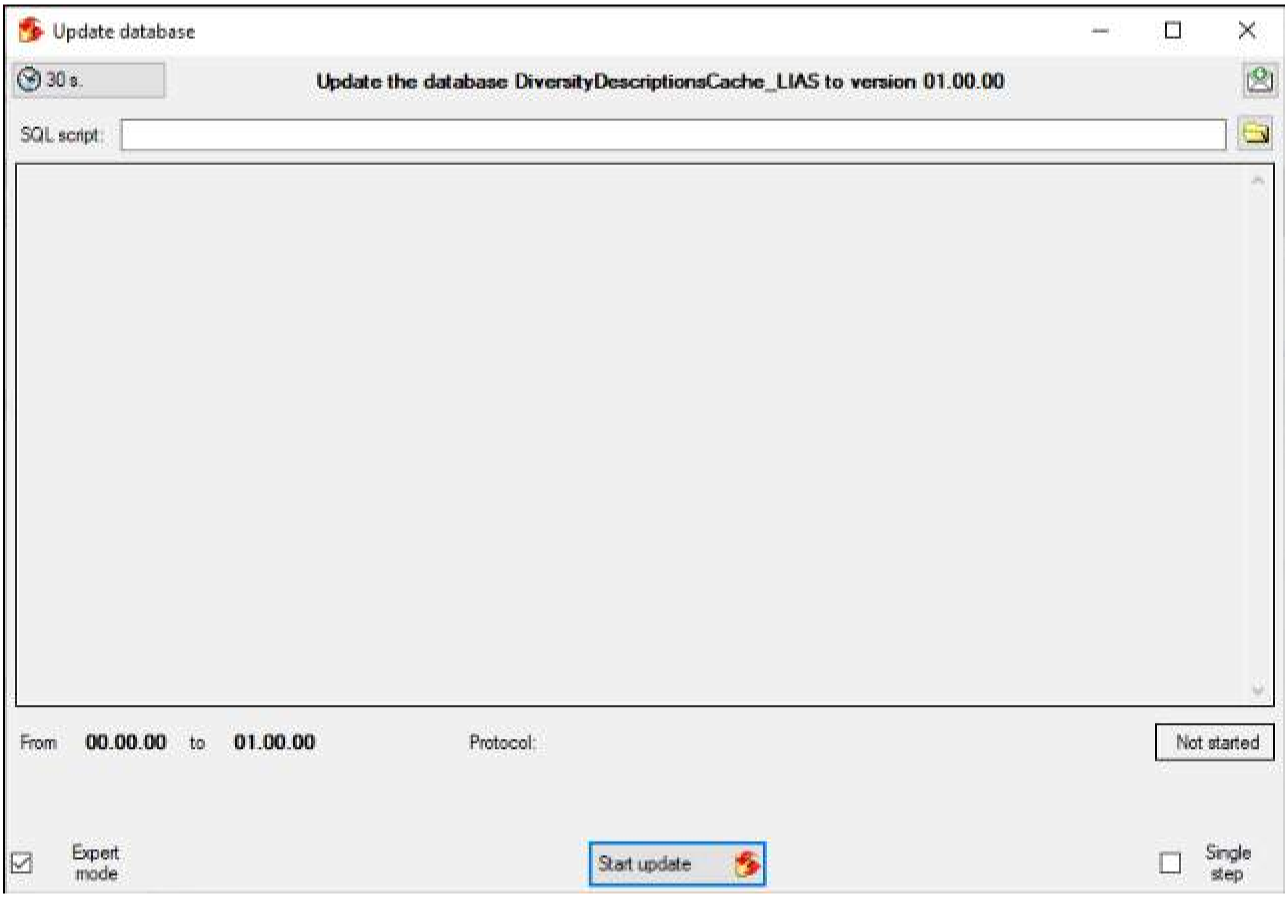
Create the cache database

To create a cache database you need to be a system administrator (s. Login administration). To create the cache database, choose **Data -> Cache database ....** from the menu. If so far no cache database exists, you will be asked if a new one should be generated. After the generation of the cache database a window as shown below will open.



Current version: 00.00.00
Update: 01.00.00
Project definitions: Not defined

Click on the **Update** button to update the database to the latest version. A window as shown below will open. Click on **Start updatee** to execute all the scripts needed for the latest version of the database.



Update the database DiversityDescriptionsCache_LIAS to version 01.00.00

From 00.00.00 to 01.00.00

☑ Expert mode

☐ Single step

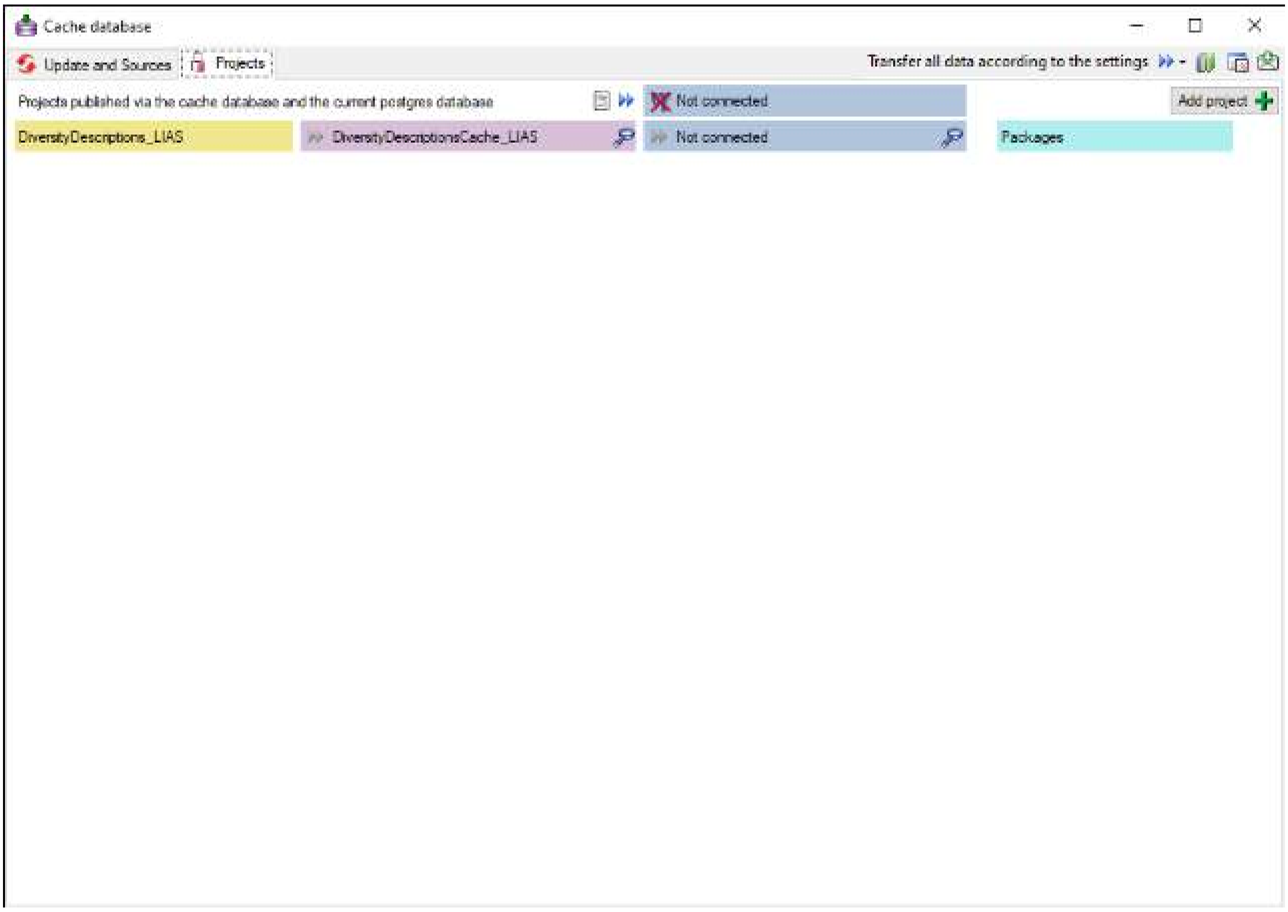
You may now continue with the Administration of the Postgres cache databasess or insert Sources from other modules. Anyway, close and re-open the cache database window before you insert Projects in the cache database.

Sources from other modules

Currently not yet supported!

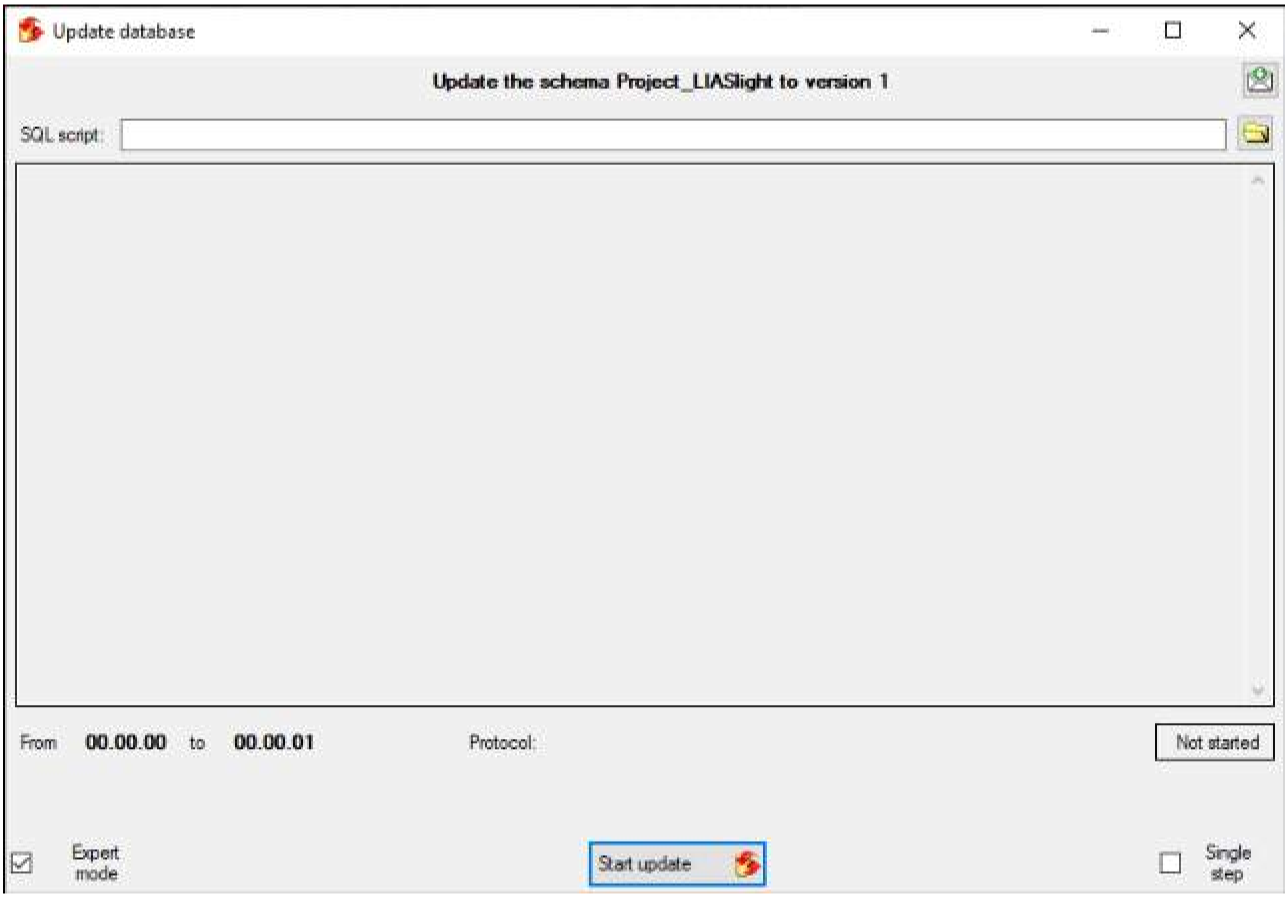
Projects in the cache database

The data transferred into the cache database are always transferred according to a project they belong to. Choose **Data -> Cache database ...** from the menu and select the tab **Projects**. If no projects were added so far the window will appear like shown below.

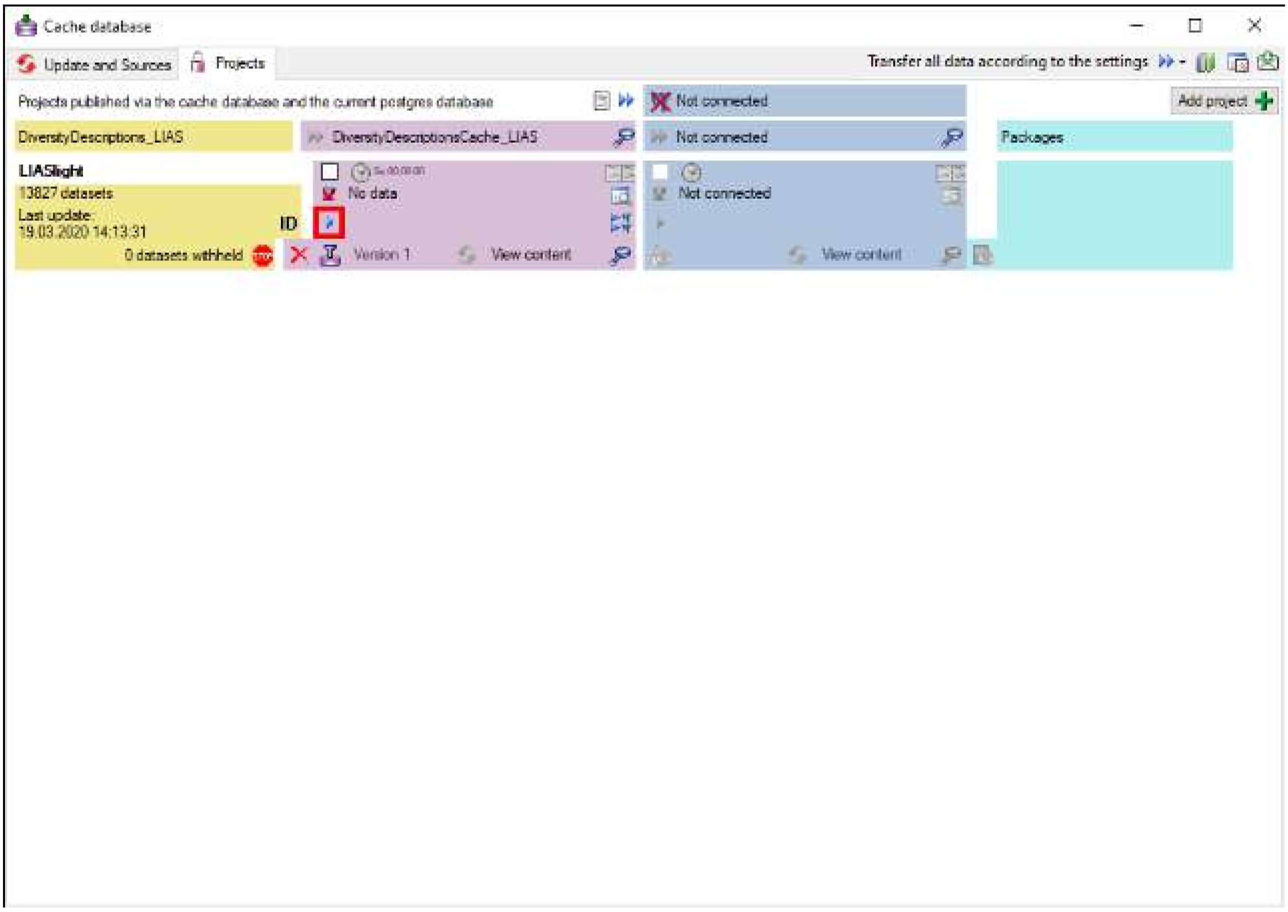


To add a new project for the transfer into the cache database, click on the **Add project** button. In the area below a new entry as shown below will appear. The area on the right shows the number of datasets in the project in the source database together with the date of the last update. To ensure the separation of the data between the projects, DiversityDescriptions creates a separate schema for every project named Project_[name of the project] together with needed roles, tables etc..

Before transferring data you have to update the project schema to the latest version, indicated by the appearance of an **update button** . Click on the button to open a window as shown below. Click on the **Start update** button to update the schema to the latest version. For adding a project and performing the database update you need to be a system administrator (s. Login administration).

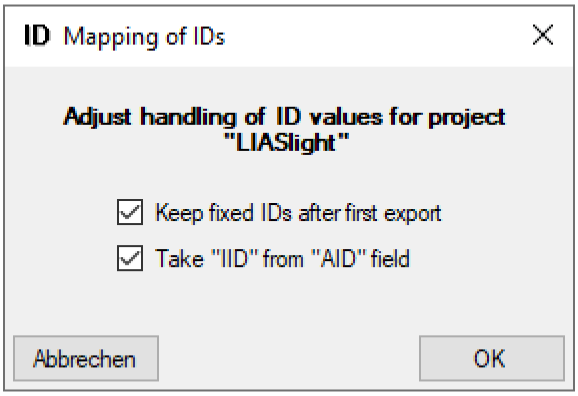


After the update the database is ready to transfer data into.



But before starting the cache transfer you should take a look on the **ID mapping**, **data withholding** and **data restrictions**. The first two items are stored in the descriptions database, the latter in the cache database.

With the ID mapping you can determine how description items, descriptors and categorical states shall be identified in the cach database and how changes are handled in subsequent cache transfers. Click on the ID button to edit the ID mapping behaviour for the data of the project (see below).

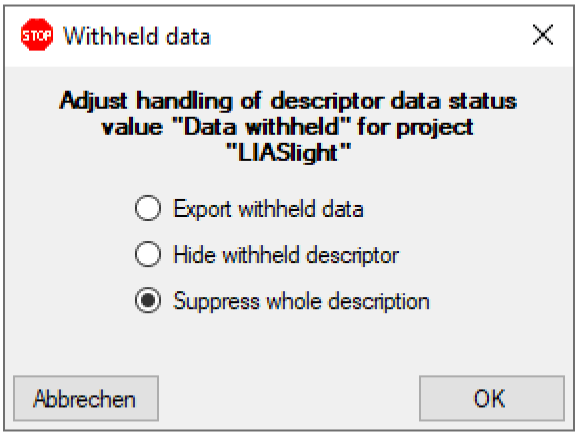


Adjust handling of ID values for project "LIASlight"

☑ Keep fixed IDs after first export

☑ Take "IID" from "AID" field

If any descriptors are marked with the data status Data withheld, you have the options to exclude the whole description the export, to hide only the marked descriptor data or to export the whole dataset. Click on the STOP button to edit the data withholding behaviour for the data of the project (see below).



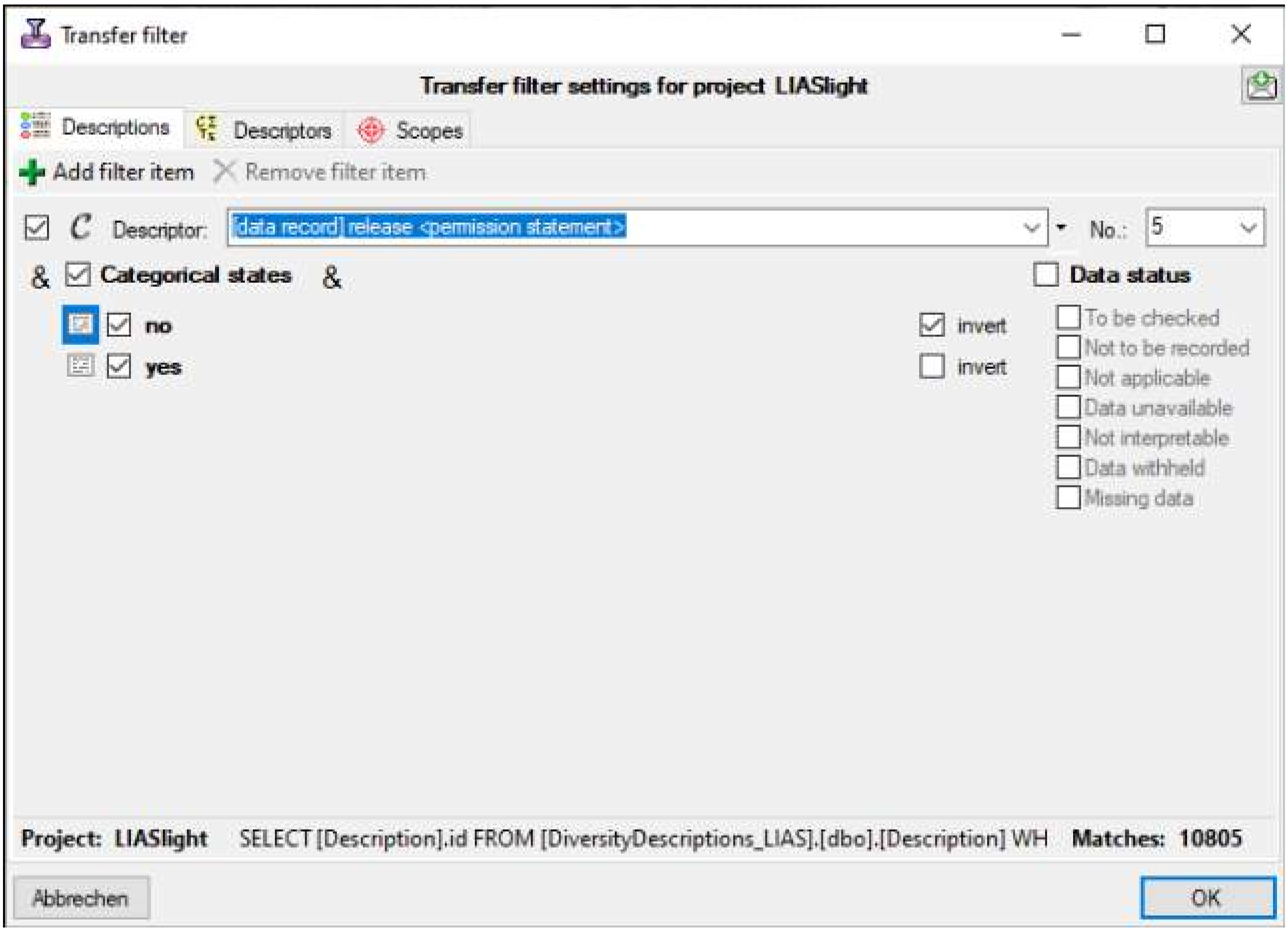
Adjust handling of descriptor data status value "Data withheld" for project "LIASlight"

○ Export withheld data

○ Hide withheld descriptor

● Suppress whole description

Besides the restrictions in the source database, you can set further data restrictions for this transfer. Click on the button and choose the data restrictions for the cache transfer (see below).



Transfer filter settings for project LIASlight

☑ Descriptor: [data record] release <permission statement> No.: 5

& ☑ **Categorical states** &

☑ no ☑ invert

☑ yes ☐ invert

☐ **Data status**

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Project: LIASlight SELECT [Description].id FROM [DiversityDescriptions_LIAS].[dbo].[Description] WH **Matches: 10805**

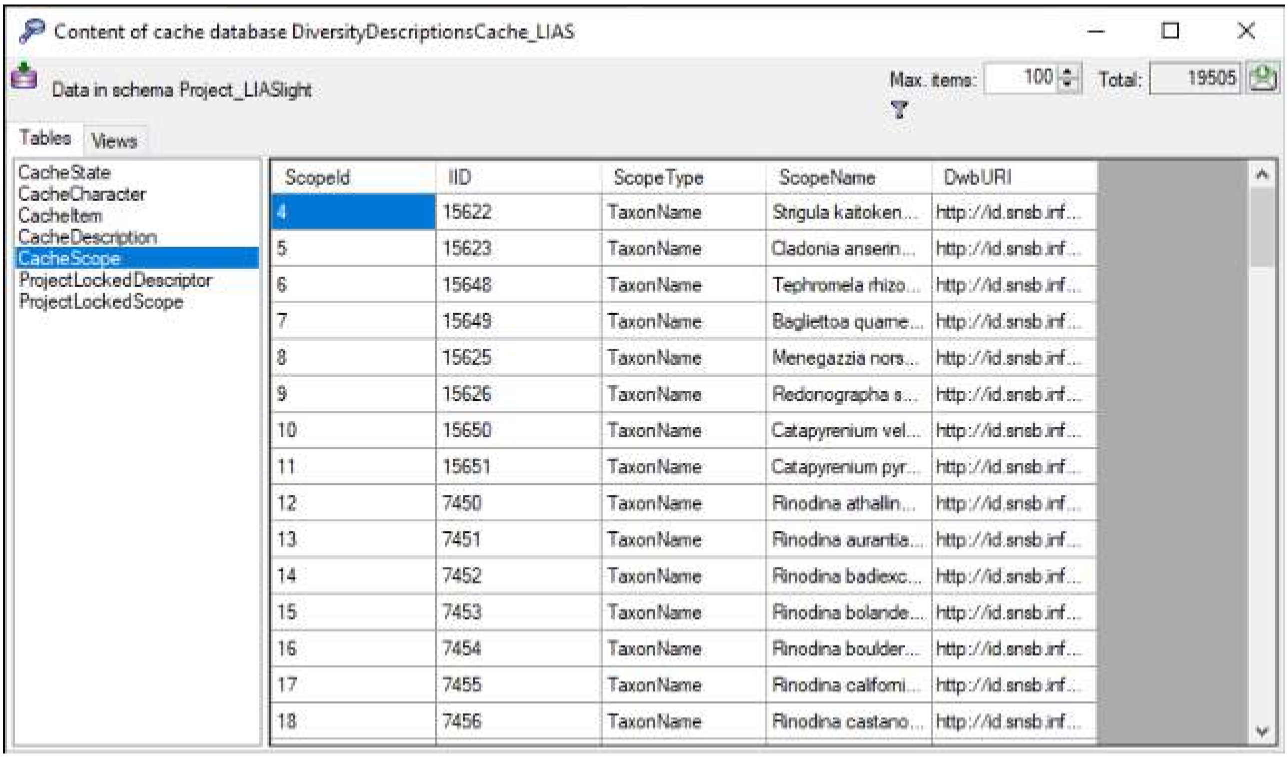
To transfer the data you have 3 options as described in the Transfer chapter.

Afterwards the number and date of the transferred data are visible as shown below.

LIASlight
13827 datasets
Last update:
19.03.2020 14:13:31
0 datasets withheld

☐ 10805 datasets
Last transfer:
2020-03-27 10:02:06

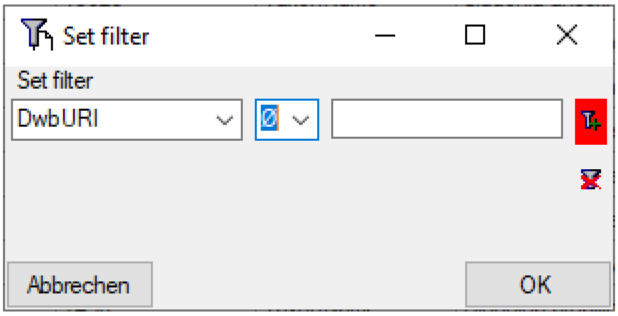
To inspect the transferred data use the **View content** button. A window as shown below will open where all tables containing the data of the project are listed.



Max. items: 100 Total: 19505

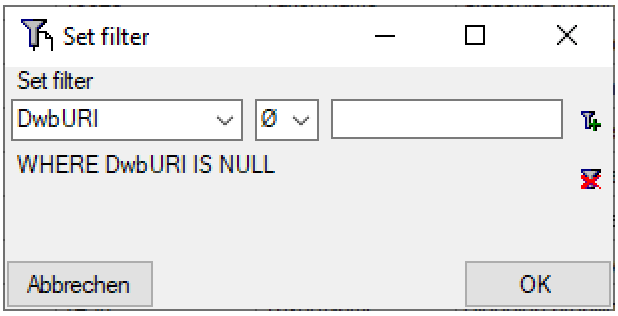
ScopeId	IID	ScopeType	ScopeName	DwbURI
4	15622	TaxonName	Strigula kaitoken...	http://id.snsb.inf...
5	15623	TaxonName	Cladonia anserin...	http://id.snsb.inf...
6	15648	TaxonName	Tephromela rhizo...	http://id.snsb.inf...
7	15649	TaxonName	Bagliettoa quame...	http://id.snsb.inf...
8	15625	TaxonName	Menegazzia nors...	http://id.snsb.inf...
9	15626	TaxonName	Redonographa s...	http://id.snsb.inf...
10	15650	TaxonName	Catapyrenium vel...	http://id.snsb.inf...
11	15651	TaxonName	Catapyrenium pyr...	http://id.snsb.inf...
12	7450	TaxonName	Rinodina athallin...	http://id.snsb.inf...
13	7451	TaxonName	Rinodina aurantia...	http://id.snsb.inf...
14	7452	TaxonName	Rinodina badiexc...	http://id.snsb.inf...
15	7453	TaxonName	Rinodina bolande...	http://id.snsb.inf...
16	7454	TaxonName	Rinodina boulder...	http://id.snsb.inf...
17	7455	TaxonName	Rinodina californi...	http://id.snsb.inf...
18	7456	TaxonName	Rinodina castano...	http://id.snsb.inf...

Click on the button to filter the content. A window as shown below will open. Choose the column for the filter, the operator (e.g. =) and the filter value (see below).



DwbURI Ø

Now click on the button to add the filter criteria to the table filter. You may add as many criteria as needed (see below). With the button you can clear the filter..



DwbURI Ø

WHERE DwbURI IS NULL

Before you can transfer the data into the Postgres database, you have to connect to the Postgres database and click on the button to establish the project and run necessary updates. After the project is established and up to date, use the button to transfer the data in the Postgres area (see below).

If a project is exported into another Postgres database on the same server, these databases will be listed underneath the Postgres block (see image below). For an overview of all target Postgres databases click on the button.

If the target is placed on the current server, the text will appear in black (see image below). Packages will be listed for the other targets as well.

In the Postgres database you can install packages to adapt the data to any needed format.

Mapping of IDs for the data transfer into the cache database

In the Diversity Descriptions database the main tables Description, Descriptor and CategoricalState have a numeric "id" as key, which is set by the MS SQL server when the dataset ist crated. All relations between the tables are set by using these unique values. For various reasons those internal IDs are not seen as suitable for all purposes of the cache database. Therefore a mapping of the internal IDs is performed before the transfer of data to the cache database.

Default mapping

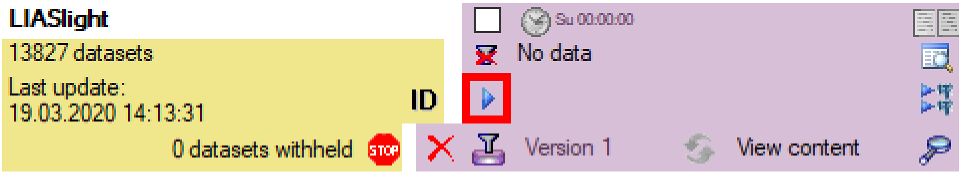
The default mapping of the IDs is mainly oriented on the way the states and characters are identified in the widely spread DELTA standard:

- **Descriptors** are numbered starting with "1" in ascending order and transferred into the cache database table **CacheCharacter**. The order is determined by the descriptor parameter "display_order" and the alphabetical order. The original "id" is stored as "CharID" in the target table, the descriptor number as "CID".
- **CategoricalStates** are numbered for each character starting with "1" in ascending order and transferred into the cache database table **CacheState**. The order is determined by the categorical state parameter "display_order" and the alphabetical order. The original "id" is stored as "StateID" in the target table, the categorical state number as "CS".
- Since the categorical state numbers ("CS") are not unique, each state is identified, e.g. in a description item, by the character and state number ("CID", "CS").
- **Descriptions** are numbered starting with "1" in ascending order and transferred into the cache database table **CacheItem**. The order is determined by the alphabetical order. The original "id" is stored as "ItemID" in the target table, the description number as "IID". As an alternative the "IID" may be derived from the field "alternate_id" of the "Description" table (see following section.

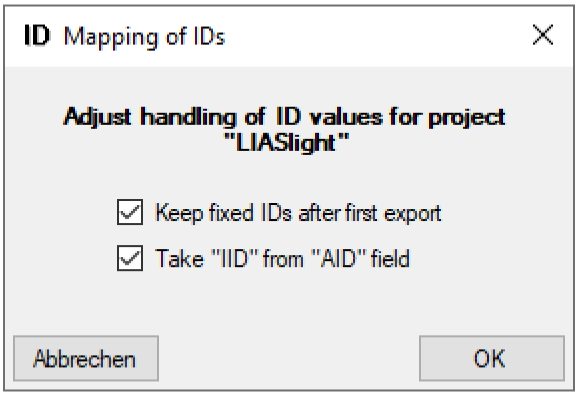
The mapping data are stored related to the project in the tables CacheMappingDescriptor, CacheMappingState and CacheMappingDescription of the original database.

ID Mapping adjustment

To set the mapping adjustments, click on the ID button (see below).



A window as shown below will open.



Adjust handling of ID values for project "LIASlight"

☑ Keep fixed IDs after first export

☑ Take "IID" from "AID" field

If **no option** is selected, the default mapping algorithm described above will be performed for every transfer to the cache database. Any changes, e.g. insertion of a descriptor or re-arrangement of categorical states, will affect the "CID", "CS" and "IID" of the cache database.

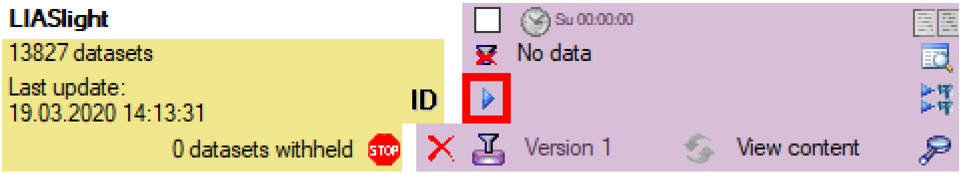
If option **Keep fixed IDs after first export** is selected, the default mapping algorithm described above will be performed only for the first transfer to the cache database. Any changes, e.g. insertion of a descriptor or re-arrangement of categorical states, will **NOT** affect the "CID", "CS" and "IID" of the cache database. New elements will get a number higher than the last one present. If an element is deleted, this will result in "missing" numbers in the cache database. Pure re-arrangements will have no effect.

The last option **Take "IID" from "AID" field** only affects the description mapping. By default the descriptions are numbered in alphabetical order. If this option is chosen, it is tried to use the field "alternate_id" ("AID" in the GUI) as item number. Preconditions are that the "AID" is a pure number and that the values are unique. If the "AID" is not supplied or an alpha-numeric string or if the number is already occupied, a new ascending value will be set. By using this option a foreign numbering scheme may be used for the cache database.

Restrictions for the data transfer into the cache database

The restrictions of the published data are defined in the main database via [local projects](#) and [data withholding](#). In the cache database further restrictions can be set for every project. You may set a filter on description data to restrict the **Descriptions**, select the **Descriptors** and the **Scopes** that are transferred.

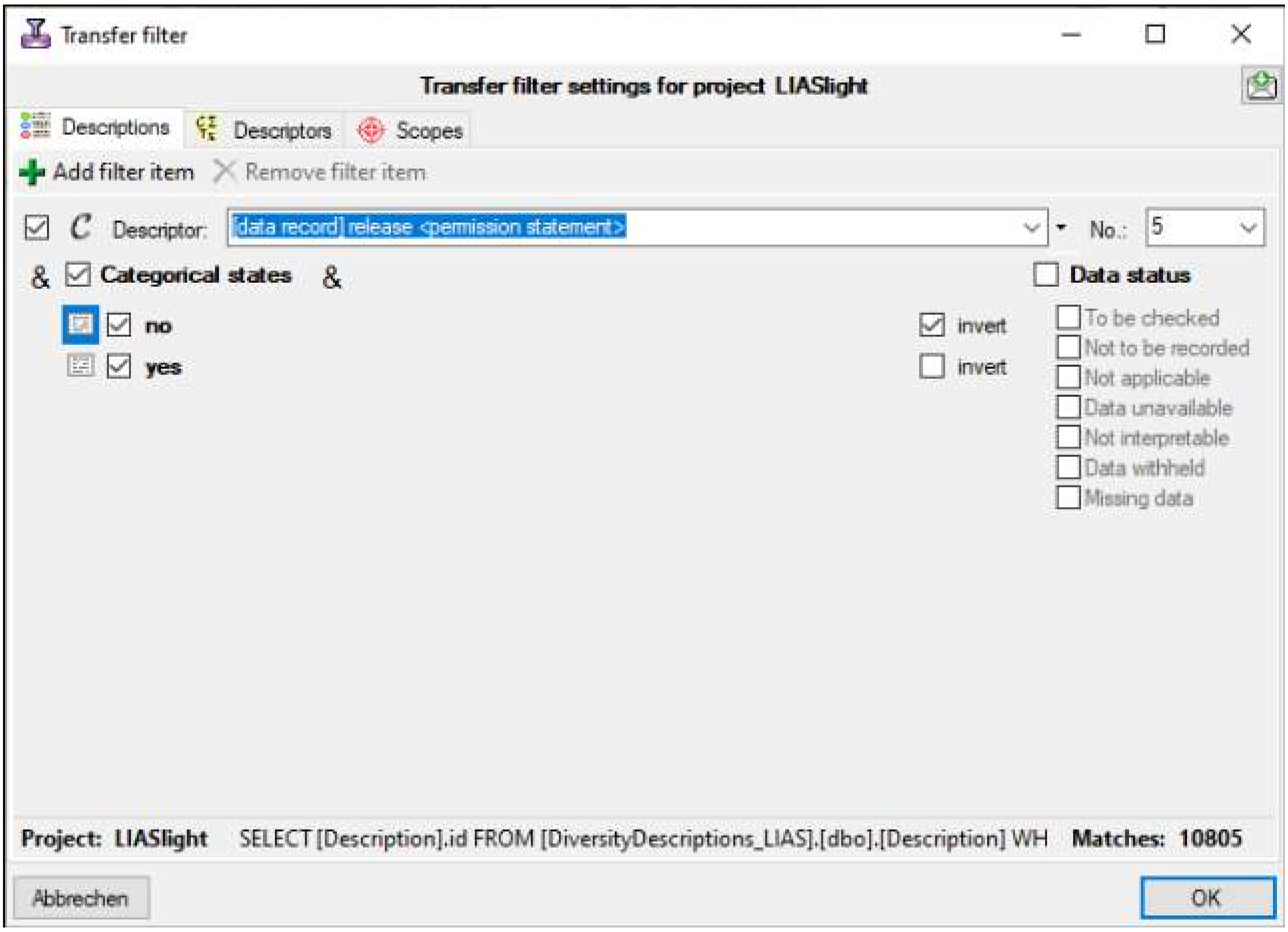
To set the restrictions, click on the button (see below).



A window as shown in the following sections will open.

Descriptions tab

The **Descriptions** filter works mainly the same way as the [Extended query](#). Use button **Add filter item** to insert a filter item, select the descriptor and set the filter conditions. With button **Remove filter item** you may remove the currently selected filter item. In the lower right corner **Matches:** shows you the current count of description items that match the adjusted filter criteria. In the center part the resulting SQL filter is shown.



Transfer filter settings for project LIASlight

☑ Descriptor: [data record] release <permission statement> No.: 5

& ☑ Categorical states &

☑ no ☑ invert

☑ yes ☐ invert

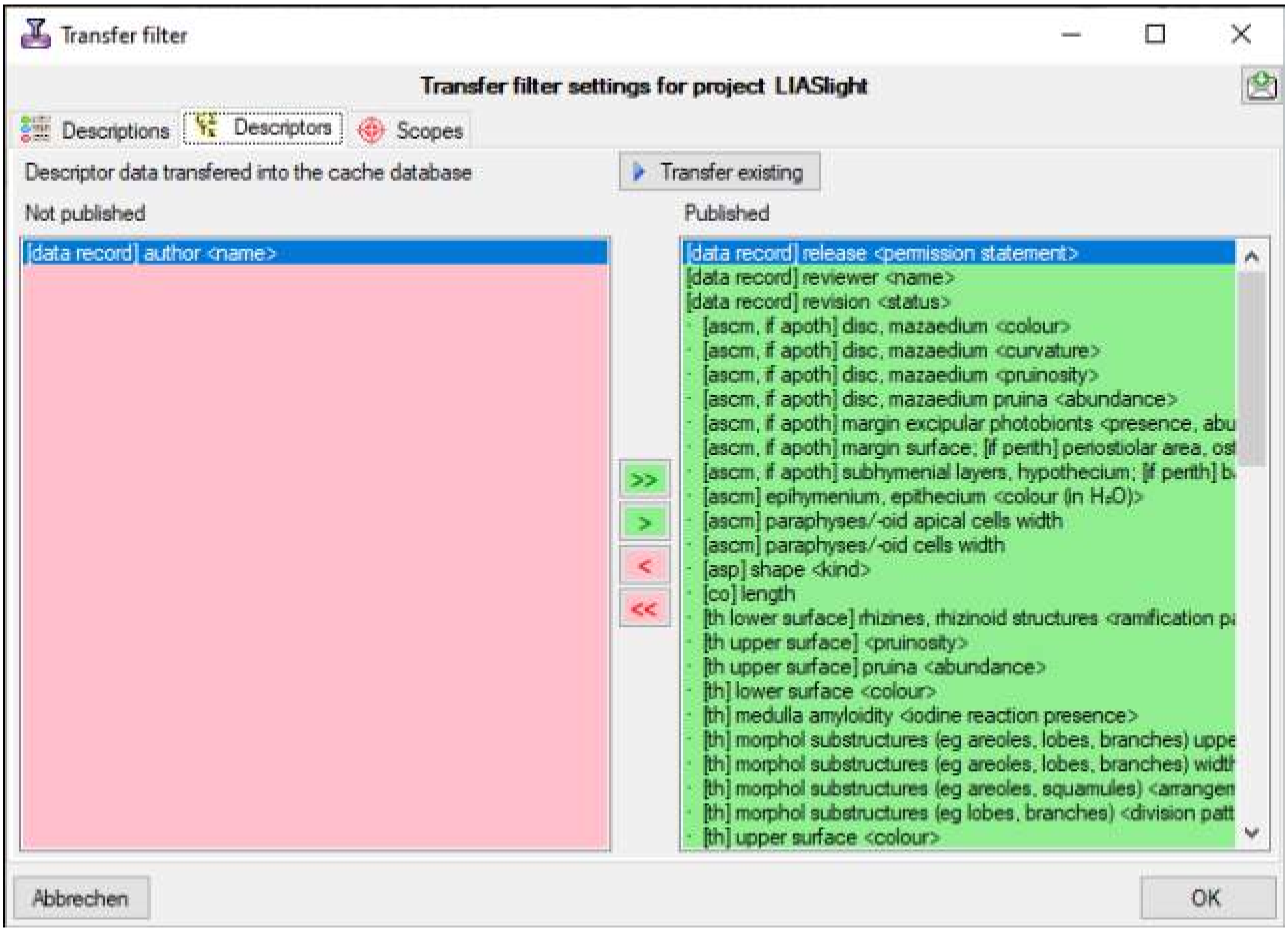
☐ Data status

☐ To be checked
☐ Not to be recorded
☐ Not applicable
☐ Data unavailable
☐ Not interpretable
☐ Data withheld
☐ Missing data

Project: LIASlight SELECT [Description].id FROM [DiversityDescriptions_LIAS].[dbo].[Description] WH **Matches: 10805**

Descriptors tab

With the **Descriptors** filter you can select the descriptors for which summary data shall be transferred. Use button the arrow buttons <<, <, > and >> for moving the entries between the Not published and Published list. Click button **Transfer existing** to move all descriptors that are used within the database to the Published list.



Descriptor data transfered into the cache database

Not published

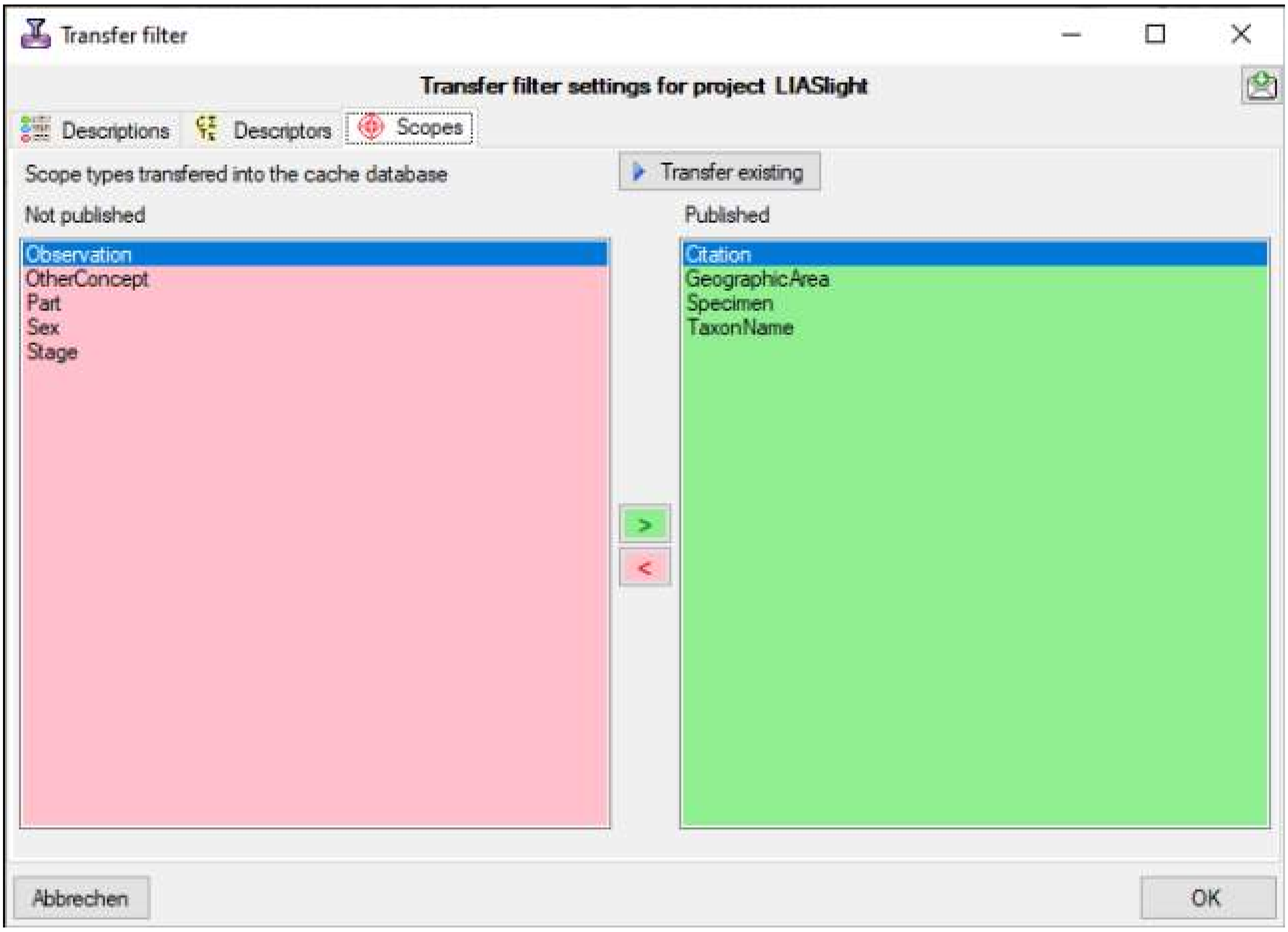
- [data record] author <name>

Published

- [data record] release <permission statement>
- [data record] reviewer <name>
- [data record] revision <status>
- [ascm, if apoth] disc, mazaedium <colour>
- [ascm, if apoth] disc, mazaedium <curvature>
- [ascm, if apoth] disc, mazaedium <pruinosity>
- [ascm, if apoth] disc, mazaedium pruina <abundance>
- [ascm, if apoth] margin excipular photobionts <presence, abu
- [ascm, if apoth] margin surface; [if perith] periostiolar area, ost
- [ascm, if apoth] subhymenial layers, hypothecium; [if perith] b
- [ascm] epihymenium, epithecium <colour (in H_2O)>
- [ascm] paraphyses/-oid apical cells width
- [ascm] paraphyses/-oid cells width
- [asp] shape <kind>
- [co] length
- [th lower surface] rhizines, rhizinoid structures <ramification p
- [th upper surface] <pruinosity>
- [th upper surface] pruina <abundance>
- [th] lower surface <colour>
- [th] medulla amyloidity <iodine reaction presence>
- [th] morphol substructures (eg areoles, lobes, branches) uppe
- [th] morphol substructures (eg areoles, lobes, branches) width
- [th] morphol substructures (eg areoles, squamules) <arrangem
- [th] morphol substructures (eg lobes, branches) <division patt
- [th] upper surface <colour>

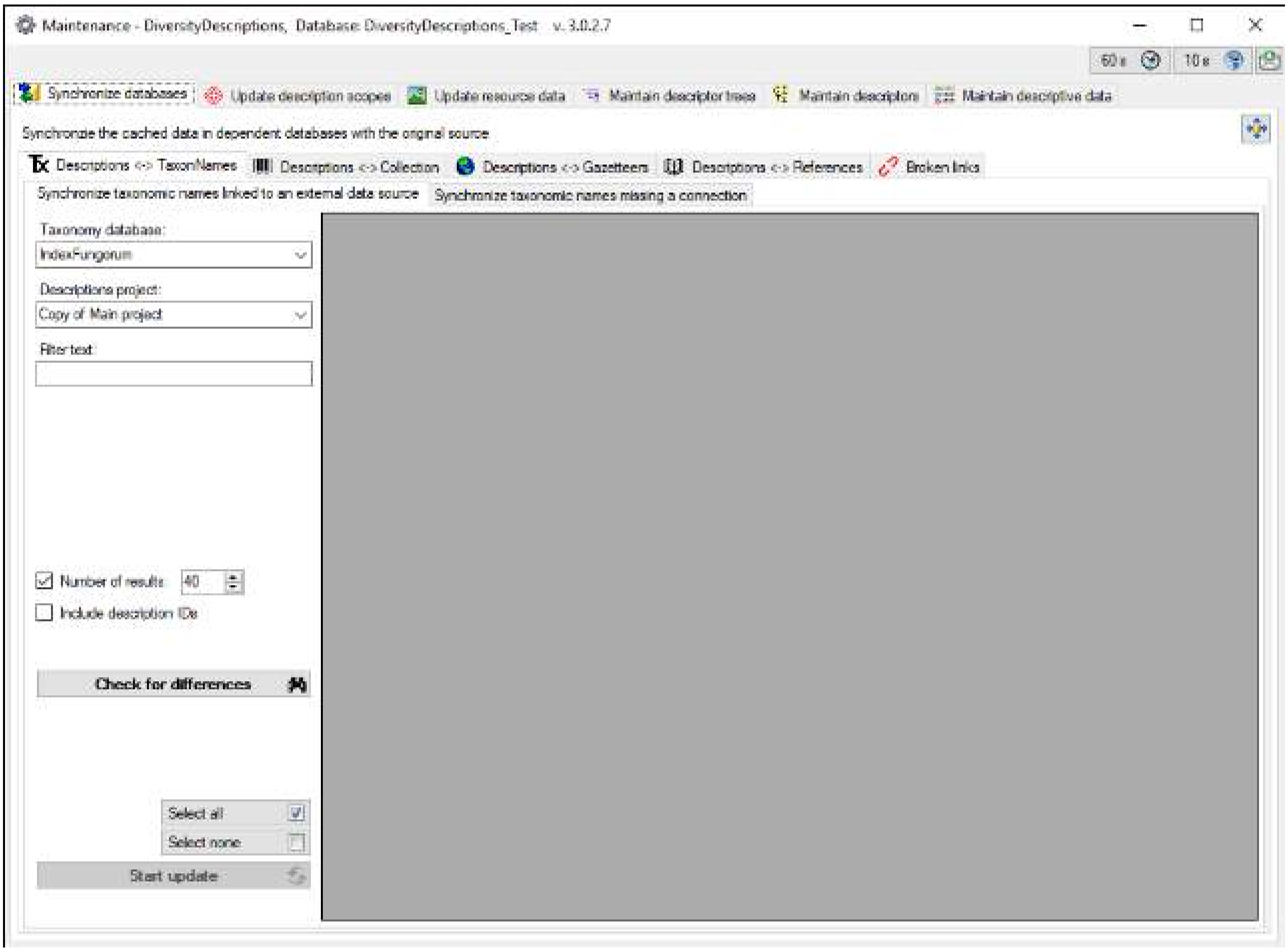
⊕Scopes tab

With the ⊕**Scope** filter you can select the scope type for description scopes shall be transferred. Use button the arrow buttons < and > for moving the entries between the Not published and Published list. Click button ▶ **Transfer existing** to move all scope types that are used within the database to the Published list.


Transfer filter
Transfer filter settings for project LIASlight
Descriptions
Descriptors
Scopes
Scope types transfered into the cache database
Transfer existing
Not published
Published
Observation
OtherConcept
Part
Sex
Stage
Citation
GeographicArea
Specimen
TaxonName
>
<
Abbrechen
OK

Maintenance

To open the maintenance form choose **Administration -> Database ... -> Maintenance ...** from the menu. The maintenance form offers functions for evaluation and update of multiple datasets that can hardly be achieved by the regular editing options, which focus on a single dataset. Currently the functions Synchronize databases, Update description scopes, Update resource data, Maintain descriptor trees, Maintain descriptors and Maintain descriptive data are available.


Maintenance - DiversityDescriptions, Database: DiversityDescriptions_Test v. 3.0.2.7

Synchronize the cached data in dependent databases with the original source

Taxonomy database: IndexFungorum

Descriptions project: Copy of Main project

Filter text:

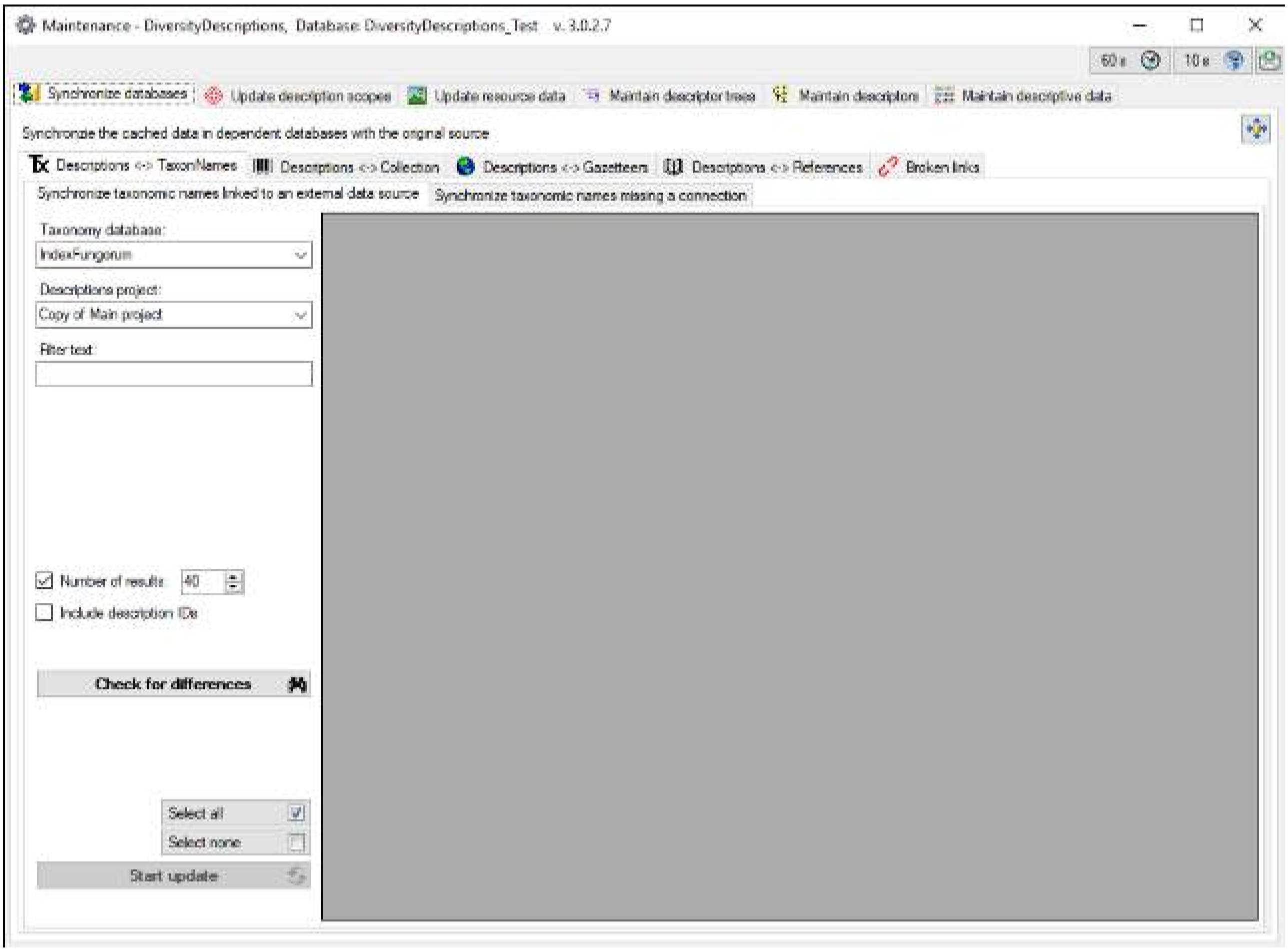
☑ Number of results 40

☐ Include description IDs

With the button you can set the timeout for critical database queries, with the button you can set the timeout for web requests used within maintenance. Feedbacks can be sent with the button .

Maintenance - Synchronize databases

To open the maintenance form choose **Administration ->** **Database ... ->** **Maintenance ...** from the menu and select the **Synchronize databases** tab. With the maintenance functions you can update values cached from other modules or external webservices. Entries in Diversity Descriptions can be linked with several other modules of the Diversity Workbench, e.g. by the **Description scopes**. If you link a data source to another module, the URI of the data set in the other module together with one or several cached values will be stored in Diversity Descriptions. Due to changes in the source modules these cached values may differ from the original values. To get the actual values you can use the synchronize functions for taxonomic names, specimen and observations, geographical names and references. Additionally broken links can be searched an repaired.



Taxonomy database: IndexFungorum

Descriptions project: Copy of Main project

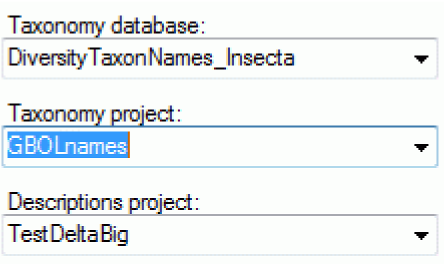
Filter text:

☑ Number of results: 40

☐ Include description IDs

Commonly used database synchronization options

In the sub-panels several commonly used options and controls are available. First the source database must be selected, where the referenced data are stored. In the example shown below this is the **Taxonomy database**. Click on button to open the connections administration form where you may connect missing databases. The second parameter that has to be specified is the **Descriptions project** that contains the datasets which have to be checked or updated. If datasets of Diversity Descriptions are not yet linked to another module, the project of the source database may be specified (**Taxonomy project** in example below).

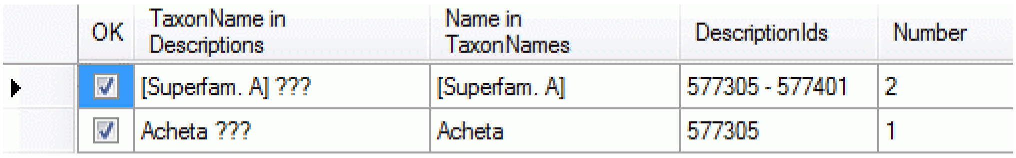


Taxonomy database: DiversityTaxonNames_Insecta

Taxonomy project: GBOLnames

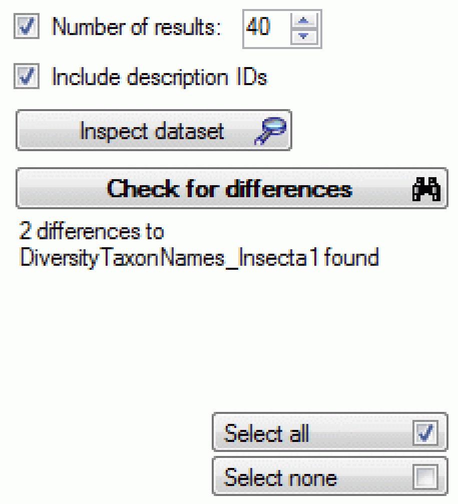
Descriptions project: TestDeltaBig

By starting a query (button **Check for differences**, **Check for identical names** or **Start check**) you will get a result list of database entries that can be updated (see image below). In this example the first result entry represents two datasets in Diversity Descriptions (column **Number**). In column **DescriptionIds** the range of the affected database internal IDs is shown. You may select or deselect single entries of the result list for the database update in column **OK**.



	OK	TaxonName in Descriptions	Name in TaxonNames	DescriptionIds	Number
▶	☑	[Superfam. A] ???	[Superfam. A]	577305 - 577401	2
	☑	Acheta ???	Acheta	577305	1

The size of the query result list may be adapted by changing the value **Number of results** or unchecking this option to get the complete list (see image below). If datasets of Diversity Descriptions are not yet linked to another module, the query in Diversity Descriptions may be restricted by specifying a value in the field **Restrict to names starting with**. You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**.

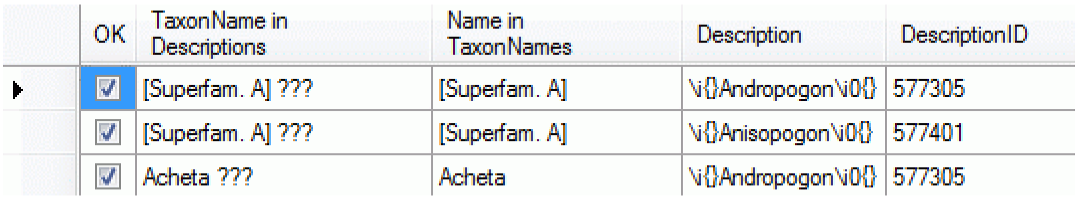


☑ Number of results: 40

☑ Include description IDs

2 differences to DiversityTaxonNames_Insecta1 found

If you select the option **Include description IDs** the button **Inspect dataset** will be shown. By starting a new query (button) the result list will now include the columns **Description** and **DescriptionID** instead of **DescriptionIds** and **Number** (see image below). Furthermore each dataset entry will now be shown in an own result line. By selecting an entry and clicking the button **Inspect dataset** you may directly navigate to that dataset.



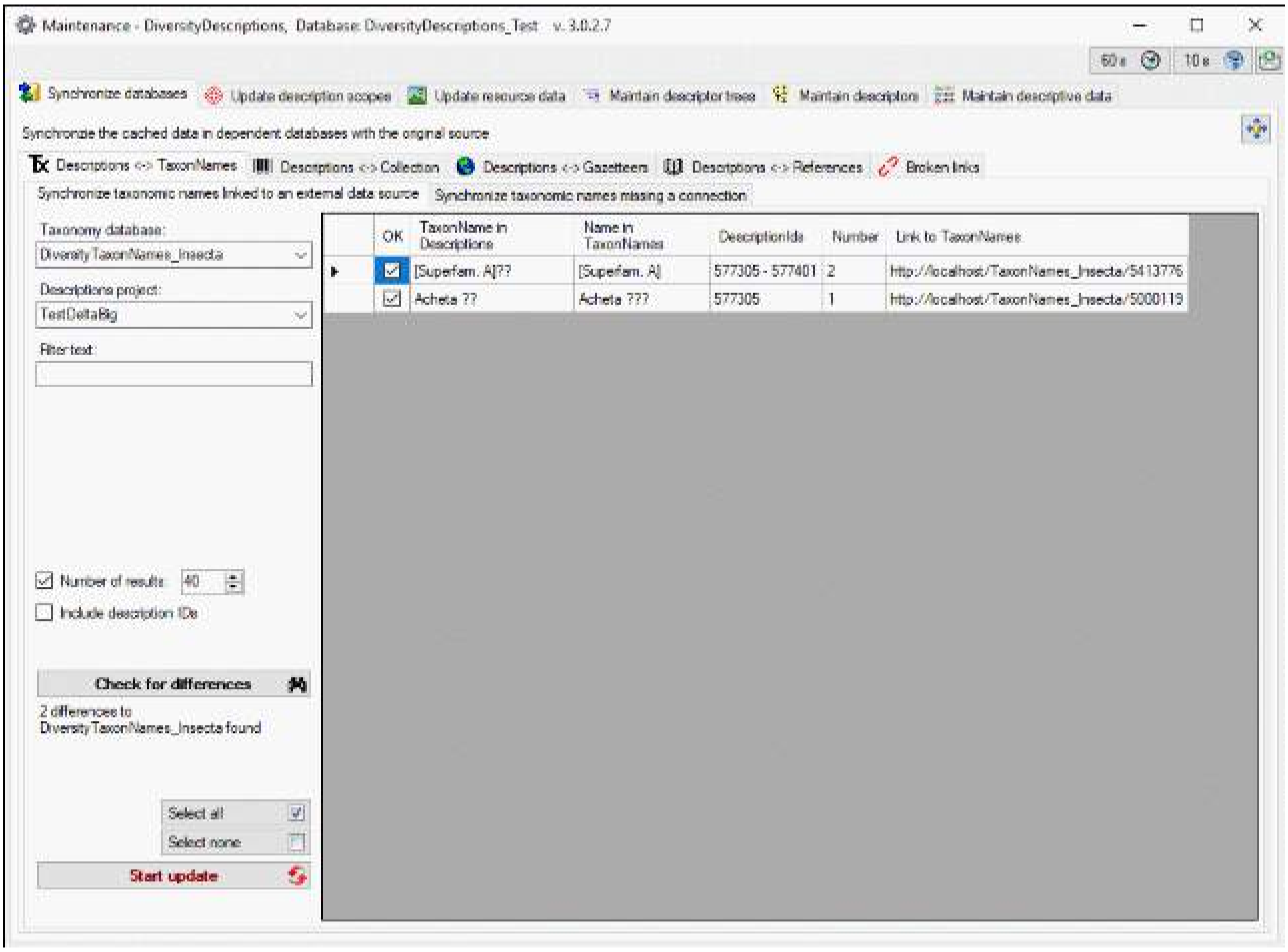
	OK	TaxonName in Descriptions	Name in TaxonNames	Description	DescriptionID
▶	☑	[Superfam. A] ???	[Superfam. A]	\i{}Andropogon\i0{}	577305
	☑	[Superfam. A] ???	[Superfam. A]	\i{}Anisopogon\i0{}	577401
	☑	Acheta ???	Acheta	\i{}Andropogon\i0{}	577305

Maintenance - Taxonomic names

To synchronize the entries for the taxonomic names derived from the module DiversityTaxonNames select the **Synchronize databases** tab and choose the tab **Descriptions <-> TaxonNames**. There are two ways to synchronize taxonomic names. You may either **Synchronize taxonomic names linked to an external data source** for entries where the link to a taxonomic database is already established or you may **Synchronize taxonomic names missing a connection** where no link is established and you can query for identical names in one of the databases. The meaning of some generally used controls is explained in the introduction page of database synchronization.

Synchronize taxonomic names linked to an external data source

The taxonomic names are stored as field "label" of table DescriptionScope, where the scope type TaxonName is specified. Select a taxonomy database and the descriptions project that shall be synchronized. Start the query with a click on the **Check for differences** button.



Synchronize the cached data in dependent databases with the original source

Taxonomy database: DiversityTaxonNames_Insecta

Descriptions project: TestDeltaBig

Filter text:

☑ Number of results 40

☐ Include description IDs

2 differences to DiversityTaxonNames_Insecta found

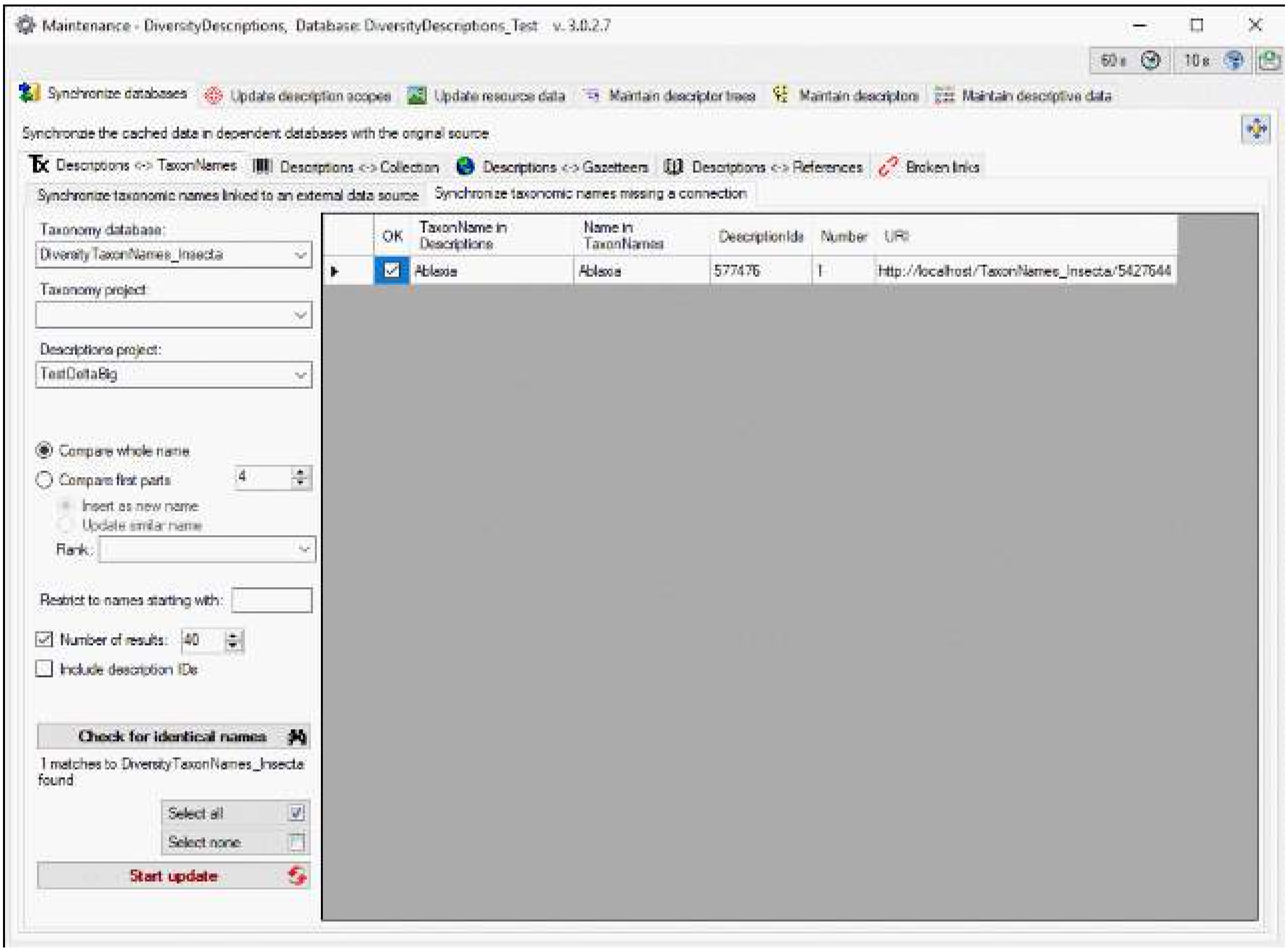
OK	TaxonName in Descriptions	Name in TaxonNames	DescriptionIds	Number	Link to TaxonNames
☑	[Superfam. A]??	[Superfam. A]	577305 - 577401	2	http://localhost/TaxonNames_Insecta/5413776
☑	Acheta ??	Acheta ???	577305	1	http://localhost/TaxonNames_Insecta/5000119

The form will list all differences found. To update the database click on the **Start update** button.

Synchronize taxonomic names missing a connection

Select a taxonomic database, optionally a project within this database and a project in the descriptions database to search for identical names. Start the query with a click on the

Check for identical names button. You may either restrict the search to an exact match (= **Compare whole name**) or to the first parts of the name (= **Compare first parts**) as shown below. If the names do not match exactly, you may either update the name (= **Update similar name**) in the descriptions database or import the name from the DiversityTaxonNames as a new scope (= **Insert as new name** - see options in the window depicted below). In the result list only matching names will be checked (column OK). The other results will be marked indicating the difference. Yellow indicates a difference in the authors while red indicates differences in main parts of the name. To use these similar names check them in the OK column.



Taxonomy database: DiversityTaxonNames_Insecta

Taxonomy project:

Descriptions project: TestDeltaBig

● Compare whole name

○ Compare first parts 4

Insert as new name

Update similar name

Rank:

Restrict to names starting with:

☑ Number of results: 40

☐ Include description IDs

1 matches to DiversityTaxonNames_Insecta found

OK	TaxonName in Descriptions	Name in TaxonNames	DescriptionIds	Number	URI
☑	Ablexia	Ablexia	577476	1	http://localhost/TaxonNames_Insecta/5427644

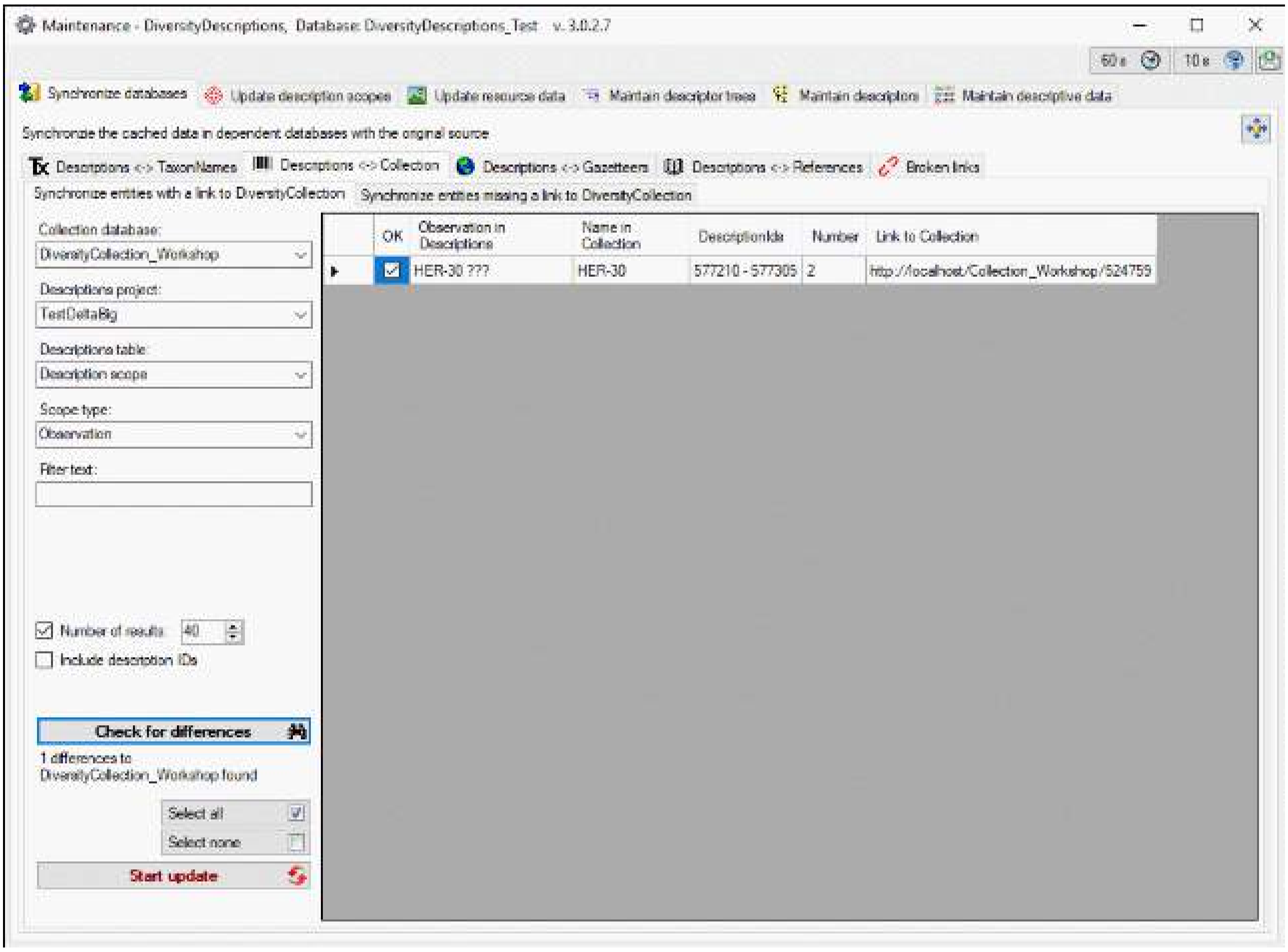
The form will list all matches found. To insert the links to the database click on the **Start update** button.

Maintenance - Collection

To synchronize the entries for the specimen or observations derived from the module DiversityCollection select the **Synchronize databases** tab and choose the tab **Descriptions <-> Collection**. There are two ways to synchronize specimen and observations. You may either **Synchronize entities with a link to DiversityCollection** for entries where the link to a taxonomic database is already established or you may **Synchronize entities missing a link to DiversityCollection** where no link is established and you can query for identical names in one of the databases. The meaning of some generally used controls is explained in the introduction page of database synchronization.

Synchronize entities with a link to DiversityCollection

The specimen and observations are stored as field "label" of table DescriptionScope, where the scope type Specimen or Observation specified. Alternatively the field collection_specimen of table SamplingUnit can be updated. Select a collection database, the descriptions project and the scope type that shall be synchronized. Start the query with a click on the **Check for differences** button.



Synchronize the cached data in dependent databases with the original source

Collection database: DiversityCollection_Workshop

Descriptions project: TestDeltaBig

Descriptions table: Description scope

Scope type: Observation

Filter text:

☑ Number of results 40

☐ Include description IDs

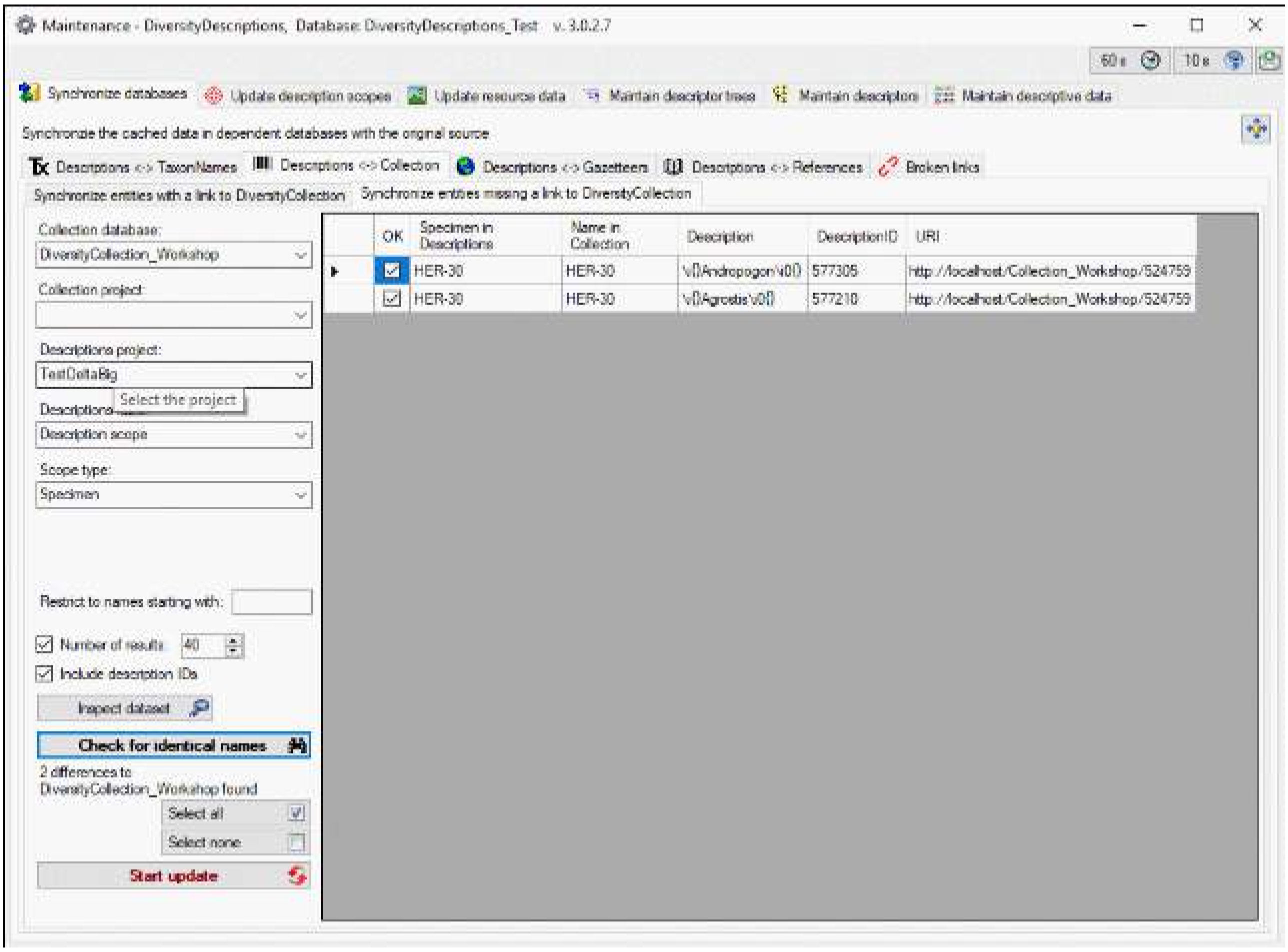
1 differences to DiversityCollection_Workshop found

OK	Observation in Descriptions	Name in Collection	DescriptionIds	Number	Link to Collection
☑	HER-30 ???	HER-30	577210 - 577305	2	http://localhost/Collection_Workshop/524759

The form will list all differences found. To update the database click on the **Start update** button.

Synchronize entities missing a link to DiversityCollection

Select the collection database, optionally a project within this database, a project in the descriptions database, the descriptions teble and the scope type Specimen or Observation to search for identical names. Start the query with a click on the **Check for identical names** button. To use these similar names check them in the OK column.



Collection database: DiversityCollection_Workshop

Collection project:

Descriptions project: TestDeltaBig

Descriptions table: Description scope

Scope type: Specimen

Restrict to names starting with:

☑ Number of results 40

☑ Include description IDs

2 differences to DiversityCollection_Workshop found

OK	Specimen in Descriptions	Name in Collection	Description	DescriptionID	URI
☑	HER-30	HER-30	\i{}Andropogon\i0{}	577305	http://localhost/Collection_Workshop/524759
☑	HER-30	HER-30	\i{}Agrostis\i0{}	577210	http://localhost/Collection_Workshop/524759

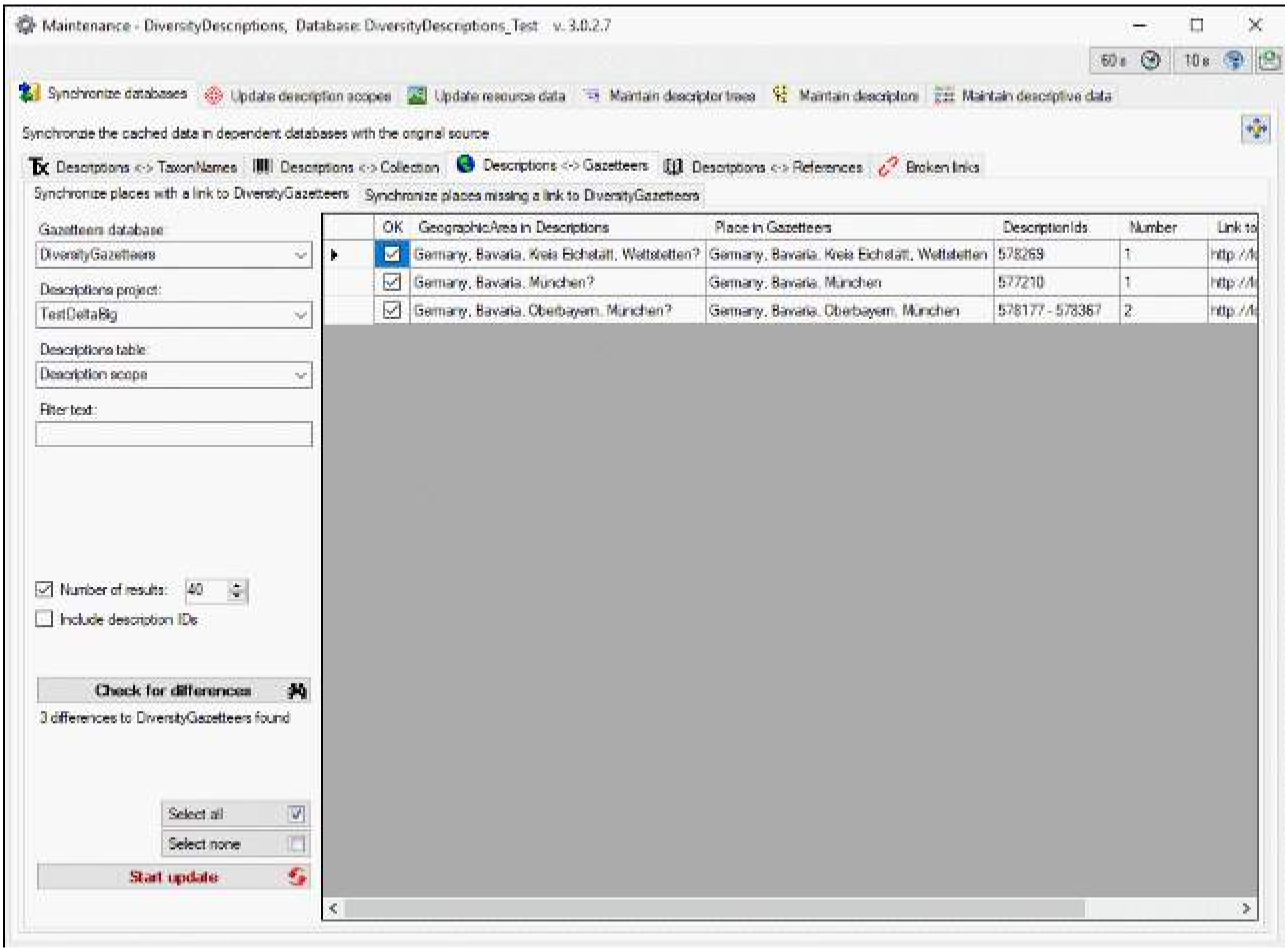
The form will list all matches found. To insert the links to the database click on the **Start update** button.

Maintenance - Gazetteers

To synchronize the entries for the geographic places derived from the module DiversityGazetteers select the **Synchronize databases** tab and choose the tab **Descriptions <-> Gazetteers**. There are two ways to synchronize geographic names. You may either **Synchronize places linked to DiversityGazetteers** for entries where the link to a gazetteers database is already established or you may **Synchronize places missing a link to DiversityGazetteers** where no link is established and you can query for identical names in one of the databases. The meaning of some generally used controls is explained in the introduction page of database synchronization.

Synchronize places linked to DiversityGazetteers

The geographic names are stored as field "label" of table Description scope with the scope type GeographicArea or in filed "geographic_area" of table SamplingEvent. Select a gazetteers database, the descriptions project and the descriptions table that shall be synchronized. Start the query with a click on the **Check for differences** button.



Maintenance - DiversityDescriptions, Database: DiversityDescriptions_Test v. 3.0.2.7

Synchronize the cached data in dependent databases with the original source

Gazetteers database: DiversityGazetteers

Descriptions project: TestDeltaBig

Descriptions table: Description scope

Filter text:

☑ Number of results: 40

☐ Include description IDs

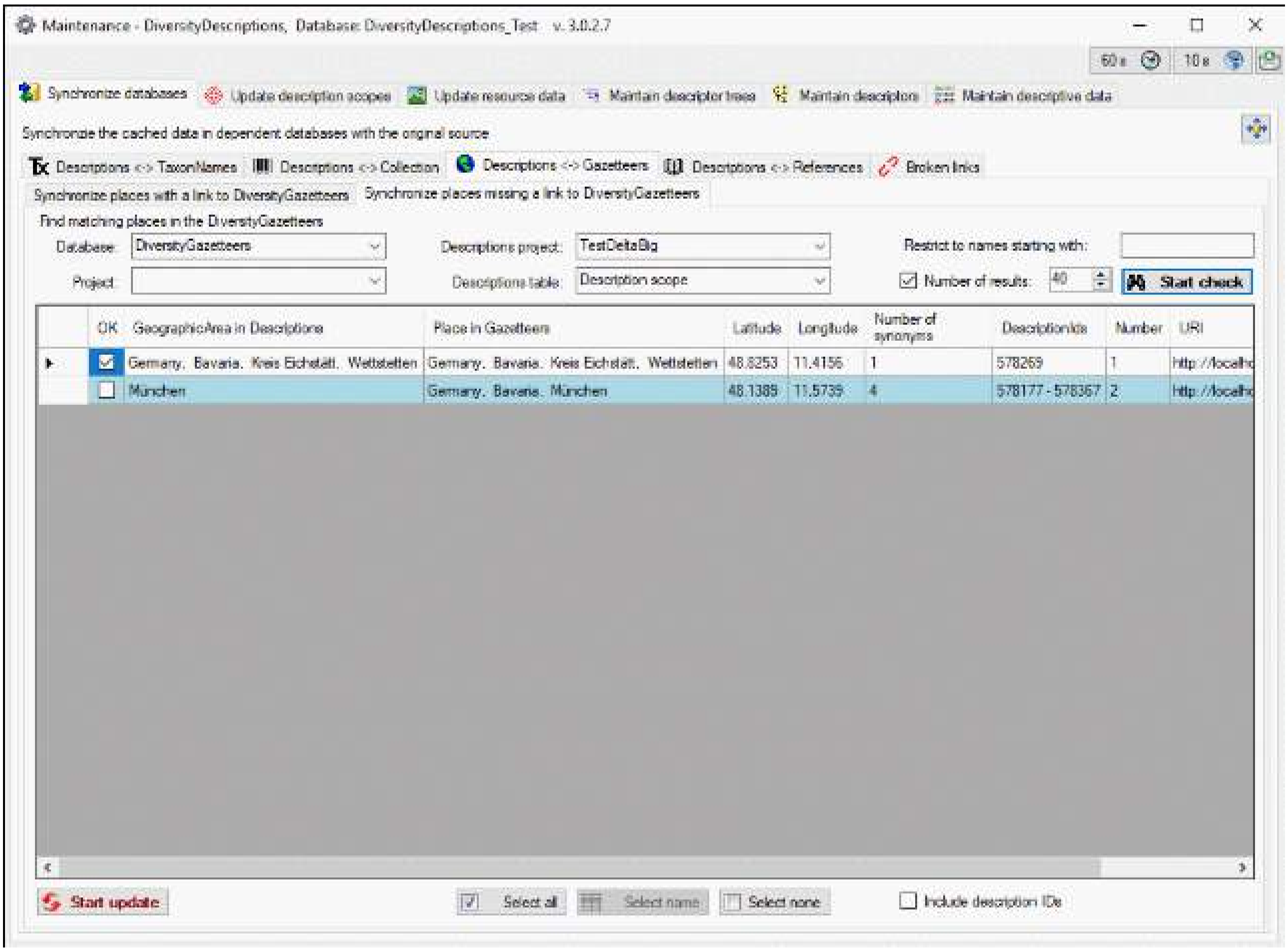
3 differences to DiversityGazetteers found

	OK	GeographicArea in Descriptions	Place in Gazetteers	DescriptionIds	Number	Link to
▶	☑	Germany, Bavaria, Kreis Eichstätt, Wettstetten?	Germany, Bavaria, Kreis Eichstätt, Wettstetten	578269	1	http://t
	☑	Germany, Bavaria, Munchen?	Germany, Bavaria, München	577210	1	http://t
	☑	Germany, Bavaria, Oberbayern, Munchen?	Germany, Bavaria, Oberbayern, München	578177 - 578367	2	http://t

The form will list all differences found. To update the database click on the **Start update** button.

Synchronize places missing a link to DiversityGazetteers

Select the gazetteers database, optionally a project within this databas, a project in the descriptions database and the descriptions table to search for identical names. Start the query with a click on the **Start check** button. To use these similar names check them in the OK column.



Synchronize the cached data in dependent databases with the original source

Find matching places in the DiversityGazetteers

Database: DiversityGazetteers

Project:

Descriptions project: TestDeltaBig

Descriptions table: Description scope

Restrict to names starting with:

☑ Number of results: 40

OK	GeographicArea in Descriptions	Place in Gazetteers	Latitude	Longitude	Number of synonyms	DescriptionIds	Number	URI
☑	Germany, Bavaria, Kreis Eichstätt, Wettstetten	Germany, Bavaria, Kreis Eichstätt, Wettstetten	48.8253	11.4156	1	578269	1	http://localho
☐	München	Germany, Bavaria, München	48.1389	11.5739	4	578177 - 578367	2	http://localho

☐ Include description IDs

Many places have identical names in different regions. Names where several results were found are marked in blue. To choose the correct name among the list of results, click on the **Select name** button and select the correct name from the list as shown below.

Please select the valid name from the list:
München

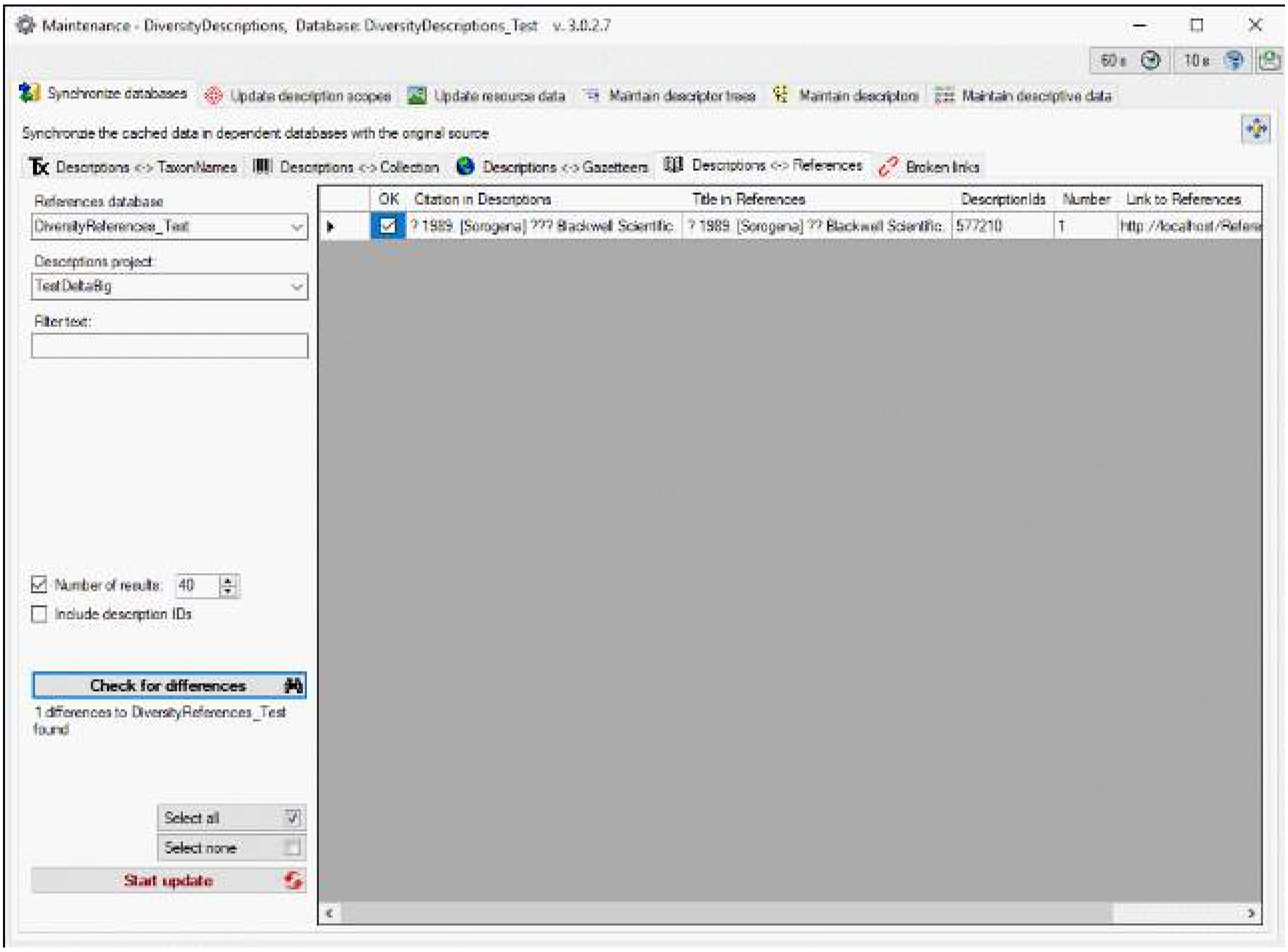
Name	Latitude	Longitude	Type
Germany, Bavaria, München	48,13890000000...	11,57389999999...	Kreis
Germany, Bavaria, Stadt-/Gemeindeteil v. Hutthurn, Kreis Passau, München	48,69720000000...	13,4644	Stadt-/Gemeinde...
Germany, Bavaria, München	48,13890000000...	11,57389999999...	inhabited place
Germany, Bavaria, Oberbayern, München	48,1333	11,5833	inhabited place

Finally, click on the **Start update** button to enter the results in the database.

Maintenance - References

To synchronize the titles of the references which are linked to the module DiversityReferences select the **Synchronize databases** tab and choose the tab **Descriptions <-> References**. Select the references database and the project for which the reference titles should be synchronized. The references are stored as field "label" of table DescriptionScope, where the scope type Citation is specified. The meaning of some generally used controls is explained in the introduction page of database synchronization.

Start the query with a click on the **Check for differences** button.



References database: DiversityReferences_Test

Descriptions project: TestDeltaBig

Filter text:

☑ Number of results: 40

☐ Include description IDs

Check for differences

1 differences to DiversityReferences_Test found

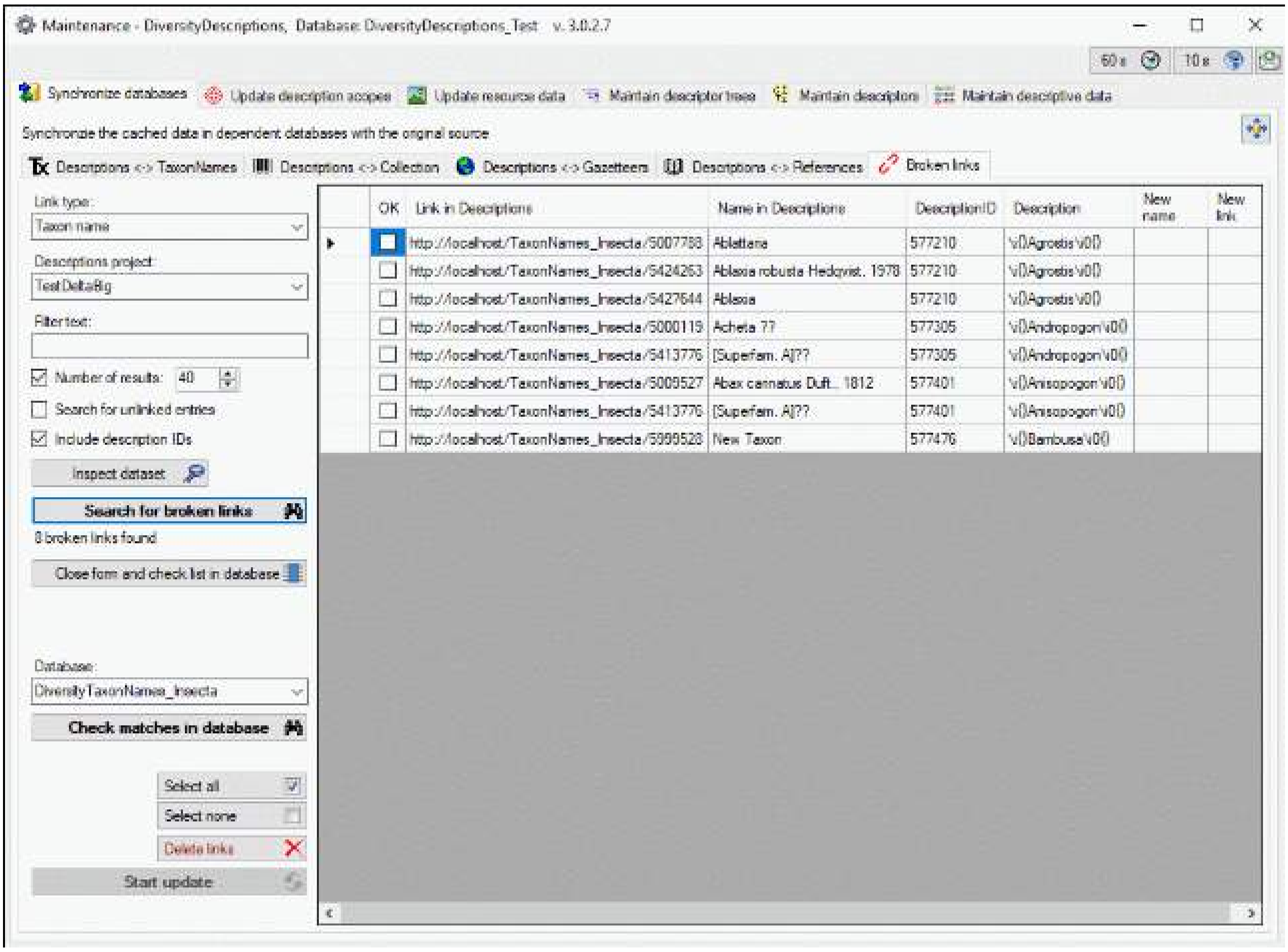
	OK	Citation in Descriptions	Title in References	DescriptionIds	Number	Link to References
▶	☑	? 1989. [Sorogena] ??? Blackwell Scientific	? 1989. [Sorogena] ?? Blackwell Scientific.	577210	1	http://localhost/Refere

The form will list all differences found. To update the database click on the **Start update** button.

Maintenance - Broken links

Broken links to other databases occur when the database's name has been change or if it was moved to a different server. To find and repair broken links to the modules of the Diversity Workbench select the **Synchronize databases** tab and choose the tab **Broken links**. The meaning of some generally used controls is explained in the introduction page of database synchronization.

Select the **Link type**, e.g. "Taxon name" to search broken links to DiversityTaxonNames and the **Descriptions project**. Start the query with a click on the **Search for broken links** button. If the link type "Geographic area" or "Specimen" has been selected, an additional selection box for the **Descriptions table** appears, where you may select from "Description scope" or " Sampling event" rsp. " Sampling unit". Each link of the selected type and project will checked if it can be connected to the referenced database and unsuccessful connection attemts will be listed in the data grid view (see image below).



Maintenance - DiversityDescriptions, Database: DiversityDescriptions_Test v. 3.0.2.7

Synchronize the cached data in dependent databases with the original source

Link type: Taxon name

Descriptions project: TestDeltaBig

Filter text:

☑ Number of results: 40

☐ Search for unlinked entries

☑ Include description IDs

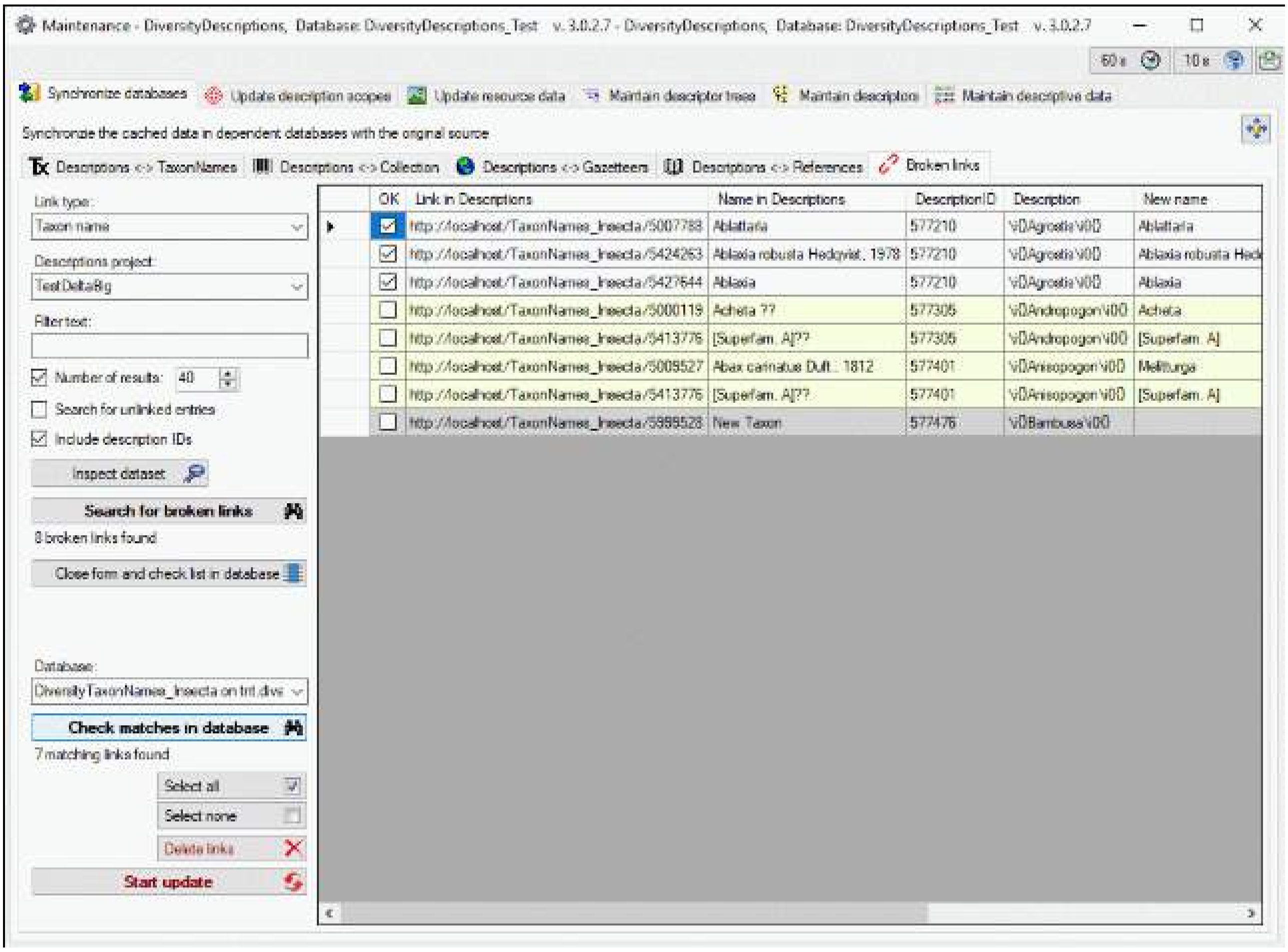
8 broken links found

Database: DiversityTaxonNames_Insecta

OK	Link in Descriptions	Name in Descriptions	DescriptionID	Description	New name	New link
☐	http://localhost/TaxonNames_Insecta/5007788	Ablattaria	577210	\i{}Agrostis\i0{}		
☐	http://localhost/TaxonNames_Insecta/5424263	Ablaxia robusta Hedqvist, 1978	577210	\i{}Agrostis\i0{}		
☐	http://localhost/TaxonNames_Insecta/5427644	Ablaxia	577210	\i{}Agrostis\i0{}		
☐	http://localhost/TaxonNames_Insecta/5000119	Acheta ??	577305	\i{}Andropogon\i0{}		
☐	http://localhost/TaxonNames_Insecta/5413776	[Superfam. A]??	577305	\i{}Andropogon\i0{}		
☐	http://localhost/TaxonNames_Insecta/5009527	Abax carinatus Duft., 1812	577401	\i{}Anisopogon\i0{}		
☐	http://localhost/TaxonNames_Insecta/5413776	[Superfam. A]??	577401	\i{}Anisopogon\i0{}		
☐	http://localhost/TaxonNames_Insecta/5999528	New Taxon	577476	\i{}Bambusa\i0{}		

Keep in mind that the connection check might be unsuccessful for remote databases, if the database connection was not set up before (see first and third entry in picture above)!

If you prefer to remove some broken links, you may now select them and then click button Delete links ✕. If you want to connect the links to a database, chose the new target in combo box Database and click the **Check matches in database** button. The check is successful, if the new databese contains an entry with the same ID and display text and the results will be selected and shown with white background (see image below).



Link type: Taxon name

Descriptions project: TestDeltaBig

Filter text:

☑ Number of results: 40

☐ Search for unlinked entries

☑ Include description IDs

8 broken links found

Database: DiversityTaxonNames_Insecta on tnt.diversityworkbench.de

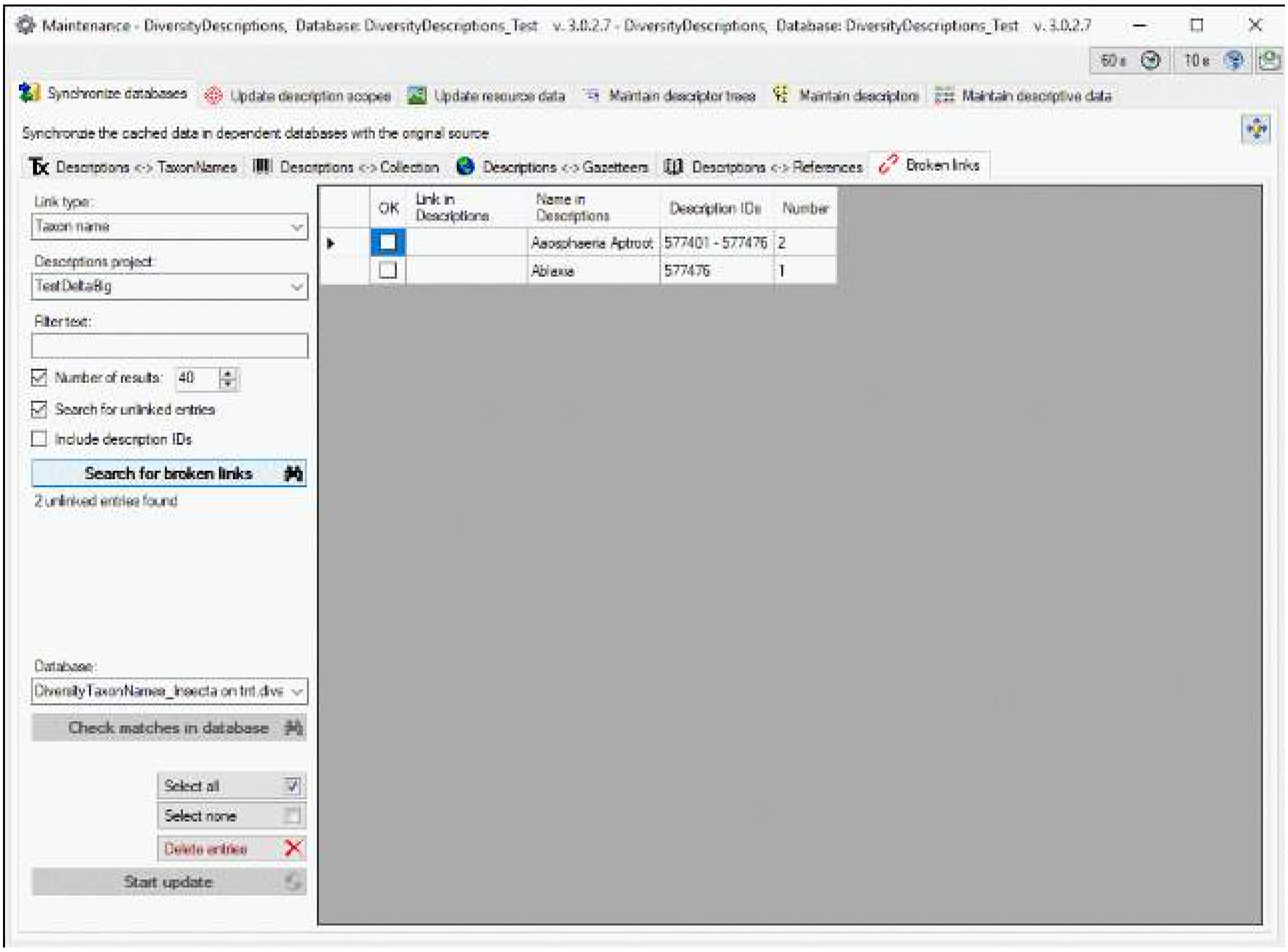
7 matching links found

OK	Link in Descriptions	Name in Descriptions	DescriptionID	Description	New name
☑	http://localhost/TaxonNames_Insecta/5007788	Ablattaria	577210	\i{}Agrostis\i0{}	Ablattaria
☑	http://localhost/TaxonNames_Insecta/5424263	Ablaxia robusta Hedqvist, 1978	577210	\i{}Agrostis\i0{}	Ablaxia robusta Hed
☑	http://localhost/TaxonNames_Insecta/5427644	Ablaxia	577210	\i{}Agrostis\i0{}	Ablaxia
☐	http://localhost/TaxonNames_Insecta/5000119	Acheta ??	577305	\i{}Andropogon\i0{}	Acheta
☐	http://localhost/TaxonNames_Insecta/5413776	[Superfam. A]??	577305	\i{}Andropogon\i0{}	[Superfam. A]
☐	http://localhost/TaxonNames_Insecta/5009527	Abax carinatus Duft., 1812	577401	\i{}Anisopogon\i0{}	Melliturga
☐	http://localhost/TaxonNames_Insecta/5413776	[Superfam. A]??	577401	\i{}Anisopogon\i0{}	[Superfam. A]
☐	http://localhost/TaxonNames_Insecta/5999528	New Taxon	577476	\i{}Bambusa\i0{}	

If in the new database a matching link was found but the display text differs, the entries are marked with yellow background. For these lines you should check the "New name" column and if the found entry is applicable you may select the entry for update. If no matching entry in the database was found, it is marked with grey background (see image above). To update the database click on the **Start update** button.

Delete unlinked scope entries

As an additional option you may search for unlinked scope entries and remove them completely from the database. Select the the **Seach for unlinked entries** and then click on the **Search for broken links** button. Deselect the entries you want to keep and click button Delete entries (see image below).



Link type: Taxon name

Descriptions project: TestDeltaBig

Filter text:

☑ Number of results: 40

☑ Search for unlinked entries

☐ Include description IDs

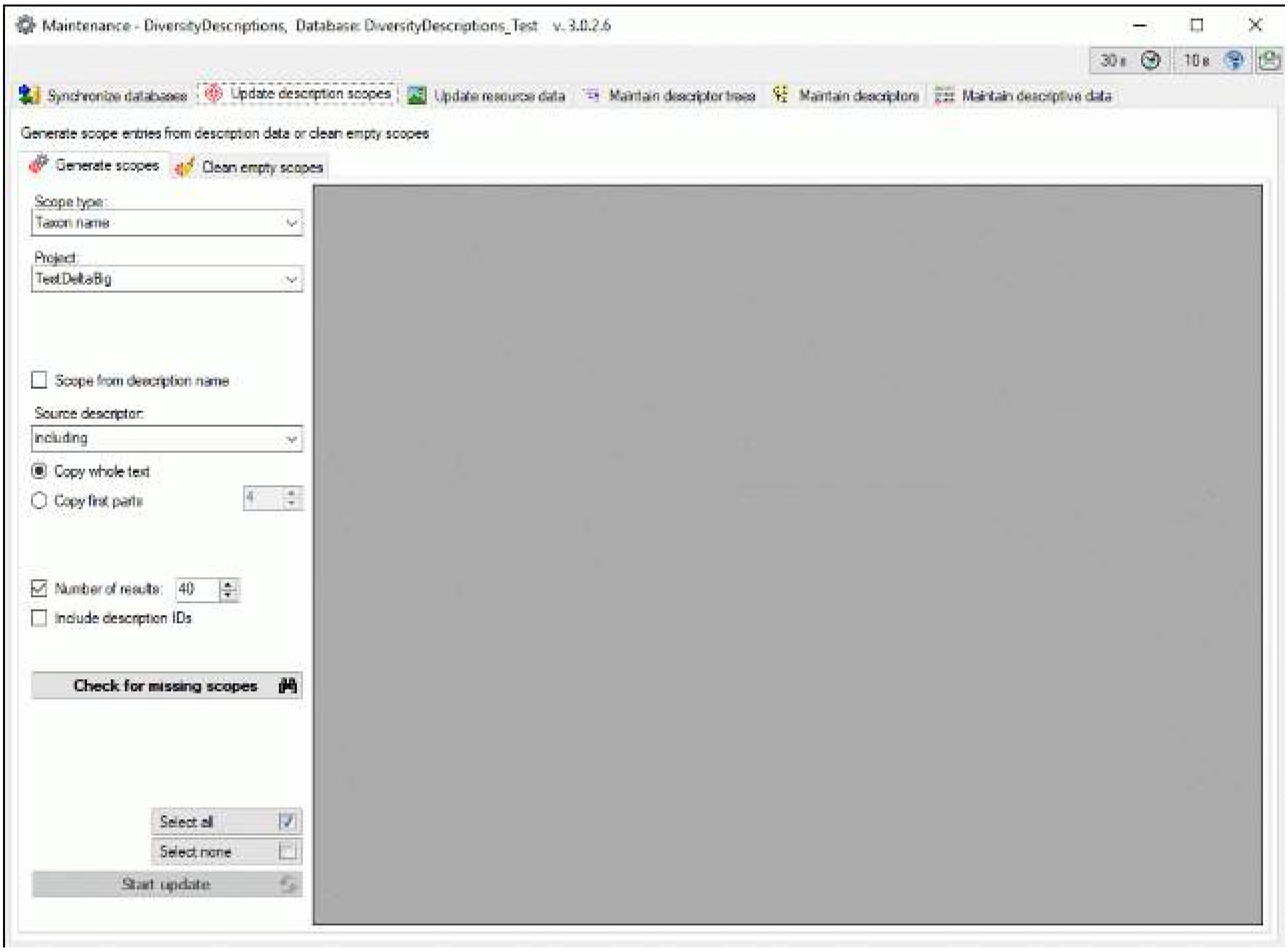
2 unlinked entries found

Database: DiversityTaxonNames_Insecta on tnt.dive

	OK	Link in Descriptions	Name in Descriptions	Description IDs	Number
▸	☐		Aaosphaeria Aptroot	577401 - 577476	2
	☐		Ablaxia	577476	1

Maintenance - Update description scopes

To open the maintenance form choose **Administration ->** **Database ... ->** **Maintenance ...** from the menu and select the **Update description scopes** tab. If you want to generate scope entries from description data, select the Generate scopes tab. To find and delete empty scopes choose the Clean empty scopes tab.



Maintenance - DiversityDescriptions, Database: DiversityDescriptions_Test v. 3.0.2.6

Generate scope entries from description data or clean empty scopes

Scope type: Taxon name

Project: TestDeltaBig

☐ Scope from description name

Source descriptor: including

● Copy whole text

○ Copy first parts 4

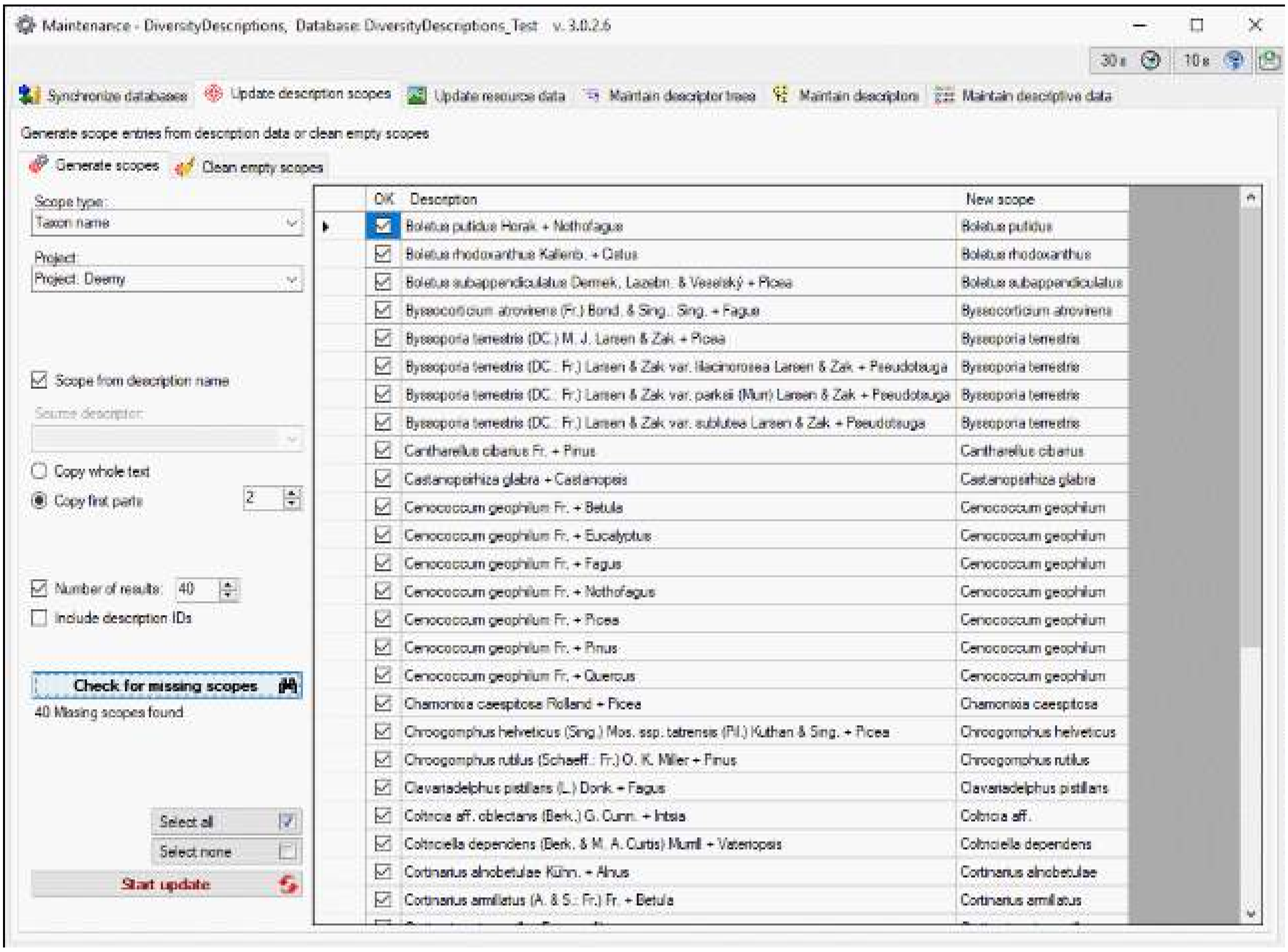
☑ Number of results: 40

☐ Include description IDs

Maintenance - Generate scopes

Especially if data are imported, e.g. from a DELTA file, data that can be stored as scope of a description are often contained in dedicated text descriptor data. For taxonomic descriptions generally the item/description names reflect the taxonomic names. To generate formal scopes from such "embedded" data select the **Update description scopes** tab and choose the tab **Generate scopes**.

Select the **Scope type**, e.g. "Taxon name" and the **Project**. You may generate the **Scope from description name** or select a **Source descriptor**. Furthermore the whole source text (description name or text descriptor data) may be selected (option **Copy whole text**) or only the first parts (option **Copy first parts**). Click on **Check for missing scopes** and all descriptions will be listed where no scope of the specified type is present and source data are available (see image below).



Generate scope entries from description data or clean empty scopes

Scope type: Taxon name

Project: Project: Deemy

☑ Scope from description name

Source descriptor:

○ Copy whole text

● Copy first parts 2

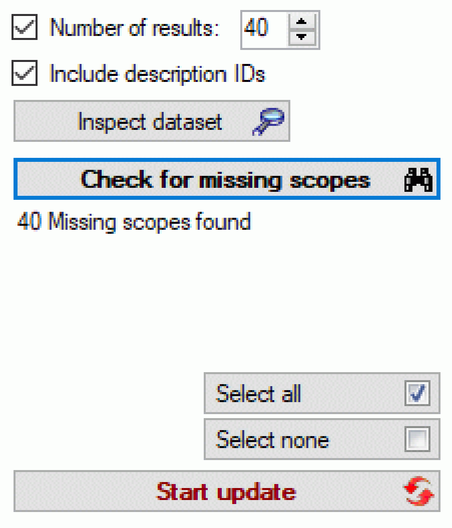
☑ Number of results: 40

☐ Include description IDs

40 Missing scopes found

OK	Description	New scope
☑	Boletus putidus Horak + Nothofagus	Boletus putidus
☑	Boletus rhodoxanthus Kallenb. + Cistus	Boletus rhodoxanthus
☑	Boletus subappendiculatus Dermek, Lazebn. & Veselský + Picea	Boletus subappendiculatus
☑	Byssocorticium atrovirens (Fr.) Bond. & Sing.: Sing. + Fagus	Byssocorticium atrovirens
☑	Byssoporia terrestris (DC.) M. J. Larsen & Zak + Picea	Byssoporia terrestris
☑	Byssoporia terrestris (DC.: Fr.) Larsen & Zak var. lilacinorosea Larsen & Zak + Pseudotsuga	Byssoporia terrestris
☑	Byssoporia terrestris (DC.: Fr.) Larsen & Zak var. parksii (Murr) Larsen & Zak + Pseudotsuga	Byssoporia terrestris
☑	Byssoporia terrestris (DC.: Fr.) Larsen & Zak var. sublutea Larsen & Zak + Pseudotsuga	Byssoporia terrestris
☑	Cantharellus cibarius Fr. + Pinus	Cantharellus cibarius
☑	Castanopsirhiza glabra + Castanopsis	Castanopsirhiza glabra
☑	Cenococcum geophilum Fr. + Betula	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Eucalyptus	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Fagus	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Nothofagus	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Picea	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Pinus	Cenococcum geophilum
☑	Cenococcum geophilum Fr. + Quercus	Cenococcum geophilum
☑	Chamonixia caespitosa Rolland + Picea	Chamonixia caespitosa
☑	Chroogomphus helveticus (Sing.) Mos. ssp. tatrensis (Pil.) Kuthan & Sing. + Picea	Chroogomphus helveticus
☑	Chroogomphus rutilus (Schaeff.: Fr.) O. K. Miller + Pinus	Chroogomphus rutilus
☑	Clavariadelphus pistillaris (L.) Donk + Fagus	Clavariadelphus pistillaris
☑	Coltricia aff. oblectans (Berk.) G. Cunn. + Intsia	Coltricia aff.
☑	Coltriciella dependens (Berk. & M. A. Curtis) Murrill + Vateriopsis	Coltriciella dependens
☑	Cortinarius alnobetulae Kühn. + Alnus	Cortinarius alnobetulae
☑	Cortinarius armillatus (A. & S.: Fr.) Fr. + Betula	Cortinarius armillatus

The size of the query result list may be adapted by changing the value **Number of results** or unchecking this option to get the complete list (see image below). You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**.



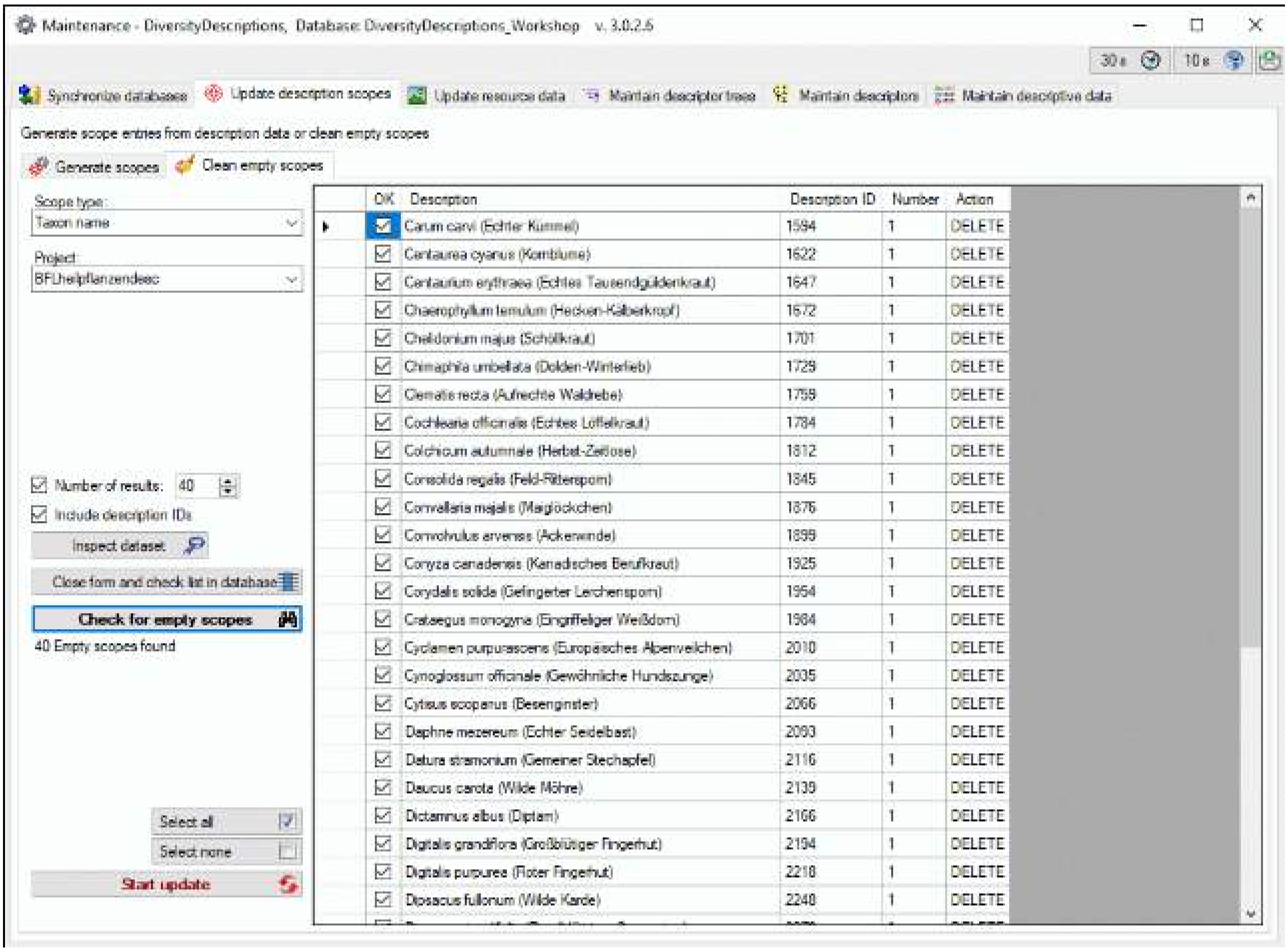
40 Missing scopes found

If you select the option **Include description IDs** the button **Inspect dataset** will be shown. By starting a new query (button **Check for missing scopes**) the result list will now include the column **DescriptionID**. By selecting an entry and clicking the button **Inspect dataset** you may directly navigate to that dataset. To update the database click on the Start update button.

Maintenance - Clean empty scopes

If you want to find and delete scope entries that do not contain any data, select the **Update description scopes** tab and choose the tab **Clean empty scopes**.

Select the **Scope type**, e.g. "Taxon name" and the **Project**. Click on **Check for empty scopes** and all descriptions will be listed where no scope of the specified type is present and source data are available (see image below).



Scope type: Taxon name

Project: BFLheilpflanzendesc

☑ Number of results: 40

☑ Include description IDs

40 Empty scopes found

OK	Description	Description ID	Number	Action
☑	Carum carvi (Echter Kümmel)	1594	1	DELETE
☑	Centaurea cyanus (Kornblume)	1622	1	DELETE
☑	Centaurium erythraea (Echtes Tausendgüldenkraut)	1647	1	DELETE
☑	Chaerophyllum temulum (Hecken-Kälberkropf)	1672	1	DELETE
☑	Chelidonium majus (Schöllkraut)	1701	1	DELETE
☑	Chimaphila umbellata (Dolden-Winterlieb)	1729	1	DELETE
☑	Clematis recta (Aufrechte Waldrebe)	1759	1	DELETE
☑	Cochlearia officinalis (Echtes Löffelkraut)	1784	1	DELETE
☑	Colchicum autumnale (Herbst-Zeitlose)	1812	1	DELETE
☑	Consolida regalis (Feld-Rittersporn)	1845	1	DELETE
☑	Convallaria majalis (Maiglöckchen)	1876	1	DELETE
☑	Convolvulus arvensis (Ackerwinde)	1899	1	DELETE
☑	Conyza canadensis (Kanadisches Berufkraut)	1925	1	DELETE
☑	Corydalis solida (Gefingerter Lerchensporn)	1954	1	DELETE
☑	Crataegus monogyna (Eingriffeliger Weißdorn)	1984	1	DELETE
☑	Cyclamen purpurascens (Europäisches Alpenveilchen)	2010	1	DELETE
☑	Cynoglossum officinale (Gewöhnliche Hundszunge)	2035	1	DELETE
☑	Cytisus scoparius (Besenginster)	2066	1	DELETE
☑	Daphne mezereum (Echter Seidelbast)	2093	1	DELETE
☑	Datura stramonium (Gemeiner Stechapfel)	2116	1	DELETE
☑	Daucus carota (Wilde Möhre)	2139	1	DELETE
☑	Dictamnus albus (Diptam)	2166	1	DELETE
☑	Digitalis grandiflora (Großblütiger Fingerhut)	2194	1	DELETE
☑	Digitalis purpurea (Roter Fingerhut)	2218	1	DELETE
☑	Dipsacus fullonum (Wilde Karde)	2240	1	DELETE

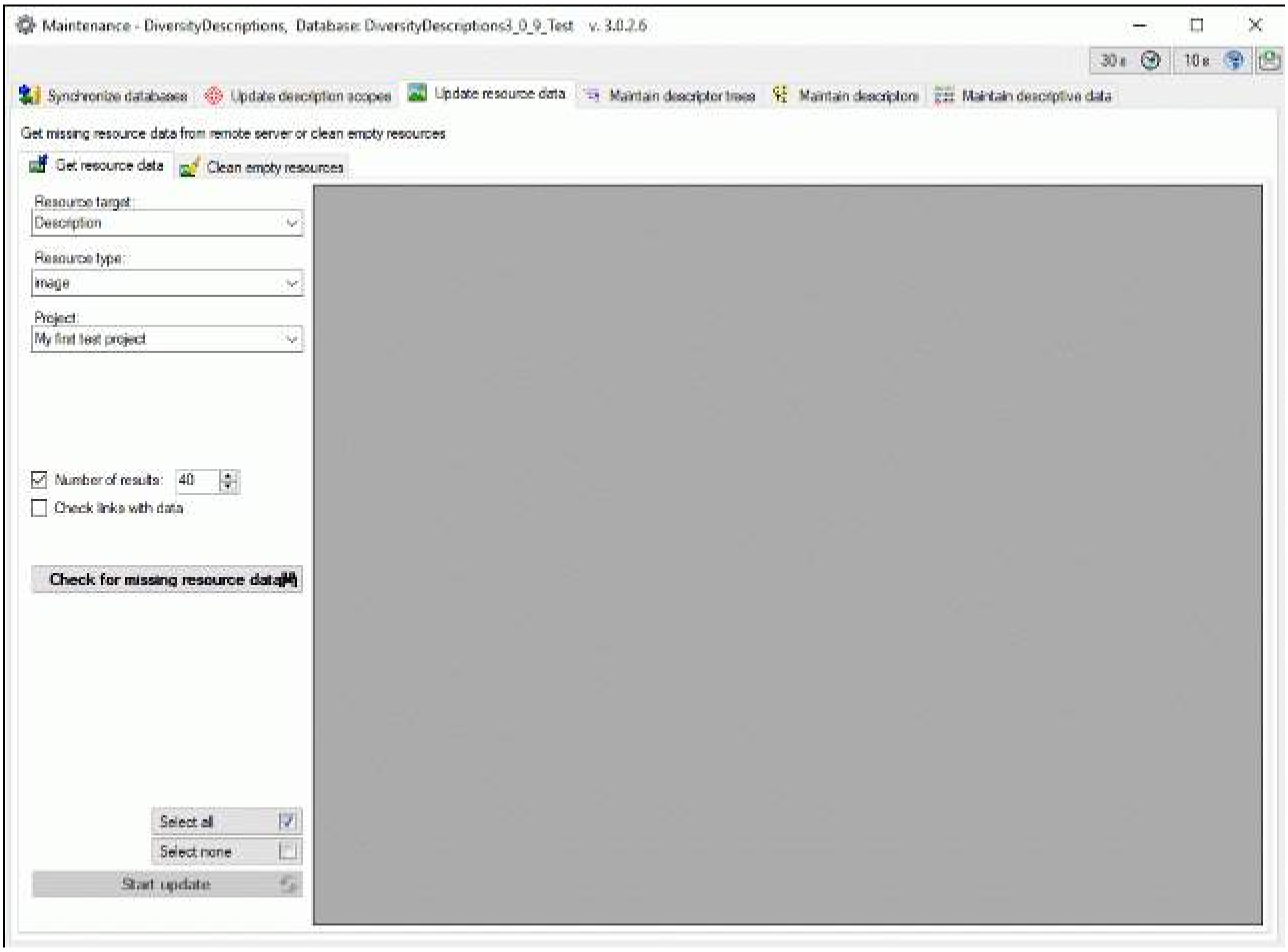
The size of the query result list may be adapted by changing the value **Number of results** or unchecking this option to get the complete list. You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**.

If you select the option **Include description IDs** and start a new query (button **Check for empty scopes**) the result list will include the column **DescriptionID**. By selecting an entry and clicking the button **Inspect dataset** you may directly navigate to that dataset. If you click on button **Close form and check list in database**, you will return to the main form and find the selected entries in the description result list.

To update the database click on the **Start update** button.

Maintenance - Update resource data

To open the maintenance form choose **Administration ->** **Database ... ->** **Maintenance ...** from the menu and select the **Update resource data** tab. In the resource edit forms the resource data, e.g. the file size, of a single resource can be obtained from the remote server addressed by the resource link. If for a large number of resouces the data shall be updated it is much easier to select the Get resource data tab. To find and delete empty resources choose the Clean empty resources tab.



Resource target: Description

Resource type: image

Project: My first test project

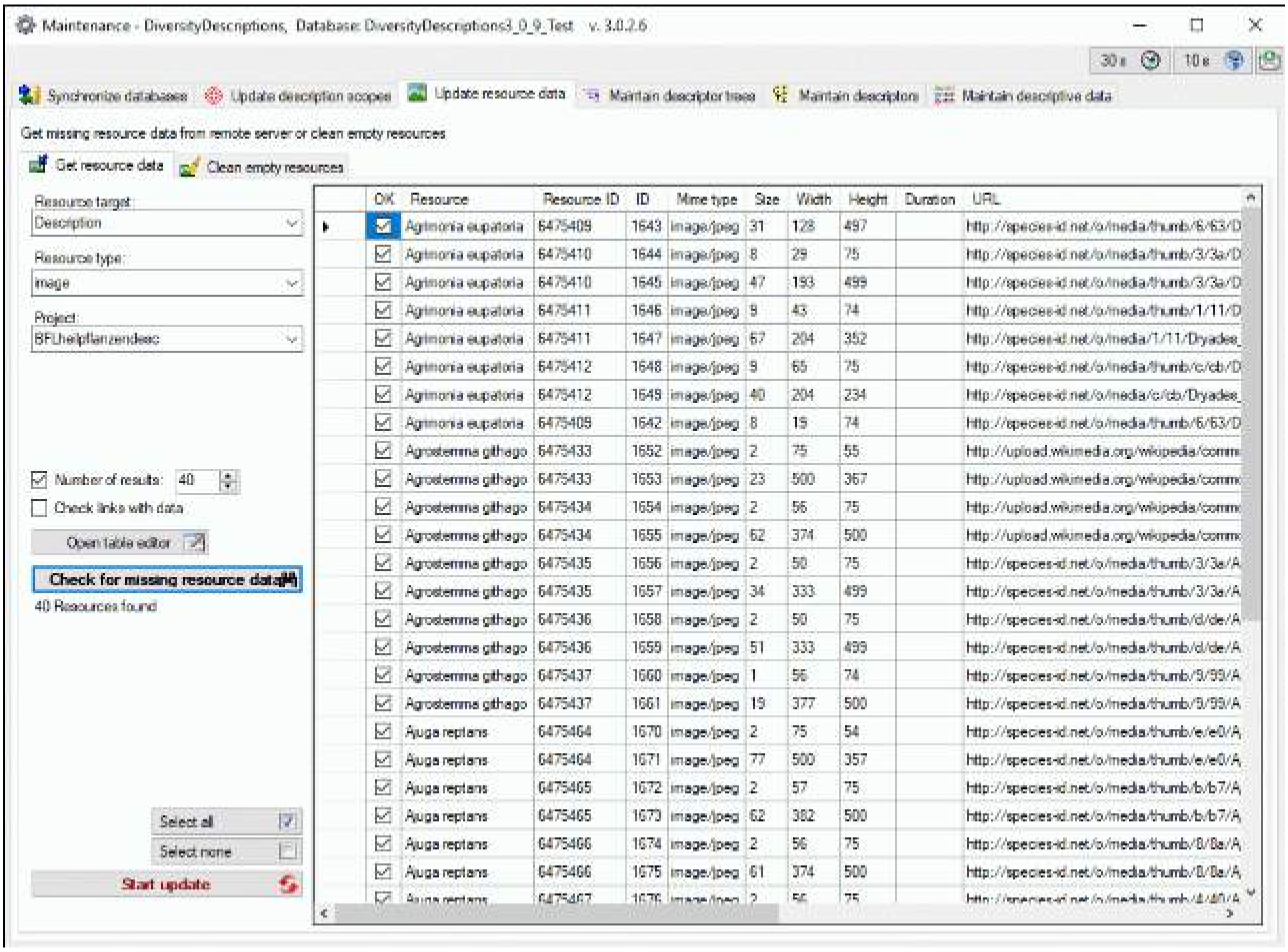
☑ Number of results: 40

☐ Check links with data

Maintenance - Get resource data

In the resource edit forms the resource data, e.g. the file size, of a single resource can be obtained from the remote server addressed by the resource link. If for a large number of resouces the data shall be updated it is much easier to select the **Update resource data** tab and choose the tab **Get resource data**.

Select the **Resource target**, ("Description", "Descriptor", "Categorical state" or "Descriptor tree node"), the **Resource type** ("image", "audio", "video", "text", "application" or "other") and the **Project**. Click on **Check for missing resource data** and all resource links of the specified type will be listed where the remote data of ("Mime type", "File size", "Width", "Height" or "Duration") differ from the database values (see image below).



Resource target: Description

Resource type: image

Project: BFLheilpflanzendesc

☑ Number of results: 40

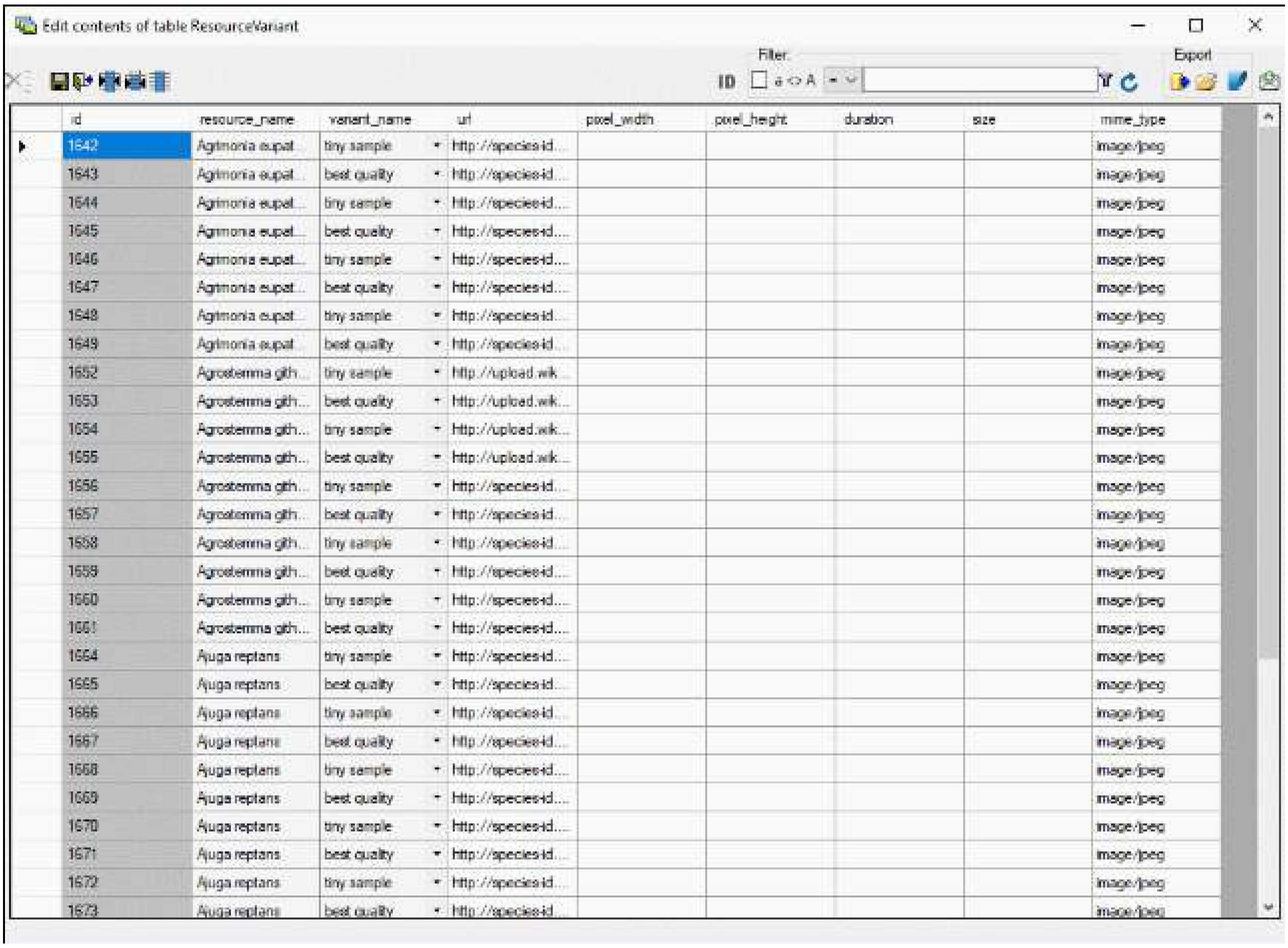
☐ Check links with data

40 Resources found

OK	Resource	Resource ID	ID	Mime type	Size	Width	Height	Duration	URL
☑	Agrimonia eupatoria	6475409	1643	image/jpeg	31	128	497		http://species-id.net/o/media/thumb/6/63/D
☑	Agrimonia eupatoria	6475410	1644	image/jpeg	8	29	75		http://species-id.net/o/media/thumb/3/3a/D
☑	Agrimonia eupatoria	6475410	1645	image/jpeg	47	193	499		http://species-id.net/o/media/thumb/3/3a/D
☑	Agrimonia eupatoria	6475411	1646	image/jpeg	9	43	74		http://species-id.net/o/media/thumb/1/11/D
☑	Agrimonia eupatoria	6475411	1647	image/jpeg	67	204	352		http://species-id.net/o/media/1/11/Dryades_
☑	Agrimonia eupatoria	6475412	1648	image/jpeg	9	65	75		http://species-id.net/o/media/thumb/c/cb/D
☑	Agrimonia eupatoria	6475412	1649	image/jpeg	40	204	234		http://species-id.net/o/media/c/cb/Dryades_
☑	Agrimonia eupatoria	6475409	1642	image/jpeg	8	19	74		http://species-id.net/o/media/thumb/6/63/D
☑	Agrostemma githago	6475433	1652	image/jpeg	2	75	55		http://upload.wikimedia.org/wikipedia/comm
☑	Agrostemma githago	6475433	1653	image/jpeg	23	500	367		http://upload.wikimedia.org/wikipedia/comm
☑	Agrostemma githago	6475434	1654	image/jpeg	2	56	75		http://upload.wikimedia.org/wikipedia/comm
☑	Agrostemma githago	6475434	1655	image/jpeg	62	374	500		http://upload.wikimedia.org/wikipedia/comm
☑	Agrostemma githago	6475435	1656	image/jpeg	2	50	75		http://species-id.net/o/media/thumb/3/3a/A
☑	Agrostemma githago	6475435	1657	image/jpeg	34	333	499		http://species-id.net/o/media/thumb/3/3a/A
☑	Agrostemma githago	6475436	1658	image/jpeg	2	50	75		http://species-id.net/o/media/thumb/d/de/A
☑	Agrostemma githago	6475436	1659	image/jpeg	51	333	499		http://species-id.net/o/media/thumb/d/de/A
☑	Agrostemma githago	6475437	1660	image/jpeg	1	56	74		http://species-id.net/o/media/thumb/9/99/A
☑	Agrostemma githago	6475437	1661	image/jpeg	19	377	500		http://species-id.net/o/media/thumb/9/99/A
☑	Ajuga reptans	6475464	1670	image/jpeg	2	75	54		http://species-id.net/o/media/thumb/e/e0/A
☑	Ajuga reptans	6475464	1671	image/jpeg	77	500	357		http://species-id.net/o/media/thumb/e/e0/A
☑	Ajuga reptans	6475465	1672	image/jpeg	2	57	75		http://species-id.net/o/media/thumb/b/b7/A
☑	Ajuga reptans	6475465	1673	image/jpeg	62	382	500		http://species-id.net/o/media/thumb/b/b7/A
☑	Ajuga reptans	6475466	1674	image/jpeg	2	56	75		http://species-id.net/o/media/thumb/8/8a/A
☑	Ajuga reptans	6475466	1675	image/jpeg	61	374	500		http://species-id.net/o/media/thumb/8/8a/A
☑	Ajuga reptans	6475467	1676	image/jpeg	2	56	75		http://species-id.net/o/media/thumb/4/40/A

The size of the query result list may be adapted by changing the value **Number of results** or unchecking this option to get the complete list. Usually only database links are checked that do not have any entry for "File size", "Width", "Height" and "Duration". Select **Check links with data** to check entries with data, e.g. to update manually entered values. You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To update the database click on the **Start update** button.

You may open a table editor for the selected resource variants by clicking the **Open table editor** button (see image below).



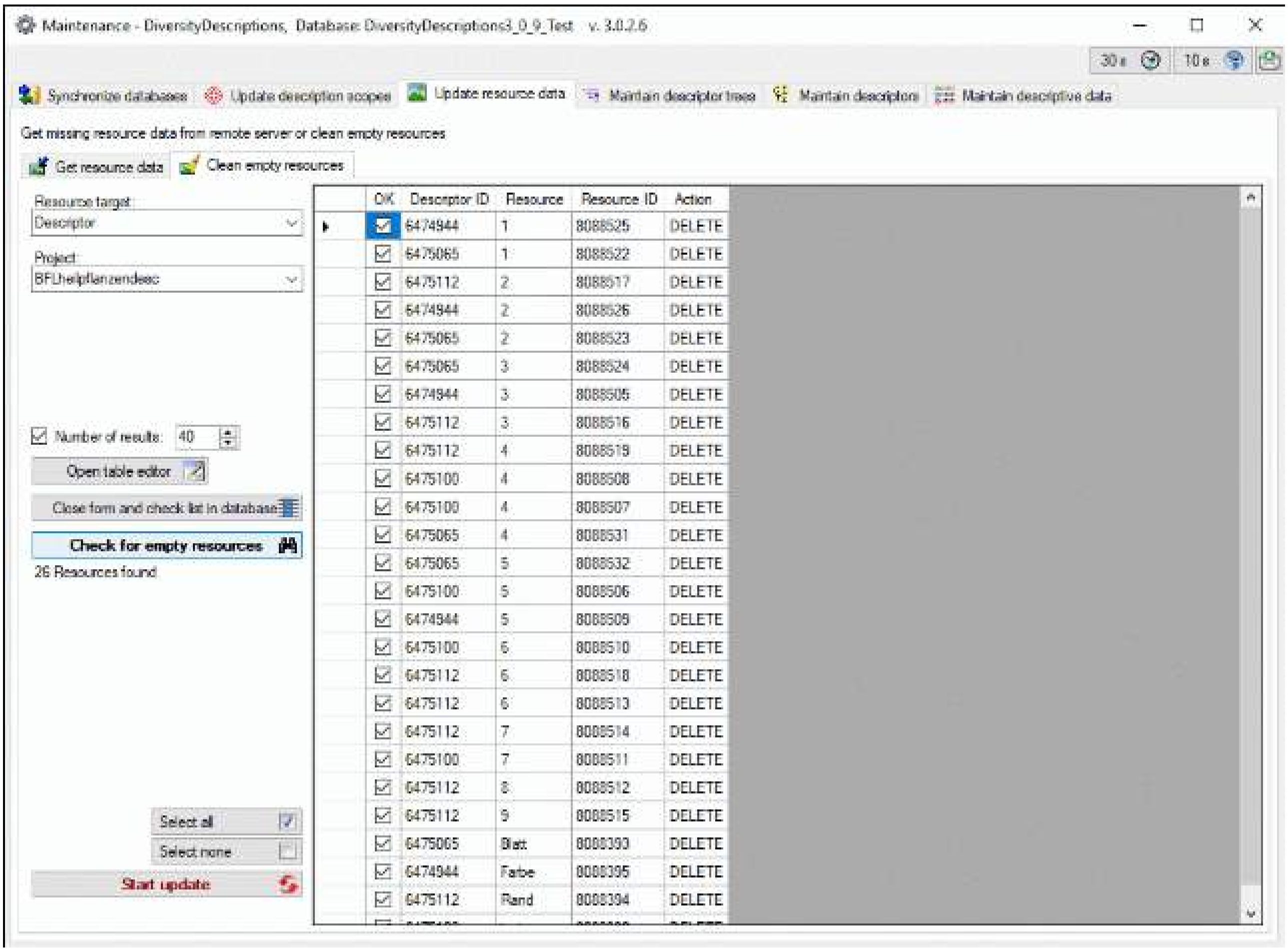
id	resource_name	variant_name	url	pixel_width	pixel_height	duration	size	mime_type
1642	Agrimonia eupat...	tiny sample	http://species-id...					image/jpeg
1643	Agrimonia eupat...	best quality	http://species-id...					image/jpeg
1644	Agrimonia eupat...	tiny sample	http://species-id...					image/jpeg
1645	Agrimonia eupat...	best quality	http://species-id...					image/jpeg
1646	Agrimonia eupat...	tiny sample	http://species-id...					image/jpeg
1647	Agrimonia eupat...	best quality	http://species-id...					image/jpeg
1648	Agrimonia eupat...	tiny sample	http://species-id...					image/jpeg
1649	Agrimonia eupat...	best quality	http://species-id...					image/jpeg
1652	Agrostemma gith...	tiny sample	http://upload.wik...					image/jpeg
1653	Agrostemma gith...	best quality	http://upload.wik...					image/jpeg
1654	Agrostemma gith...	tiny sample	http://upload.wik...					image/jpeg
1655	Agrostemma gith...	best quality	http://upload.wik...					image/jpeg
1656	Agrostemma gith...	tiny sample	http://species-id...					image/jpeg
1657	Agrostemma gith...	best quality	http://species-id...					image/jpeg
1658	Agrostemma gith...	tiny sample	http://species-id...					image/jpeg
1659	Agrostemma gith...	best quality	http://species-id...					image/jpeg
1660	Agrostemma gith...	tiny sample	http://species-id...					image/jpeg
1661	Agrostemma gith...	best quality	http://species-id...					image/jpeg
1664	Ajuga reptans	tiny sample	http://species-id...					image/jpeg
1665	Ajuga reptans	best quality	http://species-id...					image/jpeg
1666	Ajuga reptans	tiny sample	http://species-id...					image/jpeg
1667	Ajuga reptans	best quality	http://species-id...					image/jpeg
1668	Ajuga reptans	tiny sample	http://species-id...					image/jpeg
1669	Ajuga reptans	best quality	http://species-id...					image/jpeg
1670	Ajuga reptans	tiny sample	http://species-id...					image/jpeg
1671	Ajuga reptans	best quality	http://species-id...					image/jpeg
1672	Ajuga reptans	tiny sample	http://species-id...					image/jpeg
1673	Ajuga reptans	best quality	http://species-id...					image/jpeg

Some resources, especially for resource types like "text" or "application", do not even provide a file size. Therefore you might not get any new matches for subsequent check and update sequences if the number of results is limited. In those cases you should try to increase the number of results or deactivate the **Number of results** option.

Maintenance - Clean resources

In the database the "Resource" table holds the general resource data, e.g. copyright information, and links the resource to the target entity. The "ResourceVariant" table holds the link to the resource and allows to associate several links with distinguished quality levels to a single resource. To find resource entries that are not associated with any resource variant ("empty resources"), select the **Update resource data** tab and choose the tab **Clean empty resources**.

Select the **Resource target** ("Description", "Descriptor", "Categorical state" or "Descriptor tree node") and the **Project**. Click on **Check for empty resources** and all resource links of the specified type will be listed where no resource variants are present in the database (see image below).



Resource target: Descriptor

Project: BFLheilpflanzendesc

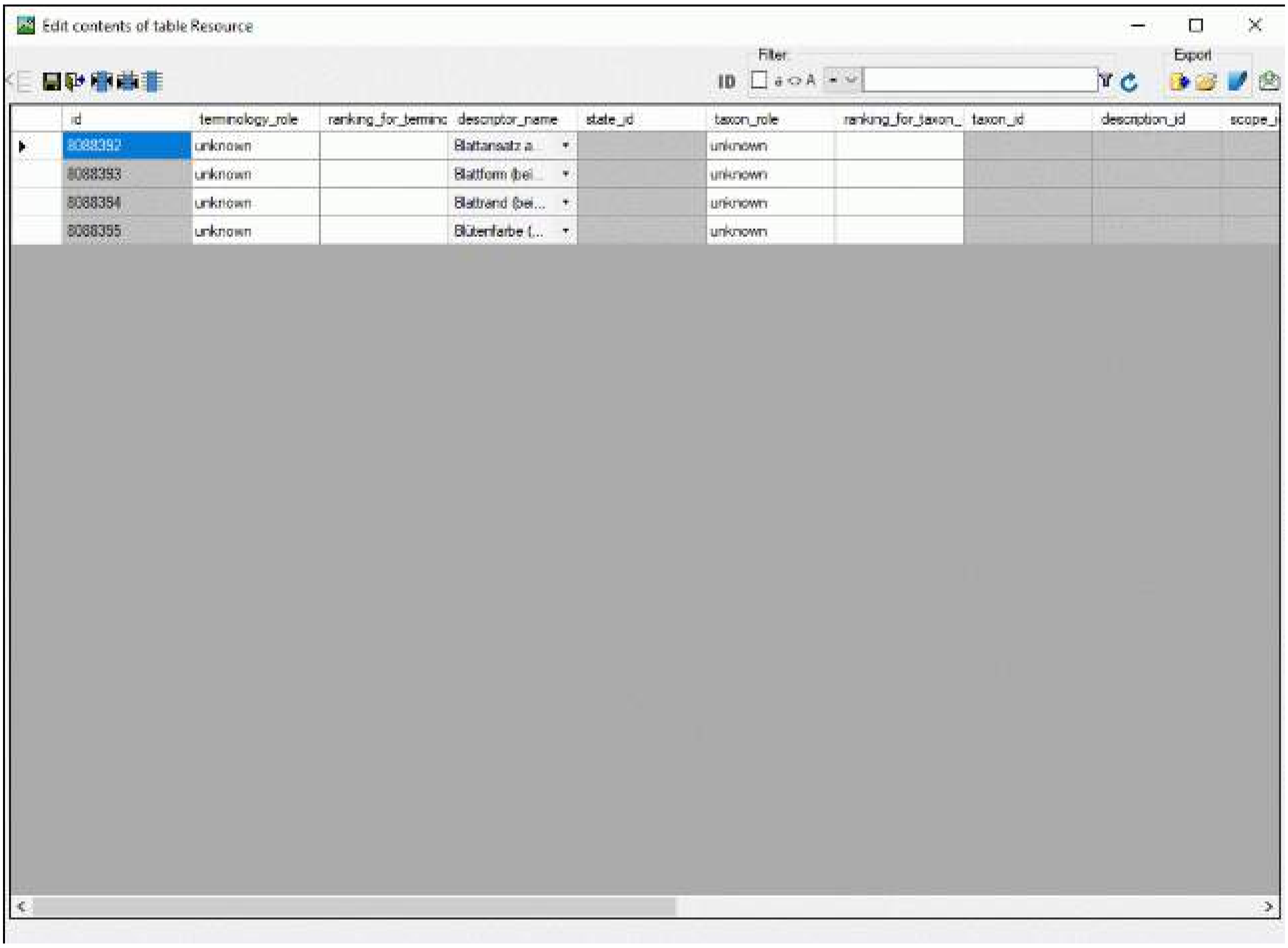
☑ Number of results: 40

26 Resources found

OK	Descriptor ID	Resource	Resource ID	Action
☑	6474944	1	8088525	DELETE
☑	6475065	1	8088522	DELETE
☑	6475112	2	8088517	DELETE
☑	6474944	2	8088526	DELETE
☑	6475065	2	8088523	DELETE
☑	6475065	3	8088524	DELETE
☑	6474944	3	8088505	DELETE
☑	6475112	3	8088516	DELETE
☑	6475112	4	8088519	DELETE
☑	6475100	4	8088508	DELETE
☑	6475100	4	8088507	DELETE
☑	6475065	4	8088531	DELETE
☑	6475065	5	8088532	DELETE
☑	6475100	5	8088506	DELETE
☑	6474944	5	8088509	DELETE
☑	6475100	6	8088510	DELETE
☑	6475112	6	8088518	DELETE
☑	6475112	6	8088513	DELETE
☑	6475112	7	8088514	DELETE
☑	6475100	7	8088511	DELETE
☑	6475112	8	8088512	DELETE
☑	6475112	9	8088515	DELETE
☑	6475065	Blatt	8088393	DELETE
☑	6474944	Farbe	8088395	DELETE
☑	6475112	Rand	8088394	DELETE

You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To delete the selected resource entries from the database click on the **Start update** button. Instead of updating the selecting entries you may click **Close form and check list in database** to return to the main program with the corresponding data sets.

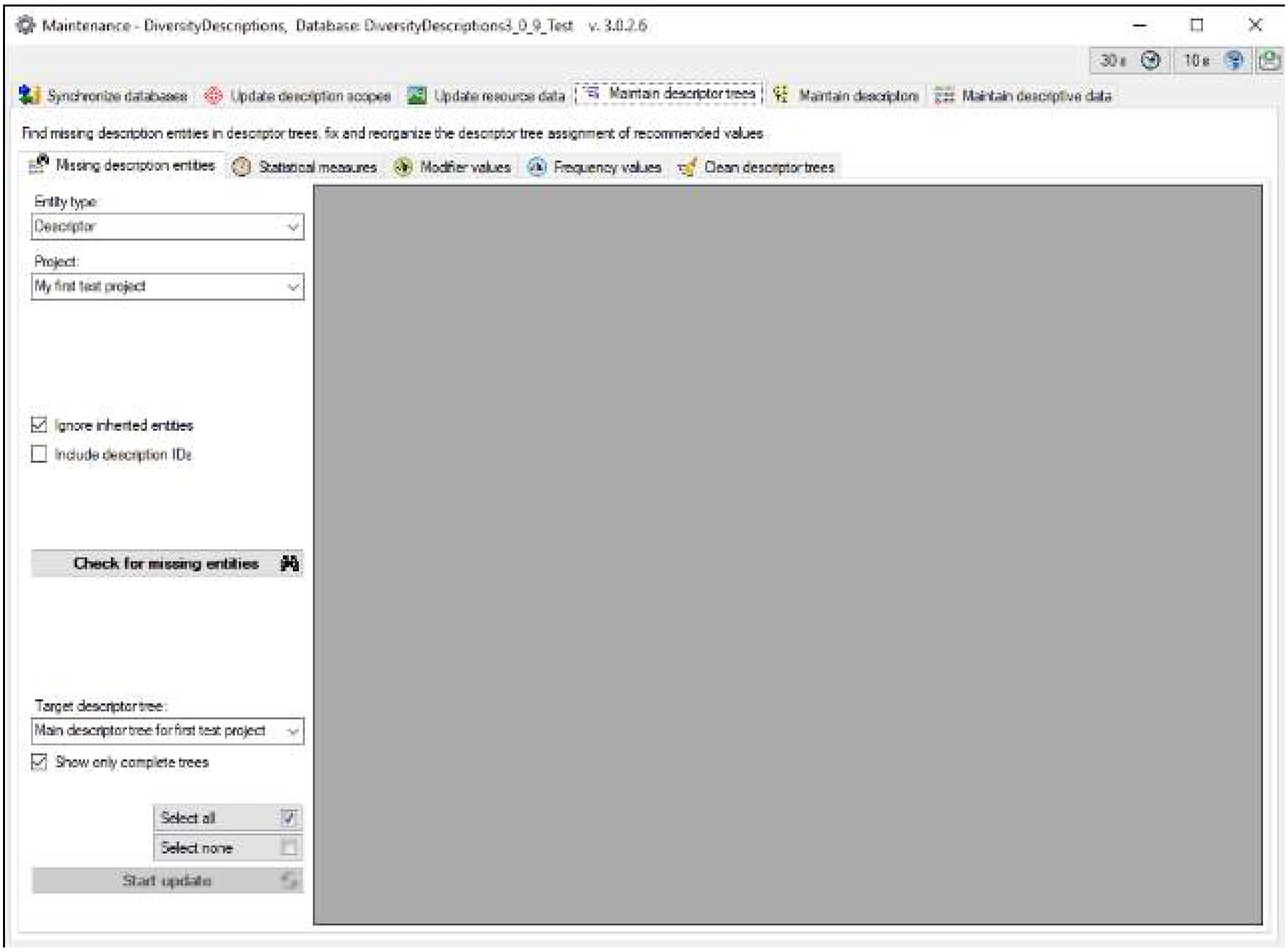
You may open a table editor for the selected resources by clicking the **Open table editor** button (see image below).



id	terminology_role	ranking_for_terminc	descriptor_name	state_id	taxon_role	ranking_for_taxon_	taxon_id	description_id	scope_
8088392	unknown		Blattansatz a...		unknown				
8088393	unknown		Blattform (bei...		unknown				
8088394	unknown		Blattrand (bei...		unknown				
8088395	unknown		Blütenfarbe (...		unknown				

Maintenance - Maintain descriptor trees

To open the maintenance form choose **Administration -> Database ... -> Maintenance ...** from the menu and select the **Maintain descriptor trees** tab. With the descriptor trees the assignment of descriptors to certain projects is done. Furthermore it is possible to administer the recommended statistical measures and modifiers for quantitive descriptors and the recommended modifier and frequency values for categorical descriptors. If a description item references entities that are not correctly assigned in the descriptor trees, this can be seen in the continious view. In the tab Missing description entities you can easily find and fix such kind of inconsistencies. Furthermore a centralized function to administer Statistical measures, Modifier values and Frequency values is provided. Finally superfluous entries may be deleted by using the Clean descriptor trees tab.



Maintenance - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.6

Find missing description entities in descriptor trees, fix and reorganize the descriptor tree assignment of recommended values

Entity type: Descriptor

Project: My first test project

☑ Ignore inherited entities

☐ Include description IDs

Target descriptor tree: Main descriptor tree for first test project

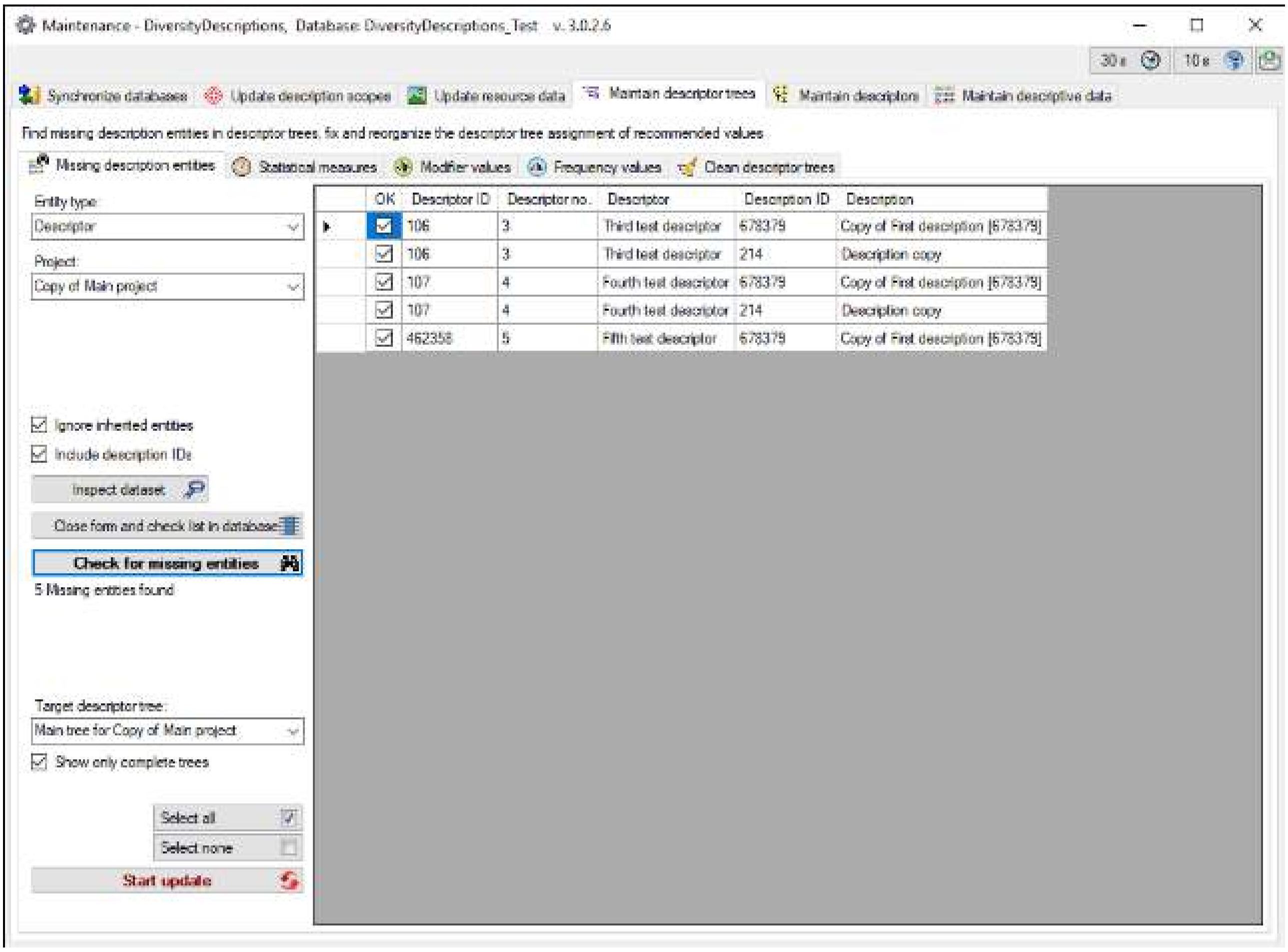
☑ Show only complete trees

Maintenance - Missing description entities

To find description entities that are not correctly assigned to the project's descriptor trees, select the **Maintain descriptor trees** tab and choose the tab **Missing description entities**. Select the **Project** and the **Entity type** that shall be checked. Currently the following entity types are supported:

- **Descriptor** - Search for descriptors that are referenced in the description data but not assigned to the project's descriptor tree
- **Statistical measure** - Search for statistical measures that are referenced in the description data but not assigned to the quantitative descriptor
- **Modifier** - Search for modifier values that are referenced in the description data but not assigned to the quantitative rsp. categorical descriptor
- **Frequency** - Search for frequency values that are referenced in the description data but not assigned to the categorical descriptor

By default the option **Ignore inherited entities** is checked, therefore only descriptors of the own project and recommended values directly assigned to the project descriptor are evaluated. If option **Include description IDs** is checked you will have the option to inspect the found data sets after the query. Start the query with a click on the **Check for missing entities** button.



Find missing description entities in descriptor trees, fix and reorganize the descriptor tree assignment of recommended values

Entity type: Descriptor

Project: Copy of Main project

☑ Ignore inherited entities

☑ Include description IDs

5 Missing entities found

Target descriptor tree: Main tree for Copy of Main project

☑ Show only complete trees

OK	Descriptor ID	Descriptor no.	Descriptor	Description ID	Description
☑	106	3	Third test descriptor	678379	Copy of First description [678379]
☑	106	3	Third test descriptor	214	Description copy
☑	107	4	Fourth test descriptor	678379	Copy of First description [678379]
☑	107	4	Fourth test descriptor	214	Description copy
☑	462358	5	Fifth test descriptor	678379	Copy of First description [678379]

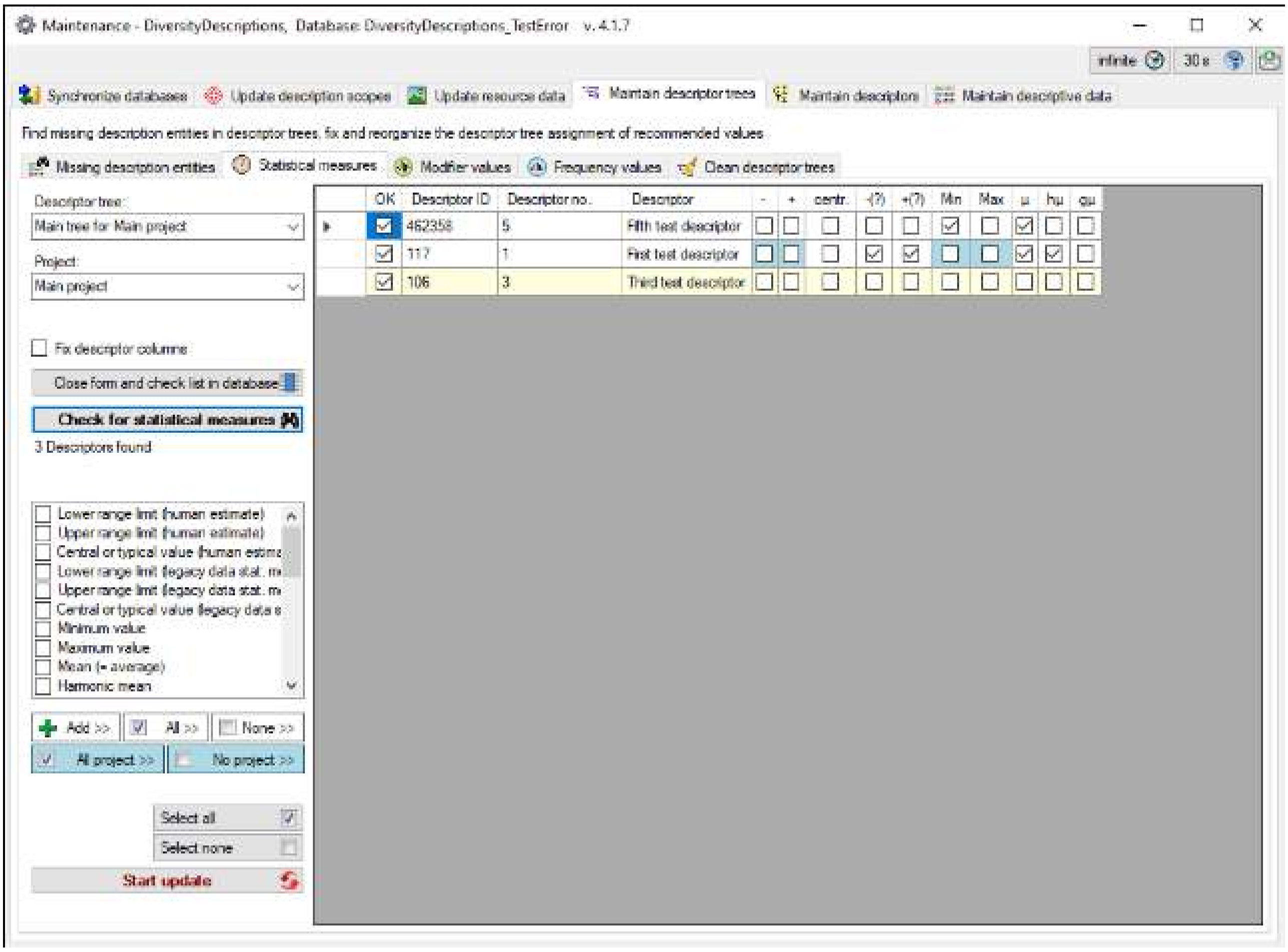
If you selected the option **Include description IDs** the button **Inspect dataset** will be shown. By selecting an entry and clicking the button **Inspect dataset** you may directly navigate to that dataset.

Before database update select the **Target descriptor tree** where missing entities shall be inserted. By default only descriptor trees that are marked as "complete" are shown. You may uncheck option **Show only complete trees** to display all present descriptor trees.

To update the database click on the Start update button. Instead of updating the selected entries you may click **Close form and check list in database** to return to the main program with the corresponding data sets.

Maintenance - Statistical measures

To administer the recommended statistical measures select the **Maintain descriptor trees** tab and choose the tab **Statistical measures**. Select the **Project** and the **Descriptor tree** that shall be checked and click on the **Check for statistical measures** button. Behind the "Descriptor" column all used statistical measures are shown in the output table. Descriptors that have not assigned any statistical measures are marked with yellow background. Values that are not assigned for the selected descriptor tree but anyway available in the project, e.g. due to a different descriptor tree or inherited by a superior tree node, are diplayed with blue background (see image below).



Find missing description entities in descriptor trees, fix and reorganize the descriptor tree assignment of recommended values

Descriptor tree: Main tree for Main project

Project: Main project

☐ Fix descriptor columns

3 Descriptors found

☐ Lower range limit (human estimate)
☐ Upper range limit (human estimate)
☐ Central or typical value (human estima
☐ Lower range limit (legacy data stat. m
☐ Upper range limit (legacy data stat. m
☐ Central or typical value (legacy data s
☐ Minimum value
☐ Maximum value
☐ Mean (= average)
☐ Harmonic mean

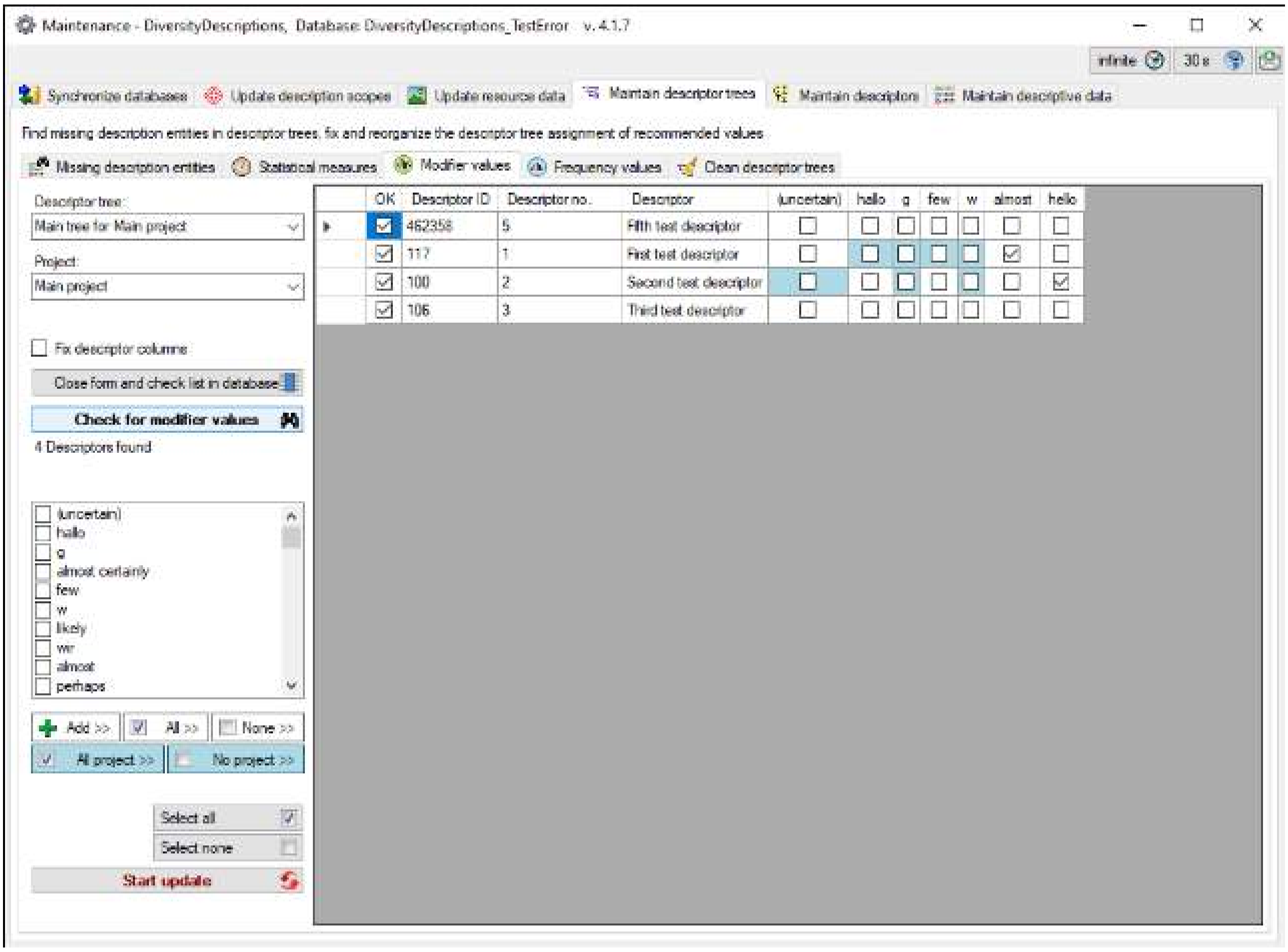
	OK	Descriptor ID	Descriptor no.	Descriptor	-	+	centr.	-(?)	+(?)	Min	Max	µ	hµ	gµ
▸	☑	462358	5	Fifth test descriptor	☐	☐	☐	☐	☐	☑	☐	☑	☐	☐
	☑	117	1	First test descriptor	☐	☐	☐	☑	☑	☐	☐	☑	☑	☐
	☑	106	3	Third test descriptor	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐

New values may be inserted in the table by selecting them in the check list on the left and clicking the **Add >>** button. By clicking the button ☑ **All >>** rsp. ☐ **None >>** may check or uncheck all checked values from the list box in the table. The buttons ☑ **All project >>** and ☐ **No project >>** check or uncheck the project specific entries with blue background in the table. If one or more lines in the output tables are selected (click on the fields before the "OK" column), the mentioned functions operate only for the selected lines, otherways for the whole table. With option **Fix descriptor columns** you may fix the first data grid columns to scroll horizontally thru the value list.

To store the modifications to the selected descriptor tree click on the **Start update** button. Instead of updating the selected entries you may click **Close form and check list in database** to return to the main program with the corresponding data sets.

Maintenance - Modifier values

To administer the recommended modifier values select the **Maintain descriptor trees** tab and choose the tab **Modifier values**. Select the **Project** and the **Descriptor tree** that shall be checked and click on the **Check for modifier values** button. Behind the "Descriptor" column all used modifier values are shown in the output table. Values that are not assigned for the selected descriptor tree but anyway available in the project, e.g. due to a different descriptor tree or inherited by a superior tree node, are diplayed with blue background (see image below).



Maintenance - DiversityDescriptions, Database: DiversityDescriptions_TestError v. 4.1.7

Find missing description entities in descriptor trees, fix and reorganize the descriptor tree assignment of recommended values

Descriptor tree: Main tree for Main project

Project: Main project

☐ Fix descriptor columns

4 Descriptors found

	OK	Descriptor ID	Descriptor no.	Descriptor	(uncertain)	hallo	g	few	w	almost	hello
▸	☑	462358	5	Fifth test descriptor	☐	☐	☐	☐	☐	☐	☐
	☑	117	1	First test descriptor	☐	☐	☐	☐	☐	☑	☐
	☑	100	2	Second test descriptor	☐	☐	☐	☐	☐	☐	☑
	☑	106	3	Third test descriptor	☐	☐	☐	☐	☐	☐	☐

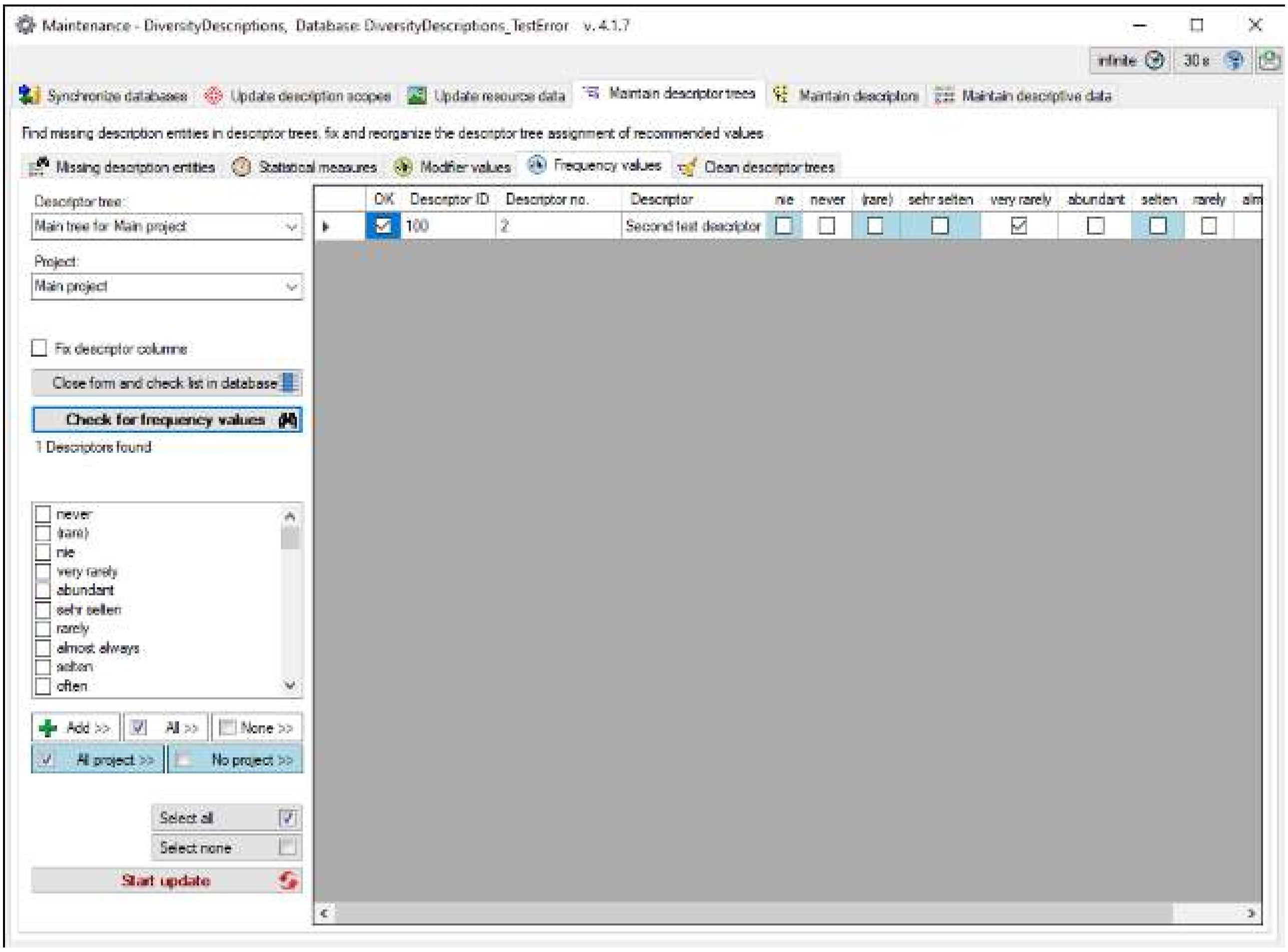
☐ (uncertain)
☐ hallo
☐ g
☐ almost certainly
☐ few
☐ w
☐ likely
☐ wir
☐ almost
☐ perhaps

New values may be inserted in the table by selecting them in the check list on the left and clicking the **Add >>** button. The check list shows the modifier values available in your database. Additional values can be inserted in the Modifier/Frequency tabs of Edit descriptor or Edit project. By clicking the button ☑ **All >>** rsp. ☐ **None >>** may check or uncheck all checked values from the list box in the table. The buttons ☑ **All project >>** and ☐ **No project >>** check or uncheck the project specific entries with blue background in the table. If one or more lines in the output tables are selected (click on the fields before the "OK" column), the mentioned functions operate only for the selected lines, otherways for the whole table. With option **Fix descriptor columns** you may fix the first data grid columns to scroll horizontally thru the value list.

To store the modifications to the selected descriptor tree click on the Start update button. Instead of updating the selected entries you may click **Close form and check list in database** to return to the main program with the corresponding data sets.

Maintenance - Frequency values

To administer the recommended frequency values select the **Maintain descriptor trees** tab and choose the tab **Frequency values**. Select the **Project** and the **Descriptor tree** that shall be checked and click on the **Check for frequency values** button. Behind the "Descriptor" column all used frequency values are shown in the output table. Values that are not assigned for the selected descriptor tree but anyway available in the project, e.g. due to a different descriptor tree or inherited by a superior tree node, are diplayed with blue background (see image below).



Descriptor tree: Main tree for Main project

Project: Main project

☐ Fix descriptor columns

1 Descriptors found

OK	Descriptor ID	Descriptor no.	Descriptor	nie	never	(rare)	sehr selten	very rarely	abundant	selten	rarely	alm
☑	100	2	Second test descriptor	☐	☐	☐	☐	☑	☐	☐	☐	

New values may be inserted in the table by selecting them in the check list on the left and clicking the **Add >>** button. The check list shows the frequency values available in your database. Additional values can be inserted in the Modifier/Frequency tabs of Edit descriptor or Edit project. By clicking the button ☑ **All >>** rsp. ☐ **None >>** may check or uncheck all checked values from the list box in the table. The buttons ☑ **All project >>** and ☐ **No project >>** check or uncheck the project specific entries with blue background in the table. If one or more lines in the output tables are selected (click on the fields before the "OK" column), the mentioned functions operate only for the selected lines, otherways for the whole table. With option **Fix descriptor columns** you may fix the first data grid columns to scroll horizontally thru the value list.

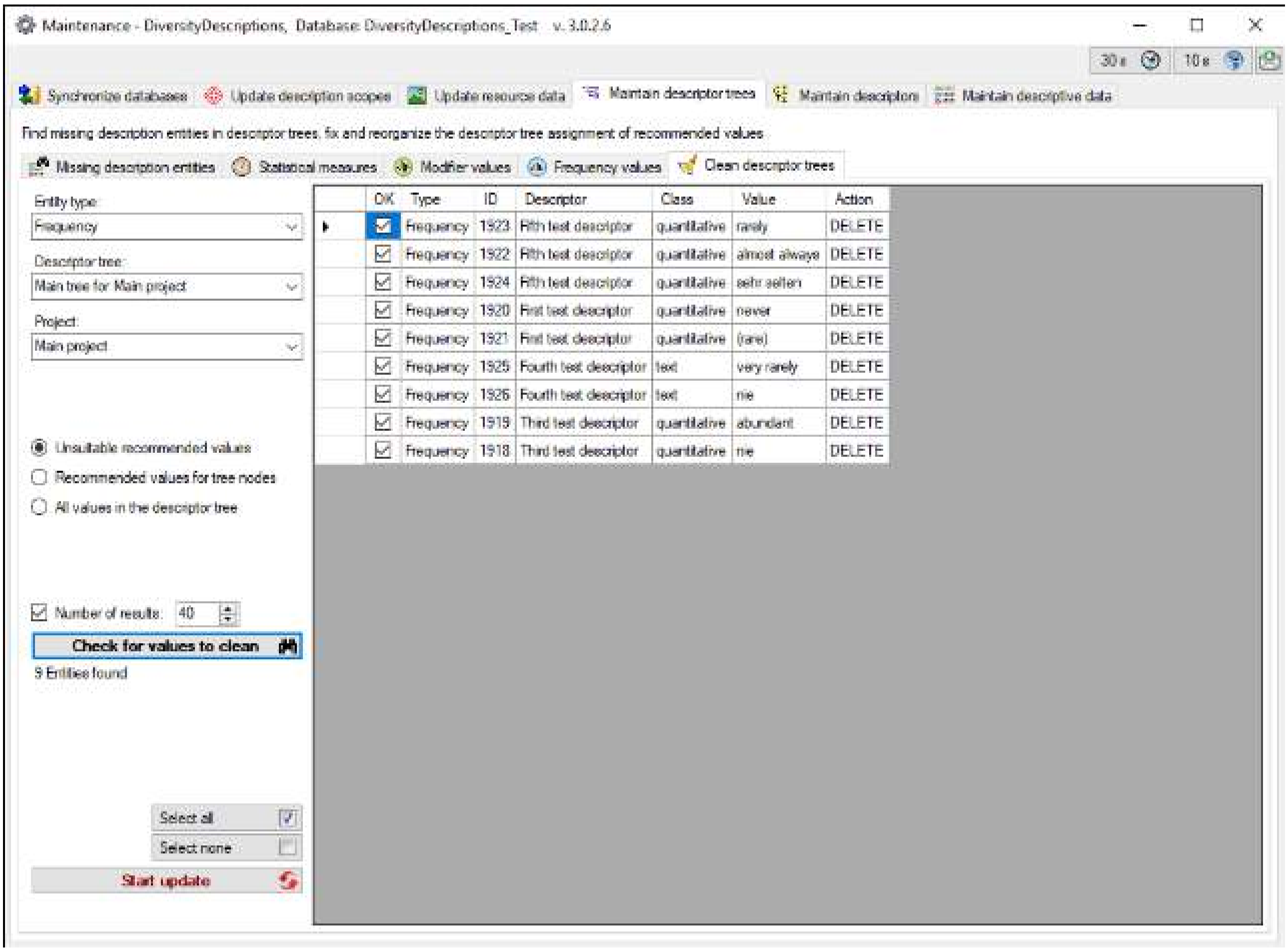
To store the modifications to the selected descriptor tree click on the **Start update** button. Instead of updating the selected entries you may click **Close form and check list in database** to return to the main program with the corresponding data sets.

Maintenance - Clean descriptor trees

To administer the recommended modifier values select the **Maintain descriptor trees** tab and choose the tab **Clean decriptor trees**. Select the **Project**, the **Descriptor tree** and the **Entity type** ("Statistical measure", "Modifier" or "Frequency") that shall be cleaned. Currently three cleaning options are supported:

- **Unsuitable recommended values** - Clear recommended values the do not match the descriptor type, e.g. statistical measures for a categorical descriptor.
- **Recommended values for tree nodes** - Clear recommended values that are not directly assigned to a descriptor, but a tree node. You should only perform this operation if you are sure that the neccessary values have been directly assigned to the approriate descriptors.
- **All values in the descriptor tree** - Delete all recommended values. Only descriptor trees can be selected for this option, that are not marked as "complete". You should only perform this operation if you are sure that the neccessary values have been assigned to a complete descriptor tree of the project.

To start the search click on the **Check for values to clean** button.



Find missing description entities in descriptor trees, fix and reorganize the descriptor tree assignment of recommended values

Entity type: Frequency

Descriptor tree: Main tree for Main project

Project: Main project

● Unsuitable recommended values
○ Recommended values for tree nodes
○ All values in the descriptor tree

☑ Number of results: 40

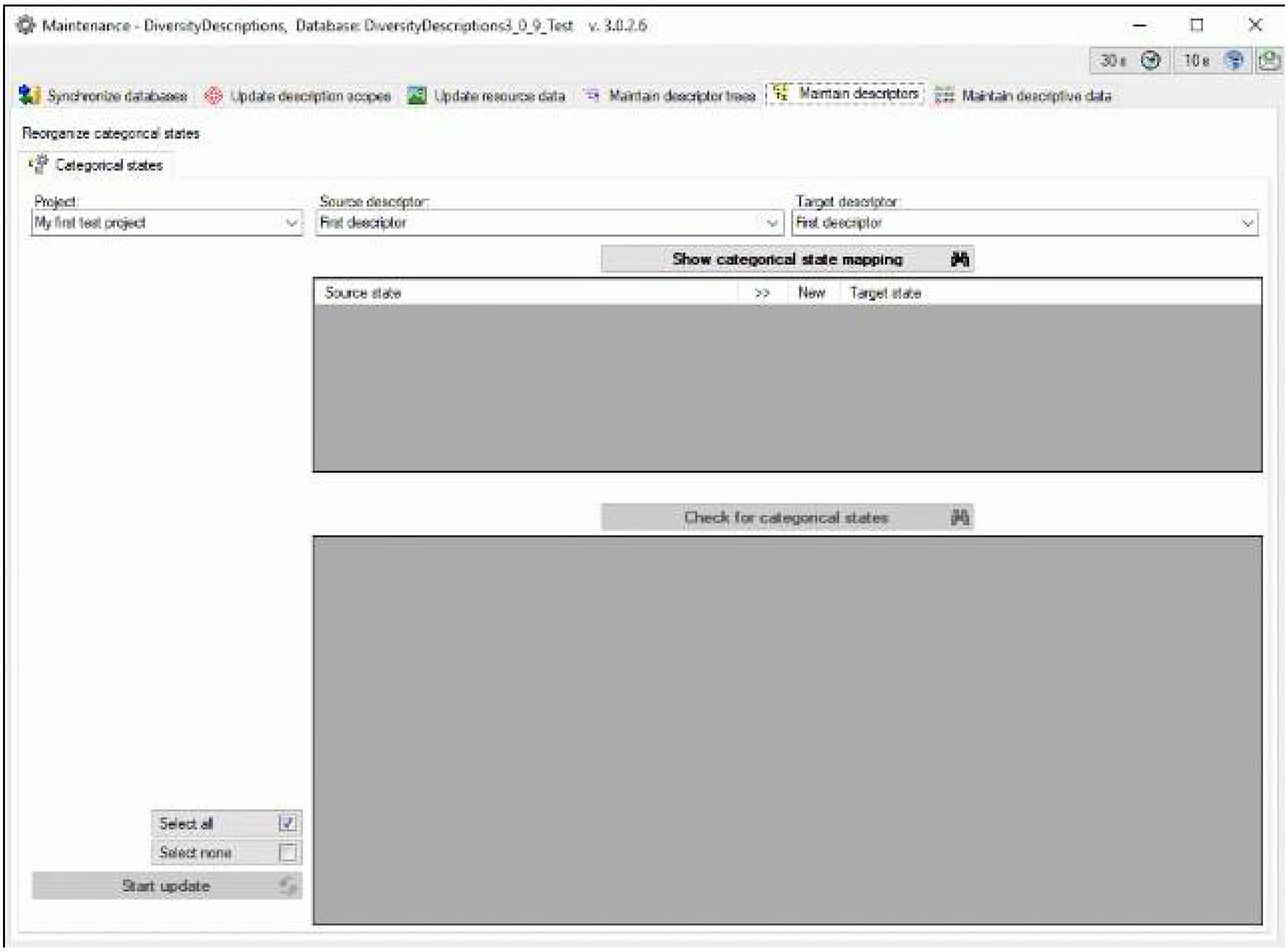
9 Entities found

OK	Type	ID	Descriptor	Class	Value	Action
☑	Frequency	1923	Fifth test descriptor	quantitative	rarely	DELETE
☑	Frequency	1922	Fifth test descriptor	quantitative	almost always	DELETE
☑	Frequency	1924	Fifth test descriptor	quantitative	sehr selten	DELETE
☑	Frequency	1920	First test descriptor	quantitative	never	DELETE
☑	Frequency	1921	First test descriptor	quantitative	(rare)	DELETE
☑	Frequency	1925	Fourth test descriptor	text	very rarely	DELETE
☑	Frequency	1926	Fourth test descriptor	text	nie	DELETE
☑	Frequency	1919	Third test descriptor	quantitative	abundant	DELETE
☑	Frequency	1918	Third test descriptor	quantitative	nie	DELETE

To start the update of the selected descriptor tree click on the **Start update** button.

Maintenance - Maintain descriptors

To open the maintenance form choose **Administration -> Database ... -> Maintenance ...** from the menu and select the **Maintain descriptors** tab. In the Categorical states tab you may shift and copy categorical states to a different descriptor or delete selected categorical states.



Maintenance - Categorical states

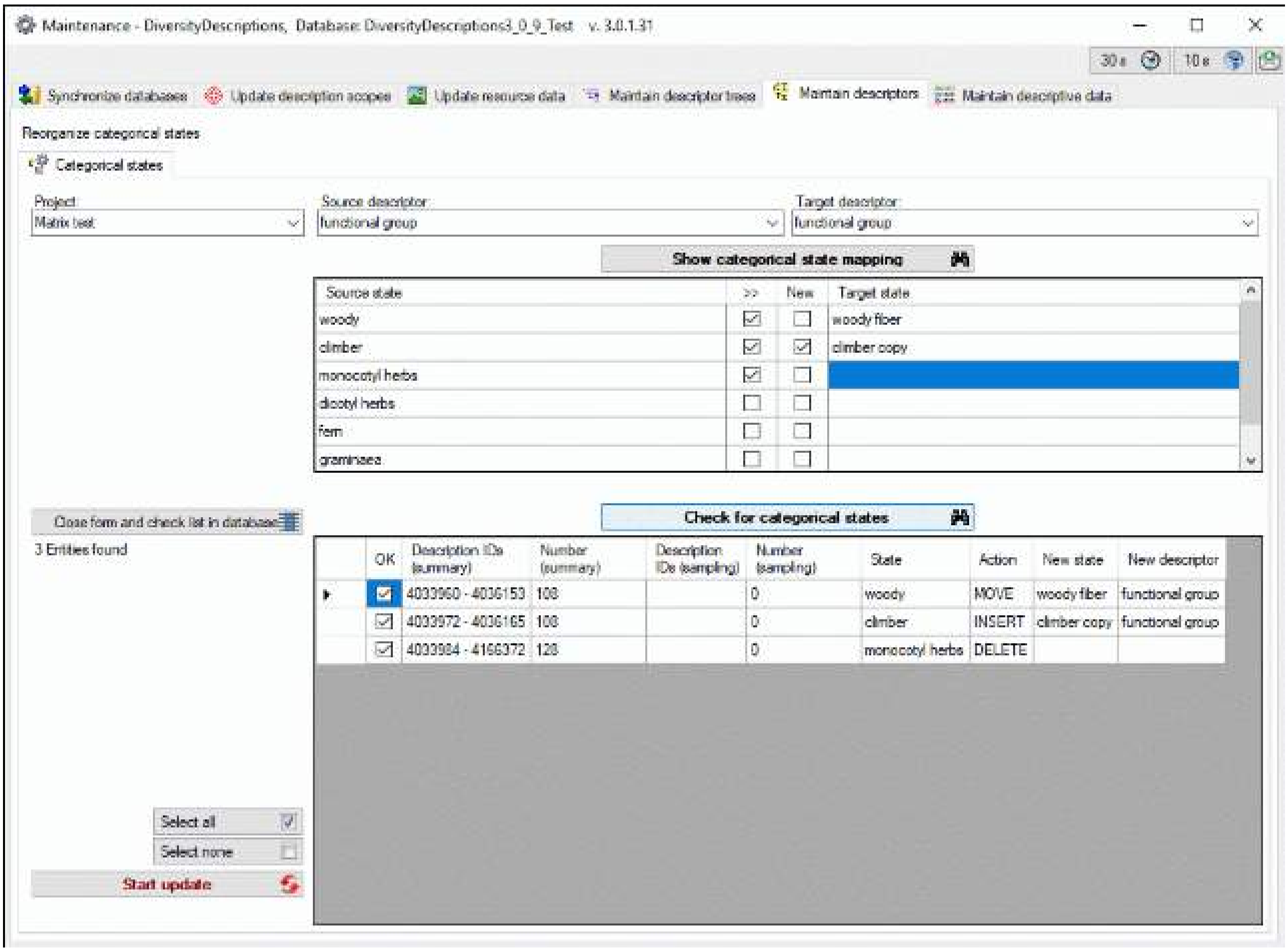
To shift and copy categorical states to a different descriptor or delete selected categorical states, select the **Maintain descriptors** tab and choose the tab **Categorical states**. In this panel you operate on the **categorical states** of the descriptors. If you want to shift or copy categorical summary data in descriptions, please use Maintenance - Categorical summary data.

Select the **Project**, the **Source descriptor** and the **Target descriptor**. Click on **Show categorical state mapping** and all categorical state values of the selected **Source descriptor** will be listed in the upper table (see image below). Select the categorical states you want to modify in column **>>**.

The following operations are available:

- **Delete** the categorical state by leaving the **Target state** empty
- **Move** the categorical state by entering the **Target state**
- **Copy** the categorical state by entering the **Target state** and selecting the **New** column

In case the categorical states are moved or copied, associated fields as **abbreviation** and **detail** will be processed. State resources will not be copied.



Project: Matrix test

Source descriptor: functional group

Target descriptor: functional group

Source state	>>	New	Target state
woody	☑	☐	woody fiber
climber	☑	☑	climber copy
monocotyl herbs	☑	☐	
dicotyl herbs	☐	☐	
fern	☐	☐	
graminaea	☐	☐	

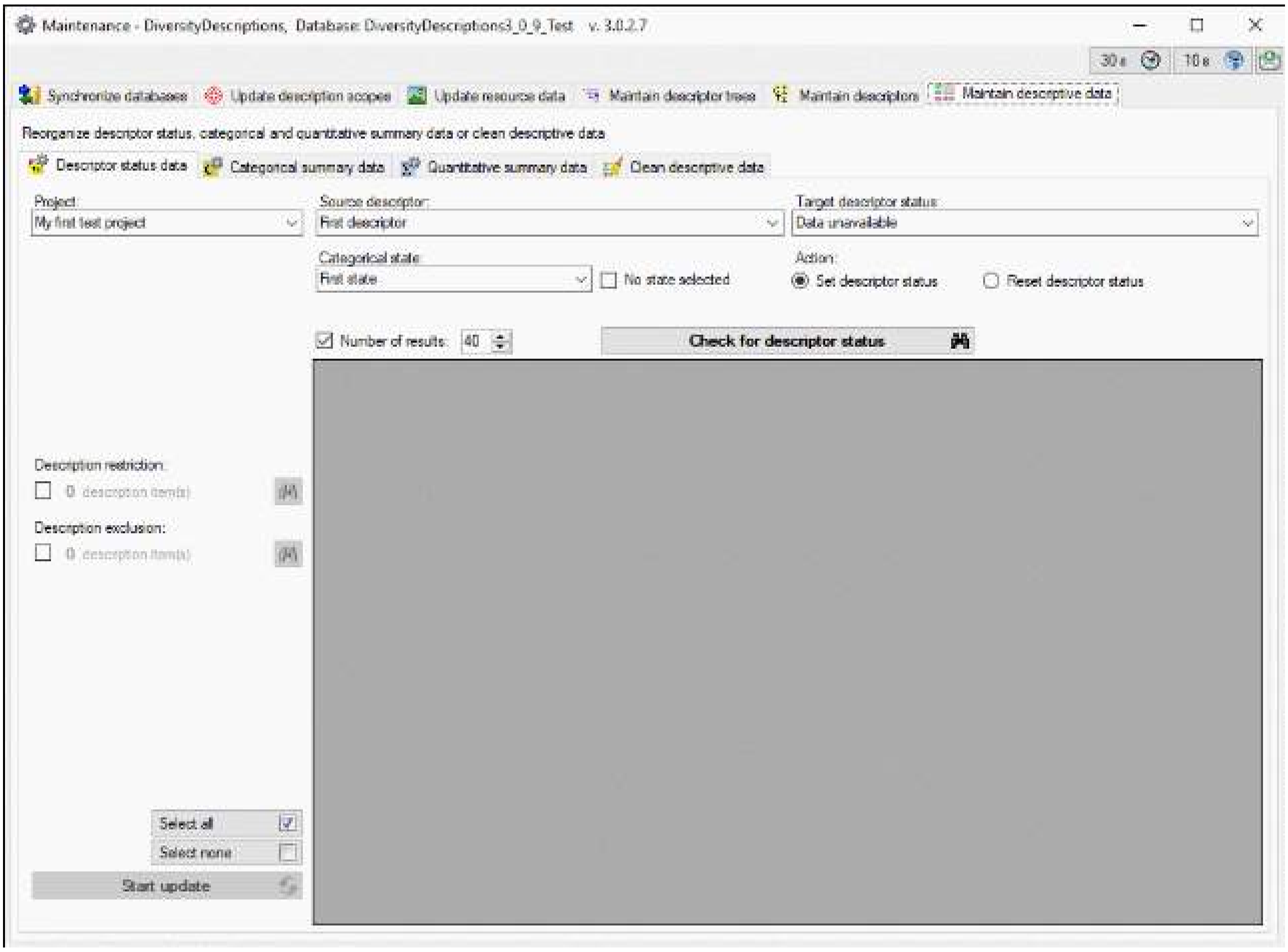
3 Entities found

	OK	Description IDs (summary)	Number (summary)	Description IDs (sampling)	Number (sampling)	State	Action	New state	New descriptor
▸	☑	4033960 - 4036153	108		0	woody	MOVE	woody fiber	functional group
	☑	4033972 - 4036165	108		0	climber	INSERT	climber copy	functional group
	☑	4033984 - 4166372	128		0	monocotyl herbs	DELETE		

After adjusting the required operations for the selected categorical states click on **Check for categorical states** and the number of affected summary and sampling data will be listed in the lower table (see image above). For each **State** the **Action** (DELETE, MOVE or INSERT) and **New state** are specified. You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To perform the selected operations click on the Start update button. If Instead updating the database you may click **Close form and check list in database** to return to the main program with the affected descriptions.

Maintenance - Maintain descriptive data

To open the maintenance form choose **Administration -> Database ... -> Maintenance ...** from the menu and select the **Maintain descriptive data** tab. In the Descriptor status data tab you may set or reset the descriptor status of a categorical descriptor depending on the categorical states in its summary data. In the Categorical summary data tab you may shift and copy categorical summary data to a different descriptor or delete values for selected categorical states. In the Quantitative summary data tab you may perform such operations concerning statistical measures. To find and delete corrupted descriptive data choose the Clean descriptive data tab.


Maintenance - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Project: My first test project

Source descriptor: First descriptor

Target descriptor status: Data unavailable

Categorical state: First state

☐ No state selected

Action: ● Set descriptor status ○ Reset descriptor status

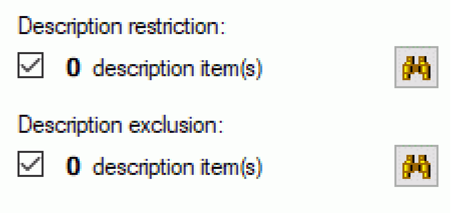
☑ Number of results: 40

Description restriction: ☐ 0 description item(s)

Description exclusion: ☐ 0 description item(s)

Commonly used description selection options

In the sub-panels you may set a descriptor status and move or copy categorical rsp. quantitative summary data. By default all descriptions from the selected project will be searched that fulfill the specified conditions, i.e. a certain categorical state or statistical measure. In certain cases it is neccessary to restrict the possibly affected descriptions by some additional conditions. For this purpose there is the option to define a restriction and/or an exclusion list (see example below).



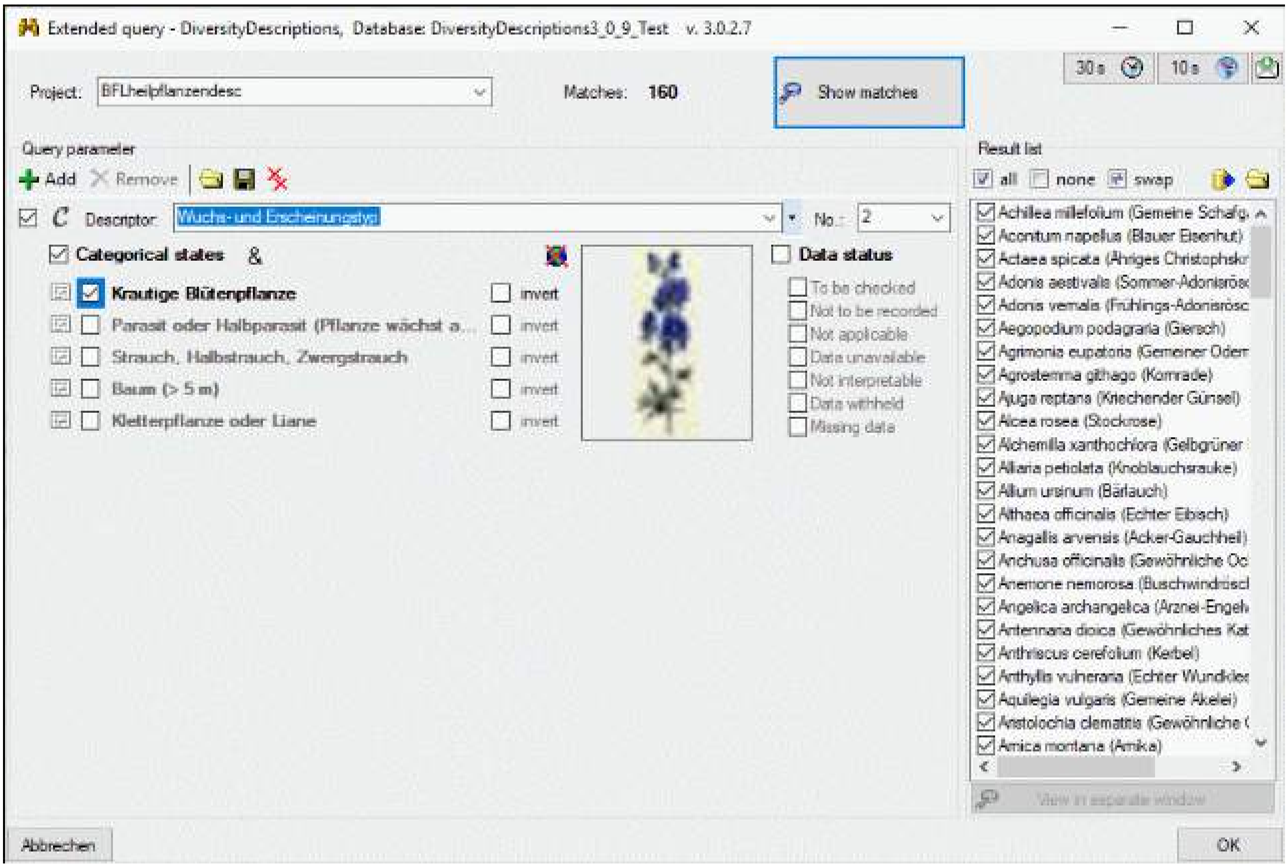
Description restriction:

☑ **0** description item(s)

Description exclusion:

☑ **0** description item(s)

By starting an extended query (button) you can generate a list of descriptions (see image below) that shall be used to restrict the search rsp. excluded from the search.



Extended query - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Project: BFLheilpflanzendesc

Matches: **160**

Query parameter

☑ Descriptor: Wuchs- und Erscheinungstyp No.: 2

☑ **Categorical states** &

☑ **Krautige Blütenpflanze** ☐ invert

☐ Parasit oder Halbparasit (Pflanze wächst a... ☐ invert

☐ Strauch, Halbstrauch, Zwergstrauch ☐ invert

☐ Baum (> 5 m) ☐ invert

☐ Kletterpflanze oder Liane ☐ invert

☐ **Data status**

☐ To be checked

☐ Not to be recorded

☐ Not applicable

☐ Data unavailable

☐ Not interpretable

☐ Data withheld

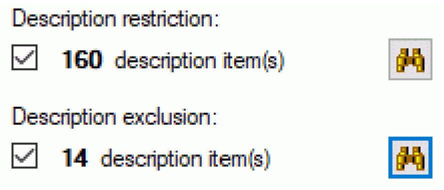
☐ Missing data

Result list

☑ all ☐ none ☑ swap

☑ Achillea millefolium (Gemeine Schafg.
☑ Aconitum napellus (Blauer Eisenhut)
☑ Actaea spicata (Ähriges Christophskr
☑ Adonis aestivalis (Sommer-Adonisrösc
☑ Adonis vernalis (Frühlings-Adonisrösc
☑ Aegopodium podagraria (Giersch)
☑ Agrimonia eupatoria (Gemeiner Oder
☑ Agrostemma githago (Kornrade)
☑ Ajuga reptans (Kriechender Günsel)
☑ Alcea rosea (Stockrose)
☑ Alchemilla xanthochlora (Gelbgrüner
☑ Alliaria petiolata (Knoblauchsrauke)
☑ Allium ursinum (Bärlauch)
☑ Althaea officinalis (Echter Eibisch)
☑ Anagallis arvensis (Acker-Gauchheil)
☑ Anchusa officinalis (Gewöhnliche Oc
☑ Anemone nemorosa (Buschwindrösc
☑ Angelica archangelica (Arznei-Engel
☑ Antennaria dioica (Gewöhnliches Kat
☑ Anthriscus cerefolium (Kerbel)
☑ Anthyllis vulneraria (Echter Wundkle
☑ Aquilegia vulgaris (Gemeine Akelei)
☑ Aristolochia clematitis (Gewöhnliche
☑ Arnica montana (Arnika)

The resulting numbers of restricted and excluded descriptions will be displayed in the controls. You may check the selected items by double-clicking the numbers (see images below below).



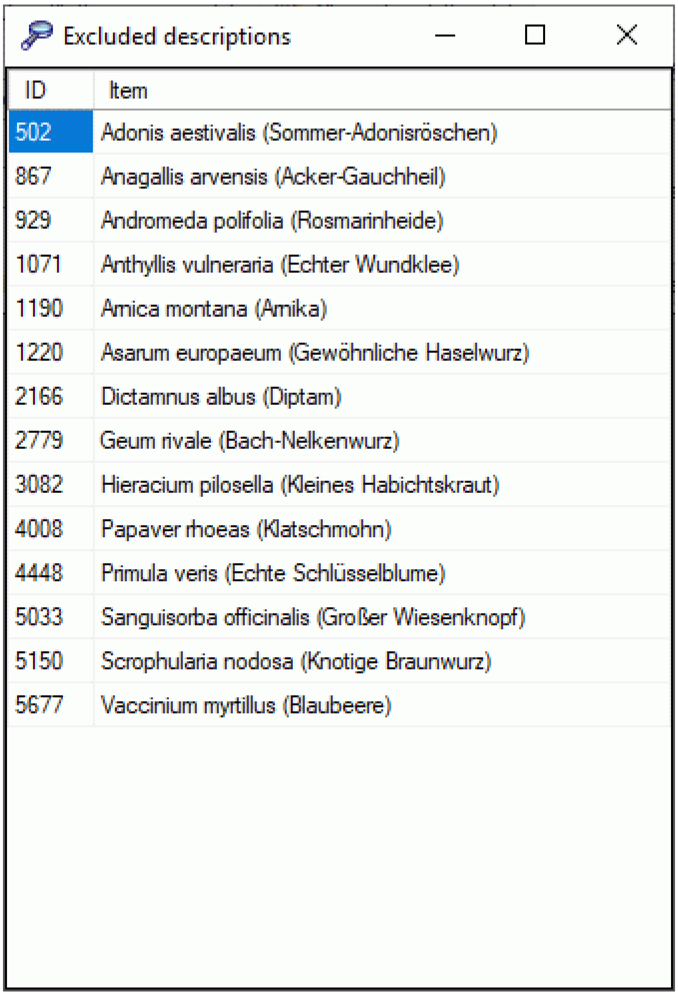
Description restriction:

☑ **160** description item(s)

Description exclusion:

☑ **14** description item(s)

ID	Item
414	Achillea millefolium (Gemeine Schafgarbe)
442	Aconitum napellus (Blauer Eisenhut)
473	Actaea spicata (Ähriges Christophskraut)
502	Adonis aestivalis (Sommer-Adonisröschen)
531	Adonis vernalis (Frühlings-Adonisröschen)
560	Aegopodium podagraria (Giersch)
625	Agrimonia eupatoria (Gemeiner Odermennig)
655	Agrostemma githago (Kornrade)
684	Ajuga reptans (Kriechender Günsel)
720	Alcea rosea (Stockrose)
752	Alchemilla xanthochlora (Gelbgrüner Frauenmantel)
781	Alliaria petiolata (Knoblauchsrauke)
809	Allium ursinum (Bärlauch)
838	Althaea officinalis (Echter Eibisch)
867	Anagallis arvensis (Acker-Gauchheil)
896	Anchusa officinalis (Gewöhnliche Ochsenzunge)
956	Anemone nemorosa (Buschwindröschen)
985	Angelica archangelica (Arznei-Engelwurz)
1014	Antennaria dioica (Gewöhnliches Katzenpfötchen)
1045	Anthriscus cerefolium (Kerbel)

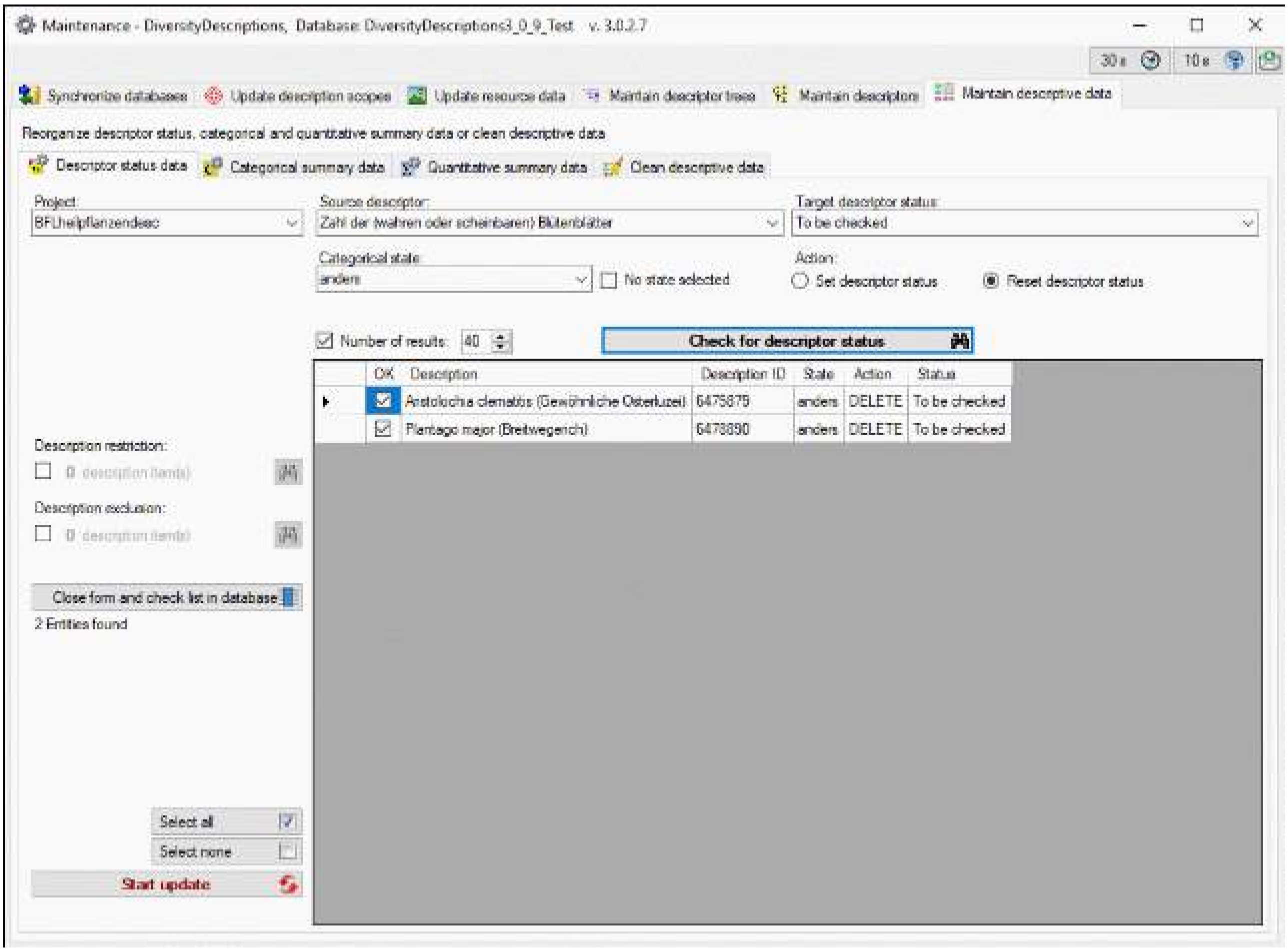


ID	Item
502	Adonis aestivalis (Sommer-Adonisröschen)
867	Anagallis arvensis (Acker-Gauchheil)
929	Andromeda polifolia (Rosmarinheide)
1071	Anthyllis vulneraria (Echter Wundklee)
1190	Arnica montana (Arnika)
1220	Asarum europaeum (Gewöhnliche Haselwurz)
2166	Dictamnus albus (Diptam)
2779	Geum rivale (Bach-Nelkenwurz)
3082	Hieracium pilosella (Kleines Habichtskraut)
4008	Papaver rhoeas (Klatschmohn)
4448	Primula veris (Echte Schlüsselblume)
5033	Sanguisorba officinalis (Großer Wiesenknopf)
5150	Scrophularia nodosa (Knotige Braunwurz)
5677	Vaccinium myrtillus (Blaubeere)

Maintenance - Descriptor status data

To set or reset a certain descriptor status for dedicated categorical summary data, select the **Maintain descriptive data** tab and choose the tab **Descriptor status data**.

Select the **Project**, the **Source descriptor** and the **Target descriptor status**. Select the **Categorical state** value for which the data status shall be set or reset and the requested **Action**.



Maintenance - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Project: BFLheilpflanzendesc

Source descriptor: Zahl der (wahren oder scheinbaren) Blütenblätter

Target descriptor status: To be checked

Categorical state: anders

☐ No state selected

Action: ○ Set descriptor status ● Reset descriptor status

☑ Number of results: 40

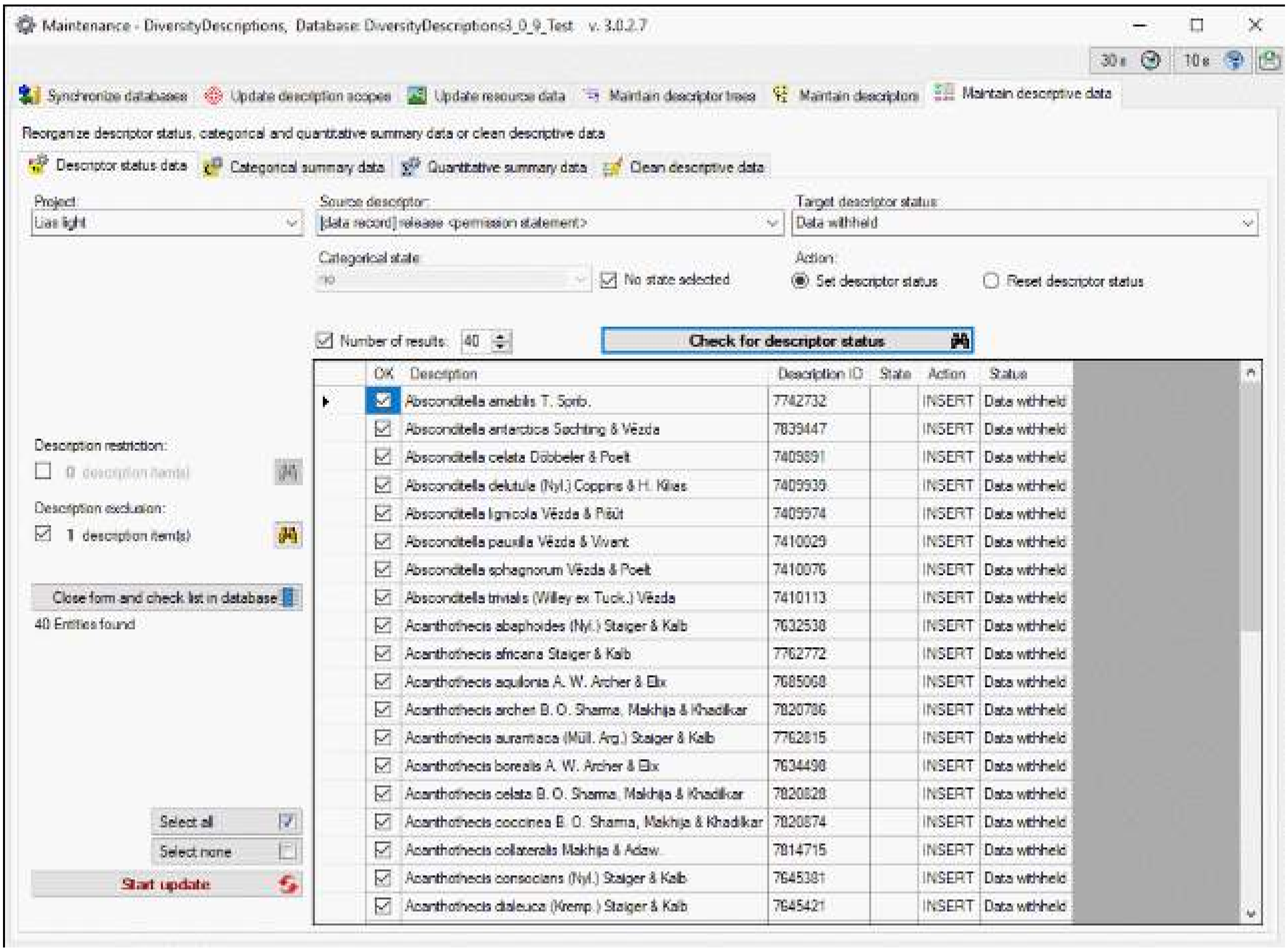
	OK	Description	Description ID	State	Action	Status
▸	☑	Aristolochia clematitis (Gewöhnliche Osterluzei)	6475879	anders	DELETE	To be checked
	☑	Plantago major (Breitwegerich)	6478890	anders	DELETE	To be checked

Description restriction: ☐ 0 description item(s)

Description exclusion: ☐ 0 description item(s)

2 Entities found

After adjusting the required operations for the selected categorical state click on **Check for descriptor status** and all affected summary data will be listed in the lower table (see image above). For each affected **Description** and **State** of the categorical summary data the **Action** (DELETE or INSERT) and the **Status** are specified. If you check the option **No state selected**, you may search for descriptions that do not reference any state of the **Source descriptor** and set the data status of the selected **Source descriptor** (see image below).



Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Project: Lias light

Source descriptor: [data record] release <permission statement>

Target descriptor status: Data withheld

Categorical state: no

☑ No state selected

Action: ● Set descriptor status ○ Reset descriptor status

☑ Number of results: 40

Description restriction:
☐ 0 description item(s)

Description exclusion:
☑ 1 description item(s)

40 Entities found

OK	Description	Description ID	State	Action	Status
☑	Absconditella amabilis T. Sprib.	7742732		INSERT	Data withheld
☑	Absconditella antarctica Sachting & Vězda	7839447		INSERT	Data withheld
☑	Absconditella celata Döbbeler & Poelt	7409891		INSERT	Data withheld
☑	Absconditella delutula (Nyl.) Coppins & H. Kilias	7409939		INSERT	Data withheld
☑	Absconditella lignicola Vězda & Pišút	7409974		INSERT	Data withheld
☑	Absconditella pauxilla Vězda & Vivant	7410029		INSERT	Data withheld
☑	Absconditella sphagnorum Vězda & Poelt	7410076		INSERT	Data withheld
☑	Absconditella trivialis (Willey ex Tuck.) Vězda	7410113		INSERT	Data withheld
☑	Acanthothecis abaphoides (Nyl.) Staiger & Kalb	7632538		INSERT	Data withheld
☑	Acanthothecis africana Staiger & Kalb	7762772		INSERT	Data withheld
☑	Acanthothecis aquilonia A. W. Archer & Elix	7685068		INSERT	Data withheld
☑	Acanthothecis archeri B. O. Sharma, Makhija & Khadilkar	7820786		INSERT	Data withheld
☑	Acanthothecis aurantiaca (Müll. Arg.) Staiger & Kalb	7762815		INSERT	Data withheld
☑	Acanthothecis borealis A. W. Archer & Elix	7634498		INSERT	Data withheld
☑	Acanthothecis celata B. O. Sharma, Makhija & Khadilkar	7820828		INSERT	Data withheld
☑	Acanthothecis coccinea B. O. Sharma, Makhija & Khadilkar	7820874		INSERT	Data withheld
☑	Acanthothecis collateralis Makhija & Adaw.	7814715		INSERT	Data withheld
☑	Acanthothecis consocians (Nyl.) Staiger & Kalb	7645381		INSERT	Data withheld
☑	Acanthothecis dialeuca (Kremp.) Staiger & Kalb	7645421		INSERT	Data withheld

You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To perform the selected operations click on the **Start update** button. If Instead updating the database you may click **Close form and check list in database** to return to the main program with the affected descriptions.

Maintenance - Categorical summary data

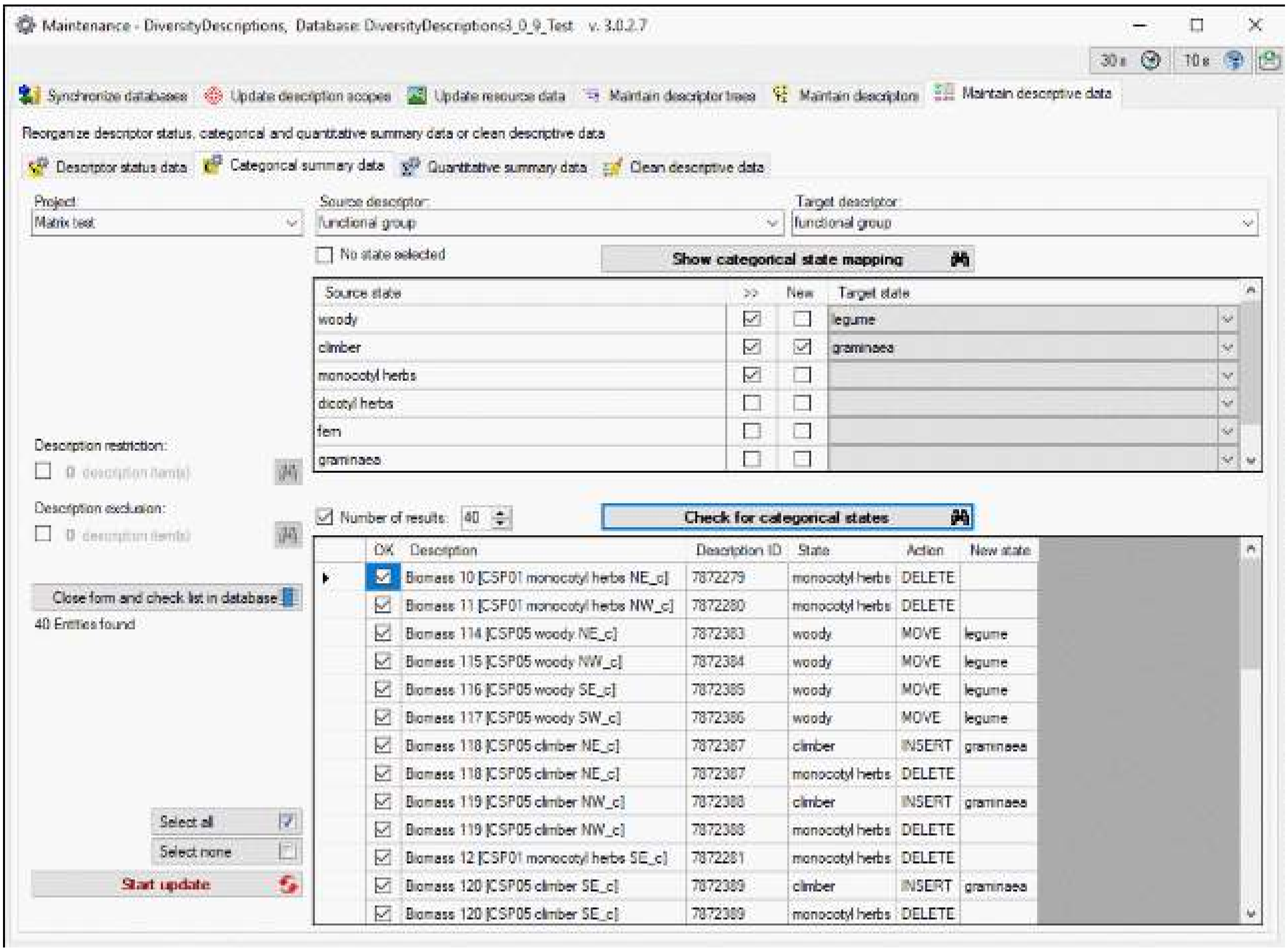
To shift and copy categorical summary data to a different descriptor or delete values for selected categorical states, select the **Maintain descriptive data** tab and choose the tab **Categorical summary data**. In this panel you operate on the **categorical summary data** of the descriptions. If you want to shift or copy categorical states between descriptors, please use Maintenance - Categorical states.

Select the **Project**, the **Source descriptor** and the **Target descriptor**. Click on **Show categorical state mapping** and all categorical state values of the selected **Source descriptor** will be listed in the upper table (see image below). Select the categorical states for which you want to modify the summary data in column **>>**.

The following operations are available:

- **Delete** the summary data by leaving the **Target state** empty
- **Move** the summary data by selecting the **Target state**
- **Copy** the summary data by selecting the **Target state** and selecting the **New** column

In case the summary data are moved or copied, all relevant data including modifier and frequency values and notes will be processed.



Project: Matrix test

Source descriptor: functional group

Target descriptor: functional group

☐ No state selected

Source state	>>	New	Target state
woody	☑	☐	legume
climber	☑	☑	graminaea
monocotyl herbs	☑	☐	
dicotyl herbs	☐	☐	
fern	☐	☐	
graminaea	☐	☐	

☐ 0 description item(s)

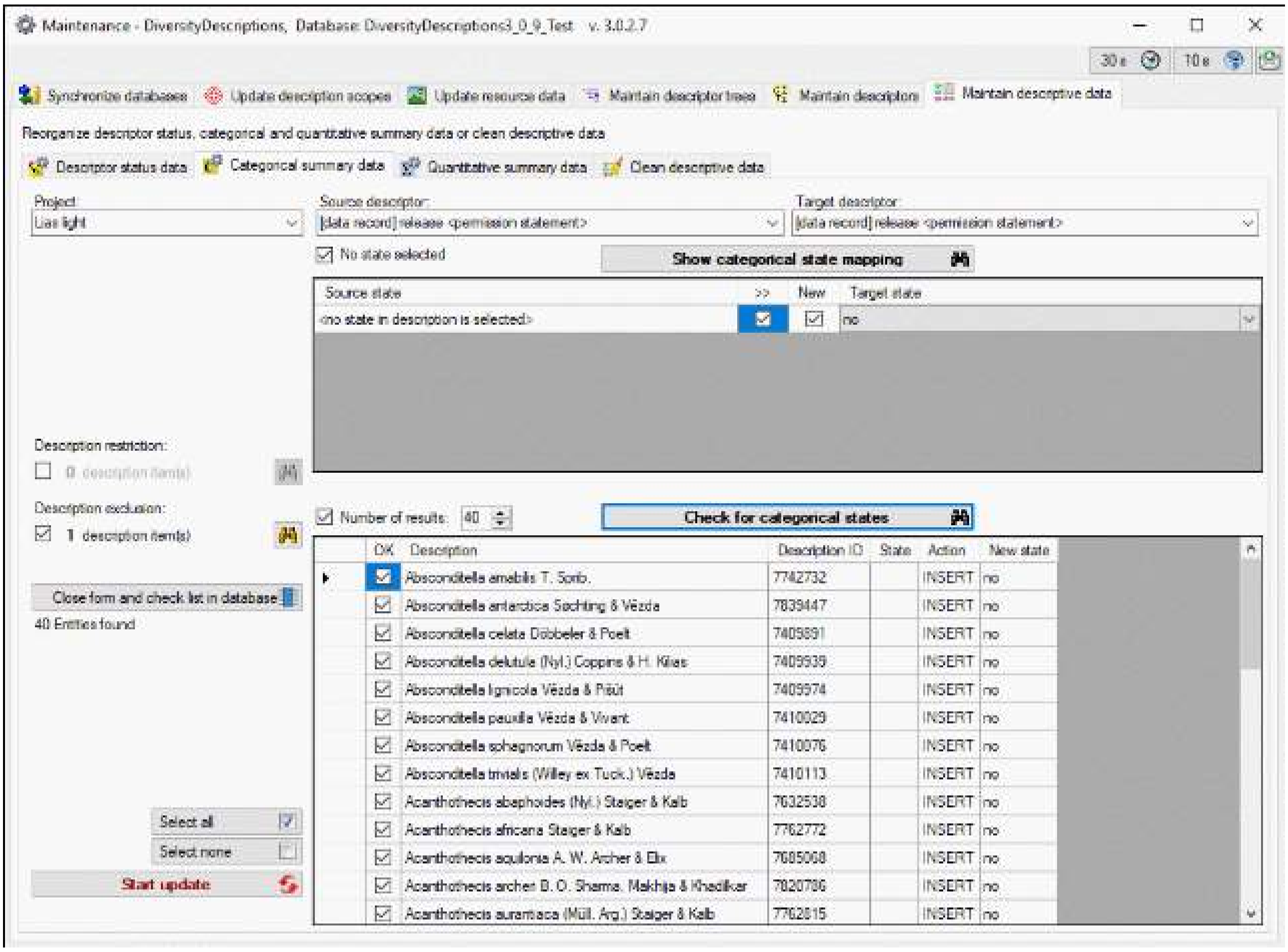
☐ 0 description item(s)

☑ Number of results: 40

40 Entities found

OK	Description	Description ID	State	Action	New state
☑	Biomass 10 [CSP01 monocotyl herbs NE_c]	7872279	monocotyl herbs	DELETE	
☑	Biomass 11 [CSP01 monocotyl herbs NW_c]	7872280	monocotyl herbs	DELETE	
☑	Biomass 114 [CSP05 woody NE_c]	7872383	woody	MOVE	legume
☑	Biomass 115 [CSP05 woody NW_c]	7872384	woody	MOVE	legume
☑	Biomass 116 [CSP05 woody SE_c]	7872385	woody	MOVE	legume
☑	Biomass 117 [CSP05 woody SW_c]	7872386	woody	MOVE	legume
☑	Biomass 118 [CSP05 climber NE_c]	7872387	climber	INSERT	graminaea
☑	Biomass 118 [CSP05 climber NE_c]	7872387	monocotyl herbs	DELETE	
☑	Biomass 119 [CSP05 climber NW_c]	7872388	climber	INSERT	graminaea
☑	Biomass 119 [CSP05 climber NW_c]	7872388	monocotyl herbs	DELETE	
☑	Biomass 12 [CSP01 monocotyl herbs SE_c]	7872281	monocotyl herbs	DELETE	
☑	Biomass 120 [CSP05 climber SE_c]	7872389	climber	INSERT	graminaea
☑	Biomass 120 [CSP05 climber SE_c]	7872389	monocotyl herbs	DELETE	

After adjusting the required operations for the selected categorical states click on **Check for categorical states** and all affected summary data will be listed in the lower table (see image above). For each affected **Description** and **State** of the categorical summary data the **Action** (DELETE, MOVE or INSERT) and **New state** are specified. If you check the option **No state selected**, you may search for descriptions that do not reference any state of the **Source descriptor** and set a state of the selected **Target descriptor** (see image below).



Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Project: Lias light

Source descriptor: [data record] release <permission statement>

Target descriptor: [data record] release <permission statement>

☑ No state selected

Source state	>>	New	Target state
<no state in description is selected>	☑	☑	no

Description restriction:
☐ 0 description item(s)

Description exclusion:
☑ 1 description item(s)

40 Entities found

☑ Number of results: 40

	OK	Description	Description ID	State	Action	New state
▸	☑	Absconditella amabilis T. Sprib.	7742732		INSERT	no
	☑	Absconditella antarctica Schting & Vězda	7839447		INSERT	no
	☑	Absconditella celata Döbbeler & Poelt	7409891		INSERT	no
	☑	Absconditella delutula (Nyl.) Coppins & H. Kilias	7409939		INSERT	no
	☑	Absconditella lignicola Vězda & Pišút	7409974		INSERT	no
	☑	Absconditella pauxilla Vězda & Vivant	7410029		INSERT	no
	☑	Absconditella sphagnorum Vězda & Poelt	7410076		INSERT	no
	☑	Absconditella trivialis (Willey ex Tuck.) Vězda	7410113		INSERT	no
	☑	Acanthothecis abaphoides (Nyl.) Staiger & Kalb	7632538		INSERT	no
	☑	Acanthothecis africana Staiger & Kalb	7762772		INSERT	no
	☑	Acanthothecis aquilonia A. W. Archer & Elix	7685068		INSERT	no
	☑	Acanthothecis archeri B. O. Sharma, Makhija & Khadilkar	7820786		INSERT	no
	☑	Acanthothecis aurantiaca (Müll. Arg.) Staiger & Kalb	7762815		INSERT	no

You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To perform the selected operations click on the **Start update** button. If Instead updating the database you may click **Close form and check list in database** to return to the main program with the affected descriptions.

Maintenance - Quantitative summary data

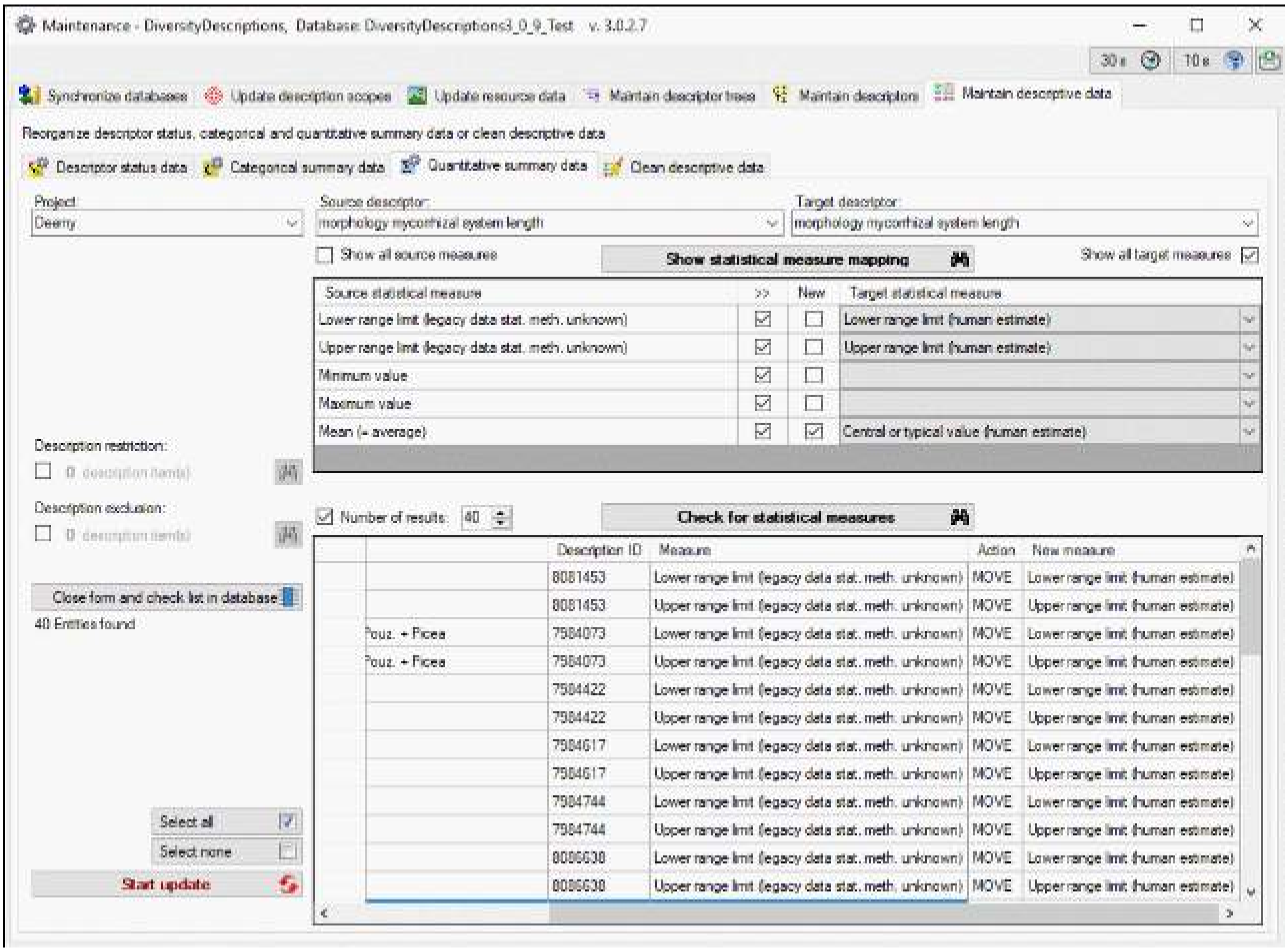
To shift and copy quantitative summary data to a different descriptor or delete values for selected statistical measures, select the **Maintain descriptive data** tab and choose the tab **Quantitative summary data**.

Select the **Project**, the **Source descriptor** and the **Target descriptor**. Click on **Show statistical measure mapping** and the assigned statistical measures of the selected **Source descriptor** will be listed in the upper table (see image below). If you want so process all available statistical measures, not only that ones assigned to the descriptors in the descriptor tree, check **Show all source measures** rsp. **Show all target measures**. Select the statistical measures for which you want to modify the summary data in column **>>**.

The following operations are available:

- **Delete** the summary data by leaving the **Target statistical measure** empty
- **Move** the summary data by selecting the **Target statistical measure**
- **Copy** the summary data by selecting the **Target statistical measure** and selecting the **New** column

In case the summary data are moved or copied, all relevant data including modifier values and notes will be processed.



Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Project: Deemy

Source descriptor: morphology mycorrhizal system length

Target descriptor: morphology mycorrhizal system length

☐ Show all source measures

Show all target measures ☑

Source statistical measure	>>	New	Target statistical measure
Lower range limit (legacy data stat. meth. unknown)	☑	☐	Lower range limit (human estimate)
Upper range limit (legacy data stat. meth. unknown)	☑	☐	Upper range limit (human estimate)
Minimum value	☑	☐	
Maximum value	☑	☐	
Mean (= average)	☑	☑	Central or typical value (human estimate)

Description restriction:
☐ 0 description item(s)

Description exclusion:
☐ 0 description item(s)

40 Entities found

☑ Number of results: 40

		Description ID	Measure	Action	New measure
		8081453	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
		8081453	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)
	Pouz. + Picea	7984073	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
	Pouz. + Picea	7984073	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)
		7984422	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
		7984422	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)
		7984617	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
		7984617	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)
		7984744	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
		7984744	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)
		8006638	Lower range limit (legacy data stat. meth. unknown)	MOVE	Lower range limit (human estimate)
		8006638	Upper range limit (legacy data stat. meth. unknown)	MOVE	Upper range limit (human estimate)

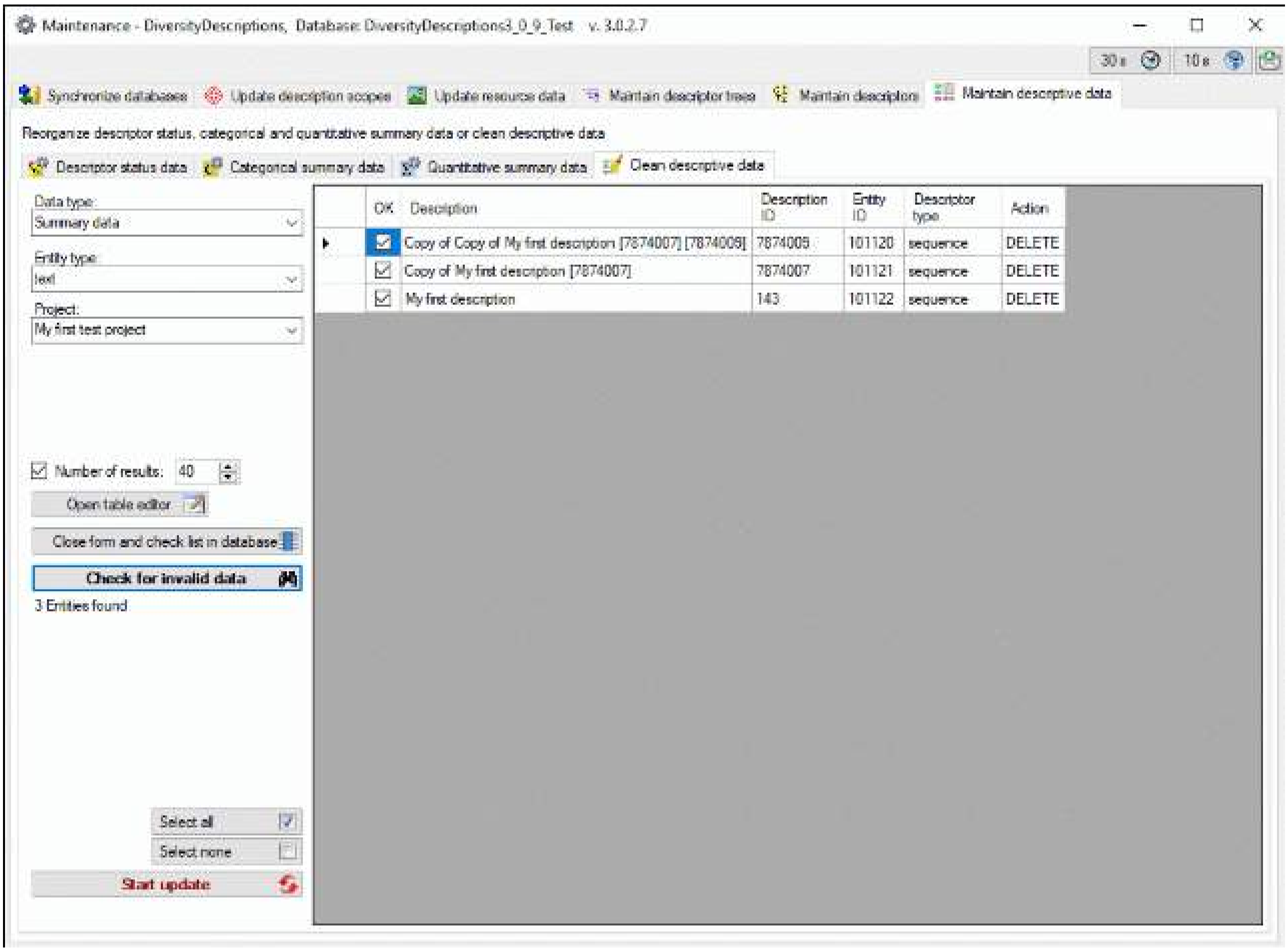
After adjusting the required operations for the selected categorical states click on **Check for statistical measures** and all affected summary data will be listed in the lower table (see image above). For each affected **Description** and **Measure** of the quantitative summary data the **Action** (DELETE, MOVE or INSERT) an **New measure** are specified. You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select**

all rsp. ☐ **Select none**. To perform the selected operations click on the Start update button. If Instead updating the database you may click **Close form and check list in database** to return to the main program with the affected descriptions.

Maintenance - Clean descriptive data

Descriptive data, which can be summary or sampling data, are stored in the database in several tables, that reference the corresponding descriptor rsp. categorical state and hold some additional data. Depending on the descriptor type - categorical, quantitative, text or sequence - different tables are used to represent the descriptive data. Although Diversity Descriptions does not allow to change the type of a descriptor if descriptive data are present, in some cases it cannot be assured that such an action is performed. The resulting data are then meaningless and will not be displayed within Diversity Descriptions. To find, check and delete such kinds of corrupted descriptive data, select the **Maintain descriptive data** tab and choose the tab **Clean descriptive data**.

Select the **Data type** ("Summary data" or "Sampling data"), the **Entity type** (i.e. the type of descriptive data in database: "categorical", "quantitative", "text" or "sequence") and the **Project**. Click on **Check for invalid data** and all invalid data will be listed (see image below).



Maintenance - DiversityDescriptions, Database: DiversityDescriptions3_0_9_Test v. 3.0.2.7

Reorganize descriptor status, categorical and quantitative summary data or clean descriptive data

Data type: Summary data

Entity type: text

Project: My first test project

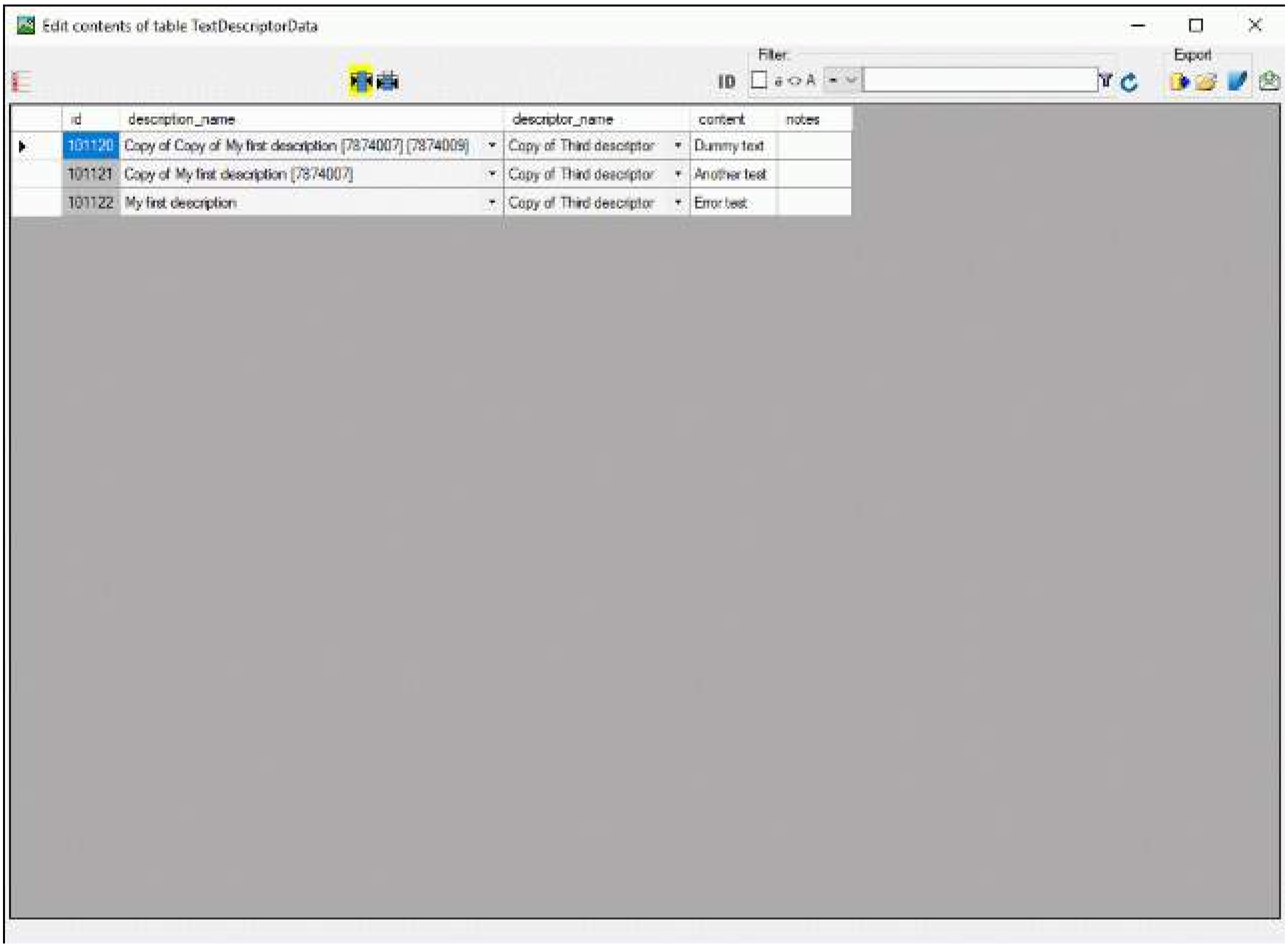
☑ Number of results: 40

3 Entities found

OK	Description	Description ID	Entity ID	Descriptor type	Action
☑	Copy of Copy of My first description [7874007] [7874008]	7874009	101120	sequence	DELETE
☑	Copy of My first description [7874007]	7874007	101121	sequence	DELETE
☑	My first description	143	101122	sequence	DELETE

You may select or deselect all entries of the result list for the database update by clicking the buttons ☑ **Select all** rsp. ☐ **Select none**. To delete the selected entries from the database click on the Start update button. Instead of deleting the selecting entries you may click **Close form and check list in database** to return to the main program with the affected descriptions.

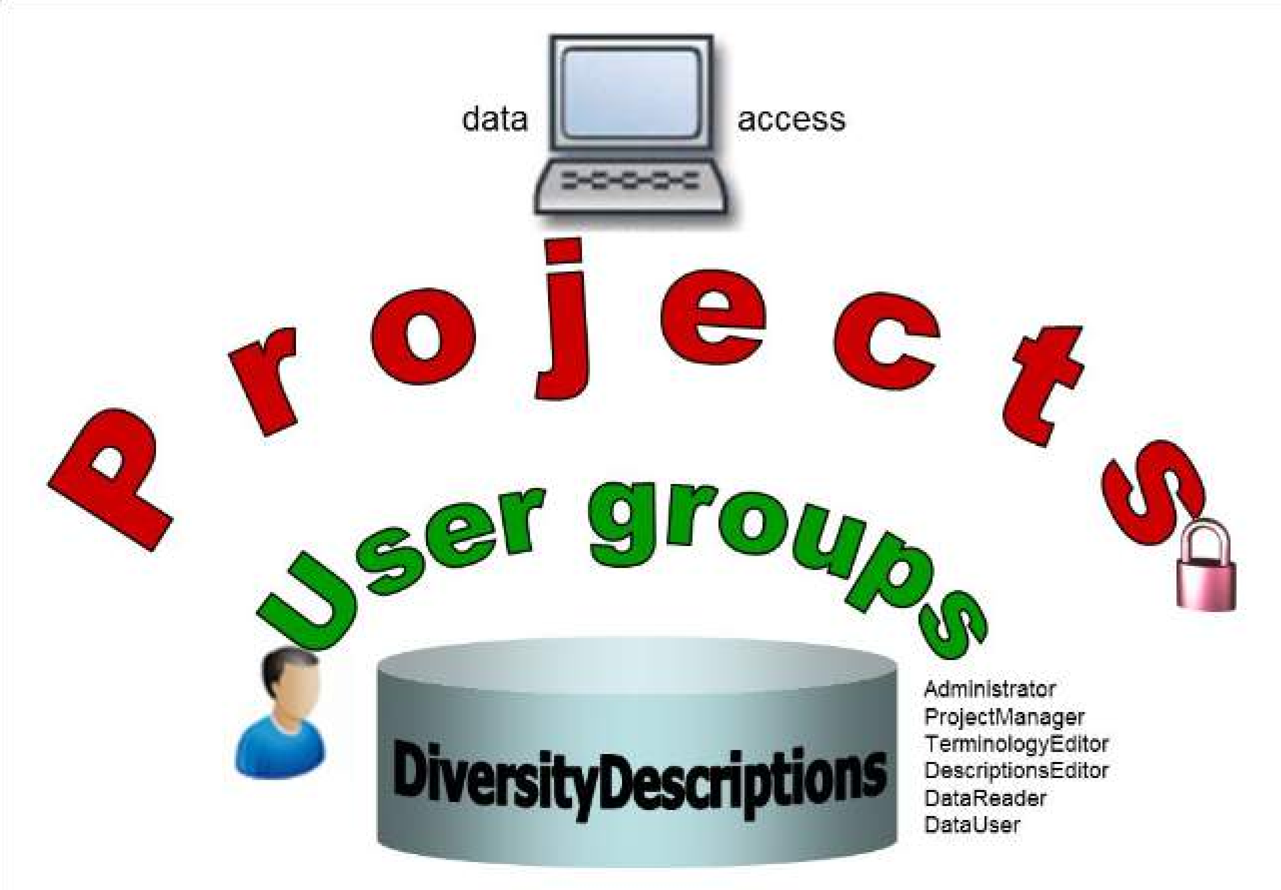
You may open a table editor for the selected entries by clicking the **Open table editor** button (see image below). Here you may check the corrupted data to decide if further measures are required.


Edit contents of table TextDescriptorData

id	description_name	descriptor_name	content	notes
101120	Copy of Copy of My first description [7874007] [7874009]	Copy of Third descriptor	Dummy text	
101121	Copy of My first description [7874007]	Copy of Third descriptor	Another test	
101122	My first description	Copy of Third descriptor	Error test	

Access to the data

To get access to the data, you have to take several hurdles. In DiversityDescriptions, you must be a member of one of the user groups. You have only access to those data, that are listed in the projects you have access to. Administration of the acces rights is done in the login administration. Depending on the user group or if a project carries the appropriate flag, a read only access to certain data is available. In the description data descriptors may be marked with the data status Data withheld, which affects export of data and document generation.



Security

A user can be in 6 groups with diverse rights in the database where certain higher groups have all rights of lower groups in addition to special rights for this group, e.g. the group DataReader can only read the data while DescriptionsEditor has the rights of DataReader and additionally can edit the data in descriptor tables - see overview below.

Summarzied overview of the permissions of the groups

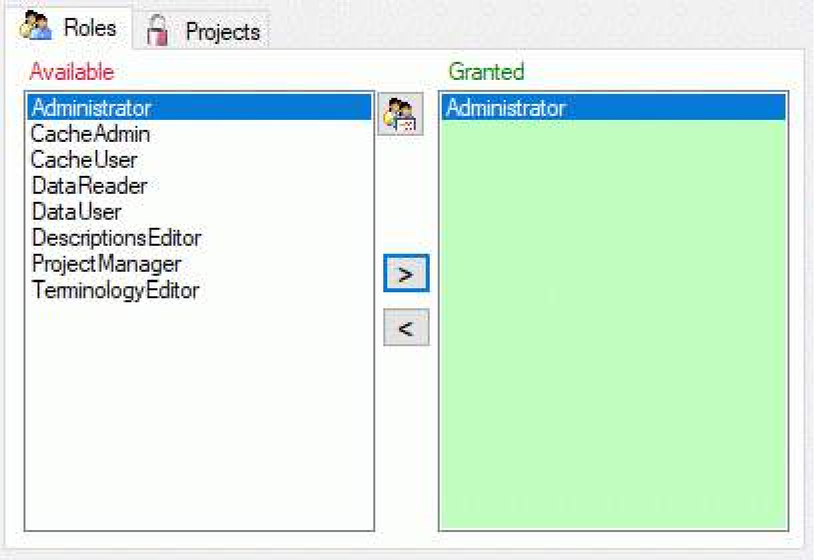
Role	**Permissions in addition to lower role resp. user group**	**Inculded rights**
Administrator	Edit own user permissions; use database maintenance functions	ProjectManager
ProjectManager	Create, edit and delete project data; import data with project information	TerminologyEditor
TerminologyEditor	Create, edit and delete descriptor data; import data without changing project information	DescriptionsEditor
DescriptionsEditor	Create, edit and delete description data	DataReader
DataReader	View description, descriptor, project and cache mapping data; export data	DataUser
DataUser	View descriptions without "withheld" descriptors and without resource data	

Two additional roles have been introduced for the handling of the cache database

Role	**Permissions in addition to lower role resp. user group**	**Inculded rights**
CacheAdmin	Edit cache related table data	CacheUser
CacheUser	View cache database and project data	DataReader

In addition to the mentioned roles a "System Aministrator" may use the Login administration to add other users to one of these groups and grant access to one ore more workbench projects . If you are an "Administrator" you have the right to modify the workbench projects assigned to your own login.

To place a user in one of the groups, go to the login administration. In the window that will open select a login and a database. The roles available in the selected database will be listed as shown below. Use the > and < buttons to add or remove roles for the login in the database (see below).



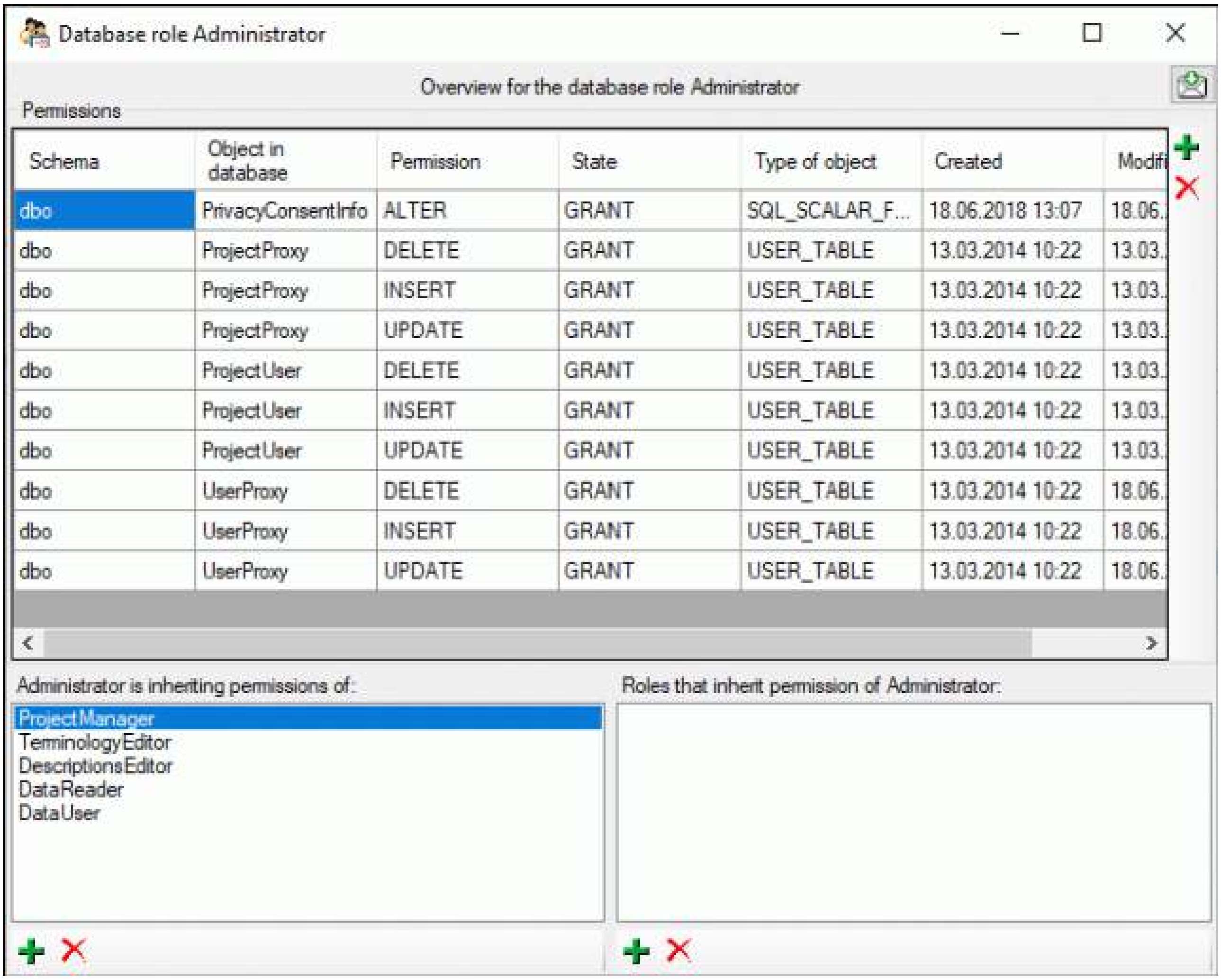
Available:

Administrator
CacheAdmin
CacheUser
DataReader
DataUser
DescriptionsEditor
ProjectManager
TerminologyEditor

Granted:

Administrator

To see the detailed permissions of a role, select it in the list of Available roles and click on the button. A window as shown below will open listing all objects in the database the role has permissions for (see below).



Schema	Object in database	Permission	State	Type of object	Created	Modifi
dbo	PrivacyConsentInfo	ALTER	GRANT	SQL_SCALAR_F...	18.06.2018 13:07	18.06.
dbo	ProjectProxy	DELETE	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	ProjectProxy	INSERT	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	ProjectProxy	UPDATE	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	ProjectUser	DELETE	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	ProjectUser	INSERT	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	ProjectUser	UPDATE	GRANT	USER_TABLE	13.03.2014 10:22	13.03.
dbo	UserProxy	DELETE	GRANT	USER_TABLE	13.03.2014 10:22	18.06.
dbo	UserProxy	INSERT	GRANT	USER_TABLE	13.03.2014 10:22	18.06.
dbo	UserProxy	UPDATE	GRANT	USER_TABLE	13.03.2014 10:22	18.06.

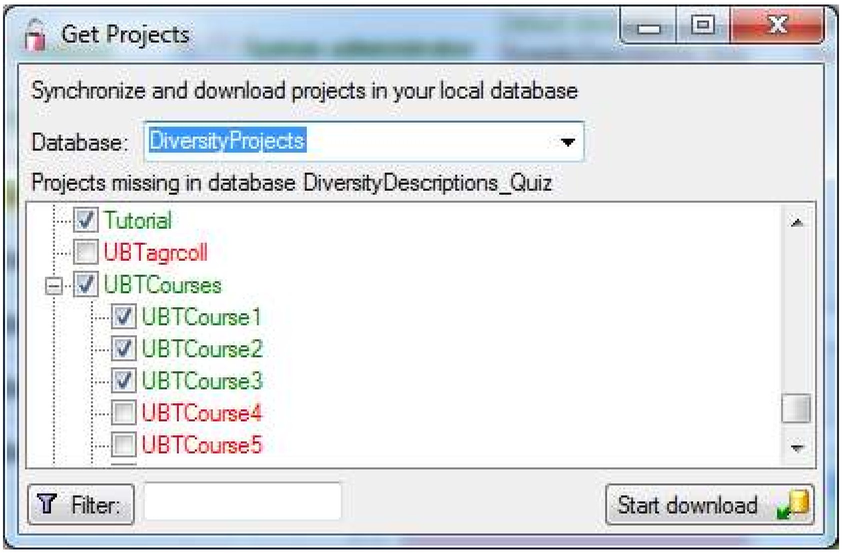
Administrator is inheriting permissions of:

ProjectManager
TerminologyEditor
DescriptionsEditor
DataReader
DataUser

Roles that inherit permission of Administrator:

Projects

Within DeversityDescriptions you have to distinguish the locally defined projects, that can be created, edited and deleted in edit projects mode, from the workbench projects, which are references to data stored in module DiversityProjects. Each local project is uniquely assigned to a workbench project that determines the access rights for the database users (see login administration). As a general default the workbench project "DiversityWorkbench" is present in the descriptions database. It should only be used if DiversityDescriptions shall be used as a stand-alone application without DiversityProjects.



Synchronize and download projects in your local database

Database: DiversityProjects

Projects missing in database DiversityDescriptions_Quiz

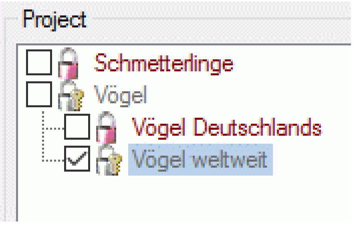
- ☑ Tutorial
- ☐ UBTagrcoll
- ☑ UBTCourses
  - ☑ UBTCourse1
  - ☑ UBTCourse2
  - ☑ UBTCourse3
  - ☐ UBTCourse4
  - ☐ UBTCourse5

If in your installation DiversityProjects is available you may load additional workbench projects with menu item **Administration -> Projects...**. A window as shown above will open. Workbench projects already in the database will be listed in green, missing projects in red (see below). Check all projects you need in your database and click the **Start download** button.

The **local project** is assigned to exactly one workbench project, which can be adjusted in the Edit project panel. Assumed you use DiversityProject for project administration, it is reasonable to have a 1:1 relation between the local projects and the workbench project. Since in the Login administration the access rights are done based on the workbench project, you can give each user individual rights for every single local project.

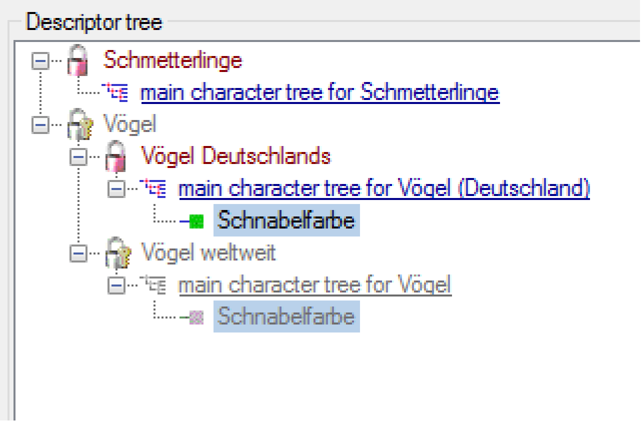
If you use Diversity Descriptions as stand-alone application, the only available workbench project will be the predefined "DiversityWorkbench". In this case every local project must be assigned to this single workbench project. As a consequence you may assign an individual database role to each user but you will not be able to distinguish the access rights according the local project.

Each **description** is uniquely assigned to a local project (see picture below from Edit description). Usually only projects that are assigned to the user are displayed in the project tree. The example above shows two projects assigned to the user that have a parent that is not assigned to the user. Therefore the parent ("Vögel") is displayed with grey text colour to indicate missing access rights.

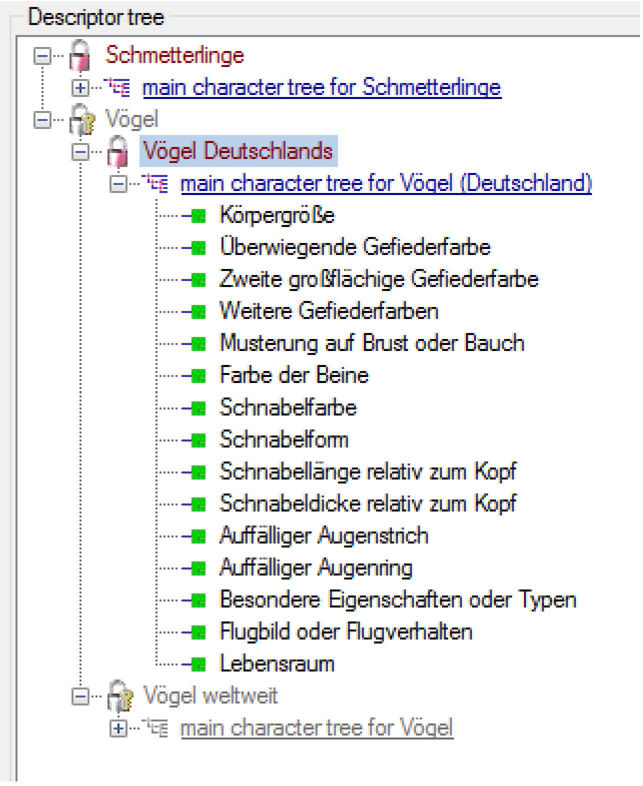


- ☐ Schmetterlinge
- ☐ Vögel
  - ☐ Vögel Deutschlands
  - ☑ Vögel weltweit

A **descriptor** is **not directly** assigned to a project, instead "descriptor trees" are used. One descriptor may be included in several descriptor trees and therefore belong to several projects or it might be unassigned. The picture below (from Edit descriptor) shows that one descriptor belongs to two projects, since it is part of two different descriptor trees. As in the description example, the picture shows a parent project ("Vögel") that is not read-only for the actual user and therefore displayed in grey text colour. Contained in that parent project therea are two parallel projects that include the same descriptor: "Vögel Deutschlands" and "Vögel weltweit", which is read-only and therefore displayed in grey colour.

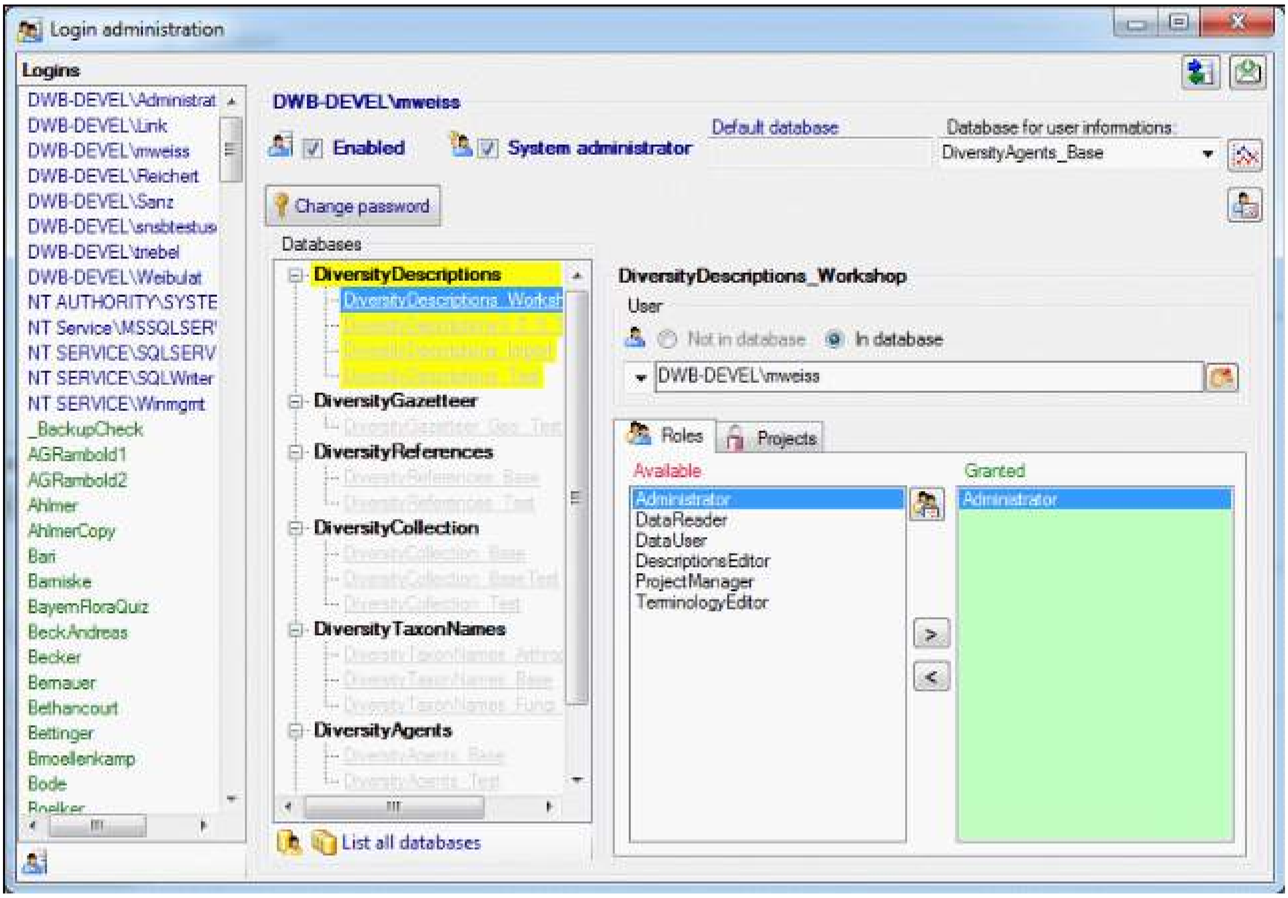


The **project** is assigned to exactly one workbench project. The Edit project panel provides the panel to edit descriptor trees, too. But here all descriptors visible for the project are displayed (see picture below).



Login administration

To administrate the logins on the database server, their permissions resp. roles and access to projects choose **Administration -> Database ... -> Logins** ... from the menu. A window as shown below will open.



☑ Enabled ☑ System administrator

Database for user informations: DiversityAgents_Base

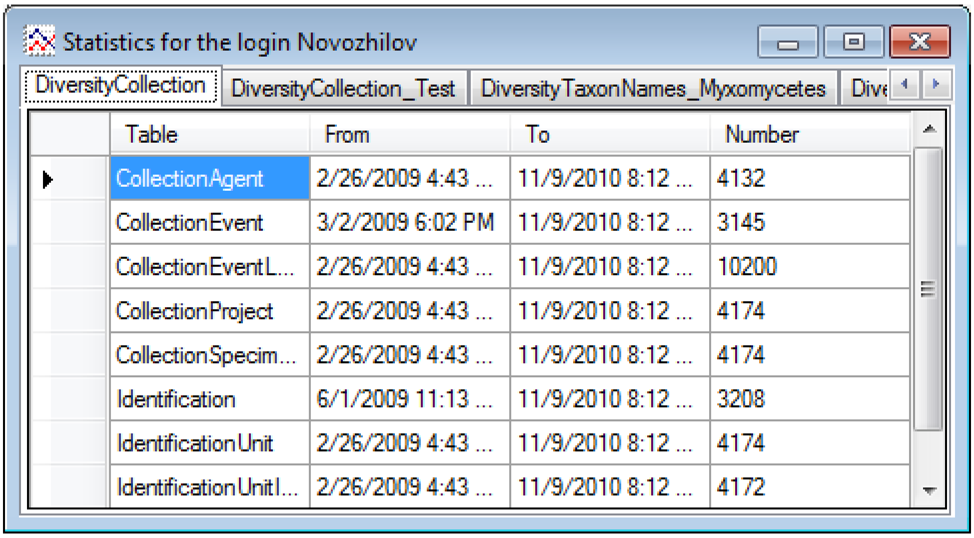
User: ○ Not in database ● In database

DWB-DEVEL\mweiss

Available	Granted
Administrator	Administrator
DataReader	
DataUser	
DescriptionsEditor	
ProjectManager	
TerminologyEditor	

Statistics

To see the activity of a login click on the button. A window will open as shown below listing all databases and tables together with the timespan (From - To) and the number of data sets where any activity of the current login has been found.

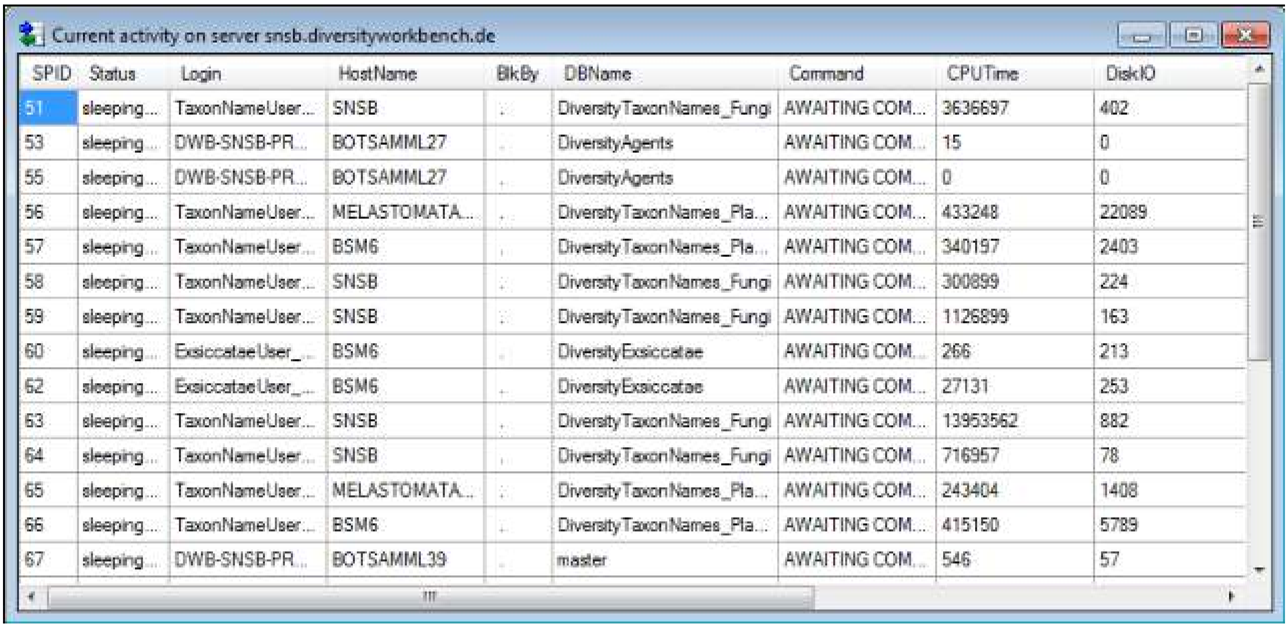


Statistics for the login Novozhilov

DiversityCollection | DiversityCollection_Test | DiversityTaxonNames_Myxomycetes | Dive

Table	From	To	Number
CollectionAgent	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4132
CollectionEvent	3/2/2009 6:02 PM	11/9/2010 8:12 ...	3145
CollectionEventL...	2/26/2009 4:43 ...	11/9/2010 8:12 ...	10200
CollectionProject	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4174
CollectionSpecim...	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4174
Identification	6/1/2009 11:13 ...	11/9/2010 8:12 ...	3208
IdentificationUnit	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4174
IdentificationUnitI...	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4172

To see the current activity on the server click on the button. A window as shown below will open listing all user related processes on the server.

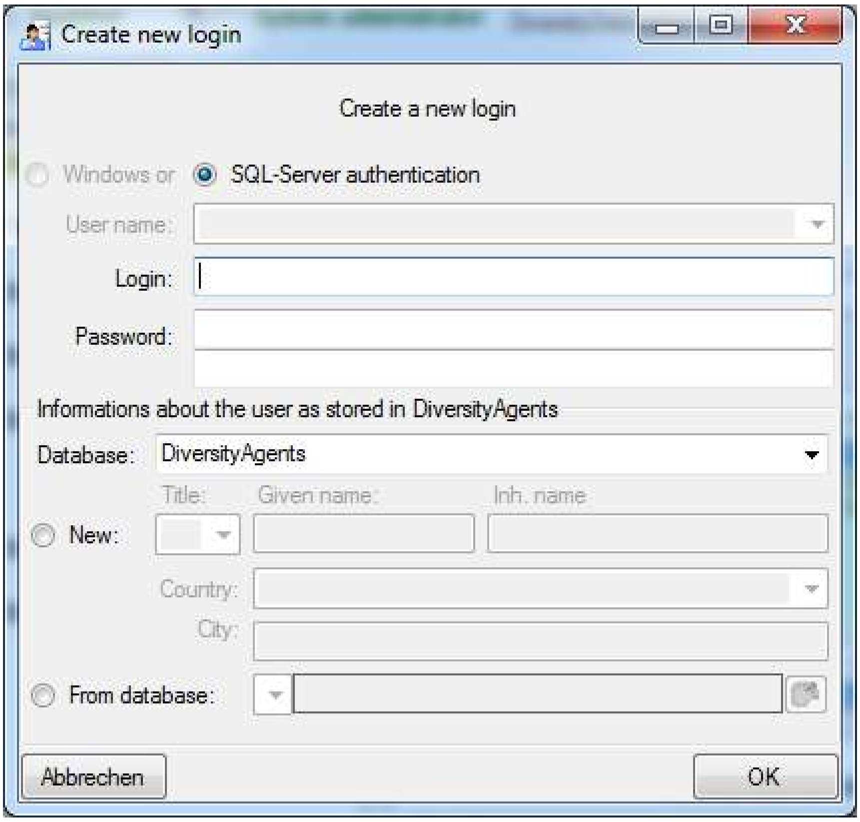


Current activity on server snsb.diversityworkbench.de

SPID	Status	Login	HostName	BlkBy	DBName	Command	CPUTime	DiskIO
51	sleeping...	TaxonNameUser...	SNSB	.	DiversityTaxonNames_Fungi	AWAITING COM...	3636697	402
53	sleeping...	DWB-SNSB-PR...	BOTSAMML27	.	DiversityAgents	AWAITING COM...	15	0
55	sleeping...	DWB-SNSB-PR...	BOTSAMML27	.	DiversityAgents	AWAITING COM...	0	0
56	sleeping...	TaxonNameUser...	MELASTOMATA...	.	DiversityTaxonNames_Pla...	AWAITING COM...	433248	22089
57	sleeping...	TaxonNameUser...	BSM6	.	DiversityTaxonNames_Pla...	AWAITING COM...	340197	2403
58	sleeping...	TaxonNameUser...	SNSB	.	DiversityTaxonNames_Fungi	AWAITING COM...	300899	224
59	sleeping...	TaxonNameUser...	SNSB	.	DiversityTaxonNames_Fungi	AWAITING COM...	1126899	163
60	sleeping...	ExsiccataeUser_...	BSM6	.	DiversityExsiccatae	AWAITING COM...	266	213
62	sleeping...	ExsiccataeUser_...	BSM6	.	DiversityExsiccatae	AWAITING COM...	27131	253
63	sleeping...	TaxonNameUser...	SNSB	.	DiversityTaxonNames_Fungi	AWAITING COM...	13953562	882
64	sleeping...	TaxonNameUser...	SNSB	.	DiversityTaxonNames_Fungi	AWAITING COM...	716957	78
65	sleeping...	TaxonNameUser...	MELASTOMATA...	.	DiversityTaxonNames_Pla...	AWAITING COM...	243404	1408
66	sleeping...	TaxonNameUser...	BSM6	.	DiversityTaxonNames_Pla...	AWAITING COM...	415150	5789
67	sleeping...	DWB-SNSB-PR...	BOTSAMML39	.	master	AWAITING COM...	546	57

Create a login

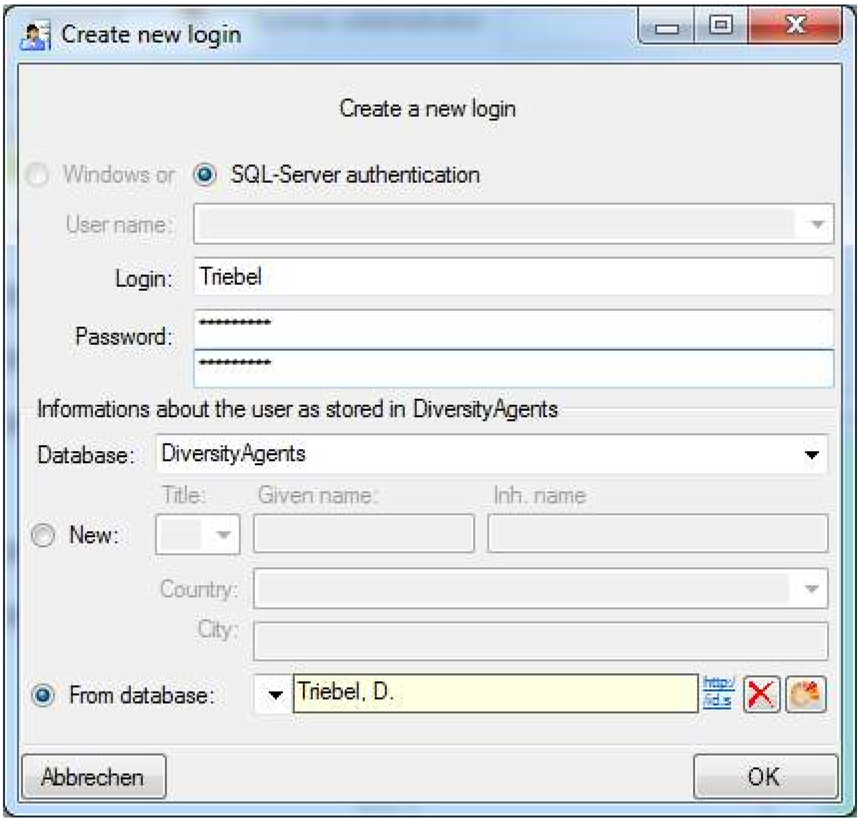
To create a new login, click on the button in the lower left corner. Another window will open.



○ Windows or ● SQL-Server authentication

Database: DiversityAgents

Here you can enter the name of the new login, the password and the informations about the user which will be stored in a DiversityAgents database. Either create a new entry in this database or select an existing one: Click on the button to search for a name in the database (see below).



○ Windows or ● SQL-Server authentication

Login: Triebel

Password: **********

****

Database: DiversityAgents

○ New:

● From database: Triebel, D.

Copy a login

To copy a login including all permissions etc. into a new login, select the original login in the list and click on the button.

Edit login data

To edit the access for a login on the server, select the login in the list. If a login should be disabled , uncheck the enabled checkbox.

☐ Enabled

All databases on the server will be listed, with the current database showing a yellow background. The databases where the login has no access will be listed in gray while the databases accessible for a login are black.

- DiversityDescriptions
  - DiversityDescriptions_Quiz
- DiversityGazetteer
  - DiversityGazetteer_Geo2
- DiversityReferences
  - DiversityReferences_Test
- DiversityCollection
  - DiversityCollection_Workshop
- DiversityTaxonNames
  - DiversityTaxonNames_Insecta
  - DiversityTaxonNames_Plants
  - DiversityTaxonNames_Vertebrata
- DiversityAgents
  - DiversityAgents
- DiversityProjects
  - DiversityProjects

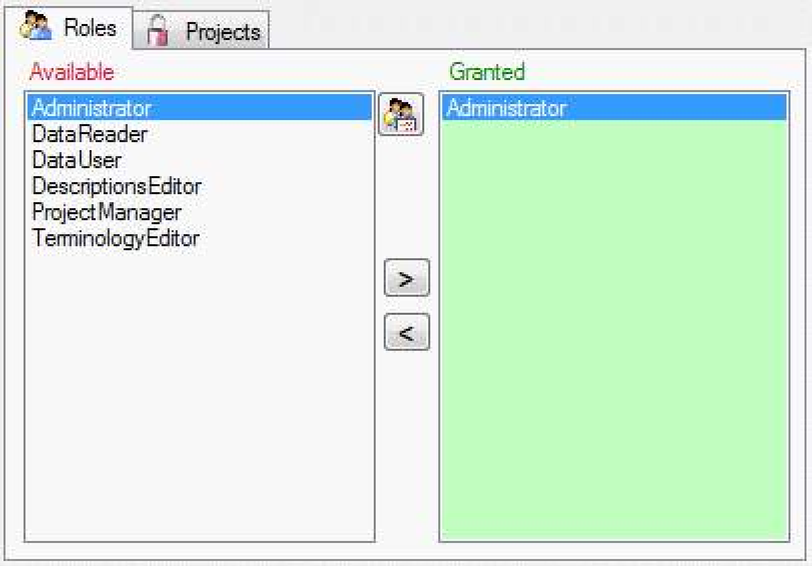
Access of a login to a database

To allow a login the access to a database, select the database from the list and choose the database as shown below.

● Not in database ○ In database

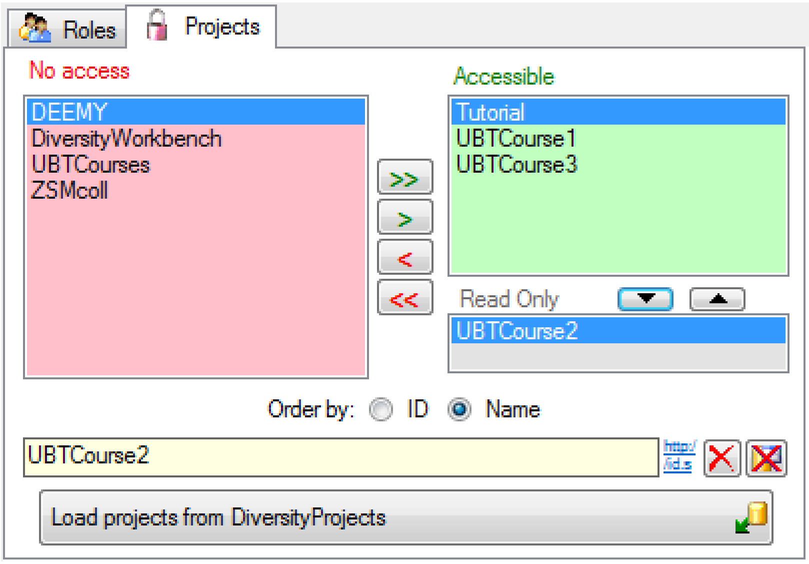
Roles of a login in a database

Use the **>** and **<** buttons to add or remove roles for the login in the database (see below). By clicking the button you get an overview of the access rights for the selected role.

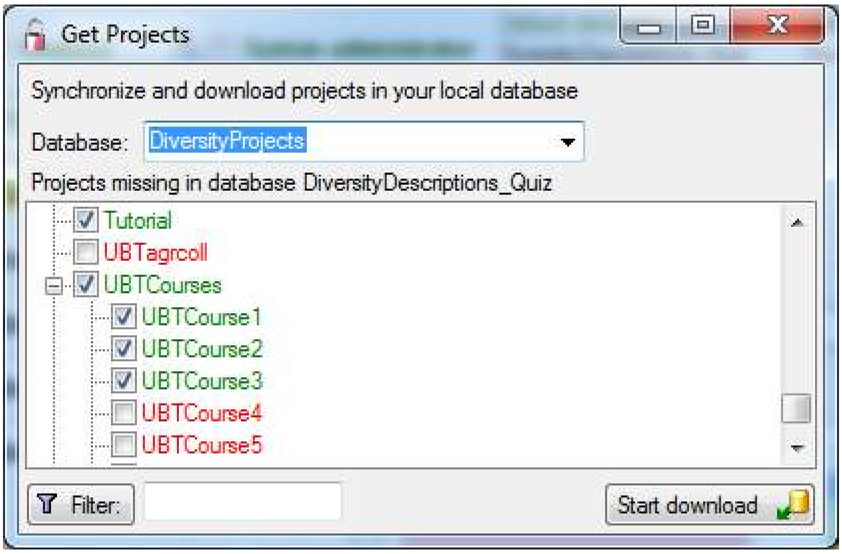


Projects for a login in a database

Depending on the database you can edit the list of [projects]() accessible for a login (see below). Next to the projects with **full access** a second list provides projects with **Read Only** access (see image below). Use the ▲and ▼buttons to move projects between **Accessible** and **Read Only**. Projects are related to the module DiversityProjects. To get additional informations about a project, select it in the list and click on the button.



To load additional projects, click on the **Load projects** button. A window as shown below will open. Projects already in the database will be listed in green, missing projects in red (see below). Check all projects you need in your database and click the **Start download** button.



Get Projects

Synchronize and download projects in your local database

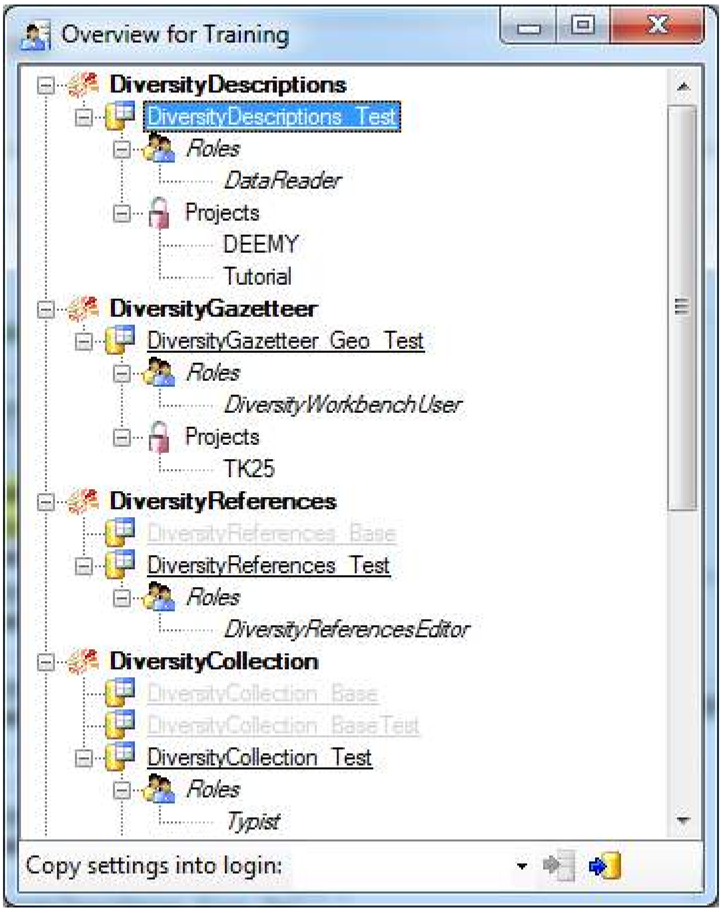
Database: DiversityProjects

Projects missing in database DiversityDescriptions_Quiz

- ☑ Tutorial
- ☐ UBTagrcoll
- ☑ UBTCourses
  - ☑ UBTCourse1
  - ☑ UBTCourse2
  - ☑ UBTCourse3
  - ☐ UBTCourse4
  - ☐ UBTCourse5

Overview for a login

If you want to se see an overview of all permissions and project for a login, click on the button. A window as shown below will open. It lists all modules and their databases, the roles, accessible projects and read only projects for a login.



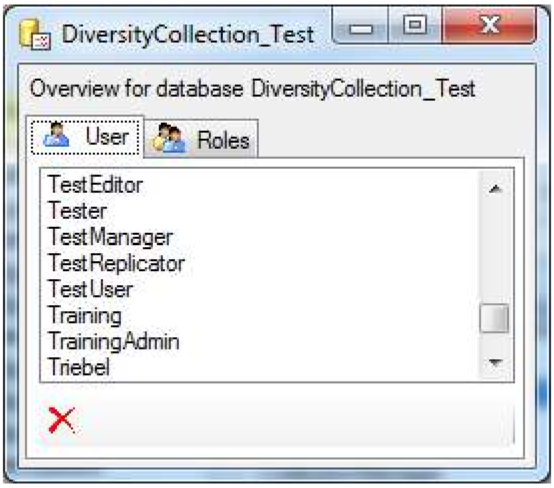
Overview for Training

- DiversityDescriptions
  - DiversityDescriptions_Test
    - *Roles*
      - *DataReader*
    - Projects
      - DEEMY
      - Tutorial
- DiversityGazetteer
  - DiversityGazetteer_Geo_Test
    - *Roles*
      - *DiversityWorkbenchUser*
    - Projects
      - TK25
- DiversityReferences
  - DiversityReferences_Base
  - DiversityReferences_Test
    - *Roles*
      - *DiversityReferencesEditor*
- DiversityCollection
  - DiversityCollection_Base
  - DiversityCollection_BaseTest
  - DiversityCollection_Test
    - *Roles*
      - *Typist*

To copy the permissions and projects of the current login to another login, select the login where the settings should be copied to from the list at the base of the window and click on the button to copy the settings for all databases or the button to copy the settings of the selected database into this login.

Overview for a database

If you see an overview of all user and roles in a database, click on the button. A window a shown below will open. It lists all user and roles in the database.



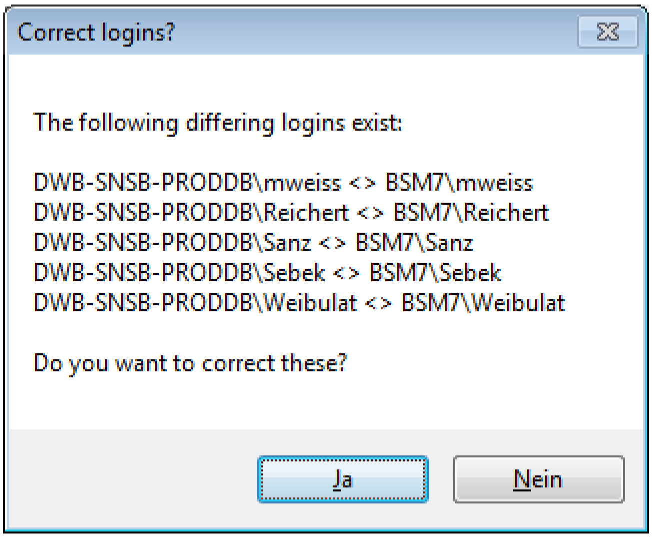
Overview for database DiversityCollection_Test

TestEditor
Tester
TestManager
TestReplicator
TestUser
Training
TrainingAdmin
Triebel

To remove a user, select it in the list and click on the ✕ button.

Correction of logins

If you select one of the databases, at the base a button may appear. This indicates, that there are windows logins listed where the name of the login does not match the logins of the server. This may happen if e.g. a database was moved from one server to another. To correct this, click on the button. A list of deviating logins will be shown, that can be corrected automatically.

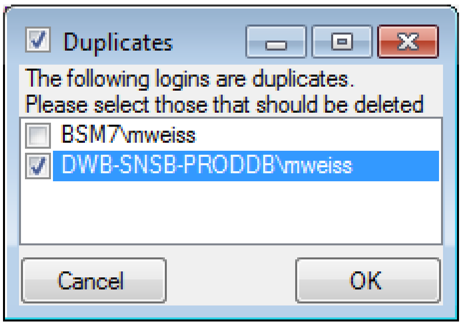


The following differing logins exist:

DWB-SNSB-PRODDB\mweiss <> BSM7\mweiss
DWB-SNSB-PRODDB\Reichert <> BSM7\Reichert
DWB-SNSB-PRODDB\Sanz <> BSM7\Sanz
DWB-SNSB-PRODDB\Sebek <> BSM7\Sebek
DWB-SNSB-PRODDB\Weibulat <> BSM7\Weibulat

Do you want to correct these?

If logins with the same name but different server are found, one of them has to be deleted to make the correction possible. You will get a list where you can select those that should be removed.



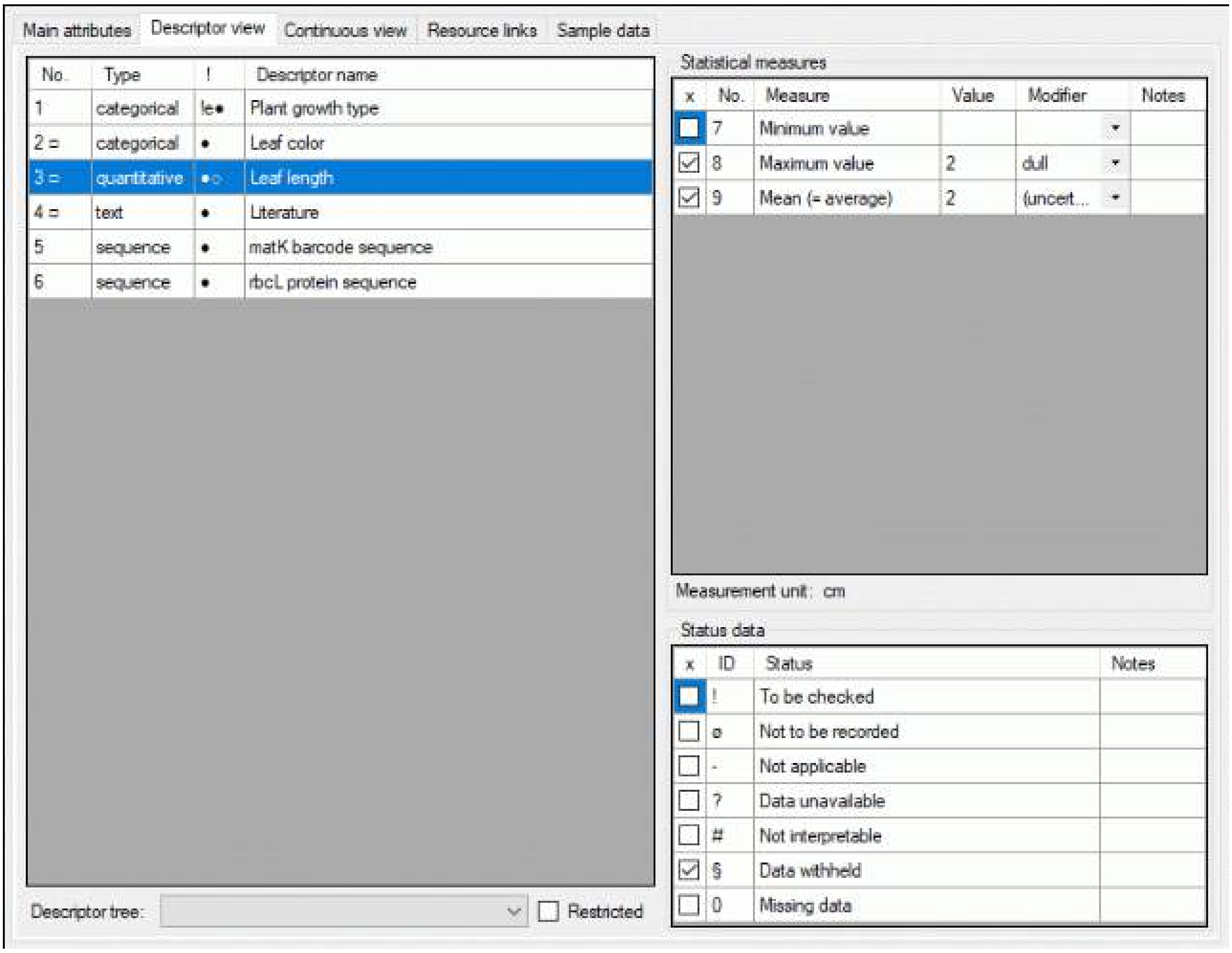
The following logins are duplicates.
Please select those that should be deleted

☐ BSM7\mweiss
☑ DWB-SNSB-PRODDB\mweiss

Select the duplicate logins that should be removed and click OK.

Availability of the data

In the description data descriptors may be marked with the data status **Data withheld** (see below).



No.	Type	!	Descriptor name
1	categorical	!e•	Plant growth type
2 =	categorical	•	Leaf color
3 =	quantitative	•○	Leaf length
4 =	text	•	Literature
5	sequence	•	matK barcode sequence
6	sequence	•	rbcL protein sequence

Descriptor tree: ☐ Restricted

Statistical measures

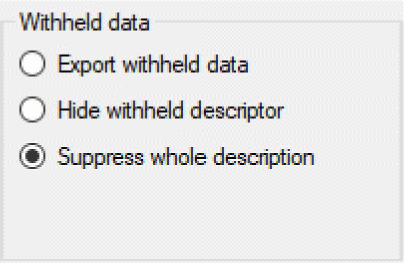
x	No.	Measure	Value	Modifier	Notes
☐	7	Minimum value			
☑	8	Maximum value	2	dull	
☑	9	Mean (= average)	2	(uncert...	

Measurement unit: cm

Status data

x	ID	Status	Notes
☐	!	To be checked	
☐	ø	Not to be recorded	
☐	-	Not applicable	
☐	?	Data unavailable	
☐	#	Not interpretable	
☑	§	Data withheld	
☐	0	Missing data	

When you export data the export forms include the "Withheld data" options where you can decide how to handle those data (see below).


Withheld data
○ Export withheld data
○ Hide withheld descriptor
● Suppress whole description

- The default setting **Suppress whole description** will exclude the whole description dataset from the export.
- The setting **Hide withheld descriptor** will include the description dataset in the export, but descriptor data that are marked as "Data withheld" will be suppressed.
- The setting **Export withheld data** will include all data in the export.

The options mentioned above are also available for the cache database. Additionally there are powerful filters to restrict the exported description items and dedicated descriptor and scope data may be excluded from export.

Finally the document generation by default excludes all descriptions that have any descriptor with data status "Data withheld". This is indicated by the STOP button in the upper right corner of the form. By clicking this button the descriptions may be included, which is indicated with the inactive icon STOP. Withheld descriptors will be skipped. For the document generators there is no option to include them.

Database

The database for DiversityDescriptions is based on Microsoft SQL-Server 2008 and higher.

Organisation of the data

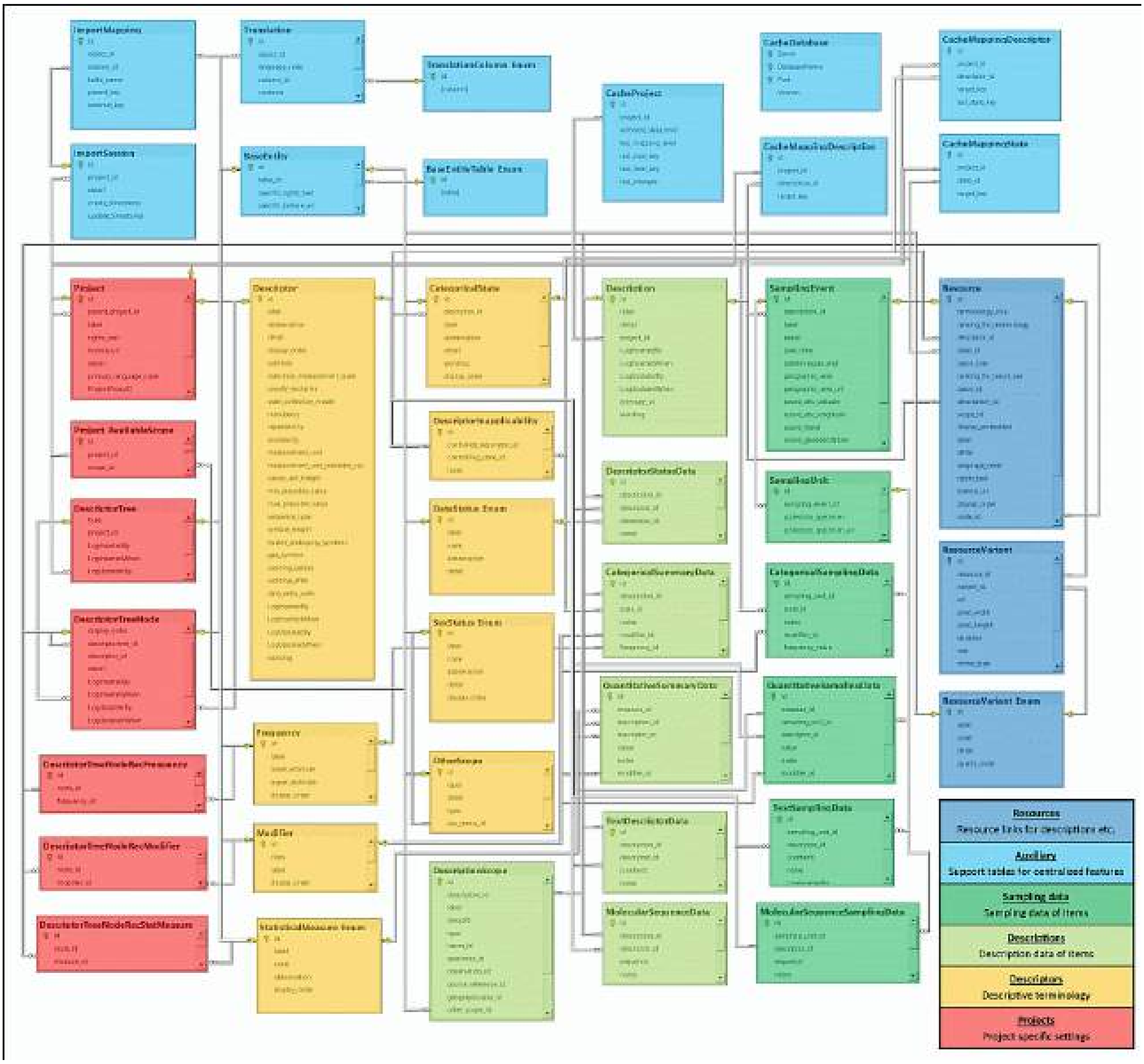
The database consits of three major parts:

1. The "Descriptive terminology" with the main tables "Descriptor" and "CategoricalState" provides the means to express the description details. The two fixed enumeration tables "DataStatus_Enum" and "StatisticalMeasure_Enum" provide values defined in the SDD standard 1.1 rev 5.

2. The "Descriptions" part with the main table "Description" reflects the items themselves. Each description must be assigned to a project (see part 3) and references entries from the descriptive terminology. These references are reflected by the tables "CategoricalSummaryData", "QuantitativeSummaryData" and "TextDescriptorData", where additional item specific data are stored.

3. The "Projects" part with the main tables "Project", "DescriptorTree" and "DescriptorTreeNode" build the anchor for the descriptions, which must be assigned to a project. Further functions are a hierarchical organization of the descriptors and restriction of the descriptive terminology to certain projects. Additionally it is possible, to define recommended values of statistical measure, modifier and frequency associated to certain branches of a descriptor tree or single descriptors. If for a certain project no descriptor tree is created, there is no restriction, i. e. all descriptors are allowed.

The image below shows the main tables of the database.



In the graphic the tables of the database are marked according to their logical groups. Additionally the database group "Resources" provides the option to assign links to resource files (pictures, audio, video) to certain descriptors, categorical states or descriptions. The "Auxilliary" group with the main table "BaseEntity" provides unique keys for the most of the other tables for building of relations. Furthermore it allowes a centralized realization of some features, e.g. support of translations supply imports and export to a cache database.

Further details: tables, projects, access.

Installation of the database

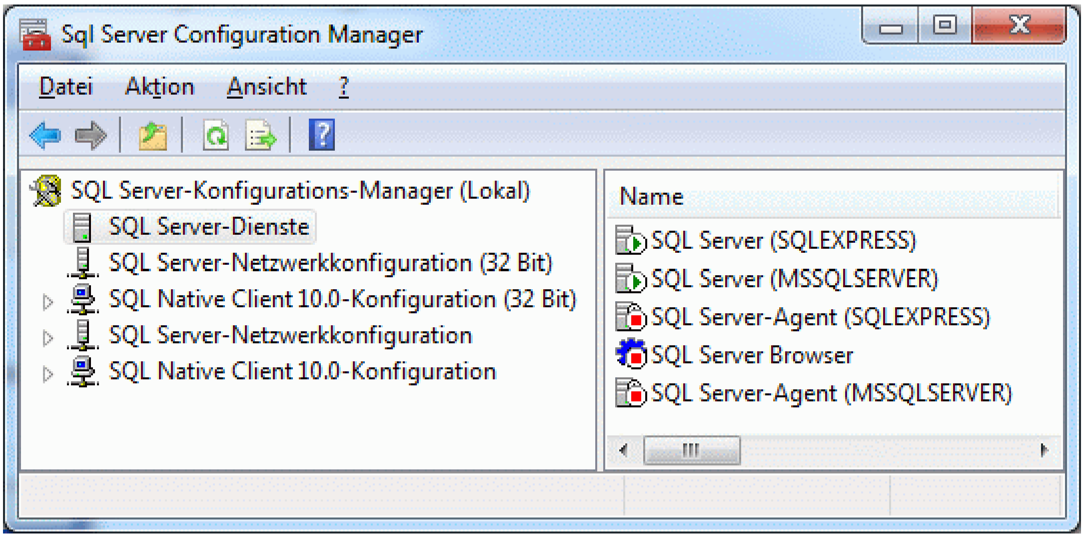
DiversityDescriptions uses Microsoft SQL-Server 2008 R2 or higher as database engine. We recommend to use one of the latest versions Microsoft SQL-Server 2012 or 2014. The database files provided at the DiversityWorkbench homepage are generated for Microsoft SQL-Server 2008 R2 but can be attached to these versions. You may use a centralized SQL-Server that is accessible by several users, e.g. over a local area network or run a local database server on your own PC.

If you do not have a database server with DiversityDescriptions already available, you have to install the database engine first. Download the free version of Microsoft SQL Server Express (e.g. SQLEXPRADV_x86_DEU.exe) from http://www.microsoft.com/downloads/. Start the program and follow the instructions for the installation. After the installation make shure to get the latest updates using Windows Update.

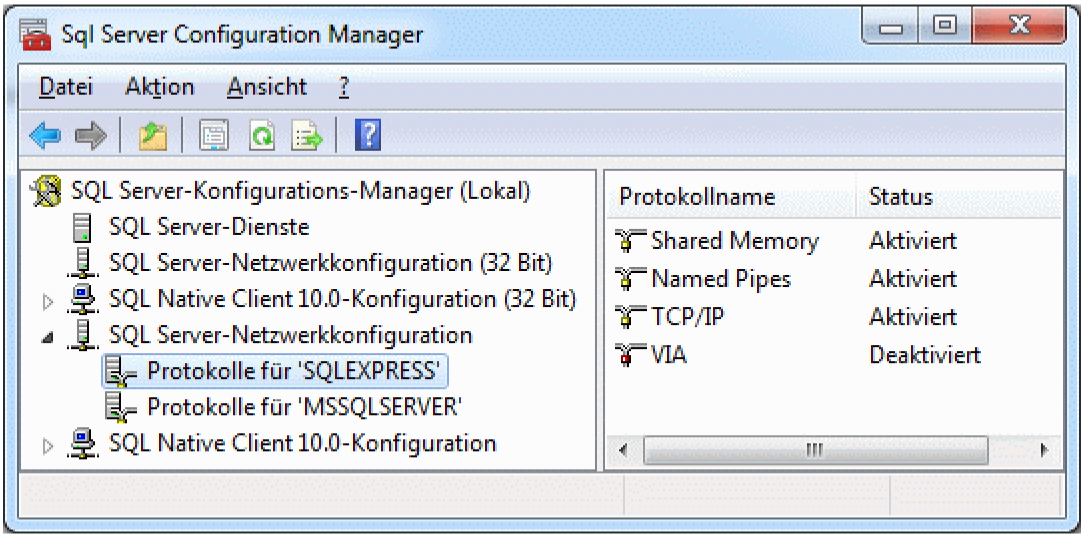
Download the database files DiversityDescriptions_Base.MDF and DiversityDescriptions_Base_log.LDF from http://www.diversityworkbench.net/Portal/ provided as a zip archive (DiversityDescriptions.zip) and copy them into your database directory.

Server configuration

To configure your server, launch the **SQL Server Configuration Manager** (see image below, please consider that in this example the two SQL-Servers "SQLEXPRESS" and "MSSQLSERVER" are installed).

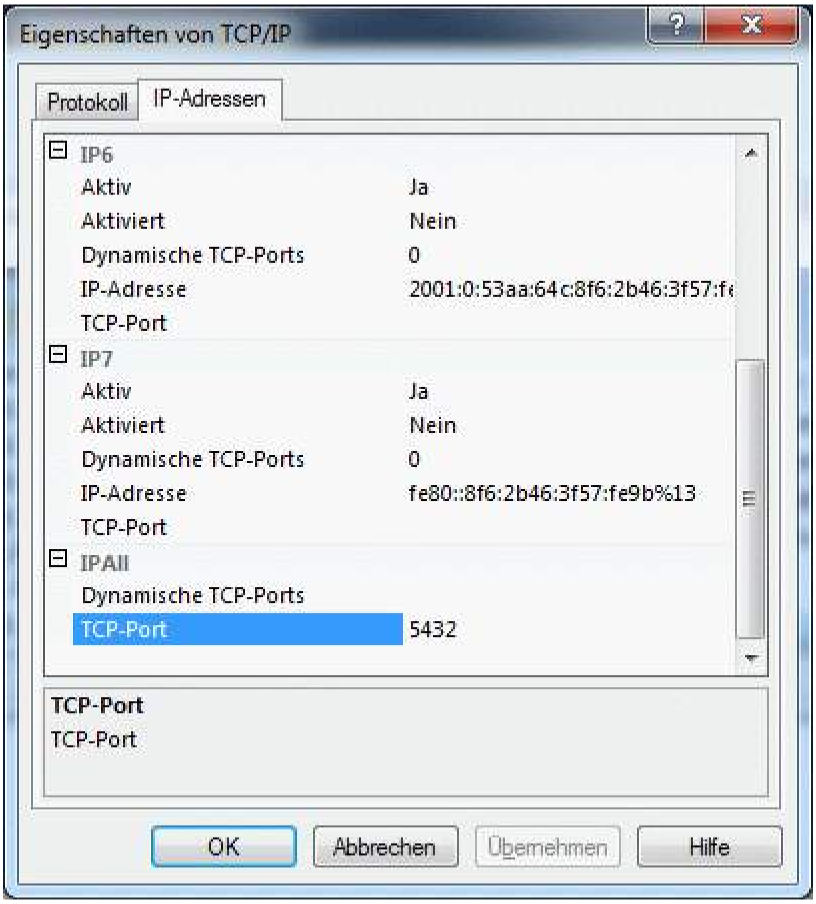


Then click on the "**Protocols** for SQLEXPRESS" node. Right click on "**TCP/IP**" in the list of Protocols and choose "enable" for TCP/IP.



Protokollname	Status
Shared Memory	Aktiviert
Named Pipes	Aktiviert
TCP/IP	Aktiviert
VIA	Deaktiviert

Right click on the TCP/IP node and select "**Properties**" to open a window as shown below.

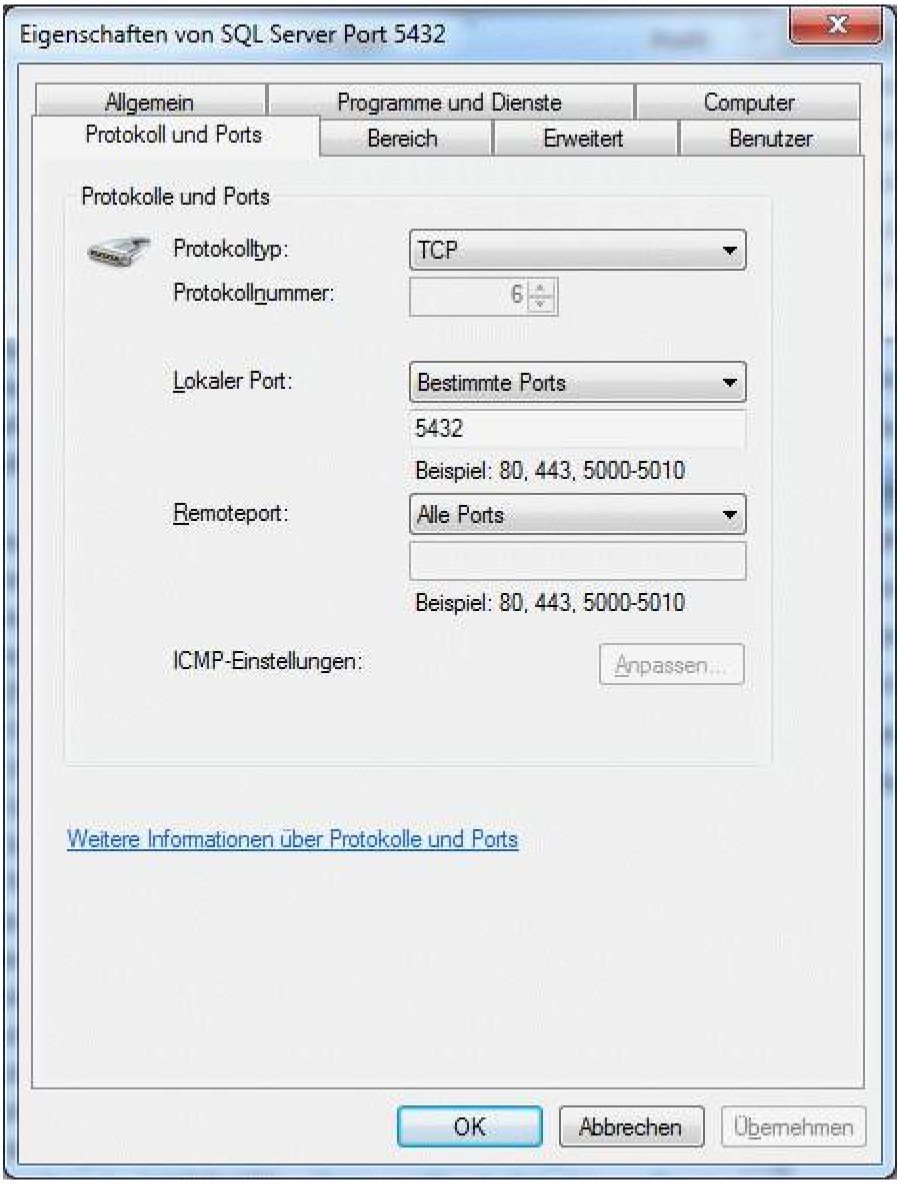


IP6	
Aktiv	Ja
Aktiviert	Nein
Dynamische TCP-Ports	0
IP-Adresse	2001:0:53aa:64c:8f6:2b46:3f57:fe
TCP-Port	
IP7	
Aktiv	Ja
Aktiviert	Nein
Dynamische TCP-Ports	0
IP-Adresse	fe80::8f6:2b46:3f57:fe9b%13
TCP-Port	
IPAll	
Dynamische TCP-Ports	
TCP-Port	5432

TCP-Port
TCP-Port

In the part **IPALL** clear out the value for "TCP Dynamic Ports". Give a **TCP-Port** number to use when making remote connections, e.g. "5432" as shown above. You have to restart the SQL Server Express service before you can connect to your database.

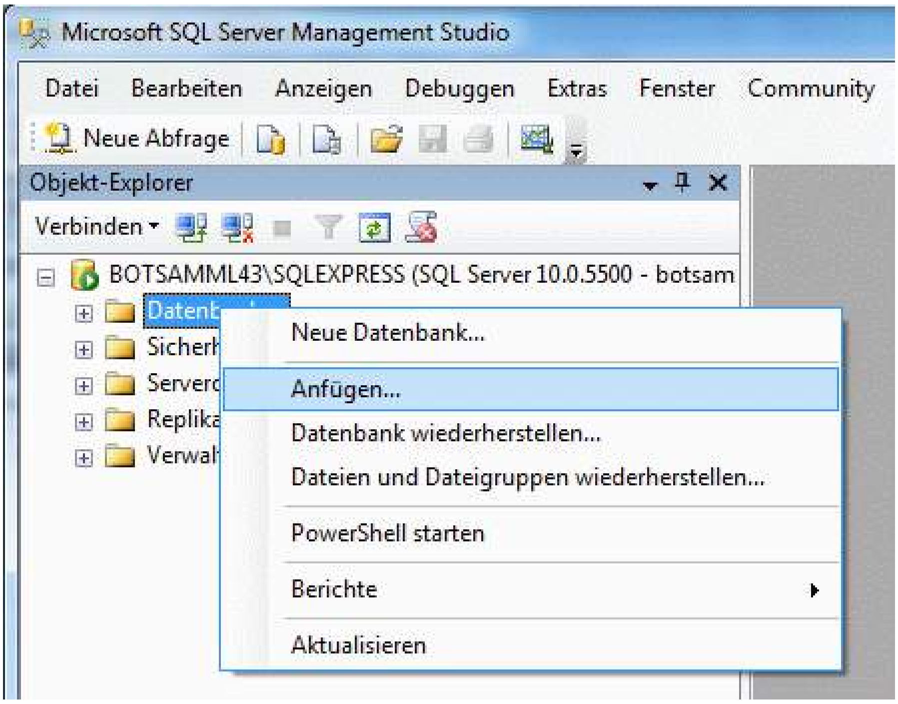
If you use a database on a centralized server that shall be reachable over a computer network, make sure that the firewall of the server allows access via the port you set for the connections (see below).



Eigenschaften von SQL Server Port 5432

Protokolltyp: TCP
Protokollnummer: 6
Lokaler Port: Bestimmte Ports
5432
Remoteport: Alle Ports

Start the Microsoft SQL Server Managment Studio and attach the database as shown below. Choose the node "databases" and right-click on it to open the context menu (see below). Then choose "attach" from the context menu. A window will open where you can choose the file DiversityDescriptions_Base.MDF from your database directory and attach it to the database engine.

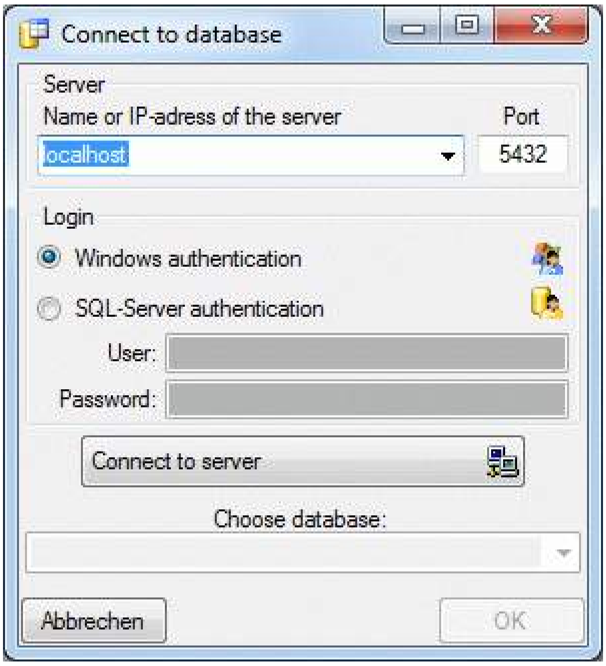


Database configuration

To configure your Database, use the Client as described in Database configuration.

Connect to database

Start the program DiversityDescriptions.exe and in the main window click on the button or choose **Connection -> Database ...** from the menu. A window as shown below will open. Here enter the server name or the IP address (here "localhost" for a local database on the own PC) and its IP port (5432 in example below) to connect to your SQL-server and select the database file in your directory.


Connect to database

Server

Name or IP-adress of the server: localhost

Port: 5432

Login

● Windows authentication

○ SQL-Server authentication

User:

Password:

Configuration of the database

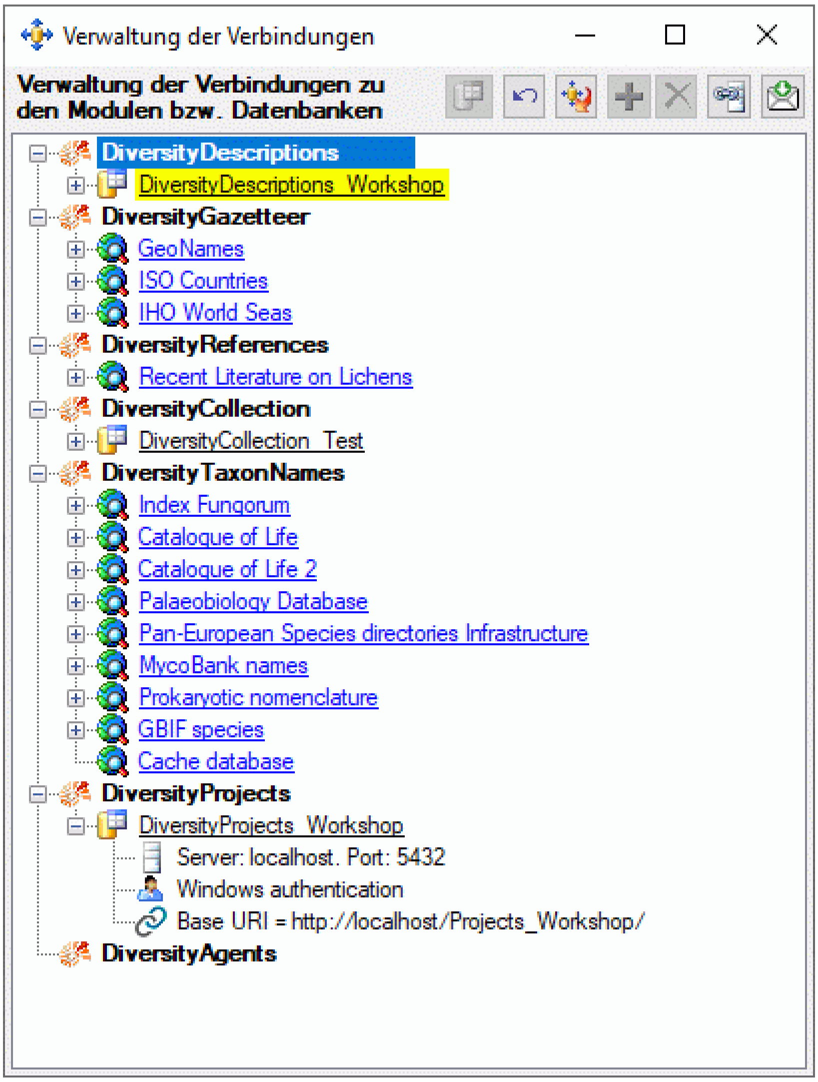
To configure your Database, choose **Administration -> Database -> Rename database ...** to change the name of the database according to your requirements. During this renaming all processes in the database will be terminated (you will get a warning if processes from other host are active).

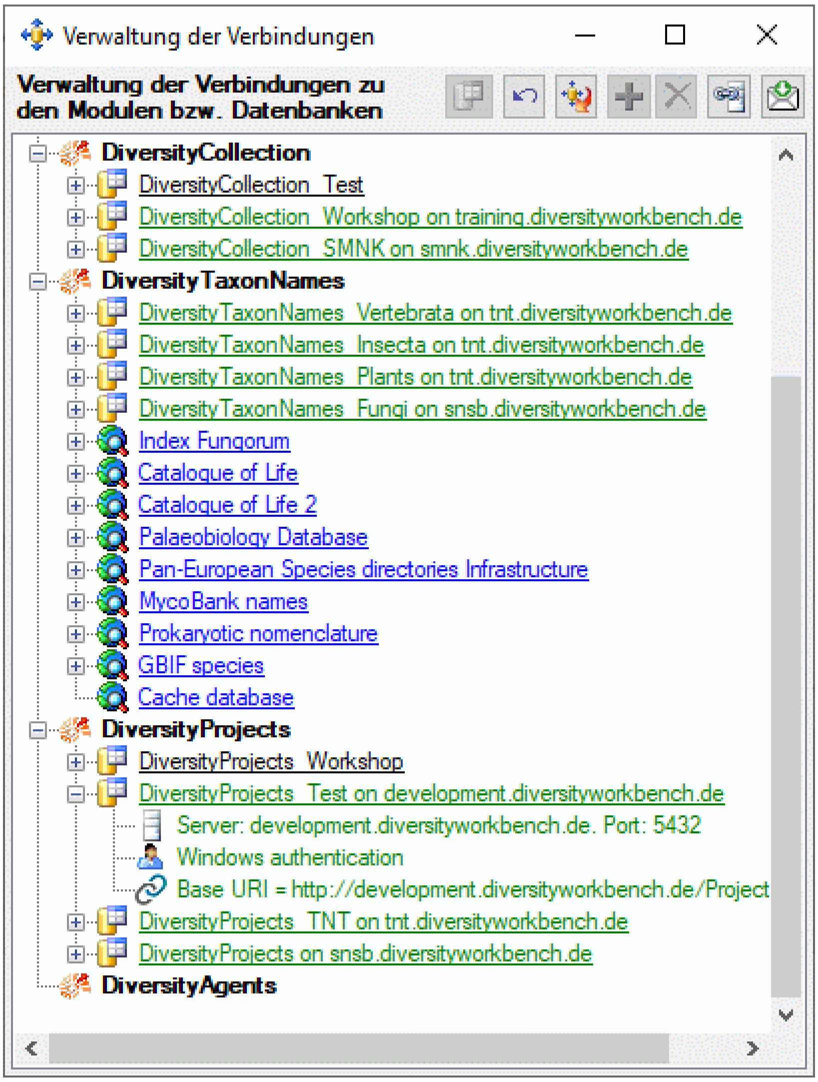
Afterwards you should adapt the address that is published by the database for access by other modules. Choose **Administration -> Database -> Set published address ...** from the menu. This will change the published address to the name of the server where your database is located and an identifier for you database, e.g. http://xy.diversityworkbench.de/Descriptions/.

Renaming of the database and adapting of the published address should be done **before you start to use the database** and name and address should **not be changed afterwards** as datasets from other modules linked to data in the database would point to outdated addresses otherwise.

Connections to the databases and services

The program will automatically try to connect to all the modules within the Diversity Workbench. To edit these connections choose **Connection ->** **Module connections ...** from the menu. A form as shown below will open, where you can edit these connections.



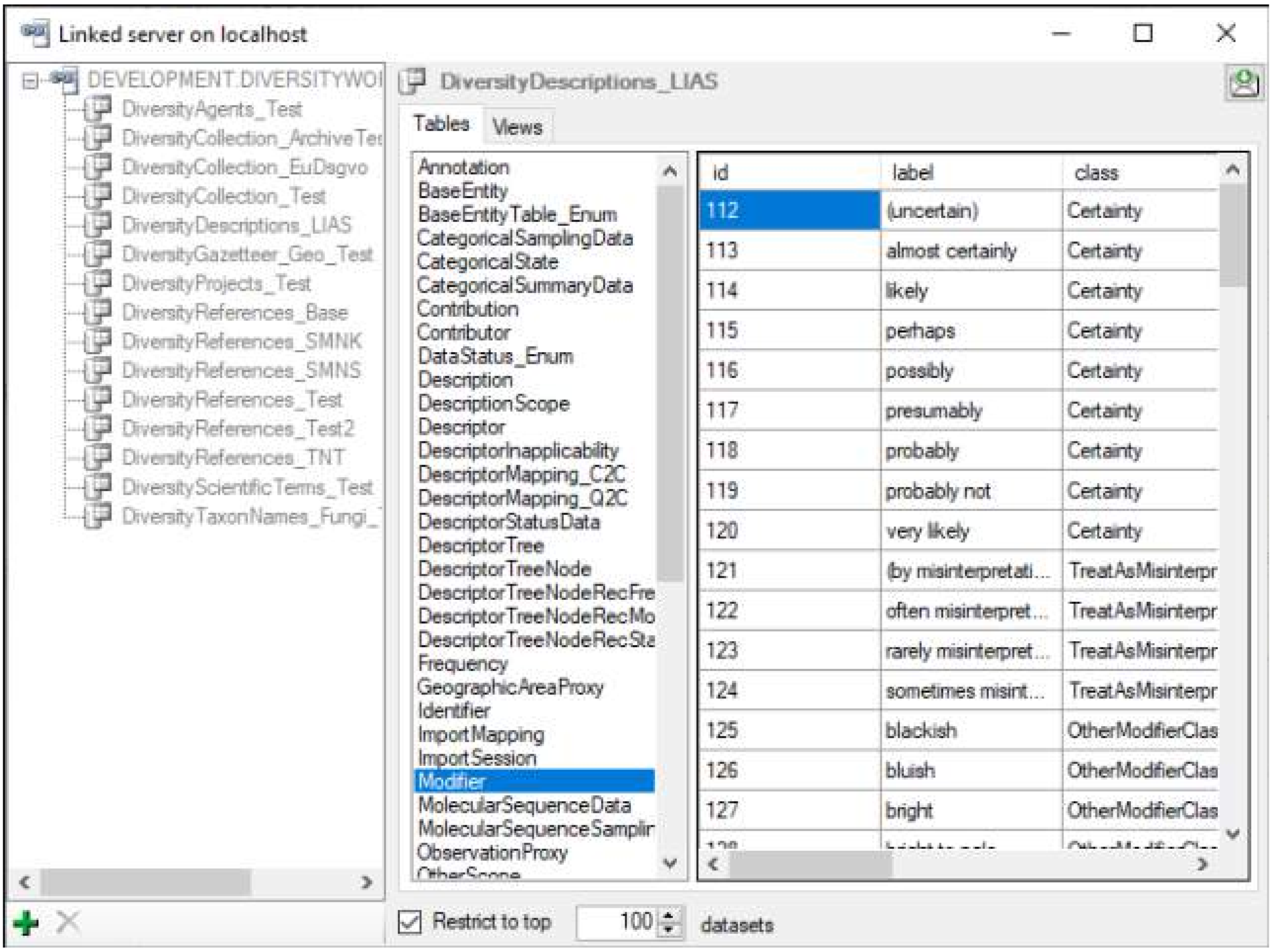


To requery the connections use the ↶ button. If you want to add a connection to a different server click on the ✚ button and connect to the database you want to add to the list. Added databases will be displayed in green. To remove a connection from the list select it and click on the ✕ button. If you have added connections in a former program run, click on button to insert them into the available connections (see right image). If an added connection misses a password, this will be indicated by a red backcolor. Click on the button to enter the missing password.

Webservices like Index Fungorum will be displayed in blue.

Linked server

Databases not available on the local server may be accessible via a linked server. To administrate the linked servers, choose **Administration -> Linked servers ...** from the menu. A form (see below) will open where you can add linked servers and inspect the content of the available databases.



id	label	class
112	(uncertain)	Certainty
113	almost certainly	Certainty
114	likely	Certainty
115	perhaps	Certainty
116	possibly	Certainty
117	presumably	Certainty
118	probably	Certainty
119	probably not	Certainty
120	very likely	Certainty
121	(by misinterpretati...	TreatAsMisinterpr
122	often misinterpret...	TreatAsMisinterpr
123	rarely misinterpret...	TreatAsMisinterpr
124	sometimes misint...	TreatAsMisinterpr
125	blackish	OtherModifierClas
126	bluish	OtherModifierClas
127	bright	OtherModifierClas

☑ Restrict to top 100 datasets

Use the ✚ resp. ✕ buttons to add or remove a linked server. To add a linked server, you need the name of the server and the port, e.g. tnt.diversityworkbench.de, 5432, the login associated with the connection of the linked server e.g. TNT and the password for this login. The available databases will be listed as shown above. To inspect the content, select among the tables or views listed in the right part as shown above. Linked servers have certain restrictions for the availability of data, e.g. XML and geography data are not available via a linked server. For a table or view containing incompatible content you may encounter a corresponding error mentioning the reason for the incompatibility.

Database - access

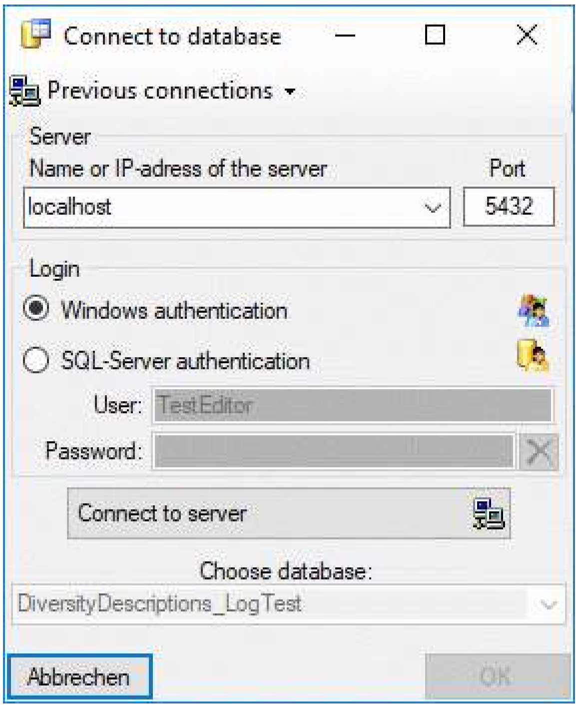
The database engine for DiversityDescriptions is Microsoft SQL-Server 2008 or higher.

If you are connected to a database this is indicated by the icon of the connection button in left upper corner. If you are not connected this will be indicated by the icon . To access any database, you must specify the server where the database is located. For the configuration of this connection choose **Connection -> Database...** from the menu or click on the button.

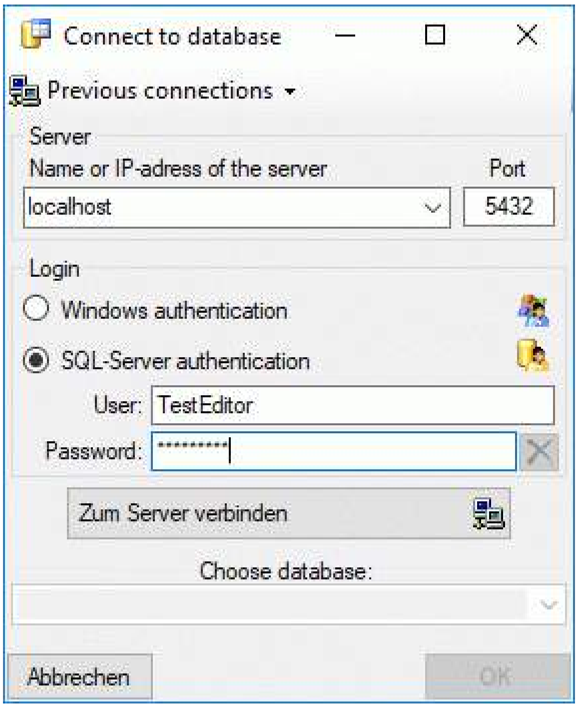
If you want to use a database on a local or remote SQL-server, start the program DiversityDescriptions.exe and in the main window click on the button or choose **Connection -> Database ...** from the menu. A window as shown below will open. Here set the connection parameters as described below.

Database name, IP-address and Port

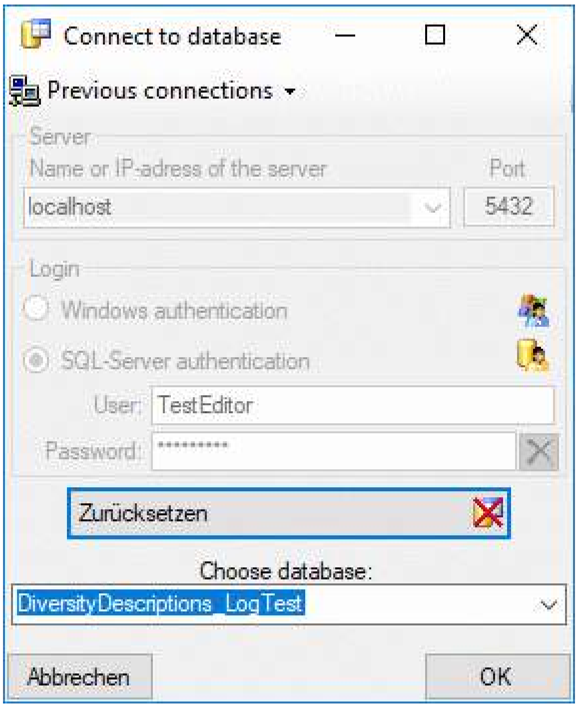
A dialog will open, to specify the name or IP-address and port number of the server and to select the authentication mode. The SQL-Server may be addressed by its IP-address, e.g. 127.0.0.1 or by its name, e.g. localhost. You can either choose Windows authentication (see left image below) or SQL-Server authentication (see below - central middle image).



Name or IP-adress of the server: localhost
Port: 5432
Login
● Windows authentication
○ SQL-Server authentication
User: TestEditor
Password:
DiversityDescriptions_LogTest



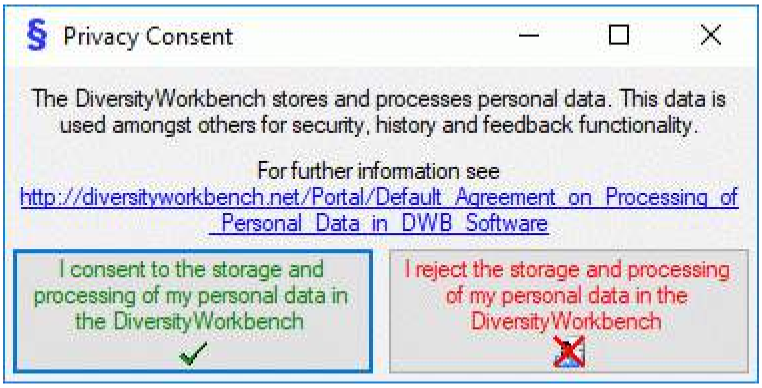
Name or IP-adress of the server: localhost
Port: 5432
Login
○ Windows authentication
● SQL-Server authentication
User: TestEditor
Password: *********



Name or IP-adress of the server: localhost
Port: 5432
○ Windows authentication
● SQL-Server authentication
User: TestEditor
Password: **********
Choose database: DiversityDescriptions_LogTest

The standard port number for SQL-Server is 1433 and will be set as a default. If the database server is configured using a port different from that port, you must give the port number in the field Port. Click on the Connect to server button to connect to the server. If the connection informations are valid, you can choose a database from the server from the combobox at the base of the window (see right image above). To restart the connecting process click on the Zurücksetzen button. In menu Previous connections you find a list of the latest login data (server and port) used.

If you access a database for the first time you will be asked to consent to the storage and processing of your personal data (see below) according to the [General Data Protection Regulation](). Without your consent the access is not possible.

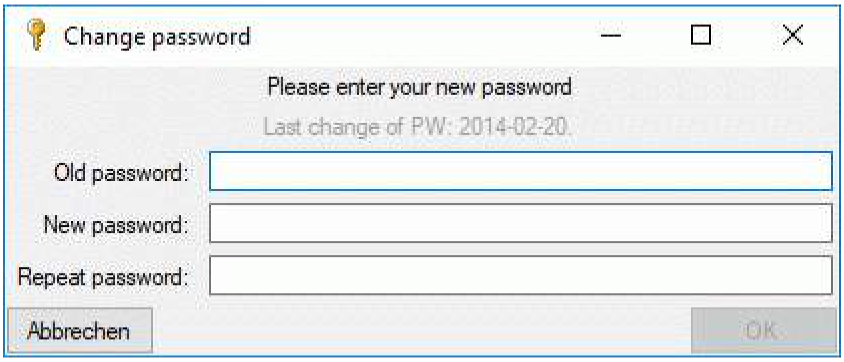


The DiversityWorkbench stores and processes personal data. This data is used amongst others for security, history and feedback functionality.

For further information see http://diversityworkbench.net/Portal/Default_Agreement_on_Processing_of_Personal_Data_in_DWB_Software

Password

If you are logged in with a SQL-Server account and are not restricted to the group **DataUser** or **DataReader**, you can change your password. Choose **Administration -> Change password...** from the menu. In the window that will open, enter your current password and the new password (see below). The password must match the restrictions set by the database server.



Please enter your new password

Last change of PW: 2014-02-20.

Old password:

New password:

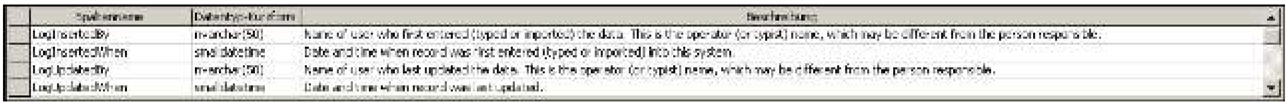
Repeat password:

Module connections

The program will automatically try to get connect to Diversity Workbench databases and webservices. For further details see the Connections section.

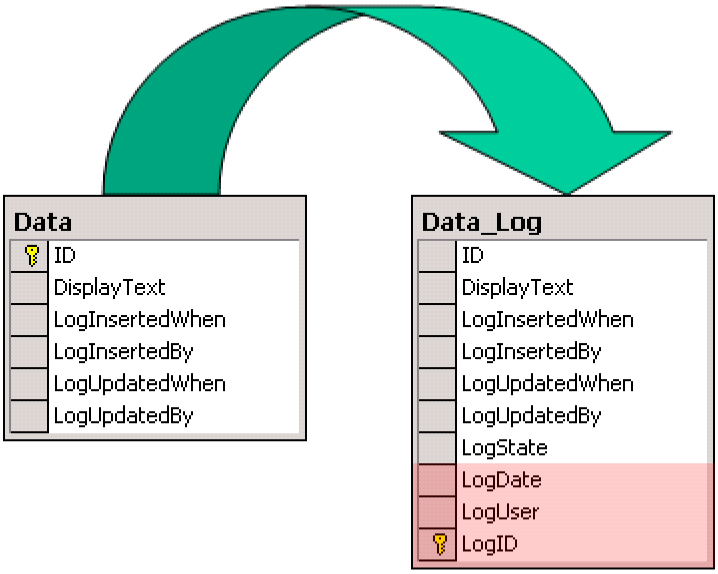
Logging

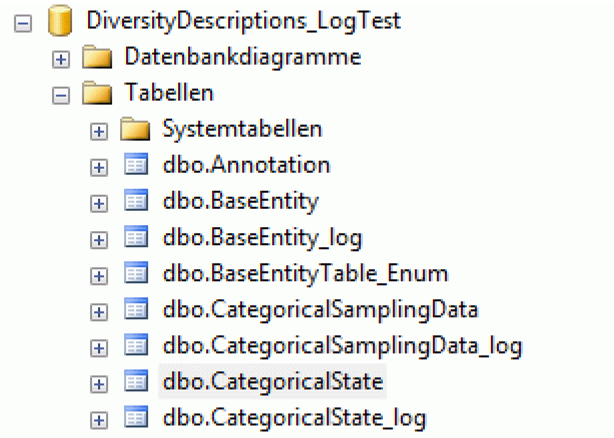
Changes within the database will be documented for each data set together with the time and the responsible user in the columns shown in the image below.



Spaltenname	Datentyp-Kurzform	Beschreibung
LogInsertedBy	nvarchar(50)	Name of user who first entered (typed or imported) the data. This is the operator (or typist) name, which may be different from the person responsible.
LogInsertedWhen	smalldatetime	Date and time when record was first entered (typed or imported) into this system.
LogUpdatedBy	nvarchar(50)	Name of user who last updated the data. This is the operator (or typist) name, which may be different from the person responsible.
LogUpdatedWhen	smalldatetime	Date and time when record was last updated.

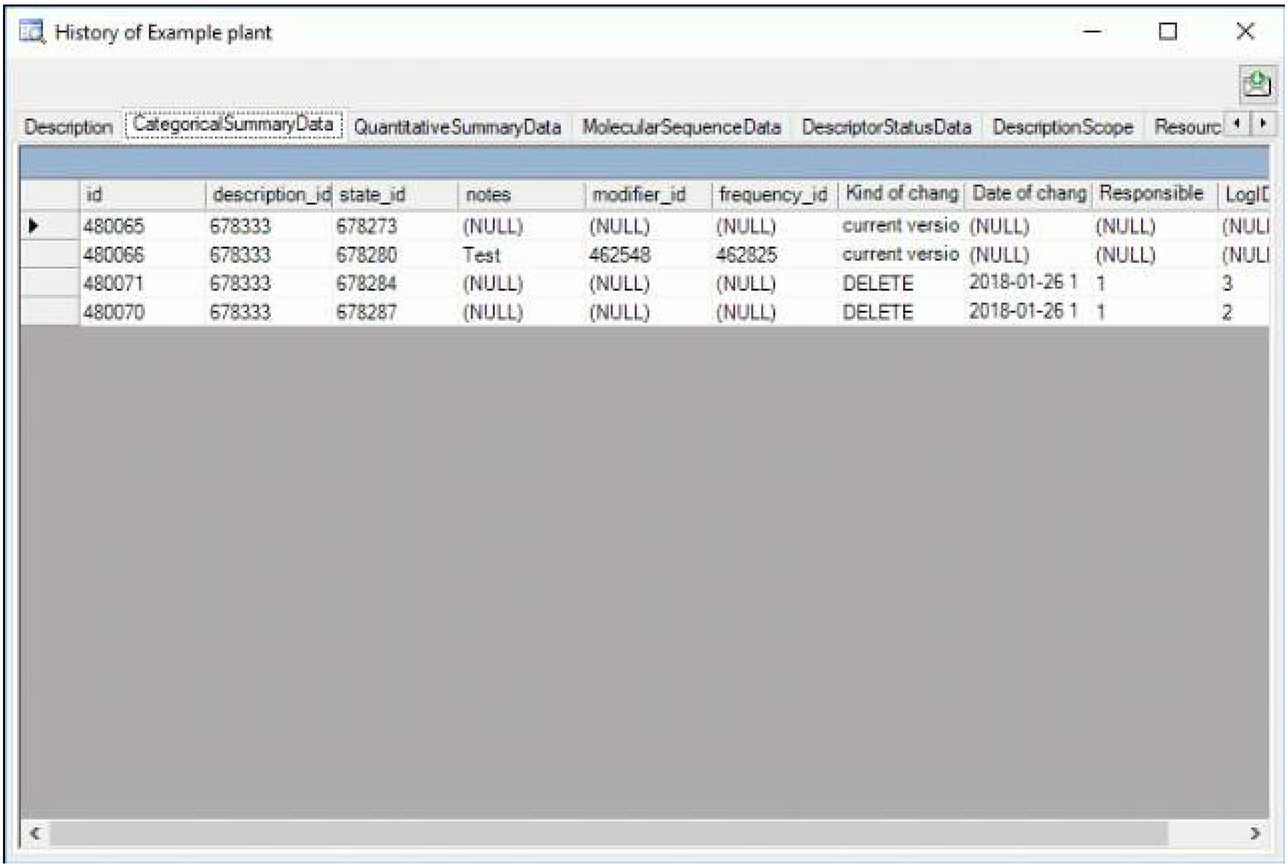
All main tables have a corresponding logging table. If you change or delete a data set, the original data set will be stored in this logging table together with information about by whom and when changes were made last.





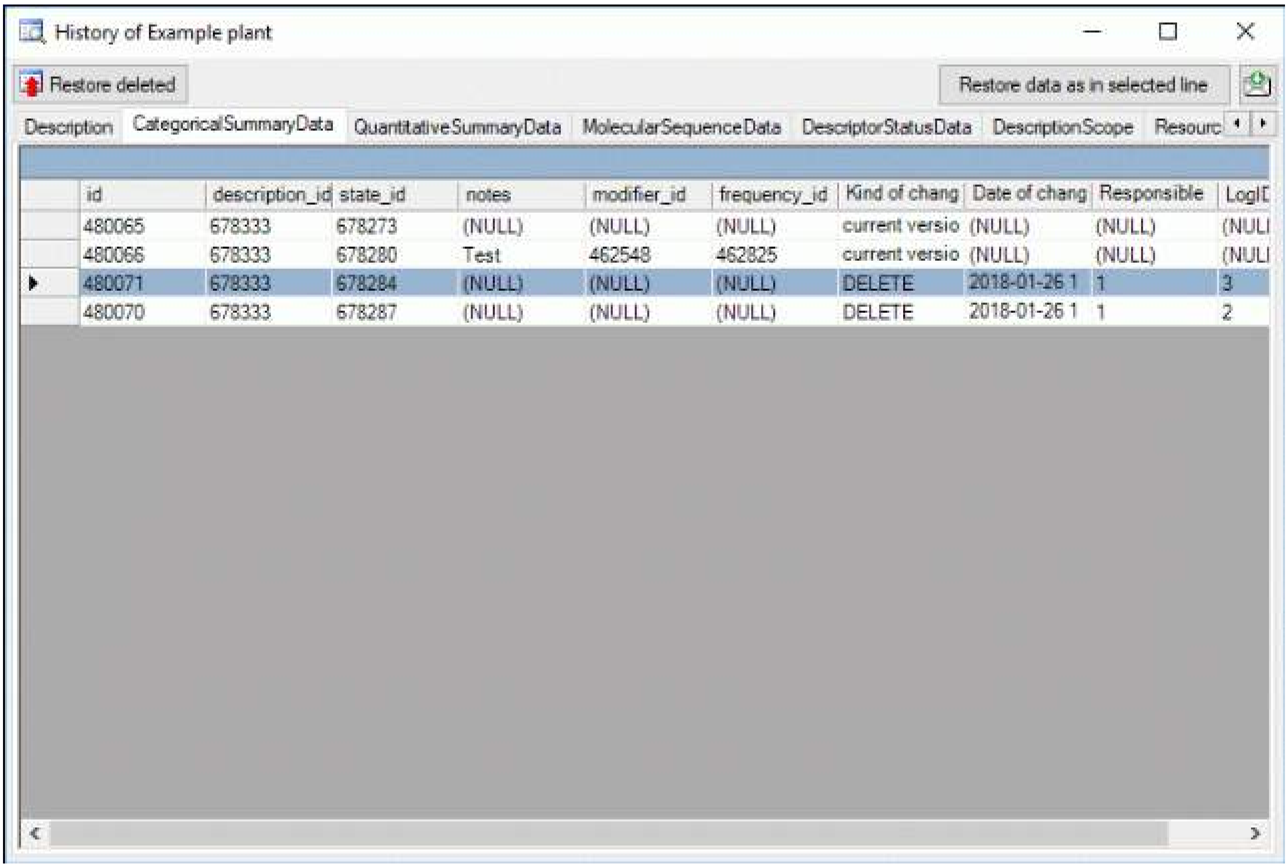
History

To inspect the history of a data set click on the button. A window will open showing all former states of the data in tables with the current data set at the top.



id	description_id	state_id	notes	modifier_id	frequency_id	Kind of chang	Date of chang	Responsible	LogI
480065	678333	678273	(NULL)	(NULL)	(NULL)	current versio	(NULL)	(NULL)	(NUL
480066	678333	678280	Test	462548	462825	current versio	(NULL)	(NULL)	(NUL
480071	678333	678284	(NULL)	(NULL)	(NULL)	DELETE	2018-01-26 1	1	3
480070	678333	678287	(NULL)	(NULL)	(NULL)	DELETE	2018-01-26 1	1	2

If you have sufficient access rights for the database (role administrator), the buttons **Restore deleted** and **Restore data as in selected line** are available (see image below). If you want to restore an old version of a data set, choose the corresponding line in the table and click on the **Restore data as in selected line** button.



	id	description_id	state_id	notes	modifier_id	frequency_id	Kind of chang	Date of chang	Responsible	LogI
	480065	678333	678273	(NULL)	(NULL)	(NULL)	current versio	(NULL)	(NULL)	(NULI
	480066	678333	678280	Test	462548	462825	current versio	(NULL)	(NULL)	(NULI
▶	480071	678333	678284	(NULL)	(NULL)	(NULL)	DELETE	2018-01-26 1	1	3
	480070	678333	678287	(NULL)	(NULL)	(NULL)	DELETE	2018-01-26 1	1	2

If you want to restore a whole data set including the dependent data, click on the **Restore deleted** button. This function is as well available from the menu **Data -> Restore from log ....** In the upcoming dialogs choose the basic table to start for the search. In the upcoming dialogs enter the date where the query should start and the number of lines from the log table that should be displayed. Finally select the datarow(s) of the root table that should be restored. After that the program will try to recover the data with all depending information.

Depending on selected edit mode ("Descriptions", "Descriptors" or "Projects") the **marked tables** in the overview below may be selected as basic tables for restorage. With "->" dependent tables are marked that will be restored automatically, if the parent has been successfully restored.

- Edit mode "Descriptions":

Translation		
Description	-> **SamplingEvent**	-> **SamplingUnit**
-> DescriptionScope		-> CategoricalSamplingData
-> CategoricalSummaryData		-> QuantitativeSamplingData
-> QuantitativeSummaryData		-> TextSamplingData
-> TextDescriptorData		-> MolecularSequenceSamplingData
-> MolecularSequenceData		
	-> **Resource** *	-> **ResourceVariant**

- Edit mode "Descriptors":

Translation

Descriptor -> **CategorialState**
-> **Resource** * -> **ResourceVariant**

- Edit mode "Projects":

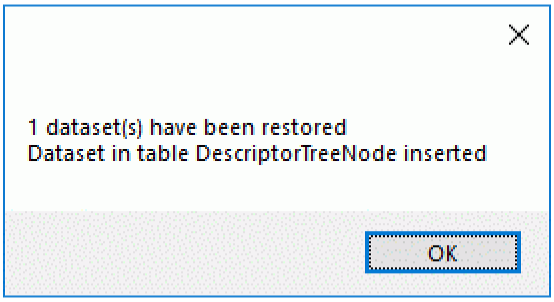
Translation

Project -> **OtherScope**

DescriptorTree -> **DescriptorTreeNode**
-> DescriptorTreeNodeRecFrequency
-> DescriptorTreeNodeRecModifier
-> DescriptorTreeNodeRecStatMeasure
-> **Resource** * -> **ResourceVariant**

***** Remark: If you restore an object that assigns resources, be aware that during delete processing in many cases the link from the resource to the deleted object was set to null before deleting the resource itself. In those cases after restoring the target object you have take a look in the history to restore the resource link using the button **Restore data as in selected line**.

After successful restorage a message will give you an overview of the performed actions.

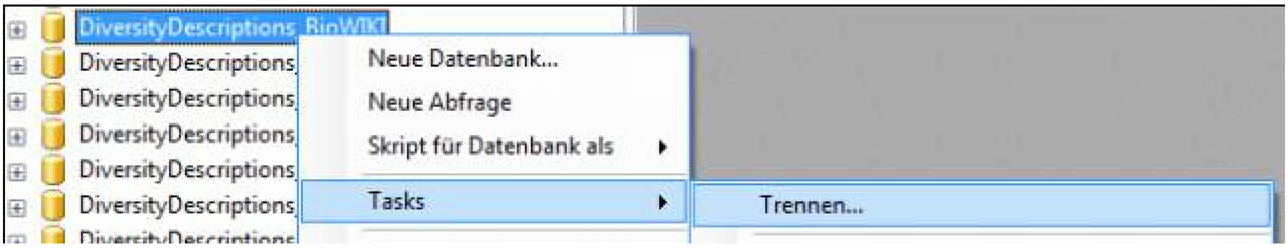


1 dataset(s) have been restored
Dataset in table DescriptorTreeNode inserted

Backup

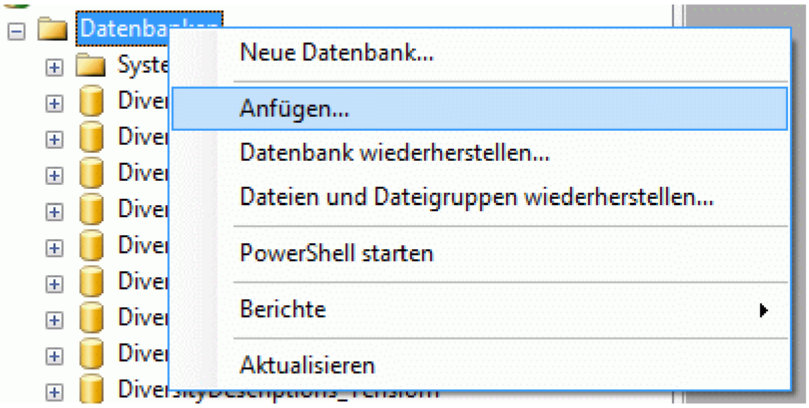
Database copy

If you need to backup your database, you have to use the functionality provided by SQL-Server. To do this, you need administration rights in the database you want to create a backup. Open the Management Studio for SQL-Server, choose the database and detach it from the server as shown in the image below.



After detaching the database, you can store a copy of the ..._Data.MDF File to keep it as a backup.

After storing the backup you have to attach the database.

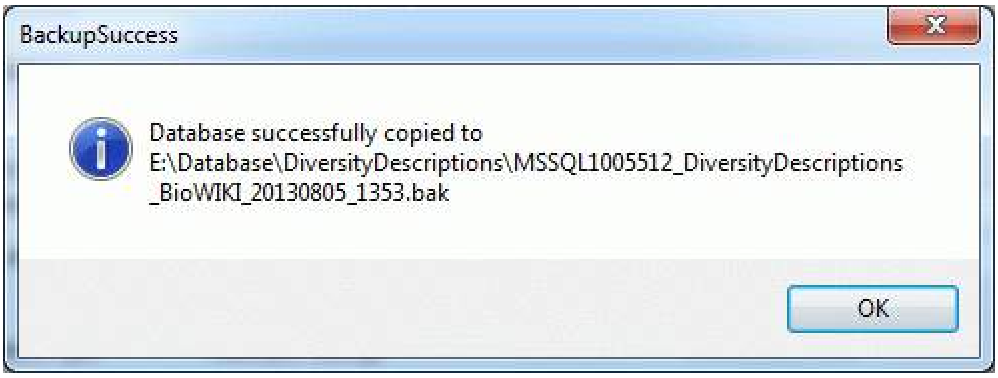


A dialog will appear where you have to select the original database file in your directory.

Note: A database copy can only be attached to an SQL server with the same or a higher version. For example if a database that was attached to an SQL-Server 2008 R2 (internal version 10.50) is copied, it is not possible to attach the copy to an SQL-Server 2008 (internal version 10.00).

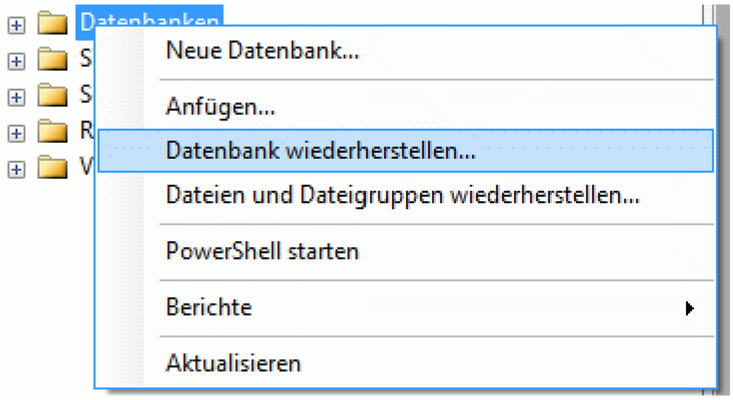
Database backup

If you are logged in to a database with administrator rights, you can start a backup within DiversityDescriptions with menu item **Data-> Backup database**. In this case the name of the backup is automaticallly generated from the SQL-server version, the database name and data/time of backup. In case of backup success the resulting file path at the SQL server disk will be displayed as in the example below.

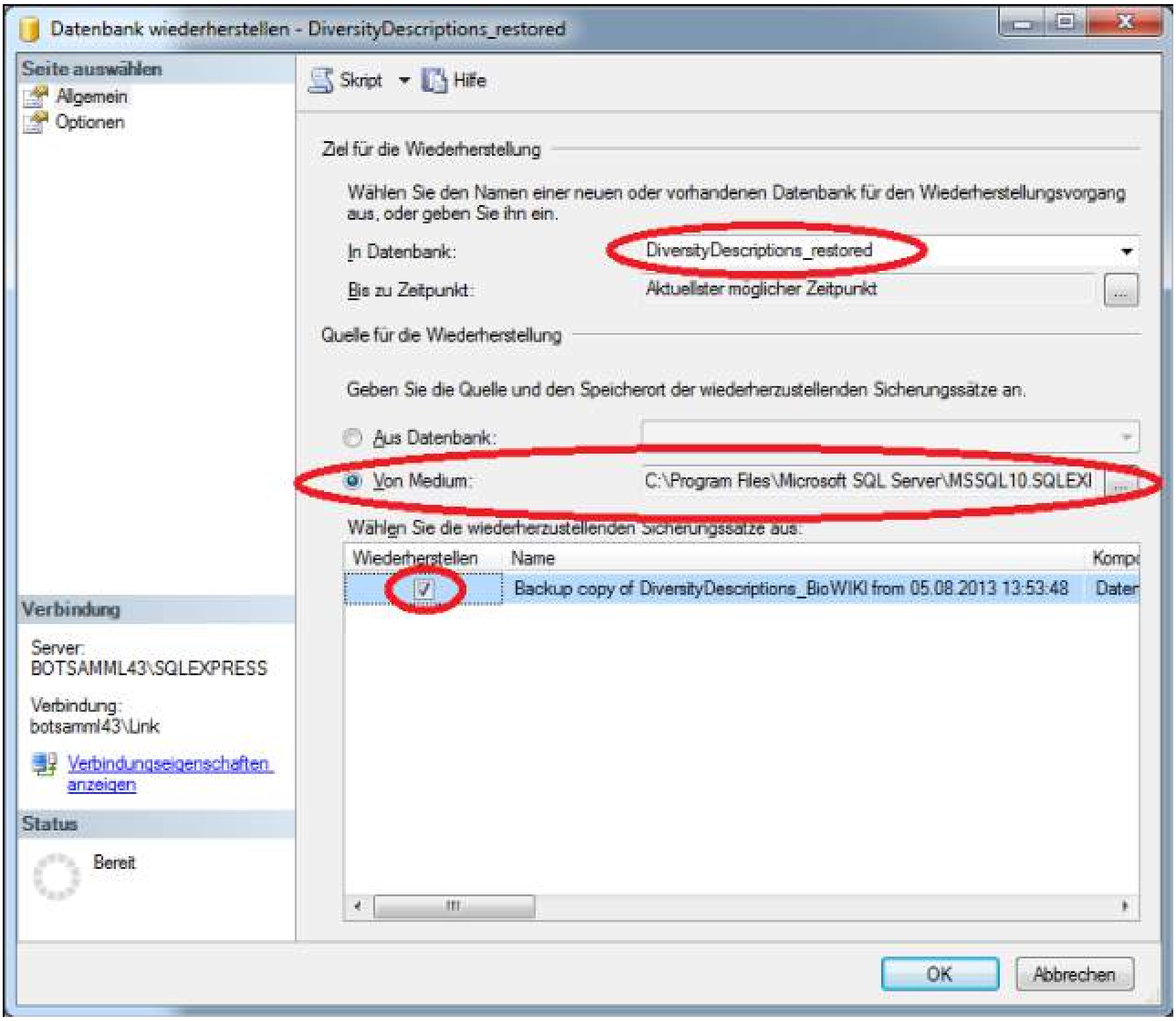


Database successfully copied to
E:\Database\DiversityDescriptions\MSSQL1005512_DiversityDescriptions
_BioWIKI_20130805_1353.bak

To restore the backup to a new database, right-click at "Database" in the Managment Studion for SQ-Server and select "Restore database...".



In the following panel specify the database name, select "Restore from medium" to specify your backup file and select the backup source (see below). You can overwrite an existing databse by selecting it in that panel instead of specifying a new database name.


Datenbank wiederherstellen - DiversityDescriptions_restored

Ziel für die Wiederherstellung

Wählen Sie den Namen einer neuen oder vorhandenen Datenbank für den Wiederherstellungsvorgang aus, oder geben Sie ihn ein.

In Datenbank: DiversityDescriptions_restored

Bis zu Zeitpunkt: Aktuellster möglicher Zeitpunkt

Quelle für die Wiederherstellung

Geben Sie die Quelle und den Speicherort der wiederherzustellenden Sicherungssätze an.

○ Aus Datenbank:

● Von Medium: C:\Program Files\Microsoft SQL Server\MSSQL10.SQLEXI

Wählen Sie die wiederherzustellenden Sicherungssätze aus:

Wiederherstellen	Name	Kompo
☑	Backup copy of DiversityDescriptions_BioWIKI from 05.08.2013 13:53:48	Dater

Verbindung

Server:
BOTSAMML43\SQLEXPRESS

Verbindung:
botsamml43\Link

Verbindungseigenschaften anzeigen

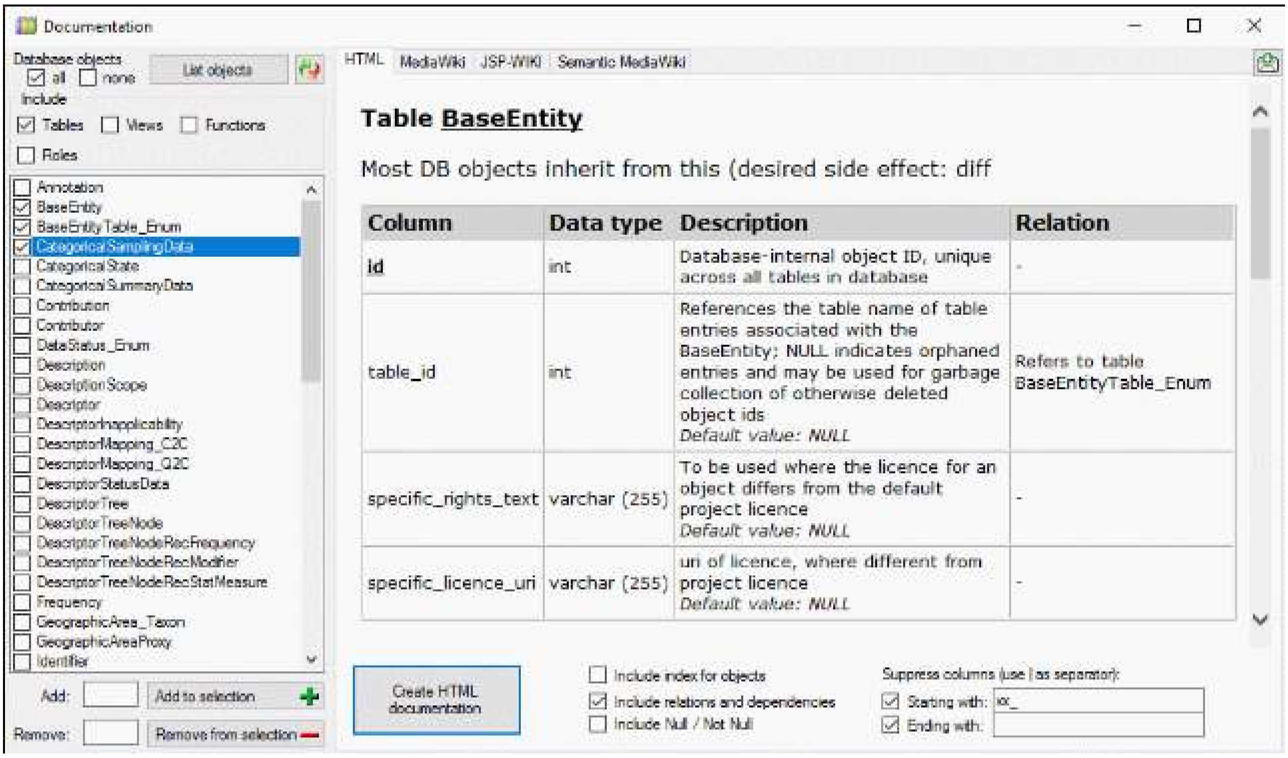
Status

Bereit

Note: The same limitations concerning the SQL-Server versions as mentioned in section "Database copy" are valid for backup handling, too. A backup can only be restored at the same or a higher version of SQL-Server.

Database documentation

This tool is used to generate a structured documentation of database parts. To use this tool, choose **Administration ->** **Database ->** **Documentation ...** from the menu. A window will open as shown below.



☑ all ☐ none

☑ Tables ☐ Views ☐ Functions

☐ Roles

- ☐ Annotation
- ☑ BaseEntity
- ☑ BaseEntityTable_Enum
- ☑ CategoricalSamplingData
- ☐ CategoricalState
- ☐ CategoricalSummaryData
- ☐ Contribution
- ☐ Contributor
- ☐ DataStatus_Enum
- ☐ Description
- ☐ DescriptionScope
- ☐ Descriptor
- ☐ DescriptorInapplicability
- ☐ DescriptorMapping_C2C
- ☐ DescriptorMapping_Q2C
- ☐ DescriptorStatusData
- ☐ DescriptorTree
- ☐ DescriptorTreeNode
- ☐ DescriptorTreeNodeRecFrequency
- ☐ DescriptorTreeNodeRecModifier
- ☐ DescriptorTreeNodeRecStatMeasure
- ☐ Frequency
- ☐ GeographicArea_Taxon
- ☐ GeographicAreaProxy
- ☐ Identifier

Table BaseEntity

Most DB objects inherit from this (desired side effect: diff

Column	Data type	Description	Relation
id	int	Database-internal object ID, unique across all tables in database	-
table_id	int	References the table name of table entries associated with the BaseEntity; NULL indicates orphaned entries and may be used for garbage collection of otherwise deleted object ids *Default value: NULL*	Refers to table BaseEntityTable_Enum
specific_rights_text	varchar (255)	To be used where the licence for an object differs from the default project licence *Default value: NULL*	-
specific_licence_uri	varchar (255)	uri of licence, where different from project licence *Default value: NULL*	-

☐ Include index for objects

☑ Include relations and dependencies

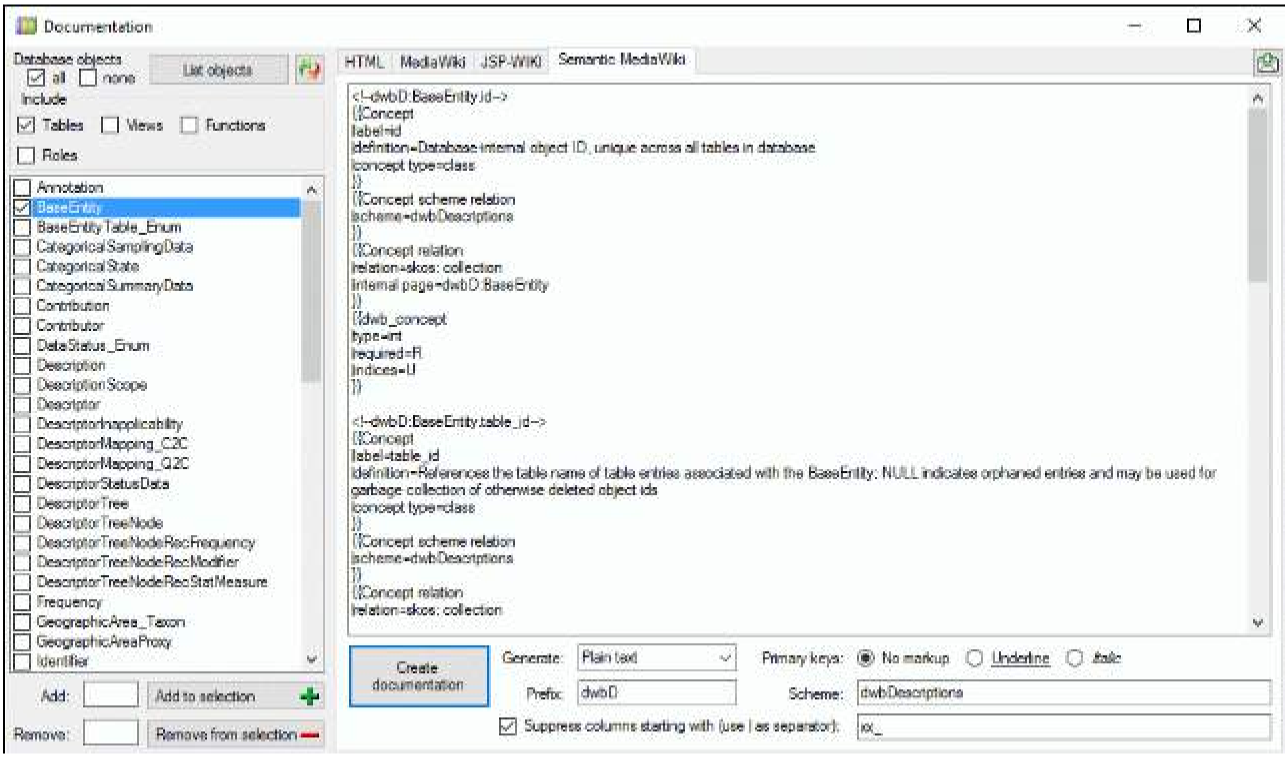
☐ Include Null / Not Null

☑ Starting with: xx_

☑ Ending with:

Select the tables that should be included in the documentation, choose among the provided options and click on the button Create ... documentation to create a documentation in one of the available formats (HTML, MediaWiki, JSP-Wiki, Semantic Media Wiki). If you create a HTML documentation, a local file named **<Database name>.htm** is generated in the application directory, that might be copied and edited for own purposes. For MediaWiki and JSP-Wiki you may simply copy and paste the needed parts from the output window.

If you select format "Semantic Media Wiki" an output is generated that fits to terminology platforms as used e.g by TDWG. In this scheme the most important entities are "Concept" and "Collection". Each "Concept" represents a single table column, which is shown on an own page named <prefix>:<table>.<column>. Each "Collection" represents a single table, which is shown on an own page named <prefix>:<table> (see image below). The "Semantic Media Wiki" option currently only supports output of **Tables**. **Views**, **Functions** and **Roles** will be ignored.



```
<!--dwbD:BaseEntity.id-->
{{Concept
|label=id
|definition=Database-internal object ID, unique across all tables in database
|concept type=class
}}
{{Concept scheme relation
|scheme=dwbDescriptions
}}
{{Concept relation
|relation=skos: collection
|internal page=dwbD:BaseEntity
}}
{{dwb_concept
|type=int
|required=R
|indices=U
}}

<!--dwbD:BaseEntity.table_id-->
{{Concept
|label=table_id
|definition=References the table name of table entries associated with the BaseEntity; NULL indicates orphaned entries and may be used for
garbage collection of otherwise deleted object ids
|concept type=class
}}
{{Concept scheme relation
|scheme=dwbDescriptions
}}
{{Concept relation
|relation=skos: collection
```

Generate: Plain text

Primary keys: ● No markup ○ Underline ○ Italic

Prefix: dwbD

Scheme: dwbDescriptions

☑ Suppress columns starting with (use | as separator): xx_

If "Generate: XML" is selected, the output is generated in an XML format that may be imported to a semantic media wiki. To show all generated data, the two templates "dwb_concept" and "dwb_relation" must be inserted in the wiki.

Index

- MolecularSequenceData
- MolecularSequenceSamplingData
- OtherScope
- Project
- Project_AvailableScope
- QuantitativeSamplingData
- QuantitativeSummaryData
- Resource
- ResourceVariant
- ResourceVariant_Enum
- SamplingEvent
- SamplingUnit
- SexStatus_Enum
- StatisticalMeasure_Enum
- TextDescriptorData
- TextSamplingData
- Translation
- TranslationColumn_Enum

Table BaseEntity

The BaseEntity is used within the database to provide unique keys

Column	Data type	Description	Nullable
id	int	Database-internal object ID, unique across all tables in database (primary key)	NO
table_id	int	References the table name of table entries associated with the BaseEntity; NULL indicates orphaned	YES

		entries and may be used for garbage collection of otherwise deleted object ids *Default value: NULL*	
specific_rights_text	nvarchar (255)	To be used where the licence for an object differs from the default project licence *Default value: NULL*	YES
specific_licence_uri	nvarchar (255)	URI of licence, where different from project licence *Default value: NULL*	YES

Table BaseEntityTable_Enum

The BaseEntityTable_Enum contains the names of tables that reference the BaseEntity table

Column	Data type	Description	Nullable
id	int	Database-internal object ID of this record (primary key)	NO
table	nvarchar (255)	Name of table that references the BaseEntity table	NO

Table CacheDatabase

Table holding the cache databases connected to the database

Column	Data type	Description	Nullable
Server	varchar (50)	The name or IP of the server where the cache database is located	NO
DatabaseName	varchar (50)	The name of the cache database	NO
Port	smallint	The port of the server where the cache database is located	NO
Version	varchar (50)	The version of the cache database	YES

Table CacheMappingDescription

Table holding the description key mappings for the cache database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Reference to the description project (foreign key)	NO
description_id	int	Reference to the description to which these data belong (foreign key)	NO
target_key	int	Mapped key value for the target of the cache database.	NO

Table CacheMappingDescriptor

Table holding the descriptor key mappings for the cache database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Reference to the descriptor project (foreign key)	NO
descriptor_id	int	Reference to the descriptor to which these data belong (foreign key)	NO
target_key	int	Mapped key value for the target of the cache database.	NO
last_state_key	int	Highest value of state key. Relevant for key_mapping_level > 0 *Default value: (0)*	YES

Table CacheMappingState

Table holding the categorical state key mappings for the cache database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Reference to the state project (foreign key)	NO
state_id	int	Reference to the categorical state to	NO

		which these data belong (foreign key)	
target_key	int	Mapped key value for the target of the cache database.	NO

Table CacheProject

Table holding the project settings for the cache database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Reference to the description project (foreign key)	NO
withheld_data_level	tinyint	Flag for handling of withheld descriptor data. 0=withhold description; 1=withhold descriptor; 2=do not withhold data *Default value: (0)*	YES
key_mapping_level	tinyint	Flag for handling of key mapping. 0=re-build mapping for each update; 1=keep first mapping; 2=additionally take numeric values of alternate ID for items; >2 as 2 but re-initialize table *Default value: (0)*	YES
last_char_key	int	Highest value of character key. Relevant for key_mapping_level > 0 *Default value: (0)*	YES
last_item_key	int	Highest value of item key. Relevant for key_mapping_level > 0 *Default value: (0)*	YES
last_changes	datetime	The recent date when data within the project had been changed *Default value: getdate()*	YES

Table CategoricalSamplingData

The categorical data recorded for a sampling event

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
sampling_unit_id	int	Reference to the sampling unit (foreign key)	NO
state_id	int	Reference to the state (descriptor is implicit in state_id) (foreign key)	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES
modifier_id	int	Optional reference to a modifier definition (e.g. "strongly", "at the base", "in autumn") (foreign key) *Default value: NULL*	YES
frequency_value	int	Number of times this category was observed within a single sampling unit *Default value: NULL*	YES

Table CategoricalState

The categorical states available for categorical descriptors

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
descriptor_id	int	Reference to the descriptor to which the state belongs (foreign key)	NO
label	nvarchar (255)	Short label (or name) of descriptor state	NO
abbreviation	nvarchar (255)	Abbreviated label of descriptor state *Default value: NULL*	YES
detail	nvarchar (MAX)	Additional detail text explaining or	YES

		commenting on the descriptor state definition	
wording	nvarchar (255)	Optional separate wording for natural language generation (label will be used if this is missing) *Default value: NULL*	YES
display_order	int	A positive number defining the sequence in which descriptor states are displayed *Default value: '0'*	NO

Table CategoricalSummaryData

The categorical data of a description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to the description to which these data belong (foreign key)	NO
state_id	int	Reference to the state (the descriptor is implicit in state_id) (foreign key)	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES
modifier_id	int	Optional reference to a modifier definition (e.g. "strongly", "at the base", "in autumn") (foreign key) *Default value: NULL*	YES
frequency_id	int	Optional reference to a frequency modifier definition (e.g. "rarely", "usually", "mostly") (foreign key) *Default value: NULL*	YES

Table DataStatus_Enum

Values of data status used for descriptions according to SDD 1.1 rev 5

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of data status	NO
code	nvarchar (255)	Code of data status	NO
abbreviation	char (1)	Single (intuitive) character	NO
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the data status definition	YES

Table Description

The description in the database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of description *Default value: NULL*	YES
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the description definition	YES
project_id	int	Each description belongs to exactly one project (required, foreign key)	NO
alternate_id	nvarchar (30)	Optional alternate id of a description item - should be unique within one project, but not checked by database *Default value: NULL*	YES
wording	nvarchar (255)	Optional separate wording for natural language generation (label will be used if this is missing) *Default value: NULL*	YES

Table DescriptionScope

The scope of the description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to the description to which these data belong (foreign key)	NO
label	nvarchar (255)	Short label (or name) of scope *Default value: NULL*	YES
dwbURI	nvarchar (255)	Reference to DiversityWorkbench component *Default value: NULL*	YES
type	nvarchar (255)	Scope type ("GeographicArea", "Citation", "Observation", "Specimen", "TaxonName", "OtherConcept", "Stage", "Part" or "Sex") *Default value: NULL*	YES
taxon_id	int	Reference to one of potentially several taxa described by the description (not used, foreign key) *Default value: NULL*	YES
specimen_id	int	Reference to one of potentially several specimens (collected and preserved) that are being described (not used, foreign key) *Default value: NULL*	YES
observation_id	int	Reference to one of potentially several observations (not preserved) that are being described (not used, foreign key) *Default value: NULL*	YES
source_reference_id	int	Reference to one or several literature references on which the description is based (not used, foreign key) *Default value: NULL*	YES
geographicarea_id	int	Reference to one of	YES

		potentially several geographic areas refered to in a description (not used, foreign key) *Default value: NULL*	
other_scope_id	int	Reference to further scopes, e.g. stage, sex etc. (foreign key) *Default value: NULL*	YES

Table <u>Descriptor</u>

Descriptor (= characters, features) define variables

Column	Data type	Description	Nullable
<u>id</u>	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of descriptor	NO
abbreviation	nvarchar (255)	Abbreviated label of descriptor *Default value: NULL*	YES
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the descriptor definition	YES
display_order	int	A positive number defining the sequence in which descriptors are displayed *Default value: '0'*	NO
subclass	nvarchar (255)	The four character subclasses of SDD are all combined here in one entity and distinguished by this attribute ("categorical", "quantitative", "text" or "sequence") *Default value: 'categorical'*	NO
statistical_measurement_scale	nvarchar (255)	Scale of descriptor: Categorical may be nominal (unordered, “red/green/blue”) or ordinal (ordered, “bad/medium/good”); Quantitative may be interval (°C) or ratio (mass, length, time, K)	NO

		Default value: 'nominal'	
usually_exclusive	tinyint	Applicable to categorical (nominal/ordinal) descriptors only. If usually exclusive = 1, then by default the user interface allows only entering one state. Nevertheless, multiple states in the data are valid. *Default value: '0'*	NO
state_collection_model	nvarchar (255)	Handling of multiple values: OrSet/AndSet: unordered set combined with or/and, OrSeq/AndSeq: ordered sequence combined with or/and, WithSeq: example is “green with brown”, Between: an example is “oval to elliptic” *Default value: 'OrSet'*	NO
mandatory	tinyint	Is the scoring of this descriptor mandatory (required) in each item? *Default value: '0'*	NO
repeatability	nvarchar (255)	How reliable and consistent are repeated measurements or scorings of the descriptor by different observers and on different objects? ("ignore", "very low", "low", "below average", "slightly below average", "standard", "slightly above average", "above average", "high" or "very high") *Default value: 'standard'*	NO
availability	nvarchar (255)	How available is the descriptor or concept for identification? ("ignore", "very low", "low", "below average", "slightly below average", "standard", "slightly above average", "above	NO

		average", "high" or "very high") *Default value: 'standard'*	
measurement_unit	nvarchar (255)	A measurement unit (mm, inch, kg, °C, m/s etc.) or dimensionless scaling factor *Default value: NULL*	YES
measurement_unit_precedes_value	tinyint	Set to 1 if the measurement unit precedes the value *Default value: '0'*	NO
values_are_integer	tinyint	Set to 1 if the values are integer *Default value: '0'*	NO
min_plausible_value	float	Applicable to quantitative descriptors only; in support of a plausibility check for values. Example: for tree height this could be 0, i.e. only positive values allowed *Default value: '-1.79e308'*	NO
max_plausible_value	float	Applicable to quantitative descriptors only; in support of a plausibility check for values. Example: for tree height this could be 99 *Default value: '1.79e308'*	NO
sequence_type	nvarchar (255)	Type of molecular sequence, "Nucleotide" or "Protein". The value "Nucleotide" covers RNA and DNA sequences *Default value: 'Nucleotide'*	NO
symbol_length	tinyint	The number of letters in each symbol. Nucleotides are always codes with 1-letter symbols, but proteins may use 1 or 3-letter codes (e.g. A or Ala for alanine) *Default value: '1'*	NO
enable_ambiguity_symbols	tinyint	Set to 1 if ambiguity symbols are supported	NO

		in the sequence string, e.g. R, Y, S, W for nucleotides or B, Z for proteins *Default value: '1'*	
gap_symbol	nvarchar (3)	A string identifying the "gap" symbol used in aligned sequences. The gap symbol must always be symbol_length long *Default value: NULL*	YES
wording_before	nvarchar (255)	Representation for natural language output, inserted before the states/value *Default value: NULL*	YES
wording_after	nvarchar (255)	Representation for natural language output, inserted after the states/value *Default value: NULL*	YES
data_entry_note	nvarchar (MAX)	A note or prompt when entering or dealing with data	YES
wording	nvarchar (255)	Optional separate wording for natural language generation (label will be used if this is missing) *Default value: NULL*	YES

Table DescriptorInapplicability

The descriptor dependency rules

Column	**Data type**	**Description**	**Nullable**
id	int	Database-internal ID of this record (primary key)	NO
controlled_descriptor_id	int	Reference to the descriptor to which the rule will apply, e.g. which will be inapplicable if controlling state applies to the same description (foreign key)	NO
controlling_state_id	int	Reference to the controlling categorical state; if present in a description, controlled	NO

		descriptor is affected according to rule	
rule	nvarchar (255)	The kind of rule creating a descriptor inapplicability ("inapplicable-if", "applicable-if", "inapplicable-computed-from-applicable") *Default value: 'inapplicable-if'*	NO

Table DescriptorStatusData

The status data of a descriptor for a certain description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to the description to which these data belong (foreign key)	NO
descriptor_id	int	Reference to the descriptor to which the status value belongs (foreign key)	NO
datastatus_id	int	Reference to a status definition. Status is like a marker why data is missing or in need of revision (examples: "unknown", "not applicable", "to be checked", "data withheld" etc.) (foreign key)	NO
notes	nvarchar (MAX)	Free-form text detailing additional information (rarely used, not multilingual)	YES

Table DescriptorTree

The root and definition of a descriptor tree

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO

is_complete	tinyint	Set to 1 if this tree includes the largest possible set of descriptors for the taxon set associated with a project (i.e. the "master-descriptor tree", other trees being subsets) *Default value: '0'*	NO
label	nvarchar (255)	Short label (or name) of descriptor tree	NO
type	nvarchar (255)	"mixed", "part-of", "property" or "generalization"	NO
project_id	int	Each tree belongs to exactly one project (required, foreign key)	NO

Table DescriptorTreeNode

The descriptor tree nodes representing either nodes of the tree or descriptors ("leafes" of the tree)

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
parent_node_id	int	Reference to a parent node, creating a true tree; NULL for a root node (foreign key) *Default value: NULL*	YES
label	nvarchar (255)	Short label (or name) of internal node associated with a concept; NULL for a descriptor node *Default value: NULL*	YES
abbreviation	nvarchar (255)	Abbreviated label of node *Default value: NULL*	YES
display_order	int	A positive number defining the sequence in which child nodes are displayed *Default value: '0'*	NO
descriptortree_id	int	Reference to a descriptor tree; all nodes must have a direct link to the tree definition (foreign key)	NO

descriptor_id	int	Reference to a descriptor; NULL if the present node is an inner concept node defining a hierarchy of nodes or descriptors (foreign key) *Default value: NULL*	YES
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the node definition	YES

Table DescriptorTreeNodeRecFrequency

Selection of recommended frequency values for descriptor tree parts or single descriptors

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
node_id	int	Reference to the descriptor tree node (foreign key)	NO
frequency_id	int	Reference to the recommended frequency modifier (foreign key)	NO

Table DescriptorTreeNodeRecModifier

Selection of recommended modifier values for descriptor tree parts or single descriptors

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
node_id	int	Reference to the descriptor tree node (foreign key)	NO
modifier_id	int	Reference to the recommended modifier (foreign key)	NO

Table DescriptorTreeNodeRecStatMeasure

Selection of recommended statistical measures for descriptor tree parts or single descriptors

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
node_id	int	Reference to the descriptor tree node (foreign key)	NO
measure_id	int	Reference to the recommended measure (foreign key)	NO

Table Frequency

Definition of frequency modifier values

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of frequency modifier (e.g. "very rare", "rare", "usually" etc.)	NO
lower_estimate	float	Each frequency modifier defines a frequency range, this is the estimated lowest frequency *Default value: '0'*	NO
upper_estimate	float	As above, estimate of upper range for the border; note: ranges may overlap! *Default value: '1'*	NO
display_order	int	A positive number defining the sequence in which frequency modifiers are to be displayed *Default value: '0'*	NO

Table ImportMapping

The import mappings to support mapping of external file keys to database keys

Column	Data type	Description	Nullable
id	int	Database-internal ID	NO

		of this record (primary key)	
object_id	int	Reference to the object to which the mapping belongs, references BaseEntity (foreign key)	NO
session_id	int	Reference to the import session to which the mapping belongs, references ImportMapping (foreign key)	NO
table_name	varchar (50)	Name of the import table	NO
parent_key	varchar (255)	Symbolic key of the parent table	NO
external_key	nvarchar (255)	External key in the import file	NO

Table ImportSession

The import sessions to support import of data spread over several files

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Each import session belongs to exactly one project (required, foreign key)	NO
detail	nvarchar (MAX)	Detail text explaining the import session definition	YES
create_timestamp	datetime	Date and time when the import session was created *Default value: getdate()*	NO
update_timestamp	datetime	Date and time when the import session was updated *Default value: getdate()*	NO

Table Modifier

Definition of modifier values

Column	Data type	Description	Nullable

id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
class	nvarchar (255)	Grouping of modifiers into classes ("Certainty", "Seasonal", "Diurnal", "TreatAsMisinterpretation" or "OtherModifierClass")	NO
label	nvarchar (255)	Short label (or name) of modifier (e.g. "strong", "probably" etc.)	NO
display_order	int	A positive number defining the sequence in which modifiers are to be displayed *Default value: '0'*	NO

Table MolecularSequenceData

The molecular sequence data of a description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to description to which these data belong (foreign key)	NO
descriptor_id	int	Reference to a molecular sequence descriptor to which the sequence text belongs (foreign key)	NO
sequence	nvarchar (MAX)	Molecular sequence text referring to information on one descriptor	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES

Table MolecularSequenceSamplingData

The molecular sequence data recorded for a sampling event

Column	Data type	Description	Nullable

id	int	Database-internal ID of this record (primary key)	NO
sampling_unit_id	int	Reference to a sampling unit (foreign key)	NO
descriptor_id	int	Reference to a molecular sequence descriptor to which the sequence text belongs (foreign key)	NO
sequence	nvarchar (MAX)	Molecular sequence text referring to information on one descriptor	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES

Table OtherScope

Scope values for description scope values for scope types "Other scope", "Part", "Stage" and "Sex"

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of scope (e.g. "male", "female", "adult", "juvenile" etc.)	NO
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the scope and delimitation of the present description	YES
type	nvarchar (255)	Describes the scope type ("sex", "stage", "part" or "other")	NO
sex_status_id	int	Reference to sex status value according SDD V5.1 (foreign key) *Default value: NULL*	YES

Table Project

Projects define separated workareas in a single database

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
parent_project_id	int	Reference to a parent project, creating a subproject; NULL for a root project (foreign key) *Default value: NULL*	YES
label	nvarchar (255)	Short label (or name) of project (or subproject); each project defines a separate work environment within a shared database by means of defining sets of descriptors (through DescriptorTree)	NO
rights_text	nvarchar (255)	The default rights and licence statement for the entire project; BaseEntity provides means to override this for individual objects *Default value: NULL*	YES
licence_uri	nvarchar (255)	URI of licence for the project; BaseEntity provides means to override this for individual objects *Default value: NULL*	YES
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the project (or subproject)	YES
primary_language_code	nvarchar (3)	Language of primary text version (fields directly in tables, may be translated in table Translation); Examples: "de", "en" etc. (ISO 639 language code)	NO
ProjectProxyID	int	Reference to a project definition of DiversityProjects that allows control of access rights *Default value: (0)*	NO

Table Project_AvailableScope

Scope values available for a certain project

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
project_id	int	Reference to the project for which a shall be available (foreign key)	NO
scope_id	int	Reference to a scope definition in OtherScope (foreign key)	NO

Table QuantitativeSamplingData

The quantitative data recorded for a sampling event

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
measure_id	int	Optional statistical measure (minimum, mean, maximum, ranges, sample size, variance etc.) recorded in value; if NULL, value is a direct measurement (foreign key) *Default value: NULL*	YES
sampling_unit_id	int	Reference to a sampling unit (foreign key)	NO
descriptor_id	int	Reference to descriptor which the values record (foreign key)	NO
value	float	The value for the statistical measure or single measurement/recording	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES
modifier_id	int	Optional reference to a modifier definition	YES

		(e.g. "strongly", "at the base", "in autumn") (foreign key) *Default value: NULL*	

Table QuantitativeSummaryData

The quantitative data of a description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
measure_id	int	Reference to the statistical measure (minimum, mean, maximum, ranges, sample size, variance etc.) recorded in value (foreign key)	NO
description_id	int	Reference to the description to which these data belong (foreign key)	NO
descriptor_id	int	Reference to the descriptor which the values record (foreign key)	NO
value	float	The value of the statistical measure	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES
modifier_id	int	Optional reference to a modifier definition (e.g. "strongly", "at the base", "in autumn") (foreign key) *Default value: NULL*	YES

Table Resource

Hyperlinks to separate rich text/media objects

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
terminology_role	nvarchar (255)	Role in relation to	NO

		descriptors or states ("unknown"=role not known or not specified; "diagnostic"=optimized for identification; "iconic"=icon/thumbnail, needs text; "normative"=defines a resource object; "primary"=display always, informative without text; "secondary"=display only on request) *Default value: 'unknown'*	
ranking_for_terminology	tinyint	Ranking of the resource with respect to terminology; range: 0 to 10 *Default value: NULL*	YES
descriptor_id	int	Optional reference to a descriptor (at least 1 of description_id, node_id, descriptor_id, state_id or taxon_id must be present) (foreign key) *Default value: NULL*	YES
state_id	int	Optional reference to a categorical state (at least 1 of description_id, node_id, descriptor_id, state_id or taxon_id must be present) (foreign key) *Default value: NULL*	YES
taxon_role	nvarchar (255)	Role in relation to taxa or descriptions ("unknown"=role not known or not specified; "diagnostic"=optimized for identification; "iconic"=icon/thumbnail, needs text; "normative"=defines a resource object; "primary"=display always, informative without text; "secondary"=display only on request) *Default value: 'unknown'*	NO

ranking_for_taxon_use	tinyint	Ranking of the resource with respect to taxa or descriptions; range: 0 to 10 *Default value: NULL*	YES
taxon_id	int	Optional reference to a taxon (at least 1 of description_id, node_id, descriptor_id, state_id or taxon_id must be present) (foreign key) *Default value: NULL*	YES
description_id	int	Optional reference to a description (at least 1 of description_id, node_id, descriptor_id, state_id or taxon_id must be present) (foreign key) *Default value: NULL*	YES
scope_id	int	Reference to the scope of the resource (e.g. "sex", "stage", "season" etc.) *Default value: NULL*	YES
display_embedded	tinyint	false/0: display as link, true/1: display as embedded media object *Default value: '0'*	NO
label	nvarchar (255)	Short label of (or caption for) the resource, e.g. a text displayed below an image or instead of the link	NO
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the resource definition	YES
language_code	nvarchar (3)	Language of the resource itself, use zxx for language neutral/no linguistic content (ISO 639-1) *Default value: NULL*	YES
rights_text	nvarchar (255)	The rights and licence statement for the resource *Default value: NULL*	YES
licence_uri	nvarchar (255)	URI of licence for the resource *Default value: NULL*	YES

display_order	int	A positive number defining the sequence in which multiple resources are displayed *Default value: '0'*	NO
node_id	int	Optional reference to a descriptor tree node (at least 1 of description_id, node_id, descriptor_id, state_id or taxon_id must be present) (foreign key) *Default value: NULL*	YES

Table ResourceVariant

Different resource variants/instances/service access points

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
resource_id	int	Reference to the resource to which these variants provide access points (foreign key)	NO
variant_id	int	Reference to the definition of a variant class e.g. "tiny sample", "small sample", "lower quality", "medium quality", "good quality" or "best quality" (foreign key)	NO
url	nvarchar (255)	URL of the resource variant	NO
pixel_width	int	Where applicable (still- or moving image): the width in pixel *Default value: NULL*	YES
pixel_height	int	Where applicable (still- or moving image): the height in pixel *Default value: NULL*	YES
duration	int	Where applicable (sound or moving image): the duration in seconds *Default value: NULL*	YES

size	int	The size of the resource in bytes *Default value: NULL*	YES
mime_type	nvarchar (255)	Type of the resource as MIME type like image/jpeg; color as color/hexrgb *Default value: NULL*	YES

Table <u>ResourceVariant_Enum</u>

Classes for resource variants, values are predefined in the database

Column	Data type	Description	Nullable
<u>id</u>	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of resource variant class ("tiny sample", "small sample", "lower quality", "medium quality", "good quality" or "best quality")	NO
code	nvarchar (255)	Brief code equivalent to the (longer) label	NO
detail	nvarchar (MAX)	Additional detail text explaining the resource variant class	YES
quality_order	int	A positive number providing a filter mechanism for "tiny sample" to "best quality"; the smaller the number, the less quality a resource has *Default value: '0'*	NO

Table <u>SamplingEvent</u>

A sampling event may contain many sampling units

Column	Data type	Description	Nullable
<u>id</u>	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to the description to which these sampling data belong (foreign key)	NO

label	nvarchar (255)	Free-form text identifying a sampling event to humans. Sampling events have time, location, perhaps purpose and act as a container for multiple sampling units. *Default value: NULL*	YES
detail	nvarchar (MAX)	Free-form text giving detail or description of sampling event	YES
date_time	datetime	Date and time when the event occurred; single point or start of duration *Default value: NULL*	YES
datetimespan_end	datetime	Optional end of a time span or duration within which or during which the event occurred *Default value: NULL*	YES
geographic_area	nvarchar (255)	A geographic area at which the event occurred *Default value: NULL*	YES
geographic_area_uri	nvarchar (255)	Reference to a geographic area in DiversityGazetteers *Default value: NULL*	YES
coord_dec_latitude	float	Latitude of geographical coordinates in signed decimal degrees *Default value: NULL*	YES
coord_dec_longitude	float	Longitude of geographical coordinates in decimal degrees *Default value: NULL*	YES
coord_literal	nvarchar (255)	Free-form string, either in addition to or instead of code (a mapping to the controlled vocabulary may be unavailable or considered ambiguous) *Default value: NULL*	YES
coord_geodeticdatum	nvarchar (50)	Optional, only where knowledge of the geodetic datum is readily available; defaults to WGS84 used in GPS *Default value: NULL*	YES

Table <u>SamplingUnit</u>

Sampling unit data

Column	Data type	Description	Nullable
<u>id</u>	int	Database-internal ID of this record (primary key)	NO
sampling_event_id	int	Reference to a sampling event; keeps paired measurements together (several categorical or quantitative observations at the same time on the same object or object part) (foreign key)	NO
collection_specimen	nvarchar (255)	A collection specimen that is represented by the sampling unit *Default value: NULL*	YES
collection_specimen_uri	nvarchar (255)	Reference to a collection specimen in DiversityCollection *Default value: NULL*	YES

Table <u>SexStatus_Enum</u>

Values of sex status predefined according to SDD 1.1 rev 5

Column	Data type	Description	Nullable
<u>id</u>	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of sex status	NO
code	nvarchar (255)	Code of sex status	NO
abbreviation	nvarchar (255)	One or two (intuitive) characters	NO
detail	nvarchar (MAX)	Additional detail text explaining or commenting on the sex status definition	YES
display_order	int	A positive number defining the sequence in which sex status values are displayed *Default value: '0'*	NO

Table StatisticalMeasure_Enum

The statistical measures predefined according SDD 1.1 rev 5

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record, references BaseEntity (primary key)	NO
label	nvarchar (255)	Short label (or name) of statistical measure	NO
code	nvarchar (255)	Code of statistical measure according SDD 1.1 rev 5	NO
abbreviation	nvarchar (255)	Abbreviation of statistical measure	NO
display_order	int	A positive number defining the sequence in which statistical measures are displayed *Default value: '0'*	NO

Table TextDescriptorData

The text data of a description

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
description_id	int	Reference to description to which these data belong (foreign key)	NO
descriptor_id	int	Reference to a text descriptor to which the free-form text belongs (foreign key)	NO
content	nvarchar (MAX)	Free-form text referring to information on one descriptor	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the values	YES

Table TextSamplingData

Free-form text data recorded for a sampling event

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
sampling_unit_id	int	Reference to a sampling unit (foreign key)	NO
descriptor_id	int	Reference to descriptor to which the free-form text belongs (foreign key)	NO
content	nvarchar (MAX)	Free-form text referring to information on one descriptor	NO
notes	nvarchar (MAX)	Free-form text detailing special cases or additional data beyond the data	YES

Table Translation

The translations of entries related to BaseEntity

Column	Data type	Description	Nullable
id	int	Database-internal ID of this record (primary key)	NO
object_id	int	Reference to the object to which the translation belongs, references BaseEntity (foreign key)	NO
language_code	nvarchar (3)	Language of representation translation (ISO 639 language code)	NO
column_id	int	References the translated column name	NO
contents	nvarchar (MAX)	Translated contents	YES

Table TranslationColumn_Enum

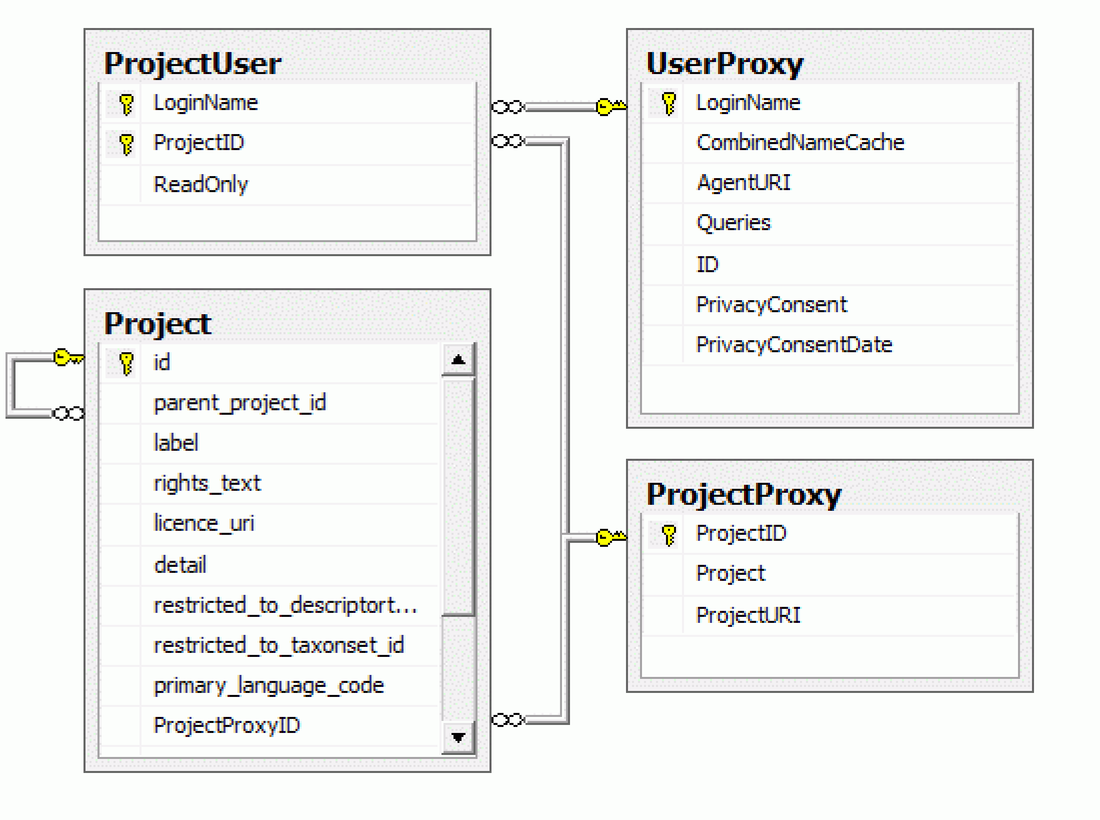
The TranslationColumn_Enum contains the column names that are translated in the Translation table

Column	Data type	Description	Nullable
id	int	Database-internal	NO

		object ID of this record (primary key)	
column	nvarchar (255)	Name of column that is translated in the Translation table	NO

Workbench project related tables

Information concerning the workbench projects and related tables are stored in the tables shown in the diagram below. The local project (table "Project") relates the workbench project (table "ProjectProxy") with attribute "ProjectProxyID". The tables "UserProxy", "ProjectUser" and "ProjectProxy" allow a independent administration of the basic functions related to projects and users.



Index

- ProjectProxy
- ProjectUser
- UserProxy

Table ProjectProxy

The projects as stored in the module DiversityProjects

Column	Data type	Description
ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
Project	nvarchar (50)	The name or title of the project as shown in a user interface (Projects are defined in DiversityProjects)

ProjectURI	nvarchar (255)	URI of a project in a remote module, e.g. refering to database DiversityProjects

Table <u>ProjectUser</u>

The projects that a user can access

Column	Data type	Description
<u>LoginName</u>	nvarchar (50)	A login name which the user uses for access the DivesityWorkbench, Microsoft domains, etc..
<u>ProjectID</u>	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
ReadOnly	bit	If the user has only read access to data of this project *Default value: (0)*

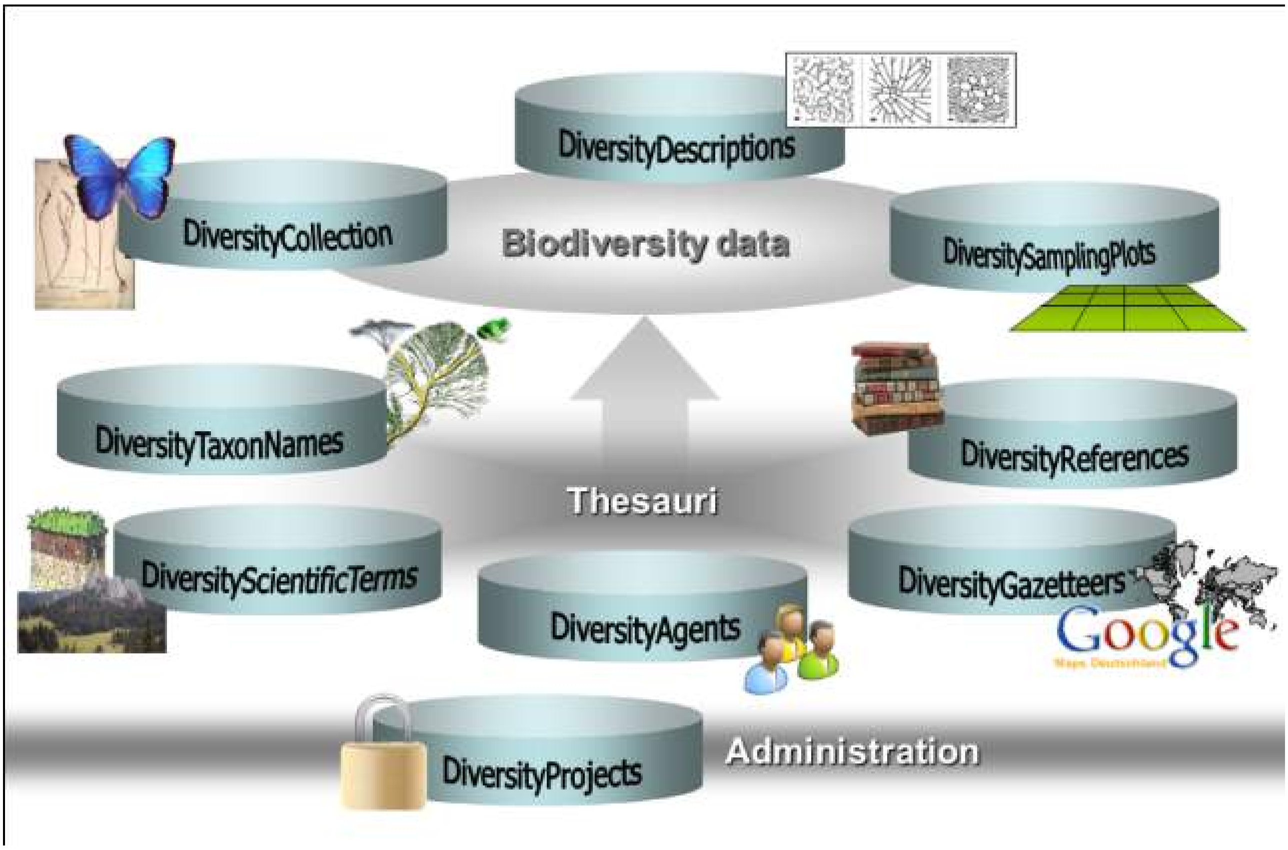
Table <u>UserProxy</u>

The user as stored in the module DiversityAgents

Column	Data type	Description
<u>LoginName</u>	nvarchar (50)	A login name which the user uses for access the DivesityWorkbench, Microsoft domains, etc..
CombinedNameCache	nvarchar (255)	The short name of the user, e.g. P. Smith
AgentURI	nvarchar (255)	URI of a user in a remote module, e.g. refering to database DiversityAgents
Queries	xml (MAX)	Queries created by the user
ID	int	ID of the user
PrivacyConsent	bit	If the user consents the storage of his user name in the database
PrivacyConsentDate	datetime	The time and date when the user consented or refused the storage of his user name in the database

Diversity Workbench

The Diversity Workbench is composed of components for building and managing biodiversity information, each of which focuses on a particular domain. Each component can provide services to the other components. DiversityDescriptions can link data to the modules DiversityCollection, DiversityTaxonNames, DiversityGazetteers and DiversityReferences as illustrated in the image below. DiversityProjects together with DiversityAgents provide support for administration of data access rights.



The modules communicate with each other to provide their services for the other modules.

Modules

The Diversity Workbench is a set of components for building and managing biodiversity information, each of which focuses on a particular domain.

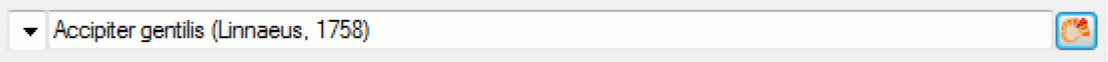
DiversityAgents	Administration of the agents, i.e. people and institutions which should be documented with e.g. th
DiversityCollection	Administration of the scientific collections, specimens within these collections and observations
DiversityDescriptions	Administration of the descriptive data
DiversityGazetteers	A data collection to enable the linking of geographical records with the Getty Thesaurus of Geogra German GN250 database and other sources of geographical names
DiversityProjects	Administration of projects
DiversityReferences	Administration of litarature references
DiversityTaxonNames	Administration of taxonomic names, their synonyms and hierarchical position

Each module provides services for the other modules. To use the service of a module, you need access to the database of the module and optionally the module application placed in your application directory.

Module related entry

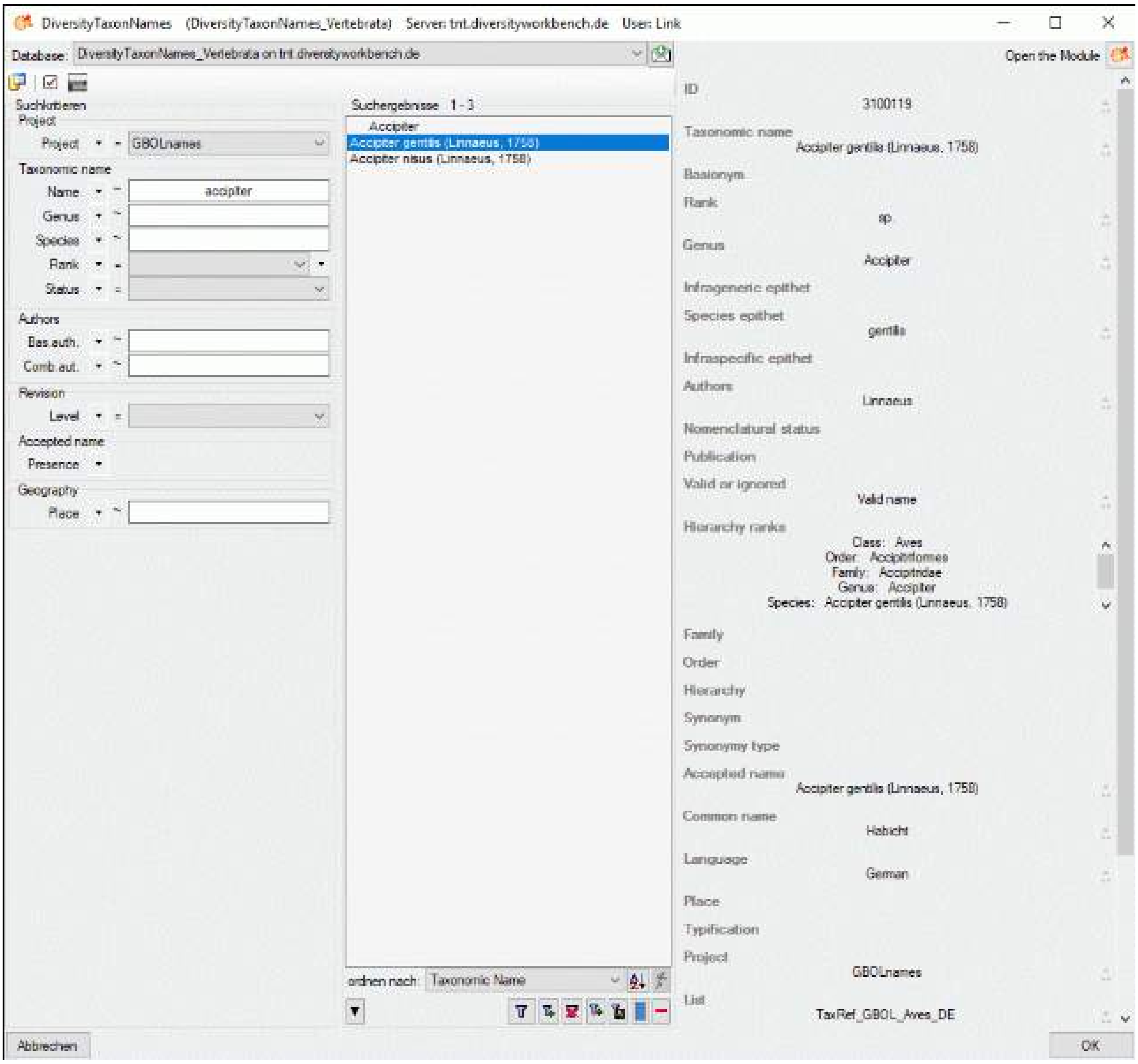
The Diversity Workbench is a set of components for building and managing biodiversity information, each of which focuses on a particular domain. Each module provides services for the other modules. To use the service of a module, you need access to the database of the module and optionally the module application placed in your application directory. Entries related to an external module have a standard interface in the main form. There are 2 states of this interface:

1 - the value is only set in the local database with no connection to the remote module



Accipiter gentilis (Linnaeus, 1758)

In this state, you can either type the value or select it from the values that are already available in the database. To get a list of the available values type the beginning of the value (you may use wildcards) and click on the ▾ button. If you want to set a relation to the remote module, click on the button. A window will open where you may select an entry from the foreign database.



DiversityTaxonNames (DiversityTaxonNames_Vertebrata) Server: tnt.diversityworkbench.de User: Link

Database: DiversityTaxonNames_Vertebrata on tnt.diversityworkbench.de

Project = GBOLnames

Name ~ accipiter

Suchergebnisse 1 - 3

- Accipiter
- Accipiter gentilis (Linnaeus, 1758)
- Accipiter nisus (Linnaeus, 1758)

ordnen nach: Taxonomic Name

ID: 3100119

Taxonomic name: Accipiter gentilis (Linnaeus, 1758)

Rank: sp

Genus: Accipiter

Species epithet: gentilis

Authors: Linnaeus

Valid or ignored: Valid name

Hierarchy ranks:
Class: Aves
Order: Accipitriformes
Family: Accipitridae
Genus: Accipiter
Species: Accipiter gentilis (Linnaeus, 1758)

Accepted name: Accipiter gentilis (Linnaeus, 1758)

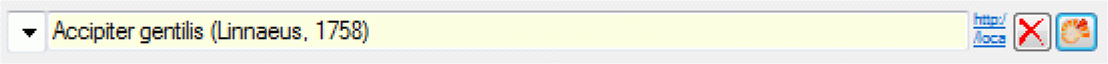
Common name: Habicht

Language: German

Project: GBOLnames

List: TaxRef_GBOL_Aves_DE

2 - the value is related to the remote module


Accipiter gentilis (Linnaeus, 1758)

If the value has a relation to the remote module, the interface will appear as shown above. To release the connection to the remote module click on the ✕button. If you need further information about the value, click on the button. This will open a form, showing an overview of the related value.

ID	3100119
Taxonomic name	Accipiter gentilis (Linnaeus, 1758)
Basionym	
Rank	sp.
Genus	Accipiter
Infrageneric epithet	
Species epithet	gentilis
Infraspecific epithet	
Authors	Linnaeus
Nomenclatural status	
Publication	
Valid or ignored	Valid name
Hierarchy ranks	Class: Aves Order: Accipitriformes Family: Accipitridae Genus: Accipiter Species: Accipiter gentilis (Linnaeus, 1758)
Family	
Order	
Hierarchy	
Synonym	
Synonymy type	
Accepted name	Accipiter gentilis (Linnaeus, 1758)
Common name	Habicht
Language	German
Place	
Typification	
Project	GBOLnames
List	TaxRef_GBOL_Aves_DE
Analysis	
Distribution	
Collection specimen	
List reference	
External database	Barthel & Helbig (2005)
External name URI	

If the client application of the module is available you can inspect the details of the entry.

3 - relation to a webservice

Some modules provide the possibility to link your data to an external webservice. For example DiversityTaxonNames gives you access to the taxonomic names of IndexFungorum. To establish a connection to an external webservice, click on the button. As with the link to modules within the Diversity Workbench a window will open where you can choose from either Diversity Workbench modules or external Webservices. See Webservice for further details

Webservice - foreign sources

Some modules within the Diversity Workbench provide the possibility to link your data to an external webservice. For example DiversityTaxonNames gives you access to the taxonomic names of IndexFungorum. To establish a connection to an external webservice, click on the button. A window will open where you can choose from either Diversity Workbench modules or external Webservices. The currently provided webservices are:

The Catalogue of Life

Index Fungorum

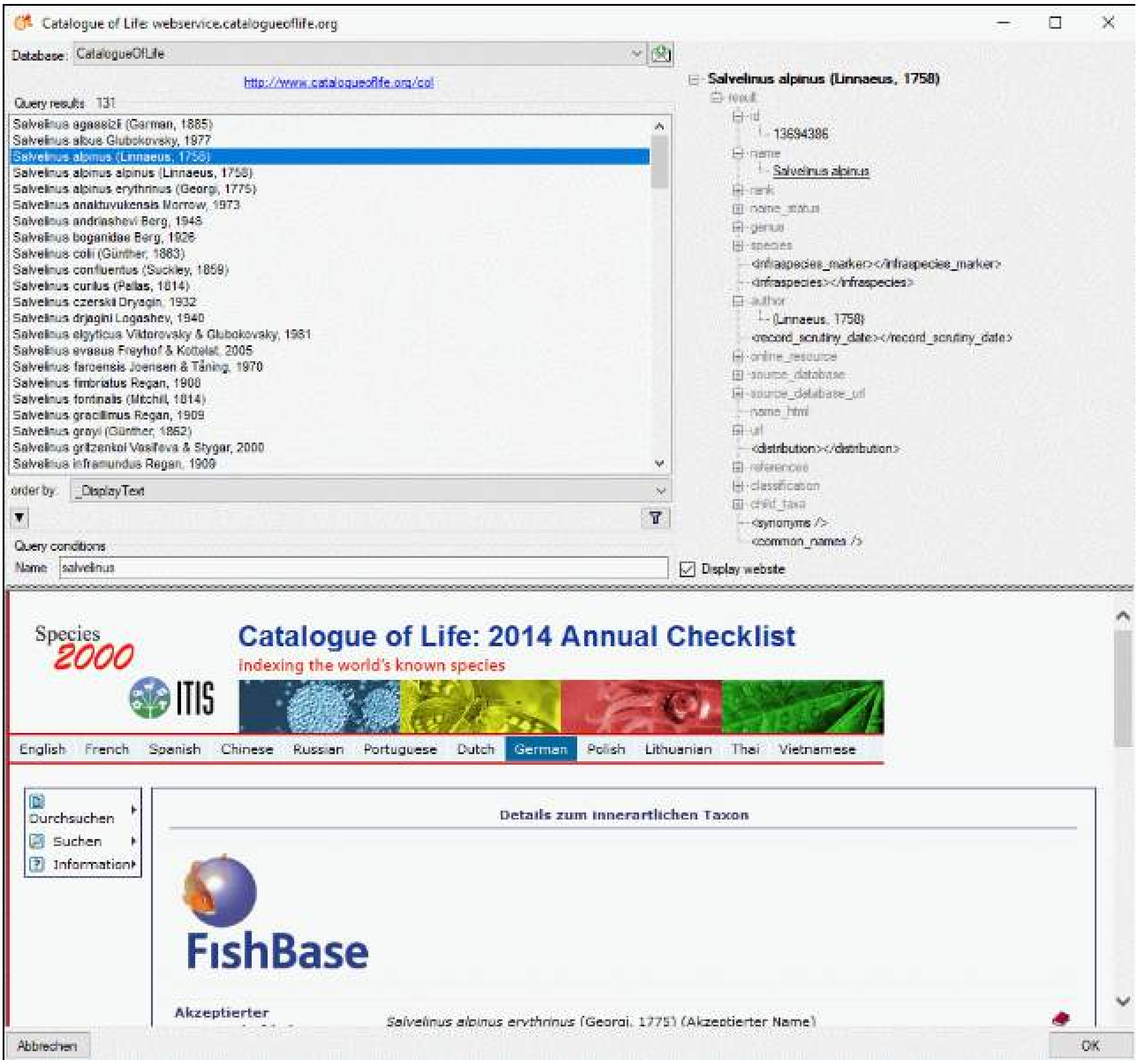
MycoBank Database

The Palaeontology Database

Pan-European Species directories Infrastructure

Catalogue of Life - webservice

Diversity Workbench provides the possibility to link your data to an external webservice. The webservice provided by the Catalogue of Life allows linkage of taxon names. To establish a connection to this external webservice, click on the button. A window will open where you can choose this webservice (see below). **Remark:** By selecting "CatalogueOfLife" you can search in the 2014 annual check list, by selecting "CatalogueOfLife_2" you can search in a newed, updated edition, which includes higher taxa.



Catalogue of Life: webservice.catalogueoflife.org

Database: CatalogueOfLife

http://www.catalogueoflife.org/col

Query results 131

```
Salvelinus agassizii (Garman, 1885)
Salvelinus albus Glubokovsky, 1977
Salvelinus alpinus (Linnaeus, 1758)
Salvelinus alpinus alpinus (Linnaeus, 1758)
Salvelinus alpinus erythrinus (Georgi, 1775)
Salvelinus anaktuvukensis Morrow, 1973
Salvelinus andriashevi Berg, 1948
Salvelinus boganidae Berg, 1926
Salvelinus colii (Günther, 1863)
Salvelinus confluentus (Suckley, 1859)
Salvelinus curilus (Pallas, 1814)
Salvelinus czerskii Dryagin, 1932
Salvelinus drjagini Logashev, 1940
Salvelinus elgyticus Viktorovsky & Glubokovsky, 1981
Salvelinus evasus Freyhof & Kottelat, 2005
Salvelinus faroensis Joensen & Tåning, 1970
Salvelinus fimbriatus Regan, 1908
Salvelinus fontinalis (Mitchill, 1814)
Salvelinus gracillimus Regan, 1909
Salvelinus grayi (Günther, 1862)
Salvelinus gritzenkoi Vasil'eva & Stygar, 2000
Salvelinus inframundus Regan, 1909
```

order by: _DisplayText

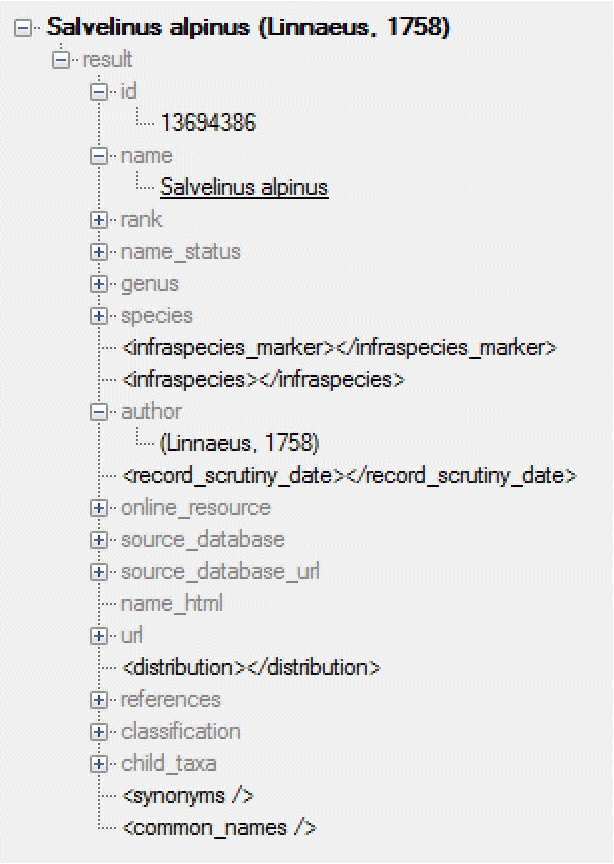
Query conditions

Name: salvelinus

```
Salvelinus alpinus (Linnaeus, 1758)
  result
    id
      13694386
    name
      Salvelinus alpinus
    rank
    name_status
    genus
    species
    <infraspecies_marker></infraspecies_marker>
    <infraspecies></infraspecies>
    author
      (Linnaeus, 1758)
    <record_scrutiny_date></record_scrutiny_date>
    online_resource
    source_database
    source_database_url
    name_html
    url
    <distribution></distribution>
    references
    classification
    child_taxa
    <synonyms />
    <common_names />
```

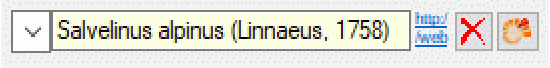
☑ Display website

In the field **Name** in Query conditions enter you search string and click on the button to start the query. In the list of the left upper part the results of the query will be listed. In the right part of the window additional information is shown as provided by the webservice. If available, the lower part of the window will show the webpage of the related information.



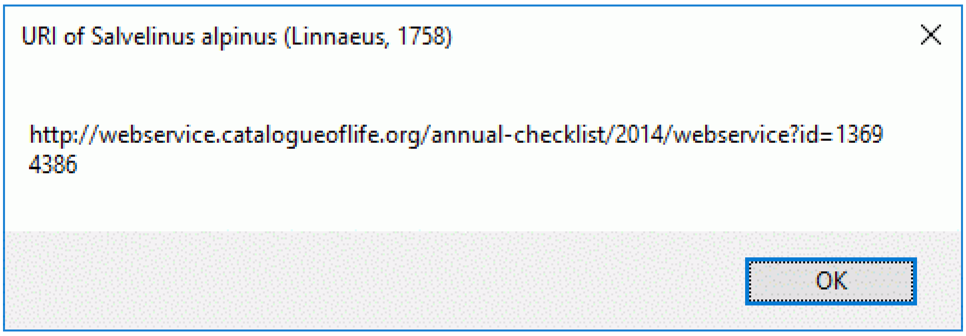
```
Salvelinus alpinus (Linnaeus, 1758)
  result
    id
      13694386
    name
      Salvelinus alpinus
    rank
    name_status
    genus
    species
    <infraspecies_marker></infraspecies_marker>
    <infraspecies></infraspecies>
    author
      (Linnaeus, 1758)
    <record_scrutiny_date></record_scrutiny_date>
    online_resource
    source_database
    source_database_url
    name_html
    url
    <distribution></distribution>
    references
    classification
    child_taxa
    <synonyms />
    <common_names />
```

Higher taxa and for synonyms the accepted name will be shown as e.g. shown above. To inspect one of these entries, click on the linked entry of the ID. To take the link from the webservice into your database choose one of the entries in the list and click OK. The entry will change as shown below.



Salvelinus alpinus (Linnaeus, 1758)

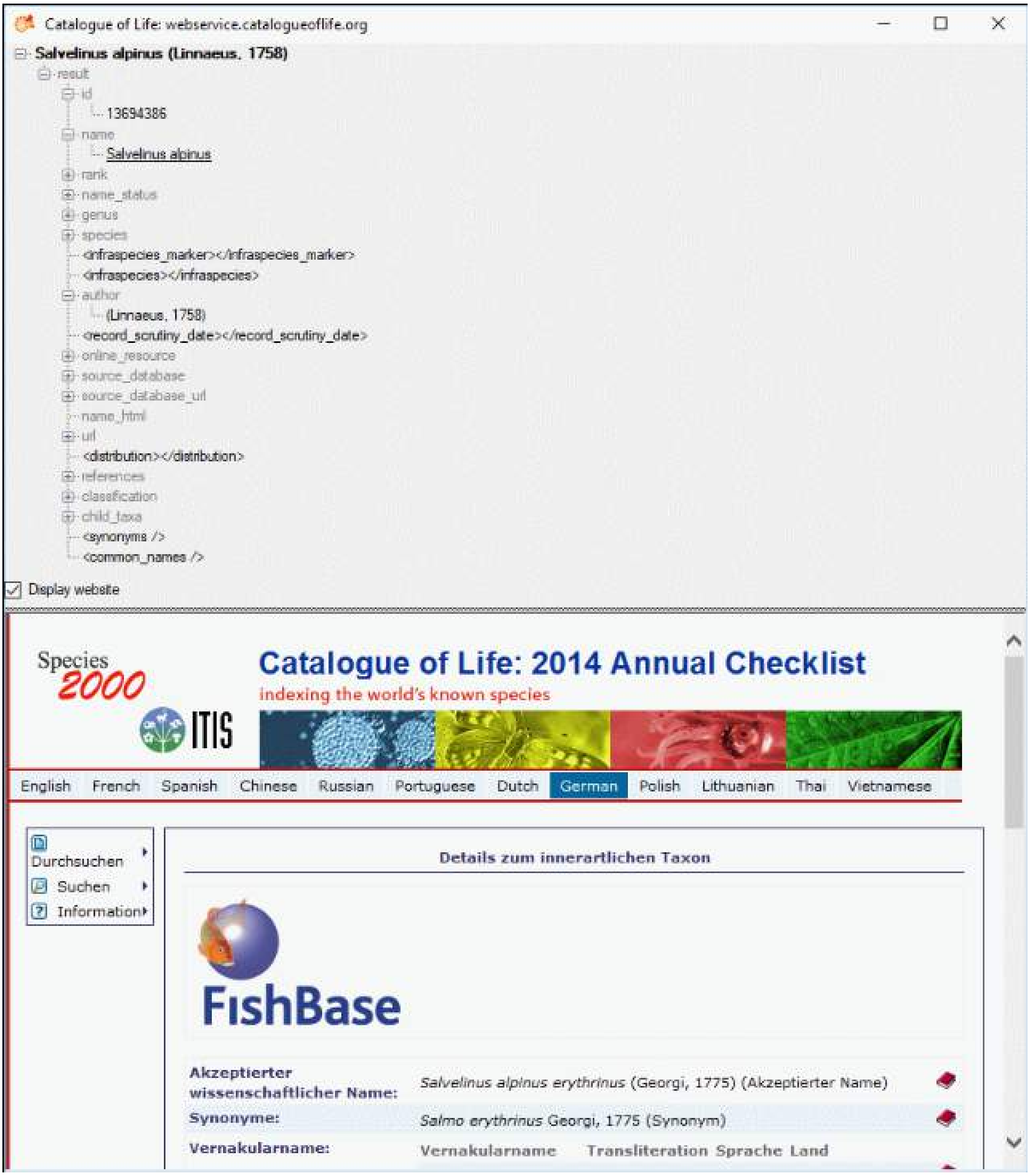
If you double-click on the link area a window will open, providing you with the retrieval information of the webservice.



URI of Salvelinus alpinus (Linnaeus, 1758)

http://webservice.catalogueoflife.org/annual-checklist/2014/webservice?id=13694386

To get the information related to an entry as provided by the webservice, click on the button. A window will open as shown below where the informations of the webservice are listed in the upper part. If available, additional informations provided on a corresponding website will be shown in the lower part.



```
Salvelinus alpinus (Linnaeus, 1758)
  result
    id
      13694386
    name
      Salvelinus alpinus
    rank
    name_status
    genus
    species
    <infraspecies_marker></infraspecies_marker>
    <infraspecies></infraspecies>
    author
      (Linnaeus, 1758)
    <record_scrutiny_date></record_scrutiny_date>
    online_resource
    source_database
    source_database_url
    name_html
    url
    <distribution></distribution>
    references
    classification
    child_taxa
    <synonyms />
    <common_names />
```

☑ Display website

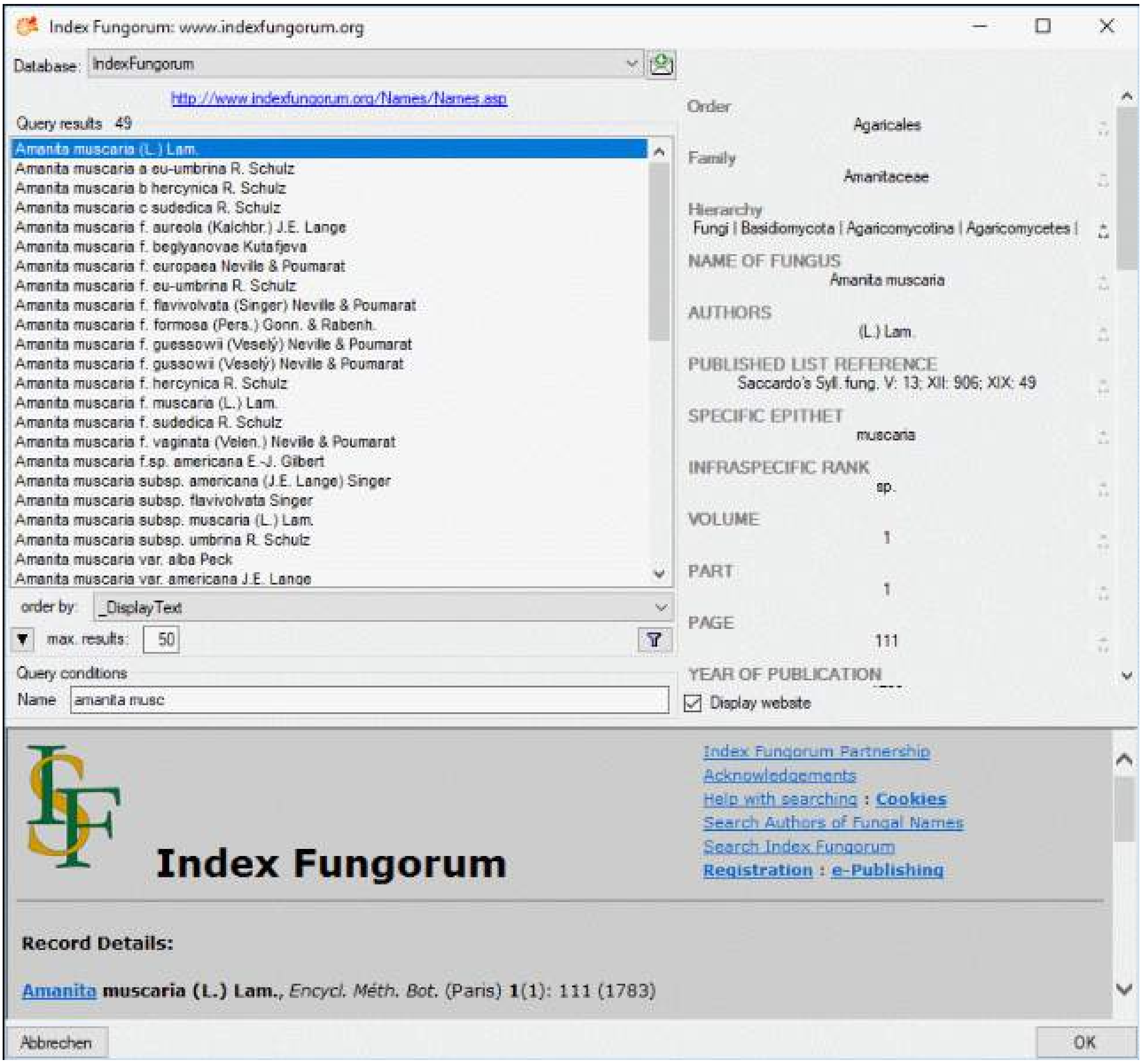
Details zum innerartlichen Taxon

Akzeptierter wissenschaftlicher Name:	*Salvelinus alpinus erythrinus* (Georgi, 1775) (Akzeptierter Name)
Synonyme:	*Salmo erythrinus* Georgi, 1775 (Synonym)
Vernakularname:	Vernakularname Transliteration Sprache Land

If you want to remove the link to the webservice, click on the ✕ button. This will only remove the relation to the webservice, not the cached name.

Index Fungorum - webservice

Diversity Workbench provides the possibility to link your data to an external webservice. The webservice provided by the IndexFungorum allows linkage of taxon names. To establish a connection to this external webservice, click on the button. A window will open where you can choose this webservice (see below).



Index Fungorum: www.indexfungorum.org

Database: IndexFungorum

http://www.indexfungorum.org/Names/Names.asp

Query results 49

Amanita muscaria (L.) Lam.
Amanita muscaria a eu-umbrina R. Schulz
Amanita muscaria b hercynica R. Schulz
Amanita muscaria c sudedica R. Schulz
Amanita muscaria f. aureola (Kalchbr.) J.E. Lange
Amanita muscaria f. beglyanovae Kutafjeva
Amanita muscaria f. europaea Nevile & Poumarat
Amanita muscaria f. eu-umbrina R. Schulz
Amanita muscaria f. flavivolvata (Singer) Neville & Poumarat
Amanita muscaria f. formosa (Pers.) Gonn. & Rabenh.
Amanita muscaria f. guessowii (Veselý) Neville & Poumarat
Amanita muscaria f. gussowii (Veselý) Neville & Poumarat
Amanita muscaria f. hercynica R. Schulz
Amanita muscaria f. muscaria (L.) Lam.
Amanita muscaria f. sudedica R. Schulz
Amanita muscaria f. vaginata (Velen.) Neville & Poumarat
Amanita muscaria f.sp. americana E.-J. Gilbert
Amanita muscaria subsp. americana (J.E. Lange) Singer
Amanita muscaria subsp. flavivolvata Singer
Amanita muscaria subsp. muscaria (L.) Lam.
Amanita muscaria subsp. umbrina R. Schulz
Amanita muscaria var. alba Peck
Amanita muscaria var. americana J.E. Lange

order by: _DisplayText

max. results: 50

Query conditions

Name: amanita musc

Order: Agaricales
Family: Amanitaceae
Hierarchy: Fungi | Basidiomycota | Agaricomycotina | Agaricomycetes |
NAME OF FUNGUS: Amanita muscaria
AUTHORS: (L.) Lam.
PUBLISHED LIST REFERENCE: Saccardo's Syll. fung. V: 13; XII: 906; XIX: 49
SPECIFIC EPITHET: muscaria
INFRASPECIFIC RANK: sp.
VOLUME: 1
PART: 1
PAGE: 111
YEAR OF PUBLICATION

☑ Display website

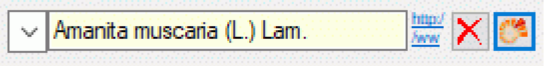
Index Fungorum

Index Fungorum Partnership
Acknowledgements
Help with searching : Cookies
Search Authors of Fungal Names
Search Index Fungorum
Registration : e-Publishing

Record Details:

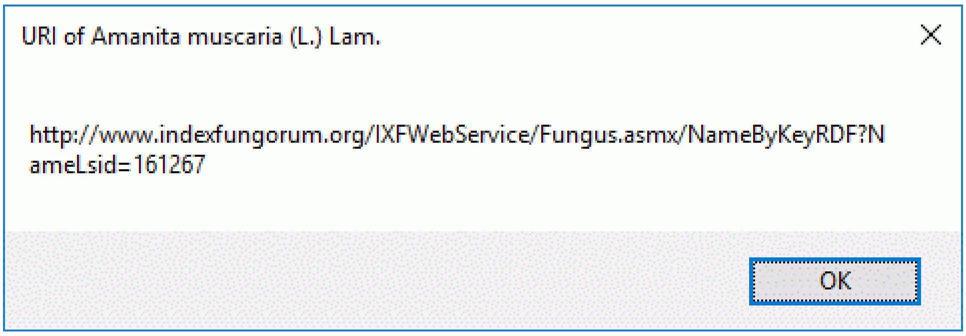
Amanita muscaria (L.) Lam., *Encycl. Méth. Bot.* (Paris) 1(1): 111 (1783)

Enter the query restriction for the name in the Name field in Query conditions. The maximal number of records you get can be set in the max. results field max. results: 50 (choose a low number if you have a slow connection to the internet). Then click on the search button to start the query. In the list of the left upper part the results of the query will be listed. In the right part of the window additional information is shown as provided by the webservice. For certain entries buttons will appear, as e.g. shown above for the basionym and the current name of a scientific name. Click on these buttons if you want to change to one of these related datasets from the webservice. If available, the informations provided on the corresponding website is shown in the lower part. To take the link from the webservice into your database choose one of the entries and click OK. The entry will change as shown below.



Amanita muscaria (L.) Lam.

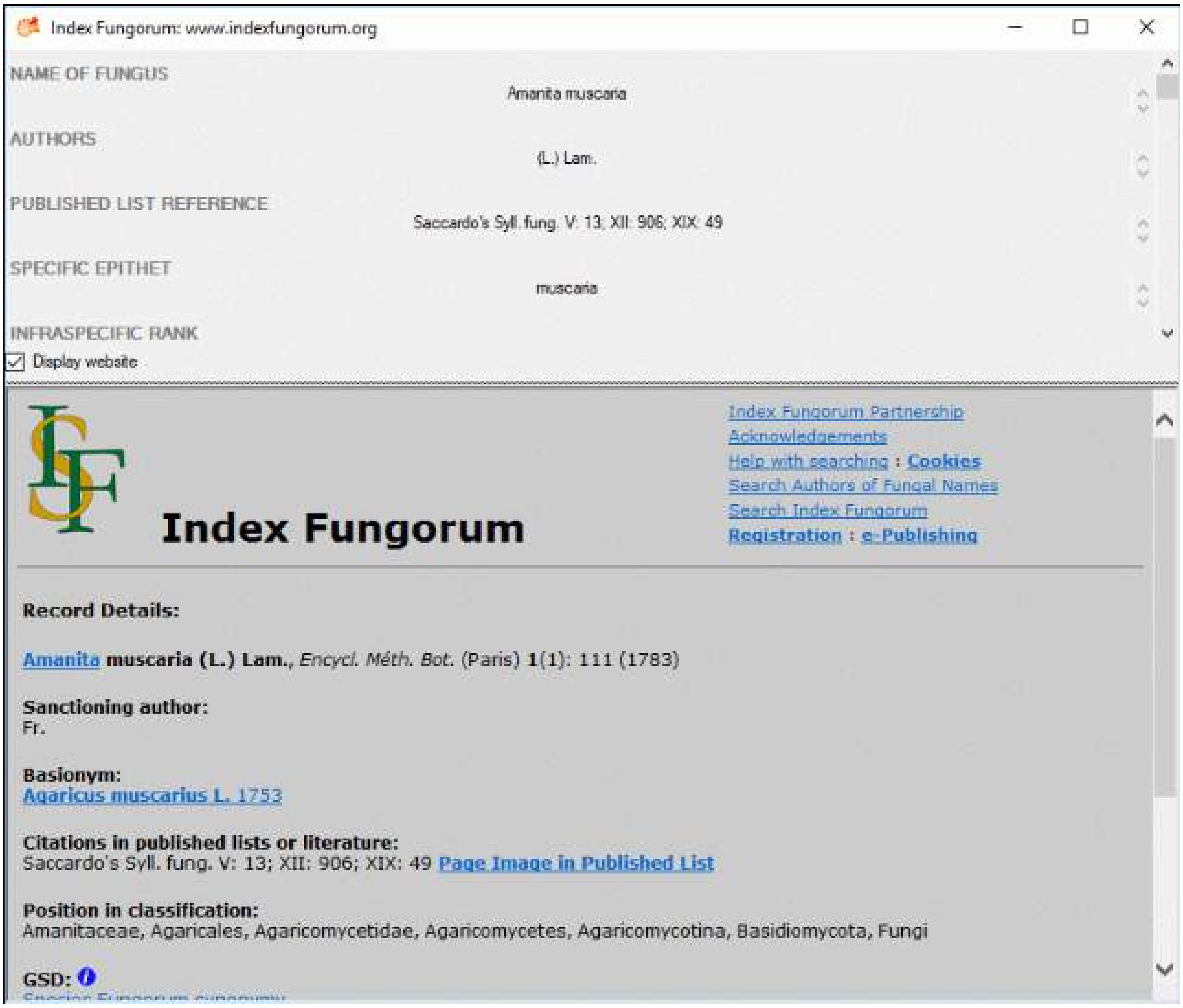
If you double-click on the link area http://www a window will open, providing you with the retrieval information of the webservice.



URI of Amanita muscaria (L.) Lam.

http://www.indexfungorum.org/IXFWebService/Fungus.asmx/NameByKeyRDF?NameLsid=161267

To get the whole information related to this entry as provided by the webservice, click on the button. A window will open as shown below where the informations of the webservice are listed, If available, the lower part will show the corresponding informations of a website.



Index Fungorum: www.indexfungorum.org

NAME OF FUNGUS: Amanita muscaria

AUTHORS: (L.) Lam.

PUBLISHED LIST REFERENCE: Saccardo's Syll. fung. V: 13; XII: 906; XIX: 49

SPECIFIC EPITHET: muscaria

INFRASPECIFIC RANK

☑ Display website

Record Details:

Amanita muscaria (L.) Lam., *Encycl. Méth. Bot.* (Paris) **1**(1): 111 (1783)

Sanctioning author:
Fr.

Basionym:
Agaricus muscarius L. 1753

Citations in published lists or literature:
Saccardo's Syll. fung. V: 13; XII: 906; XIX: 49 Page Image in Published List

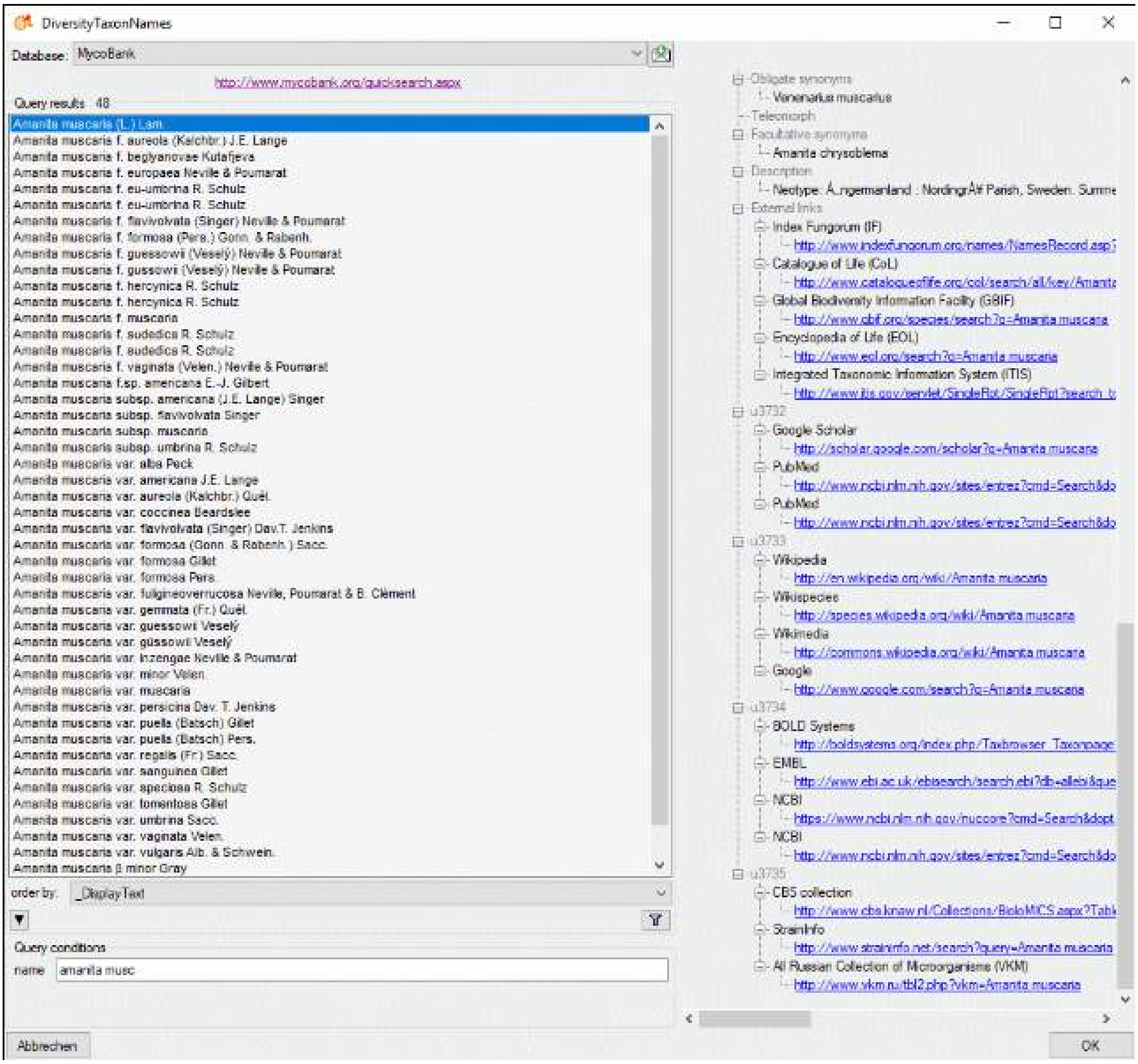
Position in classification:
Amanitaceae, Agaricales, Agaricomycetidae, Agaricomycetes, Agaricomycotina, Basidiomycota, Fungi

GSD:

If you want to remove the link to the webservice, click on the the ✗ button. This will only remove the relation to the webservice, not the cached name.

MycoBank Database - webservice

Some modules within the DiversityWorkbench provide the possibility to link your data to an external webservice. For example DiversityTaxonNames gives you access to the taxonomic names of the MycoBank database. To establish a connection to this webservice, click on the button. A window will open where you can choose MycoBank from the database list (see below).



Database: MycoBank

http://www.mycobank.org/quicksearch.aspx

Query results 48

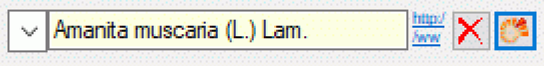
Amanita muscaria (L.) Lam.
Amanita muscaria f. aureola (Kalchbr.) J.E. Lange
Amanita muscaria f. beglyanovae Kutafjeva
Amanita muscaria f. europaea Neville & Poumarat
Amanita muscaria f. eu-umbrina R. Schulz
Amanita muscaria f. eu-umbrina R. Schulz
Amanita muscaria f. flavivolvata (Singer) Neville & Poumarat
Amanita muscaria f. formosa (Pers.) Gonn. & Rabenh.
Amanita muscaria f. guessowii (Veselý) Neville & Poumarat
Amanita muscaria f. gussowii (Veselý) Neville & Poumarat
Amanita muscaria f. hercynica R. Schulz
Amanita muscaria f. hercynica R. Schulz
Amanita muscaria f. muscaria
Amanita muscaria f. sudedica R. Schulz
Amanita muscaria f. sudedica R. Schulz
Amanita muscaria f. vaginata (Velen.) Neville & Poumarat
Amanita muscaria f.sp. americana E.-J. Gilbert
Amanita muscaria subsp. americana (J.E. Lange) Singer
Amanita muscaria subsp. flavivolvata Singer
Amanita muscaria subsp. muscaria
Amanita muscaria subsp. umbrina R. Schulz
Amanita muscaria var. alba Peck
Amanita muscaria var. americana J.E. Lange
Amanita muscaria var. aureola (Kalchbr.) Quél.
Amanita muscaria var. coccinea Beardslee
Amanita muscaria var. flavivolvata (Singer) Dav.T. Jenkins
Amanita muscaria var. formosa (Gonn. & Rabenh.) Sacc.
Amanita muscaria var. formosa Gillet
Amanita muscaria var. formosa Pers.
Amanita muscaria var. fuligineoverrucosa Neville, Poumarat & B. Clément
Amanita muscaria var. gemmata (Fr.) Quél.
Amanita muscaria var. guessowii Veselý
Amanita muscaria var. güssowii Veselý
Amanita muscaria var. inzengae Neville & Poumarat
Amanita muscaria var. minor Velen.
Amanita muscaria var. muscaria
Amanita muscaria var. persicina Dav. T. Jenkins
Amanita muscaria var. puella (Batsch) Gillet
Amanita muscaria var. puella (Batsch) Pers.
Amanita muscaria var. regalis (Fr.) Sacc.
Amanita muscaria var. sanguinea Gillet
Amanita muscaria var. speciosa R. Schulz
Amanita muscaria var. tomentosa Gillet
Amanita muscaria var. umbrina Sacc.
Amanita muscaria var. vaginata Velen.
Amanita muscaria var. vulgaris Alb. & Schwein.
Amanita muscaria β minor Gray

order by: _DisplayText

Query conditions
name: amanita musc

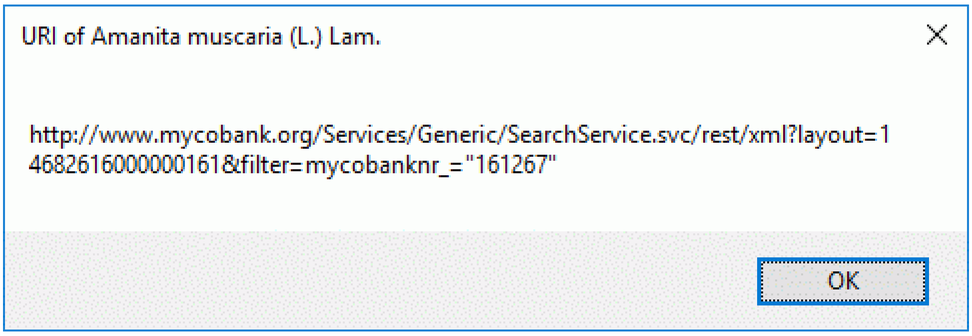
```
Obligate synonyms
    Venenarius muscarius
Teleomorph
Facultative synonyms
    Amanita chrysoblema
Description
    Neotype: Ã‚ngermanland : NordingrÃ¥ Parish, Sweden. Summe
External links
    Index Fungorum (IF)
        http://www.indexfungorum.org/names/NamesRecord.asp?
    Catalogue of Life (CoL)
        http://www.catalogueoflife.org/col/search/all/key/Amanita
    Global Biodiversity Information Facility (GBIF)
        http://www.gbif.org/species/search?q=Amanita muscaria
    Encyclopedia of Life (EOL)
        http://www.eol.org/search?q=Amanita muscaria
    Integrated Taxonomic Information System (ITIS)
        http://www.itis.gov/servlet/SingleRpt/SingleRpt?search_t
u3732
    Google Scholar
        http://scholar.google.com/scholar?q=Amanita muscaria
    PubMed
        http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=Search&do
    PubMed
        http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=Search&do
u3733
    Wikipedia
        http://en.wikipedia.org/wiki/Amanita muscaria
    Wikispecies
        http://species.wikipedia.org/wiki/Amanita muscaria
    Wikimedia
        http://commons.wikipedia.org/wiki/Amanita muscaria
    Google
        http://www.google.com/search?q=Amanita muscaria
u3734
    BOLD Systems
        http://boldsystems.org/index.php/Taxbrowser_Taxonpage
    EMBL
        http://www.ebi.ac.uk/ebisearch/search.ebi?db=allebi&que
    NCBI
        https://www.ncbi.nlm.nih.gov/nuccore?cmd=Search&dopt
    NCBI
        http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=Search&do
u3735
    CBS collection
        http://www.cbs.knaw.nl/Collections/BioloMICS.aspx?Tabl
    StrainInfo
        http://www.straininfo.net/search?query=Amanita muscaria
    All Russian Collection of Microorganisms (VKM)
        http://www.vkm.ru/tbl2.php?vkm=Amanita muscaria
```

Enter the query restriction for the name in the **Name** field in Query conditions. Click on the search button to start the query. In the list in the left upper part the results of the query will be listed. On the right part of the window additional information is shown as provided by the webservice. If available, the information provided on the corresponding website is shown in the lower part. To include the link from the webservice into your database choose one of the entries and click OK. The entry will change as shown below.



Amanita muscaria (L.) Lam.

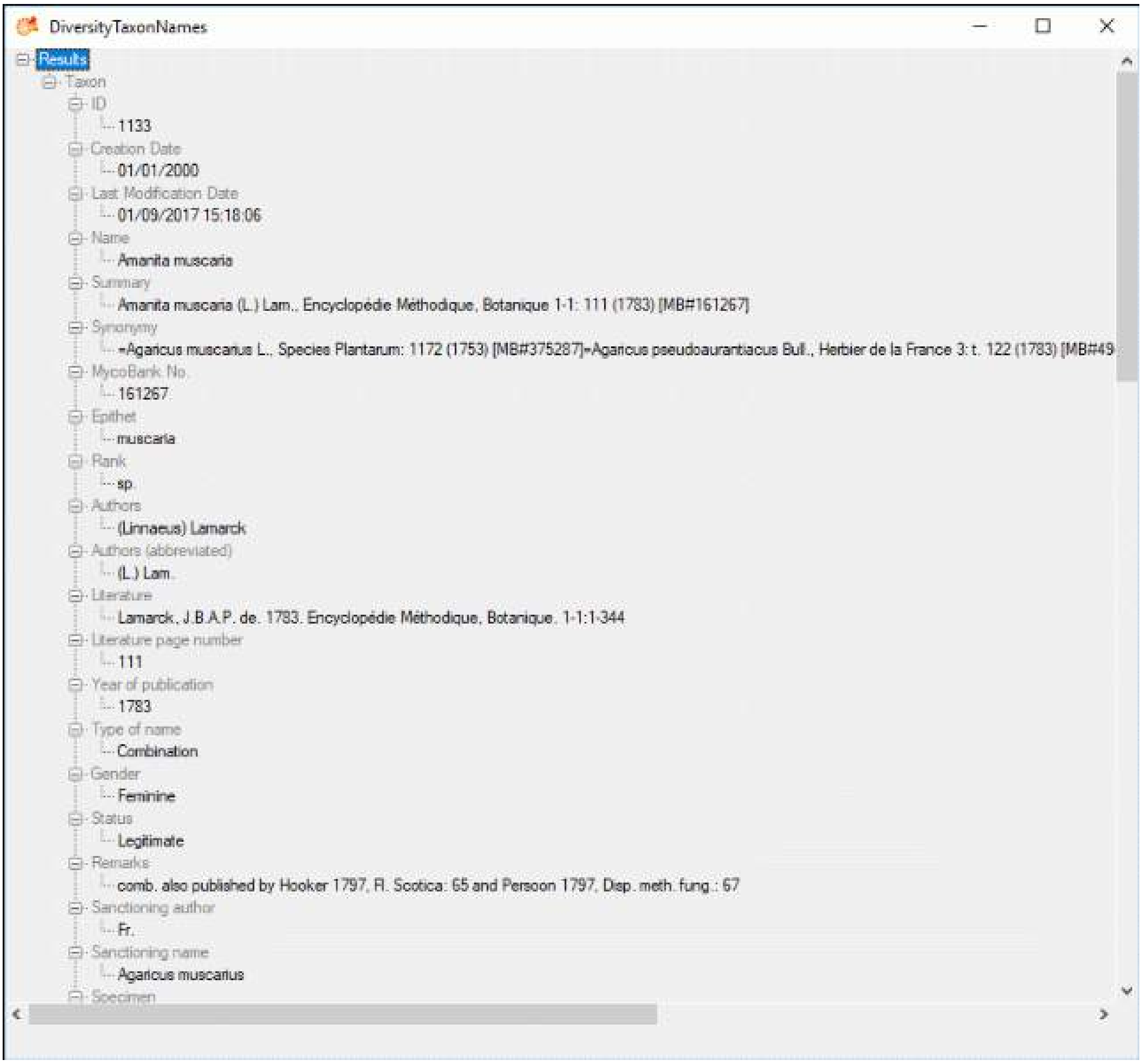
If you double-click on the link area , a window will open providing you with the retrieval information of the webservice.



URI of Amanita muscaria (L.) Lam.

http://www.mycobank.org/Services/Generic/SearchService.svc/rest/xml?layout=14682616000000161&filter=mycobanknr_="161267"

To receive the entire information related to this entry as provided by the webservice click on the button. A window will open as shown below where information on the webservice is listed. If available, the lower part will show the corresponding information of a website.

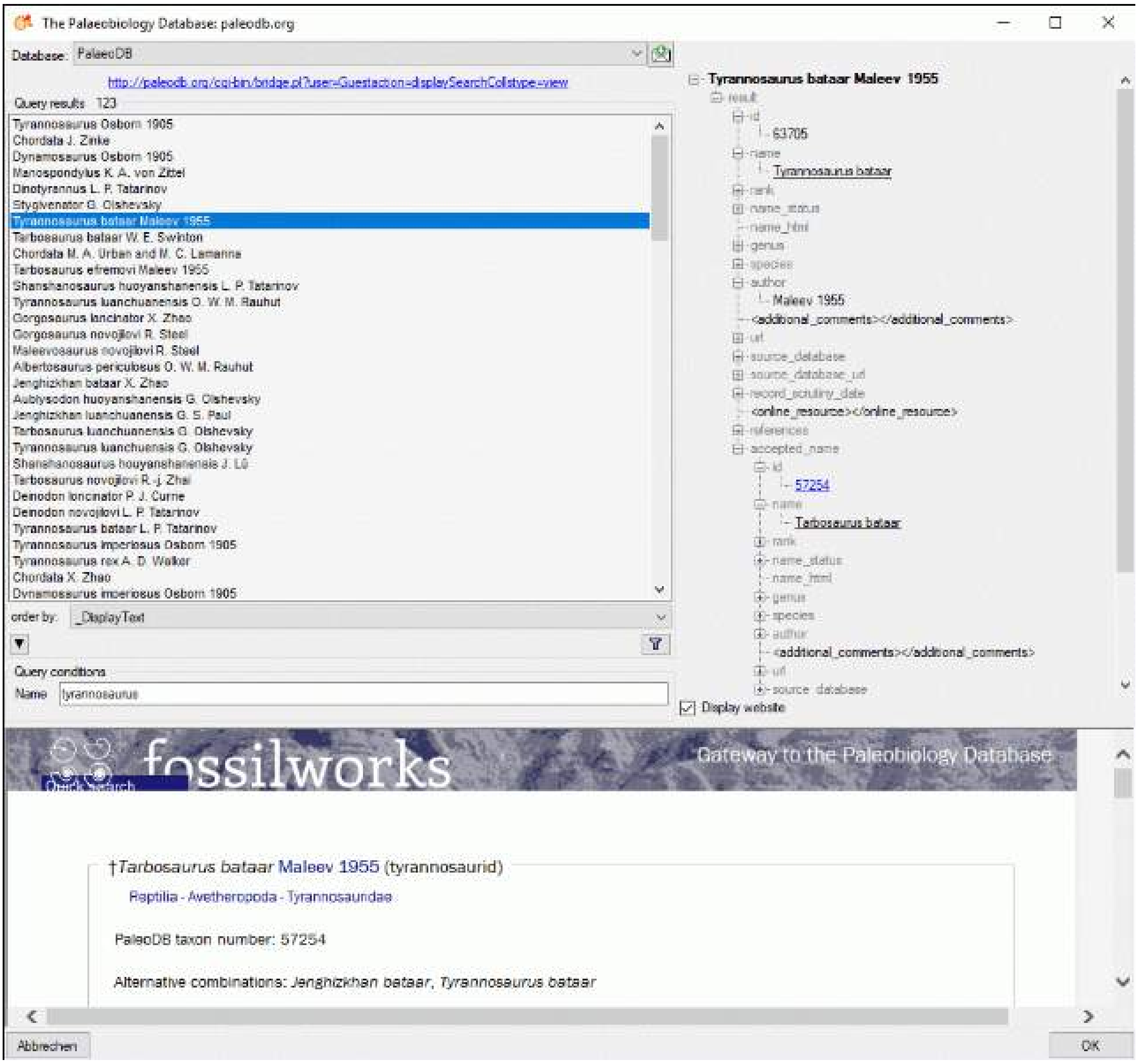


```
Results
  Taxon
    ID
      1133
    Creation Date
      01/01/2000
    Last Modification Date
      01/09/2017 15:18:06
    Name
      Amanita muscaria
    Summary
      Amanita muscaria (L.) Lam., Encyclopédie Méthodique, Botanique 1-1: 111 (1783) [MB#161267]
    Synonymy
      =Agaricus muscarius L., Species Plantarum: 1172 (1753) [MB#375287]=Agaricus pseudoaurantiacus Bull., Herbier de la France 3: t. 122 (1783) [MB#49
    MycoBank No.
      161267
    Epithet
      muscaria
    Rank
      sp.
    Authors
      (Linnaeus) Lamarck
    Authors (abbreviated)
      (L.) Lam.
    Literature
      Lamarck, J.B.A.P. de. 1783. Encyclopédie Méthodique, Botanique. 1-1:1-344
    Literature page number
      111
    Year of publication
      1783
    Type of name
      Combination
    Gender
      Feminine
    Status
      Legitimate
    Remarks
      comb. also published by Hooker 1797, Fl. Scotica: 65 and Persoon 1797, Disp. meth. fung.: 67
    Sanctioning author
      Fr.
    Sanctioning name
      Agaricus muscarius
    Specimen
```

If you wish to remove the link to the webservice, click on the ✗ button. This will only remove the relation to the webservice, not the cached name.

The Palaeontolgy Database - webservice

Diversity Workbench provides the possibility to link your data to an external webservice. The webservice provided by the Palaeontology Database allows linkage of taxon names. To establish a connection to this external webservice, click on the button. A window will open where you can choose this webservice (see below).



Database: PaleoDB

http://paleodb.org/cgi-bin/bridge.pl?user=Guestaction=displaySearchCollstype=view

Query results 123

Tyrannosaurus Osborn 1905
Chordata J. Zinke
Dynamosaurus Osborn 1905
Manospondylus K. A. von Zittel
Dinotyrannus L. P. Tatarinov
Stygivenator G. Olshevsky
Tyrannosaurus bataar Maleev 1955
Tarbosaurus bataar W. E. Swinton
Chordata M. A. Urban and M. C. Lamanna
Tarbosaurus efremovi Maleev 1955
Shanshanosaurus huoyanshanensis L. P. Tatarinov
Tyrannosaurus luanchuanensis O. W. M. Rauhut
Gorgosaurus lancinator X. Zhao
Gorgosaurus novojilovi R. Steel
Maleevosaurus novojilovi R. Steel
Albertosaurus periculosus O. W. M. Rauhut
Jenghizkhan bataar X. Zhao
Aublysodon huoyanshanensis G. Olshevsky
Jenghizkhan luanchuanensis G. S. Paul
Tarbosaurus luanchuanensis G. Olshevsky
Tyrannosaurus luanchuensis G. Olshevsky
Shanshanosaurus houyanshanensis J. Lü
Tarbosaurus novojilovi R.-j. Zhai
Deinodon lancinator P. J. Currie
Deinodon novojilovi L. P. Tatarinov
Tyrannosaurus bataar L. P. Tatarinov
Tyrannosaurus imperiosus Osborn 1905
Tyrannosaurus rex A. D. Walker
Chordata X. Zhao
Dynamosaurus imperiosus Osborn 1905

order by: _DisplayText

Query conditions

Name: tyrannosaurus

```
Tyrannosaurus bataar Maleev 1955
  result
    id
      63705
    name
      Tyrannosaurus bataar
    rank
    name_status
    name_html
    genus
    species
    author
      Maleev 1955
    <additional_comments></additional_comments>
    url
    source_database
    source_database_url
    record_scrutiny_date
    <online_resource></online_resource>
    references
    accepted_name
      id
        57254
      name
        Tarbosaurus bataar
      rank
      name_status
      name_html
      genus
      species
      author
      <additional_comments></additional_comments>
      url
      source_database
```

☑ Display website

fossilworks

Quick Search

Gateway to the Paleobiology Database

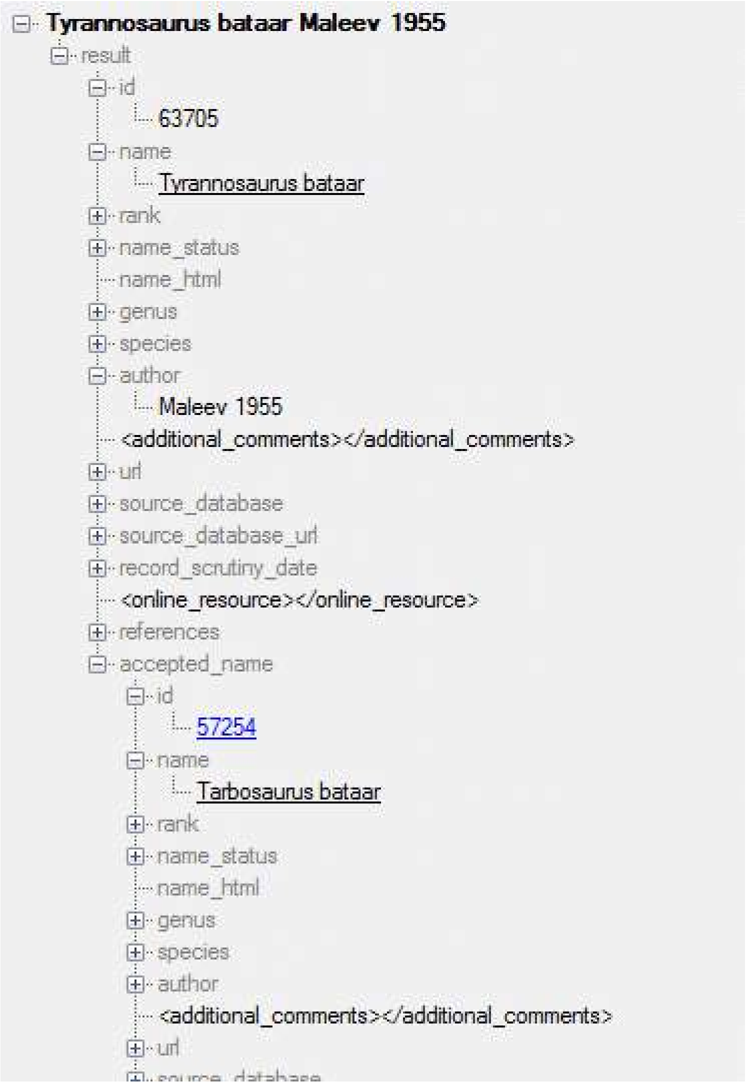
†*Tarbosaurus bataar* Maleev 1955 (tyrannosaurid)

Reptilia - Avetheropoda - Tyrannosauridae

PaleoDB taxon number: 57254

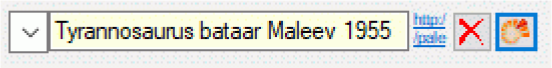
Alternative combinations: *Jenghizkhan bataar, Tyrannosaurus bataar*

In the field **Name** in Query conditions enter you search string and click on the button to start the query. In the list of the left upper part the results of the query will be listed. In the right part of the window additional information is shown as provided by the webservice. The lower part of the window will show the webpage of the related information.



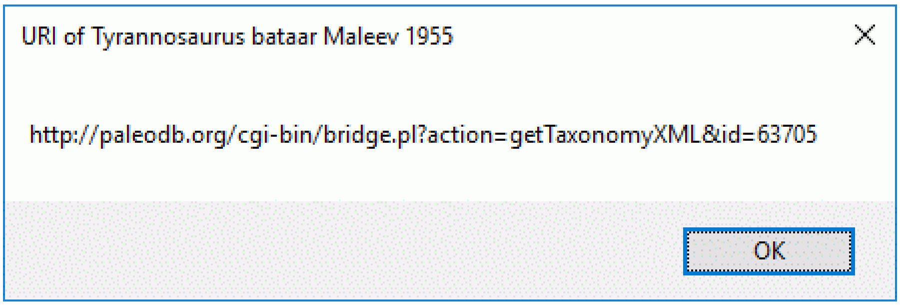
```
Tyrannosaurus bataar Maleev 1955
    result
        id
            63705
        name
            Tyrannosaurus bataar
        rank
        name_status
        name_html
        genus
        species
        author
            Maleev 1955
        <additional_comments></additional_comments>
        url
        source_database
        source_database_url
        record_scrutiny_date
        <online_resource></online_resource>
        references
        accepted_name
            id
                57254
            name
                Tarbosaurus bataar
            rank
            name_status
            name_html
            genus
            species
            author
            <additional_comments></additional_comments>
            url
            source_database
```

For synonyms, the accepted name will be shown as well as e.g. shown above. To change to the accepted name, click on the linked entry of the ID - in the example above id: 57254. To take the link from the webservice into your database choose one of the entries in the list and click OK. The entry will change as shown below.



Tyrannosaurus bataar Maleev 1955

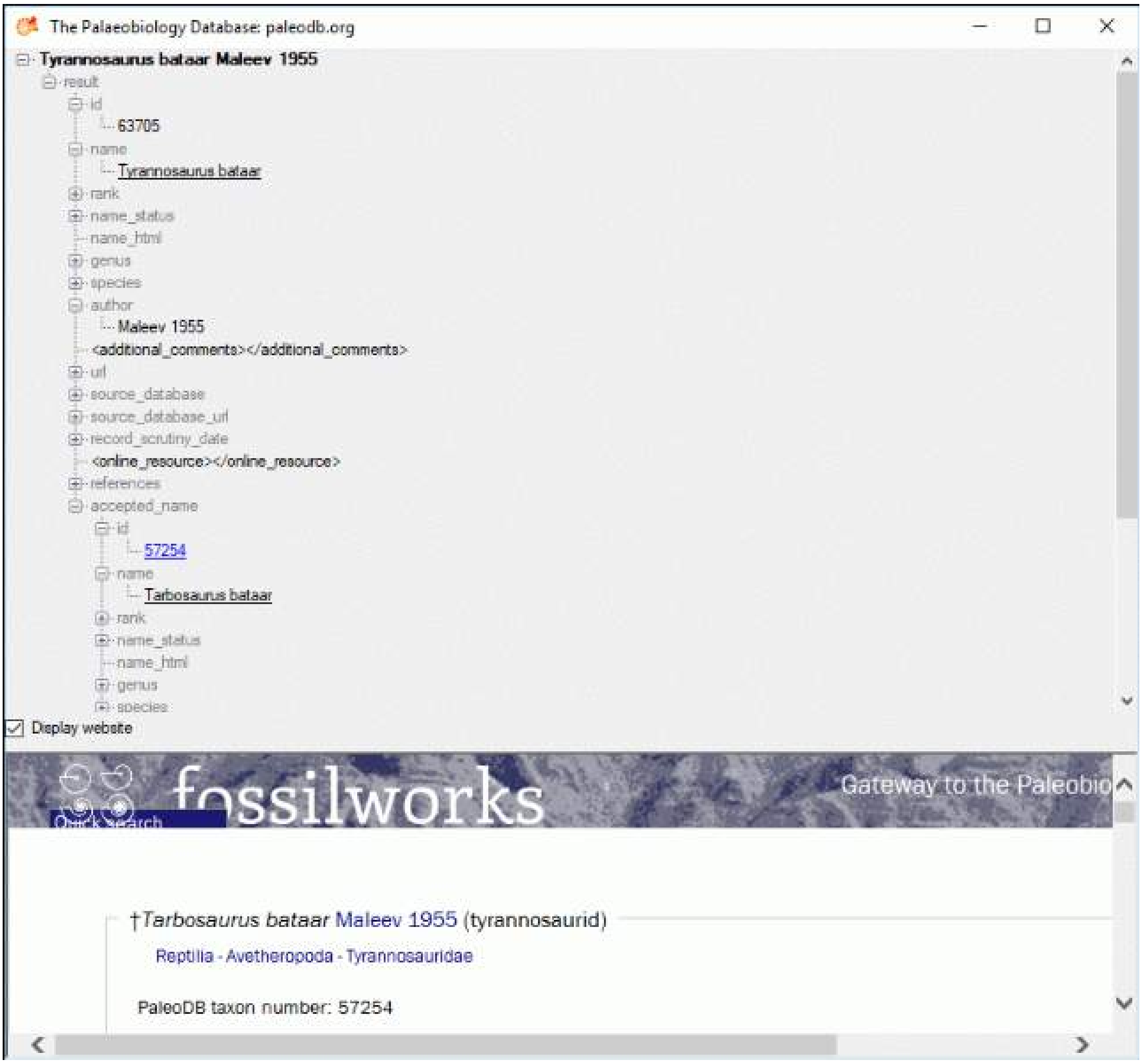
If you double-click on the link area a window will open, providing you with the retrieval information of the webservice.



URI of Tyrannosaurus bataar Maleev 1955

http://paleodb.org/cgi-bin/bridge.pl?action=getTaxonomyXML&id=63705

To get the information related to an entry as provided by the webservice, click on the button. A window will open as shown below where the informations of the webservice are listed in the upper part. If available, additional informations provided on a corresponding website will be shown in the lower part.



```
⊟ Tyrannosaurus bataar Maleev 1955
    ⊟ result
        ⊟ id
            63705
        ⊟ name
            Tyrannosaurus bataar
        ⊞ rank
        ⊞ name_status
          name_html
        ⊞ genus
        ⊞ species
        ⊟ author
            Maleev 1955
          <additional_comments></additional_comments>
        ⊞ url
        ⊞ source_database
        ⊞ source_database_url
        ⊞ record_scrutiny_date
          <online_resource></online_resource>
        ⊞ references
        ⊟ accepted_name
            ⊟ id
                57254
            ⊟ name
                Tarbosaurus bataar
            ⊞ rank
            ⊞ name_status
              name_html
            ⊞ genus
            ⊞ species
```

☑ Display website

†*Tarbosaurus bataar* Maleev 1955 (tyrannosaurid)

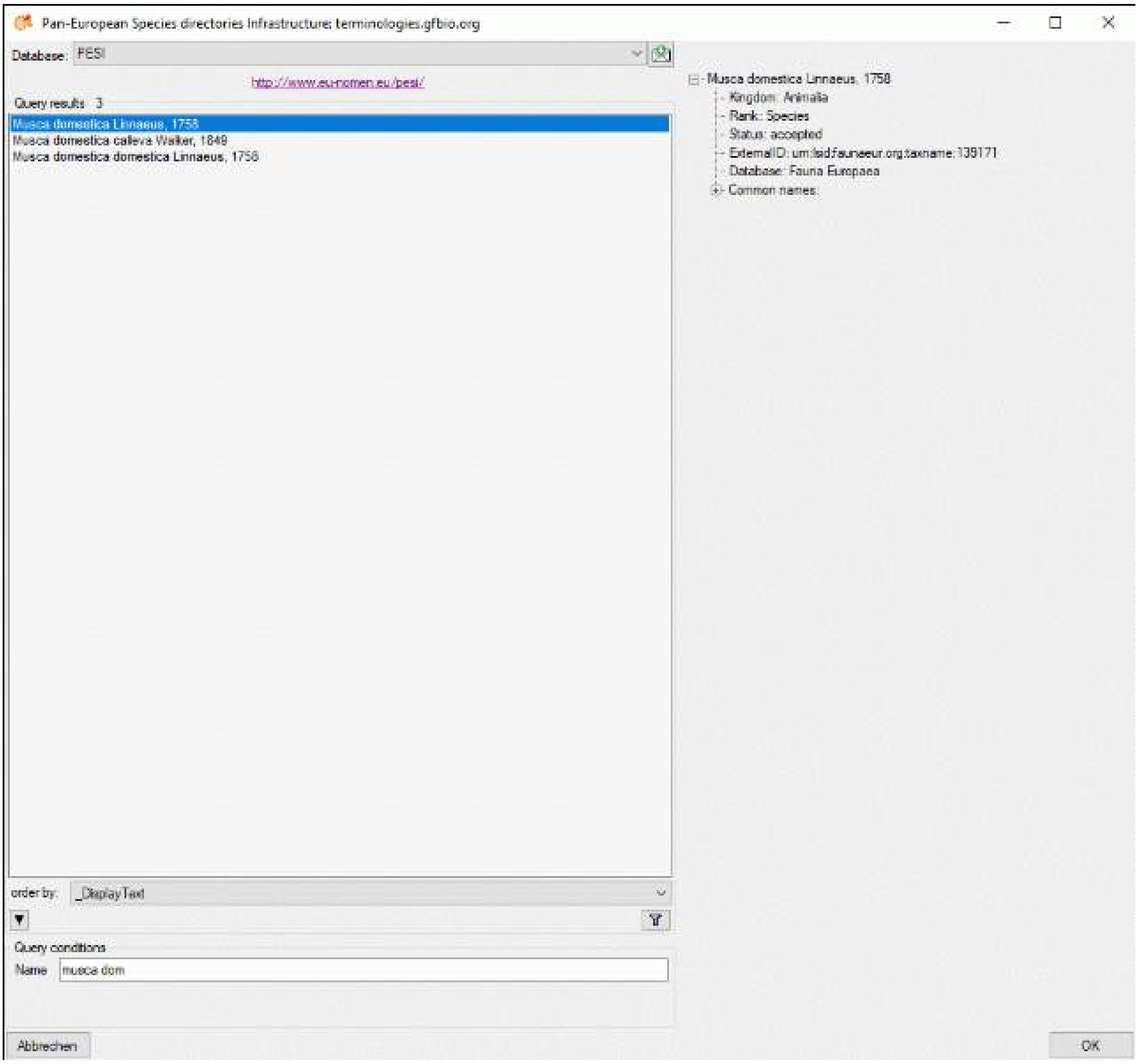
Reptilia - Avetheropoda - Tyrannosauridae

PaleoDB taxon number: 57254

If you want to remove the link to the webservice, click on the ✕ button. This will only remove the relation to the webservice, not the cached name.

Pan-European Species directories Infrastructure - webservice

Some modules within the DiversityWorkbench provide the possibility to link your data to an external webservice. For example DiversityTaxonNames gives you access to the taxonomic names of the Pan-European Species directories Infrastructure (PESI). To establish a connection to this webservice, click on the button. A window will open where you can choose PESI from the database list (see below).



Database: PESI

http://www.eu-nomen.eu/pesi/

Query results 3

Musca domestica Linnaeus, 1758
Musca domestica calleva Walker, 1849
Musca domestica domestica Linnaeus, 1758

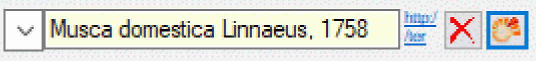
Musca domestica Linnaeus, 1758
- Kingdom: Animalia
- Rank: Species
- Status: accepted
- ExternalID: urn:lsid:faunaeur.org:taxname:139171
- Database: Fauna Europaea
- Common names:

order by: _DisplayText

Query conditions

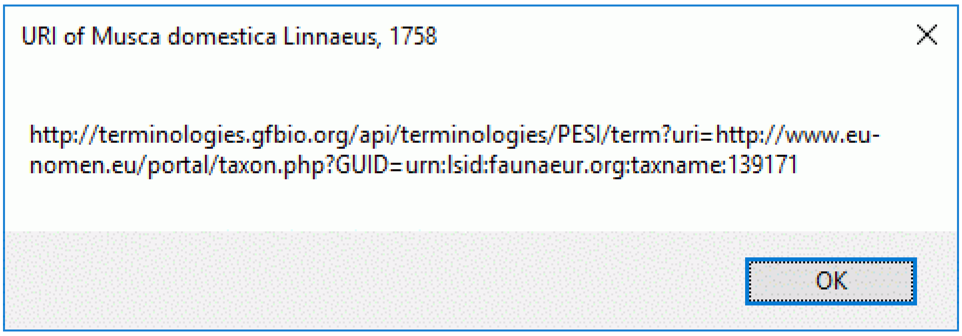
Name: musca dom

Enter the query restriction for the name in the **Name** field in Query conditions. Click on the search button to start the query. In the list in the left upper part the results of the query will be listed. On the right part of the window additional information is shown as provided by the webservice. If available, the information provided on the corresponding website is shown in the lower part. To include the link from the webservice into your database choose one of the entries and click OK. The entry will change as shown below.



Musca domestica Linnaeus, 1758

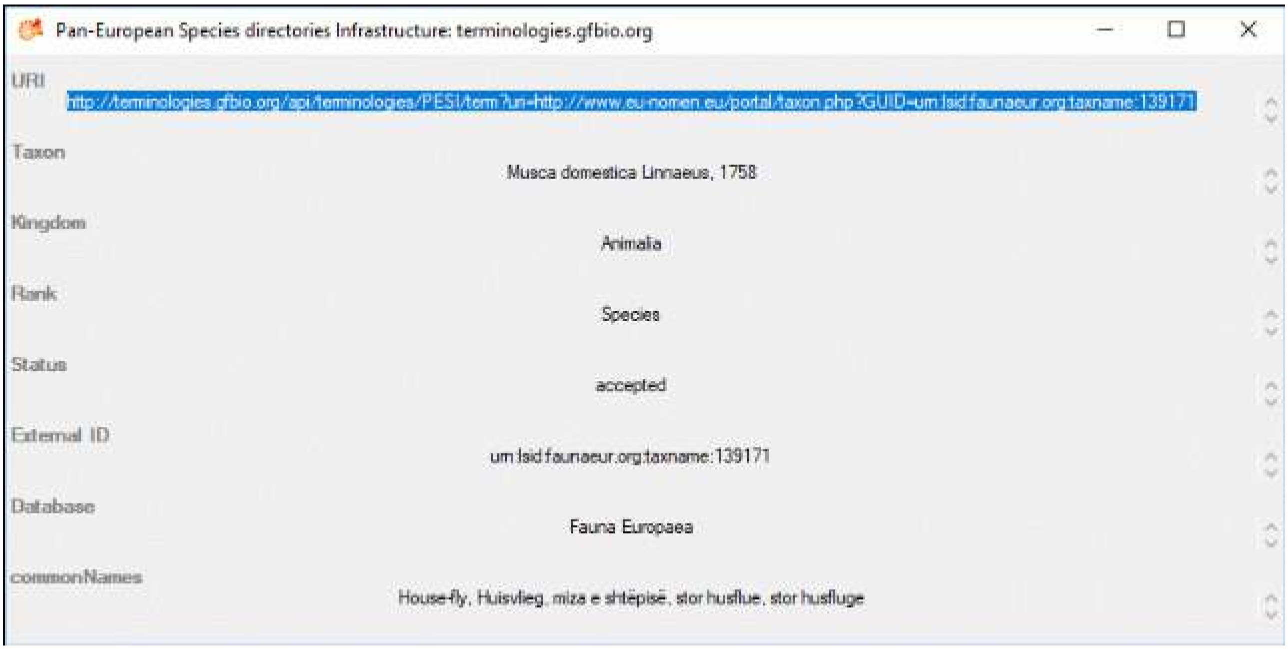
If you double-click on the link area , a window will open providing you with the retrieval information of the webservice.



URI of Musca domestica Linnaeus, 1758

http://terminologies.gfbio.org/api/terminologies/PESI/term?uri=http://www.eu-nomen.eu/portal/taxon.php?GUID=urn:lsid:faunaeur.org:taxname:139171

To receive the entire information related to this entry as provided by the webservice click on the button. A window will open as shown below where information on the webservice is listed. If available, the lower part will show the corresponding information of a website.



Pan-European Species directories Infrastructure: terminologies.gfbio.org

URI: http://terminologies.gfbio.org/api/terminologies/PESI/term?uri=http://www.eu-nomen.eu/portal/taxon.php?GUID=urn:lsid:faunaeur.org:taxname:139171
Taxon: Musca domestica Linnaeus, 1758
Kingdom: Animalia
Rank: Species
Status: accepted
External ID: urn:lsid:faunaeur.org:taxname:139171
Database: Fauna Europaea
commonNames: House-fly, Huisvlieg, miza e shtëpisë, stor husflue, stor husfluge

If you wish to remove the link to the webservice, click on the ✗button. This will only remove the relation to the webservice, not the cached name.