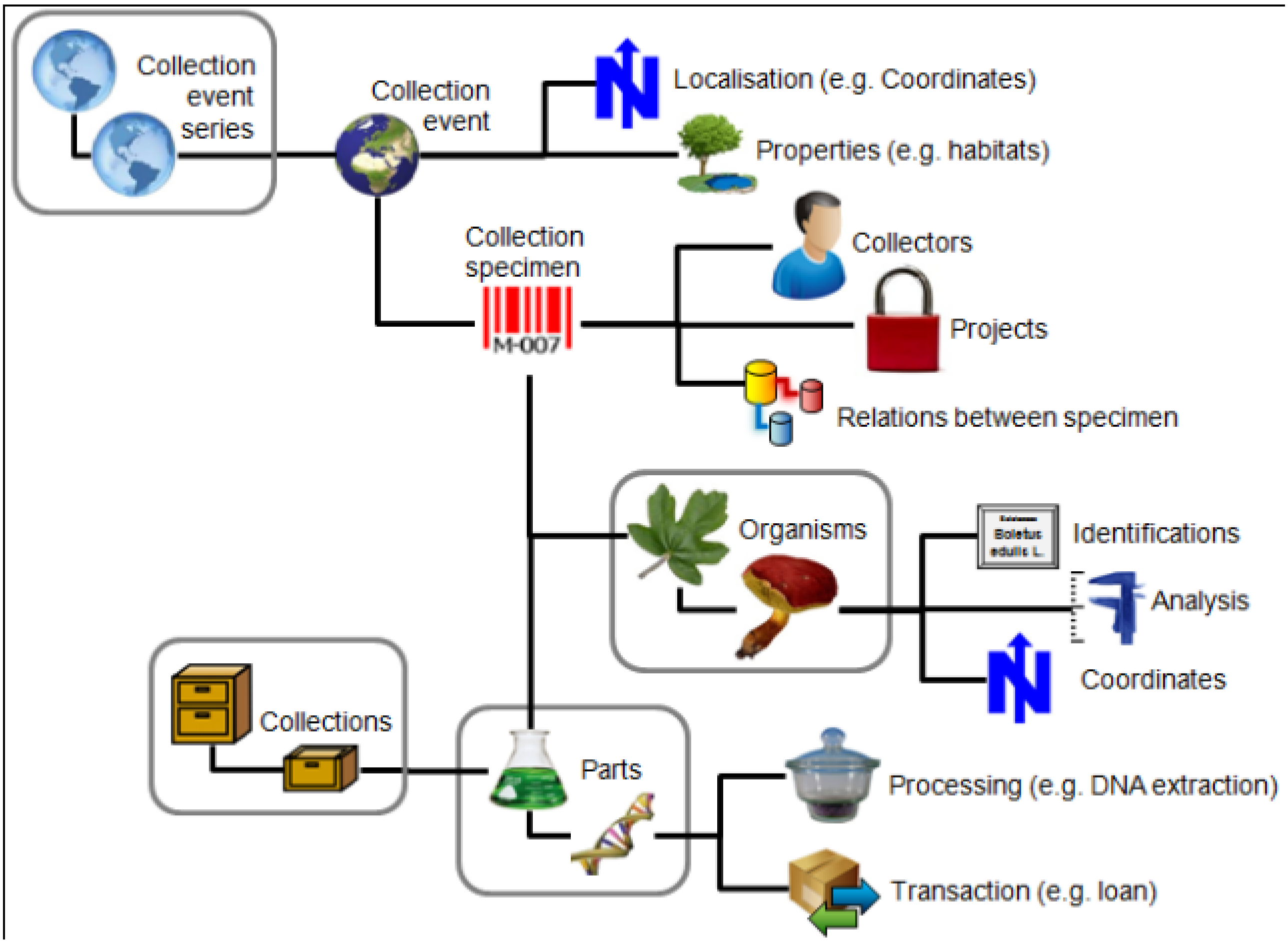
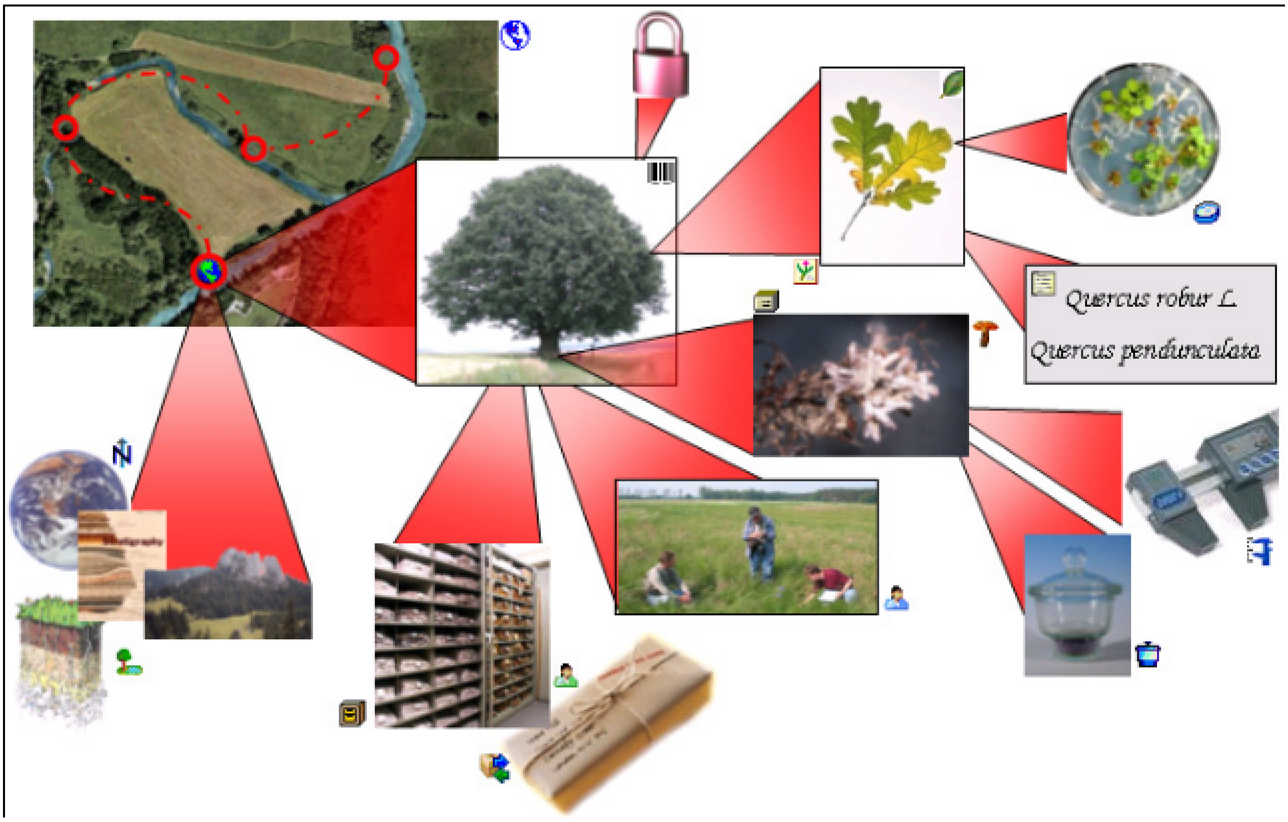
DiversityCollection

DiversityCollection (Version 3) is part of the database framework DiversityWorkbench. Within this framework the application DiversityCollection is confined to the management of specimens in scientific collections. In this context it is designed to document any action concerning the collection, storage, exchange and treatment of specimens in a collection and is also appropriate to store observation data. DiversityCollection is distinguished from other collection management systems by its focus on biological relations between organisms collected together as one or more specimens (e.g. host, parasite and hyperparasite, symbionts etc.). Any module within the Diversity Workbench is focused on a specific data domain. DiversityCollection keeps only data connected with the handling of collection specimens and observations. Data of other realms like e.g. taxonomy are handled in separate modules. For an overview of the available modules see DiversityWorkbench. DiversityCollection might also be used as a stand-alone application.

The image below gives you an overview of the main parts of DiversityCollection. The 4 squares indicate the possibility of a hierarchy where for example one organism can grow on another.



The image below gives an overview of some typical data depicted in DiversityCollection together with the symbols used throughout the program. A typical specimen may have been collected at a CollectionEvent during an expedition. The site of the CollectionEvent may be localized and characterized. The collectors collected twigs of the plant and fungi from the roots. They store the samples as herbarium sheets and specimens preserved by other methods in a collection. The manager sent some of the samples for which he had a request from a requester to another collection. The samples were collected as part of a project. Certain parts were cultivated, analysed and processed. The organisms on the specimen were identified several times. Images were taken for the EventSeries, the CollectionEvent, the CollectionSpecimen as well as organisms and part of this specimen.



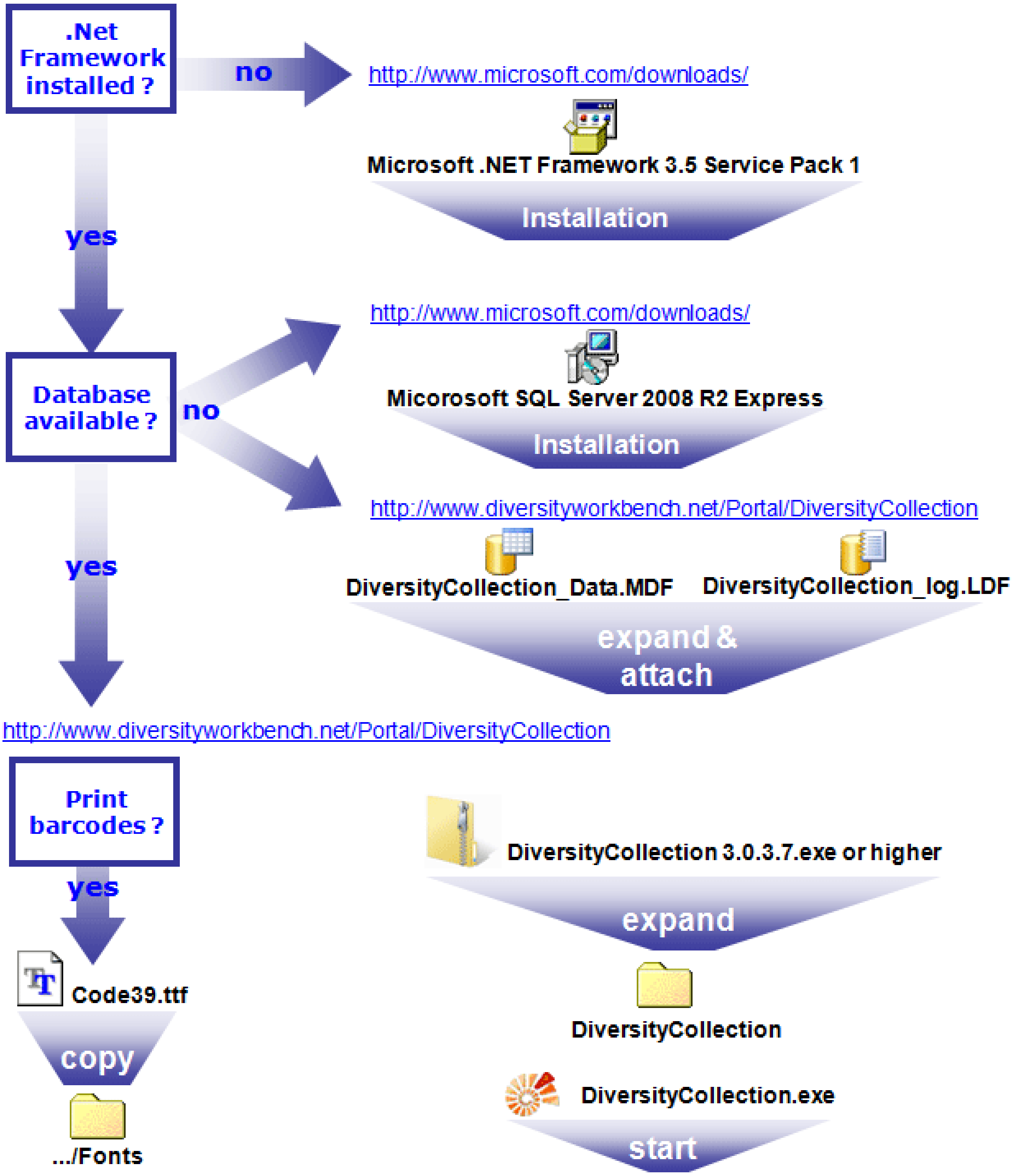
DiversityCollection 3 is based on Microsoft SQL-Server 2008 and the .Net Framework, Version 3.5.

For licence and copyright see the licence section.

Installation

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

The image below gives an overview of the installations and files needed.



Client

The client is based on the .Net framework version 3.5 from Microsoft. If not already present, you need to install the framework first. Download and install the Microsoft .NET Framework (e.g. dotnetfx35.exe) - start the program and follow the installation instructions (see http://www.microsoft.com/downloads/ for the latest versions). Version 2.0 is compatible with older operating systems like Windows 2000. For later operating systems use the latest version available.

Download the files for DiversityCollection from http://www.diversityworkbench.net/Portal/ provided as a zip archive. Copy all files (DiversityCollection.exe , DiversityCollection.chm , DiversityWorkbench.dll) into your DiversityWorkbench directory. To print barcodes of the font Code 39 the file Code39.ttf must be copied to the folder C:\WINNT\Fonts.

After the installation make sure to get the latest updates from http://windowsupdate.microsoft.com/.

Database

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

Menu

Overview of the menu in DiversityCollection

Connection

Database ...	Choose one of the databases available on the server. Only databases to which the user has access permission will be listed.
Module connections ...	Edit the connections to the other modules within the DiversityWorkbench.
Transfer previous settings	Transfer the settings for IP-Address and port of the server, name of the database, login etc. of a previous version of the client to the current version.
Quit	Quit the application and stop all processes started by the application.

Query

Show query	Show or hide the query list.
Predefined queries	All predefined queries will be listed.
Scan mode	Change to scan mode to open the data set of a specimen by scanning the barcode.

Grid

Specimen ...	Change to the grid mode to edit the data set of the Specimen in a list.
Organisms ...	Change to the grid mode to edit the data set of the Organisms in a list.
Parts ...	Change to the grid mode to edit the data set of the SpecimenParts in a list.
Collection events ...	Change to the grid mode to edit the data set of the CollectionEvents in a list.
Event series ...	Change to the grid mode to edit the data set of the CollectionEventSeries in a list.

Data

Import	
Import wizard ...	Import data from tab-separated text files.
Specimen scans ...	Import scans of specimen labels.
Import list ...	Import tab-separated lists.
Reimport list ...	Reimport tab-separated lists which have been exported including the key columns.
Export	
Export list ...	Export a tab-separated file with the data of the specimen.
XML	Export data as an XML-file.
ABCD	Export data as an XML-file according to the ABCD standard.
GPI/JSTOR	Export data as an XML-file according to the GPI/JSTOR standard.
Floristic lists	Export data in a specific format.
BIB ...	Export data according to the demands of the BIB portal.
Naturgucker ...	Export data according to the demands of the Naturgucker portal.
CSV (bcp)	Export data of the entire database as csv files.
Cache DB	Export data of selected projects into a cache database.

Withhold data	Edit the withholding reasons for the selected data.
Replication ...	Synchronisze the content of 2 databases.
Set server ...	Define the replication provider and server respectively for the replication.
Download ...	Download data from the data provider and server respectively in your local database.
Upload ...	Upload data from your local database to the replication provider and server respectively.
Clean database ...	Clean your local database.
Backup database ...	Create a backup of the entire database.
Transfer	Transfer data sets.
To project ...	Transfer the selected specimen into an additional project.
To transaction ...	Transfer the selected specimen into an additional transaction.
All annotations ...	Edit all annotations in the database.
Remove specimen ...	Remove the selected specimen from the database.
Remove from project ...	Remove the selected specimen from an additional project.
Save data set	Save current data set.

Administration

Change password ...	Changing the password of a user.
Analysis ...	Administration of the analysis methods used for the specimens.
Collections ...	Administration used for the collections.
Customize display ...	Customizing the display of the window e.g. the material categories and taxoniomc groups which should be visible when creating a new entry.
Database	Administration of the database.
Descritption ...	Administration of the descriptions and messages within the application.
Documentation ...	Documentation of the structure of the database.
Logins ...	Administration of the logins of the server and their permissions in the databases.
Maintenance ...	Maintenance of database entries, especially, if connected to other modules.
Queries ...	Creating and editing predefined queries.
Rename database	Rename the current database.
Set published address	Setting the address published for links by other modules.
External datasources ...	Administration of the external data sources of data imported into DiversityCollection.
Methods ...	Administration of the methods used for CollectionEvents, Analysis and Processing.
Processing ...	Administration of the processing procedures applied in the collection.
Projects ...	Administration of the projects.
Tools ...	Administration of the tools used for analysis and processing.
Transaction management	Management of transactions, managers, loans etc.
Transactions ...	Administration of the transactions e.g. loans, exchange etc.
Expired loans ...	Administration of expired loans. This menu entry will appear when there are expired loans in collections where the current user is a curator.
Loan requests ...	Administration of loan requests for the collections for which a user

	is a collection manager. This menu entry will appear when there are loan requests for the managed collections where the current user is a collection manager.
My requests ...	Administration of the loan requests of a user. This menu entry will appear when a user placed requests for specimen.
Requesters ...	User having the right to place requests for specimen of a collection.
Managers ...	Administration of the users who manage collections and are e.g. responsible for the administration of the transactions.

Help

Manual	Opens the online manual.
Feedback ...	Opens a window for sending feedback.
Feedback history ...	Opens a window for browsing former feedback.
Statistics ...	Overview of changes within the projects and edited specimen.
Info	Show the version of the program and corresponding information.
Websites< /td>	Websites related to DiversityCollection.
Download applications ...	Download DiversityCollection from the website of the DiveristyWorkbench project.
Information model ...	Inspect the information model on the website of the DiveristyWorkbench project.
Diversity mobile ...	Website of DiversityMobile, the mobile application for collecting data stored in DiversityCollection.

Update

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

Manual

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

Version

For information on the version of the client application choose **Help**, **Info...**

DiversityCollection

Management system for collections and observations

Version: 2.5.3.6

Institution: Staatliche Naturwissenschaftliche Sammlungen Bayerns, IT Centre http://www.snsb.info/

Authors: Markus Weiss

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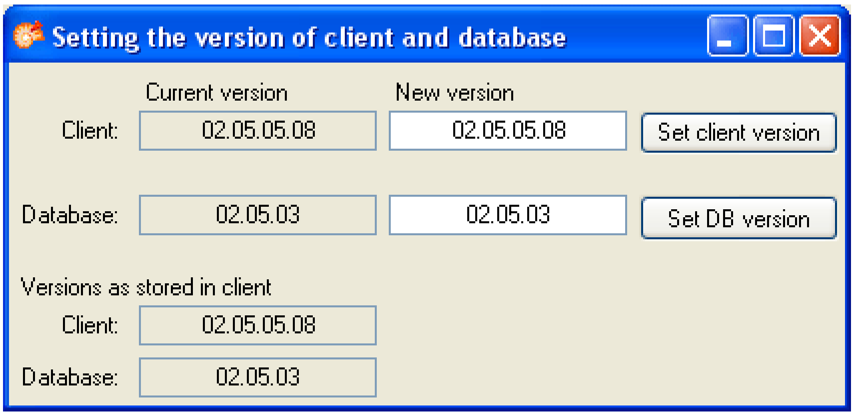
The current version in the example above is 2.5.3.6. As an administrator you may set the versions of the database and the client. Choose **Administration** - **Versions** from the menu. A form will open as shown below giving you an overview of the version settings.



	Current version	New version
Client:	02.05.05.08	02.05.05.08
Database:	02.05.03	02.05.03

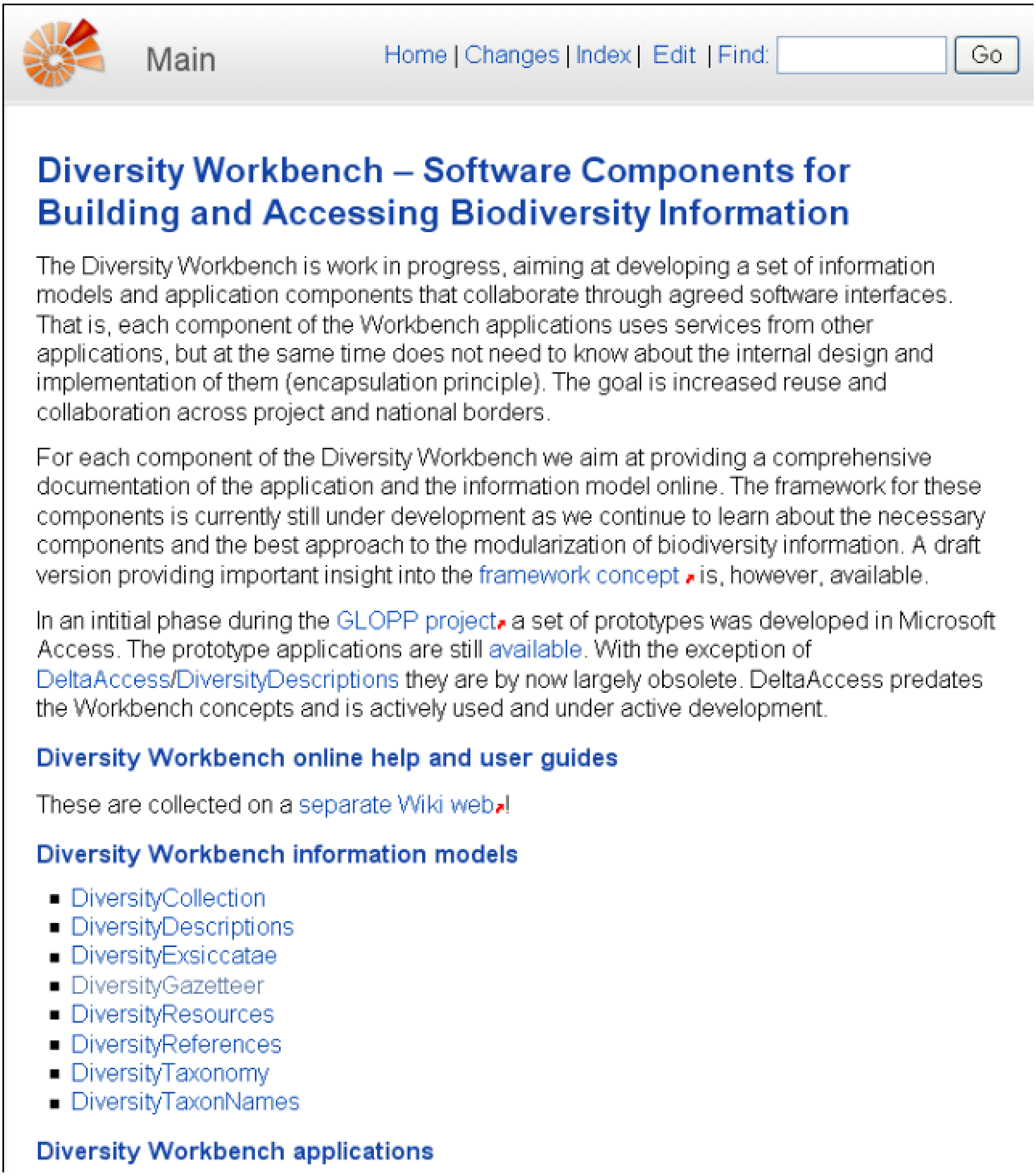
Versions as stored in client

Client: 02.05.05.08

Database: 02.05.03

Update of database and client

DiversityCollection 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 an **update** entry in the menu will appear. If a new version of the client is available, this menu will contain an **update client ...** entry. Click on it to open the webpage where you may download the client as shown below.



Diversity Workbench – Software Components for Building and Accessing Biodiversity Information

The Diversity Workbench is work in progress, aiming at developing a set of information models and application components that collaborate through agreed software interfaces. That is, each component of the Workbench applications uses services from other applications, but at the same time does not need to know about the internal design and implementation of them (encapsulation principle). The goal is increased reuse and collaboration across project and national borders.

For each component of the Diversity Workbench we aim at providing a comprehensive documentation of the application and the information model online. The framework for these components is currently still under development as we continue to learn about the necessary components and the best approach to the modularization of biodiversity information. A draft version providing important insight into the framework concept is, however, available.

In an intitial phase during the GLOPP project a set of prototypes was developed in Microsoft Access. The prototype applications are still available. With the exception of DeltaAccess/DiversityDescriptions they are by now largely obsolete. DeltaAccess predates the Workbench concepts and is actively used and under active development.

Diversity Workbench online help and user guides

These are collected on a separate Wiki web!

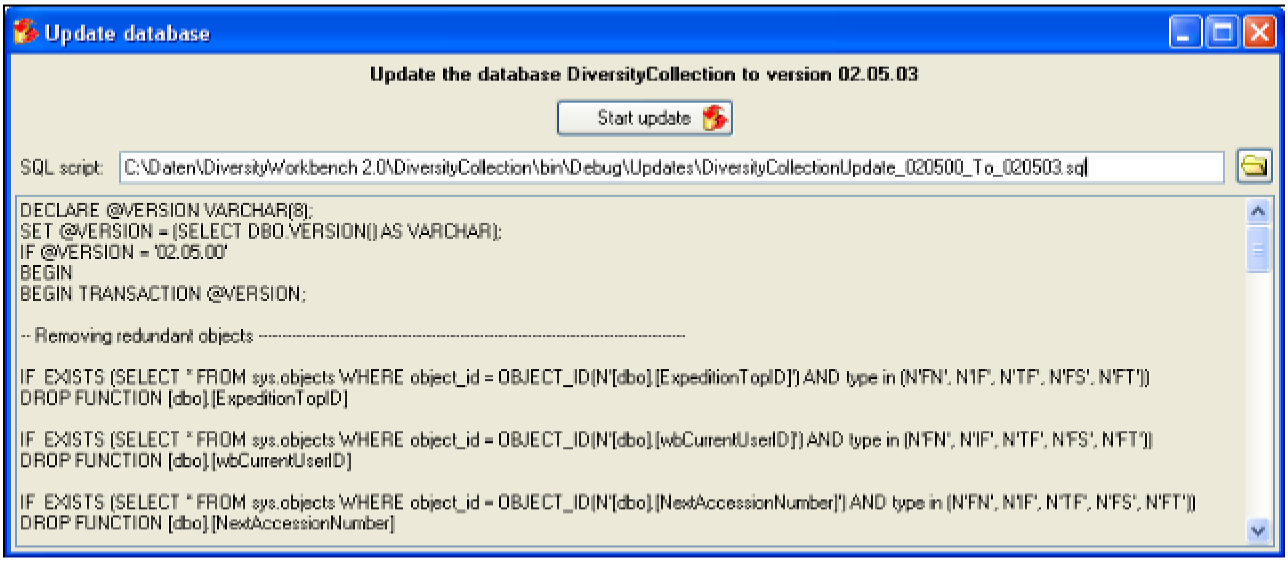
Diversity Workbench information models

- DiversityCollection
- DiversityDescriptions
- DiversityExsiccatae
- DiversityGazetteer
- DiversityResources
- DiversityReferences
- DiversityTaxonomy
- DiversityTaxonNames

Diversity Workbench applications

If you are the owner of the database (Database role = dbo) and the database needs to be updated, the menu will 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 need to run consecutively, so e.g. to update from version 2.5.1 to 2.5.4 you either have to run the script DiversityCollectionUpdate_020501_To_020504 or the scripts DiversityCollectionUpdate_020501_To_020502, DiversityCollectionUpdate_020502_To_020503 and DiversityCollectionUpdate_020503_To_020504. The program will guide you through these steps and check for the scripts. All you need to do is click the **Start update** button.



SQL script: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Updates\DiversityCollectionUpdate_020500_To_020503.sql

```
DECLARE @VERSION VARCHAR(8);
SET @VERSION = (SELECT DBO.VERSION() AS VARCHAR);
IF @VERSION = '02.05.00'
BEGIN
BEGIN TRANSACTION @VERSION;

-- Removing redundant objects ---------------------------------------------------------------------------

IF  EXISTS (SELECT * FROM sys.objects WHERE object_id = OBJECT_ID(N'[dbo].[ExpeditionTopID]') AND type in (N'FN', N'IF', N'TF', N'FS', N'FT'))
DROP FUNCTION [dbo].[ExpeditionTopID]

IF  EXISTS (SELECT * FROM sys.objects WHERE object_id = OBJECT_ID(N'[dbo].[wbCurrentUserID]') AND type in (N'FN', N'IF', N'TF', N'FS', N'FT'))
DROP FUNCTION [dbo].[wbCurrentUserID]

IF  EXISTS (SELECT * FROM sys.objects WHERE object_id = OBJECT_ID(N'[dbo].[NextAccessionNumber]') AND type in (N'FN', N'IF', N'TF', N'FS', N'FT'))
DROP FUNCTION [dbo].[NextAccessionNumber]
```

License

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For information about the license of the client software choose **Help**, **Info...**

DiversityWorkbench

DiversityCollection

Management system for collections and observations

Version: 2.5.3.6

Institution: Staatliche Naturwissenschaftliche Sammlungen Bayerns, IT Centre
http://www.snsb.info/

Authors: Markus Weiss

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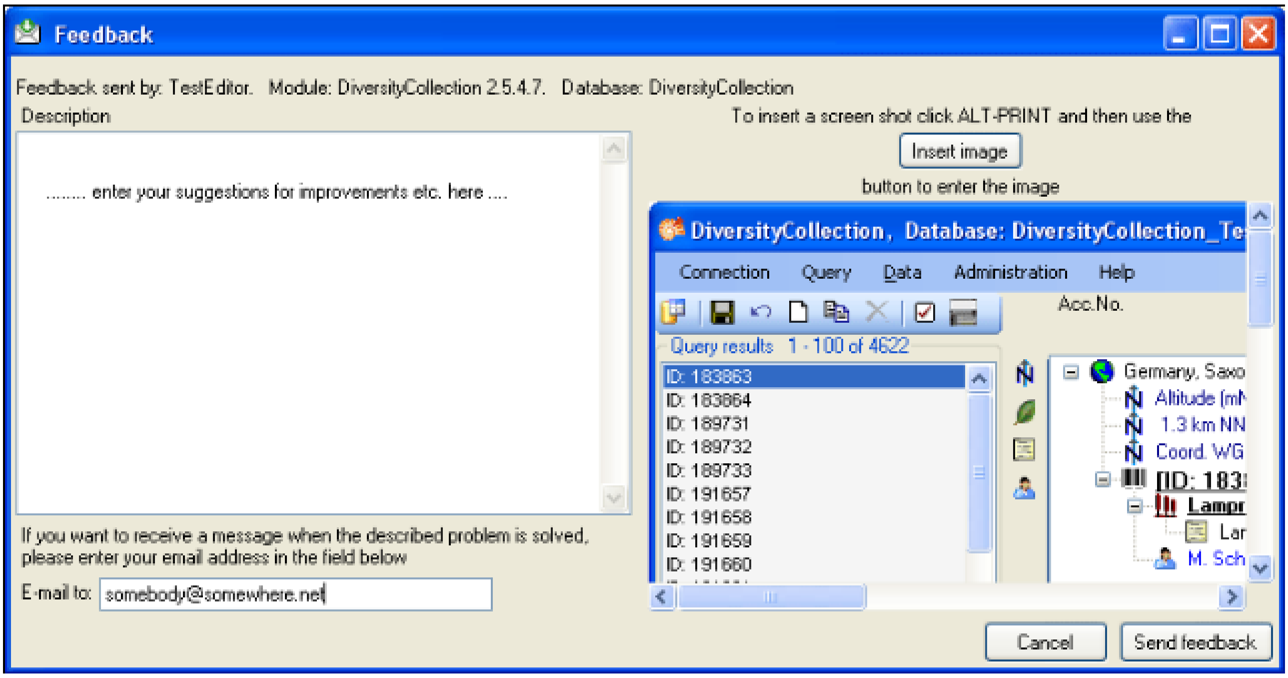
Feedback

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: TestEditor. Module: DiversityCollection 2.5.4.7. Database: DiversityCollection

Description

.... enter your suggestions for improvements etc. here ....

To insert a screen shot click ALT-PRINT and then use the Insert image button to enter the image

If you want to receive a message when the described problem is solved, please enter your email address in the field below

E-mail to: somebody@somewhere.net

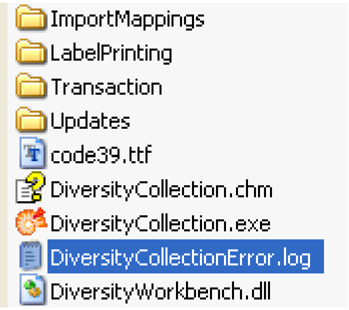
Click on the Insert image button to insert the screen shot and give a comment about your problem. Then click on the Send feedback button to send your feedback to the administrator. If you would like to receive a message when the problem you described is solved, please enter you e-mail address in the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

To inspect your former feedbacks choose **Feedback history...** from the menu. A window will open where you can browse your past 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 be helpful, if you attached the file **DiversityCollectionError.log** located in your application directory (see image below).

Error logging

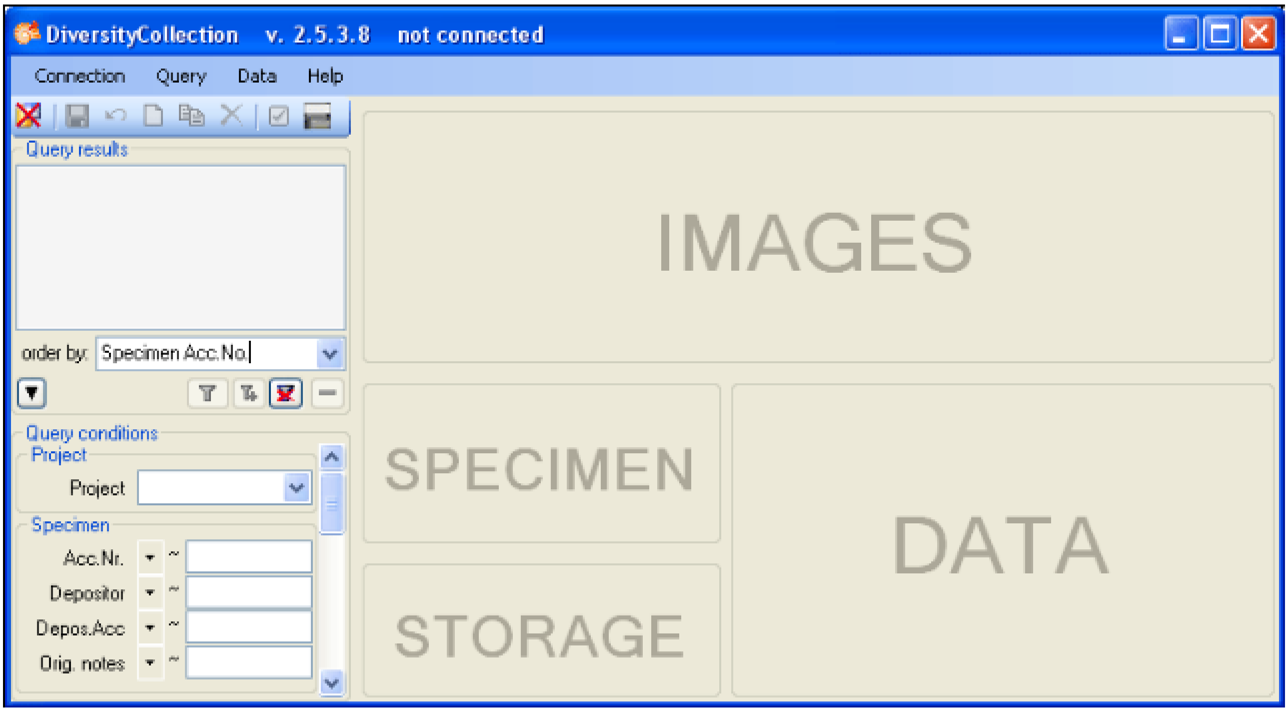
If any error messages show up while working with the application, you can find further details concerning the part of the application where the error occured and the parameters involved in the file **DiversityCollectionError.log** located in your application directory.



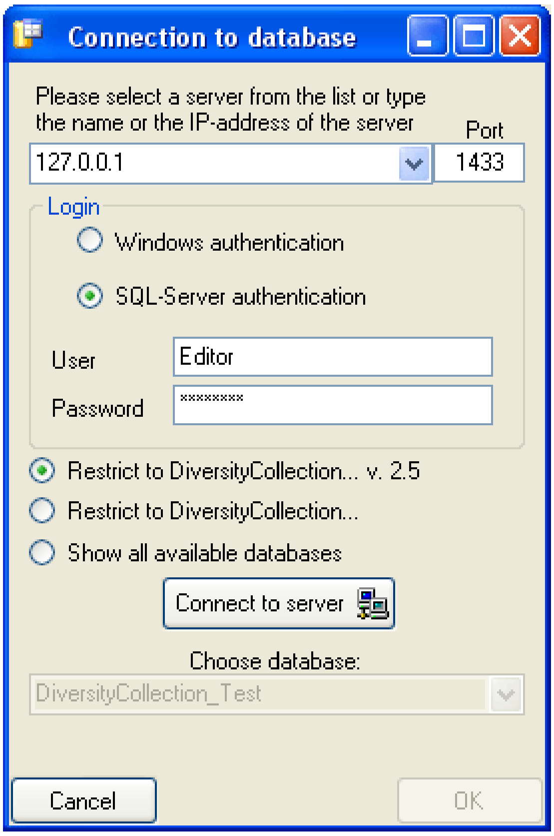
ImportMappings
LabelPrinting
Transaction
Updates
code39.ttf
DiversityCollection.chm
DiversityCollection.exe
DiversityCollectionError.log
DiversityWorkbench.dll

Tutorial - first steps

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



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).



Please select a server from the list or type the name or the IP-address of the server

127.0.0.1 Port 1433

○ Windows authentication

● SQL-Server authentication

User Editor

Password ********

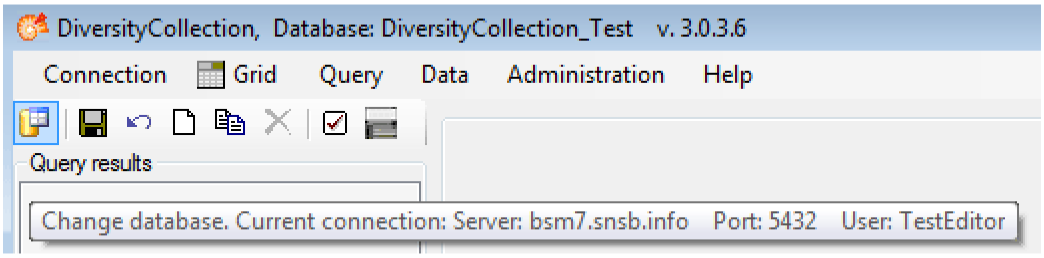
● Restrict to DiversityCollection... v. 2.5

○ Restrict to DiversityCollection...

○ Show all available databases

Choose database: DiversityCollection_Test

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).



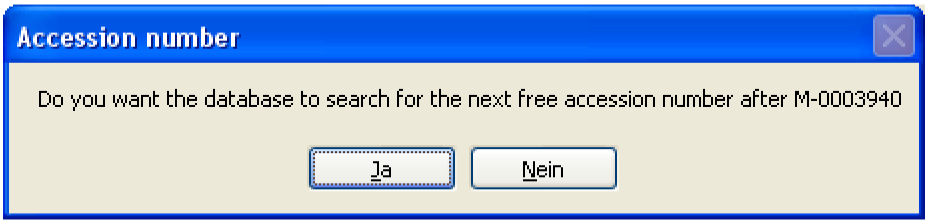
Change database. Current connection: Server: bsm7.snsb.info Port: 5432 User: TestEditor

This tutorial is continued in the sections listed below.

- section New data set
- section CollectionEvent
- section Localisation
- section CollectionEventSeries
- section CollectionSpecimen
- section Collector
- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

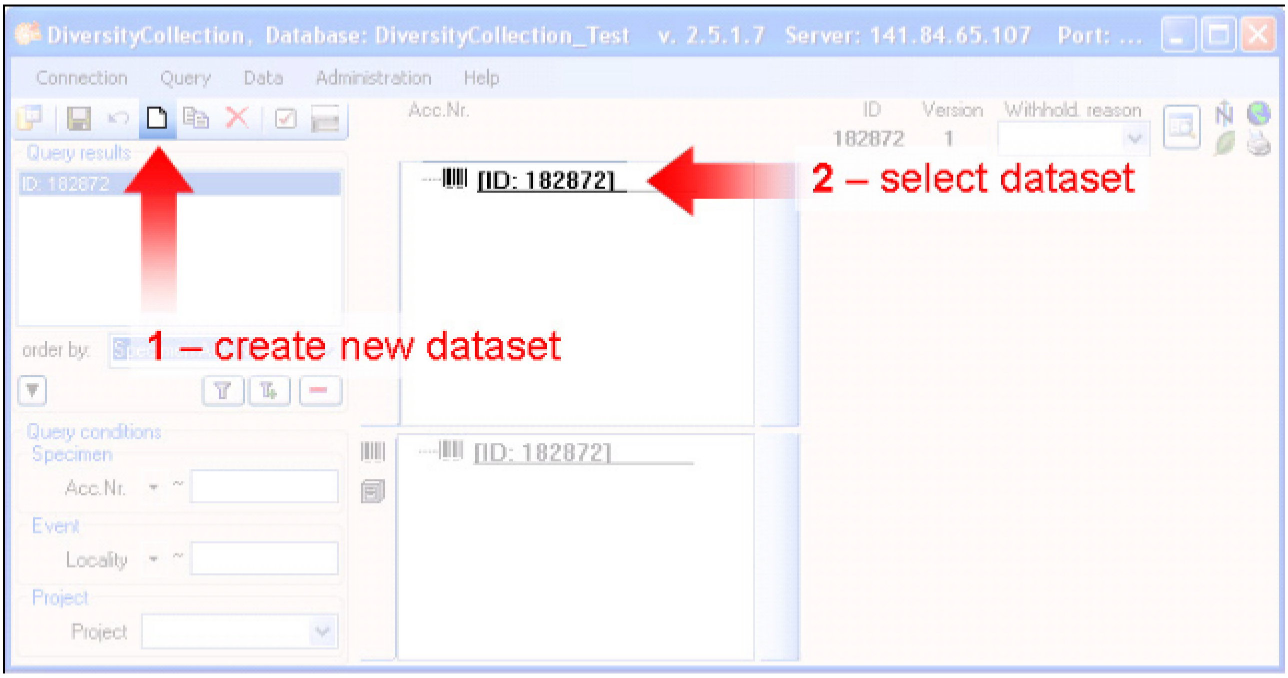
Tutorial - Creation of a new data set 🗋

To enter a new data set click on the 🗋button in the upper left panel (see point **1** in image below). In case of accession numbers being available in the database, the software will ask whether you wish to take the next free number (see accession for further information). If you click on the OK button, the program will try to find the next free accession number starting with your current accession number.



Do you want the database to search for the next free accession number after M-0003940

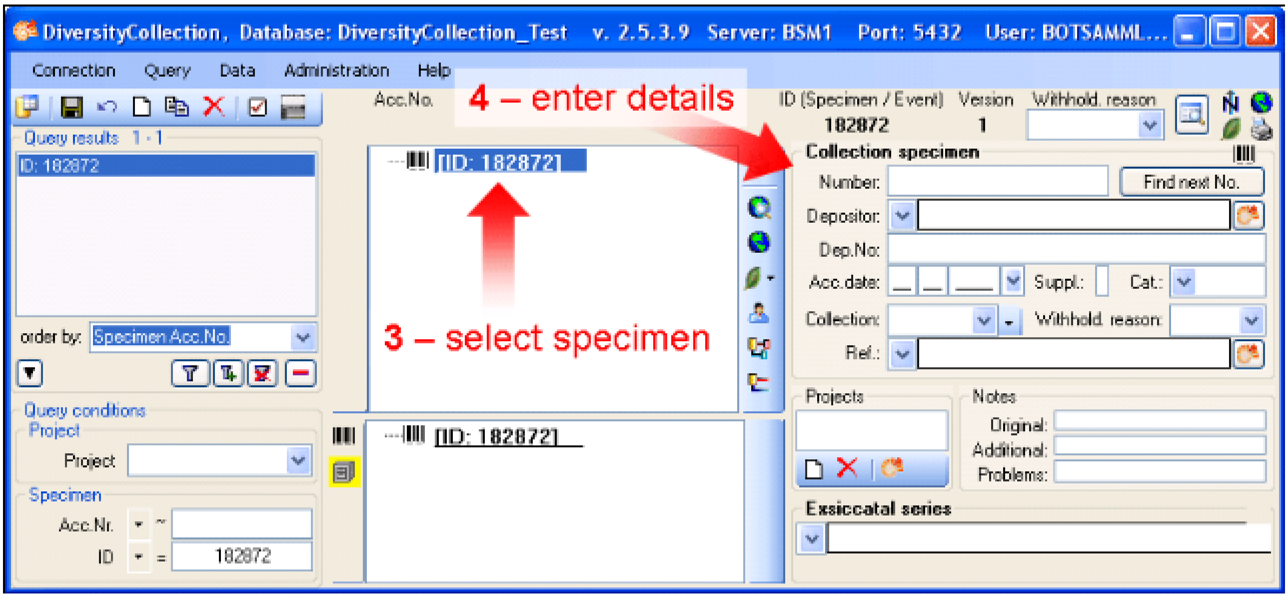
Finally you will find a new entry in the specimen list on the left and the trees for the specimen (see point **2** in image below) and the storage as shown below.



1 – create new dataset

2 – select dataset

If you did not specify an accession number, the entries will look like in the image above, otherwise the accession number will be shown. To enter your data for the specimen click on the entry in the upper tree as shown below (see point **3** in image below). This will open the fields where you may enter the details for the specimen in the area on the right of the tree (see point **4** in image below).



4 – enter details

3 – select specimen

In the panel in the middle of the form several buttons will appear where you may enter additional information for this specimen.

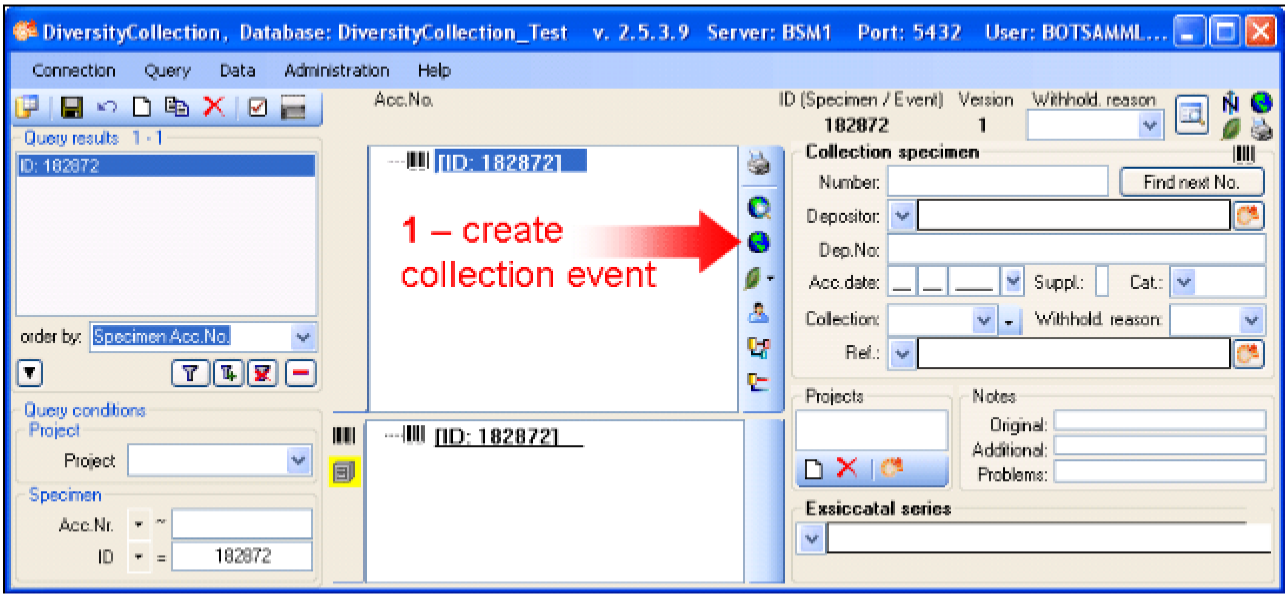
With these buttons you may enter information for the:
- CollectionEvent
- CollectionSpecimen
- Relation between specimen
- Organisms and identifications

This tutorial is continued in the sections listed below.

- section CollectionEvent
- section Localisation
- section CollectionEventSeries
- section CollectionSpecimen
- section Collector
- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - CollectionEvent

To enter information about the CollectionEvent (when and where the specimen was collected) click on the button (see point **1** in image below).



ID: 182872

order by: Specimen Acc.No.

ID = 182872

[ID: 182872]

ID (Specimen / Event): 182872

Version: 1

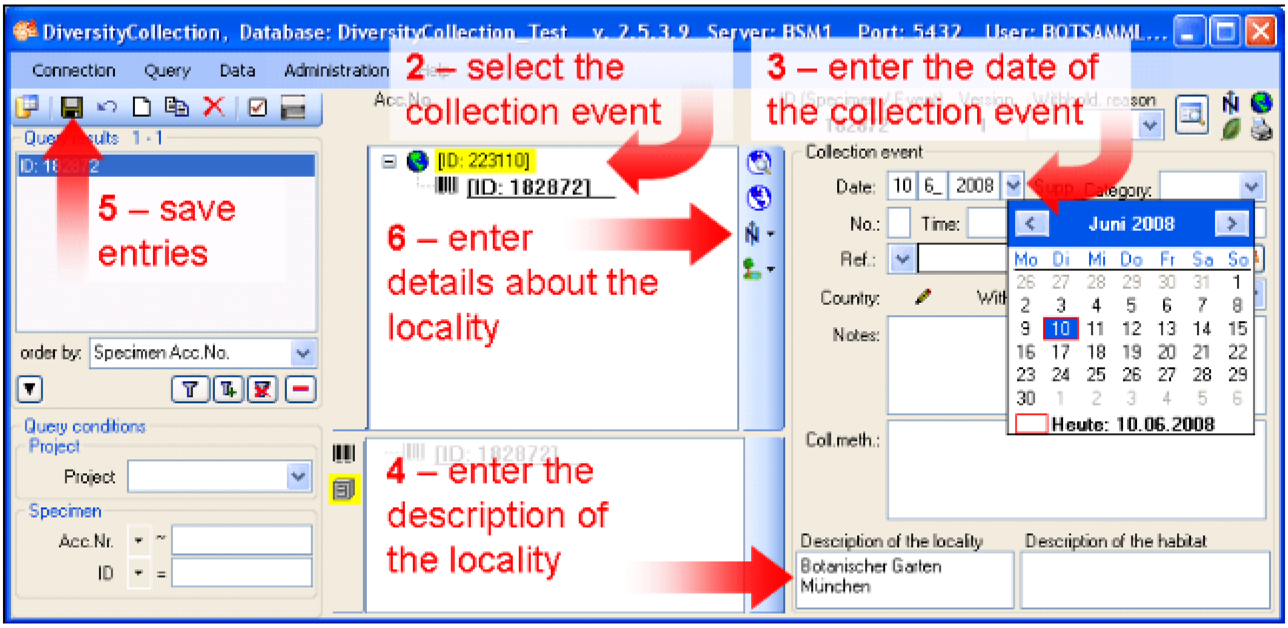
1 – create collection event

This will add an entry for the CollectionEvent in the upper tree as shown below. Select this entry in the tree (see point **2** in image below) to open the fields for the CollectionEvent. To see the projected contents of any data field simply place your mouse in the field. An explanation will appear as for the field **Description of the locality**:

Locality description of the locality, exactly as written on the original label (i.e. without corrections during data entry)

See the Event part for further details.

Then enter the date (see point **3** in image below) of the CollectionEvent. If you click on the drop-down button as shown in the image below, a calendar will open where you may select the date. Then enter the description of the locality (see point **4** in image below). To store the data entered so far click on the button (see point **5** in image below).



2 – select the collection event

3 – enter the date of the collection event

5 – save entries

6 – enter details about the locality

4 – enter the description of the locality

ID: 182872

order by: Specimen Acc.No.

[ID: 223110]

[ID: 182872]

Date: 10 6 2008

Heute: 10.06.2008

Description of the locality: Botanischer Garten München

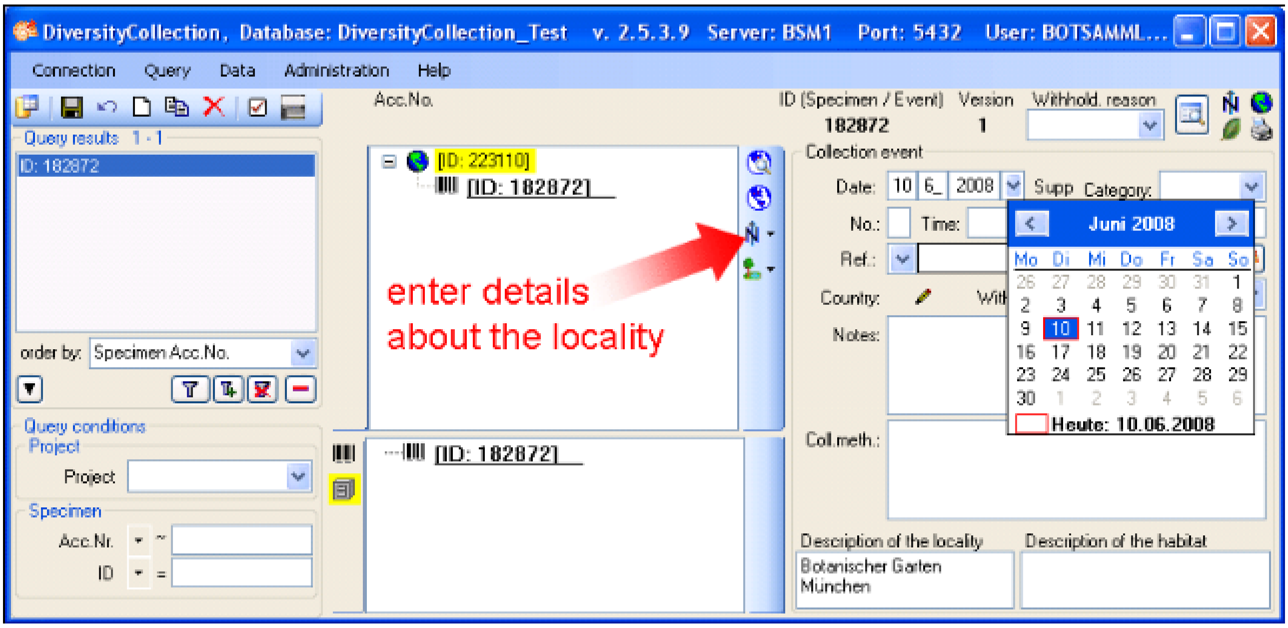
Now you have the possibility to enter more details about the locality like coordinates, named places, etc. by clicking on the N button (see point **6** in image above).

This tutorial is continued in the sections listed below.

- section Localisation
- section CollectionEventSeries
- section CollectionSpecimen
- section Collector
- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - Localisation

To enter more information on the CollectionEvent like coordinates, named places, etc. click on the button (see image below).



ID: 182872

order by: Specimen Acc.No.

[ID: 223110]

[ID: 182872]

ID (Specimen / Event): 182872

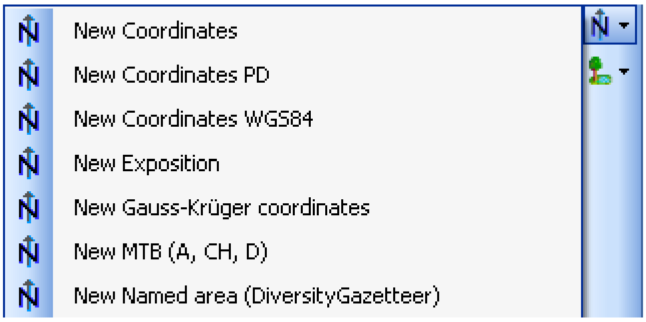
Version: 1

Date: 10 6 2008

Description of the locality: Botanischer Garten München

enter details about the locality

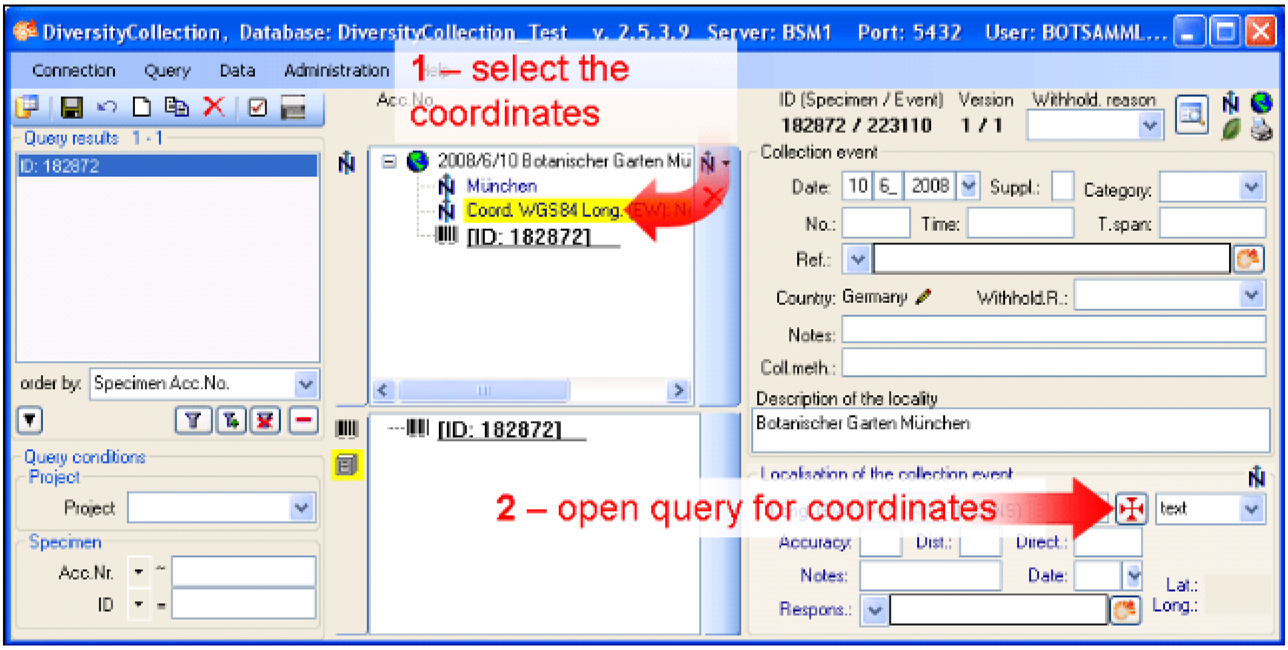
Now you may select an option from the following list:



The three most important options are:
- New Coordinates WGS84
- New Named Area (Diversity Gazetteer)
- New Altitude (mNN)

New Coordinates WGS84

You may add the exact coordinates for the locality with the assistance of Google Maps. Click on the button (see first image of this site) and choose **New Coordinates WGS84** (Google Maps uses WGS84). This will add a new entry in the overview. Select it (see point **1** in the image below) to open the details for this entry. Here click on the button (see point **2** in image below).



1 – select the coordinates

2 – open query for coordinates

ID: 182872

2008/6/10 Botanischer Garten Mü

München

Coord. WGS84 Long. (E/W): N

[ID: 182872]

ID (Specimen / Event): 182872 / 223110

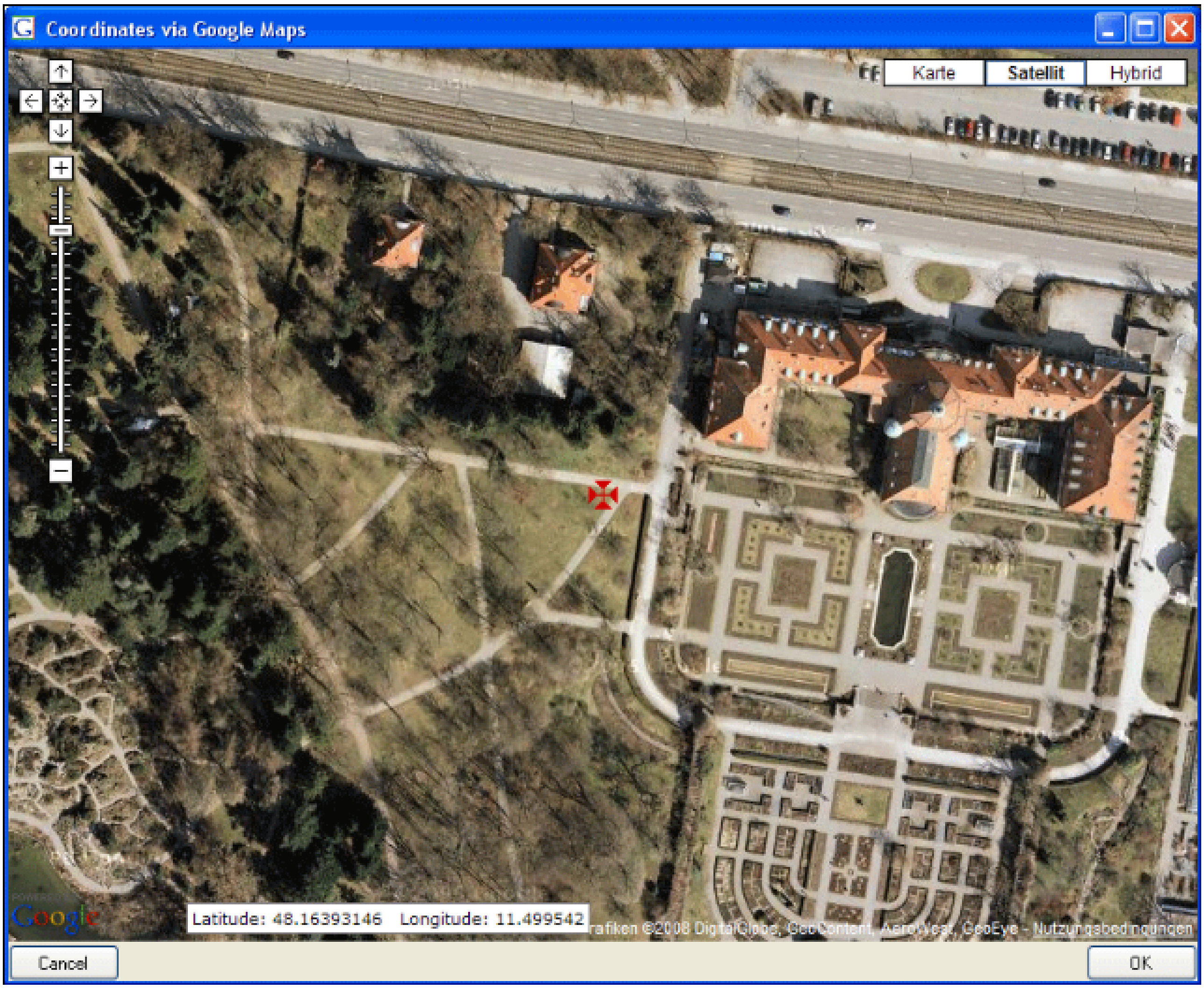
Version: 1 / 1

Date: 10 6 2008

Country: Germany

Description of the locality: Botanischer Garten München

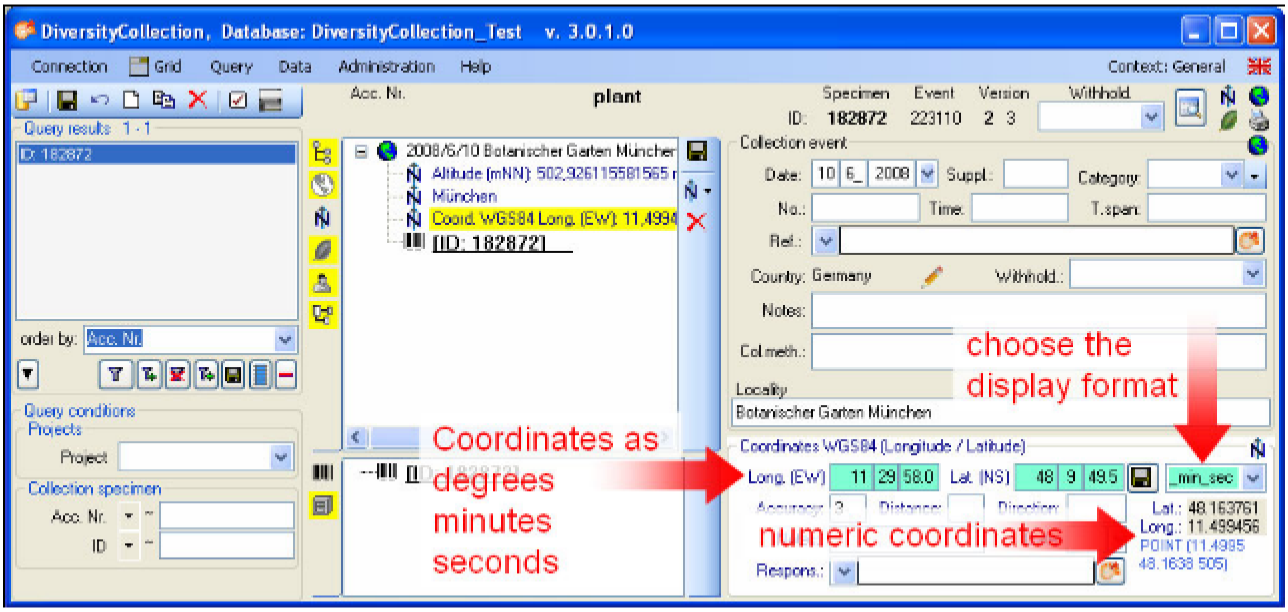
A window will open as shown below where you may set the coordintes simply by dragging the map with your mouse. The coordinates correspond to the center of the map, symbolized with the ✠. Click on the OK button to store the coordinates.



Latitude: 48.16393146 Longitude: 11.499542

rafiken ©2008 DigitalGlobe, GeoContent, AeroWest, GeoEye - Nutzungsbedingungen

In the main window the coordinates will be stored at two positions - see image below. In the upper area you may set the values and choose a different format for display as shown here - the more familiar form with degrees, minutes and seconds. Change the values and click on the 💾button to change the original entry. At the same time the numeric values are stored in fields which can not be edited by the user (see below). If not already present, the program using the webservice GeoNames will enter the altitide and the name of the closest named locality.



ID: 182872 223110 2 3

Date: 10 6 2008 Suppl.: Category:

No.: Time: T.span:

Ref.:

Country: Germany Withhold.:

Locality: Botanischer Garten München

Long. (EW) 11 29 58.0 Lat. (NS) 48 9 49.5 min_sec

Accuracy: 2

Lat.: 48.163761
Long.: 11.499456
POINT (11.4995 48.1638 505)

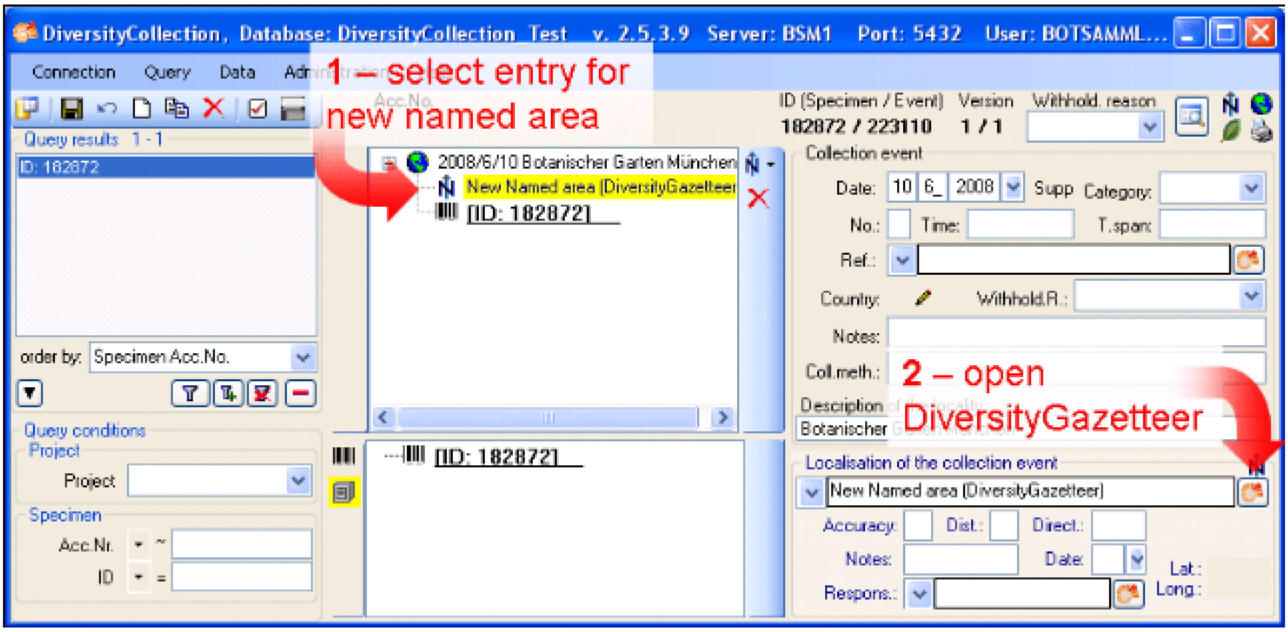
choose the display format

Coordinates as degrees minutes seconds

numeric coordinates

New Named Area (Diversity Gazetteer)

To enter a name of a place using the DiversityGazetteer choose **New Named Area (DiversityGazetteer)** from the list. In the overview tree in the middle of the window an entry will be inserted as shown below. Select it to open the detail fields for this entry (see point **1** in image below).



182872 / 223110 1 / 1

Date: 10 6 2008 Supp Category:

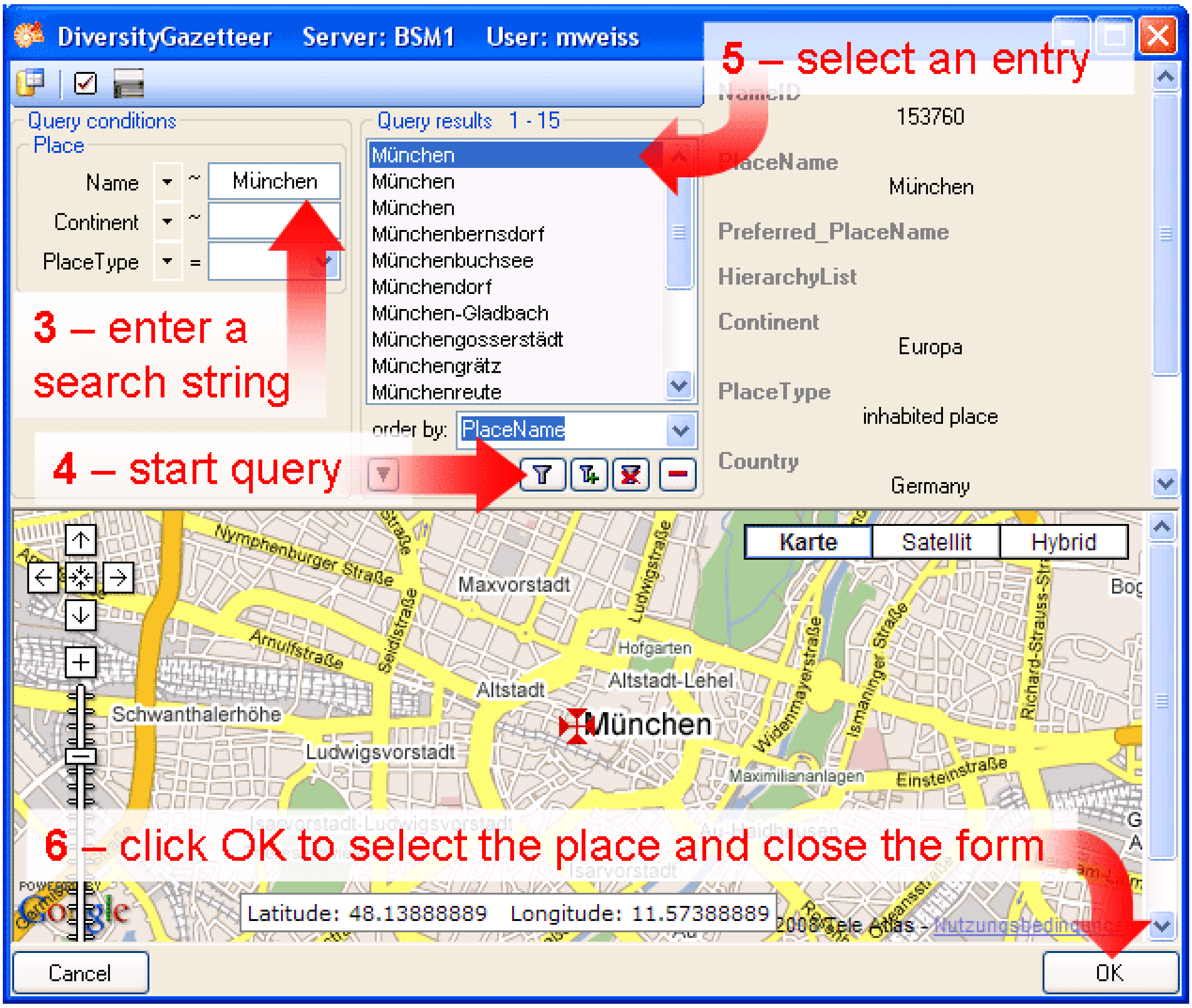
Description: Botanischer

New Named area (DiversityGazetteer)

1 – select entry for new named area

2 – open DiversityGazetteer

To open the connection to the DiversityGazetteer click on the button (see point **2** in image above). A window will open as shown below. Enter a search string - for example the city you wish to find (see point **3** in image below) - and start the query with a click on the button (see point **4** in image below).



DiversityGazetteer Server: BSM1 User: mweiss

Query conditions

Place

Name ~ München

Continent ~

PlaceType =

Query results 1 - 15

München
München
München
Münchenbernsdorf
Münchenbuchsee
Münchendorf
München-Gladbach
Münchengosserstädt
Münchengrätz
Münchenreute

order by: PlaceName

NameID 153760

PlaceName München

Preferred_PlaceName

HierarchyList

Continent Europa

PlaceType inhabited place

Country Germany

Latitude: 48.13888889 Longitude: 11.57388889

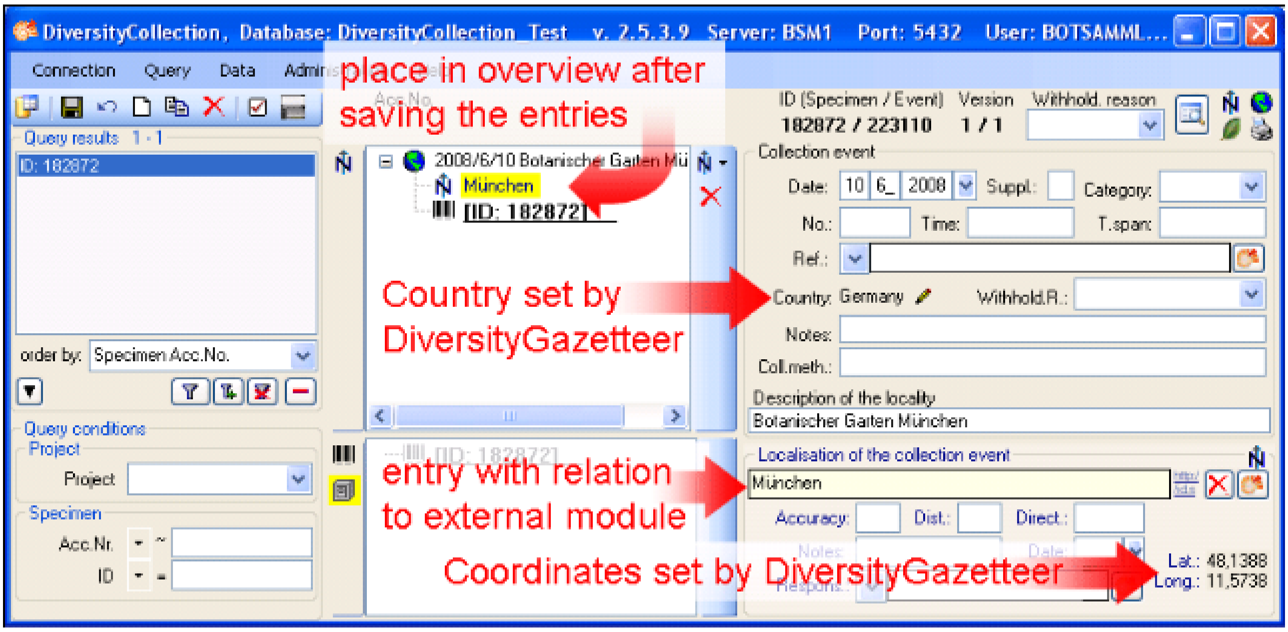
3 – enter a search string

4 – start query

5 – select an entry

6 – click OK to select the place and close the form

In the middle of the form the results of the query will be listed. Select one of these. To guide you to the correct entry details to this place are listed in the area right of the list. The base will show a map corresponding to the coordinates connected to this entry. After selecting the correct entry (see point **5** in image above) click on the OK button to return to the main window (see point **6** in image above). As shown below the data retrieved from the gazetteer will be written in several areas. Next to the name of the place the DiversityGazetteer provides the coordinates and the country as shown below.



place in overview after saving the entries

Country set by DiversityGazetteer

entry with relation to external module

Coordinates set by DiversityGazetteer

ID: 182872

order by: Specimen Acc.No.

2008/6/10 Botanischer Garten Mü
München
[ID: 182872]

ID (Specimen / Event): 182872 / 223110
Version: 1 / 1

Date: 10 6_ 2008

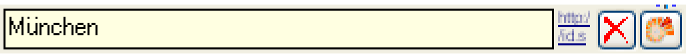
Country: Germany

Description of the locality: Botanischer Garten München

Localisation of the collection event: München

Lat.: 48,1388
Long.: 11,5738

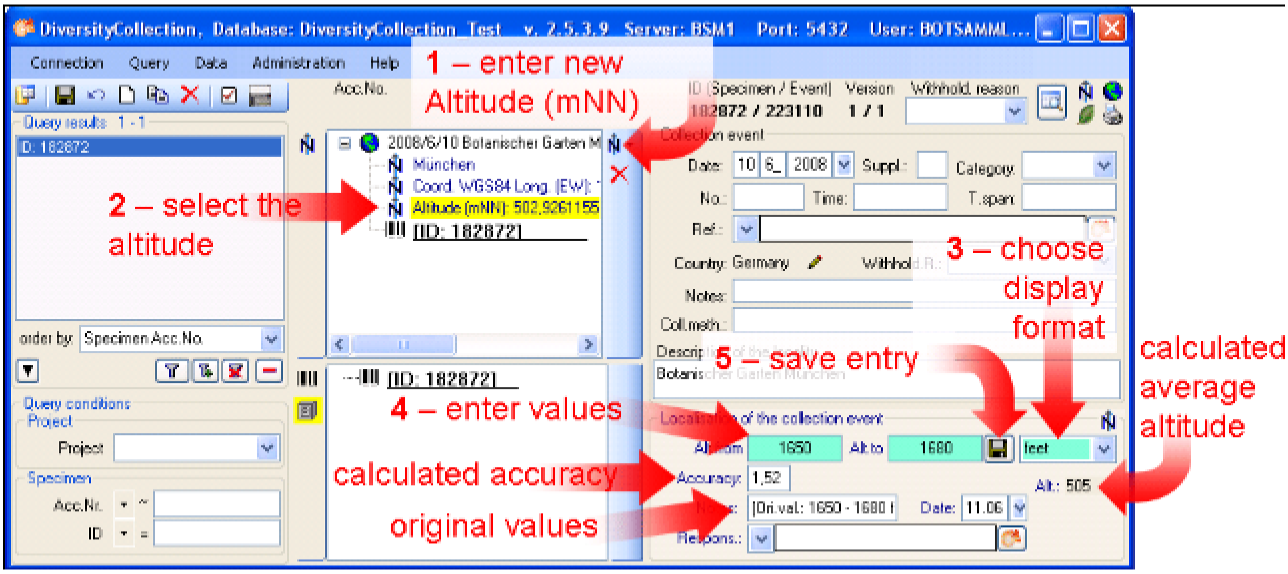
The area where you entered the name now changed to a locked state and will prevent you from changing the entry (see image below). Next to the field with the place you find the link to the external module. Double-click it for more details.


München

If you wish to remove the connection to the external module click on the ✕button. This will keep all entries (country, place, coordinates) but remove the connection to DiversityGazetteer.

New Altitude (mNN)

As a last information about the locality we enter the altitude. Click on the button (see first image of this site) and choose **New Altitude (mNN)** (see point **1** in the image below). Select the new entry in the overview to open the data fields (see point **2** in the image below). Let's suppose you have only feet values available - change the display format to feet (see point **3** in the image below). Enter your values (see point **4** in the image below) and click on the 💾 button (see point **5** in the image below) to save your entries. Now your values are converted to meter (the internal format of DiversityCollection) automatically. If you now change the display format to meter, you can see the result. The program calculates an average value for the altitude and accuracy in meter corresponding to the accuracy of your original values (see below). The original values of your entry are saved in the **Notes** field.


DiversityCollection, Database: DiversityCollection_Test v. 2.5.3.9 Server: BSM1 Port: 5432 User: BOTSAMML...

ID: 182672

order by: Specimen.Acc.No.

2008/6/10 Botanischer Garten M
München
Coord. WGS84 Long. (E/W): 1
Altitude (mNN): 502,9261155
[ID: 182872]

182872 / 223110 1 / 1

Date: 10 6_ 2008
Country: Germany
Description: Botanischer Garten München

Alt. from: 1650 Alt.to: 1680 feet
Accuracy: 1,52
Notes: [Ori.val.: 1650 - 1680 f Date: 11.06
Alt.: 505

1 – enter new Altitude (mNN)

2 – select the altitude

3 – choose display format

4 – enter values

5 – save entry

calculated accuracy

original values

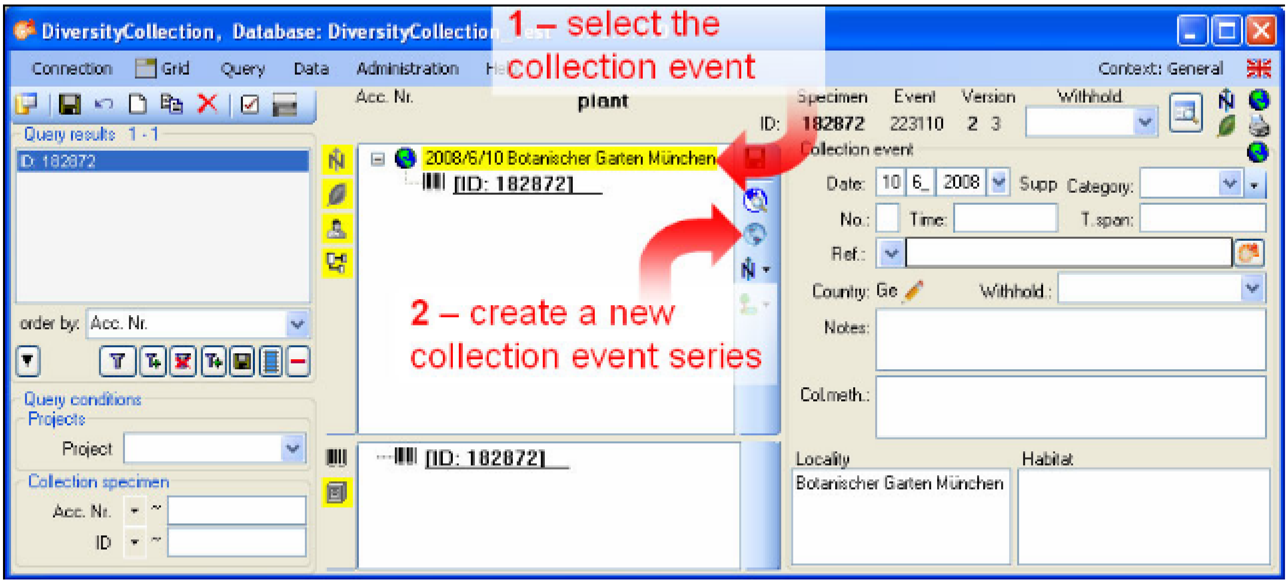
calculated average altitude

This tutorial is continued in the sections listed below.

- section CollectionEventSeries
- section CollectionSpecimen
- section Collector
- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - CollectionEventSeries

If you wish to organize your CollectionEvents, you may use the CollectionEventSeries. To create a new EventSeries select the ColletionEvent (see point **1** in image below) and click on the button (see point **2** in image below).



ID: 182872

order by: Acc. Nr.

Acc. Nr. plant

2008/6/10 Botanischer Garten München

[ID: 182872]

ID: 182872

Specimen 182872, Event 223110, Version 2 3

Date: 10 6 2008

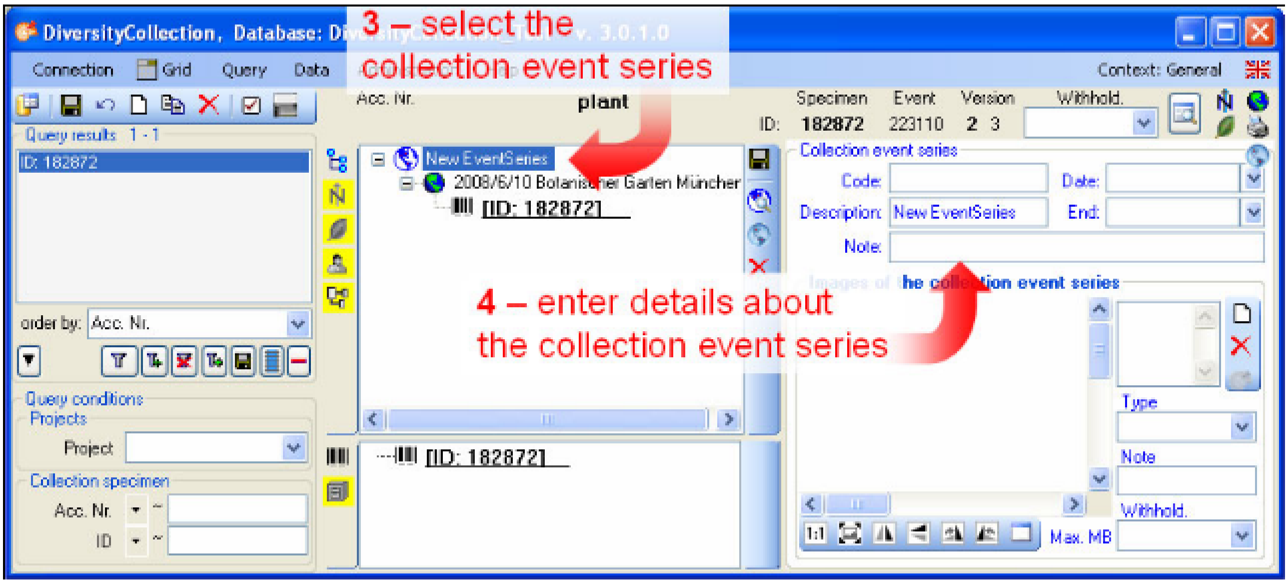
Country: Ge

Locality: Botanischer Garten München

1 – select the collection event

2 – create a new collection event series

In the tree the entry for the new EventSeries will appear (see point **3** in image below). Select this entry in the tree to enter the details about the EventSeries (see point **4** in image below).



ID: 182872

order by: Acc. Nr.

Acc. Nr. plant

New EventSeries

2008/6/10 Botanischer Garten München

[ID: 182872]

Specimen 182872, Event 223110, Version 2 3

Description: New EventSeries

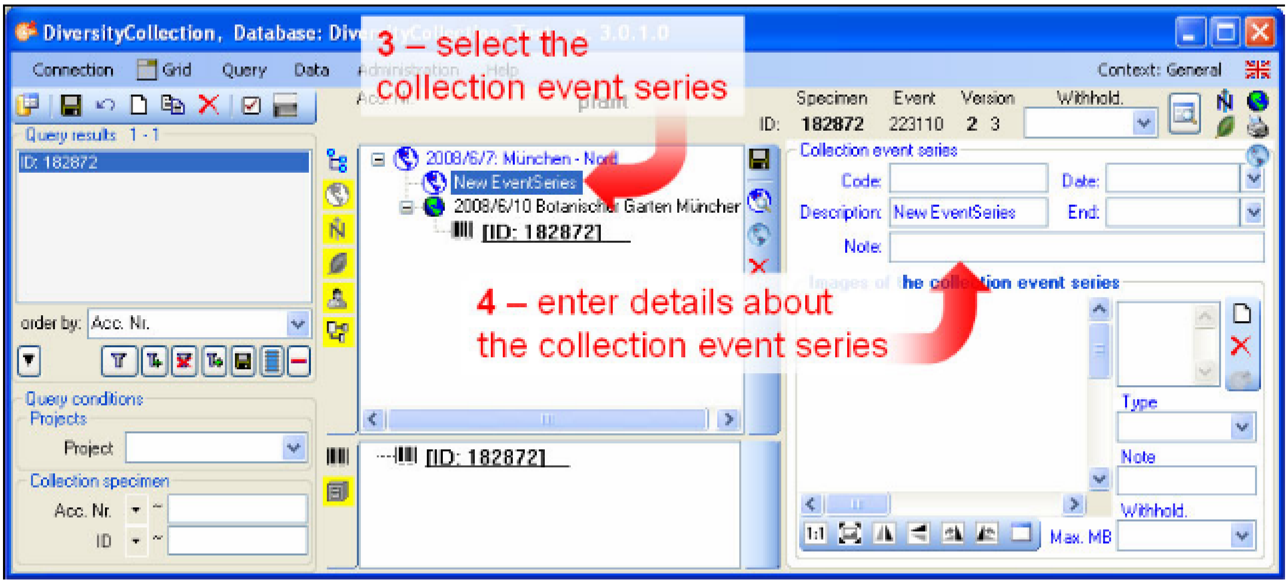
3 – select the collection event series

4 – enter details about the collection event series

To build a hierarchy for your CollectionEvents and CollectionEventSeries choose the created EventSeries in the tree (see point **1** in image below) and create a new secondary EventSeries (see point **2** in image below).

Then enter the date (see point **5** in image below) of the CollectionEvent. If you click on the drop-down button as shown in the image below, a calendar will open where you may select the date. Then enter the description of the locality (see point **6** in image below). To store the data entered so far click on the button (see point **7** in image below).

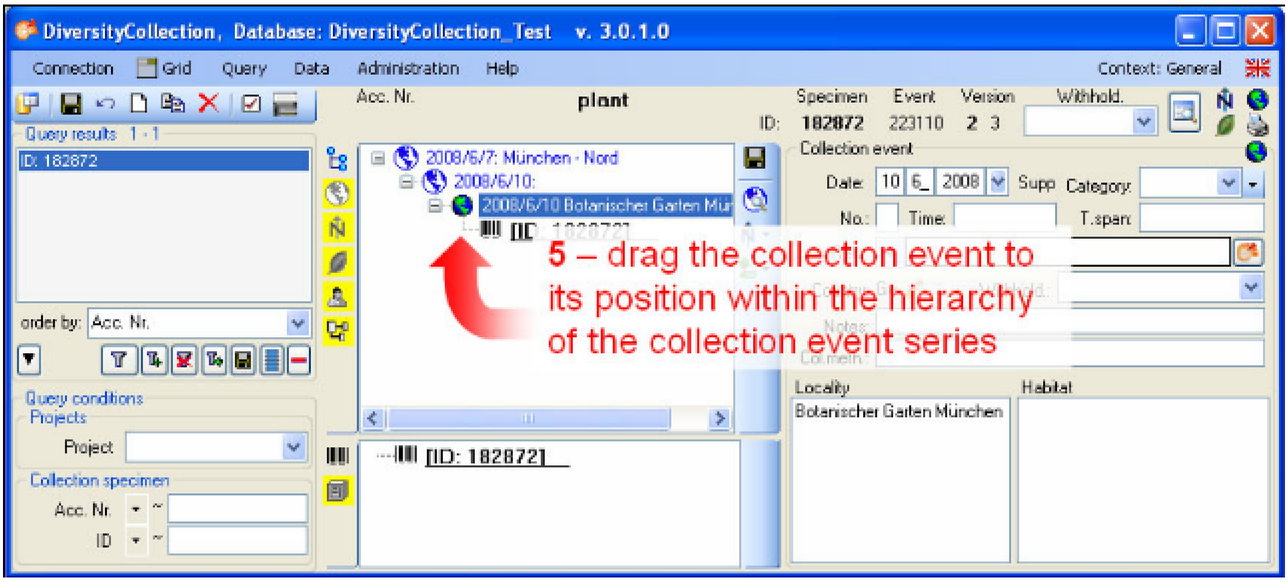
Select the entry of the new EventSeries (see point **3** in image below) and enter the details of the EventSeries (see point **4** in image below).


3 – select the collection event series

4 – enter details about the collection event series

Description: New EventSeries

Finally drag the CollectionEvent to its position within the hierarchy of the CollectionEventSeries entries (see point **5** in image below).


5 – drag the collection event to its position within the hierarchy of the collection event series

To include an extisting event in a hierarchy of the CollectionEventSeries select the CollectionEvent and click on the button. For more details see the section CollectionEventSeries.

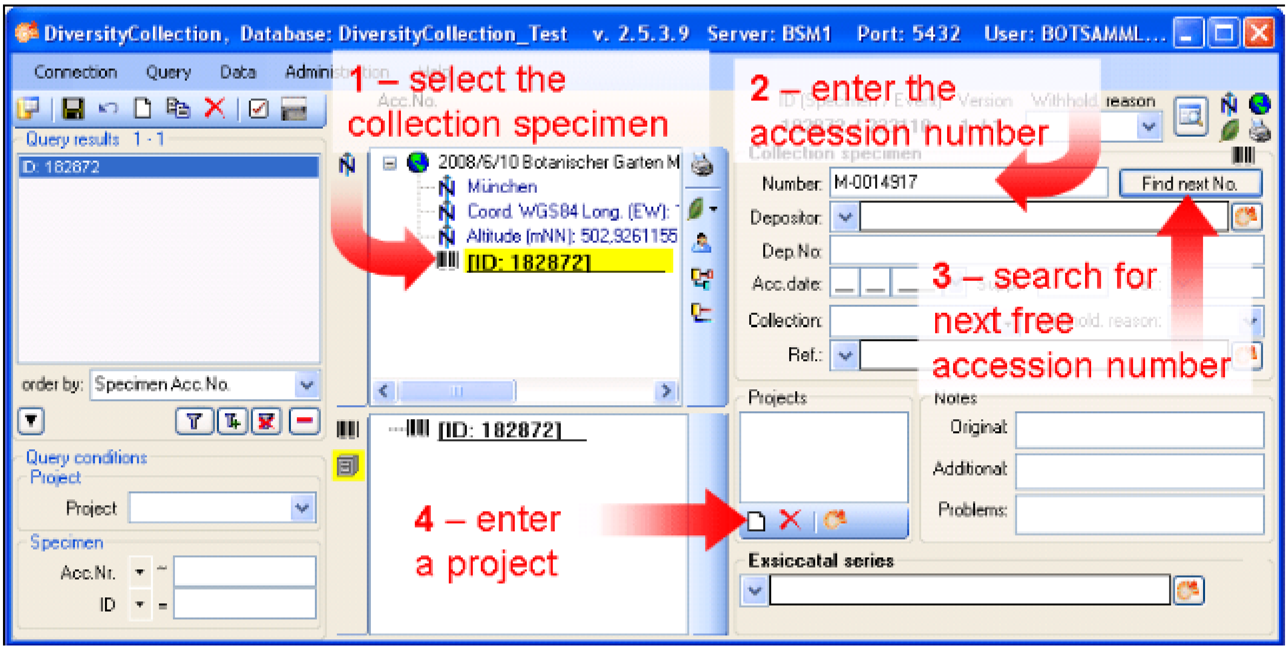
This tutorial is continued in the sections listed below.

- section CollectionSpecimen
- section Collector
- section Collection specimen relations

- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - CollectionSpecimen

To set the accession number for the CollectionSpecimen select it in the overview (see point **1** in image below) and enter the accession number (see point **2** in image below).



DiversityCollection, Database: DiversityCollection_Test v. 2.5.3.9 Server: BSM1 Port: 5432 User: BOTSAMML...

Query results 1 - 1

ID: 182872

2008/6/10 Botanischer Garten M

München

Coord. WGS84 Long. (EW):

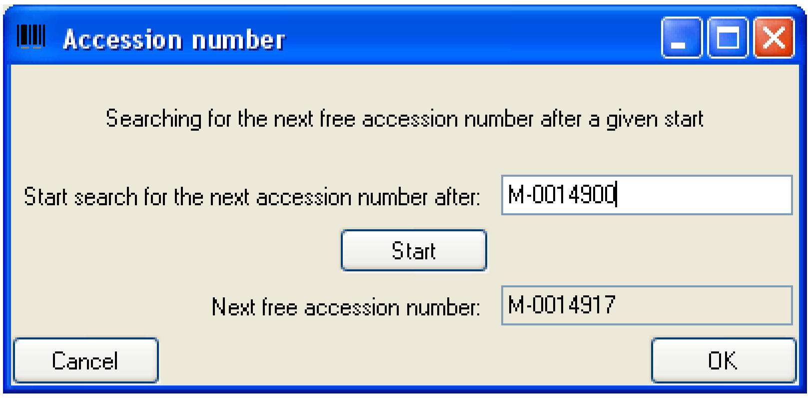
Altitude [mNN]: 502.9261155

[ID: 182872]

Number: M-0014917

order by: Specimen Acc.No.

To search for the next free accession number click on the corresponding button as shown above (see point **3** in image above). A window will open as shown below. Start the search for a free accession number. If the query ended successful, click **OK** to include the new accession number in your data set.



Accession number

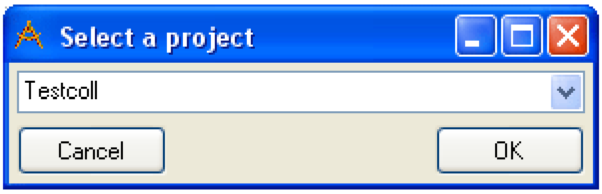
Searching for the next free accession number after a given start

Start search for the next accession number after: M-0014900

Next free accession number: M-0014917

Project

To restrict the access to your data set add it to a project (click on the 🗋button - see point **4** in image above). A dialog will open where you may select a project from the projects defined in DiversityCollection (see image below). The project will then be added to the list of the projects for this specimen.



Select a project

Testcoll

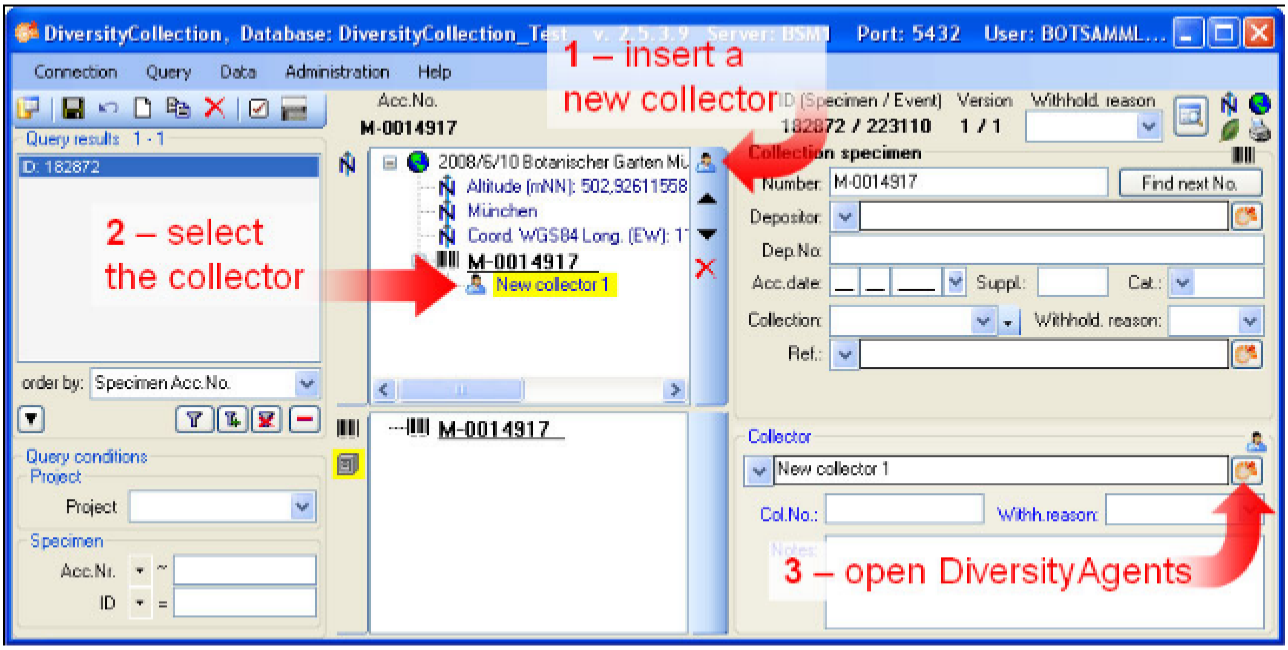
This tutorial is continued in the sections listed below.

- section Collector
- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - Collector

Collectors

Now we will add the collectors of the specimen. In the overview select the specimen and click on the 👤button to insert a new collector (see point **1** in image below). Select the collector in the overview (see point **2** in image below). Now we use the module DiversityAgents to search for a certain person. Click on the button to open the interface of the module (see point **3** in image below).



DiversityCollection, Database: DiversityCollection_Test v. 2.5.3.9 Server: BSM1 Port: 5432 User: BOTSAMML...

Query results 1 - 1: ID: 182872

order by: Specimen Acc.No.

Acc.No.: M-0014917

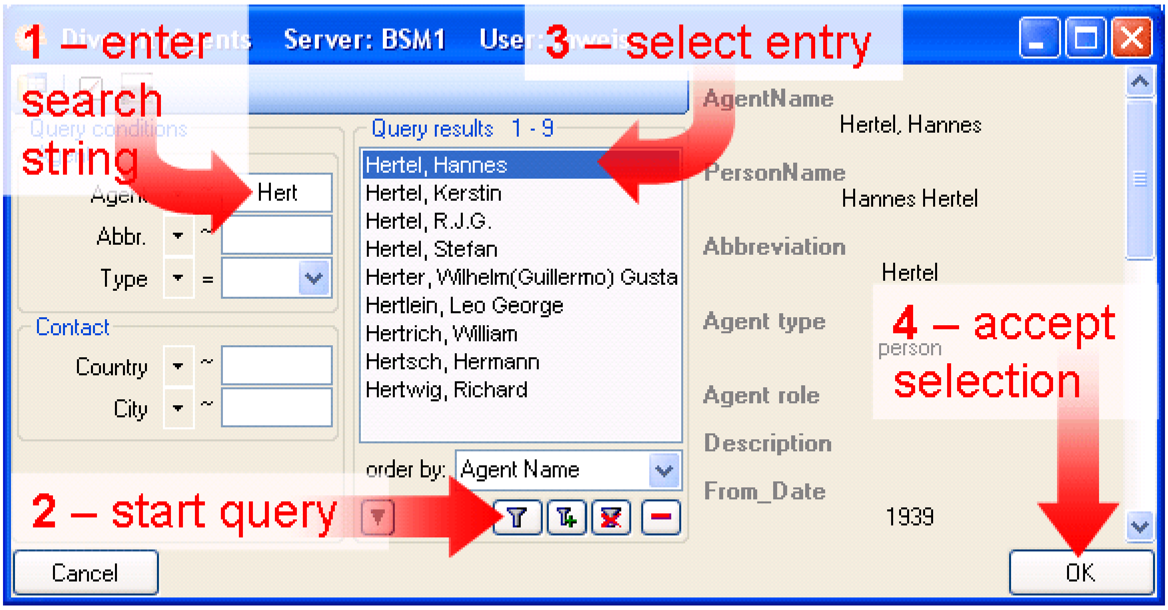
ID (Specimen / Event): 182872 / 223110 Version: 1 / 1

2008/6/10 Botanischer Garten Mü...
Altitude (mNN): 502.92611558
München
Coord. WGS84 Long. (EW): 1...
M-0014917
New collector 1

Collection specimen
Number: M-0014917

Collector: New collector 1

In the interface for DiversityAgents enter search criteria (see point **1** in image below) and click on the button to start the query (see point **2** in image below).



Agent: Hert

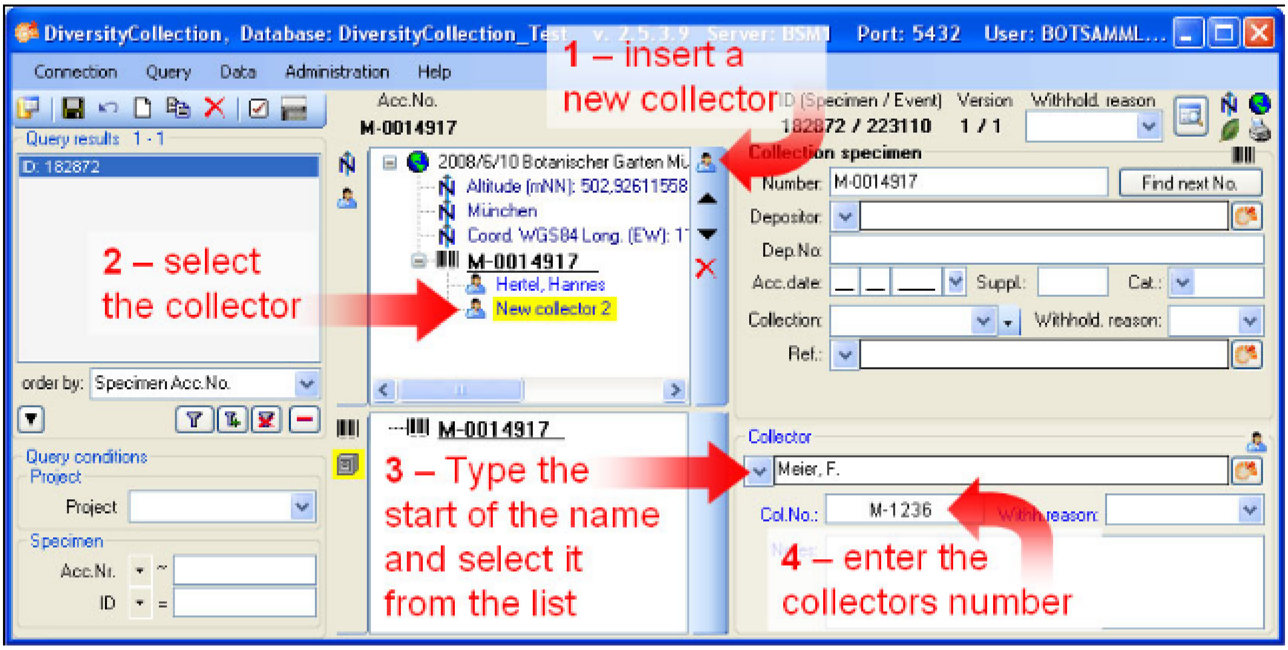
Query results 1 - 9
Hertel, Hannes
Hertel, Kerstin
Hertel, R.J.G.
Hertel, Stefan
Herter, Wilhelm(Guillermo) Gusta
Hertlein, Leo George
Hertrich, William
Hertsch, Hermann
Hertwig, Richard

order by: Agent Name

AgentName: Hertel, Hannes
PersonName: Hannes Hertel
Abbreviation: Hertel
Agent type: person
From_Date: 1939

Select the correct entry from the query result (see point **3** in image above) and click on the OK button (see point **4** in image above) to store the name in DiversityCollection.

The next collector will have no connection to the module DiversityAgents. To insert this collector click on the button again (see point **1** in image below) and select it (see point **2** in image below). Type the start of the name in the field for the name (in this example "Mei" would be a good choice) and click on the drop-down button (see point **3** in image below) to select a name from the list of collectors already stored in the database. Finally if the collector has a field number, enter said number (see point **4** in image below).



1 – insert a new collector

2 – select the collector

3 – Type the start of the name and select it from the list

4 – enter the collectors number

ID: 182872

order by: Specimen Acc.No.

Acc.No. M-0014917

ID (Specimen / Event) 182872 / 223110

Version 1 / 1

2008/6/10 Botanischer Garten Mü

Altitude (mNN): 502,92611558

München

Coord. WGS84 Long. (EW): 1

M-0014917

Hertel, Hannes

New collector 2

Number: M-0014917

Collector: Meier, F.

Col.No.: M-1236

This tutorial is continued in the sections listed below.

- section Collection specimen relations
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - Relations between specimen

There are two types of relations possible:

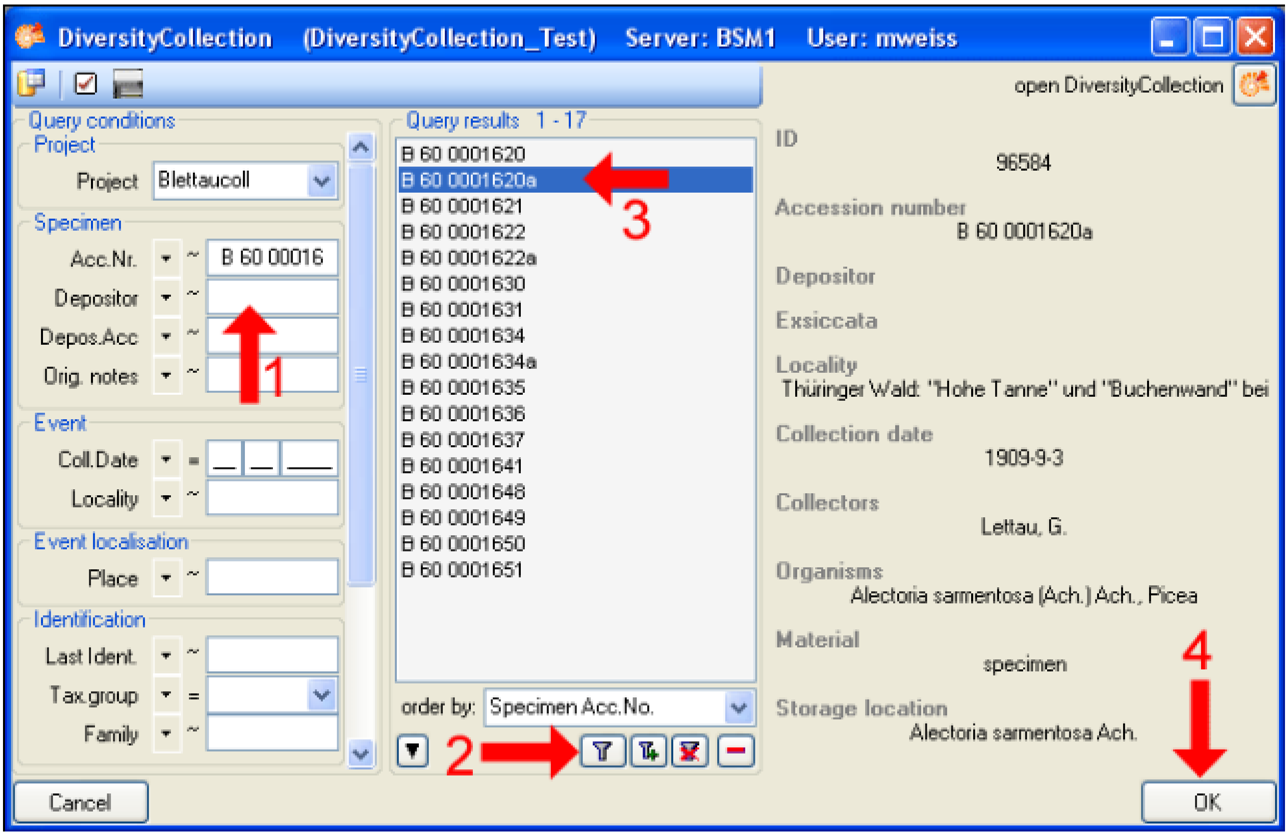
1. relation to a specimen within DiversityCollection
2. relation to a specimen not administrated in the local database.

1. Internal relations

To enter a relation to a specimen in DiverisityCollection select the specimen in the tree (see point **1** in image below) and click on the button (see point **2** in image below).

1908/9/27 Thüringer Wald: "Hohe Tanne" und "Buchenwand" bei Stützerbach, 750 m
Altitude (mNN): 750 m NN
Greenwich Coordinates Long. (EW): 10.8625 Lat. (NS): 50.6364
Stützerbach, Ilm-Kreis, Germany
B 60 0001620
Picea
Picea sp.
Alectoria sarmentosa (Ach.) Ach.
Alectoria sarmentosa (Ach.) Ach. [respons.: Sipman, H.]
Alectoria sarmentosa Ach. [respons.: Sipman, H.]

A window will open where you can search for the related specimen. In the window enter your restrictions (see point **1** in image below) and start the query (see point **2** in image below). Select the related specimen from the result list (see point **3** in image below) and click OK (see point **4** in image below) to insert the relation.



DiversityCollection (DiversityCollection_Test) Server: BSM1 User: mweiss

Query conditions

Project: Blettaucoll

Specimen

Acc.Nr. ~ B 60 00016

Query results 1 - 17

B 60 0001620
B 60 0001620a
B 60 0001621
B 60 0001622
B 60 0001622a
B 60 0001630
B 60 0001631
B 60 0001634
B 60 0001634a
B 60 0001635
B 60 0001636
B 60 0001637
B 60 0001641
B 60 0001648
B 60 0001649
B 60 0001650
B 60 0001651

order by: Specimen Acc.No.

ID: 96584

Accession number: B 60 0001620a

Depositor

Exsiccata

Locality: Thüringer Wald: "Hohe Tanne" und "Buchenwand" bei

Collection date: 1909-9-3

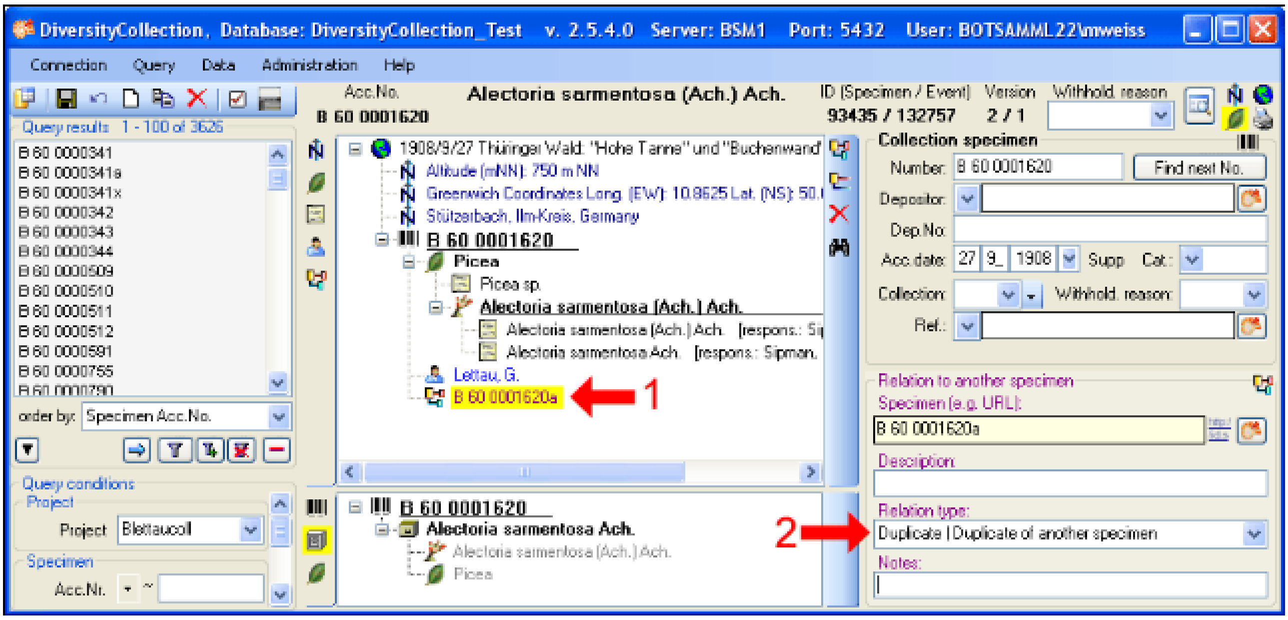
Collectors: Lettau, G.

Organisms: Alectoria sarmentosa (Ach.) Ach., Picea

Material: specimen

Storage location: Alectoria sarmentosa Ach.

In the window select the entry for the relation (see point **1** in image below) to display the fields for the details. Then enter the type of the relation (see point **2** in image below).



Acc.No. B 60 0001620 Alectoria sarmentosa (Ach.) Ach.

ID (Specimen / Event): 93435 / 132757

Version: 2 / 1

Query results: B 60 0000341, B 60 0000341a, B 60 0000341x, B 60 0000342, B 60 0000343, B 60 0000344, B 60 0000509, B 60 0000510, B 60 0000511, B 60 0000512, B 60 0000591, B 60 0000755, B 60 0000790

order by: Specimen Acc.No.

Project: Blettaucoll

1908/9/27 Thüringer Wald: "Hohe Tanne" und "Buchenwand"
- Altitude (mNN): 750 m NN
- Greenwich Coordinates Long. (EW): 10.8625 Lat. (NS): 50.1
- Stützerbach, Ilm-Kreis, Germany
- B 60 0001620
  - Picea
    - Picea sp.
  - Alectoria sarmentosa (Ach.) Ach.
    - Alectoria sarmentosa (Ach.) Ach. [respons.: Si
    - Alectoria sarmentosa Ach. [respons.: Sipman,
  - Lettau, G.
  - B 60 0001620a

B 60 0001620
- Alectoria sarmentosa Ach.
  - Alectoria sarmentosa (Ach.) Ach.
  - Picea

Number: B 60 0001620

Acc. date: 27 9_ 1908

Specimen (e.g. URL): B 60 0001620a

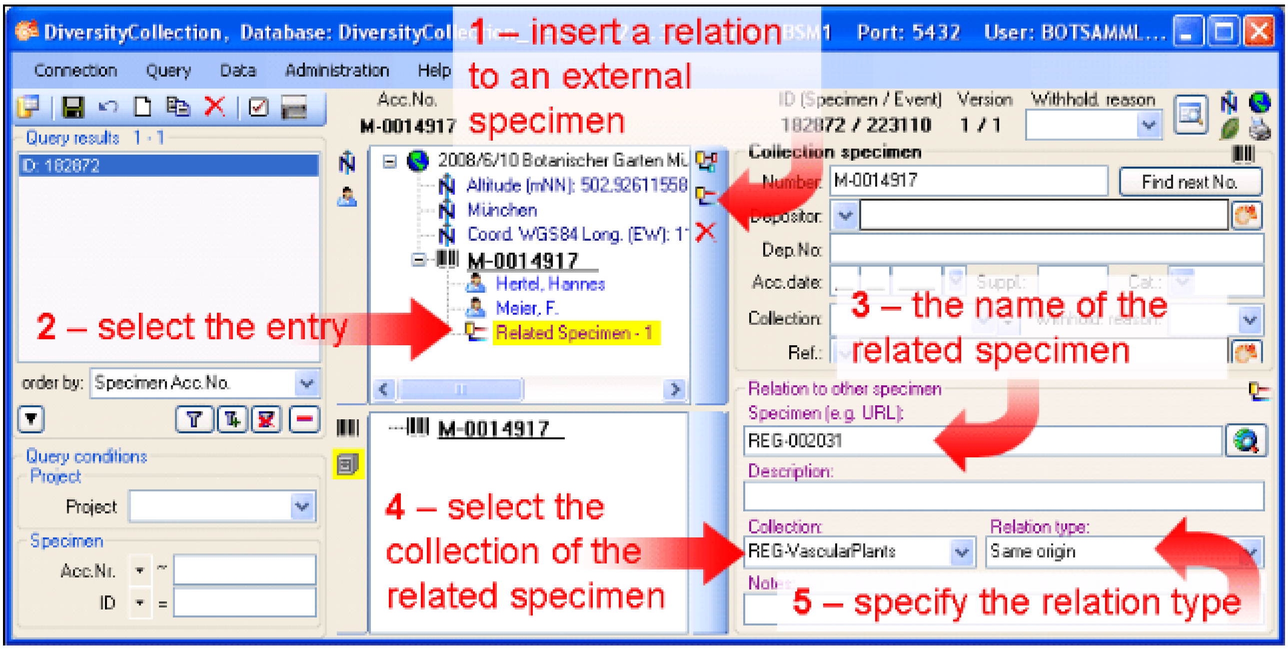
Description:

Relation type: Duplicate | Duplicate of another specimen

Notes:

2. External relations

To enter a relation to a specimen in a foreign collection insert a relation (see point **1** in image below) and select it in the overview (see point **2** in image below). Enter the name of the specimen (see point **3** in image below) and the type of the relation (see point **5** in image below).



Acc.No. M-0014917

ID (Specimen / Event): 182872 / 223110

Version: 1 / 1

Query results: ID: 182872

order by: Specimen Acc.No.

2008/6/10 Botanischer Garten Mü
- Altitude (mNN): 502.92611558
- München
- Coord. WGS84 Long. (EW): 1
- M-0014917
  - Hertel, Hannes
  - Meier, F.
  - Related Specimen - 1

M-0014917

Number: M-0014917

Specimen (e.g. URL): REG-002031

Description:

Collection: REG-VascularPlants

Relation type: Same origin

If there is a data set for the collection available you may select it from the list (see point **4** in image above). Otherwise you first have to add this collection to the list. If you have permission to edit the collections, choose Administration -> Collections from the menu to add a collection. See the section Collection for details.

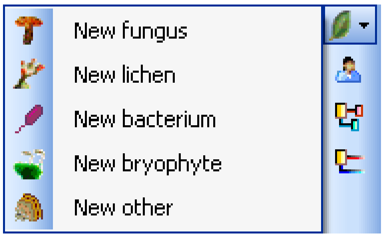
For further information on relations turn to the section Relation.

This tutorial is continued in the sections listed below.

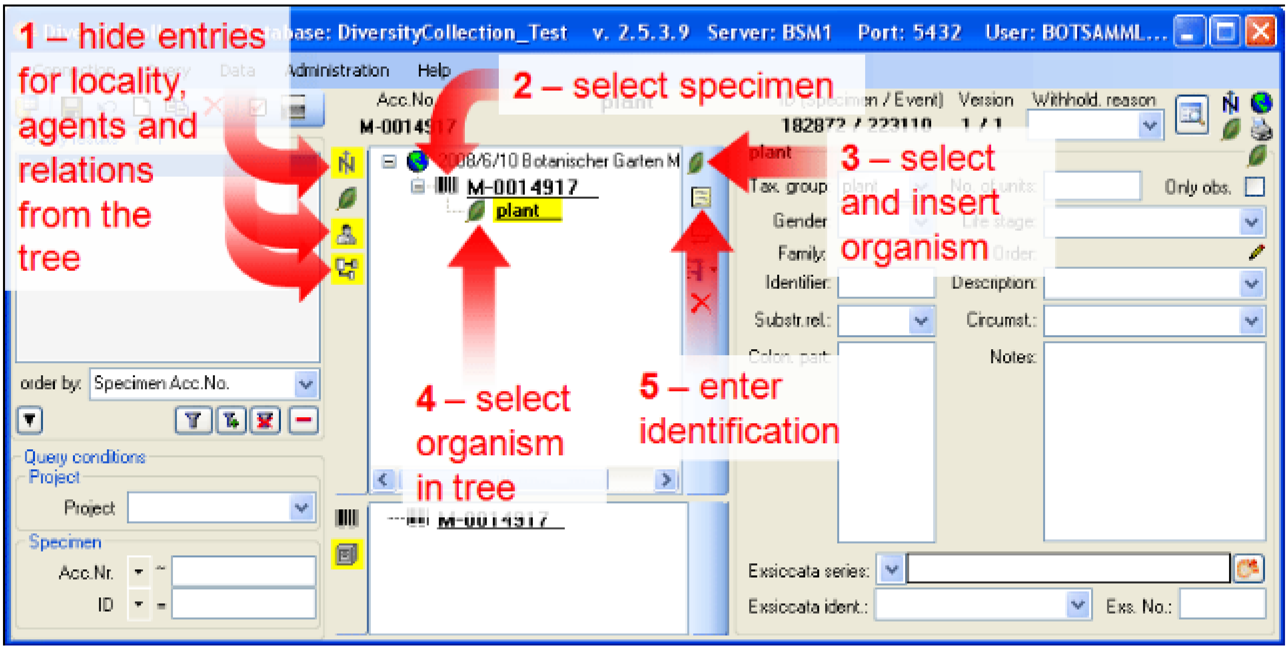
- section Organisms and identifications
- section Specimen parts and storage
- section Searching the database

Tutorial - Organisms and identifications

To focus on the specimen and its organisms hide all other entries from the tree by clicking on the corresponding buttons (see point **1** in image below). To enter the organism choose the specimen entry in the tree (see point **2** in image below). Then select the organism from the list.

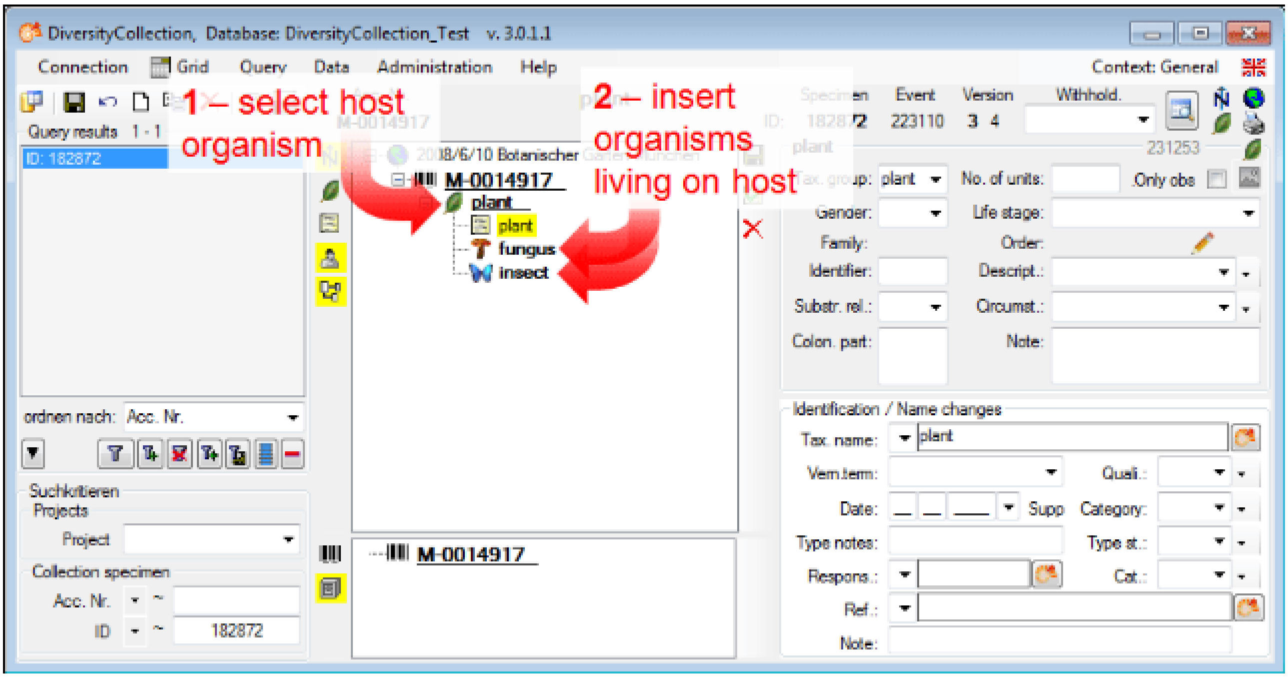


This will insert an entry for the organism underneath the entry of the specimen (see image below). To enter details for this organism select the entry in the tree (see point **3** in image below and image above).

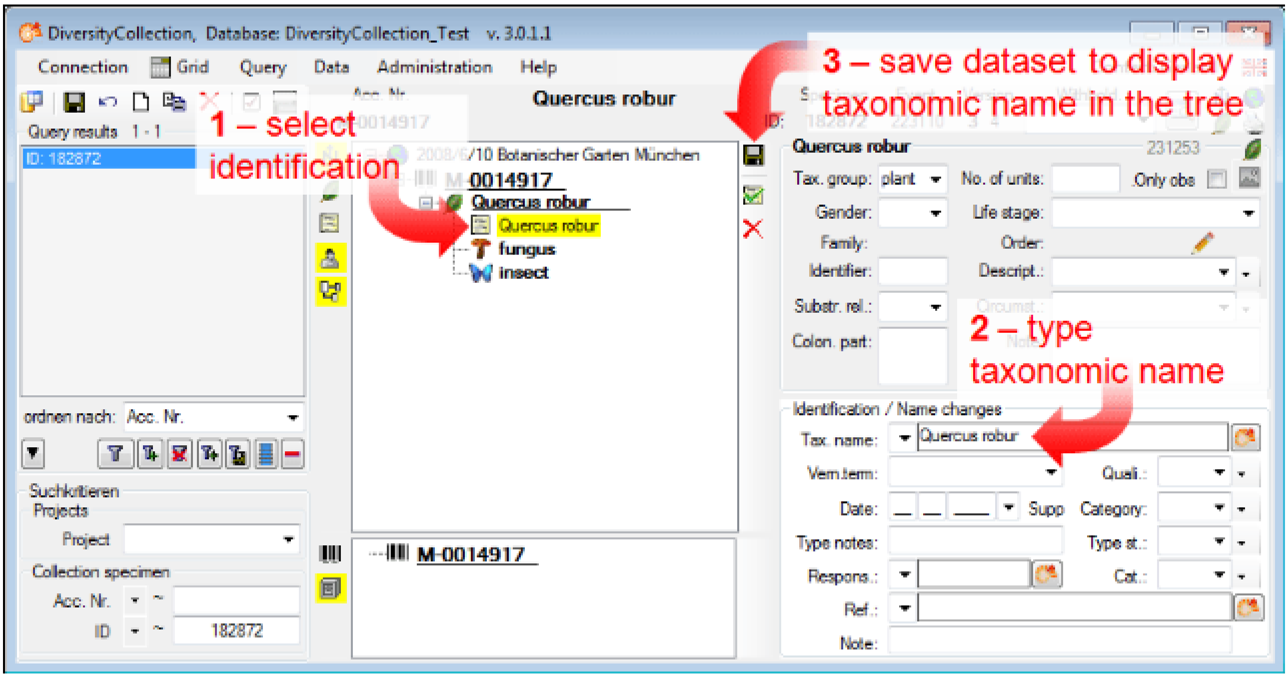


To enter an identification for this organism select it in the tree (see point **4** in image above) and click on the button (see point **5** in image above). This will insert a data set for the idenfication of the organism underneath the organism as shown above. Select this entry to enter the details of the identification.

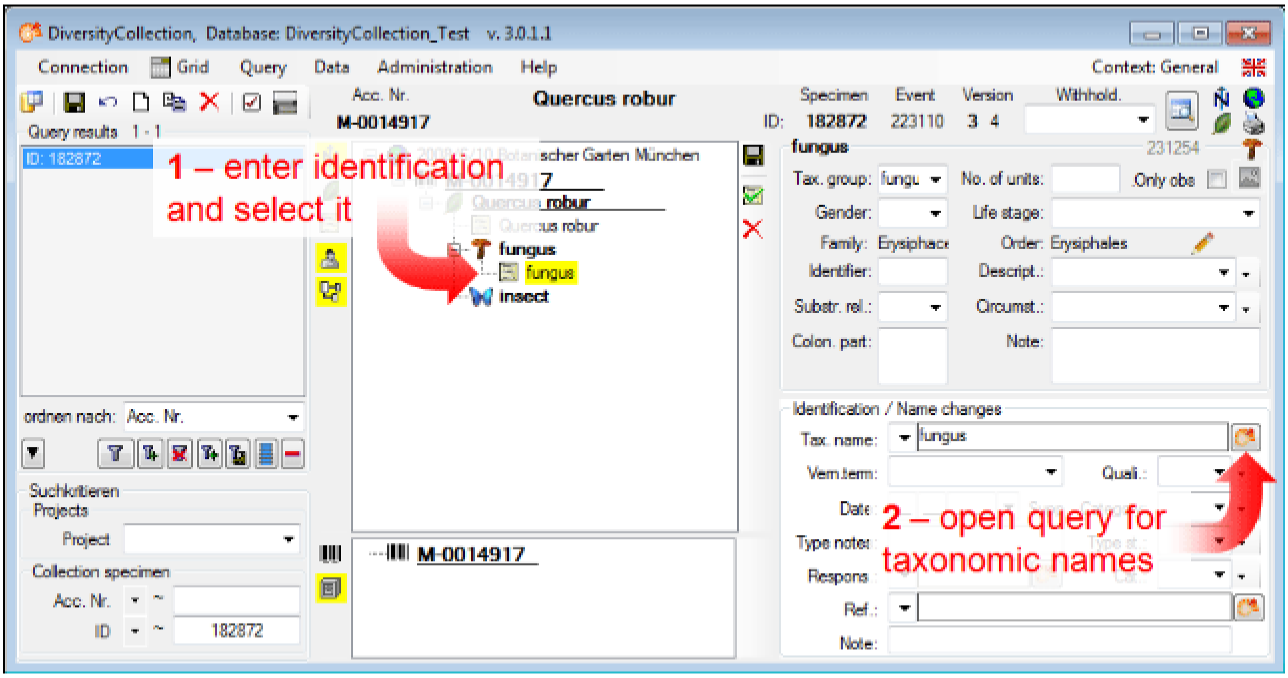
To enter more organisms living on the plant select the plant in the tree (see point **1** in image below) and create new organisms as described above (see point **2** in image below).



Now let's enter the taxonomic name of the plant. Select the entry for the identification in the tree (see point **1** in image below). As a simple method to enter a taxonomic name simply type it in the field **Tax. name** (see point **2** in image below). To save the data set and display the taxonomic name in the tree click on the button (see point **3** in image below).



Now insert an identification for the fungus (see point **1** in image below).



Acc. Nr. M-0014917 **Quercus robur**

ID: 182872 223110 3 4

ID: 182872

ordnen nach: Acc. Nr.

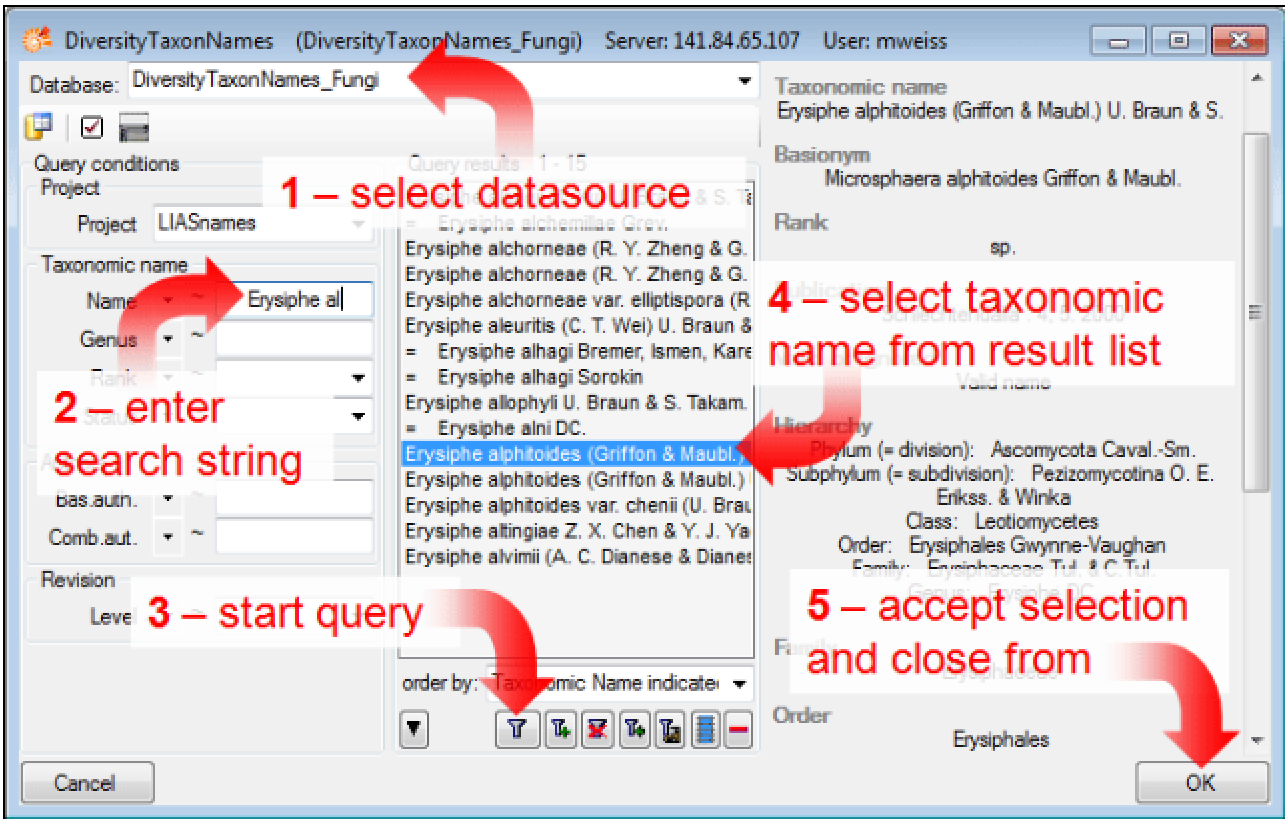
Acc. Nr. M-0014917; ID 182872

fungus; Tax. group: fungu; Family: Erysiphace; Order: Erysiphales; Tax. name: fungus

1 – enter identification and select it

2 – open query for taxonomic names

Select the identification in the tree and click on the button (see point **2** in image above) to open a [remote query](#) as shown below. Choose the database DiversityTaxonNames_Fungi (see point **1** in image below), enter the conditions for the query, e.g. the beginning of the taxonomic name (see point **2** in image below) and start the query (see point **3** in image below). From the result list select the taxonomic name (see point **4** in image below) and click OK (see point **5** in image below) to transfer the selected name to the main form.



Database: DiversityTaxonNames_Fungi

Project: LIASnames

Name: Erysiphe al

Erysiphe alchorneae (R. Y. Zheng & G.
Erysiphe alchorneae (R. Y. Zheng & G.
Erysiphe alchorneae var. ellipsispora (R
Erysiphe aleuritis (C. T. Wei) U. Braun &
= Erysiphe alhagi Bremer, Ismen, Kare
= Erysiphe alhagi Sorokin
Erysiphe allophyli U. Braun & S. Takam.
= Erysiphe alni DC.
Erysiphe alphitoides (Griffon & Maubl.)
Erysiphe alphitoides (Griffon & Maubl.)
Erysiphe alphitoides var. chenii (U. Brau
Erysiphe altingiae Z. X. Chen & Y. J. Ya
Erysiphe alvimii (A. C. Dianese & Dianes

order by: Taxonomic Name indicated

Taxonomic name: Erysiphe alphitoides (Griffon & Maubl.) U. Braun & S.

Basionym: Microsphaera alphitoides Griffon & Maubl.

Rank: sp.

Hierarchy:
Phylum (= division): Ascomycota Caval.-Sm.
Subphylum (= subdivision): Pezizomycotina O. E. Eriks. & Winka
Class: Leotiomycetes
Order: Erysiphales Gwynne-Vaughan
Family: Erysiphaceae Tul. & C. Tul.

Order: Erysiphales

1 – select datasource

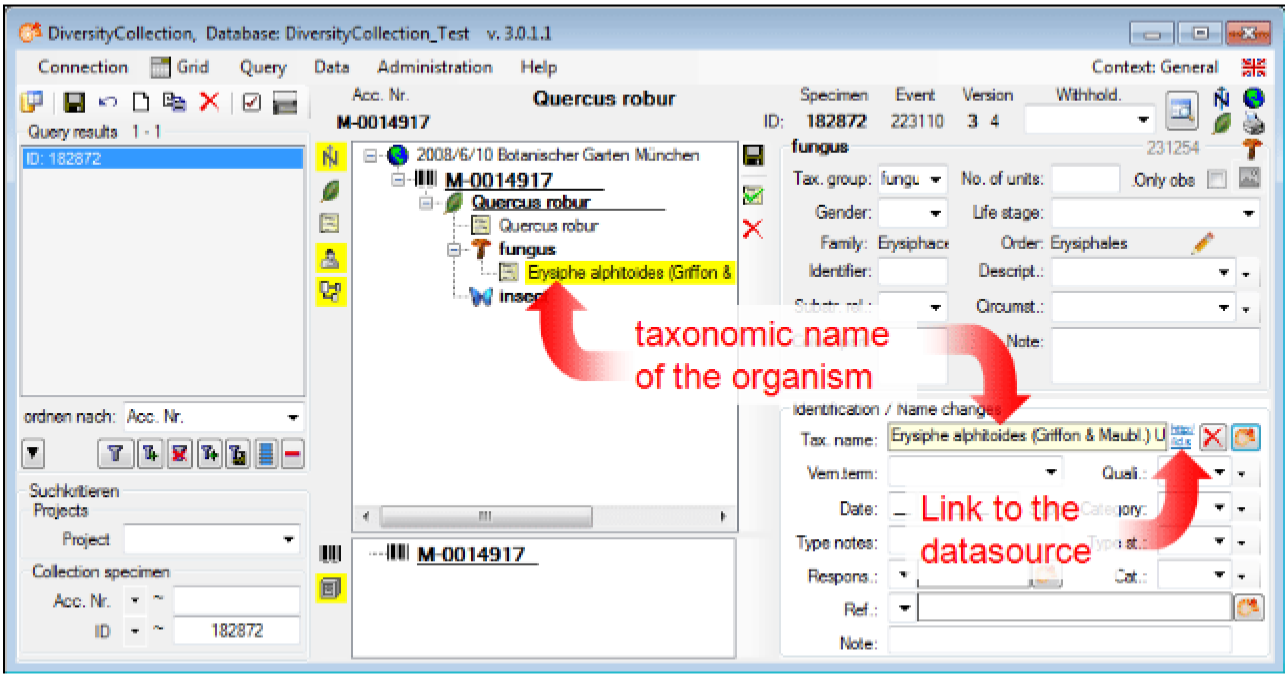
2 – enter search string

3 – start query

4 – select taxonomic name from result list

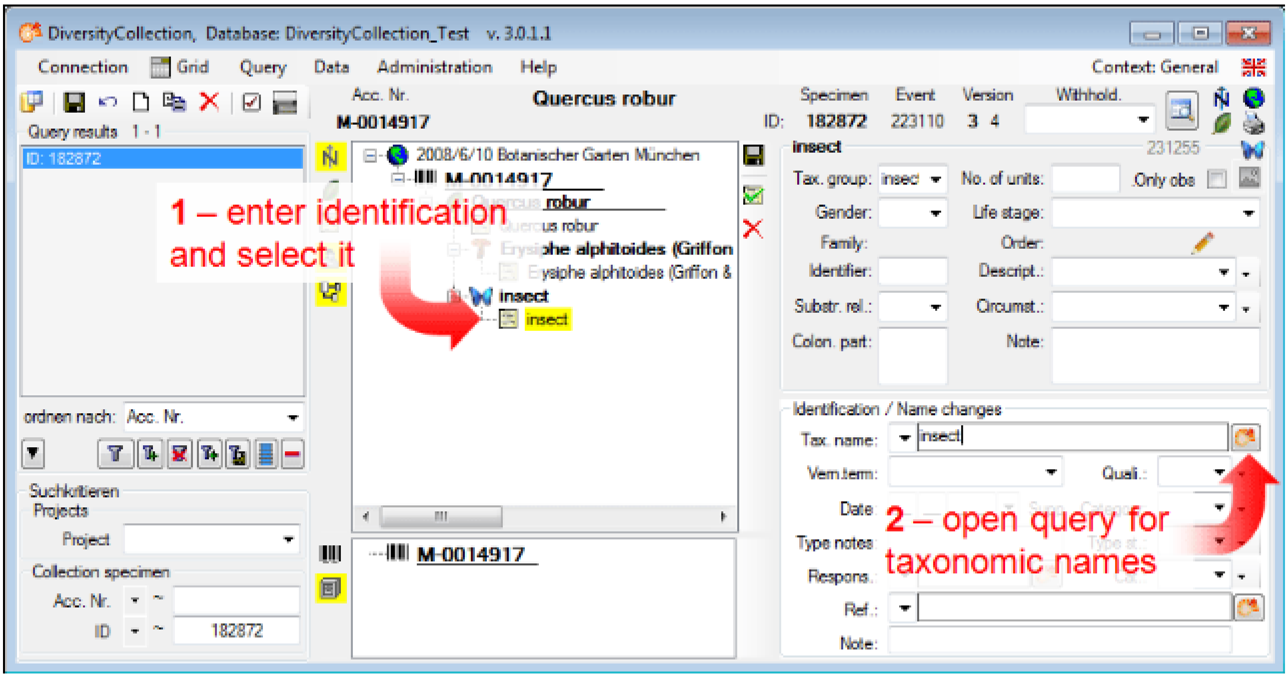
5 – accept selection and close from

The name of the selected taxon together with the link to the datasource (see image below) will be inserted in the field for the taxonomic name. The taxonomic name can not be directly edited as long as the name is linked to a datasource (indicated by the yellow background). To remove the link you need to use the ✕button. To see the entire information on the linked name as stored in the datasource click on the button.



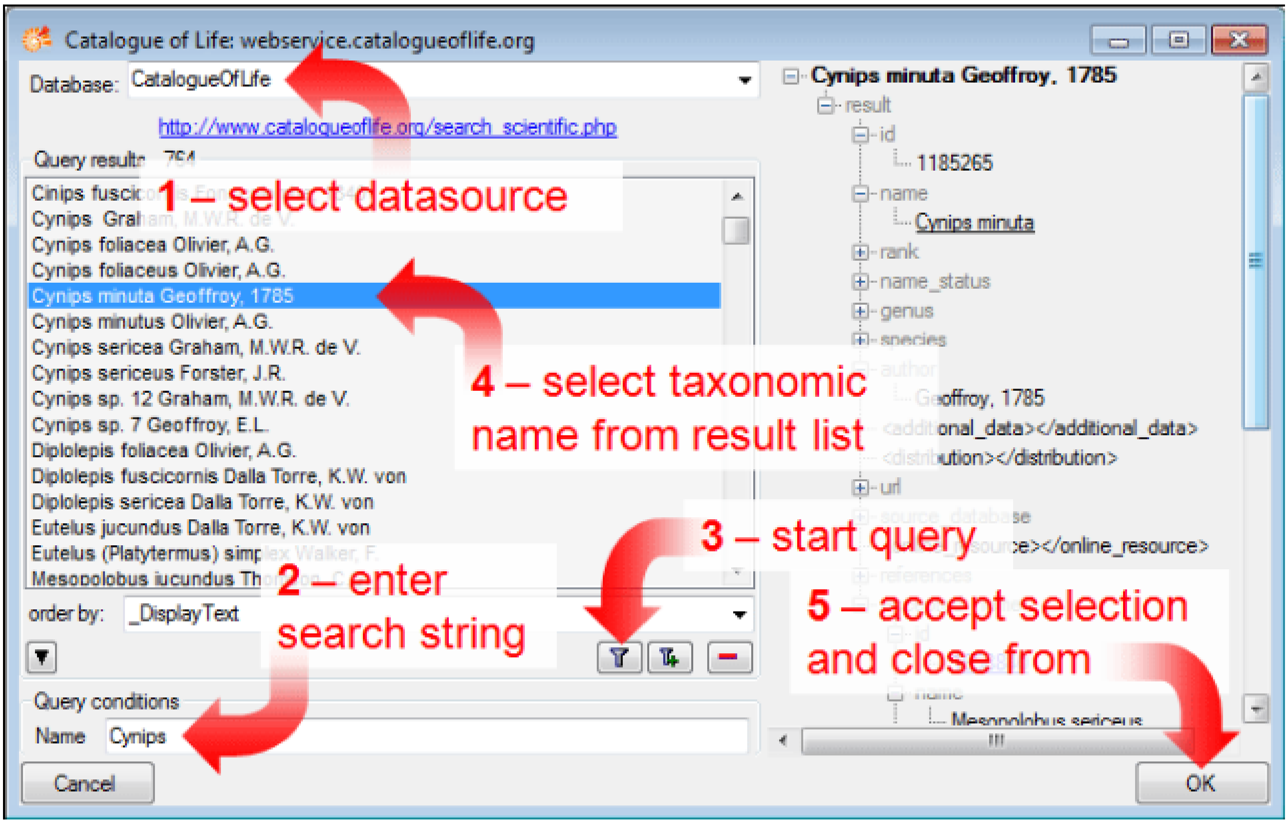
Acc. Nr.: M-0014917
Quercus robur
Specimen: 182872
Event: 223110
Version: 3 4
ID: 182872
fungus
Tax. group: fungu
Family: Erysiphace
Order: Erysiphales
Tax. name: Erysiphe alphitoides (Griffon & Maubl.) U

As as an example for the last variant enter an identification for the insect (see below). Select the identification in the tree (see point **1** in image below) and click on the button (see point **2** in image below) to open a remote query.



Acc. Nr.: M-0014917
Quercus robur
Specimen: 182872
Event: 223110
Version: 3 4
ID: 182872
insect
Tax. group: insec
Tax. name: insect

A window for the access to webservices and other modules will open as shown below. Here select CatalogueOfLife (see point **1** in image below) as a datasource. This will query the webservice of Catalogue of Life for a taxonomic name. Enter the beginning of the taxonomic name (see point **2** in image below) and start the query (see point **3** in image below). From the result list select the taxonomic name (see point **4** in image below) and click OK (see point **5** in image below) to transfer the selected name to the main form.



1 – select datasource

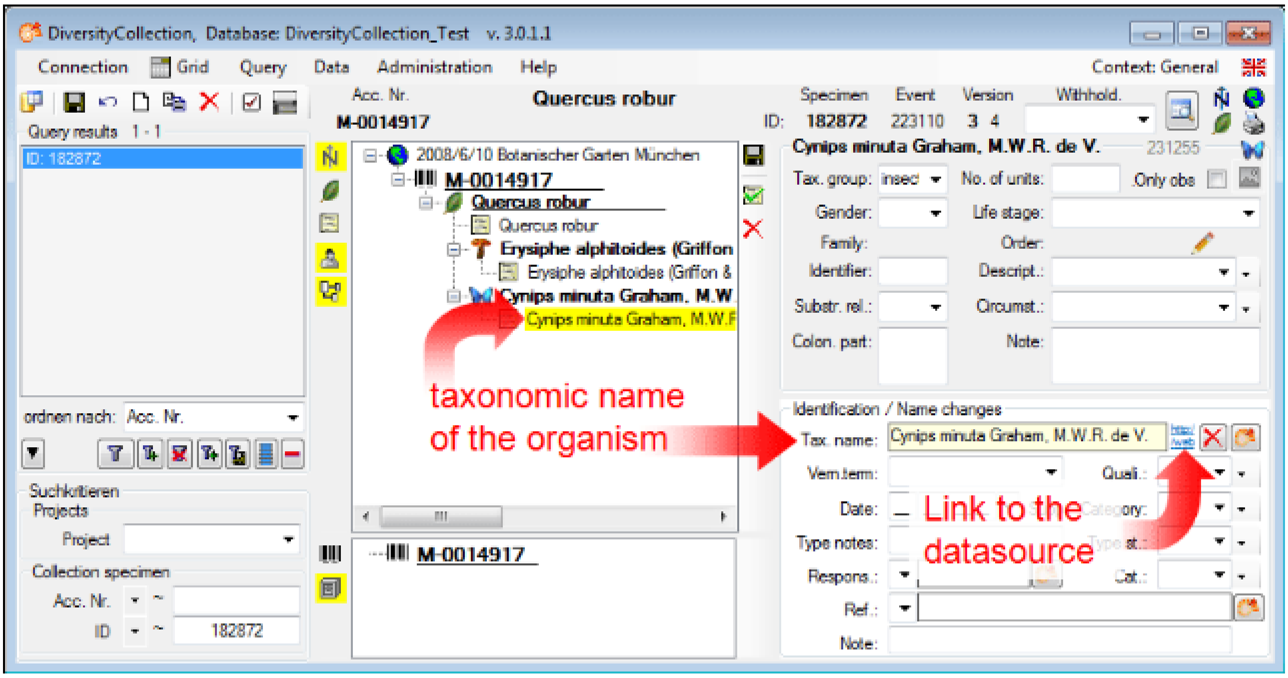
2 – enter search string

3 – start query

4 – select taxonomic name from result list

5 – accept selection and close from

The name of the selected taxon together with the link (see image below) to the data source will be inserted in the field for the taxonomic name. The taxonomic name can not be directly edited as long as the name is linked to a data source (indicated by the yellow background). To remove the link you need to use the ✕button. To see the entire information on the linked name as stored in the data source click on the button.



taxonomic name of the organism

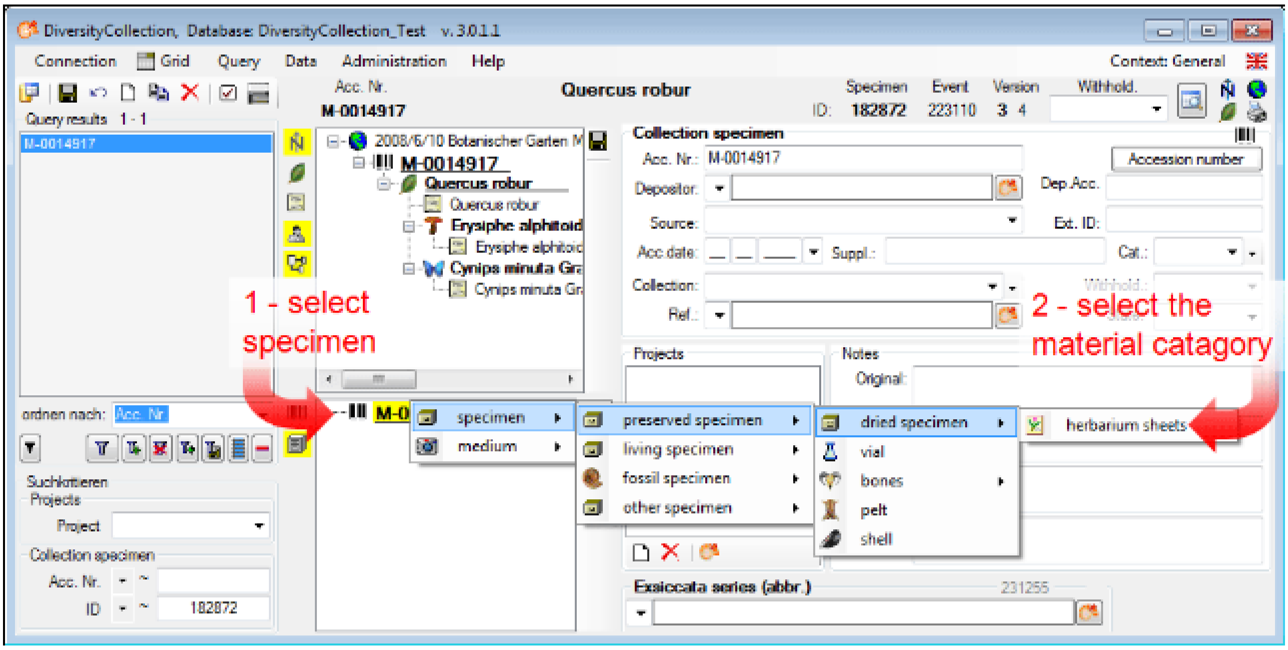
Link to the datasource

This tutorial is continued in the sections listed below.

- section Specimen parts and storage
- section Searching the database

Tutorial - Specimen parts and storage

To enter the data connected with the storage of the specimen select the specimen entry in the bottom tree view (see point **1** in image below). In the command panel at the right of the tree view a button will appear where you may select the type of the stored material. In the hierarchy select "**herbarium sheets**" as shown below (see point **2** in image below).



DiversityCollection, Database: DiversityCollection_Test v. 3.0.1.1

Acc. Nr.: M-0014917

Quercus robur

Specimen ID: 182872, Event: 223110, Version: 3 4

Context: General

Query results 1 - 1: M-0014917

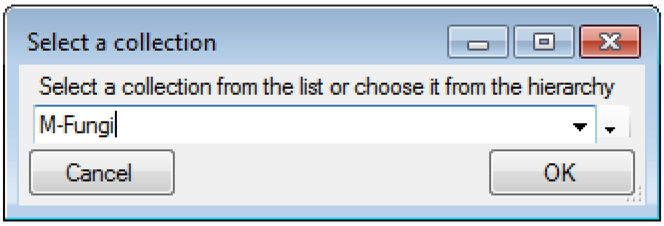
ordnen nach: Acc. Nr

Collection specimen: Acc. Nr.: M-0014917

Collection specimen: ID: 182872

Exsiccata series (abbr.): 231255

A dialog will appear where you are required to enter the collection where your specimen are stored (see below).

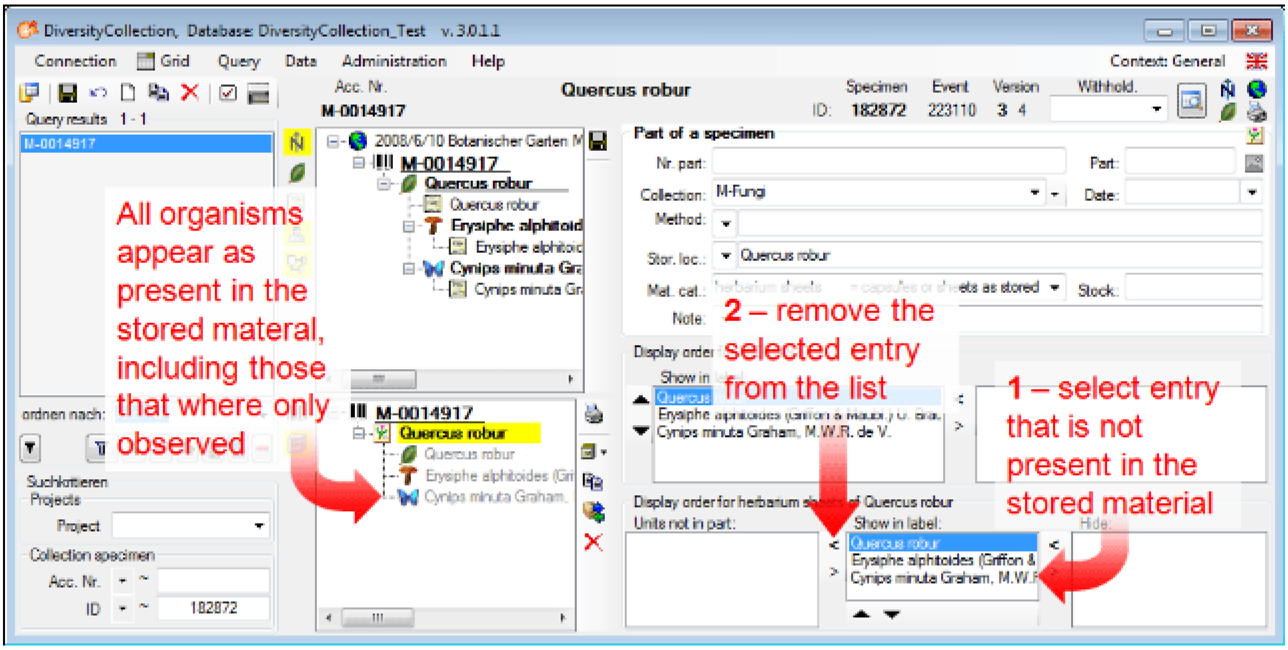


Select a collection

Select a collection from the list or choose it from the hierarchy

M-Fungi

Select the collection from the list or the hierarchy and click OK to close the dialog. The bottom tree will now contain the selected material with all organisms (see below).

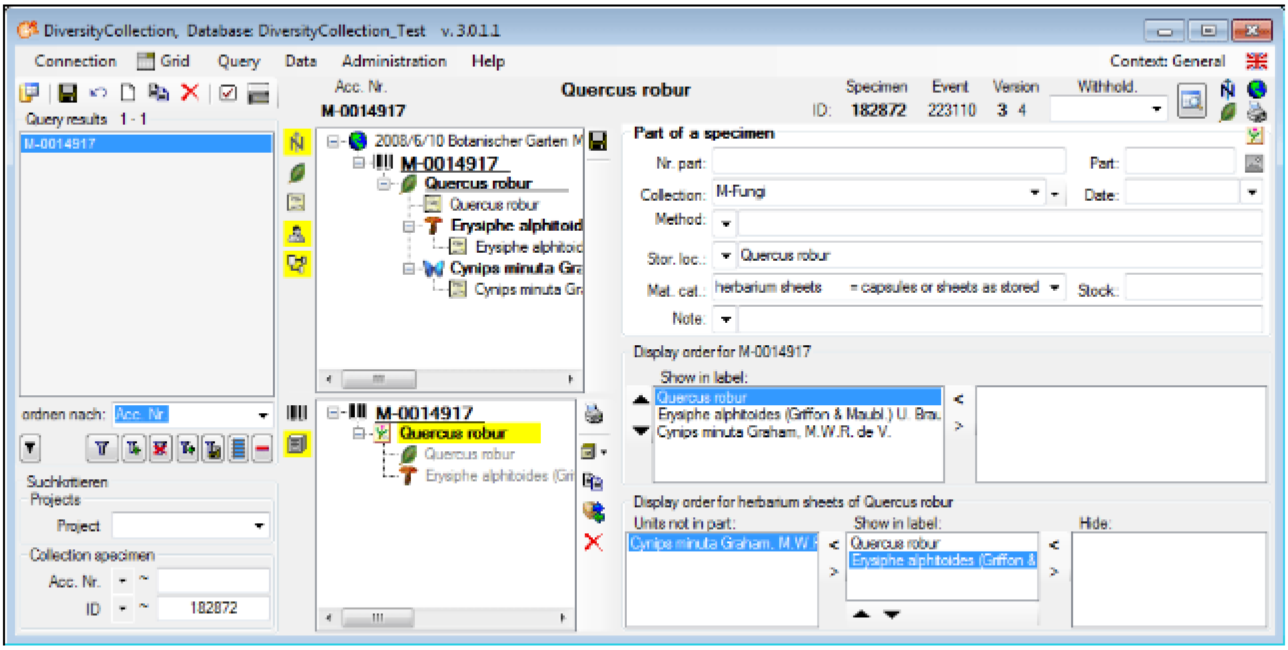


All organisms appear as present in the stored materal, including those that where only observed

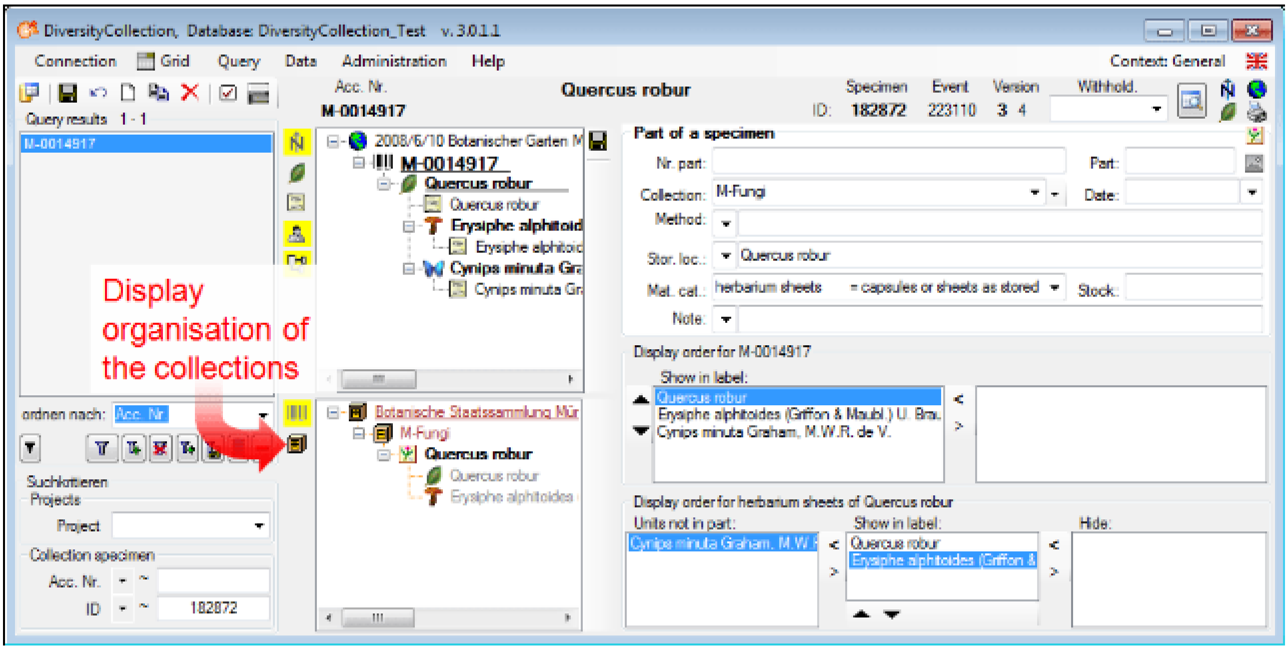
2 – remove the selected entry from the list

1 – select entry that is not present in the stored material

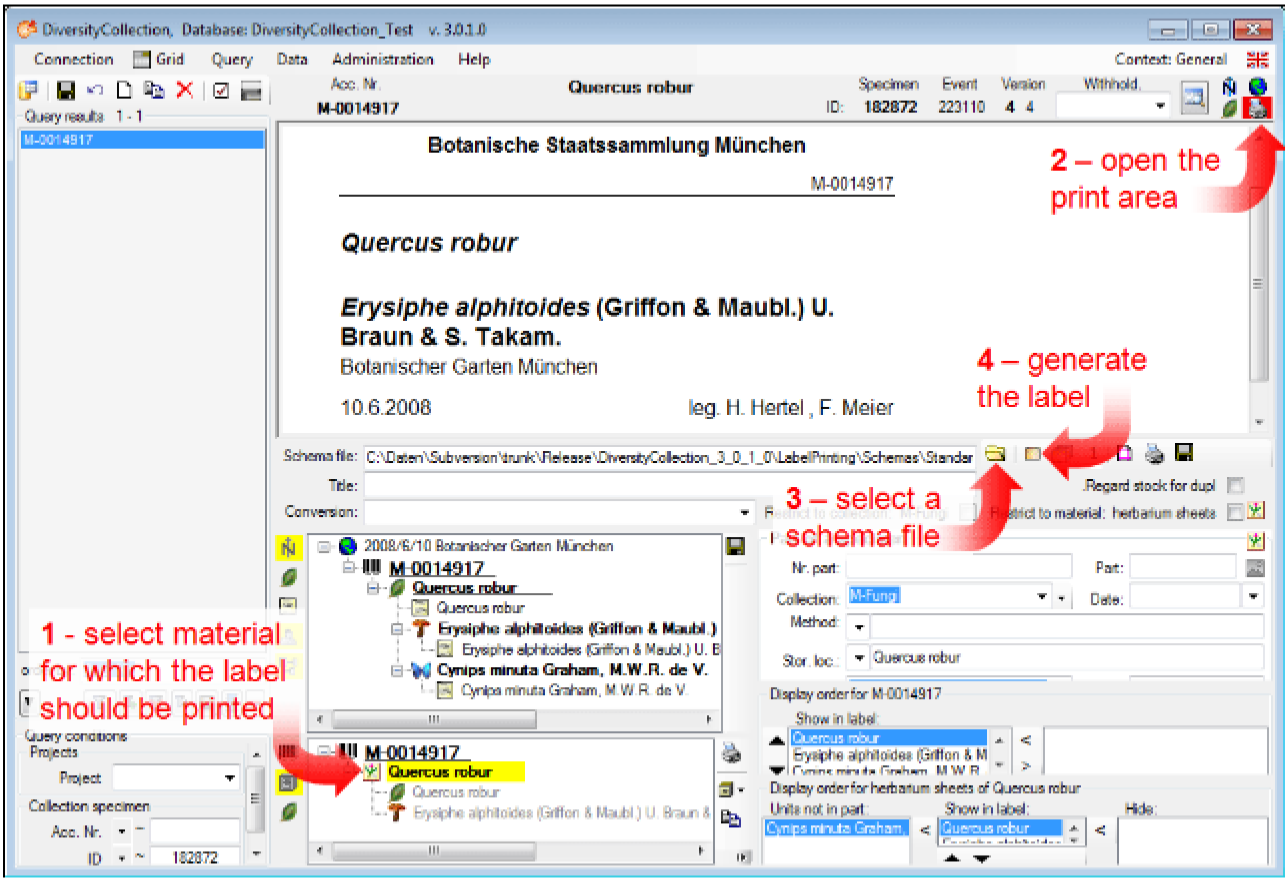
Let's assume that the insect is not present in the specimen, but e.g. has only been observed during the collection of the sample. To document this remove the entry for the insect from the **Show in label** list to the **Units not in part** list: Select it (see point **1** in image above) and remove it (see point **2** in image above) (click on the **<** button). The result is shown below.



To see the exact position within the collection click on the ▤button at the left side of the tree. The tree will change as shown below where all the collections and subcollections together with the parts of the specimen are listed (see below).



To print a label for a stored part of the specimen select it in the tree (see point **1** in image below) and click on the button in the upper right corner to open the area for the label (see point **2** in image below). Click on the button (see point **3** in image below) to select a Schema file (e.g. Standard.xslt). Then click on the button to generate a label (see point **4** in image below).



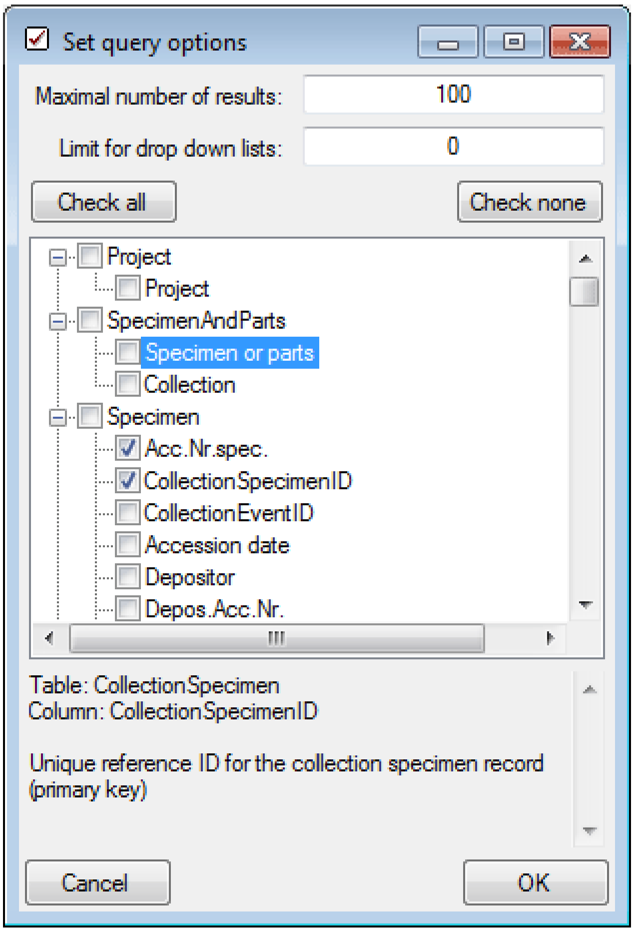
Turn to the Section part for more details.

This tutorial is continued in the sections listed below.

- section Searching the database

Tutorial - Query

To search for data in the database use the query sector in the left part of the window. 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

- ☐ Project
  - ☐ Project
- ☐ SpecimenAndParts
  - ☐ Specimen or parts
  - ☐ Collection
- ☐ Specimen
  - ☑ Acc.Nr.spec.
  - ☑ CollectionSpecimenID
  - ☐ CollectionEventID
  - ☐ Accession date
  - ☐ Depositor
  - ☐ Depos.Acc.Nr.

Table: CollectionSpecimen
Column: CollectionSpecimenID

Unique reference ID for the collection specimen record (primary key)

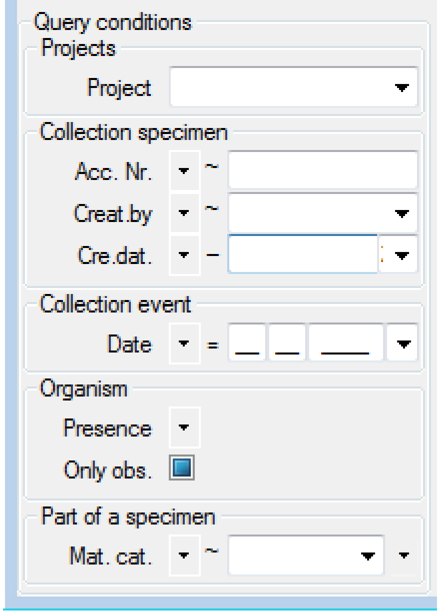
With the **Maximum number of results** you may limit the package size which should be retrieved from the server. For a slow connection to the database server choose a low value (e.g. 100 as set by default).

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. Then select the entries

- Project -> Project
- Specimen -> Accession number of specimen
- Specimen -> The user who created the data set
- Specimen -> The date when the data set was created
- Event -> Collection date
- Organism -> Organism present
- Organism -> Only observed
- Storage -> Material category
- Image -> Type

Click OK to close the window. Your query conditions will be displayed as in the image below.



Project -> Project: Here you may choose from a list of possible entries. Select your current project.

Collection specimen -> Acc. Nr.: From the operator drop-down list choose "~" and enter the first letters of your accession number. You may include wildcards. Other options are e.g. "-" for a range or ">" for a lower limit. The conditions will be interpreted as text! So 2 will appear after 10 etc.

Collection specimen -> Creat. by.: From the operator drop-down list choose "=" and choose your user name from the list.

Collection specimen -> Cre. dat.: From the operator drop-down list choose "=" and choose the current date with the help of the calender.

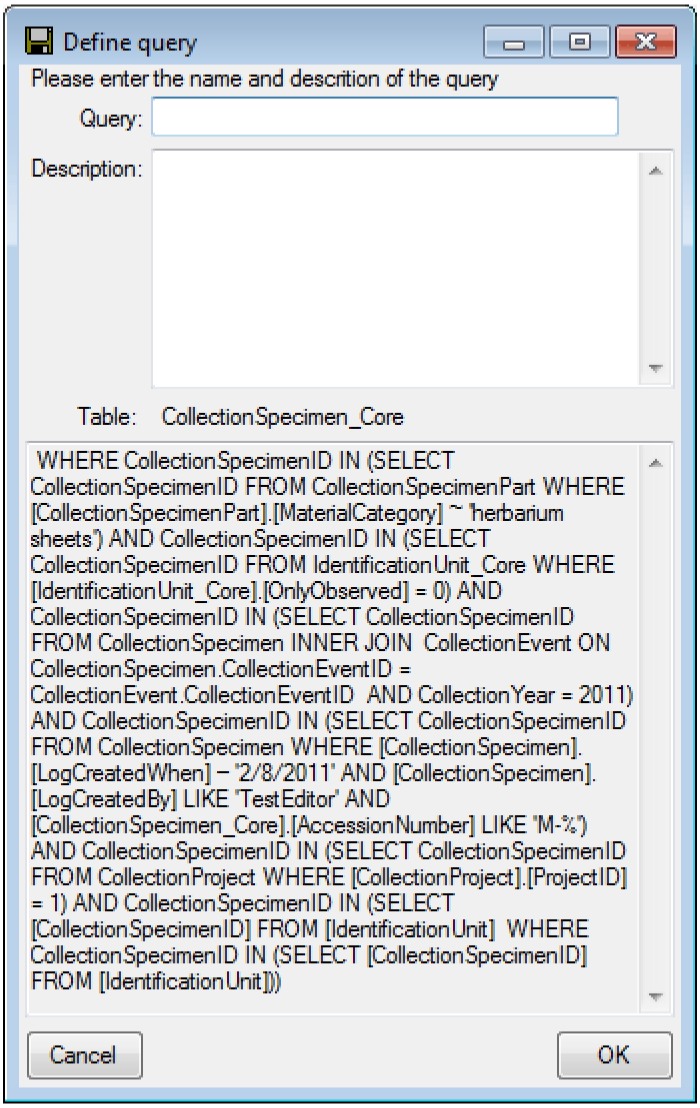
Collection event -> Date: >From the operator drop-down list choose "=" and enter the current year in the last field.

Organism -> Presence: From the operator drop-down list choose "•" which means that an organism is present.

Organism -> Only obs: Uncheck the checkbox to find organisms which were not only observed.

Part of a specimen -> Mat.cat.: Use the ▼button on the right of the combobox to open the hierarchy and select "herbarium sheet".

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



Please enter the name and descrition of the query

Query:

Description:

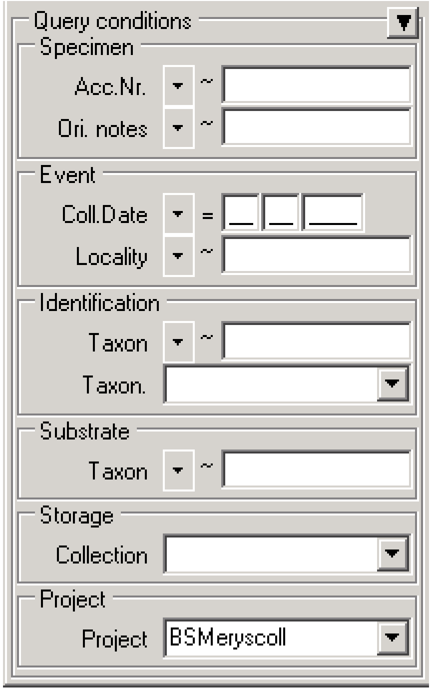
Table: CollectionSpecimen_Core

```
 WHERE CollectionSpecimenID IN (SELECT
CollectionSpecimenID FROM CollectionSpecimenPart WHERE
[CollectionSpecimenPart].[MaterialCategory] ~ 'herbarium
sheets') AND CollectionSpecimenID IN (SELECT
CollectionSpecimenID FROM IdentificationUnit_Core WHERE
[IdentificationUnit_Core].[OnlyObserved] = 0) AND
CollectionSpecimenID IN (SELECT CollectionSpecimenID
FROM CollectionSpecimen INNER JOIN  CollectionEvent ON
CollectionSpecimen.CollectionEventID =
CollectionEvent.CollectionEventID  AND CollectionYear = 2011)
AND CollectionSpecimenID IN (SELECT CollectionSpecimenID
FROM CollectionSpecimen WHERE [CollectionSpecimen].
[LogCreatedWhen] – '2/8/2011' AND [CollectionSpecimen].
[LogCreatedBy] LIKE 'TestEditor' AND
[CollectionSpecimen_Core].[AccessionNumber] LIKE 'M-%')
AND CollectionSpecimenID IN (SELECT CollectionSpecimenID
FROM CollectionProject WHERE [CollectionProject].[ProjectID]
= 1) AND CollectionSpecimenID IN (SELECT
[CollectionSpecimenID] FROM [IdentificationUnit]  WHERE
CollectionSpecimenID IN (SELECT [CollectionSpecimenID]
FROM [IdentificationUnit]))
```

Queries - overview

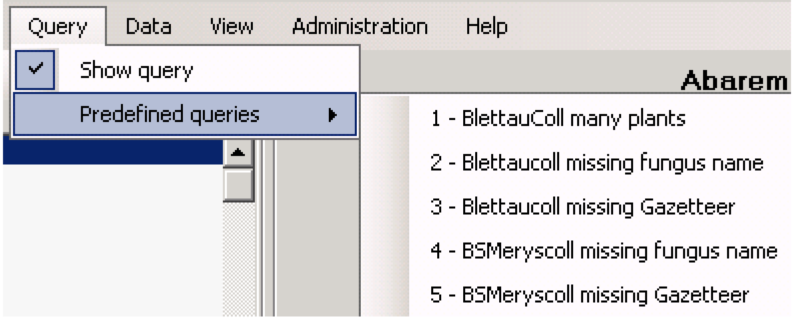
To search for specimens in the database you may choose from 3 options:

With the user defined queries you may define any query condition - this is the default query mode. You may save and load these queries.

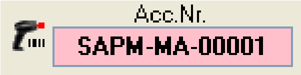


Project: BSMeryscoll

The predefined queries are defined by the system administrator and are accessible via the menu **Query** - **Predefined queries**. To return to the user-defined queries click on the **Show query conditions** ▤ button.



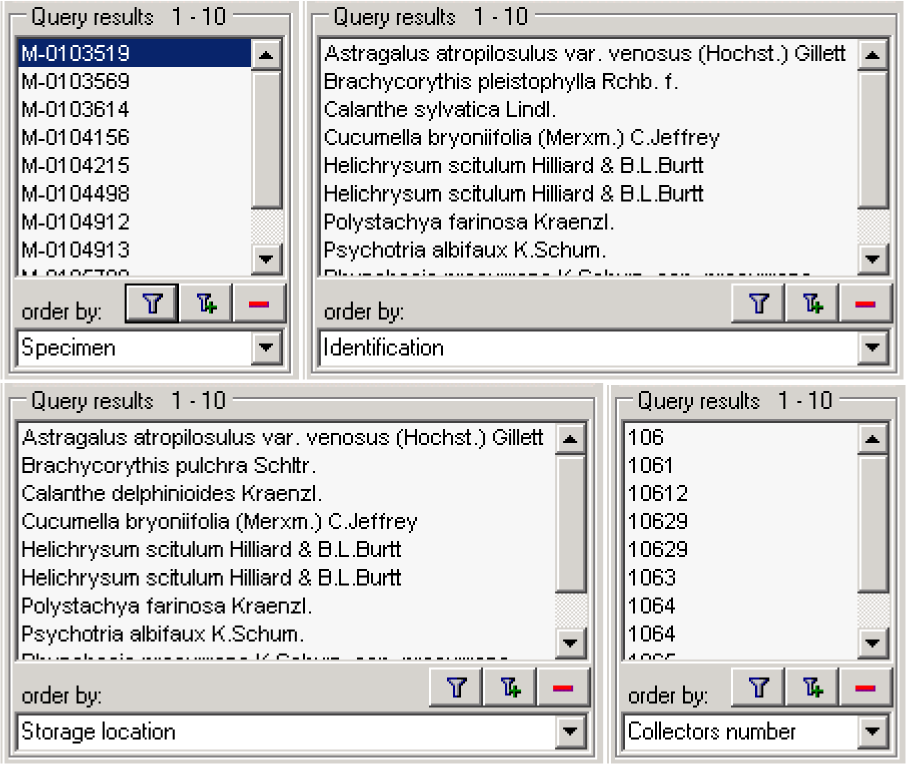
With the scan mode you may use a barcode scanner to search for a specimen. To work with the scan mode select the **Scan mode** in the **Query** menu. To return to another query mode deselect the Scan mode.



Acc.Nr. SAPM-MA-00001

Result list

The result list displays the specimens found in a query.



M-0103519
M-0103569
M-0103614
M-0104156
M-0104215
M-0104498
M-0104912
M-0104913

order by: Specimen

Astragalus atropilosulus var. venosus (Hochst.) Gillett
Brachycorythis pleistophylla Rchb. f.
Calanthe sylvatica Lindl.
Cucumella bryoniifolia (Merxm.) C.Jeffrey
Helichrysum scitulum Hilliard & B.L.Burtt
Helichrysum scitulum Hilliard & B.L.Burtt
Polystachya farinosa Kraenzl.
Psychotria albifaux K.Schum.

order by: Identification

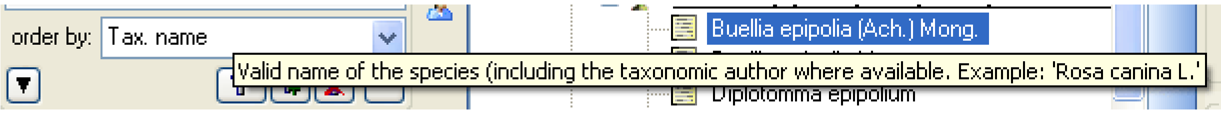
Astragalus atropilosulus var. venosus (Hochst.) Gillett
Brachycorythis pulchra Schltr.
Calanthe delphinioides Kraenzl.
Cucumella bryoniifolia (Merxm.) C.Jeffrey
Helichrysum scitulum Hilliard & B.L.Burtt
Helichrysum scitulum Hilliard & B.L.Burtt
Polystachya farinosa Kraenzl.
Psychotria albifaux K.Schum.

order by: Storage location

106
1061
10612
10629
10629
1063
1064
1064

order by: Collectors number

The specimens may be displayed with their accession number, their identifications or their storage location etc. as shown in the images above. To view further information on the chosen field simply place the mouse in the field. A text box will appear with the description of the field (see below).



order by: Tax. name

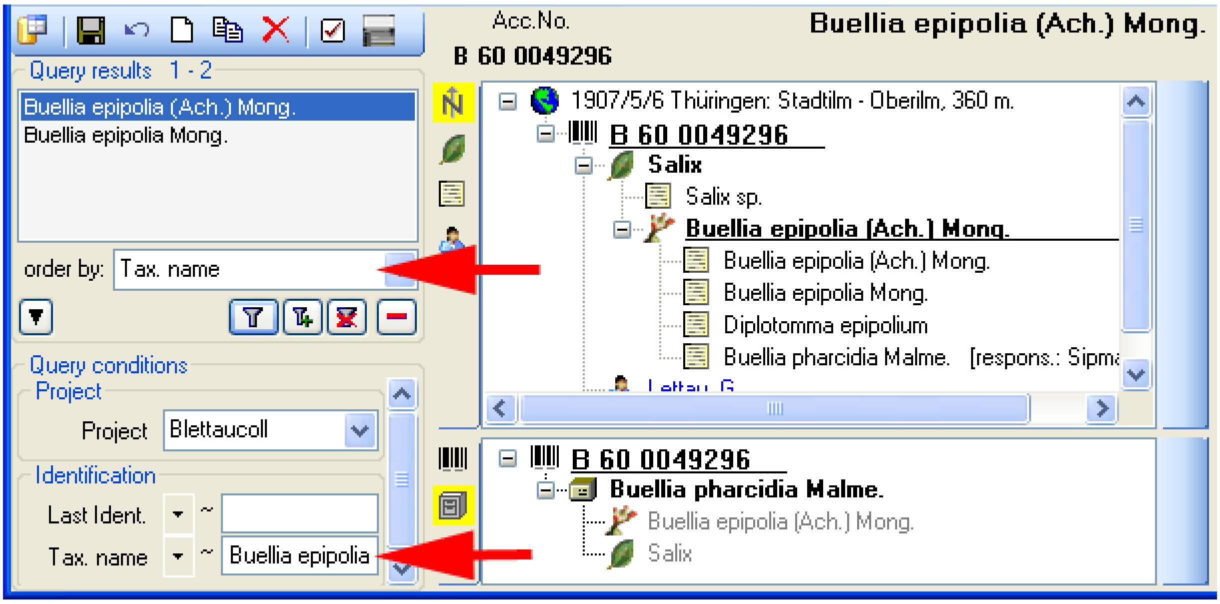
Buellia epipolia (Ach.) Mong.

Valid name of the species (including the taxonomic author where available. Example: 'Rosa canina L.'

Diplotomma epipolium

You may restrict the maximum number of specimens and query options (click on the ☑ button), if you have for example a slow connection to the database. As a default the maximum number is set to 100. If the number of data sets according to your query is higher than the maximum value set in the query options, it will be indicated in the header of the list.

To ensure that restrictions set in the query conditions will be applied to the specimen list make sure that you choose matching restrictions and order columns as shown below. In the upper example corresponding fields were used for restricting the query and the display (**Tax. name**). Here the query results will be restricted to said field.



Acc.No. B 60 0049296 — Buellia epipolia (Ach.) Mong.

Query results 1 - 2

Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.

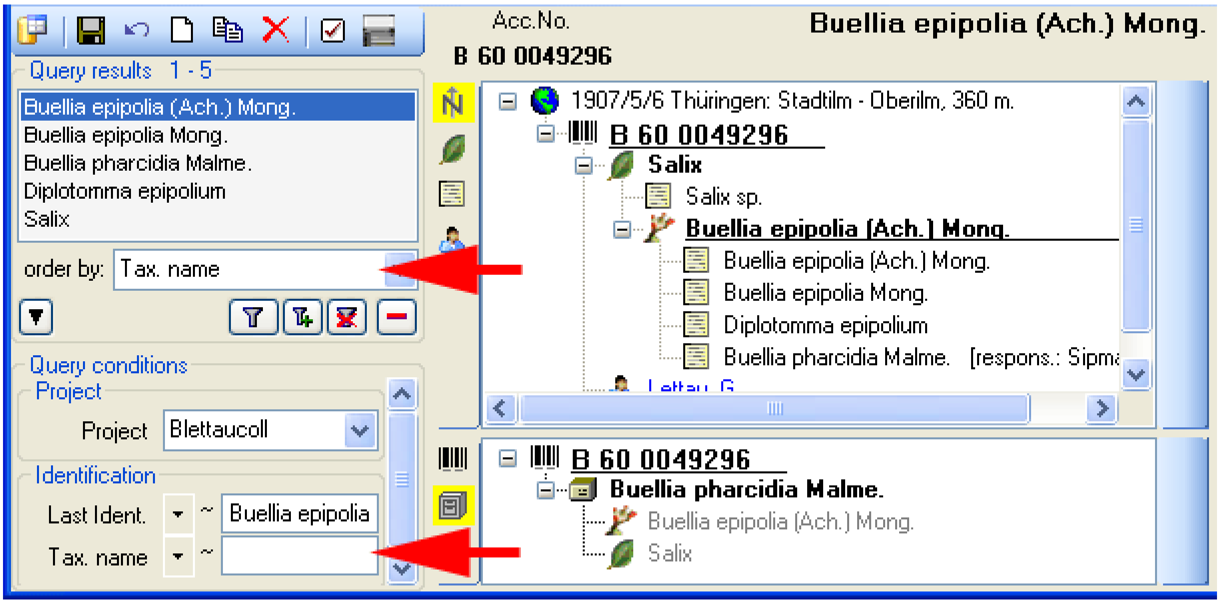
order by: Tax. name

Query conditions
Project
Project: Blettaucoll
Identification
Last Ident. ~
Tax. name ~ Buellia epipolia

1907/5/6 Thüringen: Stadtilm - Oberilm, 360 m.
B 60 0049296
Salix
Salix sp.
Buellia epipolia (Ach.) Mong.
Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.
Diplotomma epipolium
Buellia pharcidia Malme. [respons.: Sipma

B 60 0049296
Buellia pharcidia Malme.
Buellia epipolia (Ach.) Mong.
Salix

In the second example a different field for the restriction was chosen (**Last ident.** <> **Tax. name**). The query result in consequence will list all data sets with entries found in the field **Tax. name** and entries which match the restriction (see below).



Acc.No. B 60 0049296 — Buellia epipolia (Ach.) Mong.

Query results 1 - 5

Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.
Buellia pharcidia Malme.
Diplotomma epipolium
Salix

order by: Tax. name

Query conditions
Project
Project: Blettaucoll
Identification
Last Ident. ~ Buellia epipolia
Tax. name ~

1907/5/6 Thüringen: Stadtilm - Oberilm, 360 m.
B 60 0049296
Salix
Salix sp.
Buellia epipolia (Ach.) Mong.
Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.
Diplotomma epipolium
Buellia pharcidia Malme. [respons.: Sipma

B 60 0049296
Buellia pharcidia Malme.
Buellia epipolia (Ach.) Mong.
Salix

To search for specimens enter the restrictions in the fields for the search conditions and click on the ▽ button. The specimens found in the database will be shown in the result list. To add specimens with differing search conditions click on the ▽+ button. If the list of items is longer than your maximum number of returned items you may browse the next items with the ⇨ button. If you wish to remove entries from the selected list, choose them in the list and click on the ➖ button. This will not delete the data from the database but remove them from your query result.

Here are some examples you may select for display in the result list:

AccessionNumber: One entry is shown for each specimen with its corresponding accession number.

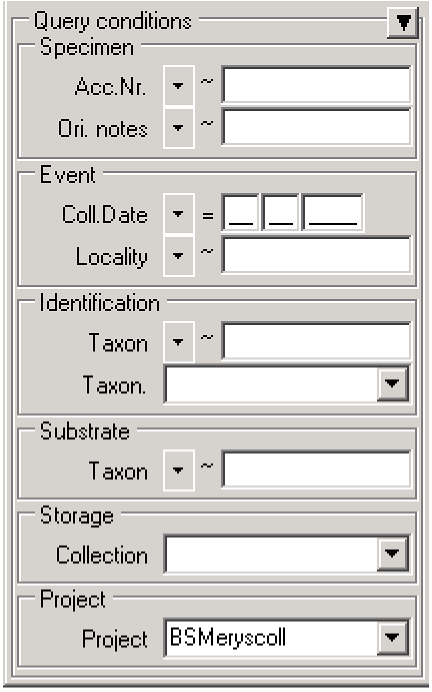
Last identification: The last identification for every unit in a specimen is shown in the list. As there can be several units in one specimen, several entries for one specimen may appear in the list.

Storage location: The storage location of every part of a specimen stored in the collections is shown in the list. As parts of a specimen can be stored in several collections under different names, several entries for one specimen may appear in the list.

Collecting number: The collecting number given by the collector of every sample of a specimen is shown in the list. A specimen may have several collectors each with a different number. Therefore, several entries for one collection specimen may appear in the list.

Query

There are two ways to search for specimens in a collection. The options for a fast search are displayed in the main window beneath the list of the items. You may change this arrangement using the / button to place the query options on the left side of the item list.



Project: BSMeryscoll

To search for specimens enter the restrictions in the fields for the search conditions and click on the button. The specimens found in the database will be shown in the specimen list. To add specimens with differing search conditions click on the button. To clear all entries in the query fields use the button. You may save and load the queries you define using the and buttons. If the list of items is longer than your maximal number of returned items, you may browse the next items with the button. To move back to the previous block of items click on the button. If you wish to remove entries from the selected list, choose them and click on the button. This will not delete the data from the database, but remove them from your query result. With the ▼and ▲buttons you may change the order of the results between ascending and descending

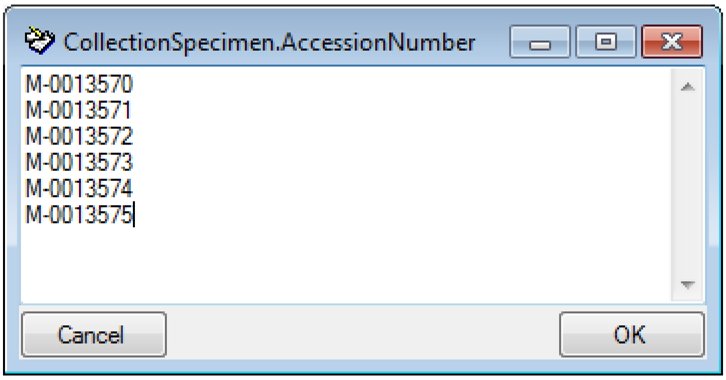
Within the query options you have several possibilities to specify your search restriction. Use the drop-down menu to switch between operators. The available operators are shown in the table below.

Operator	Meaning	Example
Text		
~	search for an entry like ...	Pinus s[iy]lvestris % (you may use wildcards)
=	search for an entry exactly equal to ...	Pinus silvestris L.
≠	search for an entry not like ...	Pinus s[iy]lvestris % (you may use wildcards)
∅	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 higher 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 higher 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 which is not equal to ...	M-Fungi
∅	search for missing entry ...	
•	search for present entry ...	
Δ	search including children 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 ...	
Geography		
Use 🌐button to set geography		
‡	Search for entries with a maximal distance of ...	POINT(24.24 45.243) | 50 km
O	Search for entries within an area	POLYGON(34.5 ...
¤	Search for entries outside an area	POLYGON(34.5 ...
•	search for present entry ...	

For yes/no fields exists a checkbox with 3 options: ☑= yes, ☐= no, 🟩= undefined

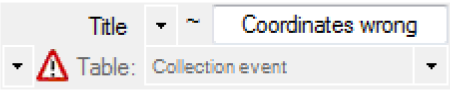
For a search within a list (using the "|" operator) you may double click in the text field to open a window where you can enter your values. To separate the values either use the "|" sign or a new line as shown in the image below.



M-0013570
M-0013571
M-0013572
M-0013573
M-0013574
M-0013575

Query annotation

The query for annotations deviate from the standard query (see below). Additionally, you may specify a type of the annotation (Annotation 📝, Problem ⚠, Reference 📖) and the linked table (see Annotation).


Title ~ Coordinates wrong

⚠ Table: Collection event

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

To change the displayed fields for searching specimens click on the ☑ button to change the query options.

Scan mode

To search for a specimen with the help of a barcode-scanner select the **Scan mode** from the Query menu. The query part will be hidden and the field for the accession number will be accessible for the entry via the scanner. If the field for the entry of the accession number Acc.Nr.: is not activated, move the mouse to the field to activate it. Once you scan the barcode the program will start the search for the specimen in the database.

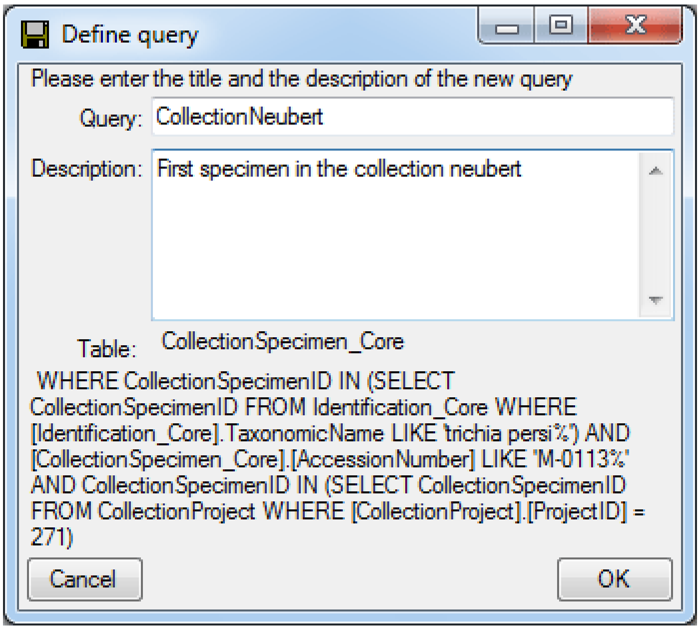
Grid mode

To edit the data in a data grid choose the **Grid mode** from the Query menu. The query part will be hidden and a table will appear where every data set from the query result list is restricted to one line. Please keep in mind, that in this view, you can only see a limited part of the data. For example, you will only see the last identifications for an organism. The selection of the visible fields can be adapted in the tree above the list.

To replace a part of a text in a column select the column, enter the text which should be replaced and enter the replacement in the corresponding fields (see below). To start the replacement click the button.

Save query

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



Please enter the title and the description of the new query

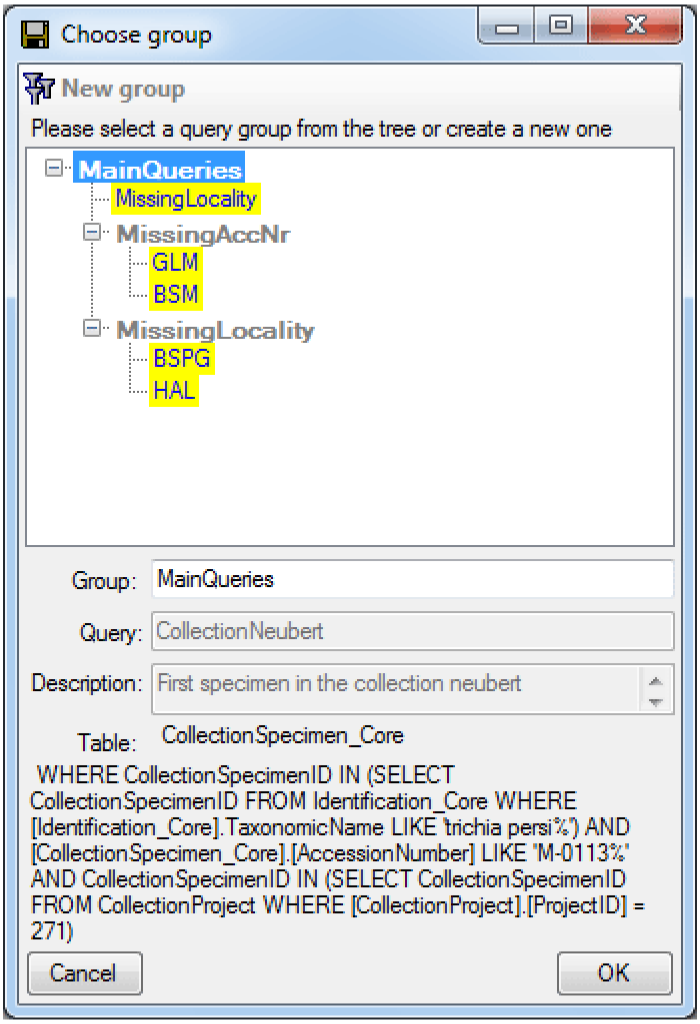
Query: CollectionNeubert

Description: First specimen in the collection neubert

Table: CollectionSpecimen_Core

```
 WHERE CollectionSpecimenID IN (SELECT
CollectionSpecimenID FROM Identification_Core WHERE
[Identification_Core].TaxonomicName LIKE 'trichia persi%') AND
[CollectionSpecimen_Core].[AccessionNumber] LIKE 'M-0113%'
AND CollectionSpecimenID IN (SELECT CollectionSpecimenID
FROM CollectionProject WHERE [CollectionProject].[ProjectID] =
271)
```

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



Please select a query group from the tree or create a new one

Group: MainQueries

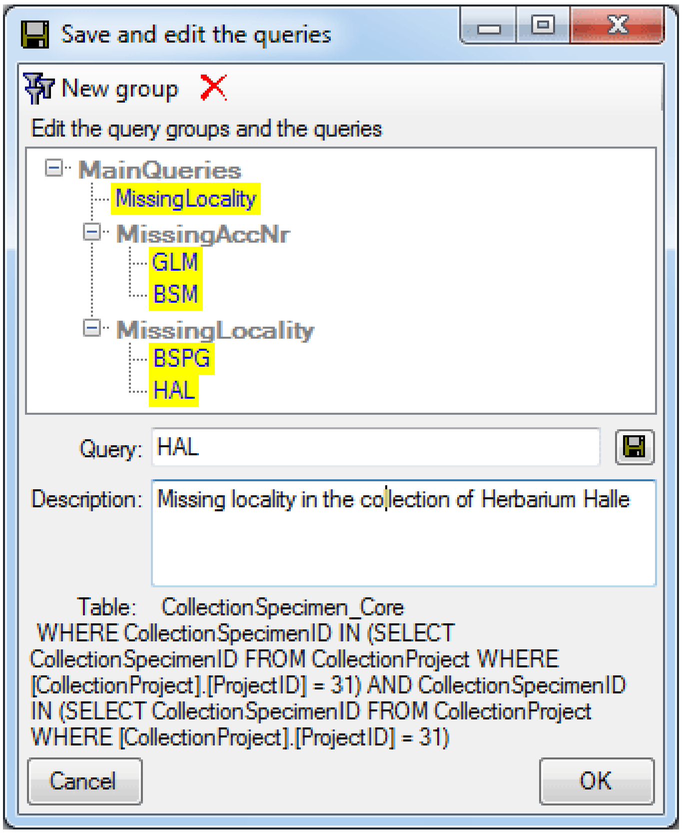
Query: CollectionNeubert

Description: First specimen in the collection neubert

Table: CollectionSpecimen_Core

WHERE CollectionSpecimenID IN (SELECT CollectionSpecimenID FROM Identification_Core WHERE [Identification_Core].TaxonomicName LIKE 'trichia persi%') AND [CollectionSpecimen_Core].[AccessionNumber] LIKE 'M-0113%' AND CollectionSpecimenID IN (SELECT CollectionSpecimenID FROM CollectionProject WHERE [CollectionProject].[ProjectID] = 271)

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



Query: HAL

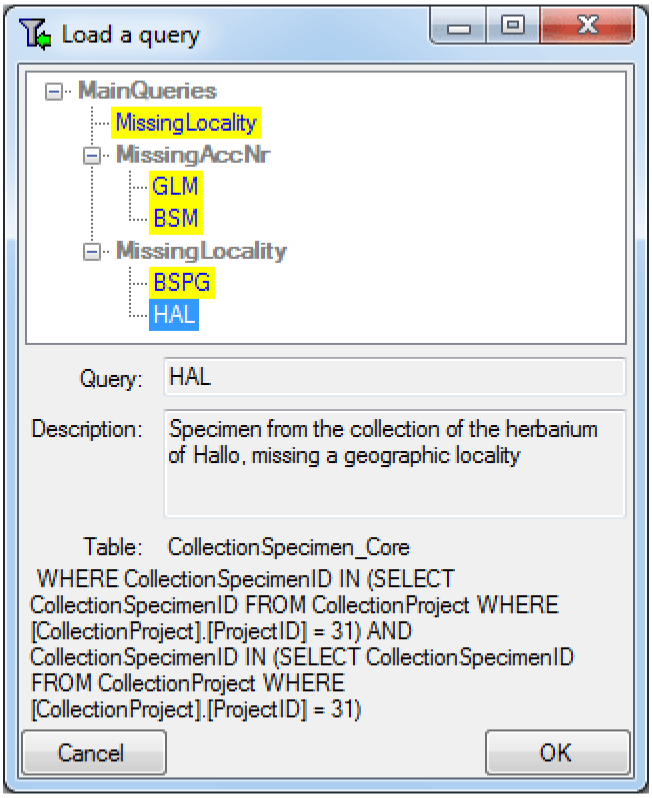
Description: Missing locality in the collection of Herbarium Halle

Table: CollectionSpecimen_Core
WHERE CollectionSpecimenID IN (SELECT CollectionSpecimenID FROM CollectionProject WHERE [CollectionProject].[ProjectID] = 31) AND CollectionSpecimenID IN (SELECT CollectionSpecimenID FROM CollectionProject WHERE [CollectionProject].[ProjectID] = 31)

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

Load query

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



Query: HAL

Description: Specimen from the collection of the herbarium of Hallo, missing a geographic locality

Table: CollectionSpecimen_Core

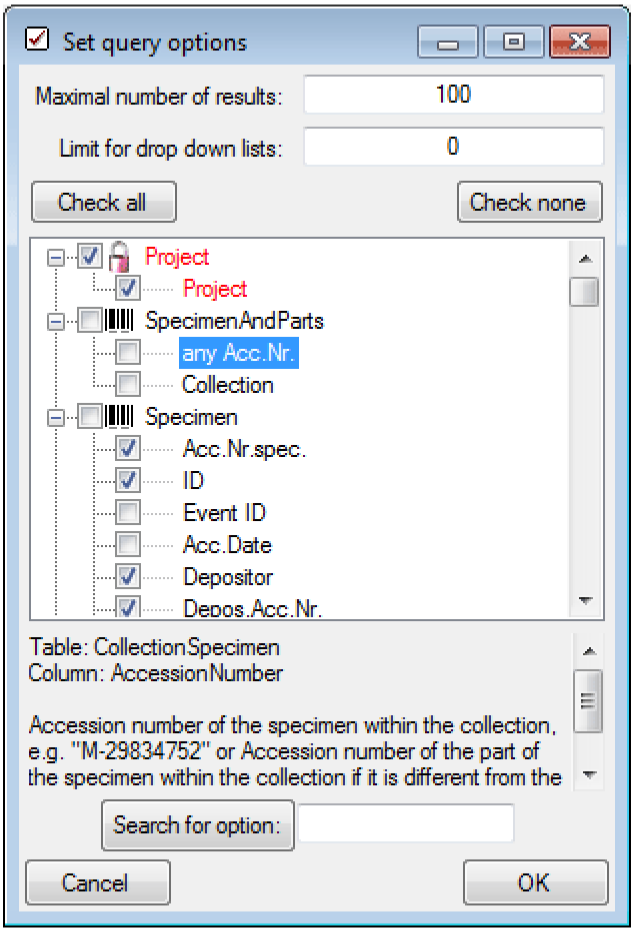
```
WHERE CollectionSpecimenID IN (SELECT
CollectionSpecimenID FROM CollectionProject WHERE
[CollectionProject].[ProjectID] = 31) AND
CollectionSpecimenID IN (SELECT CollectionSpecimenID
FROM CollectionProject WHERE
[CollectionProject].[ProjectID] = 31)
```

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

Query options

The maximum number of items shown in a query result may 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 a different number of results, you may change this value to any number.
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 which will be shown in the result list.

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



Maximal number of results: 100

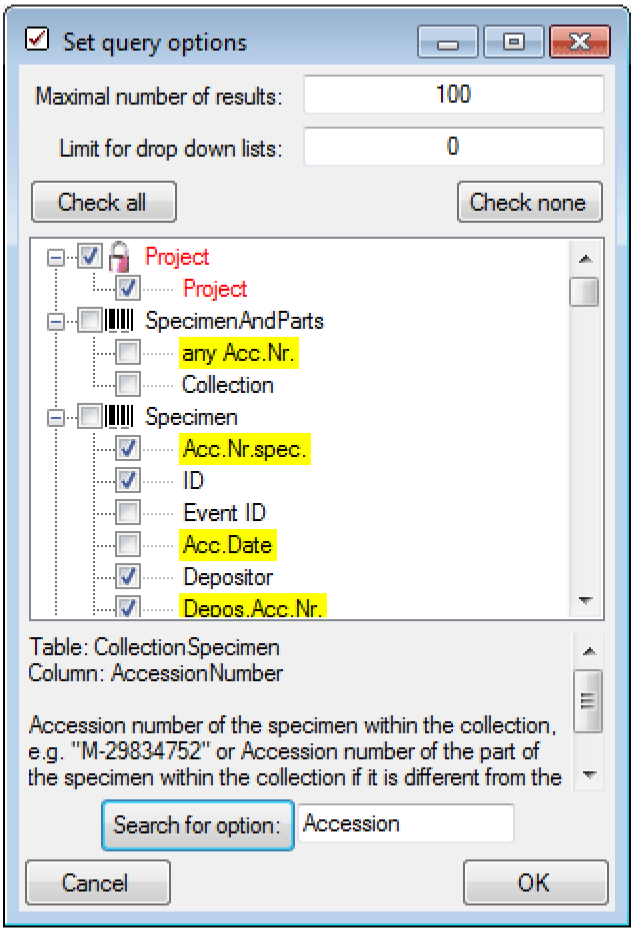
Limit for drop down lists: 0

- ☑ Project
  - ☑ Project
- ☐ SpecimenAndParts
  - ☐ any Acc.Nr.
  - ☐ Collection
- ☐ Specimen
  - ☑ Acc.Nr.spec.
  - ☑ ID
  - ☐ Event ID
  - ☐ Acc.Date
  - ☑ Depositor
  - ☑ Depos.Acc.Nr.

Table: CollectionSpecimen
Column: AccessionNumber

Accession number of the specimen within the collection, e.g. "M-29834752" or Accession number of the part of the specimen within the collection if it is different from the

To search for a field within the database use the search function which 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

- ☑ Project
  - ☑ Project
- ☐ SpecimenAndParts
  - ☐ any Acc.Nr.
  - ☐ Collection
- ☐ Specimen
  - ☑ Acc.Nr.spec.
  - ☑ ID
  - ☐ Event ID
  - ☐ Acc.Date
  - ☑ Depositor
  - ☑ Depos.Acc.Nr.

Table: CollectionSpecimen
Column: AccessionNumber

Accession number of the specimen within the collection, e.g. "M-29834752" or Accession number of the part of the specimen within the collection if it is different from the

Search for option: Accession

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.

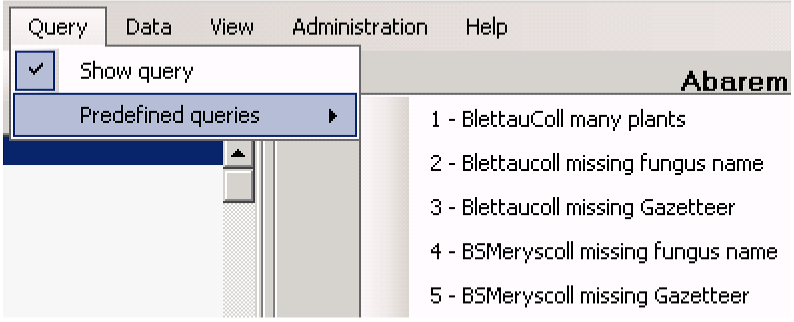
_ a single character, e.g. Pinus s**_**lvestris will find Pinus s**y**lvestris and Pinus s**i**lvestris etc.

[] 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.

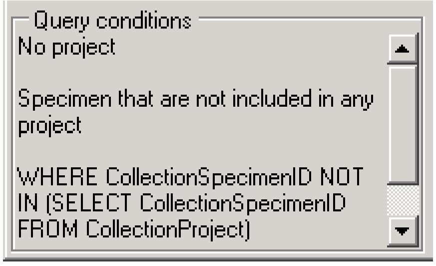
[^] any character not in a given range like **[^abcde]** or **[^a-e]**, e.g. Pinus s**[^i]**lvestris will find Pinus sylvestris but not Pinus silvestris.

Predefined queries

Besides setting queries for specimens via the query options you may define separate predefined user-specific queries. These are listed in the menu topic **Query - Predefined queries**.



If you choose one of these predefined queries, the query options will be hidden and the command of the query will be shown at the base of the specimen list. The first line shows the title of the query, the next lines contain the description followed by the part of the query command which restricts the selection of the data sets (= WHERE-clause of the SQL-statement).



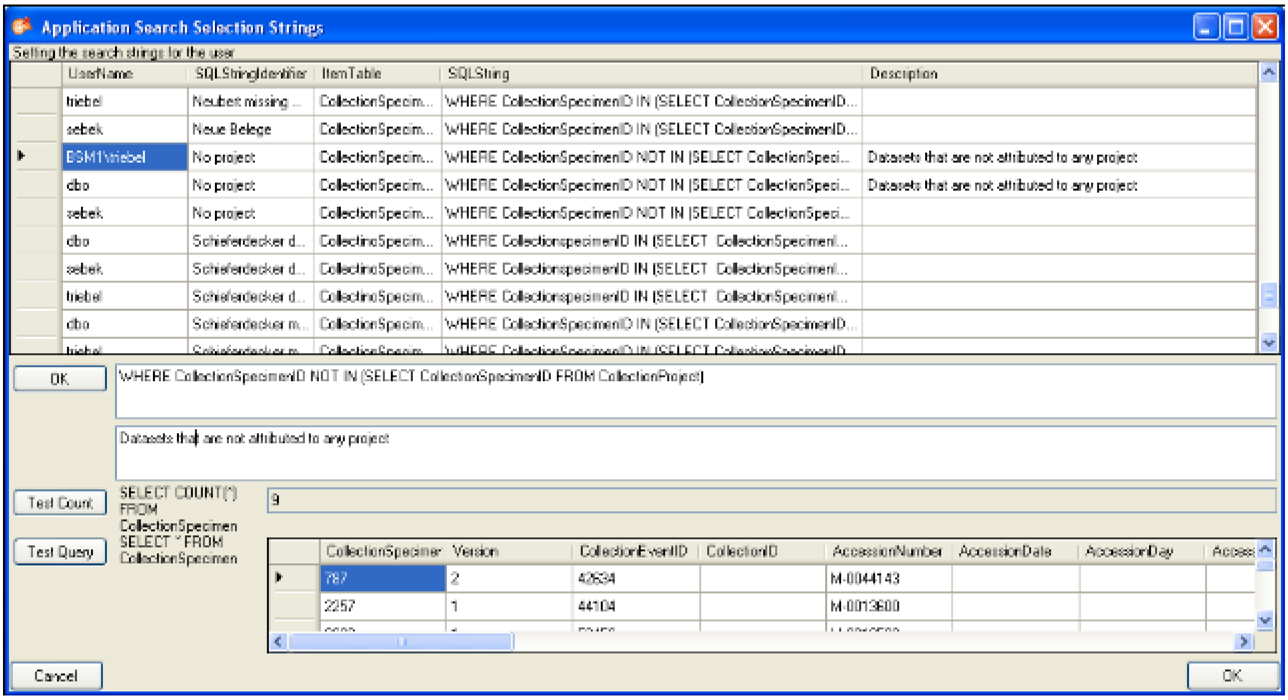
No project

Specimen that are not included in any project

```
WHERE CollectionSpecimenID NOT
IN (SELECT CollectionSpecimenID
FROM CollectionProject)
```

To return to the user-defined query click on the **Show query conditions** ▤button.

If you are an administrator, you may create new queries for users. To create a predefined query choose **Administration - Queries...** from the menu. A window will open as shown below, where you may create, edit and test your queries.



Setting the search strings for the user

	UserName	SQLStringIdentifier	ItemTable	SQLString	Description
	triebel	Neubert missing ...	CollectionSpecim...	WHERE CollectionSpecimenID IN (SELECT CollectionSpecimenID...	
	sebek	Neue Belege	CollectionSpecim...	WHERE CollectionSpecimenID IN (SELECT CollectionSpecimenID...	
▶	BSM1\triebel	No project	CollectionSpecim...	WHERE CollectionSpecimenID NOT IN (SELECT CollectionSpeci...	Datasets that are not attributed to any project
	dbo	No project	CollectionSpecim...	WHERE CollectionSpecimenID NOT IN (SELECT CollectionSpeci...	Datasets that are not attributed to any project
	sebek	No project	CollectionSpecim...	WHERE CollectionSpecimenID NOT IN (SELECT CollectionSpeci...	
	dbo	Schieferdecker d...	CollectinoSpecim...	WHERE CollectionspecimenID IN (SELECT CollectionSpecimenI...	
	sebek	Schieferdecker d...	CollectinoSpecim...	WHERE CollectionspecimenID IN (SELECT CollectionSpecimenI...	
	triebel	Schieferdecker d...	CollectinoSpecim...	WHERE CollectionspecimenID IN (SELECT CollectionSpecimenI...	
	dbo	Schieferdecker m...	CollectionSpecim...	WHERE CollectionSpecimenID IN (SELECT CollectionSpecimenID...	

```
WHERE CollectionSpecimenID NOT IN (SELECT CollectionSpecimenID FROM CollectionProject)
```

Datasets that are not attributed to any project

SELECT COUNT(*) FROM CollectionSpecimen: 9

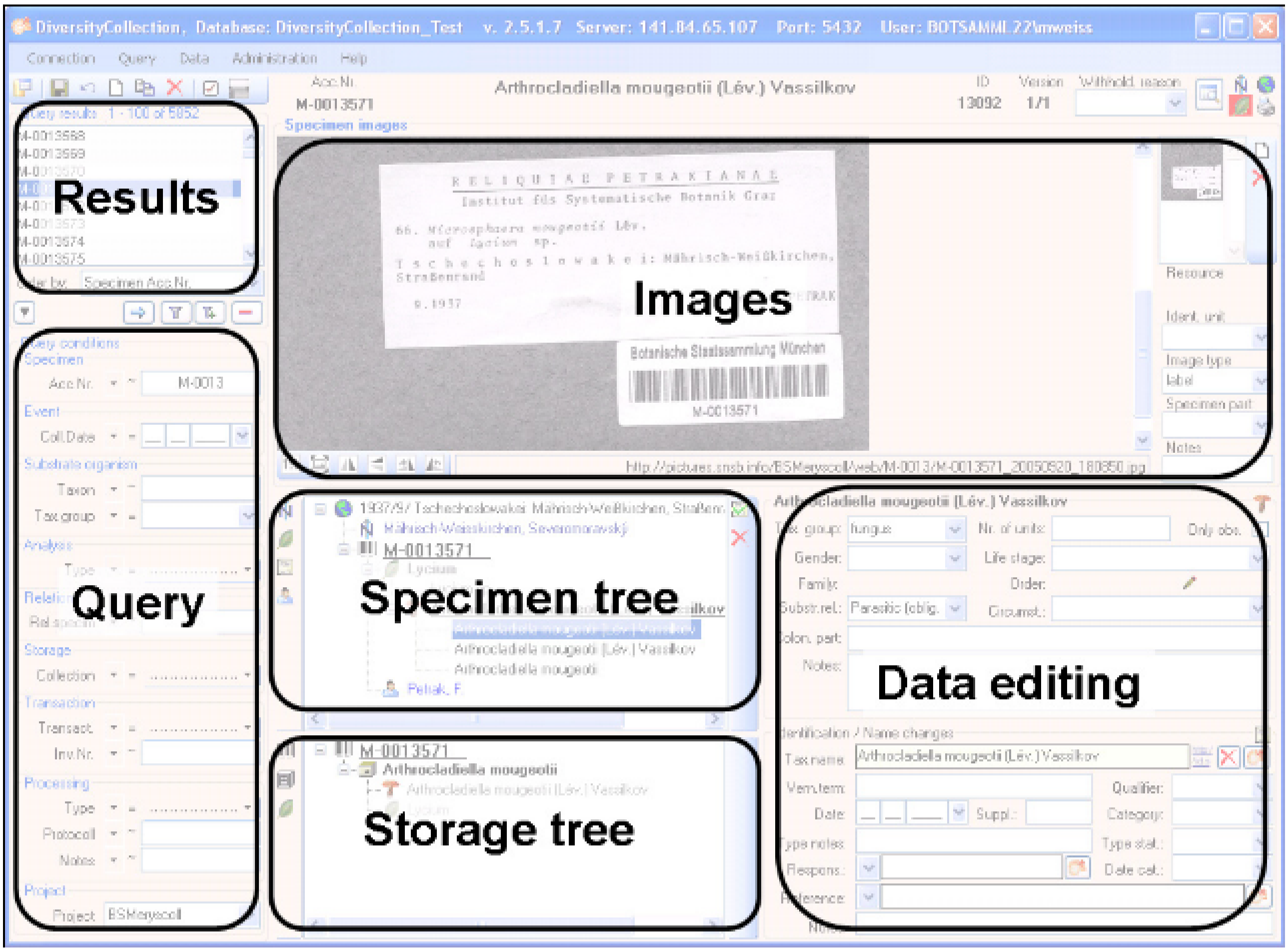
SELECT * FROM CollectionSpecimen

	CollectionSpecimen	Version	CollectionEventID	CollectionID	AccessionNumber	AccessionDate	AccessionDay	Access
▶	787	2	42634		M-0044143			
	2257	1	44104		M-0013600			

In the upper field you define the WHERE-clause of the SQL string of your query. Keep in mind that the queries can refer to different tables, depending on the order column chosen by the user. Thus, queries in DiversityCollection should start with the reference to the primary key of the main table (CollectionSpecimenID in table CollectionSpecimen and depending tables). The lower field contains the description for the query as shown in the user interface. To test a query use the **[Test count]** and **[Test query]** buttons.

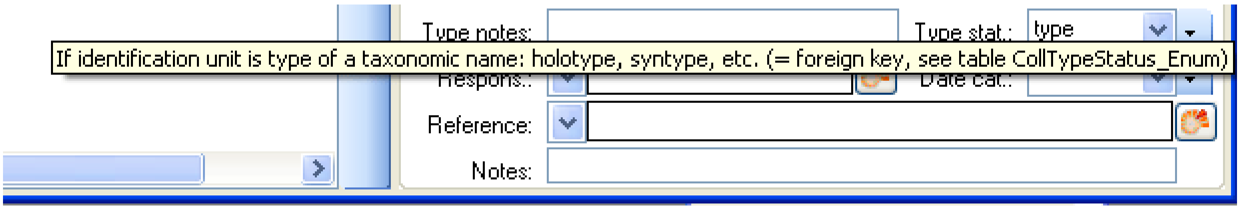
Editing the data

The main window of the DiversityCollection client contains two main areas. On the left you find the query and the results of this query. On the right the data of the data set selected in the results list is shown. The upper part of the data area shows images, labels etc. In the lower part you find two trees that give you an overview and access to the data. The data of an entry selected in one of the trees is shown in the data editing section.



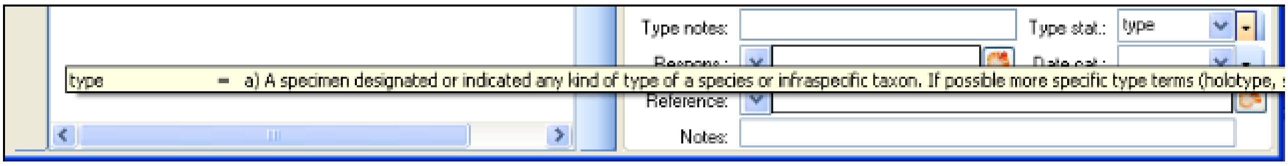
Common comments

To see the descriptions of the fields, just move the mouse over the field you want to know more about. A tip-text window will open, showing the description of the expected content of this field (see image below). These desriptions are also available in the documentation for the tables.



If identification unit is type of a taxonomic name: holotype, syntype, etc. (= foreign key, see table CollTypeStatus_Enum)

The description of some of the drop-down fields are too long to be shown in the drop-down column. However, for a selected entry you can place your mouse over the hierachy selector. A tip-text window will appear (see image below) where the full text of the description is shown.

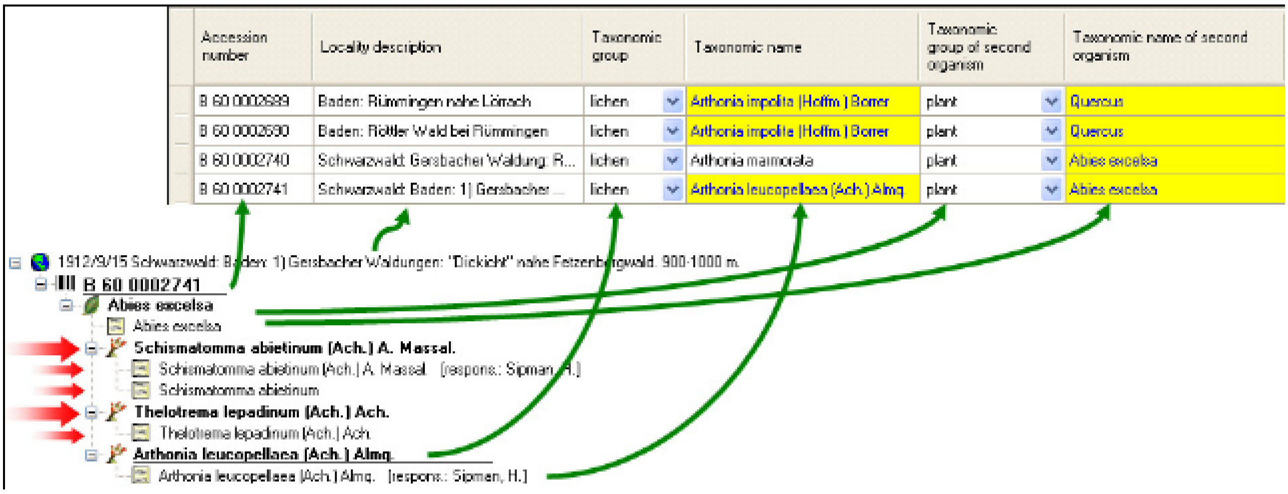


Type stat.: type

type = a) A specimen designated or indicated any kind of type of a species or infraspecific taxon. If possible more specific type terms (holotype,

Grid mode

To edit the data in a data grid choose the **Grid mode** for the specimen, the organisms, the CollectionEvents or the CollectionEventSeries from the menu. A window will open where every data set from the query result list is restricted to one line for a specimen, an organism, a CollectionEvent or a CollectionEventSeries respectively. Please keep in mind you can only see a limited part of the data while in this view. For example only the last identification of an organism will be displayed. This is demonstrated in the image below where two organisms, indicated with the red arrows, will not appear in the grid. If you use the grid mode for the organisms, all organisms will appear with their last identification.

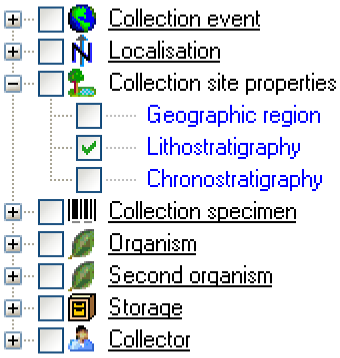


Accession number	Locality description	Taxonomic group	Taxonomic name	Taxonomic group of second organism	Taxonomic name of second organism
B 60 0002689	Baden: Rümmingen nahe Lörrach	lichen	Arthonia impolita (Hoffm.) Borrer	plant	Quercus
B 60 0002690	Baden: Röttler Wald bei Rümmingen	lichen	Arthonia impolita (Hoffm.) Borrer	plant	Quercus
B 60 0002740	Schwarzwald: Gersbacher Waldung: R...	lichen	Arthonia marmorata	plant	Abies excelsa
B 60 0002741	Schwarzwald: Baden: 1) Gersbacher ...	lichen	Arthonia leucopellaea (Ach.) Almq.	plant	Abies excelsa

1912/9/15 Schwarzwald: Baden: 1) Gersbacher Waldungen: "Dickicht" nahe Fetzenbergwald. 900-1000 m.
- B 60 0002741
  - Abies excelsa
    - Abies excelsa
  - Schismatomma abietinum (Ach.) A. Massal.
    - Schismatomma abietinum (Ach.) A. Massal. [respons.: Sipman, H.]
    - Schismatomma abietinum
  - Thelotrema lepadinum (Ach.) Ach.
    - Thelotrema lepadinum (Ach.) Ach.
  - Arthonia leucopellaea (Ach.) Almq.
    - Arthonia leucopellaea (Ach.) Almq. [respons.: Sipman, H.]

Customize visibility of fields

The selection of the visible fields can be adapted in the tree above the list. Change the selection of the columns and click on the **[Set columns]** button.



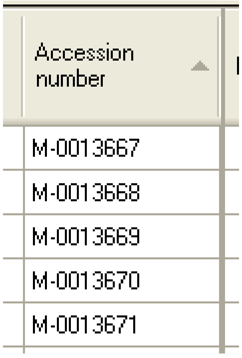
- ☐ Collection event
- ☐ Localisation
- ☐ Collection site properties
  - ☐ Geographic region
  - ☑ Lithostratigraphy
  - ☐ Chronostratigraphy
- ☐ Collection specimen
- ☐ Organism
- ☐ Second organism
- ☐ Storage
- ☐ Collector

Customize column width and sequence

To adapt the width of the columns or the height of the rows either drag the border with the mouse or double click the border to get the optimal size for one column. You may also click on the button for an optimal height of the rows or the button for an optimal width of the columns. To change the width and sequence of the columns simply use your mouse to drag the columns to the position of your choice or adapt the width to your preference. These changes will be saved for this session as well as for the next time you use the grid mode. To return to the original sequence of the columns click on the **[Reset sequence]** button.

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



Accession number

M-0013667

M-0013668

M-0013669

M-0013670

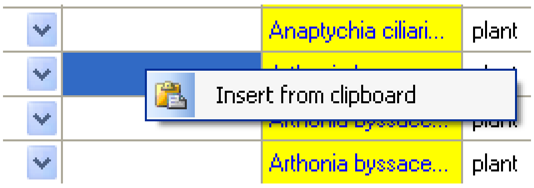
M-0013671

Find and replace

To use the find and replace functions you must either select a part of the field in this column or click on the button to select the entire column. You may then choose the function you wish to apply (remove, insert, append or replace). To replace a part of a text in the selected fields enter the text which should be replaced and enter the replacement in the corresponding fields. To start the **replacement** click the button. To insert a string to the **beginning** of all entries in the selected fields click the button. To **append** a string to all entries in the selected fields click the button. To **remove** all entries from the selected fields click the button.

Transfer from spreadsheet

You can transfer data from a spreadsheet e.g. Excel or Calc. Copy the columns of this data from the spreadsheet and then insert it in DiversityCollection. Click in the upmost left cell where this data should be transferred to and use the context menu (click the right mouse button) to insert the data.



Anaptychia ciliari... plant

Arthonia byssace... plant

Editing

Some columns can not be edited directly but are linked to external modules or services. These columns appear as buttons. Simply click on the button to call the service. If a value is linked to an entry in an external module, the background will change to yellow and you will not be able to change the text.

☐ Collector
- ☑ Collectors name
- ☐ Link to DiversityAgents
- ☐ Remove link for collector

Together with the links (in the example above Link to DiversityAgents) you can select columns that provide the posibility to release the links to the modules (e.g. Remove link for collector in image above). These columns will appear as buttons ☒. Simply click on the button related to a link to release the link to the corresponding module. After that you can edit the text field containing the linked value.

Some values are linked to a list of values. Use the drop-down list to change the value in one of these columns.

If you click in the empty line at the base of the data grid, you will be asked if you wish to create a new data set. The program will ask you for a new accession number and the project of the new data set. Another way to create a new data set is the copy button . Simply click in the line you wish to create a copy of and then click on the copy button . For details see the Data section. A copy of the data set will be inserted at the base of the data grid.

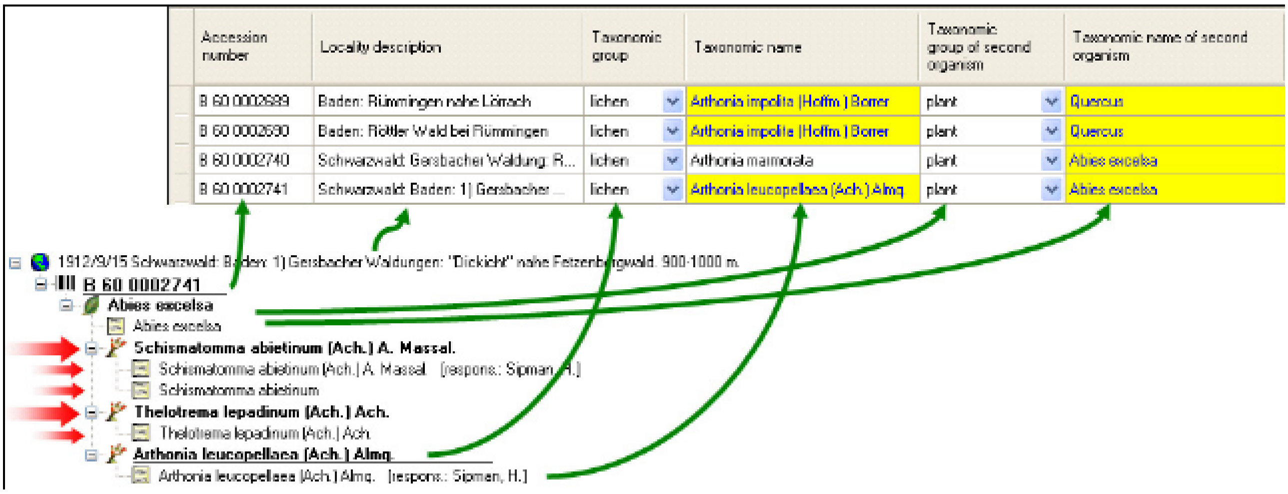
In the grid view for the organisms a part of the columns can not be edited. These columns contain data which can be related to several organisms. This is indicated by a gray background.

Saving the data

To save all changes click on the button. To undo all changes since the last time the data sets were saved click on the button. To save the changes in the current data set use the button. To undo the changes in the current data set click the button. If you click the **[OK]** button, you will be asked whether you would like to save the changes before the window will be closed. If you click the **[Cancel]** button or close the window your changes will not be saved. To save the data shown in the grid in a tab delimited file click on the button.

Grid mode for CollectionSpecimen

To edit the data of the specimens in a data grid choose the **Grid mode** for the specimen from the menu. A window will open where every data set for a specimen from the query result list is restricted to one line. Please keep in mind you can only see a limited part of the data while in this view. For example only the last identification of an organism will be displayed. This is demonstrated in the image below where two organisms, indicated with the red arrows, will not appear in the grid. If you use the grid mode for the organisms, all organisms will appear with their last identification.

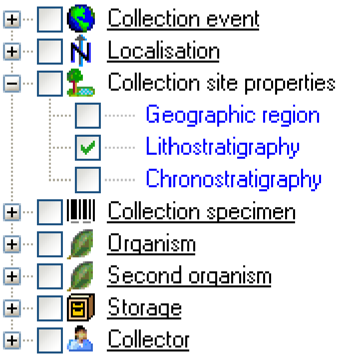


Accession number	Locality description	Taxonomic group	Taxonomic name	Taxonomic group of second organism	Taxonomic name of second organism
B 60 0002689	Baden: Rümmingen nahe Lörrach	lichen	Arthonia impolita (Hoffm.) Borrer	plant	Quercus
B 60 0002690	Baden: Röttler Wald bei Rümmingen	lichen	Arthonia impolita (Hoffm.) Borrer	plant	Quercus
B 60 0002740	Schwarzwald: Gersbacher Waldung: R...	lichen	Arthonia marmorata	plant	Abies excelsa
B 60 0002741	Schwarzwald: Baden: 1) Gersbacher ...	lichen	Arthonia leucopellaea (Ach.) Almq.	plant	Abies excelsa

- 1912/9/15 Schwarzwald: Baden: 1) Gersbacher Waldungen: "Dickicht" nahe Fetzenbergwald. 900-1000 m.
  - **B 60 0002741**
    - **Abies excelsa**
      - Abies excelsa
    - **Schismatomma abietinum (Ach.) A. Massal.**
      - Schismatomma abietinum (Ach.) A. Massal. [respons.: Sipman, H.]
      - Schismatomma abietinum
    - **Thelotrema lepadinum (Ach.) Ach.**
      - Thelotrema lepadinum (Ach.) Ach.
    - **Arthonia leucopellaea (Ach.) Almq.**
      - Arthonia leucopellaea (Ach.) Almq. [respons.: Sipman, H.]

Customize visibility of fields

The selection of the visible fields can be adapted in the tree above the list. Change the selection of the columns and click on the **[Set columns]** button.



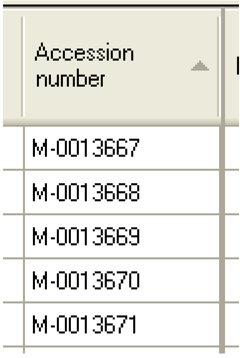
- ☐ Collection event
- ☐ Localisation
- ☐ Collection site properties
  - ☐ Geographic region
  - ☑ Lithostratigraphy
  - ☐ Chronostratigraphy
- ☐ Collection specimen
- ☐ Organism
- ☐ Second organism
- ☐ Storage
- ☐ Collector

Customize column width and sequence

To adapt the width of the columns or the height of the rows either drag the border with the mouse or double click the border to get the optimal size for one column. You may also click on the button for an optimal height of the rows or the button for an optimal width of the columns. To change the width and sequence of the columns simply use your mouse to drag the columns to the position of your choice or adapt the width to your preference. These changes will be saved for this session as well as for the next time you use the grid mode. To return to the original sequence of the columns click on the **[Reset sequence]** button.

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



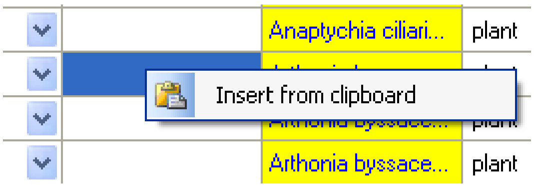
Accession number
M-0013667
M-0013668
M-0013669
M-0013670
M-0013671

Find and replace

To use the find and replace functions you must either select a part of the field in this column or click on the button to select the entire column. You may then choose the function you wish to apply (remove, insert, append or replace). To replace a part of a text in the selected fields enter the text that should be replaced and enter the replacement in the corresponding fields. To start the **replacement** click the button. To insert a string to the **beginning** of all entries in the selected fields click the button. If the selected column is a link to a module or webservice, a button will appear where you can search for a linked data set. The insert will set the selected column and related columns according to the linked data set. Thus, if you choose e.g. a value from the DiversityGazetteer, the coordinates and the country will be changed as well. Click on the link to see all related information. To reset the link use the ✕ button. To **append** a string to all entries in the selected fields click the button. To **remove** all entries from the selected fields click the button.

Transfer from spreadsheet

You can transfer data from a spreadsheet e.g. Excel or Calc. Copy the columns of this data from the spreadsheet and then insert it in DiversityCollection. Click in the upmost left cell where this data should be transferred to and use the context menu (click the right mouse button) to insert the data.



Editing

Some columns can not be edited directly but are linked to external modules or services. These columns appear as buttons. Simply click on the button to call the service. If a value is linked to an entry in an external module, the background will change to yellow and you will not be able to change the text.

☐ Collector
- ☑ Collectors name
- ☐ Link to DiversityAgents
- ☐ Remove link for collector

Together with the links (in the example above Link to DiversityAgents) you can select columns that provide the posibility to release the links to the modules (e.g. Remove link for collector in image above). These columns will appear as buttons ☒. Simply click on the button related to a link to release the link to the corresponding module. After that you can edit the text field containing the linked value.

Some values are linked to a list of values. Use the drop-down list to change the value in one of these columns.

If you click in the empty line at the base of the data grid, you will be asked if you wish to create a new data set. The program will ask you for a new accession number and the project of the new data set. Another way to create a new data set is the copy button. Simply click in the line you wish to create a copy of and then click on the copy button. For details see the Data section. A copy of the data set will be inserted at the base of the data grid.

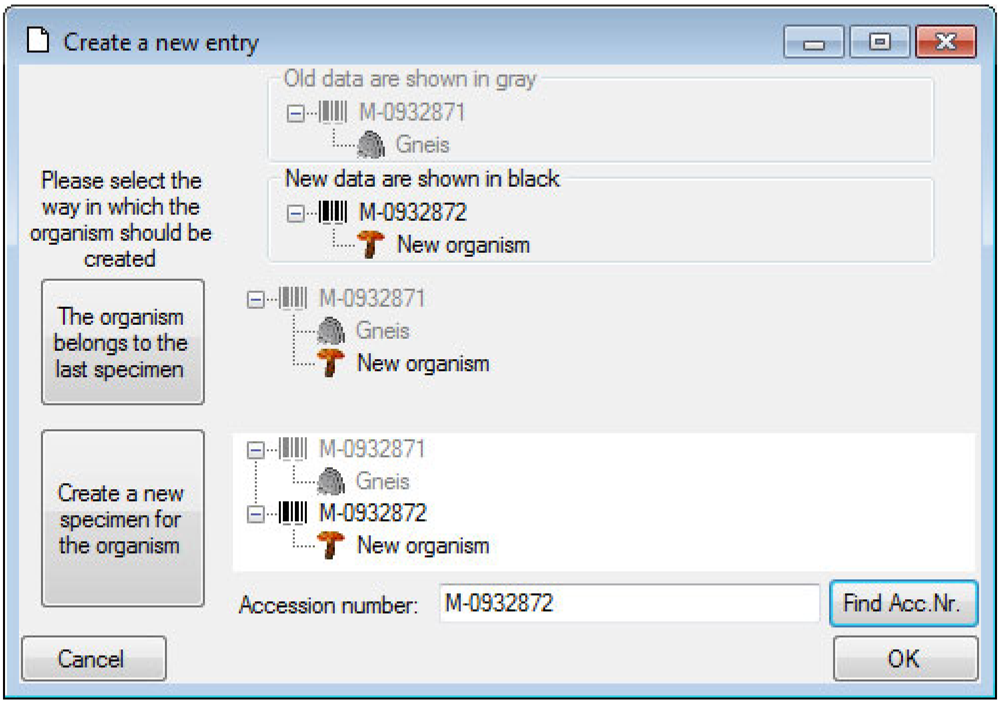
In the grid view for the organisms a part of the columns can not be edited. These columns contain data which can be related to several organisms. This is indicated by a gray background.

Saving the data

To save all changes click on the button. To undo all changes since the last time the data sets were saved click on the button. To save the changes in the current data set use the button. To undo the changes in the current data set click the button. If you click the **[OK]** button, you will be asked whether you would like to save the changes before the window will be closed. If you click the **[Cancel]** button or close the window your changes will not be saved. To save the data shown in the grid in a tab delimited file click on the button.

Inserting new data

To insert a new data set simply click in the last empty line of the data grid. The programm may ask you to specify a project in which the new data should be placed. In the grid for the organisms a window will open as shown below.



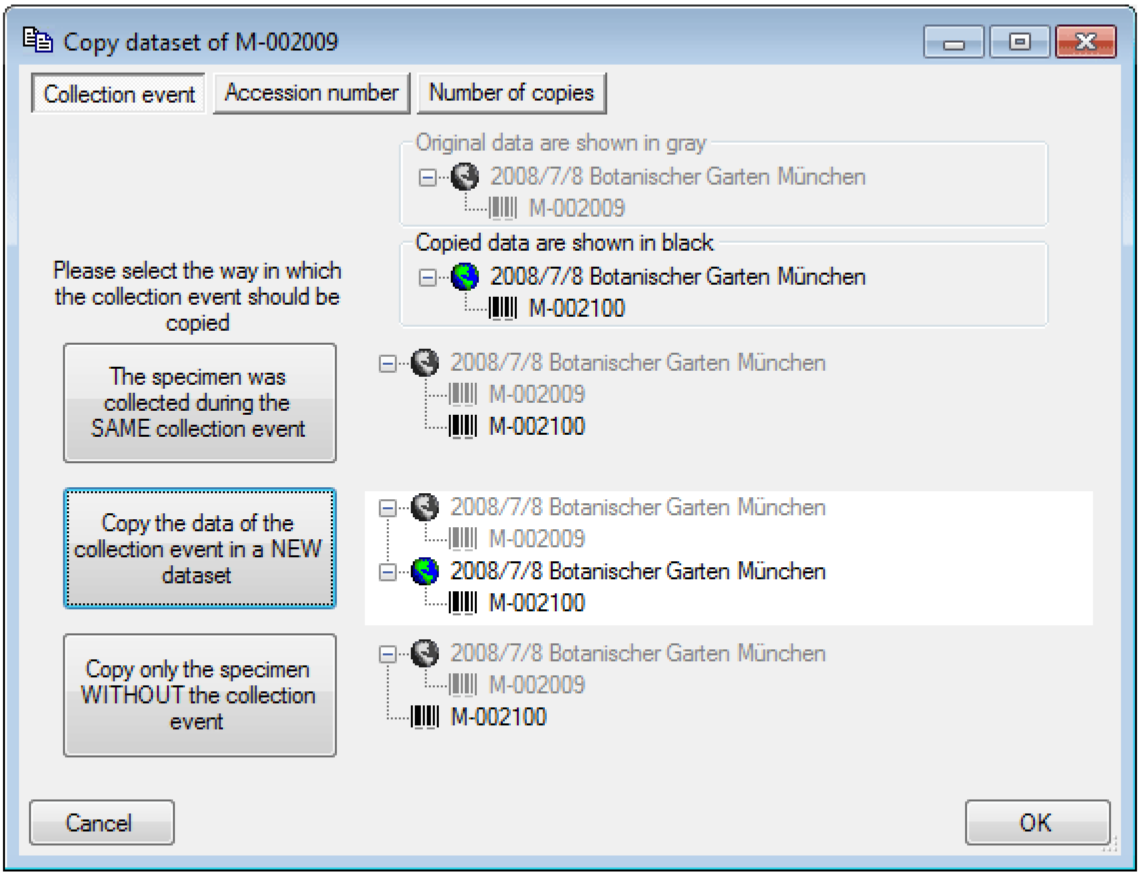
Accession number: M-0932872

Here you have the option to insert the new data set of the organism in the last specimen in the grid or to create a new specimen for the organism. In the second case you can specify the accession number of the new specimen. Use the **[Find Acc. Nr.]** button to search for the next free accession number in the database which matches your entry in the **[Accession number]** field.

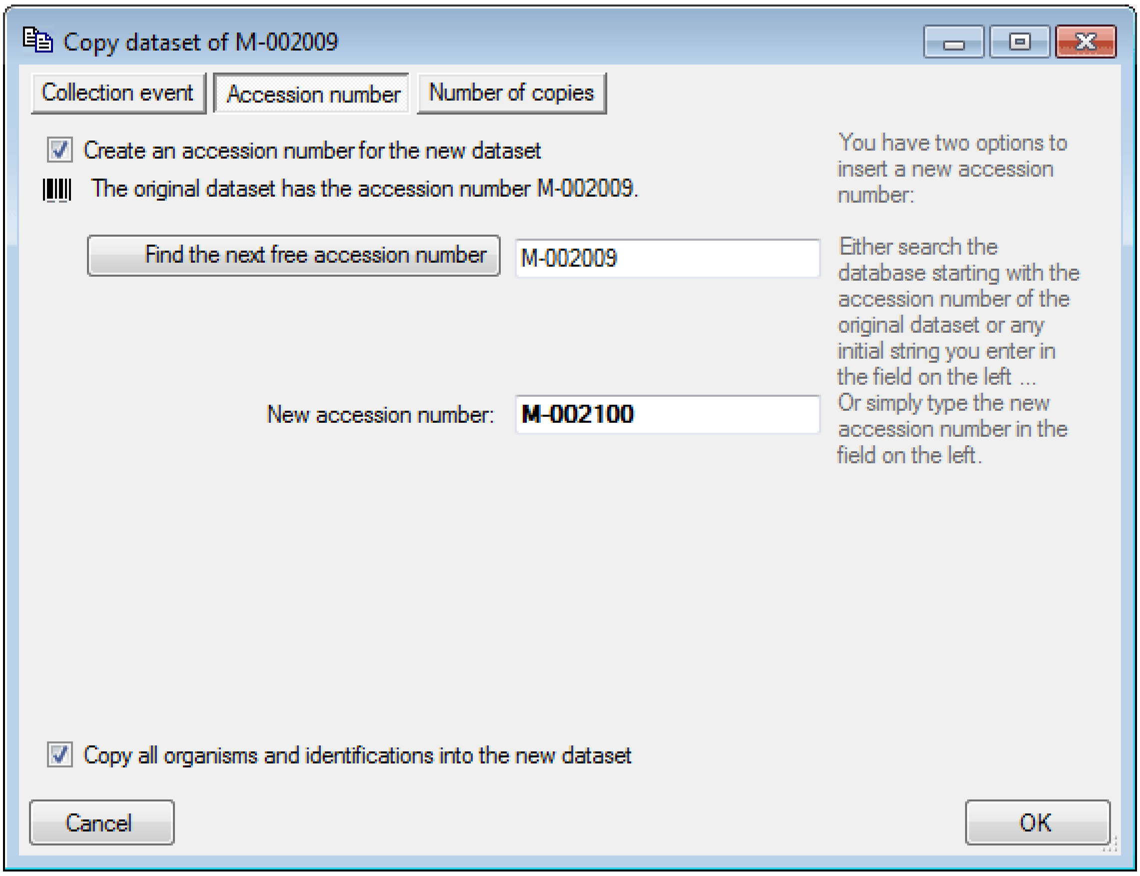
For new data sets you can specify certain **project settings** e.g. the material category of a part of the specimen. The taxonomic group of a new organism will correspond to the first organism in your last specimen unless you specify a certain taxonomic group in the project settings for the project you are working in. To enter or change a setting you need the module **DiversityProjects**. For further information please turn to the documentation provided with this module.

Copy data

To copy a data set select the line of the data grid you wish to create a copy of and click on the ⎘button. A window will open where you can choose several options for your copies. In the first tab choose in which way the **CollectionEvent** - if present - for the new data sets should be created.



In the **Accession number** tab you can search for or enter the accession number you wish to use for your new data set (see below).



☑ Create an accession number for the new dataset

The original dataset has the accession number M-002009.

M-002009

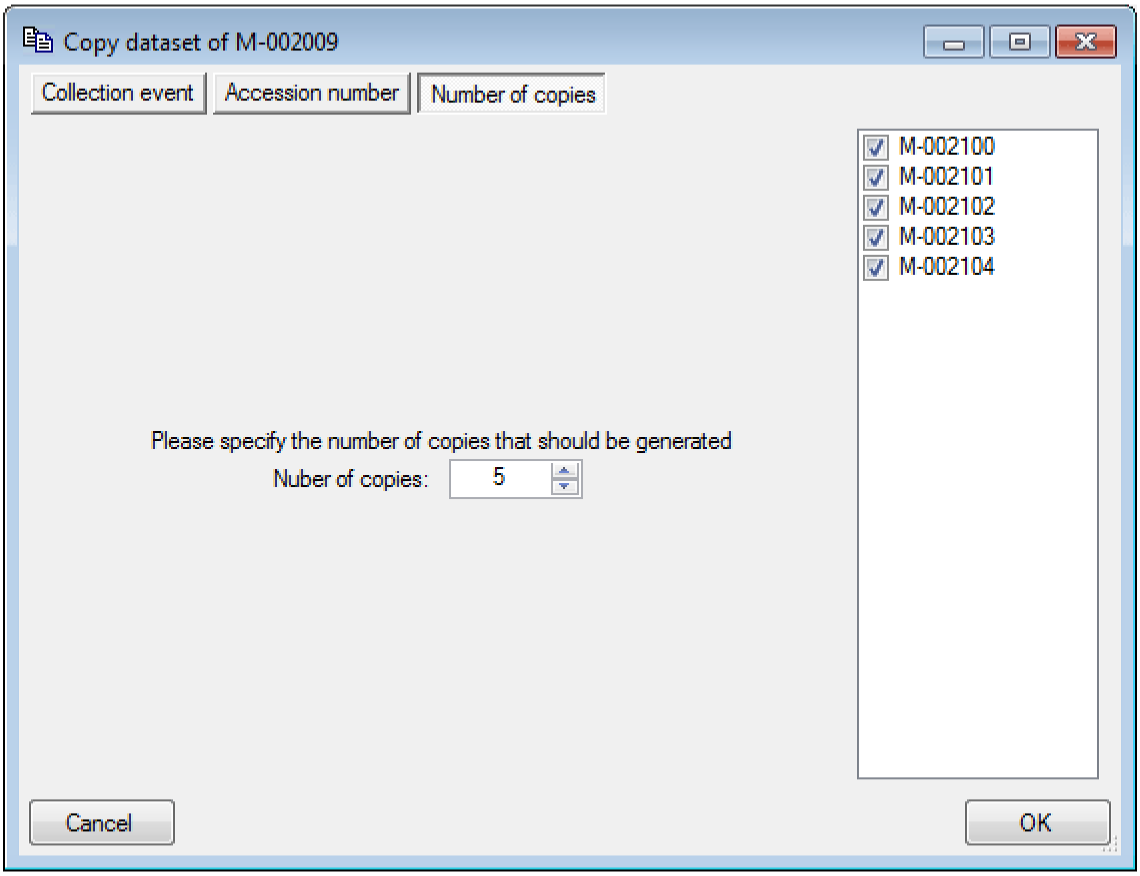
New accession number: **M-002100**

You have two options to insert a new accession number:

Either search the database starting with the accession number of the original dataset or any initial string you enter in the field on the left ...
Or simply type the new accession number in the field on the left.

☑ Copy all organisms and identifications into the new dataset

In the **Number of copies** tab you can specify the number of copies. If you checked **Create an accession number for the new data set**, the program will list all accession numbers which will be created (see below).

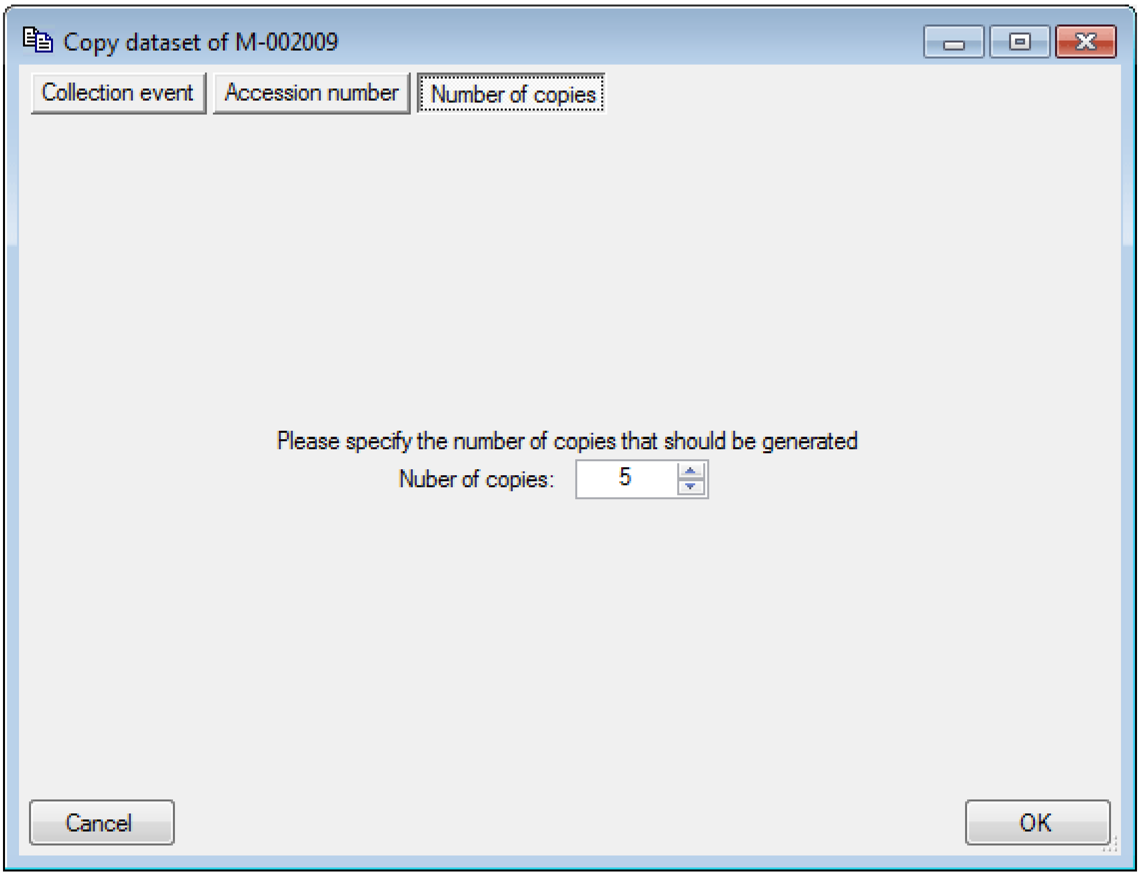


Please specify the number of copies that should be generated

Nuber of copies: 5

☑ M-002100
☑ M-002101
☑ M-002102
☑ M-002103
☑ M-002104

If you do not wish to create new accession numbers for the copies the list will not be shown (see below).



Please specify the number of copies that should be generated

Nuber of copies: 5

Grid mode for the organisms

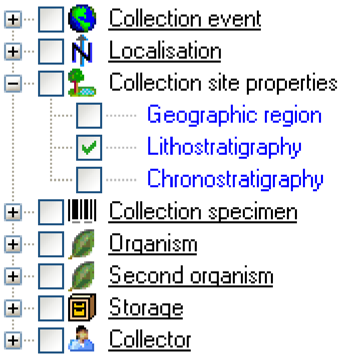
To edit the data of the organisms in a data grid choose the **Grid mode** for the organisms from the menu. A window will open where every data set for an organism from the query result list is restricted to one line. Please keep in mind you can only see a limited part of the data while in this view. For example only the last identification of an organism will be displayed.

Customize the window

To change the width and sequence of the columns simply use your mouse to drag the columns to the position of your choice or adapt the width to your preference. These changes will be saved for this session as well as for the next time you use the grid mode. To return to the original sequence of the columns click on the **[Reset sequence]** button.

To adapt the width of the columns or the height of the rows either drag the border with the mouse or double click the border to get the optimal size for one column. You may also click on the button for an optimal height of the rows or the button for an optimal width of the columns.

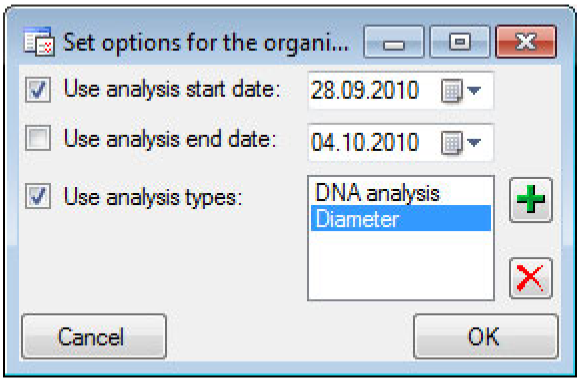
The selection of the visible fields can be adapted in the tree above the list. Change the selection of the columns and click on the **[Set columns]** button.



- ☐ Collection event
- ☐ Localisation
- ☐ Collection site properties
  - ☐ Geographic region
  - ☑ Lithostratigraphy
  - ☐ Chronostratigraphy
- ☐ Collection specimen
- ☐ Organism
- ☐ Second organism
- ☐ Storage
- ☐ Collector

Analysis

In this grid you can edit up to 10 different types of analysis, however, only the last analysis will be shown for each type. By default the available analysis types will be generated dynamically depending on the data. If you need an additional type in the grid, simply return to the main form and enter the required type in one of the data sets. If you wish to specify which analysis you want to see in the grid, you can set the list in the options. Click on the button to open a window as shown below.



☑ Use analysis start date: 28.09.2010

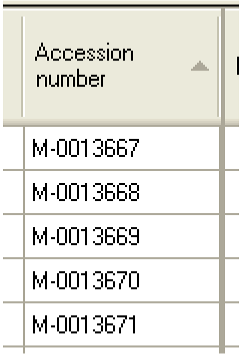
☐ Use analysis end date: 04.10.2010

☑ Use analysis types: DNA analysis, Diameter

Here you can restrict the range of the dates of the analysis and the types of the analysis which should be displayed. To change the entries in the list use the ✚and ✕buttons to add or delete entries.

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



Accession number ▲
M-0013667
M-0013668
M-0013669
M-0013670
M-0013671

Handling the data

Some columns can not be edited directly but are linked to external modules or services. These columns appear as buttons. Simply click on the button to call the service. If a value is linked to an entry in an external module, the background will change to yellow and you will not be able to change the text.

- ☐ Collector
  - ☑ Collectors name
  - ☐ Link to DiversityAgents
  - ☐ Remove link for collector

Together with the links (in the example above Link to DiversityAgents) you can select columns that provide the posibility to release the links to the modules (e.g. Remove link for collector in image above). These columns will appear as buttons ☒. Simply click on the button related to a link to release the link to the corresponding module. After that you can edit the text field containing the linked value.

Some values are linked to a list of values. Use the drop-down list to change the value in one of these columns.

If you click in the empty line at the base of the data grid, you will be asked if you wish to create a new data set. The program will ask you for a new accession number and the project of the new data set. Another way to create a new data set is the copy button ⎘. Simply click in the line you wish to create a copy of and then click on the copy button ⎘. For details see the Data section. A copy of the data set will be inserted at the base of the data grid.

In the grid view for the organisms a part of the columns can not be edited. These columns contain data which can be related to several organisms. This is indicated by a gray background.

Find and replace

To use the find and replace functions you must either select a part of the field in this column or click on the button to select the entire column. You may then choose the function you wish to apply (remove, insert, append or replace). To replace a part of a text in the selected fields enter the text which should be replaced and enter the replacement in the corresponding fields. To start the **replacement** click the button. To insert a string to the **beginning** of all entries in the selected fields click the button. To **append** a string to all entries in the selected fields click the button. To **remove** all entries from the selected fields click the button.

To **save** all changes click on the button. To undo all changes since the last time the data sets were saved click on the button. To save the changes in the current data set use the button. To undo the changes in the current data set click the button. If you click the **[OK]** button, you will be asked whether you would like to save the changes before the window will be closed. If you click the **[Cancel]** button or close the window your changes will not be saved. To save the data shown in the grid in a tab delimited file click on the button.

To copy a data set select the line of the data grid which you wish to create a copy of and click on the button. A copy of the selected data set will be added at the base of the spreadsheet.

Grid mode for the parts of the specimen

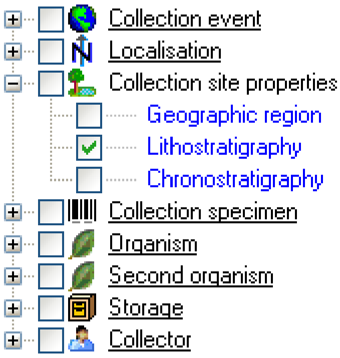
To edit the data of the parts in a data grid choose the **Grid** mode for the **Parts...** from the menu. A window will open where every data set for a part from the query result list is restricted to one line. Please keep in mind you can only see a limited part of the data while in this view. For example only the last processing or analysis of a certain type of a part will be displayed.

Customize the window

To change the width and sequence of the columns simply use your mouse to drag the columns to the position of your choice or adapt the width to your preference. These changes will be saved for this session as well as for the next time you use the grid mode. To return to the original sequence of the columns click on the **[Reset sequence]** button.

To adapt the width of the columns or the height of the rows either drag the border with the mouse or double click the border to get the optimal size for one column. You may also click on the button for an optimal height of the rows or the button for an optimal width of the columns.

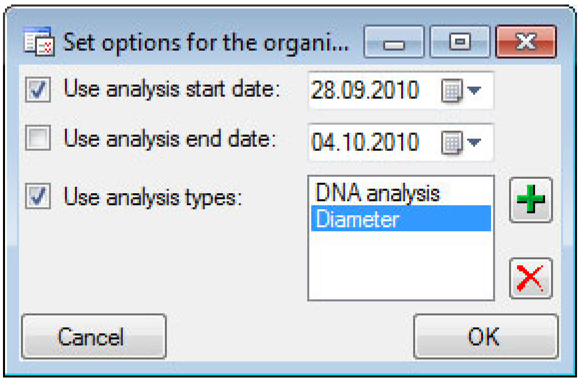
The selection of the visible fields can be adapted in the tree above the list. Change the selection of the columns and click on the **[Set columns]** button.



- ☐ Collection event
- ☐ Localisation
- ☐ Collection site properties
  - ☐ Geographic region
  - ☑ Lithostratigraphy
  - ☐ Chronostratigraphy
- ☐ Collection specimen
- ☐ Organism
- ☐ Second organism
- ☐ Storage
- ☐ Collector

Analysis

In this grid you can edit up to 10 different types of processings, however, only the last analysis will be shown for each type. To specify which analysis you wish to see in the grid click on the button to open a window as shown below.



Set options for the organi...

☑ Use analysis start date: 28.09.2010

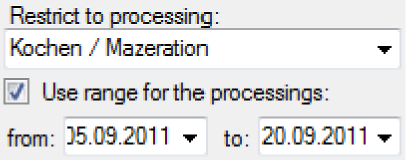
☐ Use analysis end date: 04.10.2010

☑ Use analysis types:
- DNA analysis
- Diameter

Here you can restrict the range of the dates of the analysis and the types of the analysis which should be displayed. To change the entries in the list use the ✚and ✕buttons to add or delete entries. For taxonomic groups which miss certain types of analysis the columns will be blocked.

Processing

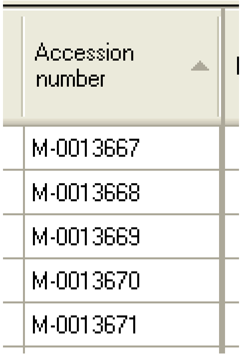
In this grid you can display up to 5 different processings, however, only the last processings will be shown. You can define a time range for the processings which should be displayed and / or restrict the processing to a certain type (see image below). For material categories which miss certain types of processings the columns will be blocked.



Restrict to processing:
Kochen / Mazeration
☑ Use range for the processings:
from: 05.09.2011 to: 20.09.2011

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



Accession number ▲
M-0013667
M-0013668
M-0013669
M-0013670
M-0013671

Selecting of the data

To restrict the data in the grid you can filter an entry. Select the entry for which you want to filter and click on the ▽button. To remove data from the grid select the rows which should be removed and click on the − button.

Handling the data

Some columns can not be edited directly but are linked to external modules or services. These columns appear as buttons. Simply click on the button to call the service. If a value is linked to an entry in an external module, the background will change to yellow and you will not be able to change the text.

☐ Collector
- ☑ Collectors name
- ☐ Link to DiversityAgents
- ☐ Remove link for collector

Together with the links (in the example above Link to DiversityAgents) you can select columns that provide the posibility to release the links to the modules (e.g. Remove link for collector in image above). These columns will appear as buttons ☒. Simply click on the button related to a link to release the link to the corresponding module. After that you can edit the text field containing the linked value.

Some values are linked to a list of values. Use the drop-down list to change the value in one of these columns.

If you click in the empty line at the base of the data grid, you will be asked if you wish to create a new data set. The program will ask you for a new accession number and the project of the new data set. Another way to create a new data set is the copy button . Simply click in the line you wish to create a copy of and then click on the copy button . For details see the Data section. A copy of the data set will be inserted at the base of the data grid.

In the grid view for the parts a part of the columns can not be edited. These columns contain data which can be related to several parts. This is indicated by a gray background.

Find and replace

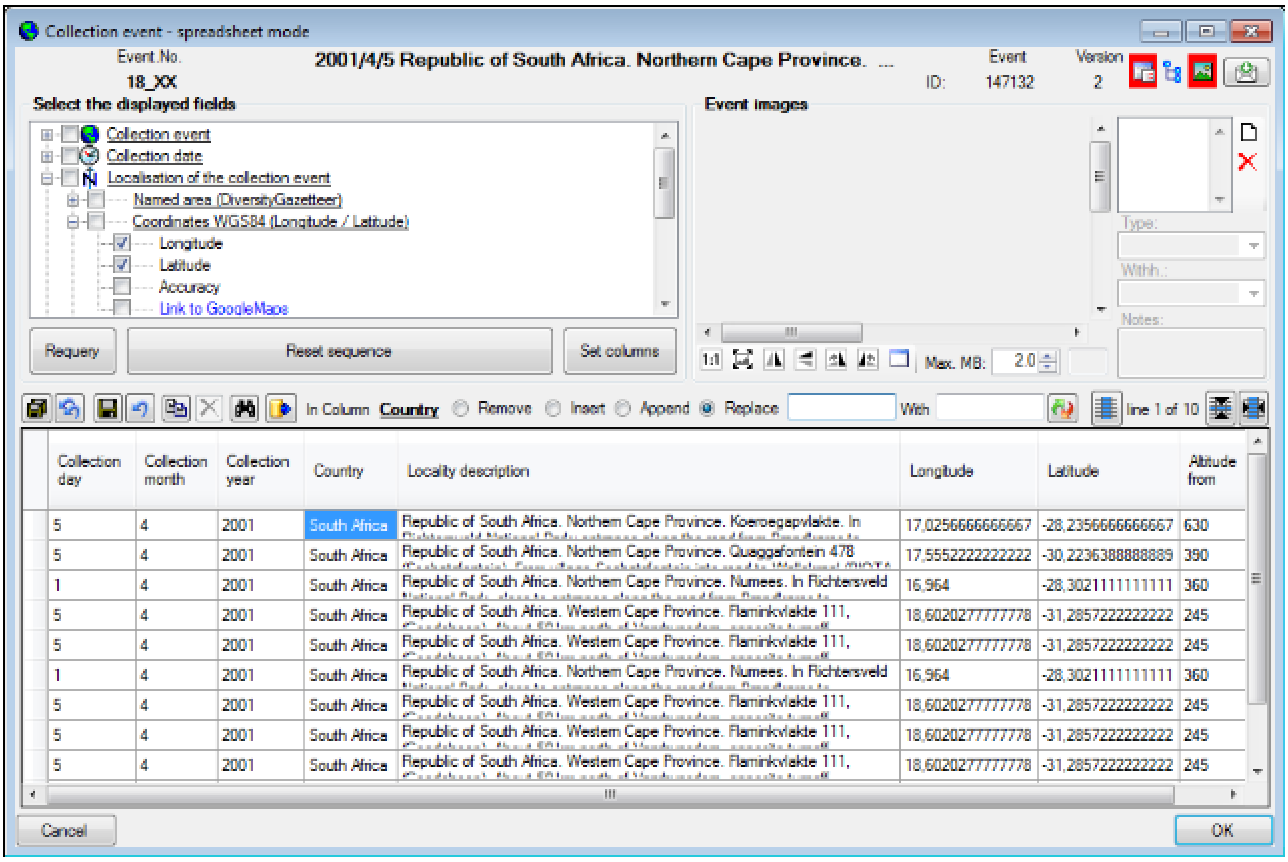
To use the find and replace functions you must either select a part of the field in this column or click on the button to select the entire column. You may then choose the function you wish to apply (remove, insert, append or replace). To replace a part of a text in the selected fields enter the text which should be replaced and enter the replacement in the corresponding fields. To start the **replacement** click the button. To insert a string to the **beginning** of all entries in the selected fields click the button. To **append** a string to all entries in the selected fields click the button. To **remove** all entries from the selected fields click the button.

To save all changes click on the button. To undo all changes since the last time the data sets were saved click on the button. To save the changes in the current data set use the button. To undo the changes in the current data set click the button. If you click the **[OK]** button, you will be asked whether you would like to save the changes before the window will be closed. If you click the **[Cancel]** button or close the window your changes will not be saved. To save the data shown in the grid in a tab delimited file click on the button.

To copy a data set select the line of the data grid which you wish to create a copy of and click on the button. A copy of the selected data set will be added at the base of the spreadsheet.

Grid mode for the CollectionEvents

To edit the data of the CollectionEvents in a data grid choose the **Grid mode** for the event from the menu. A window will open where every data set for a CollectionEvent from the query result list is restricted to one line. Please keep in mind you can only see a limited part of the data while in this view. For example only a part of the localisation will be displayed (see below).



Collection event - spreadsheet mode

Event No. 18_XX

2001/4/5 Republic of South Africa. Northern Cape Province. ...

Event ID: 147132

Version 2

Select the displayed fields

- ☐ Collection event
- ☐ Collection date
- ☐ Localisation of the collection event
  - ☐ Named area (DiversityGazetteer)
  - ☐ Coordinates WGS84 (Longitude / Latitude)
    - ☑ Longitude
    - ☑ Latitude
    - ☐ Accuracy
    - ☐ Link to GoogleMaps

Event images

Max. MB: 2.0

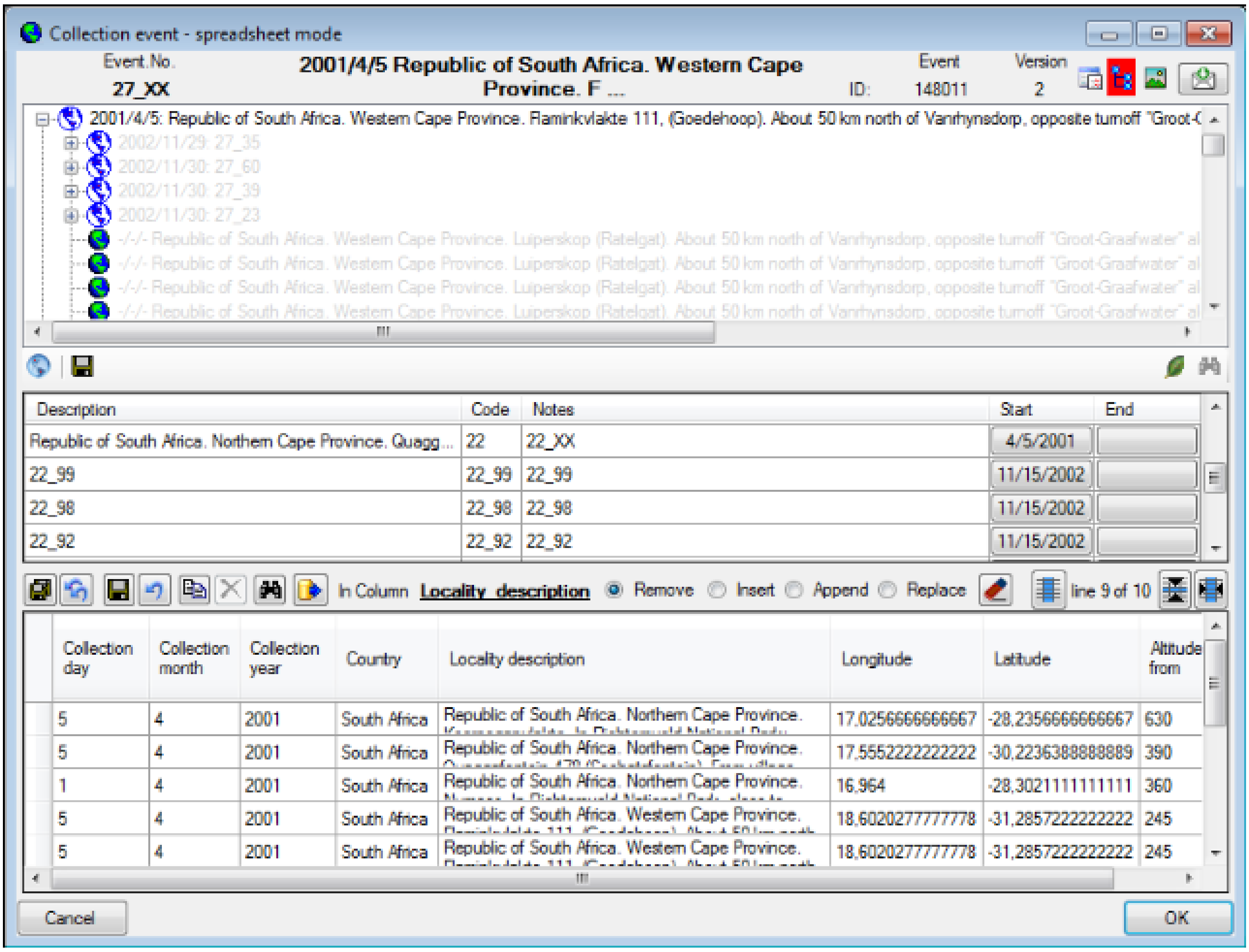
In Column **Country** ○ Remove ○ Insert ○ Append ● Replace With

line 1 of 10

Collection day	Collection month	Collection year	Country	Locality description	Longitude	Latitude	Altitude from
5	4	2001	South Africa	Republic of South Africa. Northern Cape Province. Koeroegapvlakte. In	17,0256666666667	-28,2356666666667	630
5	4	2001	South Africa	Republic of South Africa. Northern Cape Province. Quaggafontein 478	17,5552222222222	-30,2236388888889	390
1	4	2001	South Africa	Republic of South Africa. Northern Cape Province. Numees. In Richtersveld	16,964	-28,3021111111111	360
5	4	2001	South Africa	Republic of South Africa. Western Cape Province. Flaminkvlakte 111,	18,6020277777778	-31,2857222222222	245
5	4	2001	South Africa	Republic of South Africa. Western Cape Province. Flaminkvlakte 111,	18,6020277777778	-31,2857222222222	245
1	4	2001	South Africa	Republic of South Africa. Northern Cape Province. Numees. In Richtersveld	16,964	-28,3021111111111	360
5	4	2001	South Africa	Republic of South Africa. Western Cape Province. Flaminkvlakte 111,	18,6020277777778	-31,2857222222222	245
5	4	2001	South Africa	Republic of South Africa. Western Cape Province. Flaminkvlakte 111,	18,6020277777778	-31,2857222222222	245
5	4	2001	South Africa	Republic of South Africa. Western Cape Province. Flaminkvlakte 111,	18,6020277777778	-31,2857222222222	245

Customize the window

To change the width of a column simply use your mouse to adapt the width to your preference. To hide or show parts of the window use the button for the setting of the visible columns, the button for the hierarchy tree and the button for the images in the upper right corner of the window. If the hierachy tree is visible (, see below), you have access to the CollectionEventSeries which are linked to the CollectionEevents. Here you can edit the hierarchy via drag & drop. Please keep in mind that ramifications within the hierarchy can only be realized using EventSeries with CollectionEvents placed within and specimen placed within the CollectionEvents. To insert a new EventSeries use the button below the tree.



Collection event - spreadsheet mode

Event.No. 27_XX

2001/4/5 Republic of South Africa. Western Cape Province. F ...

Event ID: 148011

Version 2

2001/4/5: Republic of South Africa. Western Cape Province. Flaminkvlakte 111, (Goedehoop). About 50 km north of Vanrhynsdorp, opposite turnoff "Groot-(

- 2002/11/29: 27_35
- 2002/11/30: 27_60
- 2002/11/30: 27_39
- 2002/11/30: 27_23
- -/-/- Republic of South Africa. Western Cape Province. Luiperskop (Ratelgat). About 50 km north of Vanrhynsdorp, opposite turnoff "Groot-Graafwater" al
- -/-/- Republic of South Africa. Western Cape Province. Luiperskop (Ratelgat). About 50 km north of Vanrhynsdorp, opposite turnoff "Groot-Graafwater" al
- -/-/- Republic of South Africa. Western Cape Province. Luiperskop (Ratelgat). About 50 km north of Vanrhynsdorp, opposite turnoff "Groot-Graafwater" al
- -/-/- Republic of South Africa. Western Cape Province. Luiperskop (Ratelgat). About 50 km north of Vanrhynsdorp, opposite turnoff "Groot-Graafwater" al

Description	Code	Notes	Start	End
Republic of South Africa. Northern Cape Province. Quagg...	22	22_XX	4/5/2001	
22_99	22_99	22_99	11/15/2002	
22_98	22_98	22_98	11/15/2002	
22_92	22_92	22_92	11/15/2002	

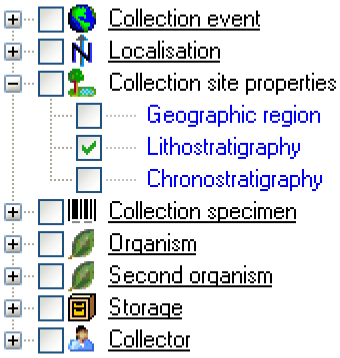
In Column **Locality_description** ● Remove ○ Insert ○ Append ○ Replace line 9 of 10

Collection day	Collection month	Collection year	Country	Locality description	Longitude	Latitude	Altitude from
5	4	2001	South Africa	Republic of South Africa. Northern Cape Province.	17,0256666666667	-28,2356666666667	630
5	4	2001	South Africa	Republic of South Africa. Northern Cape Province.	17,5552222222222	-30,2236388888889	390
1	4	2001	South Africa	Republic of South Africa. Northern Cape Province.	16,964	-28,3021111111111	360
5	4	2001	South Africa	Republic of South Africa. Western Cape Province.	18,6020277777778	-31,2857222222222	245
5	4	2001	South Africa	Republic of South Africa. Western Cape Province.	18,6020277777778	-31,2857222222222	245

To change the width and sequence of the columns simply use your mouse to drag the columns to the position of your choice or adapt the width to your preference. These changes will be saved for this session as well as for the next time you use the grid mode. To return to the original sequence of the columns click on the **[Reset sequence]** button.

Customize visibility of fields

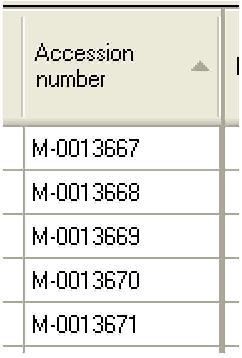
The selection of the visible fields can be adapted in the tree above the list. Change the selection of the columns and click on the **[Set columns]** button.



- ☐ Collection event
- ☐ Localisation
- ☐ Collection site properties
  - ☐ Geographic region
  - ☑ Lithostratigraphy
  - ☐ Chronostratigraphy
- ☐ Collection specimen
- ☐ Organism
- ☐ Second organism
- ☐ Storage
- ☐ Collector

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



Accession number
M-0013667
M-0013668
M-0013669
M-0013670
M-0013671

Formatting the grid

To adapt the width of the columns or the height of the rows either drag the border with the mouse or double click the border to get the optimal size for one column. You may also click on the button for an optimal height of the rows or the button for an optimal width of the columns.

Handling the data

Find and replace

To use the find and replace functions you must either select a part of the field in this column or click on the button to select the entire column. You may then choose the function you wish to apply (remove, insert, append or replace). To replace a part of a text in the selected fields enter the text which should be replaced and enter the replacement in the corresponding fields. To start the **replacement** click the button. To insert a string to the **beginning** of all entries in the selected fields click the button. To **append** a string to all entries in the selected fields click the button. To **remove** all entries from the selected fields click the button.

Editing

Some columns can not be edited directly but are linked to external modules or services. These columns appear as buttons. Simply click on the button to call the service. If a value is linked to an entry in an external module, the background will change to yellow and you will not be able to change the text.

☐ Collector
- ☑ Collectors name
- ☐ Link to DiversityAgents
- ☐ Remove link for collector

Together with the links (in the example above Link to DiversityAgents) you can select columns that provide the posibility to release the links to the modules (e.g. Remove link for collector in image above). These columns will appear as buttons ☒. Simply click on the button related to a link to release the link to the corresponding module. After that you can edit the text field containing the linked value.

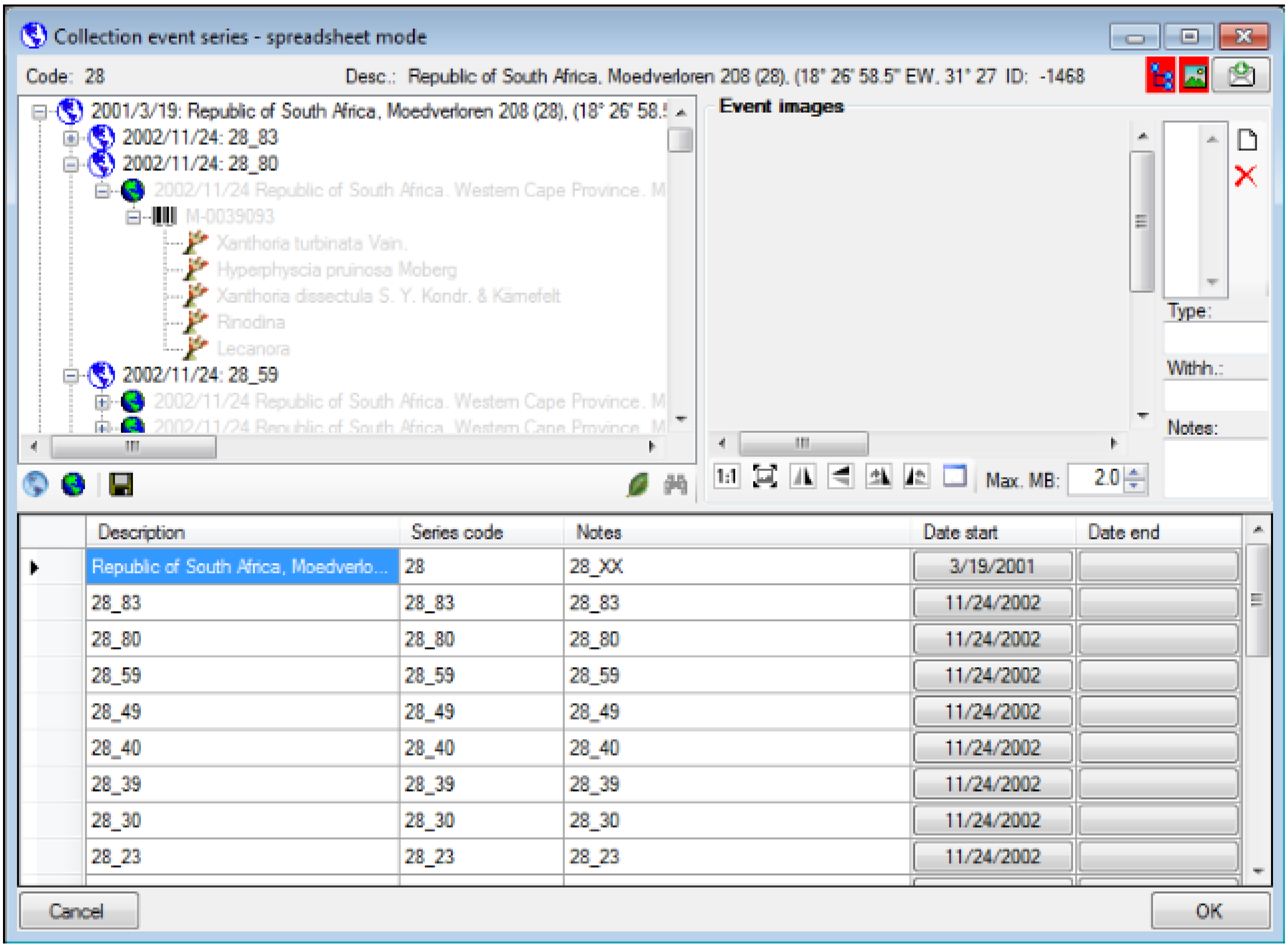
Some values are linked to a list of values. Use the drop-down list to change the value in one of these columns.

Saving the data

To save all changes click on the button. To undo the all changes since the last time the data sets were saved click on the button. To save the changes in the current data set use the button. To undo the changes in the current data set click the button. If you click the **[OK]** button, you will be asked whether you would like to save the changes before the window will be closed. If you click the **[Cancel]** button or close the window your changes will not be saved. To save the data shown in the grid in a tab delimited file click on the button.

Grid mode for the CollectionEventSeries

To edit the data in a data grid choose the **Grid mode** for the CollectionEventSeries from the menu. A window will open where every data set for a CollectionEventSeries from the query result list is restricted to one line (see below).



Collection event series - spreadsheet mode

Code: 28 Desc.: Republic of South Africa, Moedverloren 208 (28), (18° 26' 58.5" EW, 31° 27 ID: -1468

- 2001/3/19: Republic of South Africa, Moedverloren 208 (28), (18° 26' 58.5
  - 2002/11/24: 28_83
  - 2002/11/24: 28_80
    - 2002/11/24 Republic of South Africa. Western Cape Province. M
      - M-0039093
        - Xanthoria turbinata Vain.
        - Hyperphyscia pruinosa Moberg
        - Xanthoria dissectula S. Y. Kondr. & Kärnefelt
        - Rinodina
        - Lecanora
  - 2002/11/24: 28_59
    - 2002/11/24 Republic of South Africa. Western Cape Province. M
    - 2002/11/24 Republic of South Africa. Western Cape Province. M

Description	Series code	Notes	Date start	Date end
Republic of South Africa, Moedverlo...	28	28_XX	3/19/2001	
28_83	28_83	28_83	11/24/2002	
28_80	28_80	28_80	11/24/2002	
28_59	28_59	28_59	11/24/2002	
28_49	28_49	28_49	11/24/2002	
28_40	28_40	28_40	11/24/2002	
28_39	28_39	28_39	11/24/2002	
28_30	28_30	28_30	11/24/2002	
28_23	28_23	28_23	11/24/2002	

Customize the window

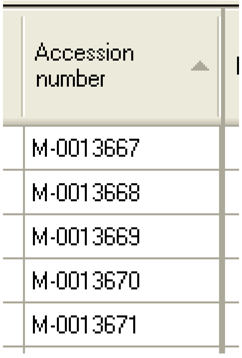
To change the width of a column simply use your mouse to adapt the width to your preference. To hide or show parts of the window use the button for the setting of the visible columns, the button for the hierarchy tree and the button for the images in the upper right corner of the window. If the parts are shown, the icon will have red backgound e.g. .

History and feedback

To inspect the history of a data set click on the button. A window will open as described in the History chapter. To send a feedback use the button. Details are described in the Feedback chapter.

Sorting of the data

To sort the data in the grid simply click in the header of the column which you want to use as sorting column. The sorting sequence will be kept even if you change values in this column. This means if you change a value in the sorting column, the changed data set will be placed at the new position according to its new value. The sorting of a column will be indicated by an arrow for the direction of the sorting (up or down) and by a thicker right border of this column (see image below).



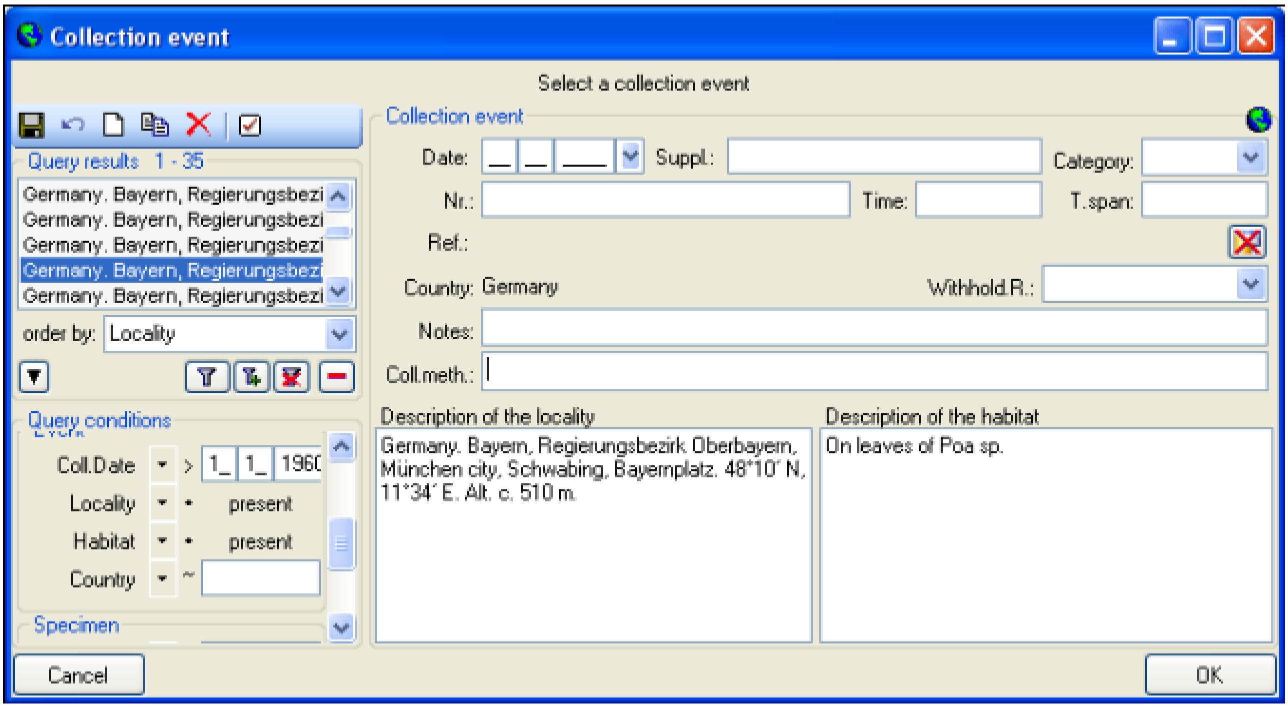
Accession number ▲
M-0013667
M-0013668
M-0013669
M-0013670
M-0013671

Handling the data

To save the changes click on the 💾button. To insert new data sets use the 🌐button for a CollectionEventSeries and the 🌐button for a CollectionEvent.

CollectionEvent

Specimens stored in a collection are gathered during a CollectionEvent. This CollectionEvent keeps information about the geographic locality, the habitat, the collection date etc. During a CollectionEvent several specimens may have been collected. To create a new event for a specimen click on the 🌍button. If a specimen has not been assigned to a CollectionEvent, you can assign the specimens to an existing event with a click on the 🔍button. If you assign the specimen to an existing event, a window will open where you can search for the events already included in the database as shown below. Choose an event and click OK to assign the specimen to this event. If you click OK without selecting any CollectionEvent, the current CollectionEvent will be removed from the CollectionSpecimen.



Germany. Bayern, Regierungsbezi
Germany. Bayern, Regierungsbezi
Germany. Bayern, Regierungsbezi
Germany. Bayern, Regierungsbezi
Germany. Bayern, Regierungsbezi

order by: Locality

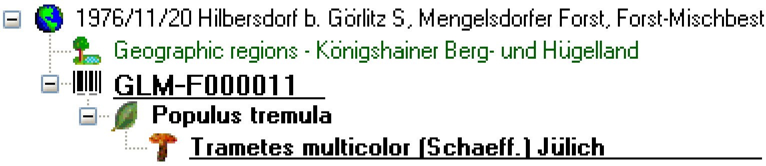
Coll.Date > 1_ 1_ 1960
Locality • present
Habitat • present
Country ~

Collection event
Date: _ _ __ Suppl.: Category:
Nr.: Time: T.span:
Ref.:
Country: Germany
Withhold R.:
Notes:
Coll.meth.:

Description of the locality: Germany. Bayern, Regierungsbezirk Oberbayern, München city, Schwabing, Bayernplatz. 48°10' N, 11°34' E. Alt. c. 510 m.

Description of the habitat: On leaves of Poa sp.

In the tree view the CollectionEvent is symbolized by a 🌍icon as shown below.

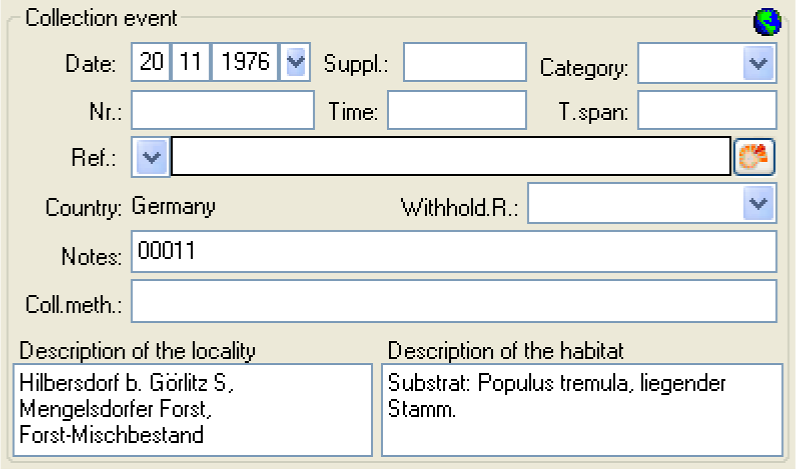


1976/11/20 Hilbersdorf b. Görlitz S, Mengelsdorfer Forst, Forst-Mischbestand
Geographic regions - Königshainer Berg- und Hügelland
GLM-F000011
Populus tremula
Trametes multicolor (Schaeff.) Jülich

The CollectionEvents can be organized in a hierarchy either by using CollectionEventSeries or sampling plots. If your CollectionEvents belong e.g. to an expedition, you should preferably use CollectionEventSeries for the organization.

If your samples are taken e.g. on a regular basis from permanent sampling plots, you may prefer to use the module DiversitySamplingPlots to document the geography and other details of the sampling plots and use the CollectionEvents only to document the collection date.

To edit the data of the CollectionEvent choose it in the tree view to open the detail fields as shown below. If the collection date does not correspond to a certain day, you may use the **Suppl.** field to enter e.g. a range or a series of dates or the **T.span** field to document a certain time span.


Collection event

Date: 20 11 1976

Suppl.:

Category:

Nr.:

Time:

T.span:

Ref.:

Country: Germany

Withhold.R.:

Notes: 00011

Coll.meth.:

Description of the locality

Hilbersdorf b. Görlitz S, Mengelsdorfer Forst, Forst-Mischbestand

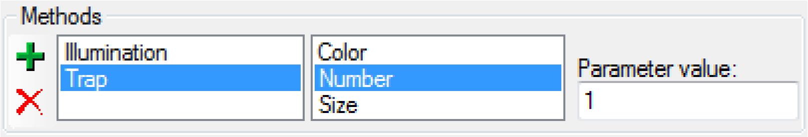
Description of the habitat

Substrat: Populus tremula, liegender Stamm.

The text shown in the tree view is composed of the date of the CollectionEvent and the description of the locality. For each CollectionEvent you can enter several geographical locations and properties. To see the locality according to the coordinates stored in the database you can check the Maps. For each CollectionEvent you can enter images related to this event.

If other specimens were collected during the same CollectionEvent, they will be displayed once the entire hierarchy of the EventSeries is shown. To do this click on the button in the panel on the left side of the tree. See EventSeries for further details. You can also move a specimen to another event by drag and drop.

Besides of a plain text description of the methods used during the CollectionEvent, you may insert methods as defined in the chapter Methods. Use the + and ✕ buttons to add or remove methods from the list (see below)


Methods

Illumination

Trap

Color

Number

Size

Parameter value:

1

Data is stored in the table CollectionEvent.

CollectionEventSeries

If you need a hierarchical order of your CollectionEvents or to organise your CollectionEvents e.g. to document expeditions respectively, you can do this with a CollectionEventSeries . For a better differentation between events and CollectionEventSeries you have a blue text in the hierarchy as well as the editing part and a different icon . A CollectionEventSeries can contain other CollectionEventSeries and CollectionEvents. Information about the geographic locality, properties of the collection site, date of collecting etc. is stored in the CollectionEvent. To show or hide the CollectionEventSeries you have two options. In the panel of the left of the tree the button will show the superior EventSeries of the current CollectionEvent as shown below.

1986/2/4: Australia New South Wales Barrington Tops National Park. 4.2.1986
1986/2/4: Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Altid.: ca. 1200 m; Koord.: 32°05' S, 151°35' E.
1986/2/4 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Altid.: ca. 1200 m; Koord.: 32°05' S, 151°35'
GR04228

The button will show the entire hierarchy of the EventSeries as shown below.

1986/2/4: Australia New South Wales Barrington Tops National Park. 4.2.1986
1986/2/4: Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Altid.: ca. 1200 m; Koord.: 32°05' S, 151°35' E.
4.2.1986 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Altid.: ca. 1200 m; Koord.: 32°05' S, 151°35' I
GR04243
1986/2/4 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Altid.: ca. 1200 m; Koord.: 32°05' S, 151°35'
GR04228
1986/2/4: Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail, on way to Gloucester Falls. Altid.: ca. 1200 m; K
4.2.1986 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail, on way to Gloucester Falls. Altid.: ca. 1200 m
GR04260
4.2.1986 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail, on way to Gloucester Falls. Altid.: ca. 1200 m
GR04264
GR04265

To edit the data of an EventSeries select it in the tree to display the detail fields as shown below.

Event series
Date
04.02.1986
Description
Australia New South Wales Barrington Tops National Park.
Code
Notes

New EventSeries

To insert a new CollectionEventSeries click on the button. If there are no CollectionEventSeries so far, the CollectionEvent will be placed within the new CollectionEventSeries. If there are CollectionEventSeries present, the new CollectionEventSeries will be placed below the selected CollectionEventSeries. To assign an CollectionEvent to an existing CollectionEventSeries already available in the database click on the icon.

To move an item within the hierarchy just drag it with the mouse to whatever position it should be placed in. Keep in mind that specimens can only be placed in CollectionEvents and CollectionEvents only in CollectionEventSeries.

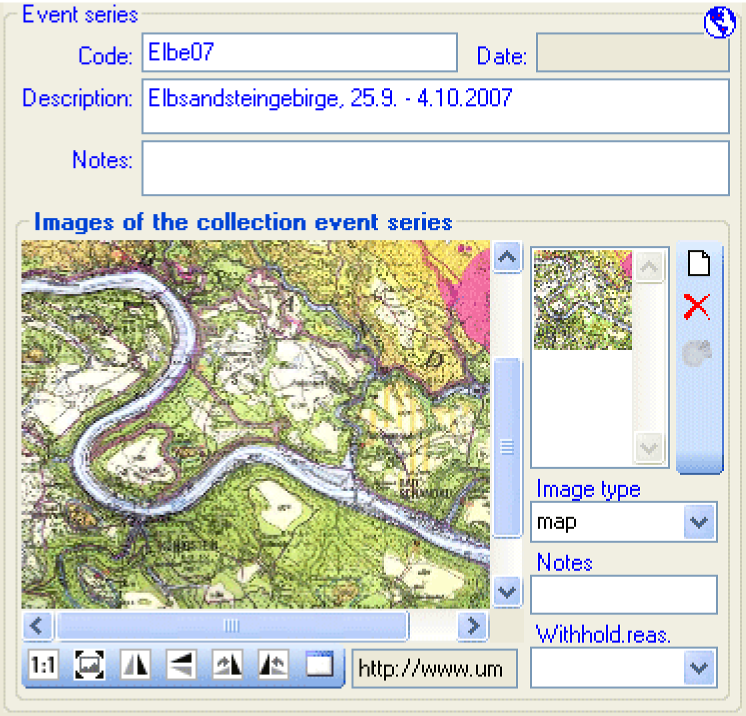
Removing EventSeries

If you want to delete a CollectionEventSeries or a CollectionEvent, remove all depending CollectionEventSeries, CollectionEvents and specimens and click on the ✕ button. A specimen can not be deleted here.

If you want to remove a CollectionEvent 🌍 from a CollectionEventSeries, click on the 🔍 button to open the window for selecting a CollectionEventSeries. Then select nothing but simply click OK to remove the link to the CollectionEventSeries.

Images

The images for a CollectionEventSeries are displayed below the data of the CollectionEventSeries (see below). To add images to a CollectionEventSeries click on the 🗋 button, to remove an image use the ✕ button.



Event series

Code: Elbe07

Date:

Description: Elbsandsteingebirge, 25.9. - 4.10.2007

Notes:

Images of the collection event series

Image type: map

Notes:

Withhold.reas.:

http://www.um

To zoom a sector of the image simply move the mouse over the image. A red square will indicate the zoomed area. To set the size of the image to the original resolution click on the 1:1 button. To adapt the size of the image to the available space in the form click on the ⛶ button. To change the orientation of the image use the appropriate buttons (◭ flip horizontally, ⧩ flip vertically, ↻ rotate right, ↺ rotate left). To view the image in a separate form click on the ☐ button. If the image should not be published e.g. on the internet, enter any reason in the **Withhold reason** field. Besides images you can also store other media.

Hierarchy

If you want to change to another specimen listed in the CollectionEventSeries, select it in the hierarchy and click on the 🔭 button.

The current specimen together with the event and all superior CollectionEventSeries will be highlighted.

Geography

The CollectionEventSeries can contain a geographical object (using WGS84) such as a point, a line, an area etc. To edit or show the geographical object related to the CollectionEventSeries either click on the N button in the details next to the notes field or click on the N button in the control to show the maps and use the GIS editor.

Storage

The data of the CollectionEventSeries is stored in the table CollectionEventSeries.

Event images

The specimens stored in a collection are gathered during a CollectionEvent. To insert an image related to a CollectionEvent click on the 🗋 button. If you want to delete an image, click on the ✕ button. For more details see the section Images.

If for any reason an image should not be published i.e. shown on a website, enter the reason in the field **Withholding reason**. Only images where this field is empty will be shown e.g. on websites.

http://bsm4.snsb.info/UBT-Mycology/Biota/pics/aufn

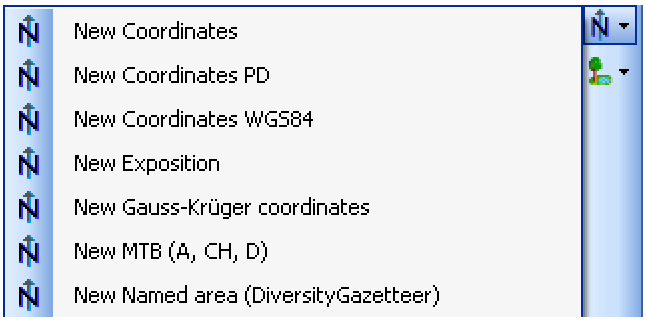
Data is stored in the table CollectionEventImage .

Geography

As additional information to the description of the locality you can use several localisation systems, e.g. georeferencing. These entries are marked with a icon in the tree as shown below.

1986/2/4: Australia New South Wales Barrington Tops National Park. 4.2.1986
1986/2/4: Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail. Alt
1986/2/4 Australia New South Wales Barrington Tops National Park, Gloucester Tops, Negrohead Beech Forest Walking Trail.
Altitude (mNN): c. 1200 m
Greenwich Coordinates Long. (EW): 151°35' E Lat. (NS): 32°05' S
GR04228

To add a new entry choose the localisation system from the drop-down list as shown below. Only items which are not already set for a CollectionEvent will be shown. The items visible in the drop-down list can be customized.



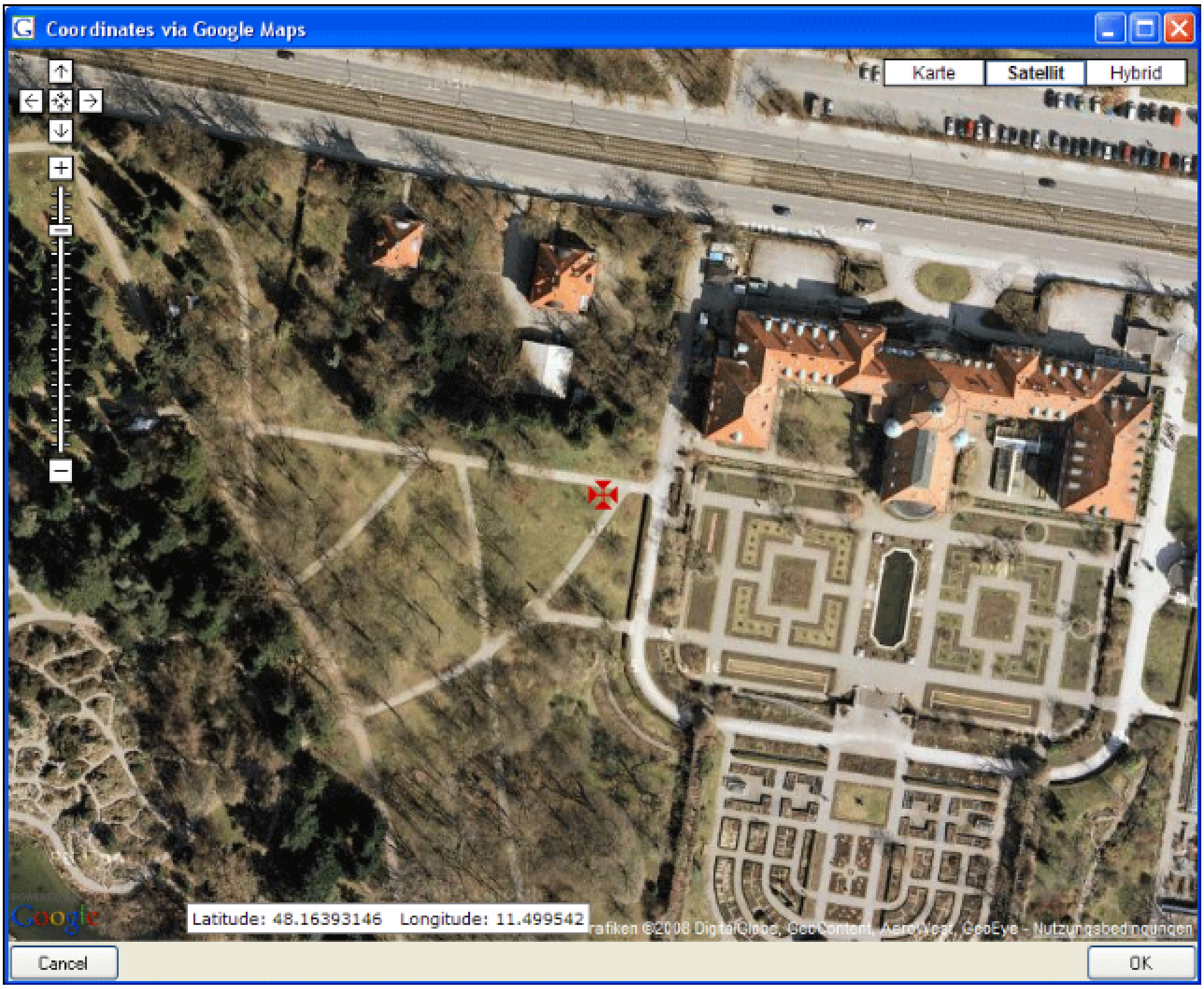
If a localisation should be removed, select it from the list and click on the button.

GIS editor

To define an area for the locality you can use the GIS editor. For further details please see the help sections for the corresponding pages.

Coordinates (WGS84)

If you use geo-coordinates as georeferencing system (coordinates WGS84), a button will appear which will provide you with the possibility to set or correct the coordinates via Google Maps. Just click on the button and a window will open with a map provided by Google Maps as shown below. If there are already coordinates provided by a different localisation e.g. by the DiversityGazetteer, these will be taken as a starting position. Thus, you may use an entry for a named area (DiversityGazetteer) as an approximate localisation and use additional coordinates for a more accurate localisation.



Latitude: 48.16393146 Longitude: 11.499542

If you start with existing geographic coordinates (WGS84) in your data, the system will use these as starting point. You can zoom the map, drag it to another position and change from map to satellite mode. The actual position is symbolized by the symbol in the middle of the map. The current coordinates are shown in the field at the buttom of the map. To include these coordinates in your data simply click OK.

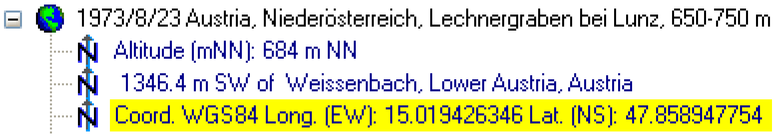
With the **Set start coordinates** button you can set the coordinates which GoogleMaps should use as a starting position.

Please keep in mind that Google Maps coordinates are based on **WGS84**.

If there are no entries for the altitude and the named area, this data will be retrieved from the webservice ws.geonames.org and entered into the database. The source will be documented in the **Notes** field. Subsequent changes in the coordinates using the GoogleMaps function will update the altitude and named area entries provided they are derived from a webservice (ws.geonames.org) as documented in the Notes field.

Please keep in mind that the place names provided by **ws.geonames.org** may differ from those depicted in **GoogleMaps**.

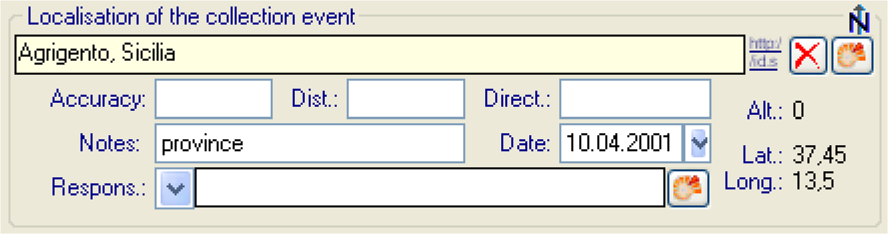
To enter the localisations listed above simply enter the **Coordinates WGS84**, the **Altitude** and **Named area** will be added automatically.



1973/8/23 Austria, Niederösterreich, Lechnergraben bei Lunz, 650-750 m
Altitude (mNN): 684 m NN
1346.4 m SW of Weissenbach, Lower Austria, Austria
Coord. WGS84 Long. (EW): 15.019426346 Lat. (NS): 47.858947754

Named areas - DiversityGazetter

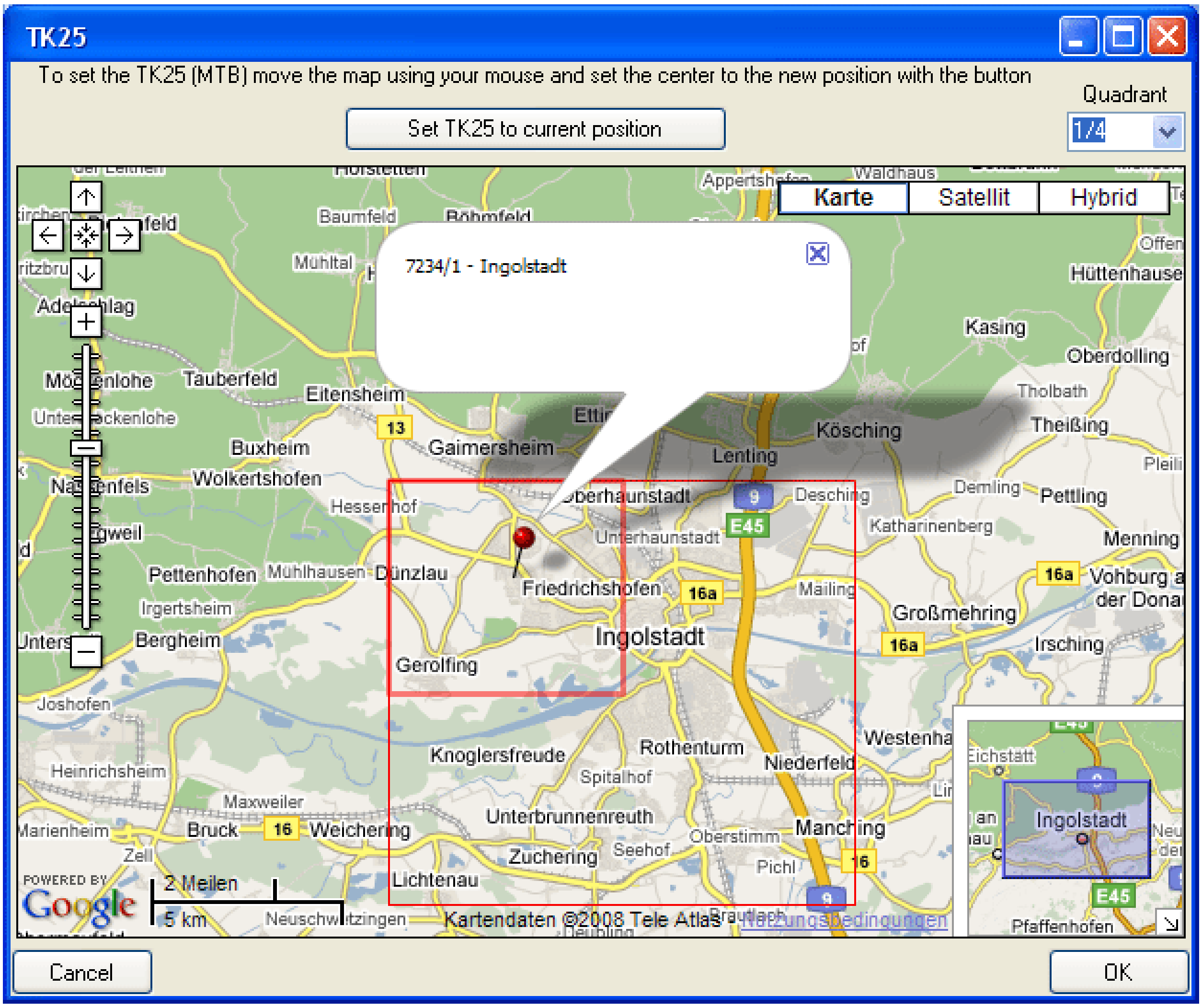
To edit the details of an entry select in the list to open the fields in the form on the right. The localisation system DiversityGazetteer is linked to the module DiversityGazetteer within the DiversityWorkbench and providing information on geographical names as shown below.



Localisation of the collection event
Agrigento, Sicilia
Accuracy:
Dist.:
Direct.:
Alt.: 0
Notes: province
Date: 10.04.2001
Lat.: 37,45
Respons.:
Long.: 13,5

TK25 (MTB)

If you choose MTB or TK25, the button will open a window where you can set the TK25 as well as the quadrant (see image below). Choose the quadrant depending on your preferred resolution. The thick line shows the current quadrant, the thin line the entire TK25. The needle in the center is placed at your current position. If you click on it, a message box will display the TK25 information as shown below.



TK25

To set the TK25 (MTB) move the map using your mouse and set the center to the new position with the button

Quadrant: 1/4

7234/1 - Ingolstadt

If you click **[OK]**, the TK25 values together with the coordinates of the center of the selected quadrant will be entered into the database.

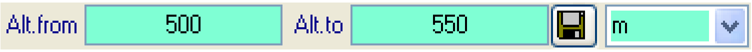
Conversion of values

The values for any localisation system are stored in two text fields. You can enter your values as simple text. This may, however, prevent any calculations with said values. Thus, you should preferably enter your values according to the measurement units available. Whatever obsolete measurement units like feet or Fahrenheit may exist, within the DiversityWorkbench measurement data is stored in units according to the *Système International d'Unités* (SI). For those who still need to use these obsolete units DiversityCollection provides a possibility to convert them into their modern counterparts. To enter a numeric value choose the unit you prefer from the list. The form will change as shown below.

Long. (EW) 18 36 1,6111111 Lat. (NS) -31 16 34,888888 deg_min_sec

You can then edit the values and click on the 💾 button to incorporate the changed values into your data. The system will calculate the corresponding value for storage in the database together with the default accuracy. You may correct this accuracy if you have more exact values. To indicate that the shown values are calculated from the values in the database the fields have a green background. When you save the data DiversityCollection will store geographic coordinates and the average altitude, if available, in separate fields.

The altitude, the exposition or the slope may be entered as one value or as a range of two values. If you use the conversion function and have only one value, make sure that the second field is empty.


Alt.from 500 Alt.to 550 m

Available units: meter and feet.


Exp. from NNE to NE orientation

Available units: Orientiation (N, NE, ...) and degree rel. to North.


Slope from 10 to 15 percent

Available units: degree and percent.

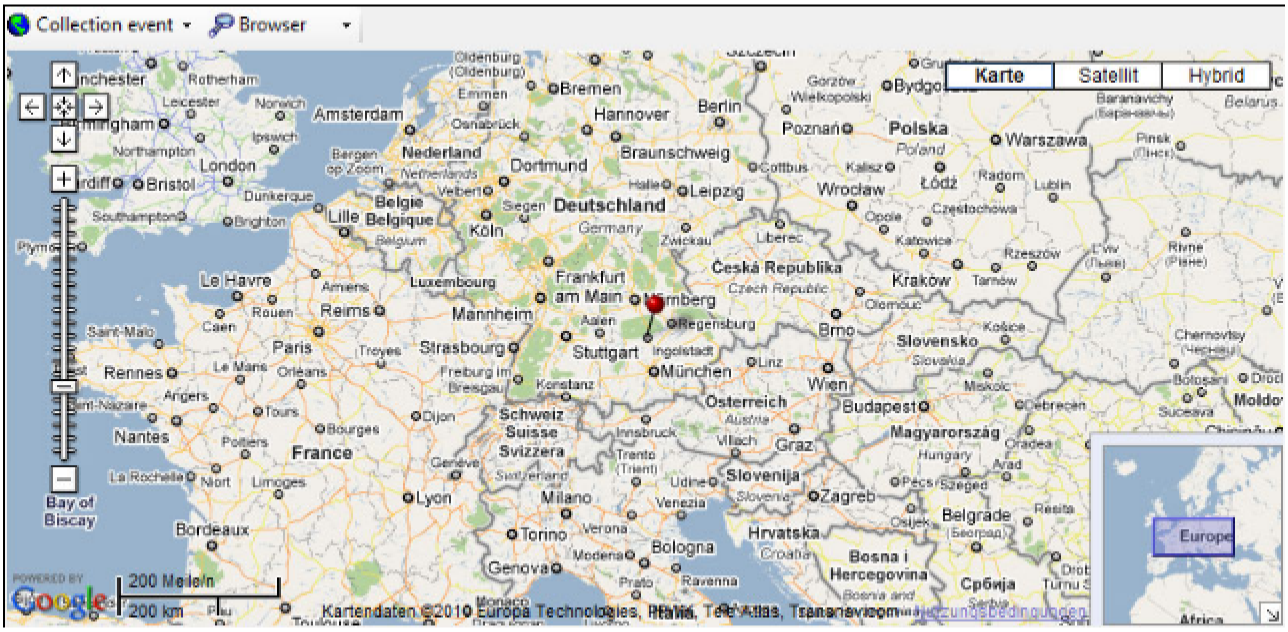
The accuracy and uncertainity respectively will be calculated as an approximation in parts derived from Wieczorek, J. 2001 (MaNIS/HerpNet/ORNIS Georeferencing Guidelines. University of California, Berkeley: Museum of Vertebrate Zoology) and in parts according to Wieczorek, J., Q. Guo, and R. Hijmans 2004 (The point-radius method for georeferencing locality descriptions and calculating associated uncertainty. International Journal of Geographical Information Science 18: 745-767). The unit of the accuracy will always be the unit stored in the database according to the *Système International d'Unités* (SI) and degrees for angles respectively.

The data for the geography is stored in the table CollectionEventLo calisation.

Maps of samples in the database

If there are WGS84 coordinates available for your collection site, an event series or single organisms, you can use GoogleMaps to display these locations.

To use this service you need access to the internet. Click on the button in the control to show the maps. Here you can display maps of CollectionEventSeries, CollectionEvent, Organism as well as [Distribution maps](). To display the maps you can either use the browser, the GIS viewer or the [GIS editor](). By default the map will show the location of the CollectionEvent using the browser as shown below.

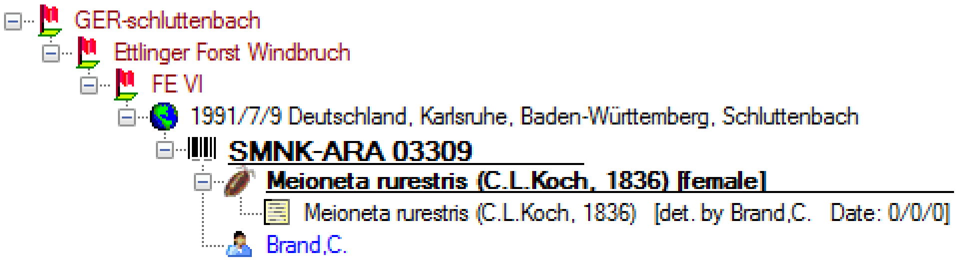


For the CollectionEventSeries, the CollectionEvent or the [Organism]() you can use any geographical object like points, lines, areas, etc. to describe the location. The browser will always display these objects as points (see left image below) whereas with the [GIS editor]() you can see and edit the real objects (see right image below).

The data of the geographical objects is stored in the table CollectionEventSeries for the collection event series,the table CollectionEventLocalisation for the colletion event and the table IdentificationUnitGeoAnalysis for the organisms.

Sampling plots

If your samples are collected at constant sampling plots, you may use the module DiversitySamplingPots to describe said SamplingPlots. For a better differentation between events and the SamplingPlots there is a brown text in the hierarchy as well as a different icon . A SamplingPlot can contain other SamplingPlots and CollectionEvents. Information about the geographic locality and properties of the collection site can be stored in the SamplingPlot, while the collecting date must be stored in the CollectionEvent. To show or hide the SamplingPlots you have two options. In the panel on the left of the tree the button will show the superior SamplingPlots of the current CollectionEvent as shown below.



- GER-schluttenbach
  - Ettlinger Forst Windbruch
    - FE VI
      - 1991/7/9 Deutschland, Karlsruhe, Baden-Württemberg, Schluttenbach
        - **SMNK-ARA 03309**
          - **Meioneta rurestris (C.L.Koch, 1836) [female]**
            - Meioneta rurestris (C.L.Koch, 1836) [det. by Brand,C. Date: 0/0/0]
          - Brand,C.

The button will show the entire hierarchy of the SamplingPlots as shown below.

- GER-schluttenbach
  - Schluttenbach
  - Ettlinger Forst Windbruch
    - FE VI
      - 1992/5/12 Deutschland, Karlsruhe, Baden-Württemberg, Schluttenbach Ettlinger Forst Windbruch
      - 1992/5/26 Deutschland, Karlsruhe, Baden-Württemberg, Schluttenbach Ettlinger Forst Windbruch
      - 1991/7/9 Deutschland, Karlsruhe, Baden-Württemberg, Schluttenbach
        - SMNK-ARA 03681
          - Neon reticulatus (Blackwall, 1853) [female]
        - SMNK-ARA 03828
          - Episinus angulatus (Blackwall, 1836) [male]
        - SMNK-ARA 03833
          - Robertus lividus (Blackwall, 1836) [male]
        - **SMNK-ARA 03309**
          - **Meioneta rurestris (C.L.Koch, 1836) [female]**
            - Meioneta rurestris (C.L.Koch, 1836) [det. by Brand,C. Date: 0/0/0]
          - Brand,C.

If you select a SamplingPlot in the hierarchy, two buttons will appear in the bar to the left of the tree. With the button you can retrieve a taxon list for the SamplingPlot. With the button you can retrieve a summary of the information on a SamplingPlot (see image below).

Description
Versuchsfläche von Alex Kehl zur Untersuchung von Gallen an Salix

Plot identifier
Salix - Versuchsfläche im ÖBG

Latitude
49.9267306925503

Longitude
11.5829768002811

Altitude

Accuracy angle
0.000156986 °

Area
0 m2

Geography
LINESTRING (11.5831805555556 49.9266444444444, 11.58277777777 49.9266444444444,

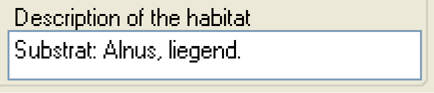
☑ Display website

To edit the data of a SamplingPlot please use the module DiversitySamplingPlots.

The link to the module DiversitySamplingPlots is stored in the table CollectionEventLocalisation.

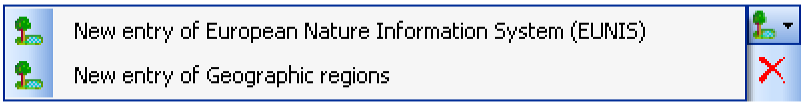
Habitats and properties of the collection site

For the description of the habitat select the CollectionEvent or an existing collection site property. The description is entered in the field **Description of the habitat** (see below).

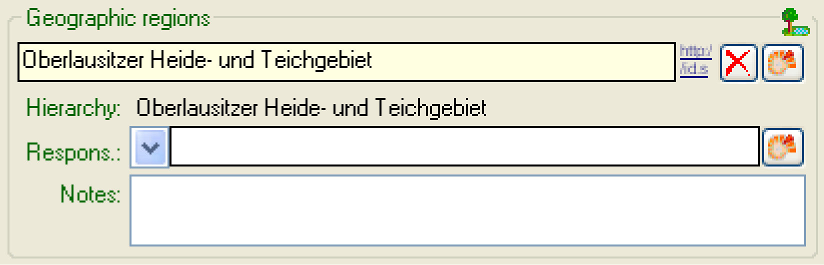

Description of the habitat

Substrat: Alnus, liegend.

To enter a new property of the collection site select the CollectionEvent or an existing collection site property. Then choose the type of the property you wish to enter from the drop-down menu as shown below. Only items which are not already set for a CollectionEvent will appear in the list. You can [customize]() the selection of visible items.



The list is dependent on the availability of terminologies for site descriptions. Details for the property can be entered if you choose the item in the hierarchy. The person responsible for the entry as well as notes can be entered in the corresponding fields as shown below.


Geographic regions

Oberlausitzer Heide- und Teichgebiet

Hierarchy: Oberlausitzer Heide- und Teichgebiet

Respons.:

Notes:

To delete entries use the ✕ button. You can enter a value by either typing the name of the collection site property or by selection from the module DiversityScientificTerms. To search for properties from this module click on the button. The current user's name will be inserted as the responsible user. You may change this by either typing or through selection from the module DiversityAgents.

The data concerning the habitats is stored in the table [CollectionEventProperty]().

Specimens

Specimens are the entities stored in a collection. For handling the data use the appropriate buttons (new specimen ,copy , delete). See the Data section for further details. Directly attached to the specimen is the data about accession, label, exsiccatae, notes, reference and the availability. A specimen may be composed of several units. Any problems concerning the specimen should be entered into the problems field.

The header of the main window shows some important parameters for the selected specimen. On the left side the **accession number** is shown. In the center you find the last identification of the main IdentificationUnit according to the display order. The next field shows the internal **ID**s (field CollectionSpecimenID in table CollectionSpecimen and CollectionEventID in table CollectionEvent) and the **Version**s for the specimen and the CollectionEvent. For details about the version of a data set see the Version topic. The availability of a specimen can be changed by entering an appropriate reason in the field **Withholding reason**.


Acc.No. M-0040397
Erysiphe aquilegiae var. ranunculi (Grev.) U. Braun
ID (Specimen / Event) 135548 / 211558
Version 3 / 1
Withhold. reason

If the specimen is a type, the header will show the type state and the identification connected with the type (see below).


Acc.No. M-0003940
Potamogeton parmatus Hagström
isotype
ID (Specimen / Event) 29432 / 72391
Version 1 / 2
Withhold. reason

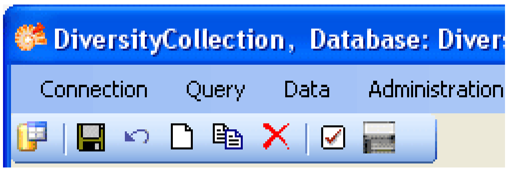
To inspect the history of a specimen click on the button. For further details see the History section.

With the buttons you may control the upper part of the window with the maps , the images for the CollectionEvent and the Specimen as well as the label print . The buttons, with the corresponding sector visible in the window, are depicted with a red background. If there are images available and they are hidden, the background will turn yellow .

The data is stored in the table CollectionSpecimen .

Data

The controls for handling data sets in the database are located in the left upper part of the window as shown in the image below. A step-by-step introduction for the creation of new data sets is provided in the Tutorial.

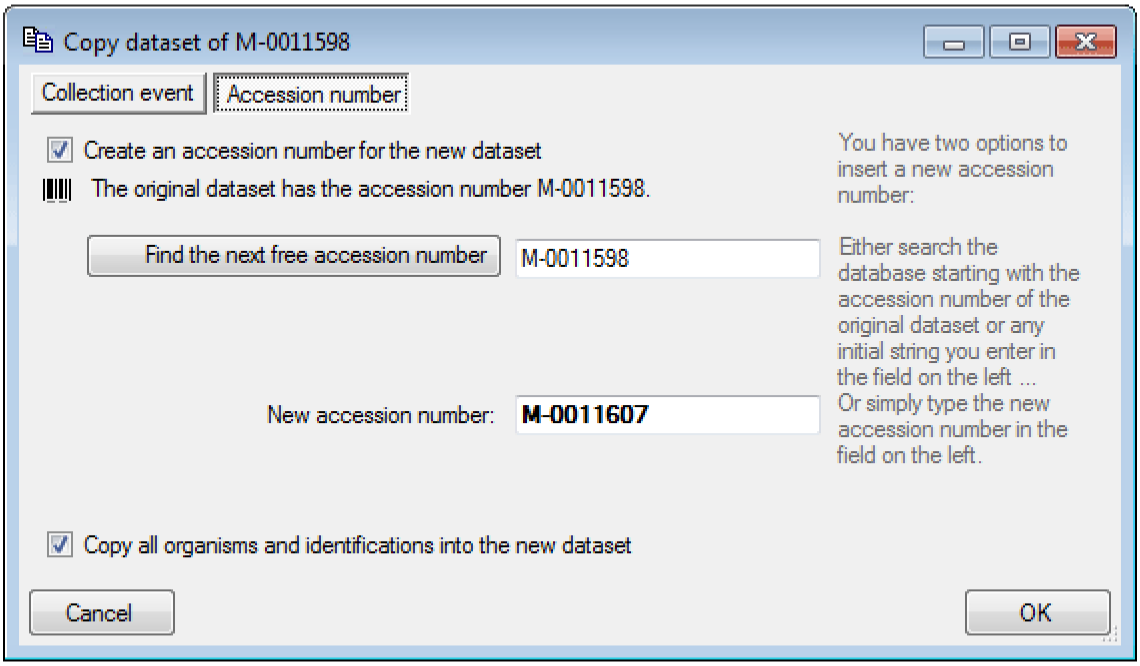


💾- To **SAVE** the changes in a data set click on the 💾button. If you select another data set from the results list, the current changes will be saved automatically.

↶- To **UNDO** the changes in a data set, click on the ↶button. This will recover the original data unless the changes have been saved or changes were done in certain tables or hierarchies were the data must be stored to display the hierarchy.

🗋- To create a **NEW** entry in the database click on the 🗋button. This will create a new record of a specimen and show it in the results list.

⧉- To **COPY** the data of a specimen record choose it from the list and click on the ⧉button. If you want to create multiple copies of your specimen, use the corresponding function in the grid mode. If the specimen you want to copy is linked to a collection event, a window will open and provide you with several copy possibilities as shown below.



☑ Create an accession number for the new dataset

The original dataset has the accession number M-0011598.

M-0011598

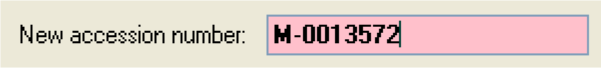
New accession number: M-0011607

You have two options to insert a new accession number:

Either search the database starting with the accession number of the original dataset or any initial string you enter in the field on the left ...
Or simply type the new accession number in the field on the left.

☑ Copy all organisms and identifications into the new dataset

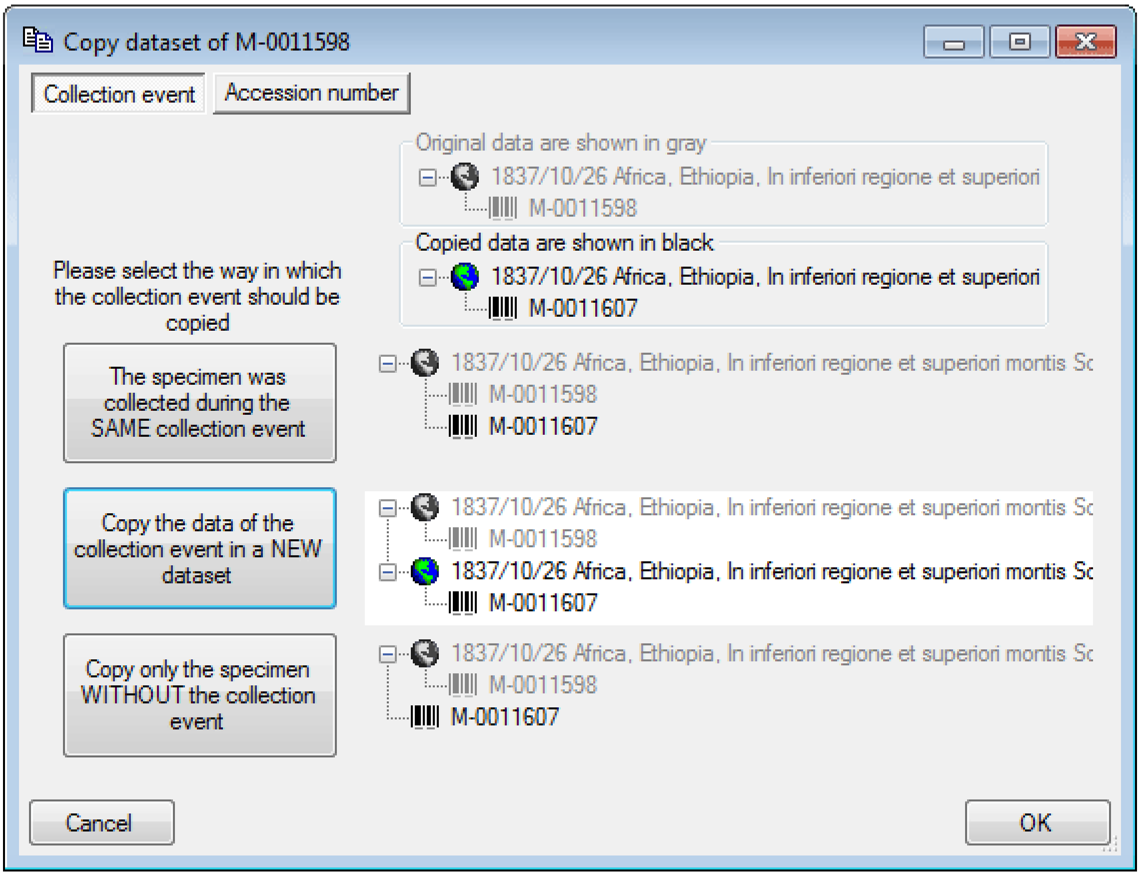
The field **[New accession number]**: You can change this number manually or search for another number using the **[Find the next free accession number after:]** button. If you change the accession number to a value that is already present in the database, you will get a warning and the color of the field will change as shown below.



New accession number: M-0013572

If you do not want to create an accession number, just uncheck the **[Create an accession number for the new dataset]** checkbox. By default all organisms and identifications will be copied into the new data set. If you dont want to copy this infomation, uncheck the **[Copy all organisms and identifications into the new data set]** checkbox.

If the original data set contains information about the collection, you have 3 options to handle the data. By default the new specimen will be placed into the same collection event, which means no new data set for the collection event will be created (see image below). The second option will create a copy of the original data for the collection event and connect the copy of the specimen record with the new event. The last option will only copy the specimen data and establish no connection to any collection event. If you decide not to copy anything, just close the window.



Please select the way in which the collection event should be copied

After all options are set just click the **OK** button to create the new entry.

✕- To **DELETE** a data set select it in the list and click on the ✕button.

Tree for the specimen

The upper tree in the window provides an overview for all the data linked with the specimen. With the buttons in the left panel you may hide or show certain nodes in the tree. If for example you do not wish to see the collectors, simply click on the button and they will be hidden in the tree. The button will change to a grey version and the background will turn yellow to show that there is hidden data of the collectors.

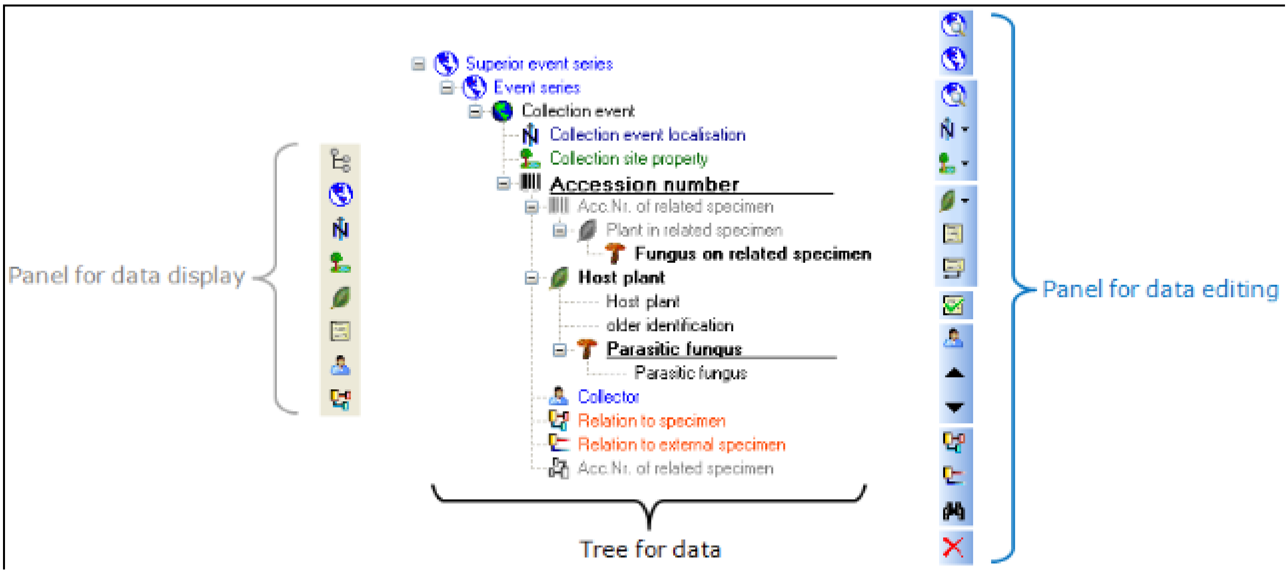
If the CollectionEvent is part of a CollectionEventSeries, a drop-down button will appear where you may select between 3 states:

- = show the parent EventSeries
- = show the entire hierarchy of the EventSeries
- = hide the EventSeries

If the CollectionEvent is linked to a SamplingPlot, a drop-down button will appear where you may select between 3 states:

- = show the parent SamplingPlots
- = show the entire hierarchy of the SamplingPlots
- = hide the SamplingPlots

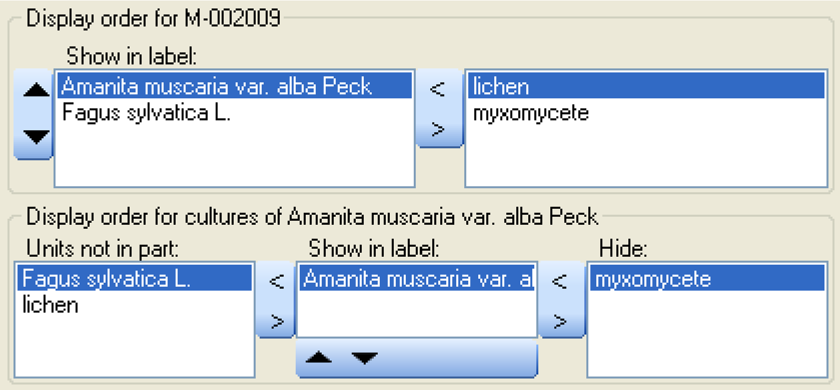
If both options are available, you may choose between the CollectionEventSeries or the SamplingPlot hierarchy. If the entire hierarchy for the EventSeries or the SamplingPlots is displayed, the items not inculded in the current data set will be desplayed with gray icons, e.g. . To change to one of these use the button. For the Events, the EventSeries, the Plots and the Specimen a button will appear which will give you access to a taxon list of the selected item.



The panel on the right side of the tree is for editing the data, for example the button will insert a new collector. For further details see the special sections.

Display order

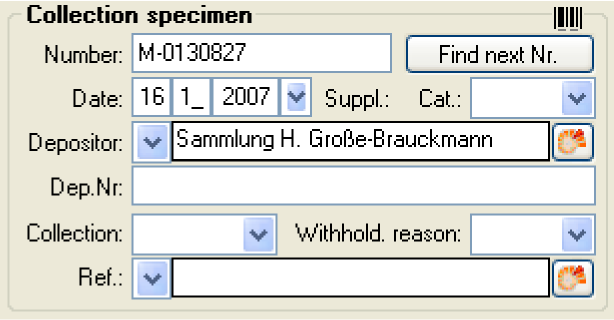
The display order defines the sequence in which the units within this specimen will appear on e.g. a label. The first unit will be printed in the header of the label, others are included in the text below. You can change the display order by using the ▲ ▼ buttons. If a unit should not appear on the label, transfer it to the hide list using the > button. The < button returns it to the list to be shown on a label. The first unit can not be transferred to the hide list. The upper section shows the display orders of the units within the whole specimen. The lower section shows the display orders in a specimen part. If you print a label without reference to a part, the display order for the entire specimen as in the upper section will be used. This part is also accessible if you click on the 🖨button in the right panel of the upper tree, which will appear if you e.g. select the specimen.



If you print a label with reference to a part, the display order for the part as in the lower section will be used. This area will be shown when you select a specimen part in the lower tree. In addition to the display order you can specify whether an organsim is present in a selected part of a specimen.

Accession

The accession of a specimen in a collection is documented with its accession number and the date of the accession if available.


Collection specimen

Number: M-0130827

Date: 16 1_ 2007

Depositor: Sammlung H. Große-Brauckmann

Dep.Nr:

Collection:

Withhold. reason:

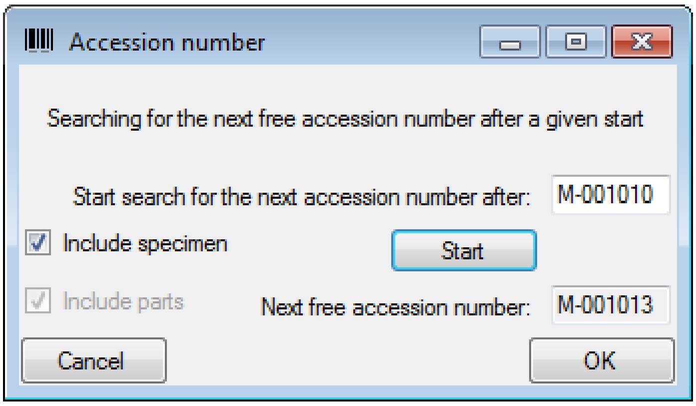
Ref.:

If the specimen was received from another collection, this may be documented with the name of the depositor and the number in the original collection (Dep.Nr).

If the current project (= as selected in the query list) contains a duplicate of the accession number, a button will appear. This gives you the opportunity to switch to the specimen with the duplicate accession number .


Acc. Nr.: M-0038380

If a new specimen is entered you can use the Find next button to search for the next free accession number. A window will open as shown below, where you can begin the search. The search will start with the number you provide as a starting point.


Accession number

Searching for the next free accession number after a given start

Start search for the next accession number after: M-001010

☑ Include specimen

☑ Include parts

Next free accession number: M-001013

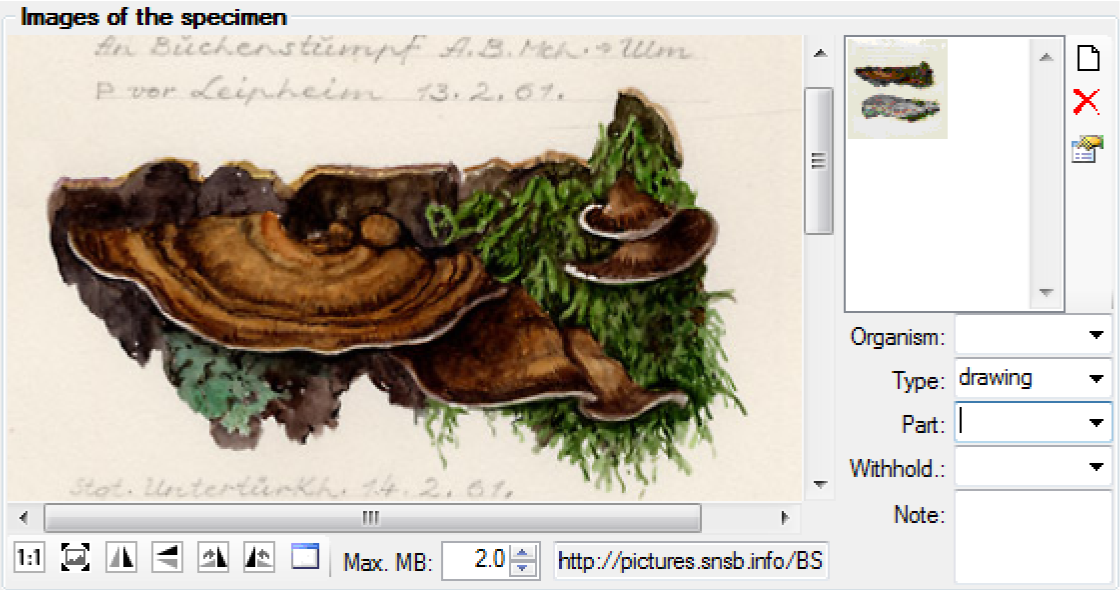
The system will try to find the next free number based on the accession numbers available in the database. As accession numbers can be assigned to a specimen as well as a part of a specimen, you have the option to include accession numbers in both places in the query. Click OK to use the recommended number for the specimen.

Data concerning the accession and deposition are stored in the table CollectionSpecimen.

Specimen images

To see the specimen images activate the icon in the image selector . If you choose the option **View - Show existing images** from the menu, the images will automatically be shown. Each specimen may be documented with several images. The images may be stored locally with its path or as a reference to the module DiversityResources within the DiversityWorkbench. To enter a new image click on the button. For more details see the section [Images](#).

To delete an image select it from the list and click on the button (see below).



Type: drawing

Max. MB: 2.0

http://pictures.snsb.info/BS

To document the relation of an image to an **organism** or a **part** of the specimen choose the corresponding entries from the drop-down lists. To restrict the display of the images to either images which are related to a certain part or a certain organism within the specimen click on the button in the corresponding areas. The buttons will receive a red backgroud to remind you of the restriction. Next to the image list a button will appear which enables you to show all images again.

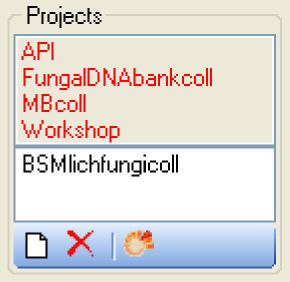
To enter a description for an image click on the button (see the chapter [Image description](#) for further details).

The data is stored in the table [CollectionSpecimenIma ge](#).

Projects

Every CollectionSpecimen may be assigned to any number of projects. To assign a specimen to a project click on the button. To remove it from a project select the project from the list and click on the button.

If there are projects, to which you have no access to, these will be listed in a separate list at the top as shown below.

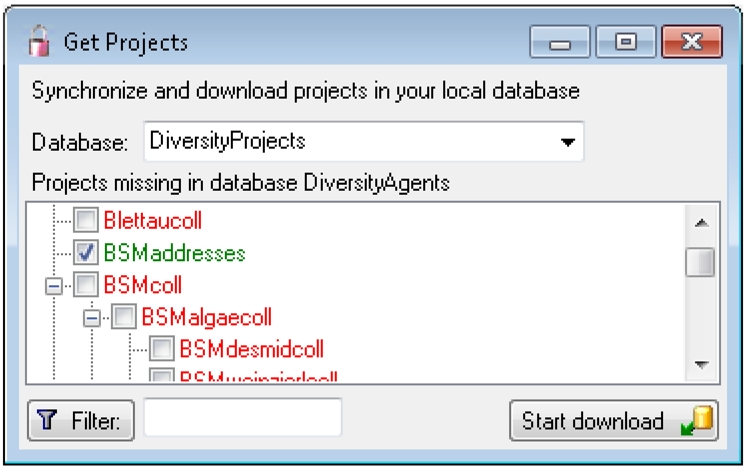


To transfer all selected specimen into an additional project choose **Data -> Transfer -> To project...** from the menu. A window will open where you can select the project to which the specimen should be added.

To remove all selected specimen from an additional project choose **Data -> Remove from project...** from the menu. A window will open where you can select the project from which the specimen should be removed. The last project in which a specimen is placed can not be removed.

The data is stored in the table CollectionProject.

Details of the projects within the DiversityWorkbench are stored in the database DiversityProjects. To access further information on a project click on the button. To edit details in projects you require the application **DiversityProjects.exe** in your application directory and access to the database DiversityProjects. To synchronize the projects listed in DiversityProjects you may use the synchronize function in the user administration window as shown below. If DiversityProjects is not available, you may create a new project by clicking the button. If DiversityProjects is available, use the synchronize function Synchronize with DiversityProjects .



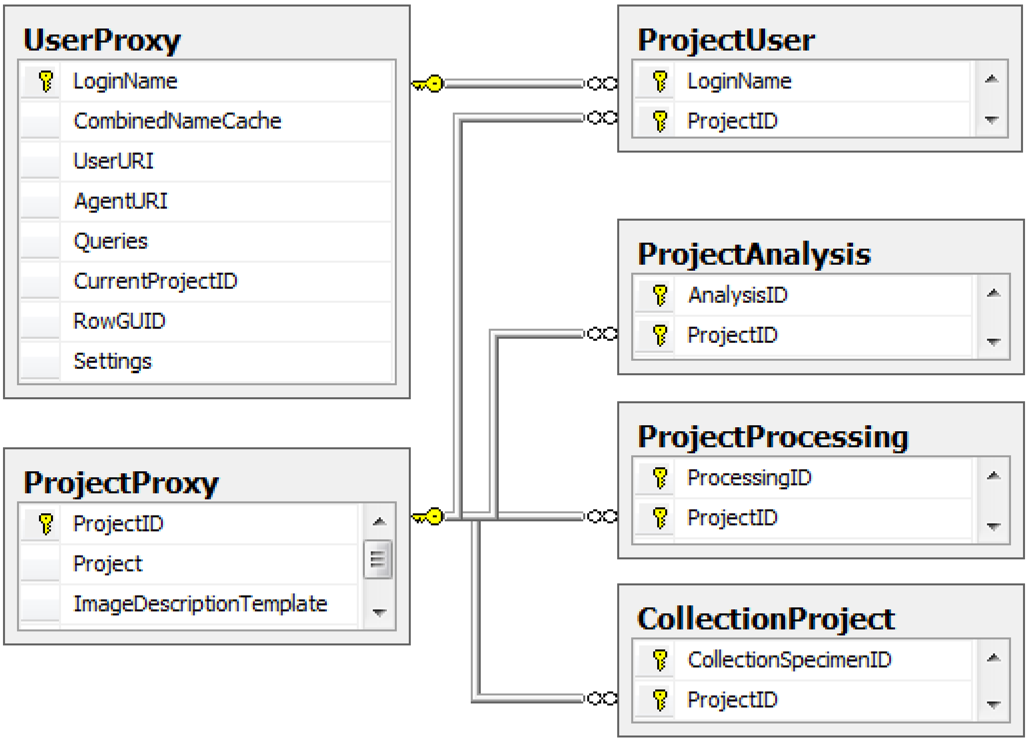
Synchronize and download projects in your local database

Database: DiversityProjects

Projects missing in database DiversityAgents

- ☐ Blettaucoll
- ☑ BSMaddresses
- ☐ BSMcoll
  - ☐ BSMalgaecoll
    - ☐ BSMdesmidcoll

The ER-chart below shows all tables with direct relations to the project tables. For more details see the sections Analysis, Processing and Image description.



Notes and problems

To enter notes or problems connected with the specimen select it in the hierarchy. The data form will open the corresponding fields. The **Original** notes are the notes found on the label of the specimen, made by the original collector or from a later revision. **Additional** notes are those made by the editor of the specimen record, e. g. doubtful identification or locality.

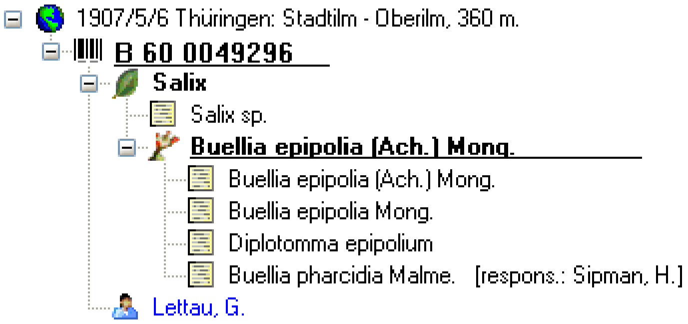
In the **Problems** area enter the description of a problem which occurred during data editing. Typically these entries should be deleted after help has been obtained. Do not enter scientific problems here. Use Additional notes for such permanent problems!

The data is stored in the table CollectionSpecimen.

For notes on data created by users with no permission for editing see the chapter Annotation
.

Organisms and identifications

Each specimen can contain several organisms and each organism may have been identified several times as shown in the image below.

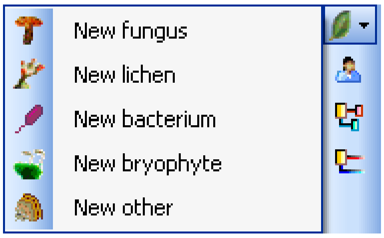


1907/5/6 Thüringen: Stadtilm - Oberilm, 360 m.
B 60 0049296
Salix
Salix sp.
Buellia epipolia (Ach.) Mong.
Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.
Diplotomma epipolium
Buellia pharcidia Malme. [respons.: Sipman, H.]
Lettau, G.

To see the list of organisms within a Specimen, CollectionEvent, EventSeries or SamplingPlot use the taxon list function.

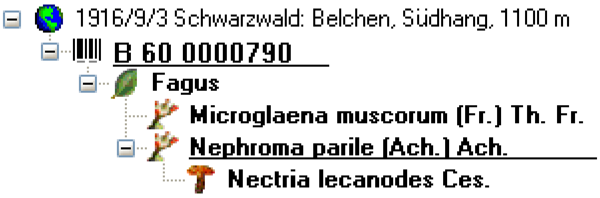
IdentificationUnit

The items or organisms in one CollectionSpecimen are regarded as IdentificationUnits. One specimen can contain several IdentificationUnits e.g. an insect (1) feeding on a fungus (2) growing as a parasit on a plant (3). To add a new organism use the drop-down menu as shown below to select the taxonomic group to which the new organism belongs to.



To specify the taxonomic groups that are shown in the drop-down menu select Administration - Customize display ... from the menu.

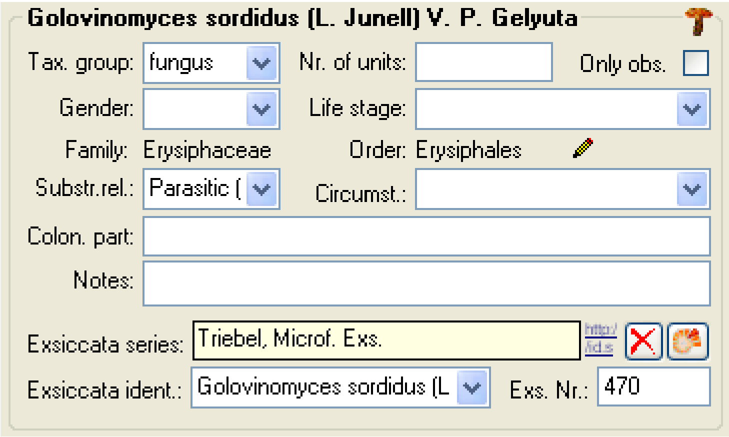
The organisms of the specimen are shown in the tree. To edit the relations between the organisms simply drag and drop. The name of the organism under which the specimen is stored in the collection is underlined. To delete an organism select it in the tree and click on the ✕ button.



1916/9/3 Schwarzwald: Belchen, Südhang, 1100 m
B 60 0000790
Fagus
Microglaena muscorum (Fr.) Th. Fr.
Nephroma parile (Ach.) Ach.
Nectria lecanodes Ces.

To enter details about one of the organisms like e.g. gender or life stage, select it in the tree. The fields for the details of this organism will be displayed in the right area of the window as shown below.

A description for an IdentificationUnit can be entered with the unit, where you can type your description. You may also use the combobox to select a description as found for the same taxonomic group in the database or select a predefined description from a hierarchy. An additional description can be entered for an IdentificationUnit within part of a CollectionSpecimen.



Golovinomyces sordidus (L. Junell) V. P. Gelyuta
Tax. group: fungus
Nr. of units:
Only obs. ☐
Gender:
Life stage:
Family: Erysiphaceae
Order: Erysiphales
Substr.rel.: Parasitic (
Circumst.:
Colon. part:
Notes:
Exsiccata series: Triebel, Microf. Exs.
Exsiccata ident.: Golovinomyces sordidus (L
Exs. Nr.: 470

Taxonomic hierarchy - family and order

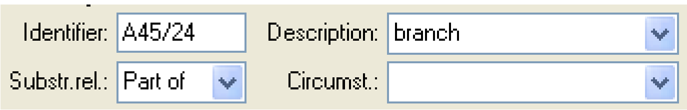
The entries for the family and the order of the taxon are either set when linking to a taxonomic database or set manually when no link to a taxonomic database exists.

Family: Erysiphaceae Order: Erysiphales

If no link to a taxonomic database exists you may enter the family and the order after clicking on the ✎button. To transfer these entries to other specimens with the same genus use the maintenance functions as described under Maintenance - family and order.

Parts of units

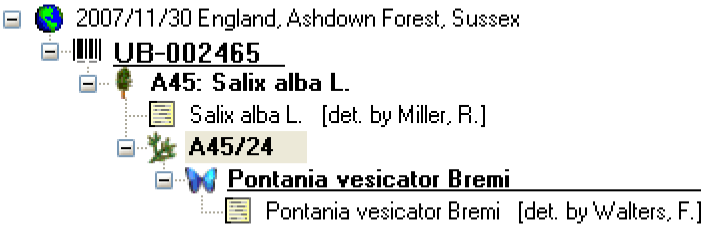
If a unit contains parts which have to be documented, you can do this by setting the relation to the substrate to "Part of".



Identifier: A45/24 Description: branch

Substr.rel.: Part of Circumst.:

In the tree the backgroud of a part will be grey as shown below for the unit-tree und the tree depicting the storage of a sample. The name of the part will correspond to the identifier set for this part. The icon will correspond to the description of the part provided you choose one of the preset options contained in the drop-down list. You may of course enter any description for the unit. A unit that is part of another unit can not get an identification. Identifications are restricted to the main unit.

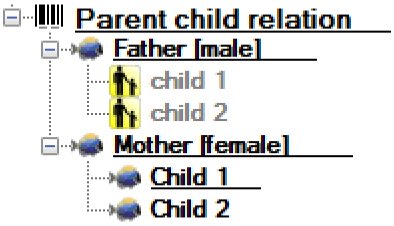


2007/11/30 England, Ashdown Forest, Sussex
- UB-002465
  - **A45: Salix alba L.**
    - Salix alba L. [det. by Miller, R.]
    - **A45/24**
      - **Pontania vesicator Bremi**
        - Pontania vesicator Bremi [det. by Walters, F.]

- UB-002465
  - **Pontania vesicator Bremi**
    - Pontania vesicator Bremi
    - A45/24

Parent-child relations

If a unit is a child of a parent in the genetical sense, choose "**Child of**" as type of the relation. If there are 2 parents like mother and father that you want to document, click on the button next to the relation type. A window will open where you can choose among the organisms (= units) in your sample. The second parent will be indicated with the symbol in the tree (see below).



- Parent child relation
  - Father [male]
    - child 1
    - child 2
  - Mother [female]
    - Child 1
    - Child 2

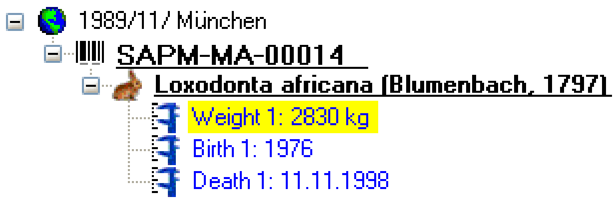
For details about exsiccatal series and analysis see the related topics. You can sort your IdentificationUnits e.g. for display on a label with the display order button. Each IdentificationUnit can have several identifications.

If there are images which are related to the current organism, the button for the restriction of the images will be enabled (→). Click on it to restrict the images to this organism. The button will get a red backgroud to remind you about the restriction and in the image list a button 🖼 will appear that enables you to show all images.

The data for the organisms is stored in the table IdentificationUnit.

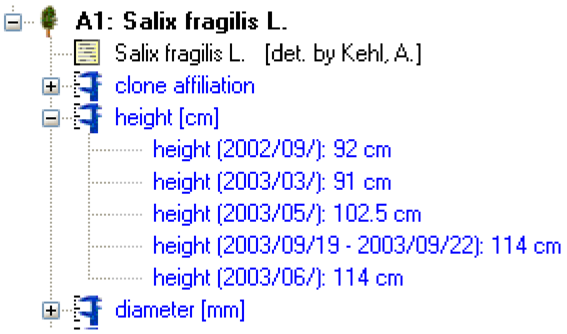
Analysis

The organisms in a specimen can be analysed by analysis types defined in the database. In the tree the analysis entries are symbolized with a icon. Only the types of analysis that were assigned to the group of the organism can be selected. An analysis always refers to an organism and may also refer to a part of a specimen. An analysis that refers to a part of a specimen will be shown in the tree for the parts as shown in the examples below.



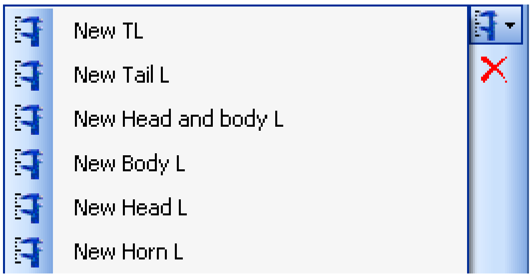
1989/11/ München
SAPM-MA-00014
Loxodonta africana (Blumenbach, 1797)
Weight 1: 2830 kg
Birth 1: 1976
Death 1: 11.11.1998

To show or hide the analysis items in the tree use the button in the left panel. This button has 3 states. In the default state the analyis entries will be shown as above. If you click a second time it will change to the hierarchy mode and the entries will appear as shown in the tree below. The last state will hide the entries.

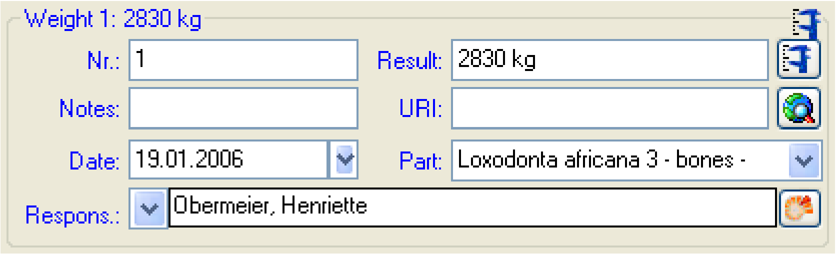


A1: Salix fragilis L.
Salix fragilis L. [det. by Kehl, A.]
clone affiliation
height [cm]
height (2002/09/): 92 cm
height (2003/03/): 91 cm
height (2003/05/): 102.5 cm
height (2003/09/19 - 2003/09/22): 114 cm
height (2003/06/): 114 cm
diameter [mm]

To insert a new analysis select the organism which has been analysed in the upper tree. Then select the type of the analysis from the drop down list as shown below.



To delete an analysis, select it in the tree and use the button in the panel on the left. To edit the details of an analysis, select it in the tree and enter data into the fields as shown below. To enter or inspect an URI given for a single analysis, click on the button.

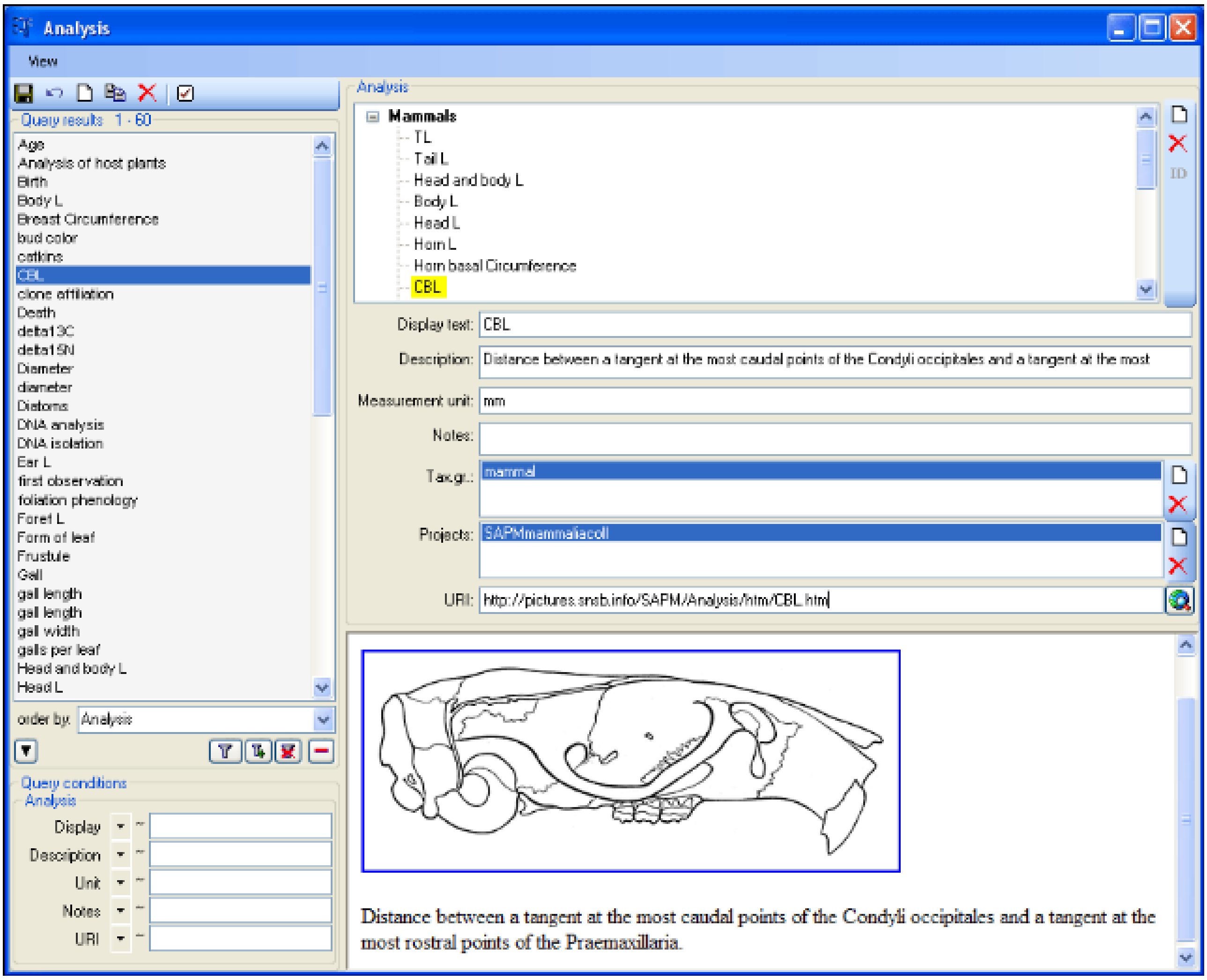


Weight 1: 2830 kg
Nr.: 1
Result: 2830 kg
Notes:
URI:
Date: 19.01.2006
Part: Loxodonta africana 3 - bones -
Respons.: Obermeier, Henriette

If an analysis refers to a part of the specimen, you can document this by choosing the respective part from the list (see field **Part** above). The analysis will then be shown in the tree for the parts of the specimen as well. Alternatively you may directly choose the organism in the part tree and create the analysis for this part of the organism in the part tree. If you used any tools defined in the tool section, you can include the usage of these tools.

SAPM-MA-00014
Loxodonta africana 3
Loxodonta africana (Blumenbach, 1797)
Weight 1: 2830 kg

If you require further information about an analysis click on the button to open the window for the analysis administration. If you have the proper rights you can edit the analysis types used in your collection as shown below. This window is also accessible via the menu entry **Administration - Analysis...**



Age
Analysis of host plants
Birth
Body L
Breast Circumference
bud color
catkins
CBL
clone affiliation
Death
delta13C
delta15N
Diameter
diameter
Diatoms
DNA analysis
DNA isolation
Ear L
first observation
foliation phenology
Forel L
Form of leaf
Frustule
Gall
gall length
gall length
gall width
galls per leaf
Head and body L
Head L

Mammals
- TL
- Tail L
- Head and body L
- Body L
- Head L
- Horn L
- Horn basal Circumference
- CBL

Display text: CBL

Description: Distance between a tangent at the most caudal points of the Condyli occipitales and a tangent at the most

Measurement unit: mm

Notes:

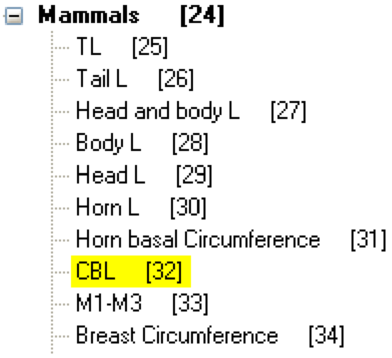
Taxa: mammal

Projects: SAPMmammaliacoll

URI: http://pictures.snsb.info/SAPM/Analysis/htm/CBL.htm

Distance between a tangent at the most caudal points of the Condyli occipitales and a tangent at the most rostral points of the Praemaxillaria.

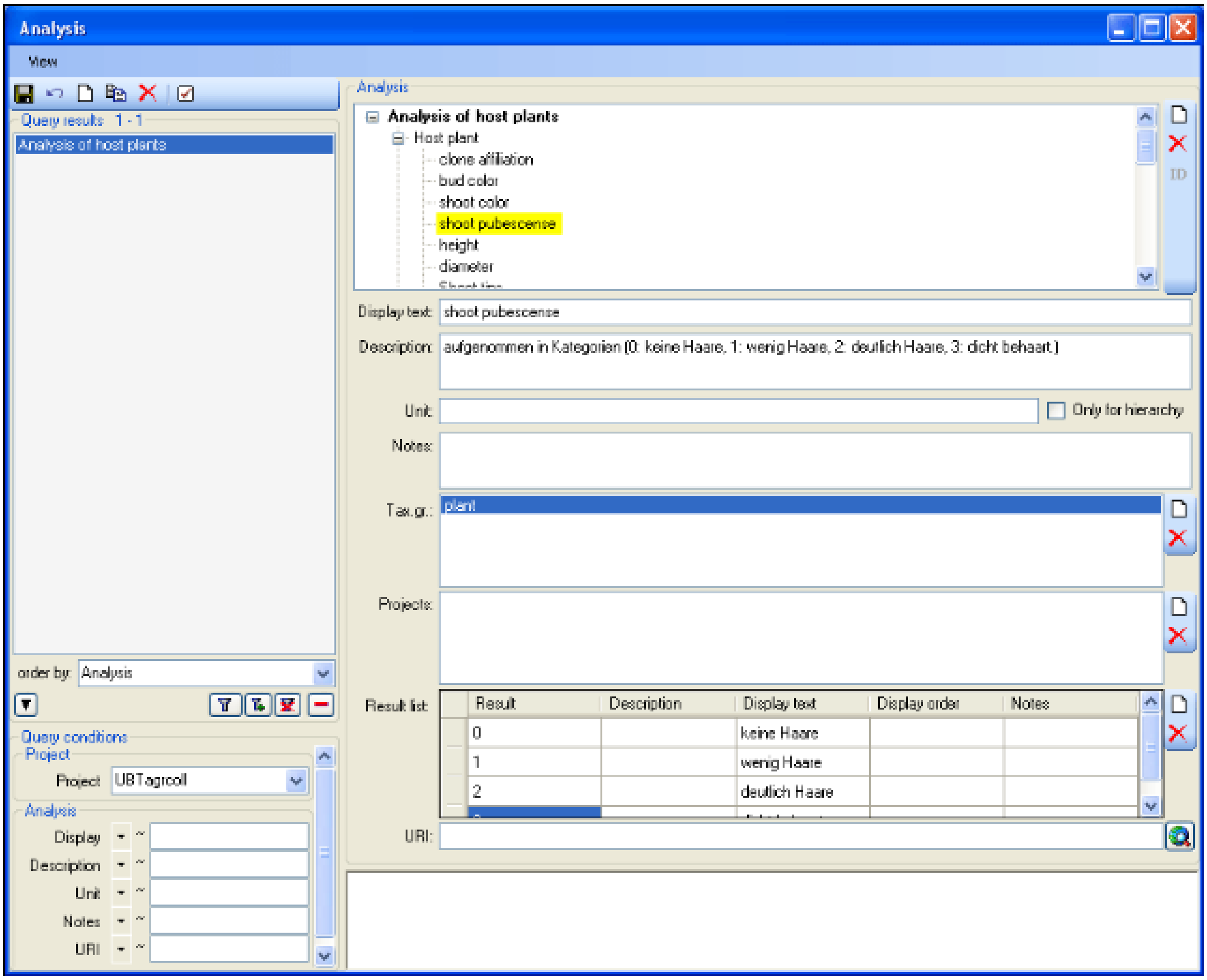
For the import and export of data it is sometimes necessary to know the IDs of the analyis types. To see the IDs, click on the **ID** button to display them as shown in the image below.



Mammals [24]
- TL [25]
- Tail L [26]
- Head and body L [27]
- Body L [28]
- Head L [29]
- Horn L [30]
- Horn basal Circumference [31]
- CBL [32]
- M1-M3 [33]
- Breast Circumference [34]

The types of an analysis are restricted by the **taxonomic group** of the organism or object to be analysed and from the **projects**. You may edit the list of taxonomic groups resp. projects, which can use a certain analysis, using the 🗋and ✕button. For details about handling data see the data section. If you add a taxonomic group or a project to an analysis, all children of this analysis will be available for these taxonomic groups resp. projects as well. Thus, in the example above it is sufficient to enter the taxonomic group and the project in the analysis Mammals to have access to all analysis within this superior analysis as shown in the tree. The different types of analysis are organized in a hierarchy. Some of the entries may only serve for structuring purposes (e.g. Mammals as shown above) and should not be used to document the analysis of the specimen. To ensure this, check the checkbox **[Only hierarchy]**.

There are 3 states for result lists in the main form. (1) No result list will be generated if a measurement unit is defined, for example if you specify "mm" as the measurement unit. (2) If no measurement unit is defined, the programm will collect all values given so far and present these values as a list. (3) Some types of analysis need categorized values. Enter these values together with their description in the **Result list** as shown below using the 🗋and ✕buttons respectively. To show values different from the entries in the **Result** column change the entries in the **Display text** column.



order by: Analysis

Project: UBTagrcoll

Display text: shoot pubescense

Description: aufgenommen in Kategorien (0: keine Haare, 1: wenig Haare, 2: deutlich Haare, 3: dicht behaart.)

Unit:

☐ Only for hierarchy

Notes:

Tax.gr.: plant

Projects:

Result list:

Result	Description	Display text	Display order	Notes
0		keine Haare		
1		wenig Haare		
2		deutlich Haare		

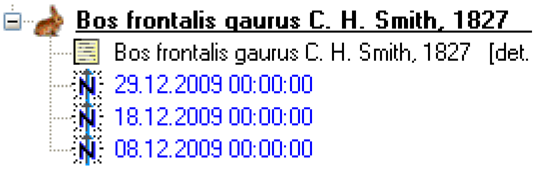
URI:

If you want to access or inspect an URI given for an analysis type, click on the button. The URI related to the analysis will then be displayed in the window below.

To view the history of a dataset, click on the button. A window with the history will open. For more details see the section History.

Geography of organisms

The geograhical position (using WGS84) of organisms can be captured related to the date to e.g. document a migration or the distribution of an organism. In the tree the geograhical entries are symbolized with a icon as shown below.

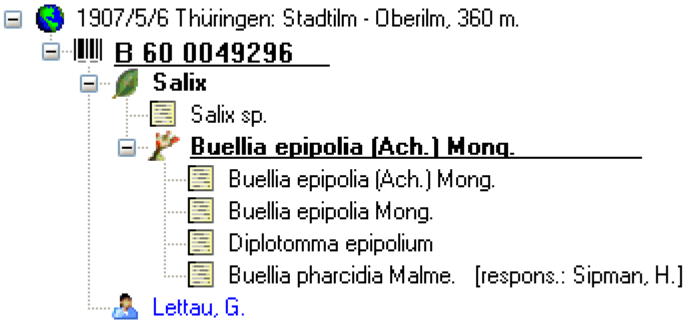


Bos frontalis gaurus C. H. Smith, 1827
Bos frontalis gaurus C. H. Smith, 1827 [det.
29.12.2009 00:00:00
18.12.2009 00:00:00
08.12.2009 00:00:00

To display the corresponding map activate Maps and click on the button. To edit an already existing geography use the GIS editor.

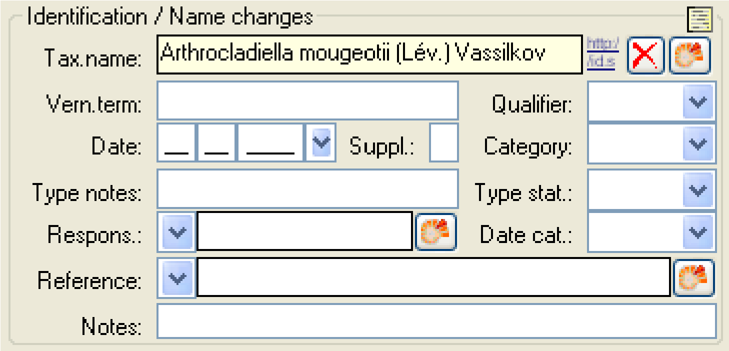
Identification

Each organism or unit may have been identified several times. The identifications are listed in the tree under the organism as shown in the image below. To create a new identification choose the organism from the tree and click on the icon. The last identification will always be taken as the valid one and set at the top of the list. To insert an older identification at the base of the list click on the icon.



1907/5/6 Thüringen: Stadtilm - Oberilm, 360 m.
B 60 0049296
Salix
Salix sp.
Buellia epipolia (Ach.) Mong.
Buellia epipolia (Ach.) Mong.
Buellia epipolia Mong.
Diplotomma epipolium
Buellia pharcidia Malme. [respons.: Sipman, H.]
Lettau, G.

To hide / show the identifications in the tree click on the icon on the right panel next to the tree. To enter a confirmation of an identification choose it in the tree and then click on the ☑ button. To move an identification to the end or the start of the list use the ▼ or ▲ button respectively. To delete an identification select it in the tree and click the ✗ button. To enter details for an identification choose it in the tree. You can then enter the details in the form opening on the right side of the tree as shown below.



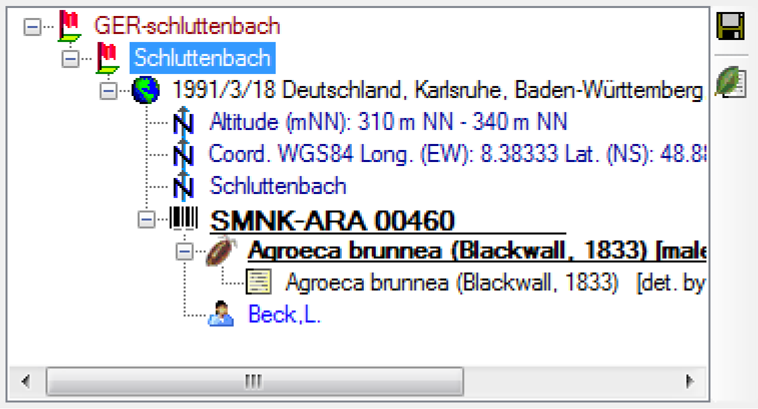
Identification / Name changes
Tax.name: Arthrocladiella mougeotii (Lév.) Vassilkov

The taxonomic name of an organism can be selected from either the names already available in DiversityCollection or from the module DiversityTaxonNames. To choose from the local names type the beginning of the name and click on the drop-down button ▼ to get a list of available names. You can use wildcards according to SQL.

To select a taxonomic name from an external database click on the button. A window will open where you can search for a taxonomic name. In the database the data for the identification is stored in the table Identification.

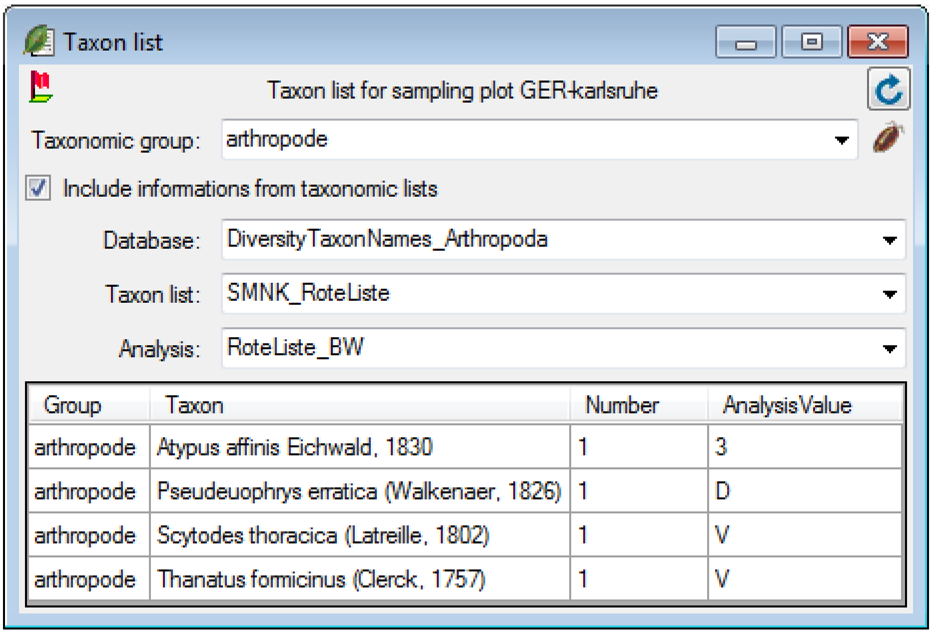
Taxon lists

To see the list of organisms within a Specimen, CollectionEvent, EventSeries or SamplingPlot click on the button which will appear, if you select one of the corresponding items in the tree (see below).



GER-schluttenbach
Schluttenbach
1991/3/18 Deutschland, Karlsruhe, Baden-Württemberg
Altitude (mNN): 310 m NN - 340 m NN
Coord. WGS84 Long. (EW): 8.38333 Lat. (NS): 48.8
Schluttenbach
SMNK-ARA 00460
Agroeca brunnea (Blackwall, 1833) [male
Agroeca brunnea (Blackwall, 1833) [det. by
Beck,L.

A window will open as shown below where you can gather additional information stored in the module DiversityTaxonNames.



Taxon list

Taxon list for sampling plot GER-karlsruhe

Taxonomic group: arthropode

☑ Include informations from taxonomic lists

Database: DiversityTaxonNames_Arthropoda

Taxon list: SMNK_RoteListe

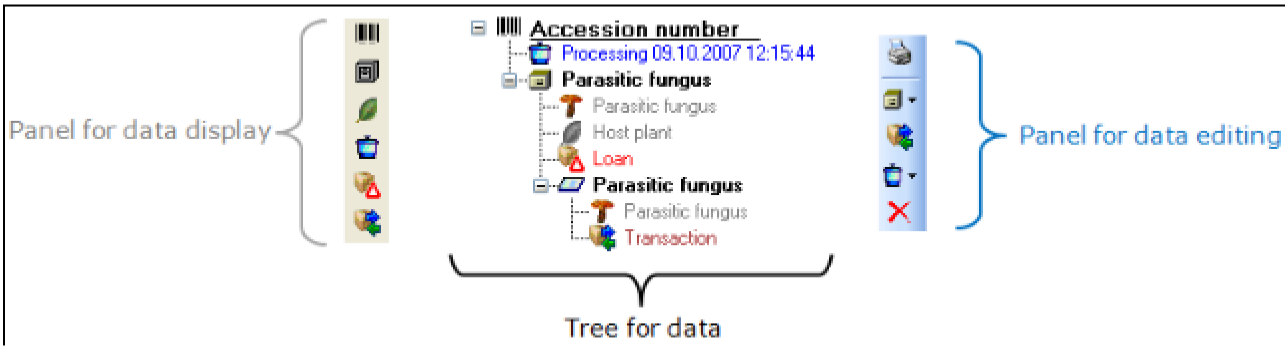
Analysis: RoteListe_BW

Group	Taxon	Number	AnalysisValue
arthropode	Atypus affinis Eichwald, 1830	1	3
arthropode	Pseudeuophrys erratica (Walkenaer, 1826)	1	D
arthropode	Scytodes thoracica (Latreille, 1802)	1	V
arthropode	Thanatus formicinus (Clerck, 1757)	1	V

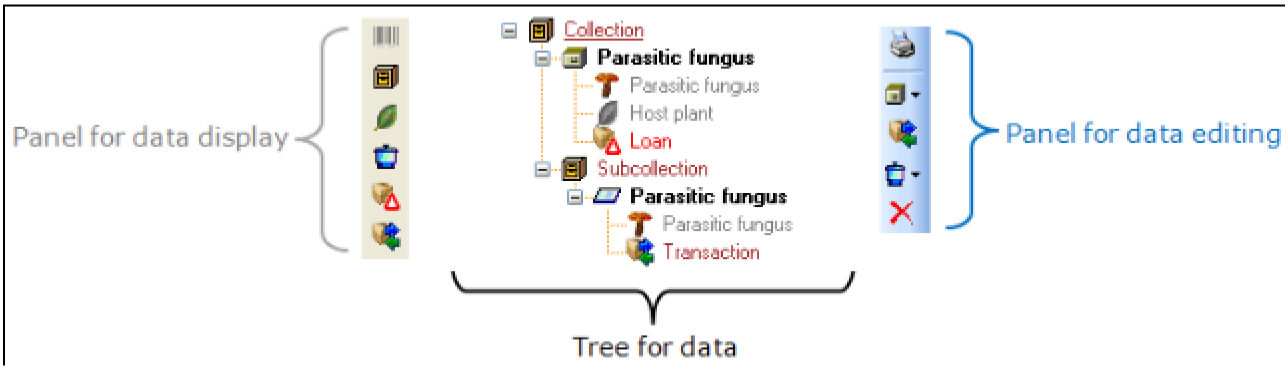
To retrieve information stored in the module DiversityTaxonNames for names which are linked to this module select the taxonomic group of the organism. Then select the option [Include information from taxonomic lists]. A combobox will appear where you may select the taxonomic database. Next, select the project in the combobox and finially the analysis. After all options are selected, click the button to requery the data. To export the results in a tab-separated list use the button.

Storage and trees for the parts of the specimen

In the tree at the base of the window the parts of the specimen with their related data are shown. This tree depicts the parts either in accordance to their relation to each other in the specimen tree (click on the icon in the panel on the left) ...



... or depending on the collections where the parts are stored (click on the icon in the panel on the left).

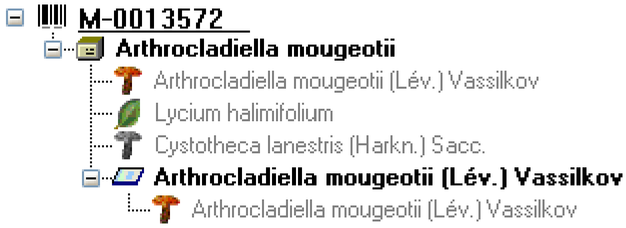


With the buttons in the left panel you may hide or show certain nodes in the tree. If e.g you do not wish to see the processings, simply click on the button and they will be hidden in the tree. The button will change to a grey version and the background will turn yellow, to show you that there is hidden data of the processings.

The panel on the right of the tree is for editing the data, for example the button will insert a new transaction. For further details see the sections Transaction and Processing.

Parts of the specimen

A specimen can contain several parts which may be stored in several collections. These parts may represent different material categories, e.g. herbarium sheets, microscopic slides etc. The parts are shown in the part tree under the main tree. This tree depicts the parts either in accordance to their relation to each other in the specimen tree (click on the icon in the panel on the left) - see first image below - or in relation to the collections where the parts are stored (click on the icon in the panel on the left) - see second image below. Here the two parts of the specimen are located in two collections. To add a new part use the drop-down field in the panel on the right of the tree and choose the material category of the new part. The material categories which appear in this list can be customized. You can set the default collection for new parts. If the default collection is not set, you will be asked to name the collection of the new part. If the part is derived from another part, select this in the tree before creating the new part. The new part will then be added as a child of the old part. You can later edit these relations by drag & drop. If you wish to create a copy of a part, use the button in the panel on the right side of the tree.

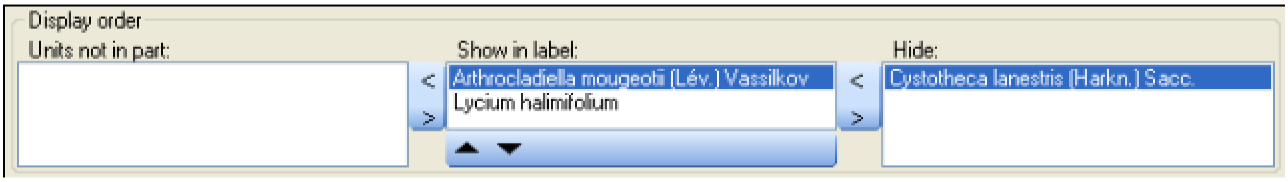


M-0013572
- **Arthrocladiella mougeotii**
  - Arthrocladiella mougeotii (Lév.) Vassilkov
  - Lycium halimifolium
  - Cystotheca lanestris (Harkn.) Sacc.
  - **Arthrocladiella mougeotii (Lév.) Vassilkov**
    - Arthrocladiella mougeotii (Lév.) Vassilkov

Botanische Staatssammlung München (M)
- M-Fungi
  - **Arthrocladiella mougeotii**
    - Arthrocladiella mougeotii (Lév.) Vassilkov
    - Lycium halimifolium
    - Cystotheca lanestris (Harkn.) Sacc.

Botanischer Garten und Botanisches Museum Berlin-Dahlem (B)
- **Arthrocladiella mougeotii (Lév.) Vassilkov**
  - Arthrocladiella mougeotii (Lév.) Vassilkov

If an organism is present in a part of the specimen, it will be shown in the tree. To edit its presence select the specimen part in the tree and edit the **Display order** as shown below.



Display order

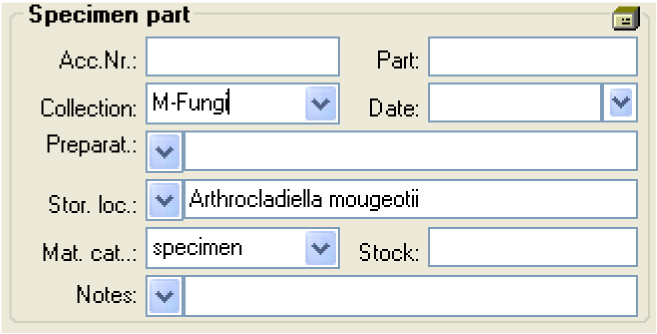
Units not in part:	Show in label:	Hide:
	Arthrocladiella mougeotii (Lév.) Vassilkov	Cystotheca lanestris (Harkn.) Sacc.
	Lycium halimifolium	

In the expample above, all organisms are present in the specimen. However, the fungus *Cystotheca lanestris* was chosen not to appear on the label and was transferred to the **Hide** list. This is symbolized by a grey icon in the tree. You may enter a description for an organism as a whole or for the organism within a certain part. The slide, symbolized by the icon, was created from the sample. Thus, in the specimen tree it is shown as a child of the specimen symbolized by the icon. Concerning the organisms only the fungus *Arthrocladiella* is found on the slide. Thus, in the tree it is the only organism shown as child of the slide. In the display order the two other organisms appear in the **Units not in part** list (see below).

Display order

Units not in part:	Show in label:	Hide:
Lycium halimifolium	Arthrocladiella mougeotii (Lév.) Vassilkov	
Cystotheca lanestris (Harkn.) Sacc.		

To move the organisms between the lists use the **>** and **<** buttons. In the list **Show in label** you may change the sequence of the organisms with the ▲and ▼buttons in the panel at the base of the list. The organism at the top will be the one taken as the main organism, e.g. for printing a label. To edit the details of a part select it in the tree to open the fields as shown below.



Specimen part

Acc.Nr.:		Part:	
Collection:	M-Fungi	Date:	
Preparat.:			
Stor. loc.:	Arthrocladiella mougeotii		
Mat. cat.:	specimen	Stock:	
Notes:			

The identifier, e.g. the taxonomic name under which the specimen can be found in the collection is entered in the field **Storage location**. You can search for this entry in the query.

To search for a free accession number use the button (see chapter Accession). To enter the **storage location** you may use the drop-down button ▼ to select from the identifications within the specimen. The drop-down button ▼ for the Notes will provide you with a list of all entries in this field, filtered with your entry in the text field. You may use wildcards like "%" or "_" (see Wildcards).

In the collection tree, the specimen are shown with their dependence upon each other based on their location in Collections. To get information about a collection simply select it in the tree. If you have the required rights, you may use the button to open the administration of the collections. This form is accessible under the menu entry **Administration - Collections...** as well.

The material category of a specimen part is indicated by the icon in the hierarchy.

Here some expamples:
bones: bones or skeleton from vertebrates
cultures: living cultures of organisms
drawing: original line or color drawing
herbarium sheets: capsules or sheets as stored in a botanical collection
icons: icons, images etc. stored in a botanical collection
micr. slide: glass plate with sections of specimen for microscopic studies
specimen: specimen stored in a collection

Specimens can be included in a transaction. Every stored part of a specimen may be treated with several processings.

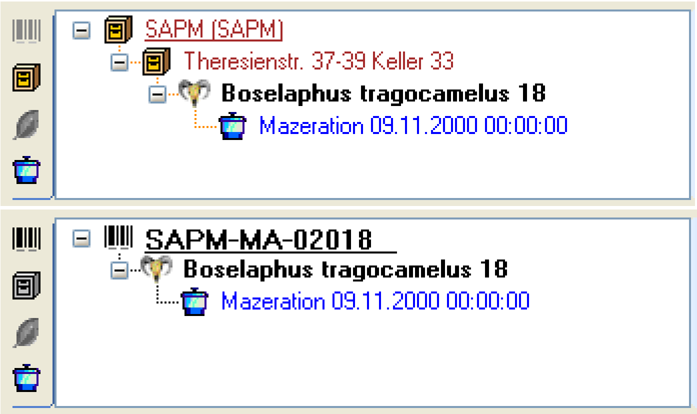
If there are images which are related to the current part, the button for the restriction of the images will be enabled (→). Click on it to restrict the images to this part. The button will recieve a red backgroud to remind you of the restriction and in the image list a button will appear which enables you to show all images.

To edit the parts of the specimens see the chapter Grid for parts.

The data is stored in the table CollectionSpecimenPart .

Processing

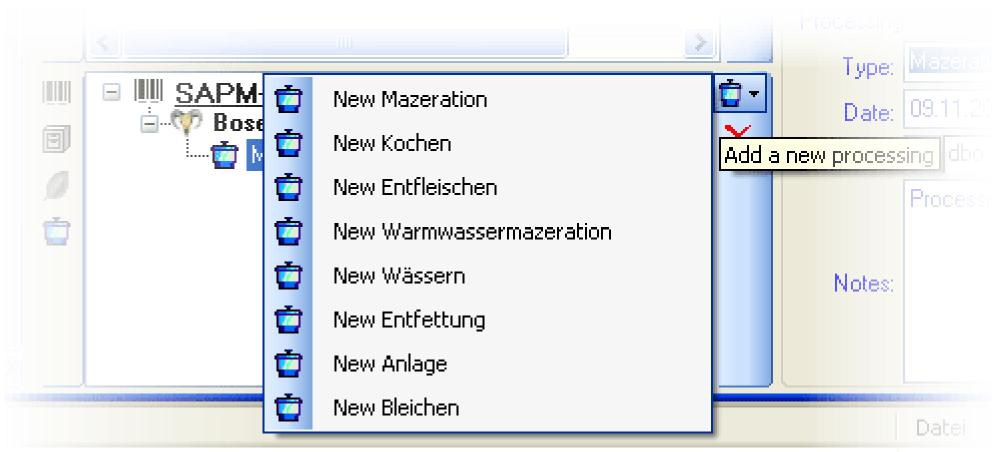
Every specimen can be processed, e.g. for preparation or preservation. Processings can be applied to a specimen or a part of a specimen. In the hierarchy for the parts the processings are indicated by the icon and a blue text. If there are any processings available, they will be indicated by the icon in the tool bar. Please keep in mind, that the **availability** of the processings depend upon the **material category** and the current **project** as described below. You can hide or show the processings in the hierarchy with a click on the icon. The images below show a processing in the collection and the specimen tree for the parts respectively.



SAPM (SAPM)
Theresienstr. 37-39 Keller 33
Boselaphus tragocamelus 18
Mazeration 09.11.2000 00:00:00

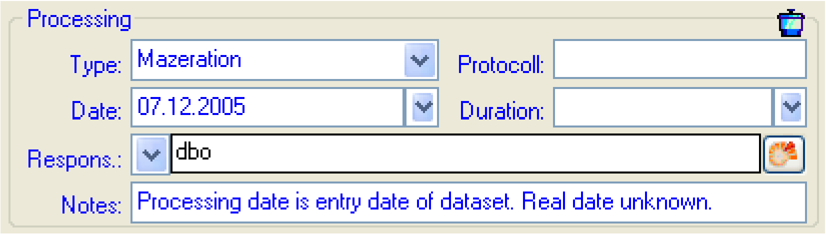
SAPM-MA-02018
Boselaphus tragocamelus 18
Mazeration 09.11.2000 00:00:00

You can enter a new processing for either the entire specimen or a part of the specimen. To do this select the specimen or part in the hierarchy and choose a processing from the list as shown below.



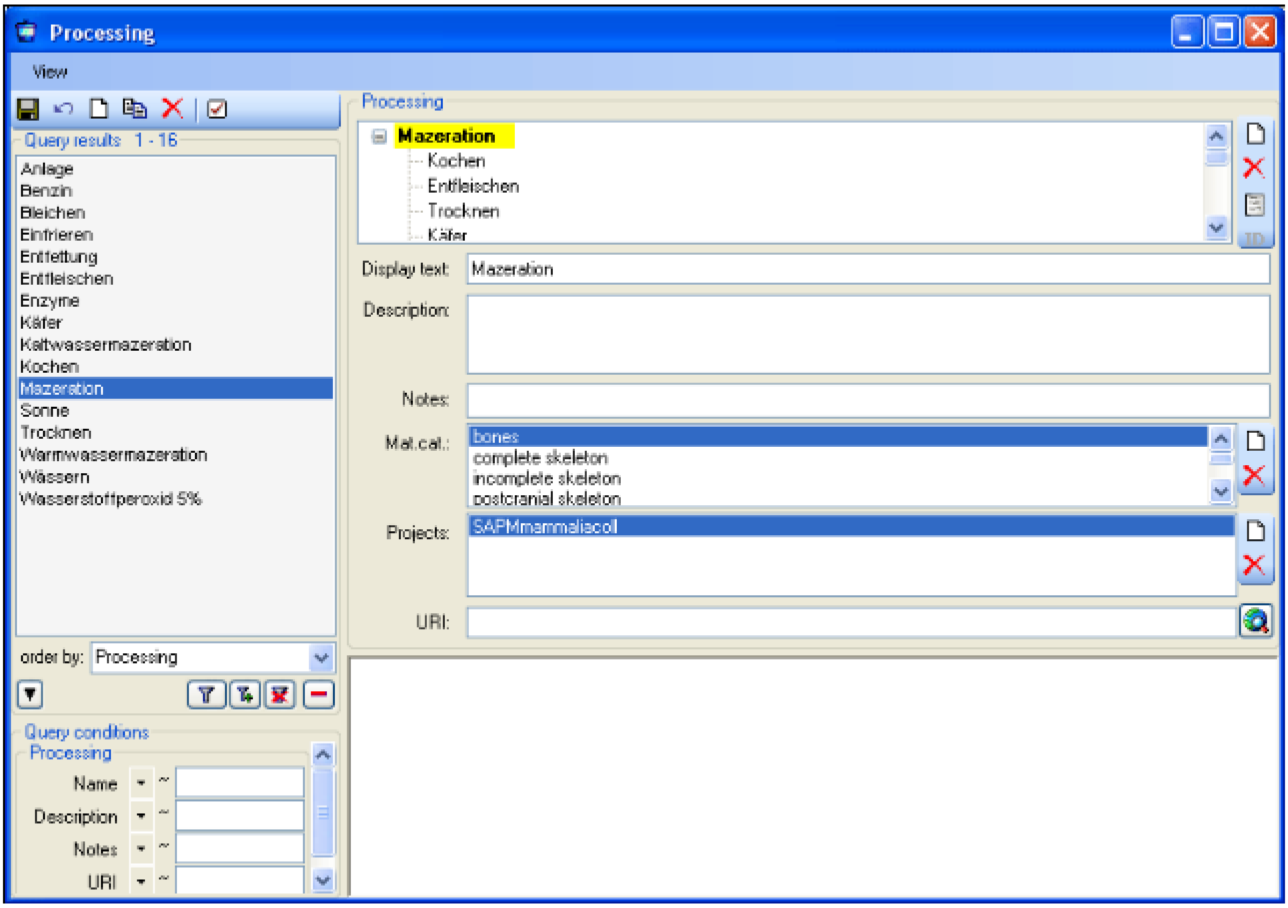
To delete a processing select it and click on the ✕ button. To edit the data for a processing select it in the hierarchy. The window will show you the fields related to the processing as shown below. If you used any tools defined in the tool section, you may include the usage of these tools.

In the window select the type of your processing from the list.



Processing
Type: Mazeration
Protocoll:
Date: 07.12.2005
Duration:
Respons.: dbo
Notes: Processing date is entry date of dataset. Real date unknown.

If you have the required rights you may edit the processing types in the menu entry **Administration - Processing...**



Query results 1 - 16:
Anlage
Benzin
Bleichen
Einfrieren
Entfettung
Entfleischen
Enzyme
Käfer
Kaltwassermazeration
Kochen
Mazeration
Sonne
Trocknen
Warmwassermazeration
Wässern
Wasserstoffperoxid 5%

order by: Processing

Processing:
- Mazeration
  - Kochen
  - Entfleischen
  - Trocknen
  - Käfer

Display text: Mazeration

Description:

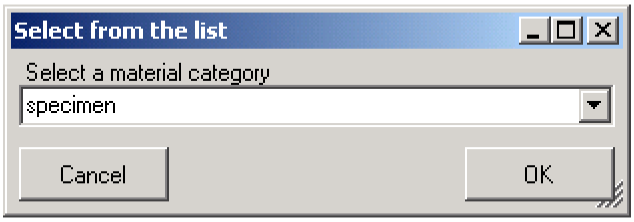
Notes:

Mat.cat.: bones, complete skeleton, incomplete skeleton, postcranial skeleton

Projects: SAPMmammaliacoll

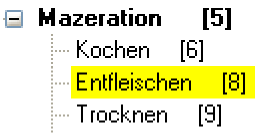
URI:

In this window you can define the processings used in your collection. To add a new processing click on the 🗋button, to delete a processing select it and click on the ✕button. The processings are related to material categories within the database. To add a new material category or projects, which should be connected to the selected processing, click on the 🗋 button in the panel right of the material categories or the projects. A window will open where you need to select the desired material category or project respectively (see below).



Select a material category: specimen

The processing types are organized in a hierarchy. Some of the entries may only serve for structuring as Mazeration in the example below and should not be used to document the processing of specimen parts. To ensure this check the checkbox **[Only hierarchy]**. For the import and export of data it is sometimes necessary to know the ID's of the analysis types. To see the ID's of the data sets click on the **ID** button. The ID's will then be displayed as in the image shown below.



- **Mazeration [5]**
  - Kochen [6]
  - Entfleischen [8]
  - Trocknen [9]

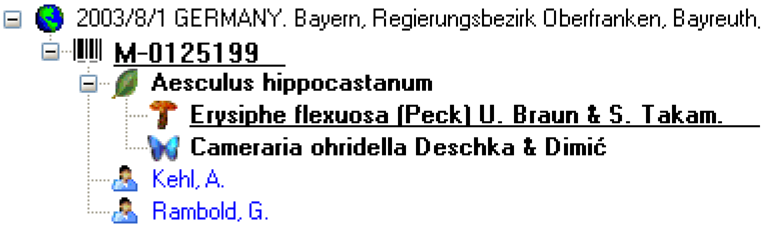
To view the history of a data set, click on the 🗒button. A window with the history will open.

For more details see the section History.

The data of the processing is stored in the table CollectionSpecimenProcessing.

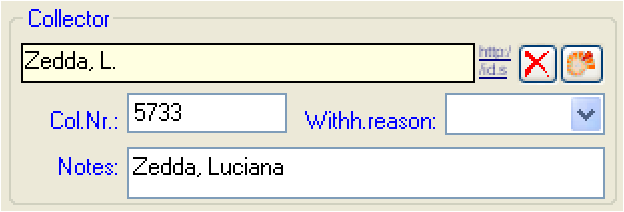
Collector

The people or groups responsible for the gathering of the specimen are stored in the table CollectionAgent. There may be several collectors for one specimen. In the tree the collectors are symbolized by the icon as shown below.



2003/8/1 GERMANY. Bayern, Regierungsbezirk Oberfranken, Bayreuth.
M-0125199
Aesculus hippocastanum
Erysiphe flexuosa (Peck) U. Braun & S. Takam.
Cameraria ohridella Deschka & Dimić
Kehl, A.
Rambold, G.

To hide or show the collectors in the tree use the icon in the left panel (it will change to a grey version with a yellow background when the authors are hidden). To insert a collector choose either the specimen or an existing collector in the tree and then click on the icon in the right panel. Select a collector in the tree to enter details. In the right part of the window the detail fields will appear as shown below.



Collector
Zedda, L.
Col.Nr.: 5733
Withh.reason:
Notes: Zedda, Luciana

If a collector should refer to a dataset in the module DiversityAgents (where more details like addresses may be stored) click on the button. The sequence of the collectors (e.g. for print on a label) as shown in the tree can be changed by with the ▲ and ▼ buttons in the panel on the right side of the tree.

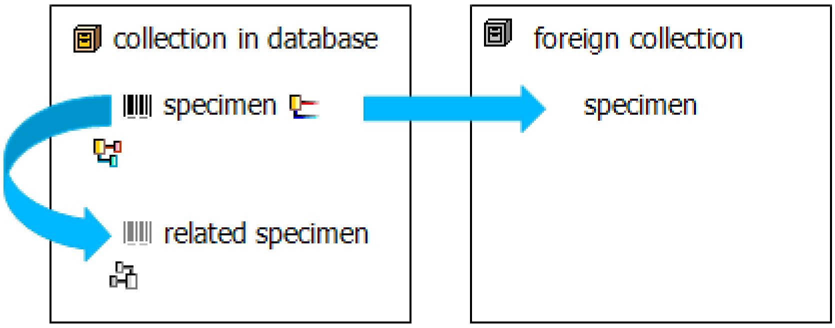
To remove a collector select the entry in the tree and click on the ✕ button.

You can search for the gathering numbers of the collectors in the query.

Data of the collectors is stored in the table CollectionAgent.

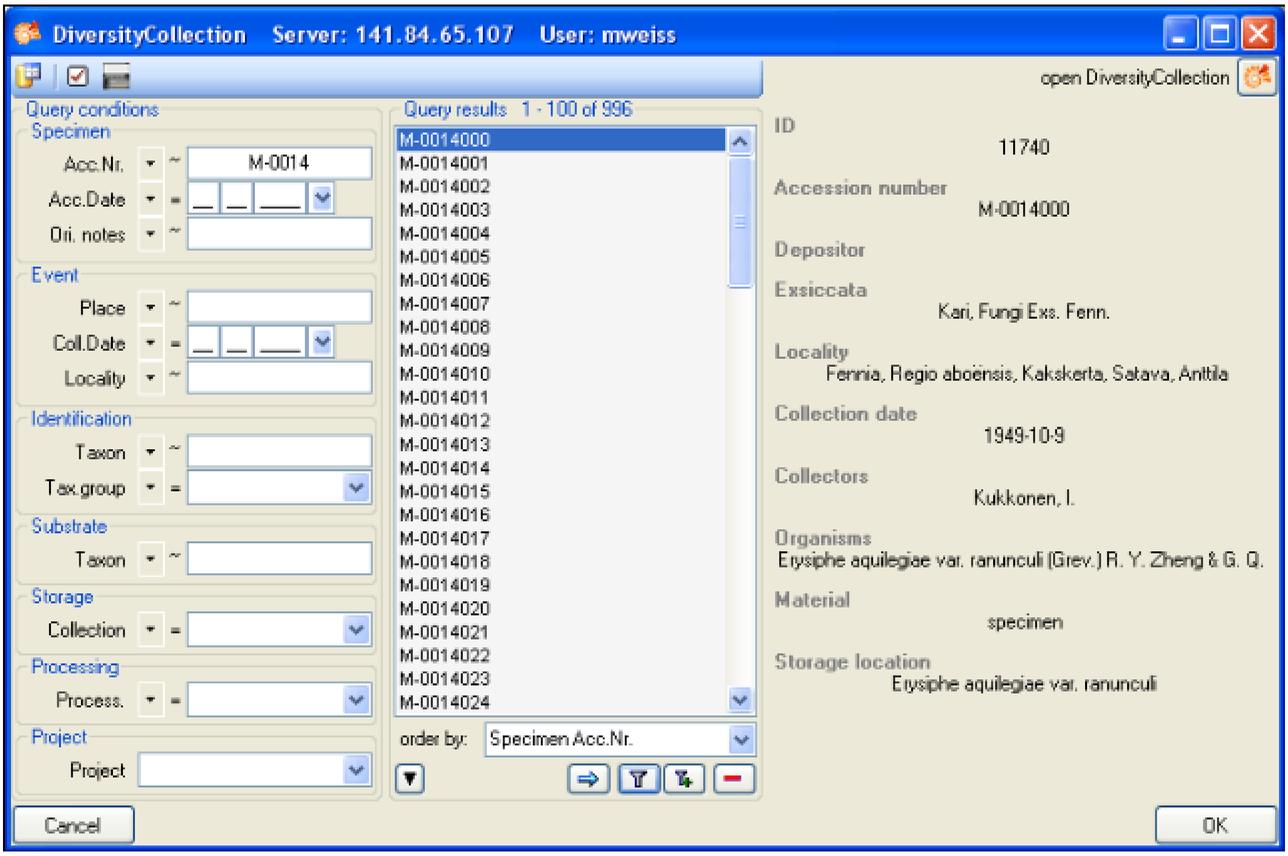
Relation

Each specimen may have relations to other specimens. This can be documented by adding relations to these specimens. To add a relation select the specimen in the tree (symbolized by the barcode). You may then either add a relation to a local specimen using the button or add a relation to a remote specimen using the button. To show or hide the relations in the tree use the and buttons.



Internal relation

To add an internal relation to a local specimen use the button. A window will open where you may search for the related specimen.



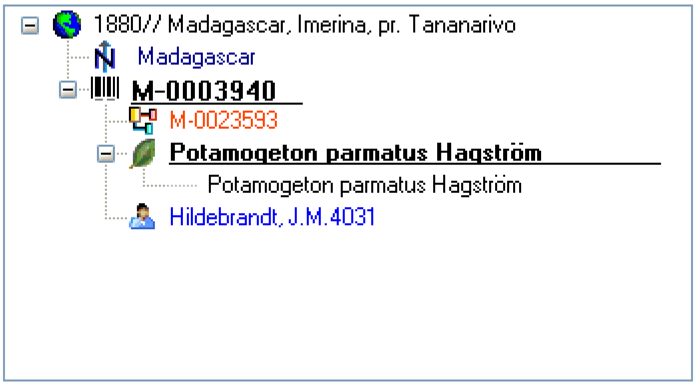
Acc.Nr. ~ M-0014

Specimen Acc.Nr.

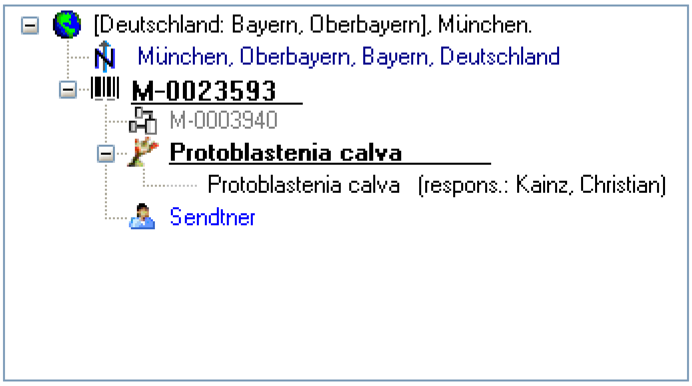
M-0014000
M-0014001
M-0014002
M-0014003
M-0014004
M-0014005
M-0014006
M-0014007
M-0014008
M-0014009
M-0014010
M-0014011
M-0014012
M-0014013
M-0014014
M-0014015
M-0014016
M-0014017
M-0014018
M-0014019
M-0014020
M-0014021
M-0014022
M-0014023
M-0014024

ID: 11740
Accession number: M-0014000
Depositor:
Exsiccata: Kari, Fungi Exs. Fenn.
Locality: Fennia, Regio aboënsis, Kakskerta, Satava, Anttila
Collection date: 1949-10-9
Collectors: Kukkonen, I.
Organisms: Erysiphe aquilegiae var. ranunculi (Grev.) R. Y. Zheng & G. Q.
Material: specimen
Storage location: Erysiphe aquilegiae var. ranunculi

Select the related specimen from the query result list and click OK to close the window and establish the relation. In the left image below you can see an internal relation while the image on the right shows a reverse relation from another specimen.



1880// Madagascar, Imerina, pr. Tananarivo
Madagascar
M-0003940
M-0023593
Potamogeton parmatus Hagström
Potamogeton parmatus Hagström
Hildebrandt, J.M.4031

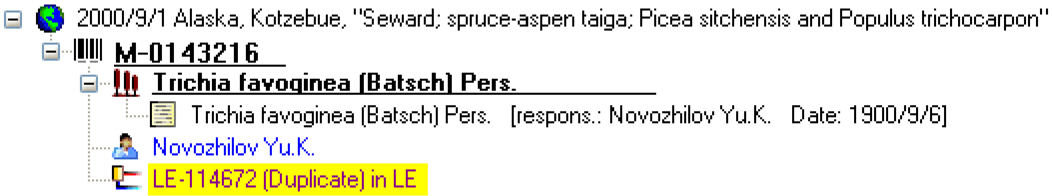


[Deutschland: Bayern, Oberbayern], München.
München, Oberbayern, Bayern, Deutschland
M-0023593
M-0003940
Protoblastenia calva
Protoblastenia calva (respons.: Kainz, Christian)
Sendtner

In the case of internal relations you can navigate to the related specimens using the button.

External relation

To add an external relation to a specimen which is not administrated in the database DiversityCollection use the button. In the image below you can see a relation to a specimen in an external collection.

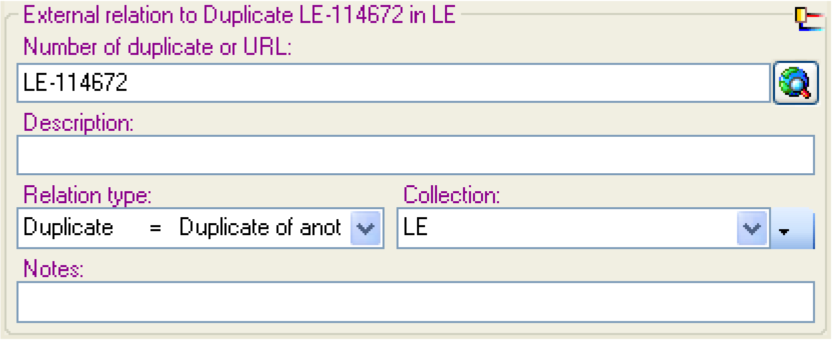


2000/9/1 Alaska, Kotzebue, "Seward; spruce-aspen taiga; Picea sitchensis and Populus trichocarpon"
M-0143216
Trichia favoginea (Batsch) Pers.
Trichia favoginea (Batsch) Pers. [respons.: Novozhilov Yu.K. Date: 1900/9/6]
Novozhilov Yu.K.
LE-114672 (Duplicate) in LE

To delete a relation select it in the tree and click on the ✕ button.

Editing the data

To edit the data for a relation click on the entry in the tree. In the right part of the window the details of the data set will be shown (see below).



External relation to Duplicate LE-114672 in LE

Number of duplicate or URL: LE-114672

Description:

Relation type: Duplicate = Duplicate of anot

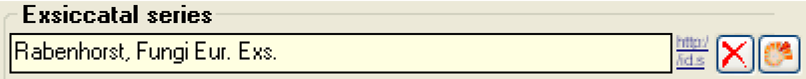
Collection: LE

Notes:

The data is stored in the table CollectionSpecimenRelation.

Exsiccatae

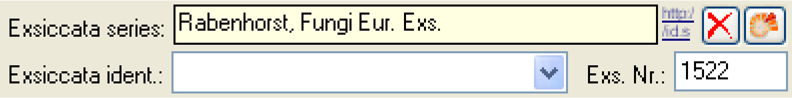
A Specimen may be part of an exsiccatal series. These series are administrated in the DiversityWorkbench module DiversityExsiccatae. To enter the exsiccatal series select the Specimen, the Organism or IdentificationUnit in the tree. With the Specimen the exsiccatal series is shown at the base of the data form as shown below.



Exsiccatal series

Rabenhorst, Fungi Eur. Exs.

As there may be several Organisms with separate exsiccatal numbers in one Specimen the numbers are handled together with the IdentificationUnits. Select the concerned Organism to enter data in the form as shown below.



Exsiccata series: Rabenhorst, Fungi Eur. Exs.

Exsiccata ident.:

Exs. Nr.: 1522

You can either type the name of the exsiccatal series or choose one from the module DiversityExsiccatae. If you click on the , a window will open showing the link to the entry as derived from the module.

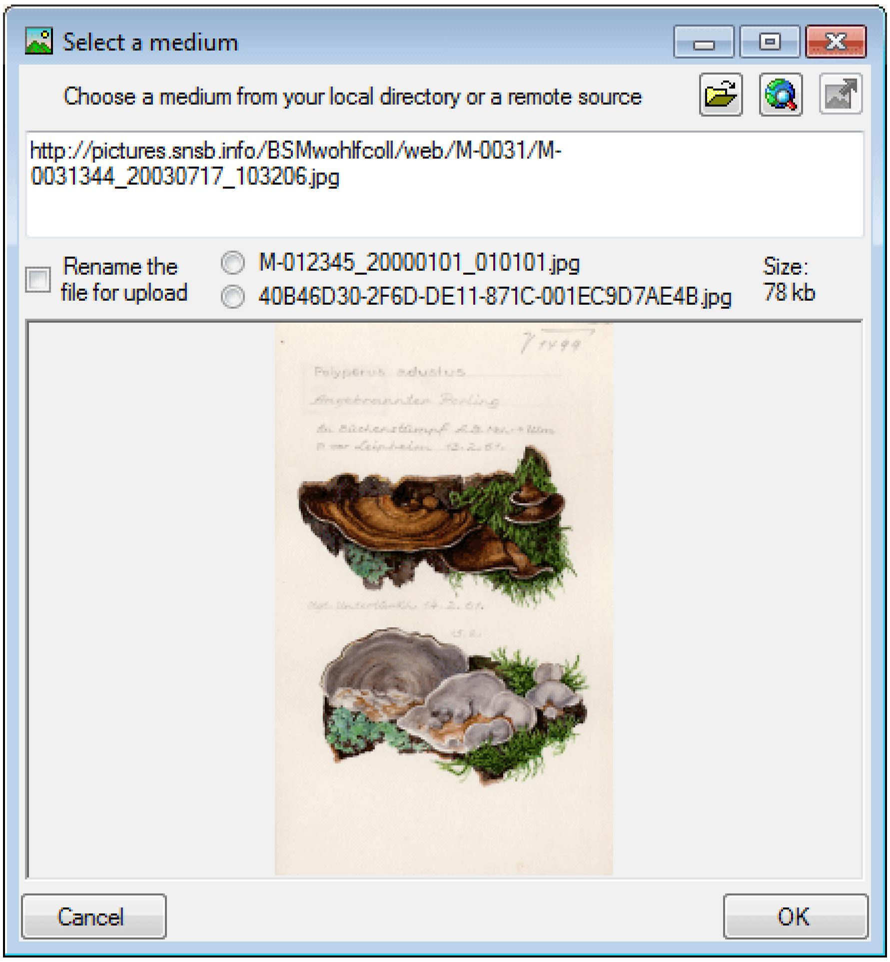
URI of Rabenhorst, Fungi Eur. Exs.

http://id.snsb.info/Exsiccatae/632034778

The data on the exsiccatal series is stored in the table CollectionSpecimen, the data on the number and the taxon is stored in the table IdentificationUnit.

Images

To insert a new image click on the 🗋 button. A window will open where you can enter the path and file name of the image. Click on the 🔍button to search for a web address of an image as shown below.



http://pictures.snsb.info/BSMwohlfcoll/web/M-0031/M-0031344_20030717_103206.jpg

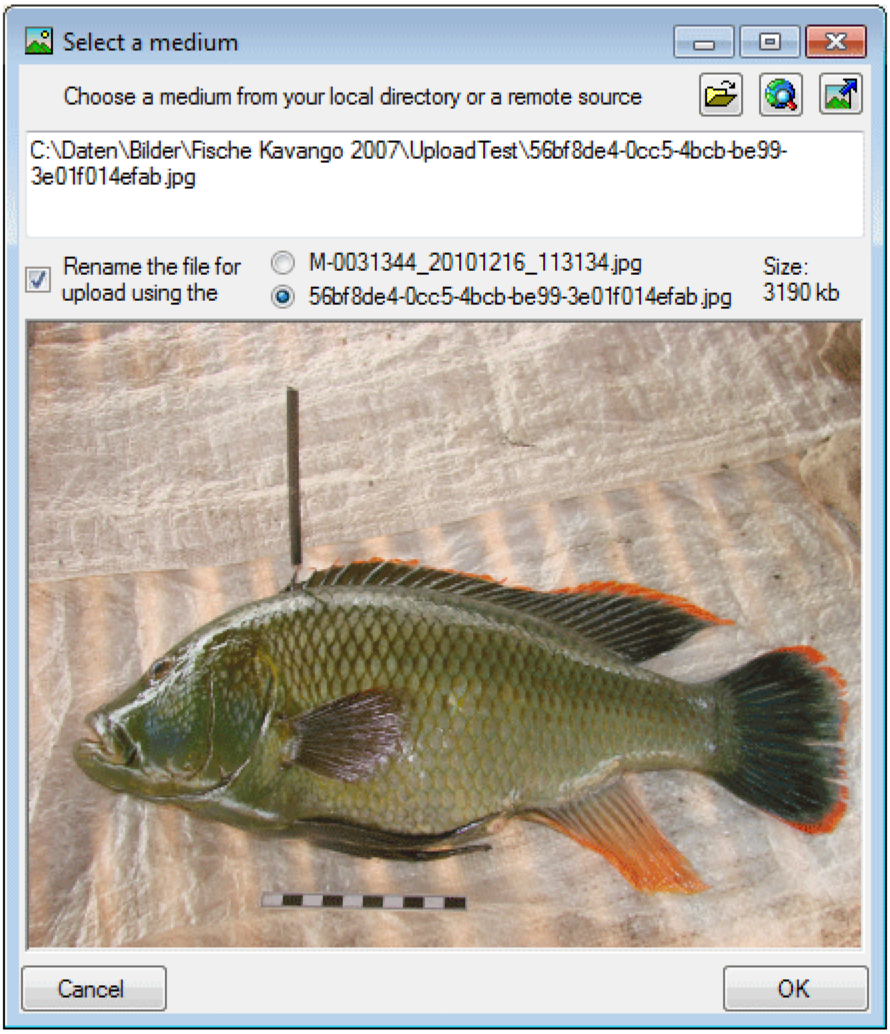
☐ Rename the file for upload

○ M-012345_20000101_010101.jpg

○ 40B46D30-2F6D-DE11-871C-001EC9D7AE4B.jpg

Size: 78 kb

To use an image available as a local file click on the 📂button to search in your local directories. You can upload this file via a webservice to the server of an institution providing the DiversityMediaService. To use this service you may rename your image either using a GUID or according to the accession number including date and time. Use the upload button to upload your image to the server.



Choose a medium from your local directory or a remote source

C:\Daten\Bilder\Fische Kavango 2007\UploadTest\56bf8de4-0cc5-4bcb-be99-3e01f014efab.jpg

☑ Rename the file for upload using the
○ M-0031344_20101216_113134.jpg
● 56bf8de4-0cc5-4bcb-be99-3e01f014efab.jpg

Size: 3190 kb

To delete an image select it from the list and click on the ✕ button.

Image size: 69920 KB

Res.:
Unit:
Type:
Part:
Withh.:
Notes:

Max. MB: 2,0

http://pictures.snsb.info/Test.jpg

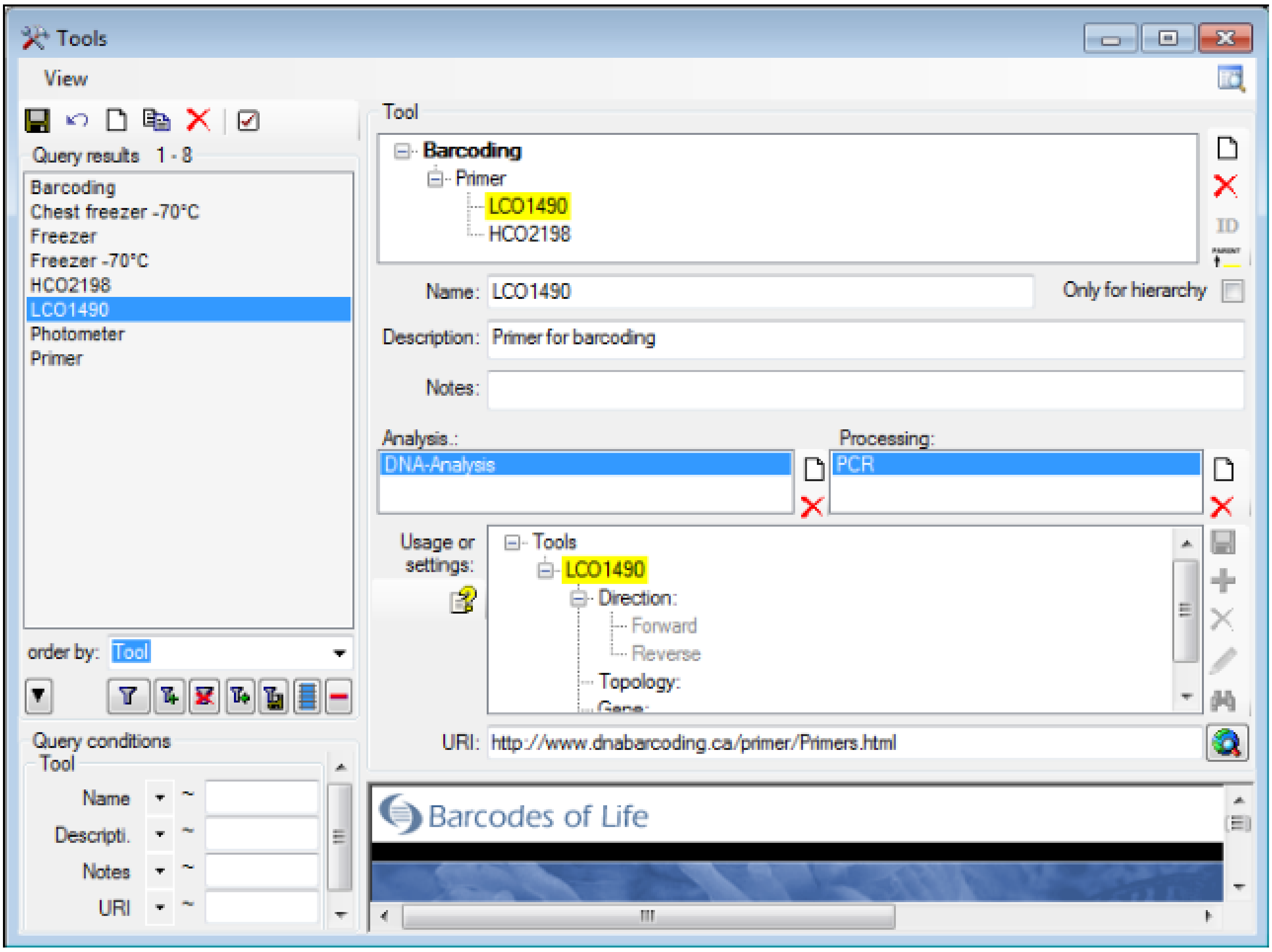
To zoom a specific sector of an image simply drag the mouse over the preferred area of the image. A red square will indicate the zoomed area. To set the size of the image to its original resolution click on the 1:1 button. To adapt the size of the image to the available space in the form click on the 🖼 button. To change the orientation of the image use the appropriate buttons (flip horizontal, flip vertical, rotate right, rotate left). To view the image in a separate form click on the button. If the image should not be published e.g. on the internet, enter any reason in the **Withhold. reason** - field. Next to images you can store other media.

For the description of a medium see the chapter Image description.

Data is stored in the tables CollectionSpecimenImage, CollectionEventImage , CollectionEventSeriesImage and CollectionImage.

Tools

The tools are used for the analysis of the organisms or the processing of the material. To administrate these tools choose **Administation ->🛠 Tools ...** from the menu. A window will open as shown below.



Name: LCO1490

Description: Primer for barcoding

Notes:

Analysis.: DNA-Analysis

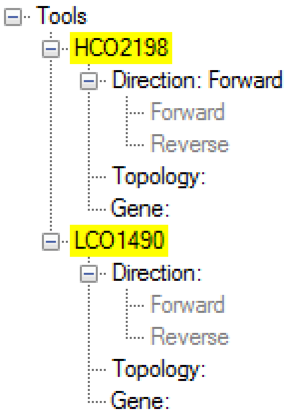
Processing: PCR

URI: http://www.dnabarcoding.ca/primer/Primers.html

There are 2 list where you can define for which analysis or processing the selected tool may be used. The tools may contain a definition for the usage defined via XML (targetNamespace="http://diversityworkbench.net/Schema/tools") (use the 📝 button to see the current definition) and depicted as a tree as shown above. To insert a previous defined usage definition click on the 🔭 button to search among the usages defined for other tools. To insert a new usage for the tool click on the ✚ button. If a usage should only allow predefined values, select the usage in the tree and click on the ✚ button to add and the ✎ button to edit the predefined values. With the ✕ button you may remove usages or predefined values.

In the main form you are able to add tools to an analysis or a processing. Choose the respective item in the tree and click on the ✚ button for the Tools (see below). Depending on the tools available for the analysis or processing respectively you may select from a list or tools.

You may add several tools for one analysis or processing as shown below. Tools are indicated with a yellow background. To edit the value of a usage or setting select it in the tree and click on the button. After changing content click on the button to save your changes.

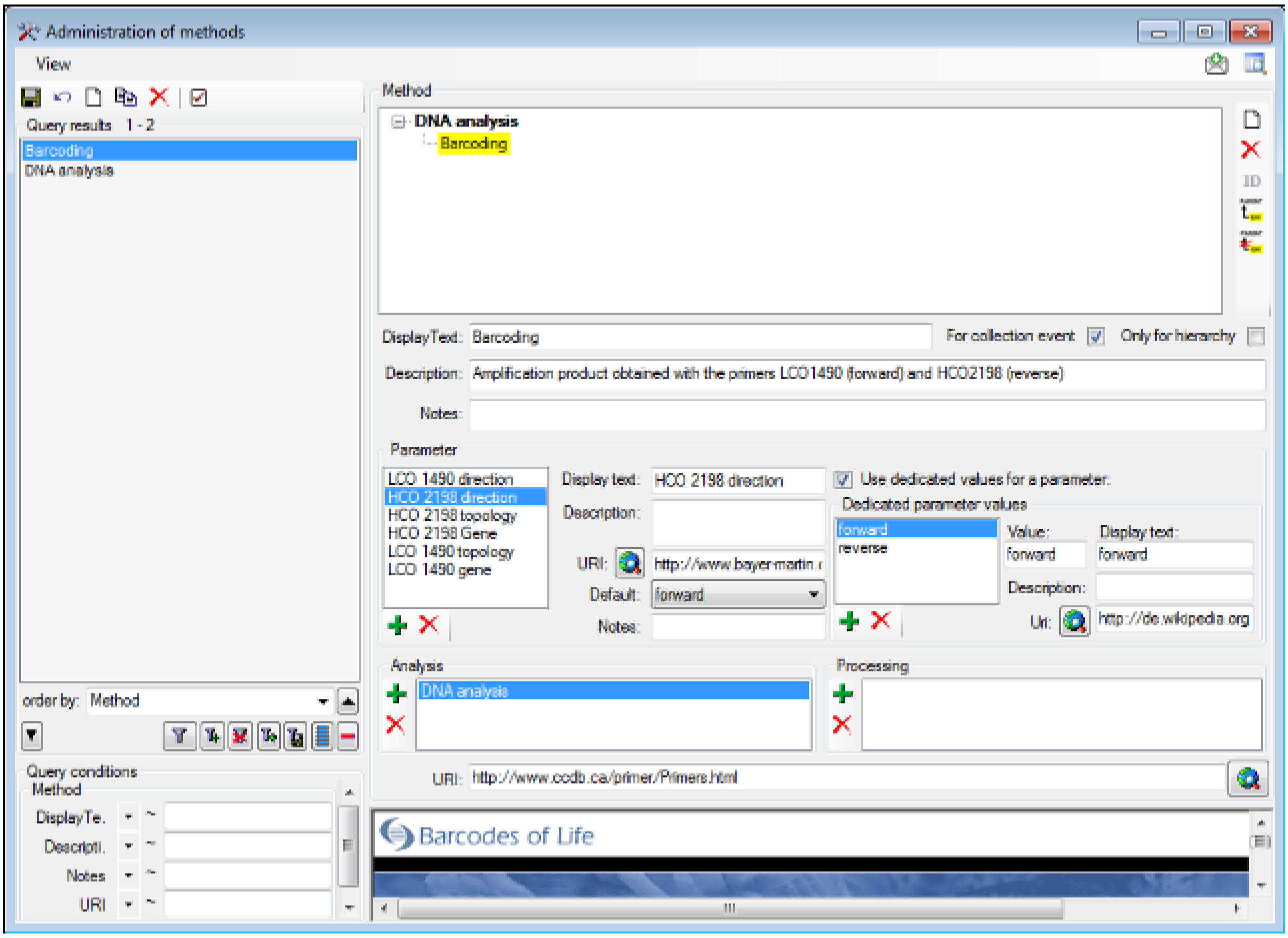


- Tools
  - HCO2198
    - Direction: Forward
      - Forward
      - Reverse
    - Topology:
    - Gene:
  - LCO1490
    - Direction:
      - Forward
      - Reverse
    - Topology:
    - Gene:

To view the history of a data set click on the button. A window with the history will open. For more details see the section History. For any comments to this part of the application use the feedback function.

Methods

The methods used for collection events, the analysis of the organisms or the processing of the material. To administrate these methods, choose **Administation -> Methods ...** from the menu. A window as shown below will open.



DisplayText: Barcoding

For collection event ☑ Only for hierarchy ☐

Description: Amplification product obtained with the primers LCO1490 (forward) and HCO2198 (reverse)

Notes:

Parameter:
- LCO 1490 direction
- HCO 2198 direction
- HCO 2198 topology
- HCO 2198 Gene
- LCO 1490 topology
- LCO 1490 gene

Display text: HCO 2198 direction

Description:

URI: http://www.bayer-martin.c

Default: forward

Notes:

☑ Use dedicated values for a parameter:

Dedicated parameter values: forward, reverse

Value: forward

Display text: forward

Description:

Uri: http://de.wikipedia.org

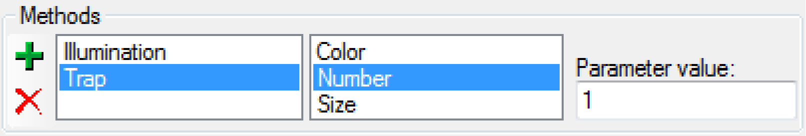
Analysis: DNA analysis

URI: http://www.ccdb.ca/primer/Primers.html

There are 2 lists where you can define for which **analysis** resp. **processing** the selected method may be used. If the checkbox **For collection event** is checked, this method may be used for collecting specimen. The methods may contain several parameters as shown above. To insert a parameter click on the ✚ button. If a parameter should only allow predefined values, check the **Use dedicated values for a parameter** checkbox and add values using the ✚ button. With the ✕buttons you can remove parameters or predefined values.

To view the history of a dataset, click on the button. A window with the history will open. For more details see the section History. For any comments to this part of the application, use the feedback function.

In the main form you can add a method to a collection event, an analysis or a processing. Choose the respective item in the tree and click on the ✚button to add a method (see below). Depending on the selected method, you get a list of parameters for which the values can be set. For the parameters where default values are available, these will be inserted when adding the method.



- Illumination
- Trap

- Color
- Number
- Size

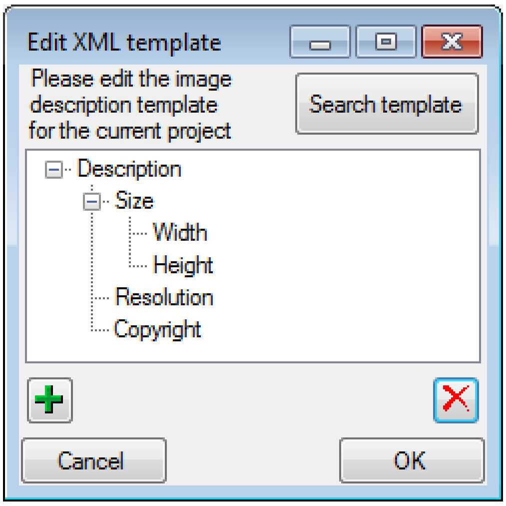
Parameter value: 1

You may add several methods for one analysis resp. processing or collection event as shown above.

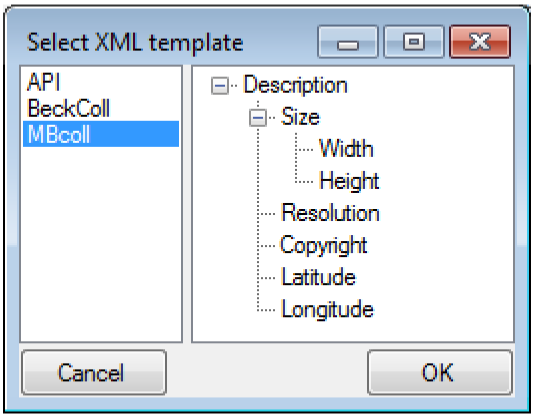
Image description

Creating and editing templates

To enter a description for an image or a medium a before designed description template for the current project is required. To be able to create a template you need to be an admininstrator or data manager. To define the template choose **Administration - Image description ...** from the menu. A window will open as shown below.

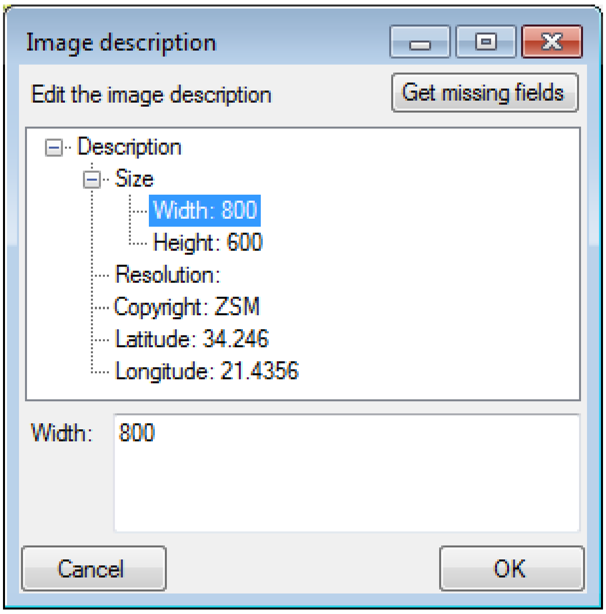


To enter or remove description fields use the + and ✕ buttons respectively. To search for a template from another project click on the **Search template** button. A window will open where you can choose from templates defined for other projects as shown below.



Description of the image

To edit a description of an image or medium select it from the list and click on the button. A window will open as shown below where you can edit the description according to the template. If the template has changed or you want to add description fields from another project, click on the **Get missing fields** button.



Edit the image description

- Description
  - Size
    - Width: 800
    - Height: 600
  - Resolution:
  - Copyright: ZSM
  - Latitude: 34.246
  - Longitude: 21.4356

Width: 800

Media

Next to images you can store audio 🔊 and video 📹 files. Click on the **[>>>]** button (see below)

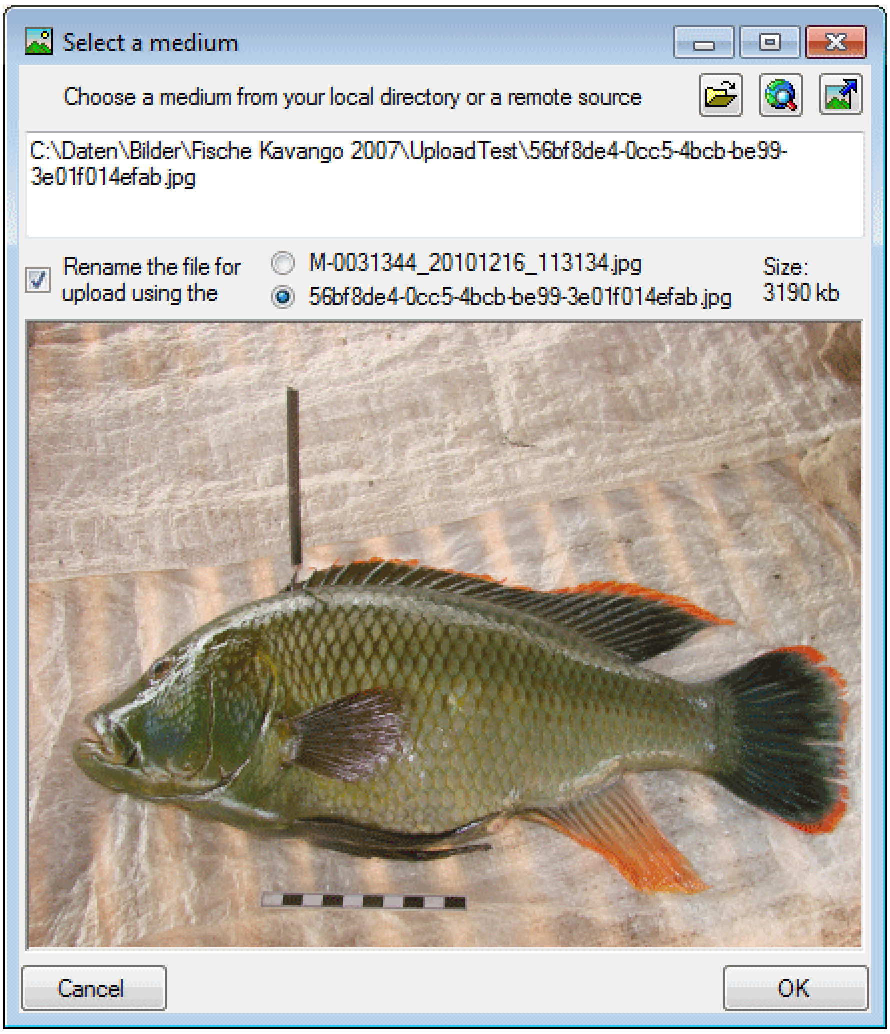
to open Windows Media Player and play the content of the media. You must have Windows Media Player installed to use this function. For the description of a medium see the chapter Image description.

DiversityMediaService

The webservice DiversityMediaService provides the possibility to upload media files like images, audio recordings, etc. to a server. The usage of this webservice includes several preconditions (please turn to your administrator):

- You need an account in the DiversityWorkbench module DiversityAgents with your login in DiversityCollection linked to this account
- Your project has to be registered on the server
- You have to rename your media file according to the settings of the server e.g. using a GUID (see image below)

Use the upload button to upload your image to the server.



Choose a medium from your local directory or a remote source

C:\Daten\Bilder\Fische Kavango 2007\UploadTest\56bf8de4-0cc5-4bcb-be99-3e01f014efab.jpg

☑ Rename the file for upload using the

○ M-0031344_20101216_113134.jpg

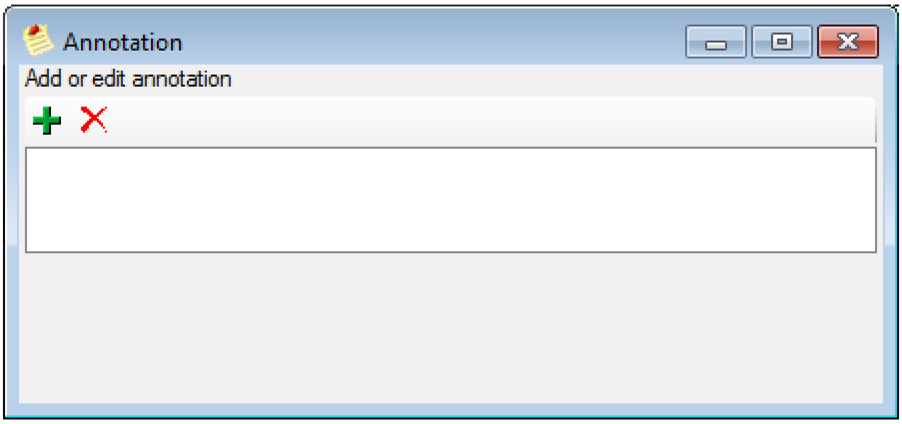
● 56bf8de4-0cc5-4bcb-be99-3e01f014efab.jpg

Size: 3190 kb

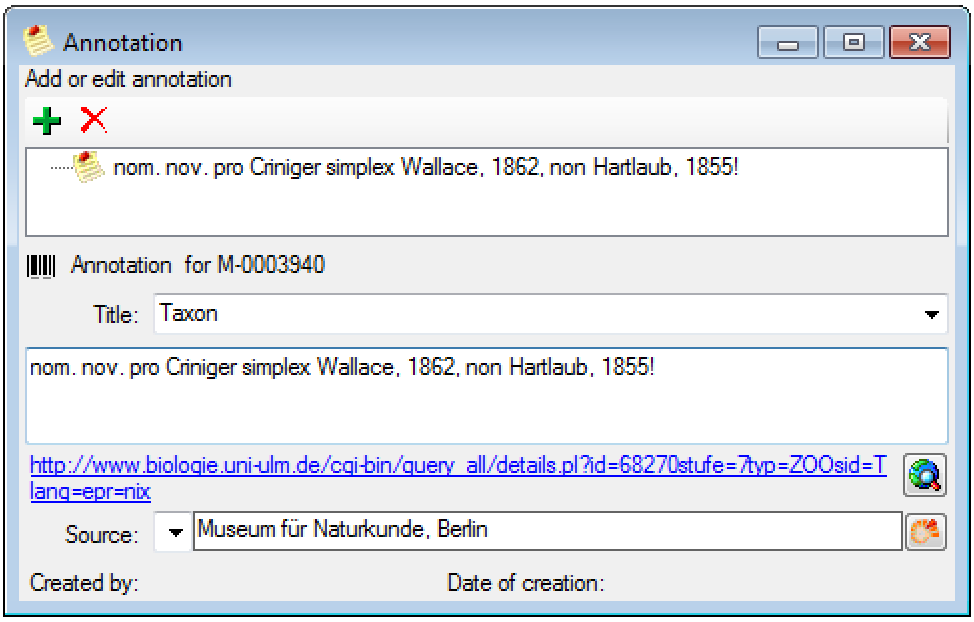
Annotation

You can add an annotation for a collection event, a collection specimen, a part of a collection specimen or an organism (= identification unit).

The available types are annotation, problem and reference. To add an annotation, select the corresponding data in the tree view. In the tool panel on the right of the tree view a button will appear: if no annotations have been added so far or if there are annotations for this entry. A window will open as shown below.



To add an annotation, click on the button and select the type of the annotation. The annotation will be shown in the tree with the details listed below (see image below).



nom. nov. pro Criniger simplex Wallace, 1862, non Hartlaub, 1855!

Annotation for M-0003940

Title: Taxon

nom. nov. pro Criniger simplex Wallace, 1862, non Hartlaub, 1855!

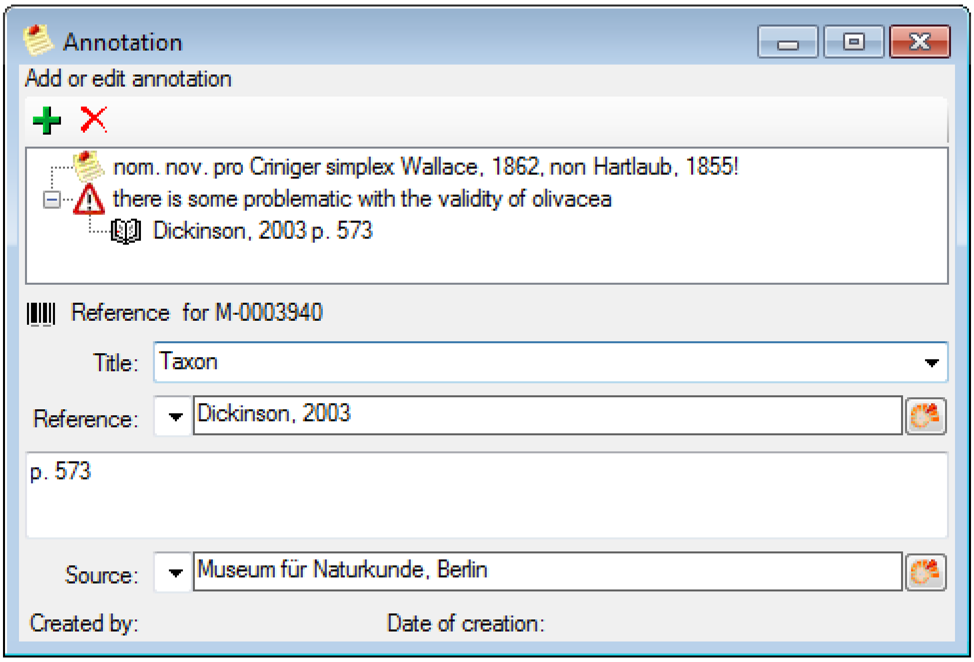
http://www.biologie.uni-ulm.de/cgi-bin/query_all/details.pl?id=68270stufe=7typ=ZOOsid=Tlang=epr=nix

Source: Museum für Naturkunde, Berlin

Created by:

Date of creation:

Enter your annotation in the text box as shown above. You can enter a title or subject for your annotation or select one from the list. You may enter a link and a source as shown above. The source may be related to the module DiversityAgents.



nom. nov. pro Criniger simplex Wallace, 1862, non Hartlaub, 1855!
there is some problematic with the validity of olivacea
Dickinson, 2003 p. 573

Reference for M-0003940

Title: Taxon

Reference: Dickinson, 2003

p. 573

Source: Museum für Naturkunde, Berlin

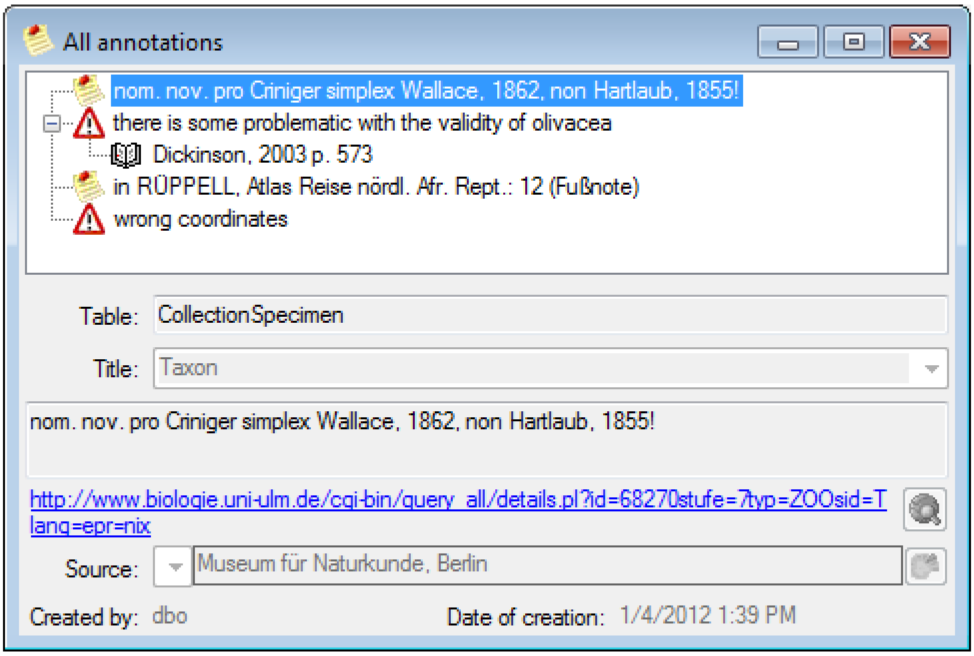
Created by:

Date of creation:

For the type reference (see above) you may enter a link to the module DiversityReferences.

To delete an annotation you have to be either an administrator or a data manager. Select the annotation and click on the ✗ button.

If you want to see all annotations of the current specimen choose **Data - All annotations...** from the menu. All annotations will be listed as shown below.



nom. nov. pro Criniger simplex Wallace, 1862, non Hartlaub, 1855!
there is some problematic with the validity of olivacea
Dickinson, 2003 p. 573
in RÜPPELL, Atlas Reise nördl. Afr. Rept.: 12 (Fußnote)
wrong coordinates

Table: CollectionSpecimen

Title: Taxon

nom. nov. pro Criniger simplex Wallace, 1862, non Hartlaub, 1855!

http://www.biologie.uni-ulm.de/cgi-bin/query_all/details.pl?id=68270stufe=7typ=ZOOsid=Tlang=epr=nix

Source: Museum für Naturkunde, Berlin

Created by: dbo

Date of creation: 1/4/2012 1:39 PM

Data for the annotations are stored in the table Annotation.

GIS editor

To use the GIS editor, click on the button in the control to show the maps and choose the appropriate option (GIS- edit) from the first drop-down list in the maps control. With this editor you can document locations with any geographical object (lines, areas, ...) different from a simple point. If coordinates are available for your data set, the GIS editor will load a map (Google Maps) as background. To insert the geographical object defined for e.g. the locality click on the + button. To set the format for point symbols use the controls for the symbol, color, size and line thickness above the GIS editor. To redraw the maps with new settings click on the button.

With the GIS editor you can edit the geographical information for the CollectionEventSeries , the CollectionEvent and an Organism . Furthermore you can create distribution maps for any sample selection.

The GIS editor has several states which are needed to handle geographical objects. For a detailed description see the GIS tutorial.

Diversity GIS Editor - Tutorial

Introduction

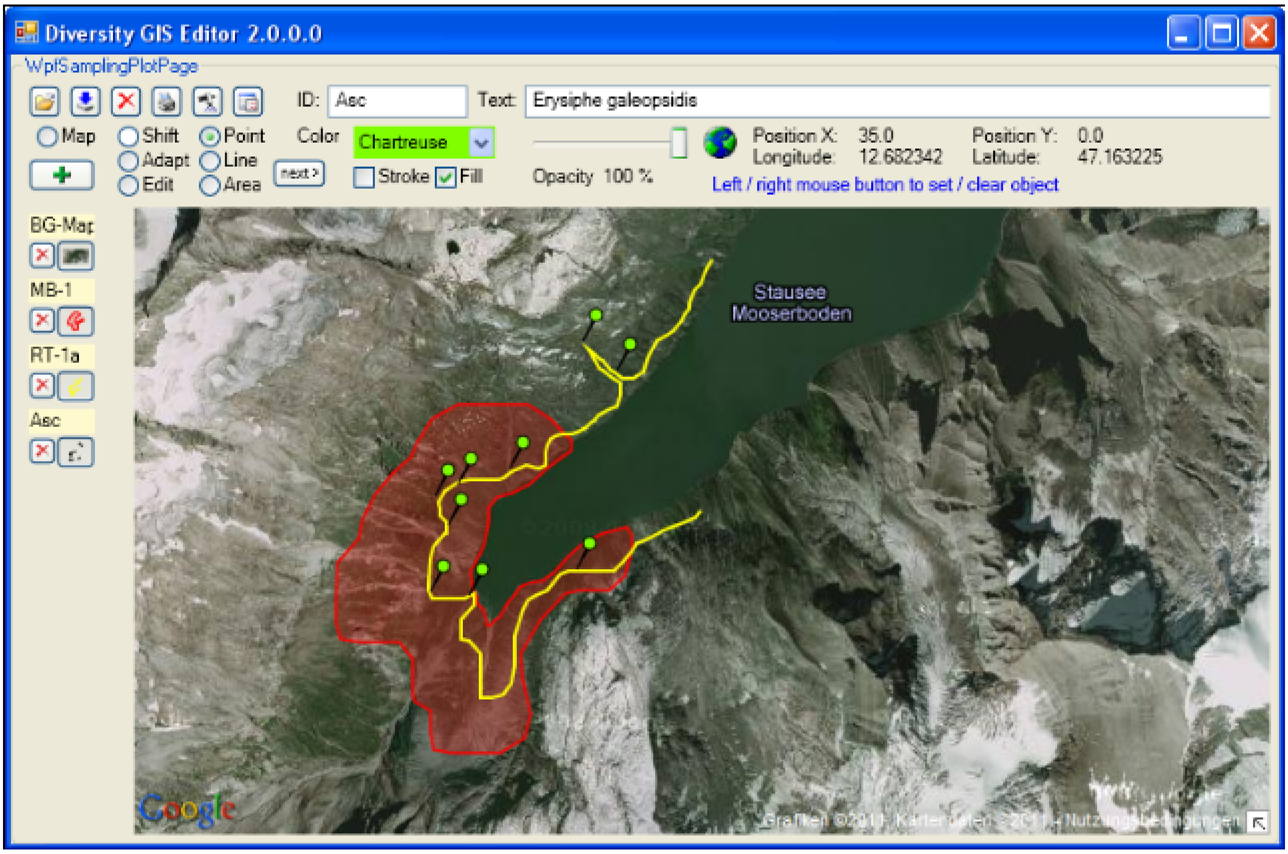
The Diversity GIS Editor is a tool to create, visualize, edit and archive samples within a geographical environment. It may be used as a stand-alone application or as a component of the Diversity Workbench by other applications, e.g. DiversityCollection or DiversitySamplingPlots.

In combination with a background map, equipped with world coordinates, collections of Microsoft SQL Geometry Objects (points, lines and areas) may be displayed and edited in their geographical context. The screen and world coordinates of the objects will be calculated and shown in the status line. Color, thickness and transparency of the elements can be adjusted. The working area which keeps the maps and objects may be shifted or zoomed.

The background map could either be loaded from a storage device or created with an online map server tool provided by the editor. Other maps without world coordinates may be adjusted to the background map easily by setting 3 pairs of reference points on the background and the new map. The calculated world coordinates will be assigned and stored when the new map is saved.

A GPS functionality has been integrated. If a GPS device is connected, the current position will be displayed and - if an applicable background map is loaded - marked on the map.

The data transfer between application and GIS editor is made by interface function calls. In that way geometry objects of a Diversity data base may be loaded to the editor, modified or extended and sent back to the application, which then updates the data base.


Diversity GIS Editor 2.0.0.0

WpfSamplingPlotPage

ID: Asc

Text: Erysiphe galeopsidis

○ Map ○ Shift ● Point ○ Adapt ○ Line ○ Edit ○ Area

Color: Chartreuse

☐ Stroke ☑ Fill

Opacity 100 %

Position X: 35.0 Position Y: 0.0

Longitude: 12.682342 Latitude: 47.163225

Left / right mouse button to set / clear object

Diversity GIS Editor - Tutorial

Chapter 1: GIS Editor Layout

The layout of the Diversity GIS Editor could be divided into 3 regions:

- Control Panel
- Sample List
- Working Area

Control Panel

ID: Asc
Text: Erysiphe galeopsidis
○ Map ○ Shift ● Point
○ Adapt ○ Line
○ Edit ○ Area
Color: Chartreuse
☐ Stroke ☑ Fill
Opacity 100 %
Position X: 662.0 Position Y: 0.0
Longitude: 12.736150 Latitude: 47.163225
Left / right mouse button to set / clear object

The Control Panel consists of the following elements:

- 7 buttons to load, save, delete, print or add samples, switch GPS and to open the Settings window
- 2 text boxes for sample Identifier (ID) and Description (Text)
- 7 radio buttons to select the operation mode (Map, Shift, Adapt, Edit, Point, Line, Area)
- 1 button next > to switch to a new object, if the current sample is composed of multiple lines or areas
- 4 controls to adjust color and transparency of the samples (for stroke and fill) or to zoom the working area
- Status lines with screen and world coordinates (if any) and an appropriate symbol Google, OSM, , or
- A hint about the user interaction, which is possible or expected

Sample List

The Sample List is the container for added maps or objects. Each entry is composed of the following elements:

- Identifier of the sample
- Delete button to remove the sample
- Toggle button to hide or show the sample

The toggle button is illustrated with a small picture of the associated sample. Switching these controls using the left mouse button will hide or show the corresponding sample. Using the right mouse button will show the corresponding sample and hide all others, except the background map. If the number of samples in the list do not fit into the window area, a scroll bar will be displayed.

Working Area

This is the drawing space containing loaded maps and objects. In Shift mode the area could be moved or zoomed.

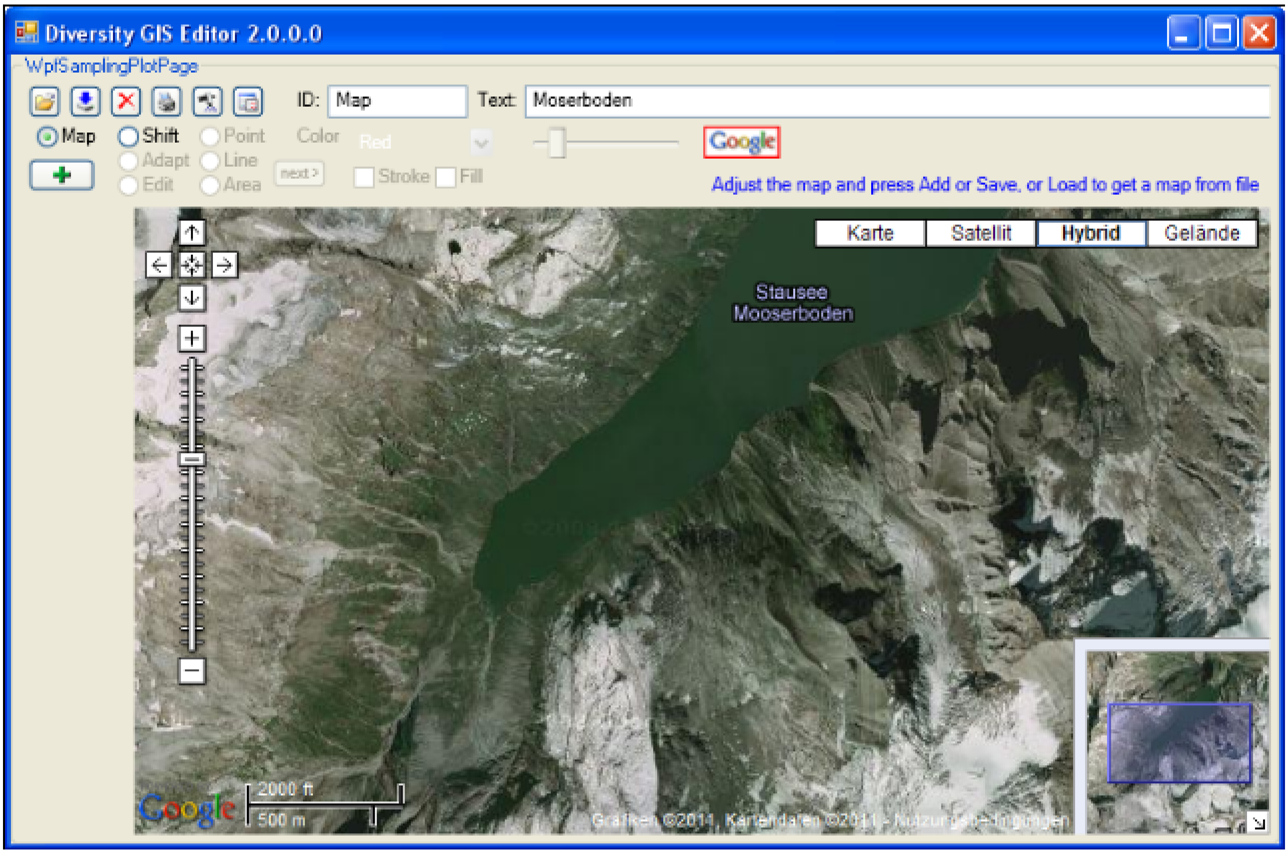
Chapter 2: GIS Editor Usage

The GIS Editor has 7 operation modes which are described in the following chapters:

- Map: Create an online map from the map server
- Shift: Move the working area with the mouse or zoom it with the slider
- Adapt: Calculate world coordinates for a new image using reference points of the background map
- Edit: Modify the current object and all visible samples of the Sample List
- Point: Create a number of object markers on the background map
- Line: Create a line string or a collection of line strings on the background map
- Area: Create an area or a collection of areas on the background map

When starting the GIS Editor as a stand-alone application the start-up operating mode usually is the Map mode. This is to remind the user that a background map with world coordinates is necessary to work with geographic objects.

Chapter 2.1: Map Mode



ID: Map

Text: Moserboden

Adjust the map and press Add or Save, or Load to get a map from file

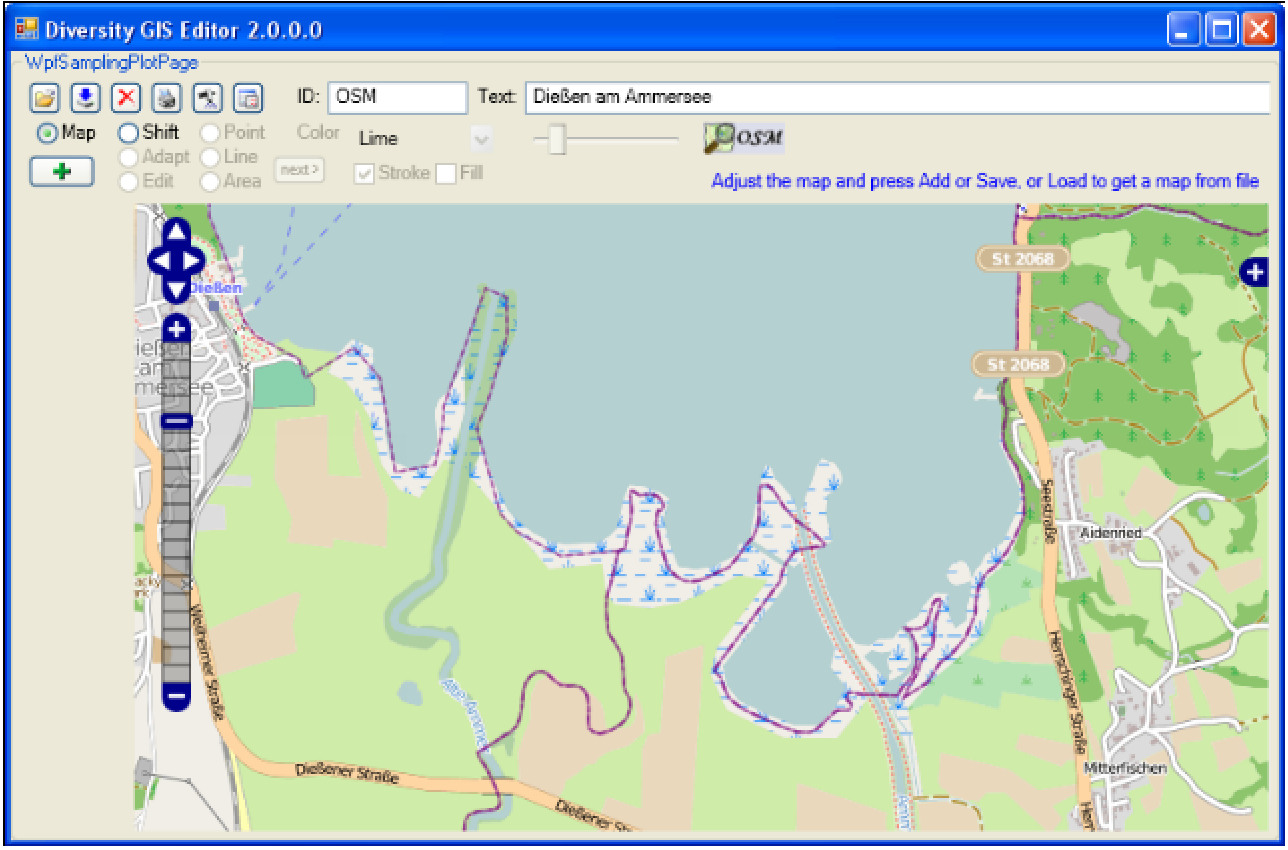
In Map mode the editor connects via Internet to the SNSB Google Maps service or alternatively to the Open Street Maps service, regarding on the [GIS-Editor Settings](), and displays an online map which can be moved, zoomed and switched as usual. The status area shows the Google or respectively the OSM symbol. The size of the map area adapts to the size of the working area, even when resizing the window.

In case of Google the controls for moving, zooming, map type, the scale and the overview window in the bottom right corner are displayed by default. The map can be adjusted to the user's needs as follows:

- Select map area: Press and hold left mouse button and move the mouse, or use the Google shift control
- Zoom map: Turn the mouse wheel (if any), double click (left mouse button) on a location or use the Google zoom control
- Switch map type: Use Google map type control
- Hide Google controls: Click right mouse button to hide, left mouse button to show them again
- Hide overview window: Toggle arrow box in the bottom right corner of the window to hide or show it

In case of Open Street Maps the pan and zoom control is displayed by default. It can be switched off or on by clicking the left mouse button anywhere within the map area. The layer switch control is hidden and can be opened by pressing the ⊕ or closed again by pressing the ▣ button on the right side. The map can be adjusted to the user's needs as follows:

- Select map area: Press and hold left mouse button and move the mouse, or use the OSM pan control
- Zoom map: Turn the mouse wheel (if any), double click (left mouse button) on a location or use the OSM zoom control
- Switch map type: Open the layer switch and select a layer
- Hide or show pan and zoom control: Click left mouse button to toggle the control


Diversity GIS Editor 2.0.0.0

WpfSamplingPlotPage

ID: OSM

Text: Dießen am Ammersee

● Map ○ Shift ○ Point ○ Adapt ○ Line ○ Edit ○ Area

Color: Lime

☑ Stroke ☐ Fill

Adjust the map and press Add or Save, or Load to get a map from file

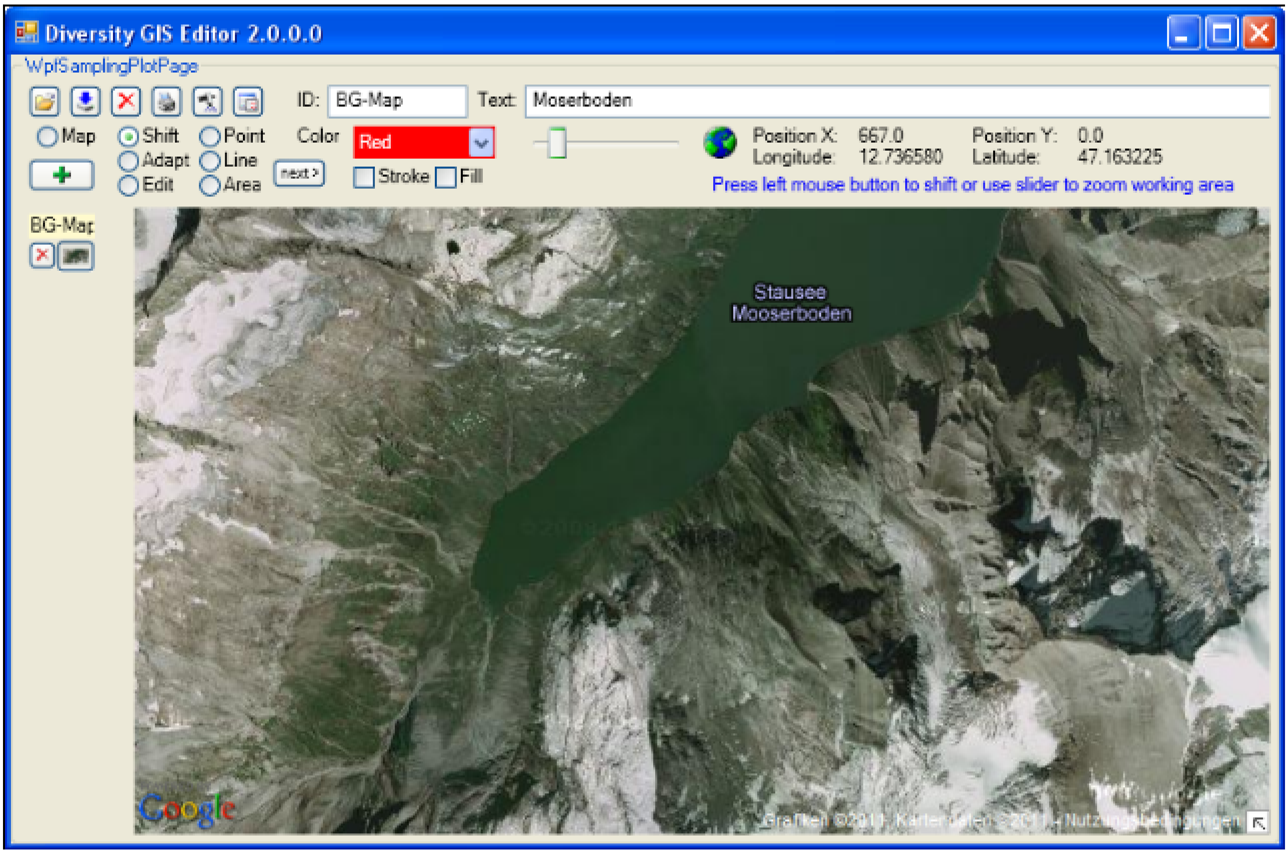
If an appropriate area has been selected, just press the Add button ✚, then the area will be scanned and added to the Sample List as a reference map. This may take a couple of seconds, depending on size of the map area and processor power. A little image of the map will appear on the toggle button in the Sample List. The Google controls should be switched off before adding to get a neat map image.

The mode will be switched to Shift mode automatically and the status symbol will change to 🌍 indicating that world coordinates are present. The screen and world coordinates will be shown in the status lines if the mouse is moved over the map surface.

The maps are subject to the Mercator projection, which is the GIS Editor's precondition for every bitmap used as a reference map. While the screen coordinates are linear in horizontal and vertical direction, the world coordinates are non linear in vertical direction.

Chapter 2: GIS Editor Usage

Chapter 2.2: Shift Mode



ID: BG-Map
Text: Moserboden
Color: Red
Position X: 667.0
Position Y: 0.0
Longitude: 12.736580
Latitude: 47.163225

Press left mouse button to shift or use slider to zoom working area

This is the quasi default mode of the GIS Editor. The cursor changes to a move shape when touching the background map. The map is "frozen" and exists as an image sample on the working area. Changing the map region or resolution is no longer possible. But the Shift Mode provides 2 features:

- Move the working area
- Zoom the working area

Moving the working area

Press and hold the left mouse button and move the mouse to shift the working area within the display window. This is useful when having loaded a map from a storage unit which is larger than the GIS Editor's window, or in combination with zooming the working area.

Zooming the working area

Place the mouse cursor at the slider control, press and hold the left mouse button and move the control left to zoom out or right to zoom in to the working area. The range of the zoom is from factor 0.6 to 3.0. The current value is displayed beneath the zoom control. Double click the slider control to reset the zoom to default value 1.0.

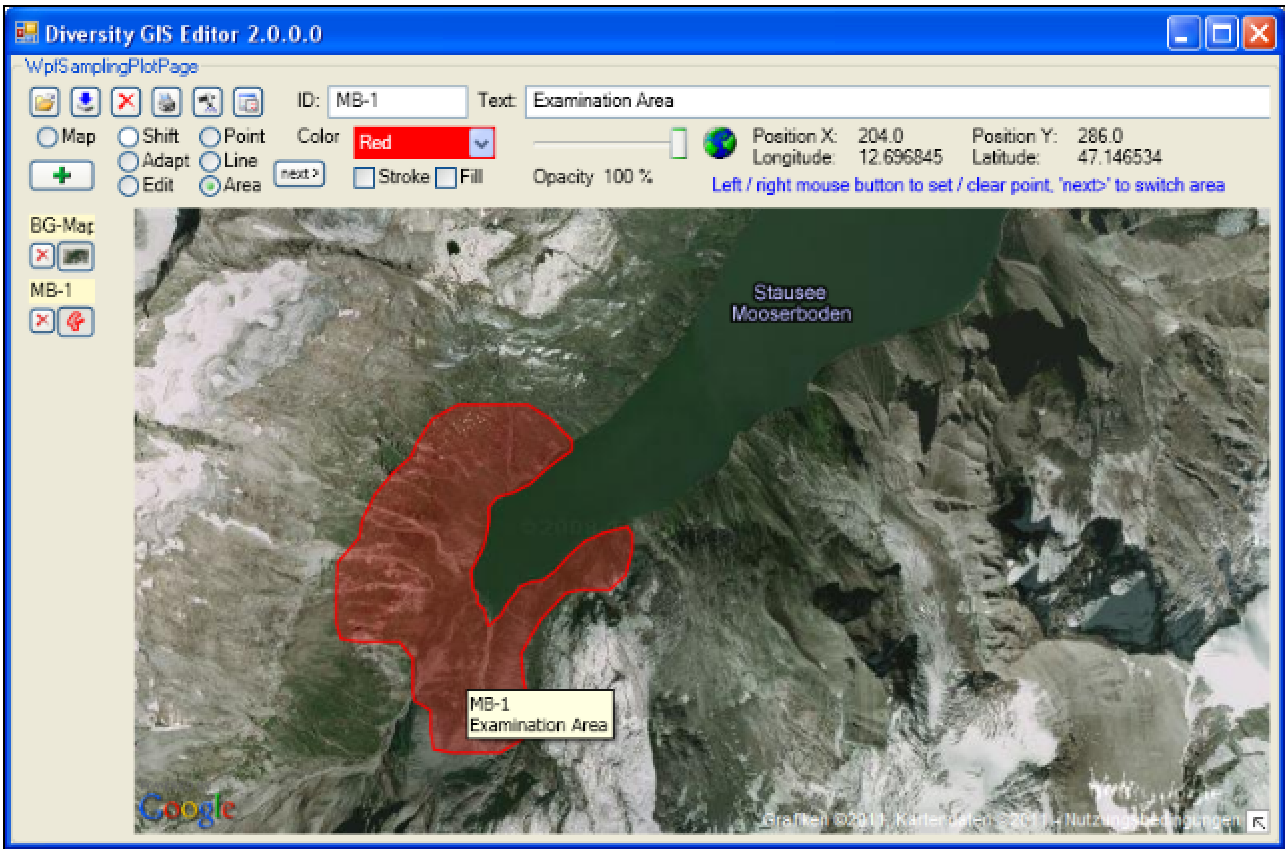
Enlarging the working area makes it more easy to place objects precisely. The relevant area then could be selected by moving the zoomed working area. Downsizing the working area gives an overview of large map regions.

Please note that the resolution of the map itself does not change any more when zooming in. But objects on the map are created in vector graphics, so the markers, lines or areas will remain sharp and clear while zooming. And they will adapt there thickness smoothly to the size.

Chapter 2: GIS Editor Usage

Chapter 2.3: Area Mode

This mode is used to create areas (polygons) on the background map. The cursor changes to a cross line when touching the background map. Each click on the left mouse button sets a new point of the polygon. Every click on the right mouse button clears the last point set. The closed polygon defined by the points is displayed completely at any time. When holding the left mouse button the point can be placed while the lines of the polygon are shown as a "rubber band" display.



Diversity GIS Editor 2.0.0.0

WpfSamplingPlotPage

ID: MB-1 Text: Examination Area

○ Map ○ Shift ○ Point ○ Adapt ○ Line ○ Edit ● Area

Color: Red

☐ Stroke ☐ Fill

Opacity 100 %

Position X: 204.0 Position Y: 286.0

Longitude: 12.696845 Latitude: 47.146534

Left / right mouse button to set / clear point, 'next>' to switch area

To create more than one area for a sample, just click the next > button. This will finish the current polygon and start another one. It could be repeated without limitation of the number of polygons.

Setting the color

The areas are created as filled polygons, this means they have a border line (stroke) and a filling. The color of stroke and filling can be set independently or simultaneously by clicking the appropriate check boxes beneath the Color list box. Clicking on the list box will open a drop down menu with the complete set of 141 predefined brushes. Use the scroll bar to navigate to the preferred color and select it with the left mouse button.

Setting the transparency

Besides the color the transparency of the area could also be set for stroke and filling. In each edit mode the slider control is used for that. The area stroke or filling changes smoothly from invisible at the left till completely opaque on the right slider position. The value beneath the slider control indicates the opaqueness in a range from 0% to 100%. The default settings are 100% for stroke and 25% for filling.

Before adding the polygon to the Sample List an Identifier (ID) and a Description (Text) should be written to the text boxes in the control panel.

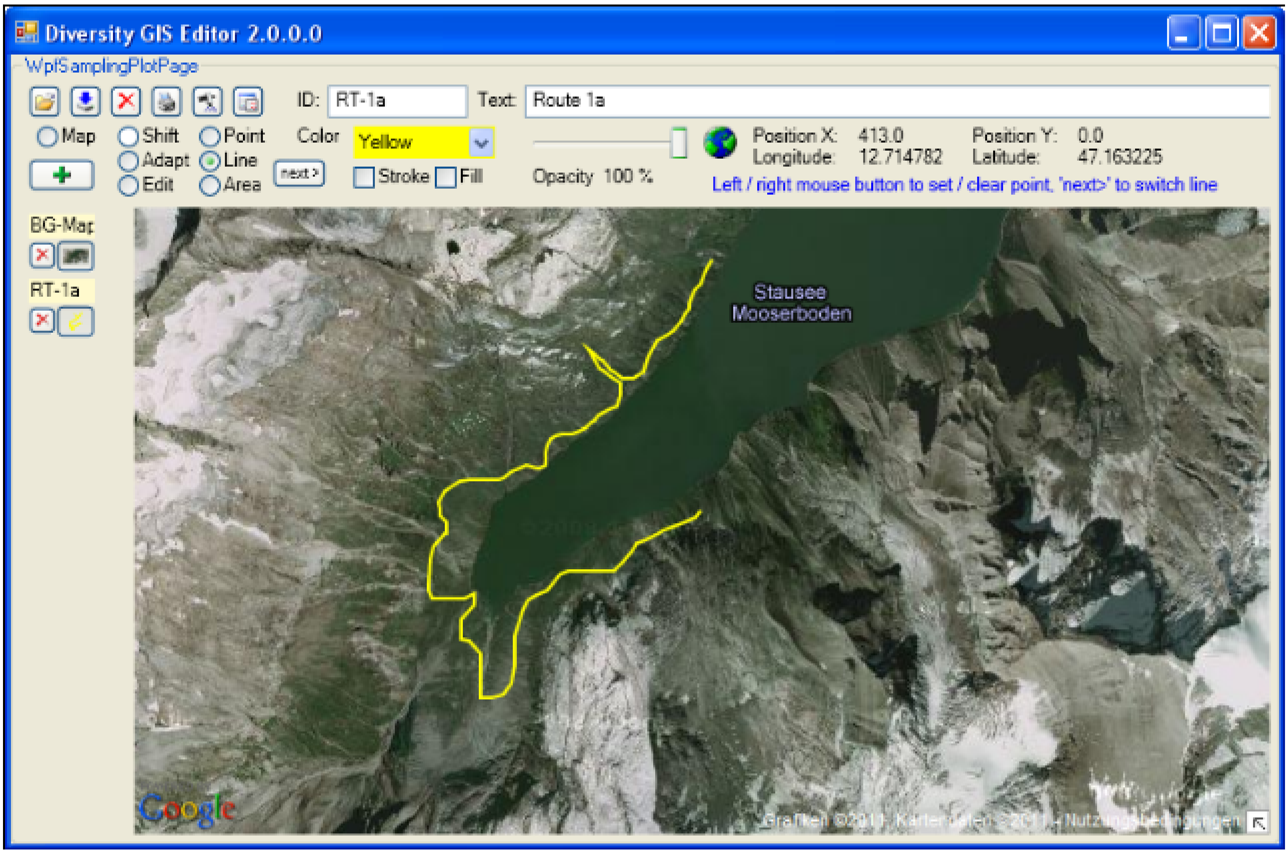
Clicking the Add button ✚ will put the current area(s) as one sample into the Sample List. The toggle button will show a small picture of the first area of the sample. The ID will be displayed above the buttons. Furthermore a tool tip will be created for the sample holding the ID and Description, which will pop up when moving the mouse over the toggle button or over the polygon in the working area.

Diversity GIS Editor - Tutorial

Chapter 2: GIS Editor Usage

Chapter 2.4: Line Mode

This mode is used to create line strings on the background map. The usage is adequate to the Area Mode. The cursor changes to a cross line when touching the background map. The points of the line strings can be set or cleared by clicking the mouse buttons. Clicking the next > button will switch to the next line string for the sample.



ID: RT-1a

Text: Route 1a

Color: Yellow

☐ Stroke ☐ Fill

Opacity 100 %

○ Map ○ Shift ○ Point ○ Adapt ● Line ○ Edit ○ Area

Position X: 413.0 Position Y: 0.0

Longitude: 12.714782 Latitude: 47.163225

Left / right mouse button to set / clear point, 'next>' to switch line

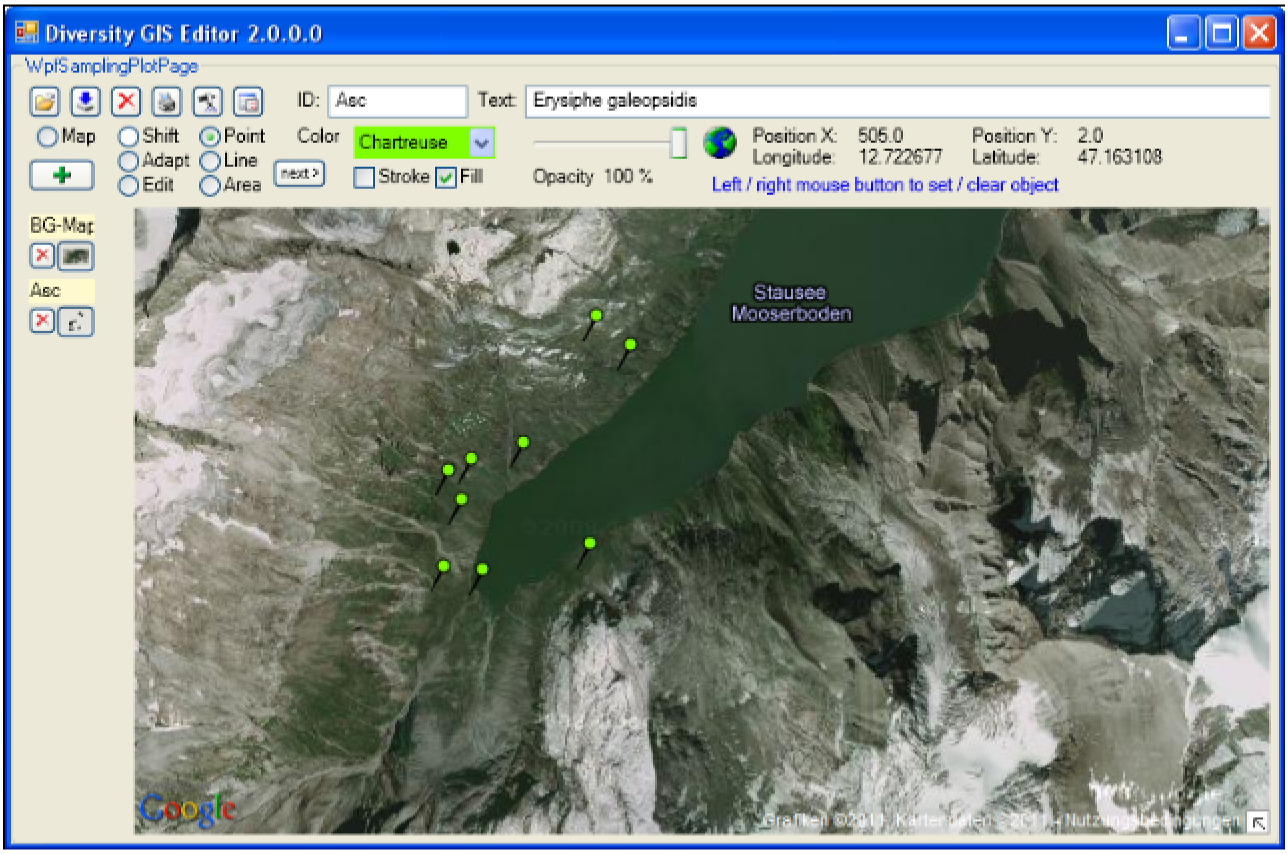
Color and transparency can be set for the line strings using the appropriate controls, but only for stroke, because the line strings do not have a filling. Thus checking the Fill box will have no effect. After adding the lines to the sample list a small picture of the first line string will appear on the toggle button.

Diversity GIS Editor - Tutorial

Chapter 2: GIS Editor Usage

Chapter 2.5: Point Mode

This mode is used to create Points (object markers) on the background map. The usage is similar to the Area Mode. The cursor changes to a cross line when touching the background map. The object markers can be set by clicking the left mouse button, clicking the right mouse button will clear the last markers one by one again. The next > button has no impact, because each Point represents a complete object and needs not to be finished before creating the next one.



Diversity GIS Editor 2.0.0.0

WpfSamplingPlotPage

ID: Asc

Text: Erysiphe galeopsidis

○ Map ○ Shift ● Point

○ Adapt ○ Line

○ Edit ○ Area

Color: Chartreuse

☐ Stroke ☑ Fill

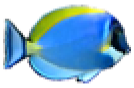
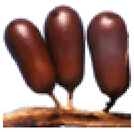
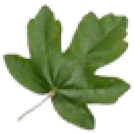
Opacity 100 %

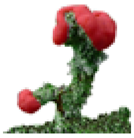
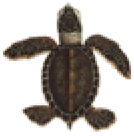
Position X: 505.0 Position Y: 2.0

Longitude: 12.722677 Latitude: 47.163108

Left / right mouse button to set / clear object

The shape of the object markers can be selected from a number of predefined Point symbols and icons within the Settings window, e.g.:

Pin:		Assel:		Fish:		Mollusc:	
Cross:	+	Bird:		Fungus:		Myxomycete:	
X:	✕	Bryophyt:		Insect:		Plant:	

Circle:	○	Echinoderm:		Lichen:		Reptile:	
Square:	□	Evertebrate:		Mammal:		Vertebrate:	
Diamond:	◇						

Color can be set for the symbol markers using the appropriate controls. It depends on the selected point symbol, whether it just has a stroke (e.g. "Cross") or also a filling (e.g. "Pin"). Transparency can be set for both, the symbol and icon markers. The stroke thickness and the size of the markers can be set in the Settings menu. After adding the object markers to the sample list a small picture of the collection will appear on the toggle button.

Chapter 2: GIS Editor Usage

Chapter 2.6: Edit Mode

This mode is used to modify all samples (objects and images) which are currently **visible** on the working area. It applies to the elements of the Sample List as well as to the current sample.

Changing the position or shape of objects (points, line strings, areas)

To change an object one has to move the vertices ("corner points") which are defining it. To do so just move the mouse close to a vertex to localize it. As soon as the corner has been grabbed the cursor changes its shape to a hand symbol 👆.

Now press the left mouse button and hold it, then move the mouse to change the position of the vertex accordingly. The shape of the object or the marker will change in the same manner. Release the mouse button when the preferred position has been set.

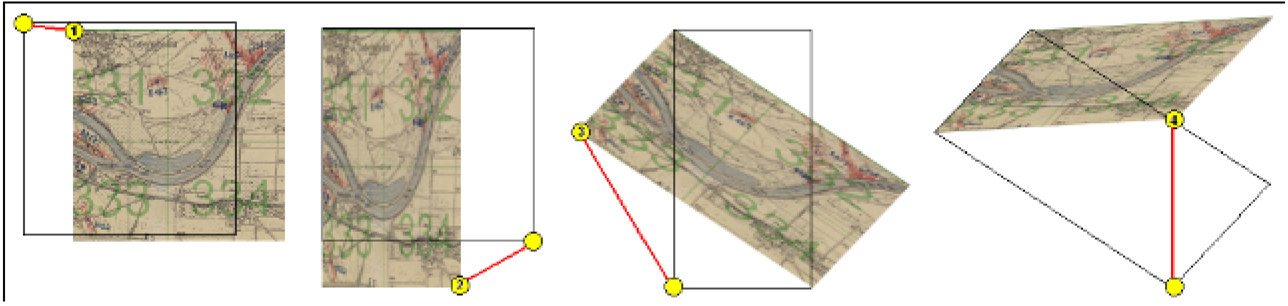
Note that areas and line strings cannot be moved in total while keeping their shapes!

Changing the position or shape of images (maps)

Images (e.g. maps) can be moved completely (keeping their aspect ratio), scaled in horizontal and vertical direction and skewed within an affine transformation. Editing an image can be divided into 4 stages by grabbing and moving the following corners:

1. Top-left: Moving the total image by keeping its aspect ratio
2. Bottom-right: Squeezing or stretching the image horizontally and vertically
3. Bottom-left, top-right: Skewing the image in an affine way by keeping the corner points top-left and bottom-right at its positions
4. Bottom-right again: Skewing the image in an affine way by keeping the corner points top-left and bottom-left at its positions

Stages 1 to 4:



Changing color and transparency

Color and transparency can be set independently (or simultaneously) for the objects using the appropriate controls and check boxes for Stroke or Fill. The setting will affect all visible objects, so objects which should not be changed have to be switched off before with their toggle buttons. The color of images could not be changed, of course, but the transparency can be set if the Fill box is checked. The transparency of the background map cannot be changed.

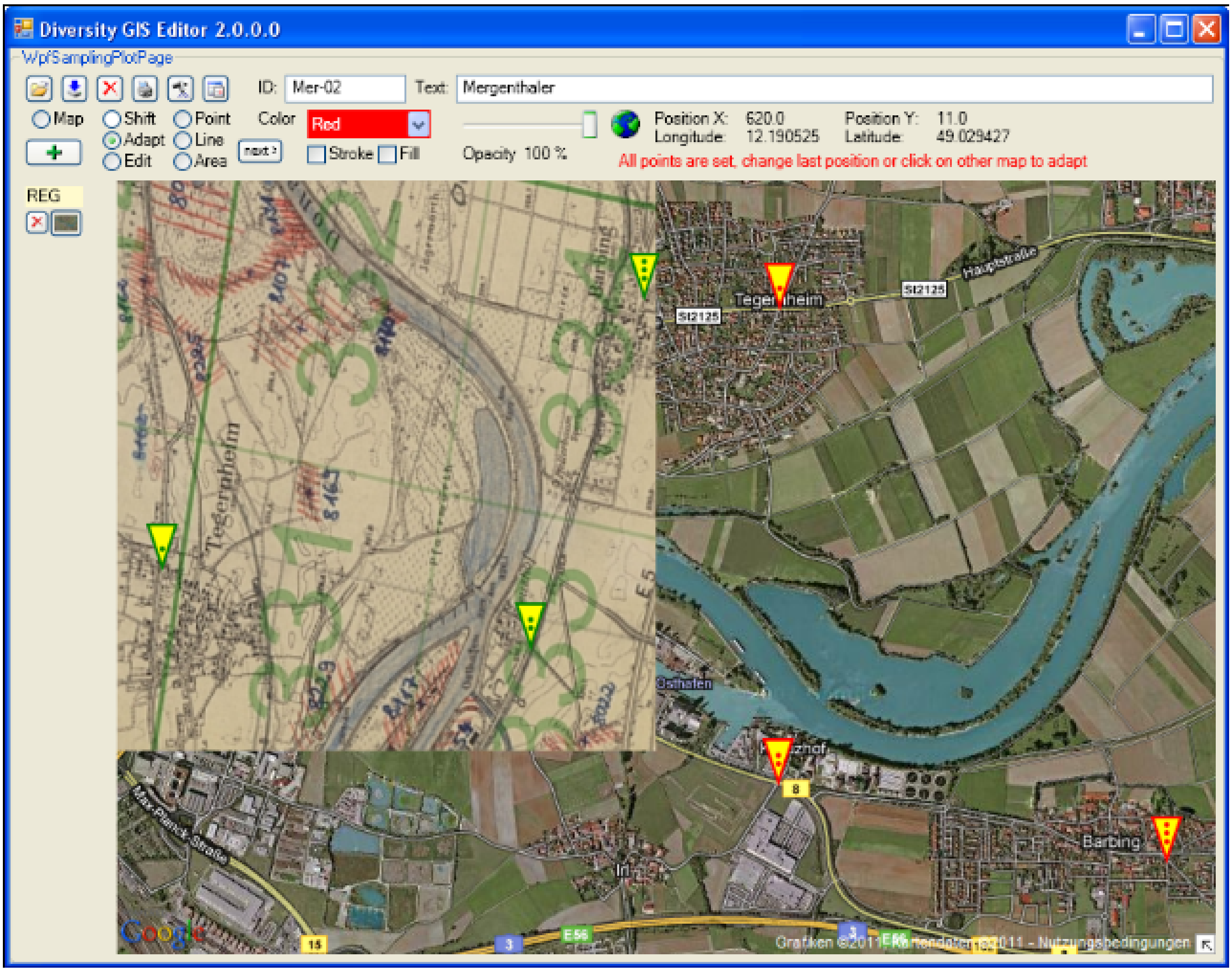
Chapter 2: GIS Editor Usage

Chapter 2.7: Adapt Mode

Essential for visualizing Geographical Objects is a background map with world coordinates. The GIS Editor's Map mode offers a convenient way to create such a map, but it is restricted for the use of Google or OSM maps which are present in the web and are providing world coordinates. It would be nice to load scans of e.g. topographical or even historical maps into the working area and use them as background maps, but the problem is how to assign world coordinates to them.

The Adapt mode solves this in an easy way by executing the following steps. As a precondition a background map having world coordinates (e.g. a Google map) must be present which covers the area of interest of the new map to be referenced.

1. Load the new map image using the Load button 📂. The image will be placed top left inside the working area.
2. Select Adapt mode by checking the Adapt radio button. The cursor changes to a pointer symbol ▽ having a green border when touching the new image and having a red one when touching the background map.
3. Now 3 reference points must be set alternately on background and new map to assign the appropriate locations (e.g. distinctive landmarks like road crossings). The last point can be modified as long as the map is not changed. The cursor always tells you what reference point will be set, according to its color and the number of dots in the middle: ▽ ▽ ▽ ▽ ▽ ▽
   Note: It is reasonable to select distant points close to the edges of the new map, because this will give more accurate results.



ID: Mer-02
Text: Mergenthaler

○ Map ○ Shift ● Adapt ○ Edit ○ Point ○ Line ○ Area

Color: Red

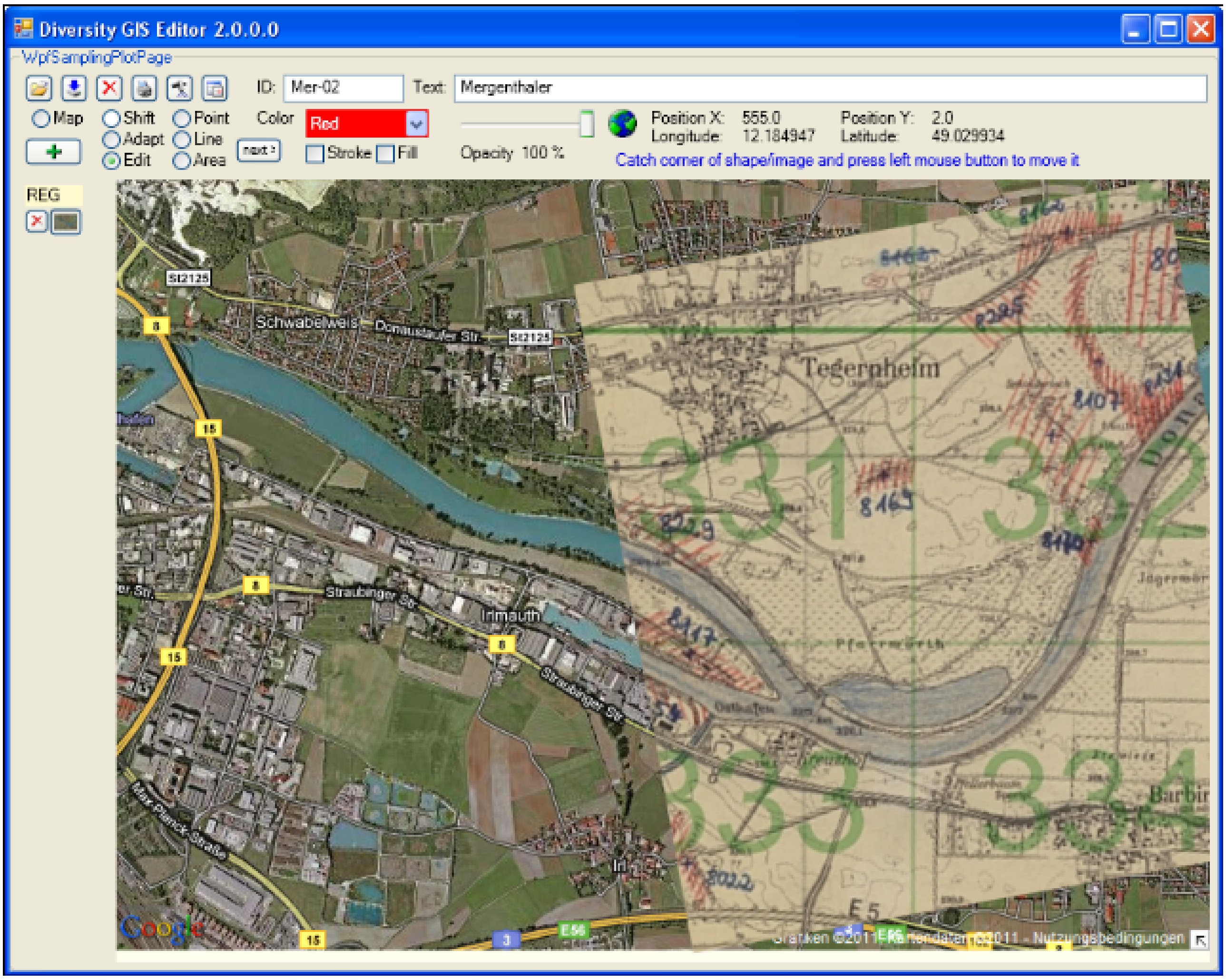
☐ Stroke ☐ Fill

Opacity 100 %

Position X: 620.0
Longitude: 12.190525
Position Y: 11.0
Latitude: 49.029427

All points are set, change last position or click on other map to adapt

4. When all reference points have been set and the cursor touches the alternate map, it changes to the finished shape ▼ . The next click will place the new map into the appropriate background map area.



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WpfSamplingPlotPage

ID: Mer-02 Text: Mergenthaler

○ Map ○ Shift ○ Point Color Red

○ Adapt ○ Line

● Edit ○ Area ☐ Stroke ☐ Fill Opacity 100 %

Position X: 555.0 Position Y: 2.0

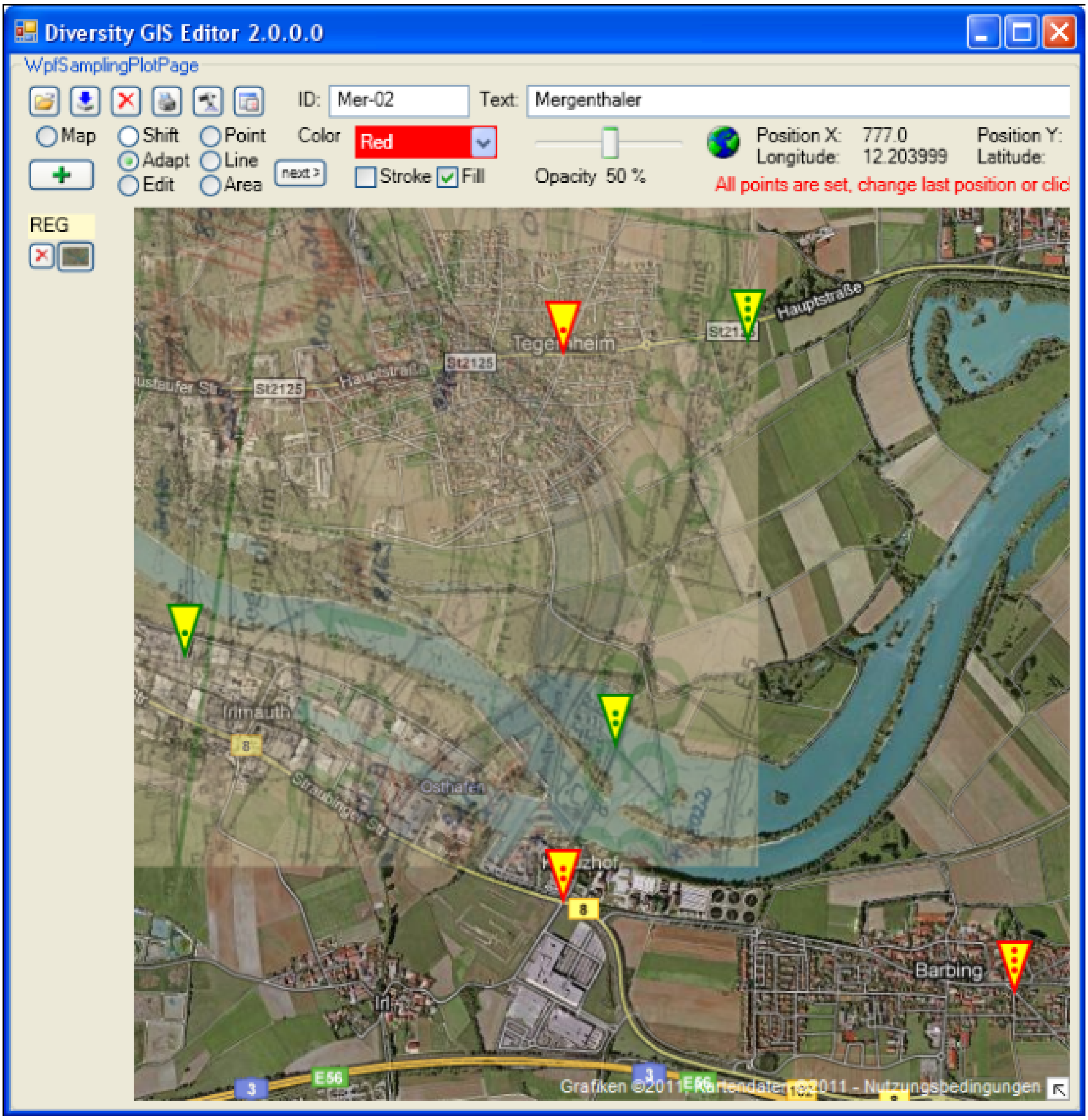
Longitude: 12.184947 Latitude: 49.029934

Catch corner of shape/image and press left mouse button to move it

The adapted image has been transformed to fit into the current world coordinates of the background map. Now the new map can be added to the sample list by pressing the Add button ✚. When it is finally saved to disk by pressing the Save button ⬇, the new assigned world coordinates will be saved, too, in an XML file with the same name (see Chapter 2.9: Save Samples).

Sometimes it is difficult to place the new map and the reference map side by side, because the window is too small, and zooming out would blur the details needed for setting the reference points. If the new map covers the background map, the reference points can be set anyway

- for the new map by making it opaque with the transparency slider
- for the background map by making the new map transparent (less than 10% opacity) with the slider



ID: Mer-02

Text: Mergenthaler

Color: Red

☐ Stroke ☑ Fill

Opacity 50 %

Position X: 777.0

Longitude: 12.203999

Position Y:

Latitude:

All points are set, change last position or clic

Note: The Fill box must be checked to change the transparency of the new map. The background map's transparency cannot be changed.

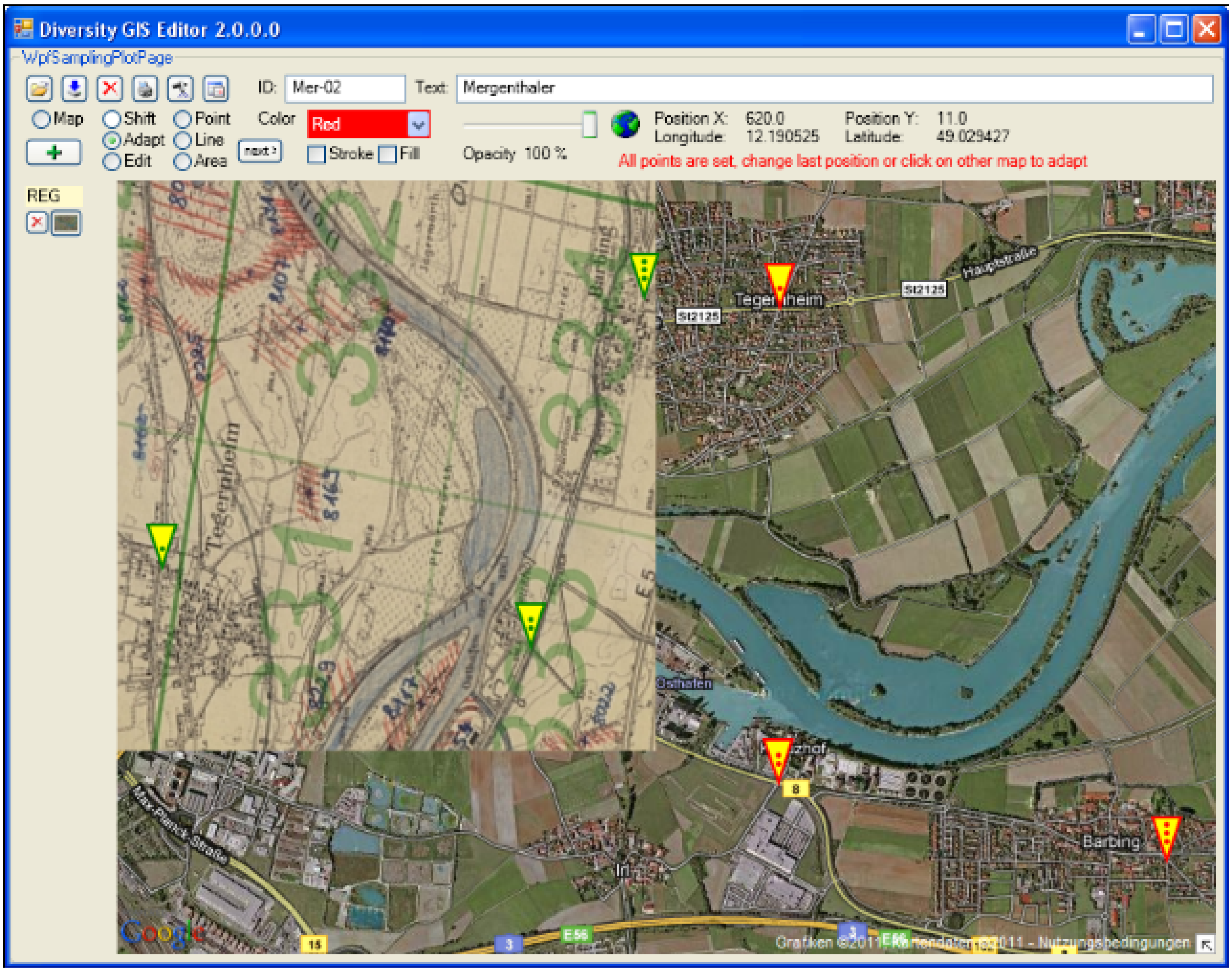
Chapter 2: GIS Editor Usage

Chapter 2.7: Adapt Mode

Essential for visualizing Geographical Objects is a background map with world coordinates. The GIS Editor's Map mode offers a convenient way to create such a map, but it is restricted for the use of Google or OSM maps which are present in the web and are providing world coordinates. It would be nice to load scans of e.g. topographical or even historical maps into the working area and use them as background maps, but the problem is how to assign world coordinates to them.

The Adapt mode solves this in an easy way by executing the following steps. As a precondition a background map having world coordinates (e.g. a Google map) must be present which covers the area of interest of the new map to be referenced.

1. Load the new map image using the Load button 📂. The image will be placed top left inside the working area.
2. Select Adapt mode by checking the Adapt radio button. The cursor changes to a pointer symbol ▽ having a green border when touching the new image and having a red one when touching the background map.
3. Now 3 reference points must be set alternately on background and new map to assign the appropriate locations (e.g. distinctive landmarks like road crossings). The last point can be modified as long as the map is not changed. The cursor always tells you what reference point will be set, according to its color and the number of dots in the middle: ▽ ▽ ▽ ▽ ▽ ▽
   Note: It is reasonable to select distant points close to the edges of the new map, because this will give more accurate results.



ID: Mer-02

Text: Mergenthaler

Color: Red

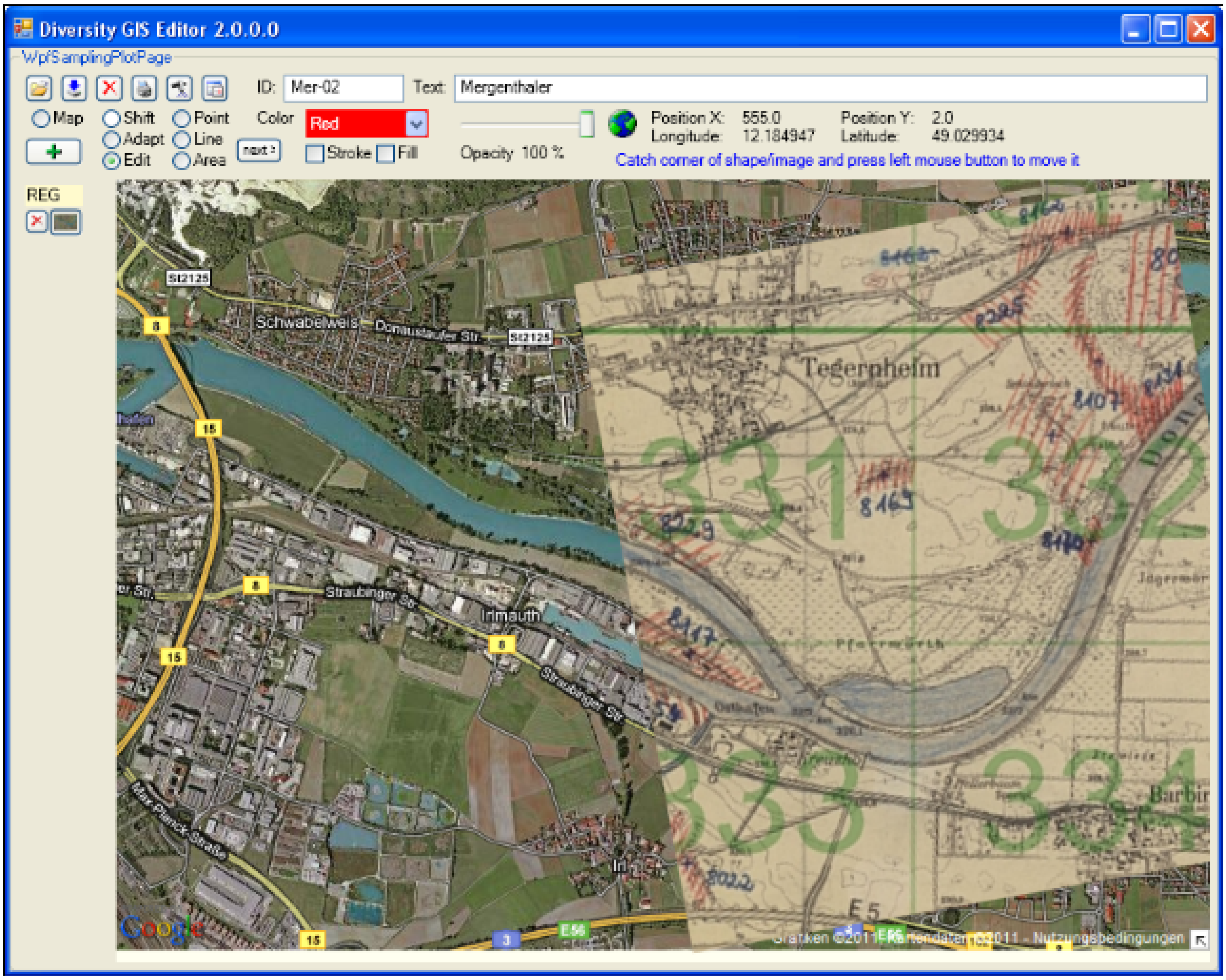
Opacity 100 %

Position X: 620.0
Longitude: 12.190525

Position Y: 11.0
Latitude: 49.029427

All points are set, change last position or click on other map to adapt

4. When all reference points have been set and the cursor touches the alternate map, it changes to the finished shape . The next click will place the new map into the appropriate background map area.



ID: Mer-02

Text: Mergenthaler

Color: Red

Opacity 100 %

Position X: 555.0 Position Y: 2.0

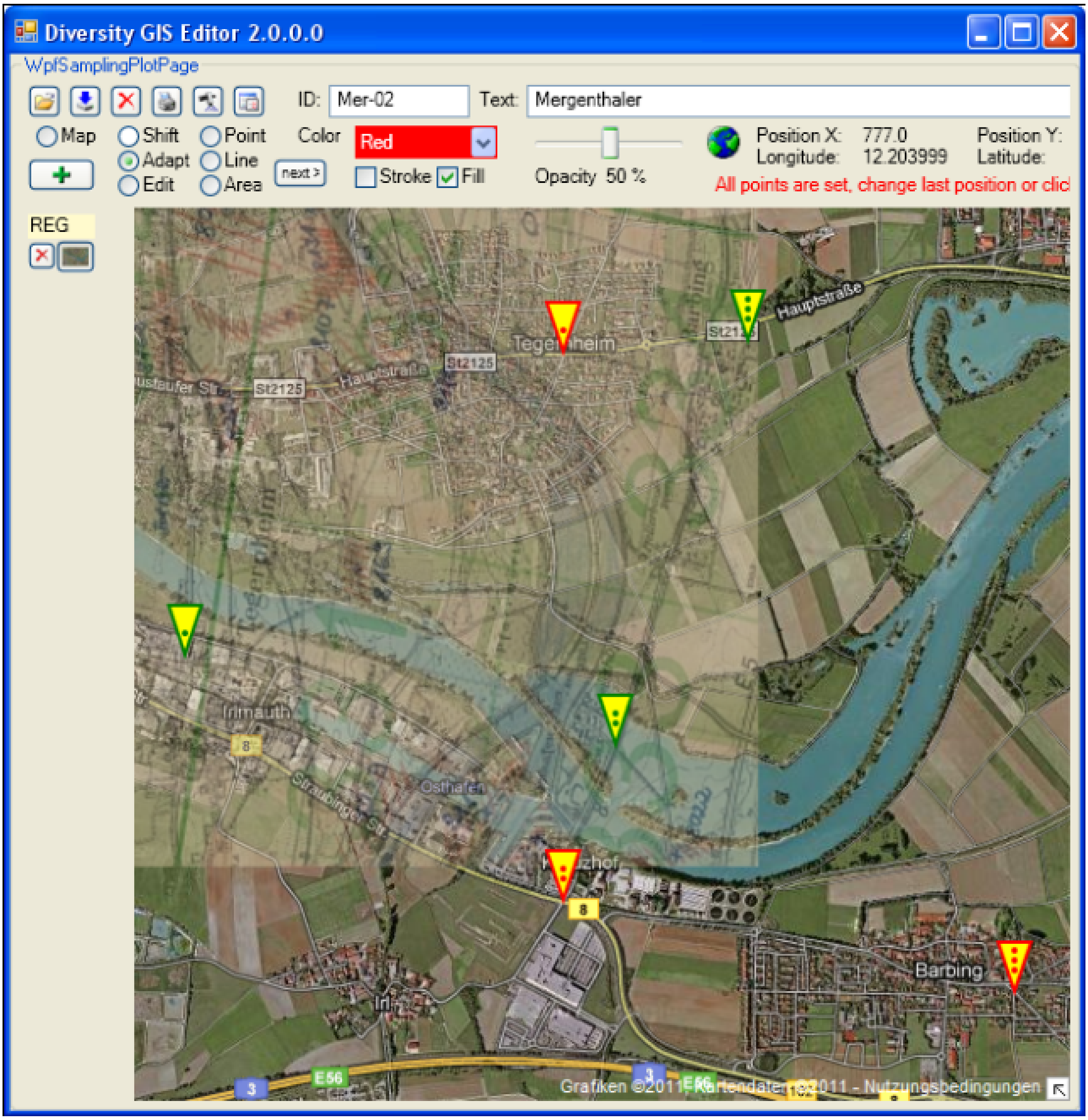
Longitude: 12.184947 Latitude: 49.029934

Catch corner of shape/image and press left mouse button to move it

The adapted image has been transformed to fit into the current world coordinates of the background map. Now the new map can be added to the sample list by pressing the Add button ✚. When it is finally saved to disk by pressing the Save button ⬇, the new assigned world coordinates will be saved, too, in an XML file with the same name (see Chapter 2.9: Save Samples).

Sometimes it is difficult to place the new map and the reference map side by side, because the window is too small, and zooming out would blur the details needed for setting the reference points. If the new map covers the background map, the reference points can be set anyway

- for the new map by making it opaque with the transparency slider
- for the background map by making the new map transparent (less than 10% opacity) with the slider



ID: Mer-02

Text: Mergenthaler

○ Map ○ Shift ○ Point

● Adapt ○ Line

○ Edit ○ Area

Color: Red

☐ Stroke ☑ Fill

Opacity 50 %

Position X: 777.0

Longitude: 12.203999

Position Y:

Latitude:

All points are set, change last position or clic

Note: The Fill box must be checked to change the transparency of the new map. The background map's transparency cannot be changed.

Chapter 2: GIS Editor Usage

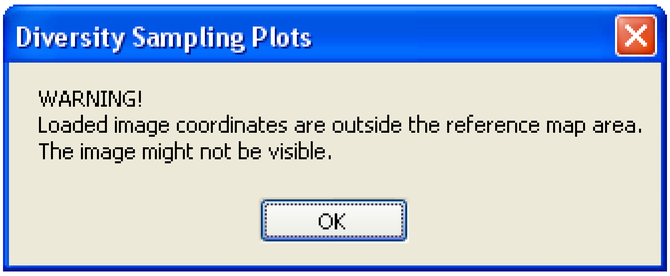
Chapter 2.8: Load Samples

A background map is required before objects (areas, line strings, points) can be loaded. When loading a shape file, the objects will be displayed at the background map according to their coordinates and added to the Sample List automatically. The GIS Editor is able to read MS-SQL Geo Object files (.shp1) as well as ArcView Shape Files (.shp), which are using geographical or Gauß-Krüger coordinates.

When loading an image without world coordinates, it will be displayed top left in the working area. If no background map is loaded yet, the Screen symbol 🖥 is shown in the status line, followed by the screen coordinates of the current cursor position.

When loading an image with world coordinates and no background reference map exists, it will be displayed top left in the working area. The World symbol 🌐 is shown in the status line, followed by the screen coordinates and the world coordinates of the current cursor position.

When loading an image with world coordinates having an existing reference map, it will be embedded in the background map according to its coordinates. If the new image does not overlap with the reference map, the image exists virtually in the coordinate system, but possibly could not be seen because it is too far away from the reference map. In this case a warning will be displayed:



WARNING!
Loaded image coordinates are outside the reference map area.
The image might not be visible.

When loading an image it is displayed, but not yet added to the Sample List. The user has to add it manually by pressing the Add button ✚. This is because the user should have the opportunity to adapt the image to the background map to be stored later on with applicable coordinates.

Chapter 2: GIS Editor Usage

Chapter 2.9: Save Samples

To save a background map which is currently displayed in Map mode just press the Save button ⬇instead of the Add button ✚. A save file dialog will pop up to name the file, the map and its coordinates will be saved and added to the sample list.

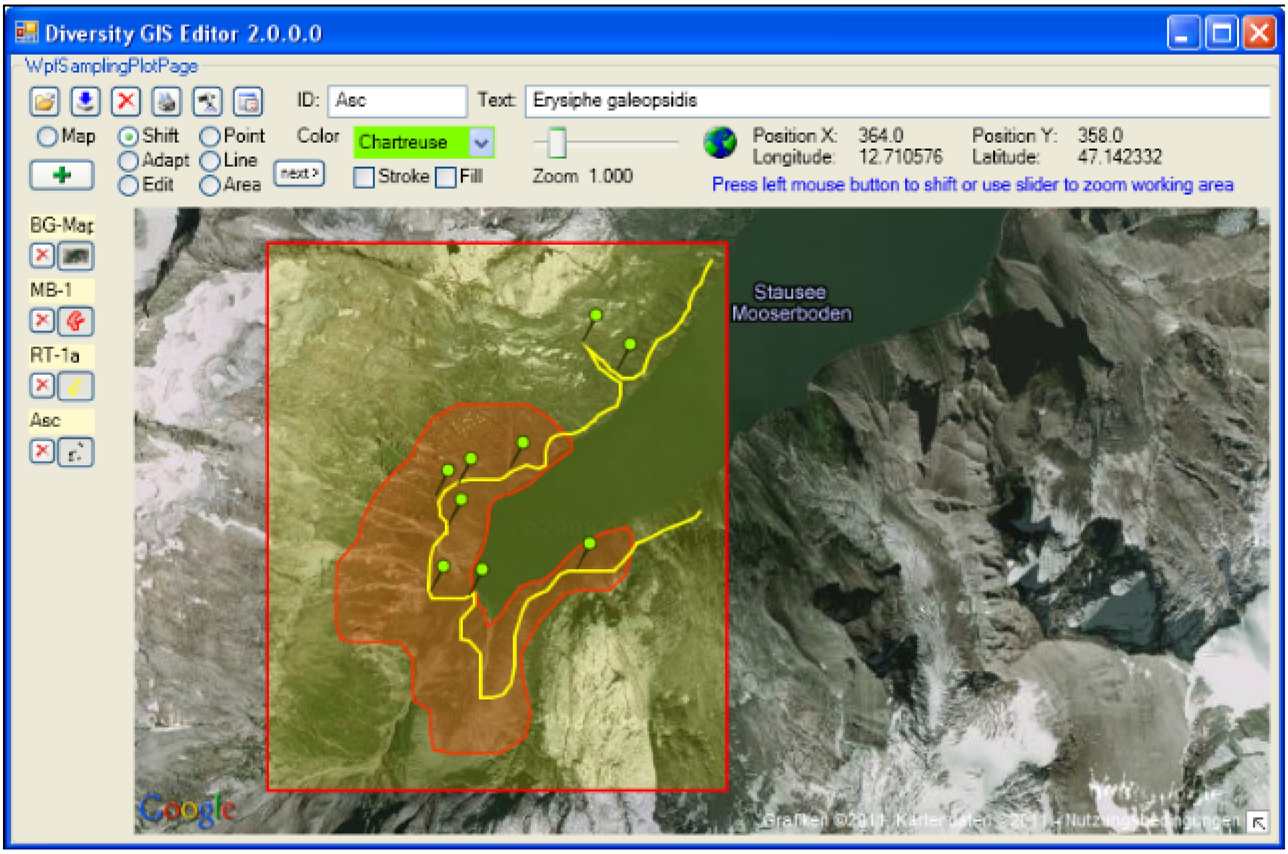
A background map is required before objects and images can be saved. Saving samples means saving their type, attributes and world coordinates in files. When pressing the Save button ⬇, it applies to all visible samples on the working area, except the background map. A current sample will be added to the sample list before it is saved.

If objects are visible, a save file dialog will open and a name for the target file(s) must be set. Objects (areas, line strings, points) will be saved in respect to the selected formats of the GIS-Editor Settings:

- If MS-SQL is enabled, all visible objects will be collected and stored in one GIS Editor shape file in ASCII text format (extension .shp1). The file contains the objects' attributes and MS-SQL Geo Object definition strings. If altitude calculation is enabled in the GIS-Editor Settings, these values are stored, too.
- If ArcView is enabled, for each object 3 ArcView compatible shape definition files in binary format will be created: A shape file, an index file and a dBase file holding the description (extensions .shp, .shx, .dbf).

If images are in the Sample List, they are already present on disk and will not be saved twice. Instead for each image an XML file will be created with the calculated world coordinates of the image and will be stored under the same location and name as the image. This does not apply to the current background map.

If Save Working Area is enabled in the GIS-Editor Settings, a scan of the complete working area including its objects is made and stored in an image file, which name has been set in the save file dialog.
To save only a part of the working area the Frame box must be checked in the GIS-Editor Settings, too. Then a rectangular frame of the given dimensions is displayed, which defines the part of the working area that will be saved. It can be dragged to the right position using the left mouse button (click, hold and shift), and it can be resized by grabbing and moving the corners of the frame.



ID: Asc
Text: Erysiphe galeopsidis
Color: Chartreuse
☐ Stroke ☐ Fill
Zoom 1.000
Position X: 364.0 Position Y: 358.0
Longitude: 12.710576 Latitude: 47.142332

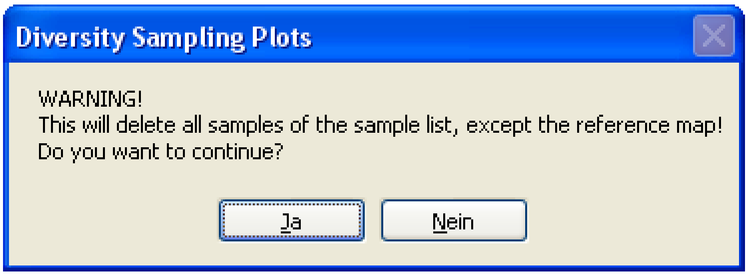
Press left mouse button to shift or use slider to zoom working area

Chapter 2: GIS Editor Usage

Chapter 2.10: Delete Samples

To delete a single object of the Sample List just press the small Delete button ✕ left of the Toggle button. The sample will be removed from the list and the working area, the other sample entries will be rearranged.

Pressing the large Delete button ✕ in the Control Panel will remove all samples of the Sample List, except the reference map. A warning is shown before:



WARNING!
This will delete all samples of the sample list, except the reference map!
Do you want to continue?

Chapter 2: GIS Editor Usage

Chapter 2.11: Print Samples

Pressing the Print button in the Control Panel will open a print dialog to select a printer and adjust the settings. Then it will print the complete working area including all visible objects. This feature is useful e.g. for documentations.

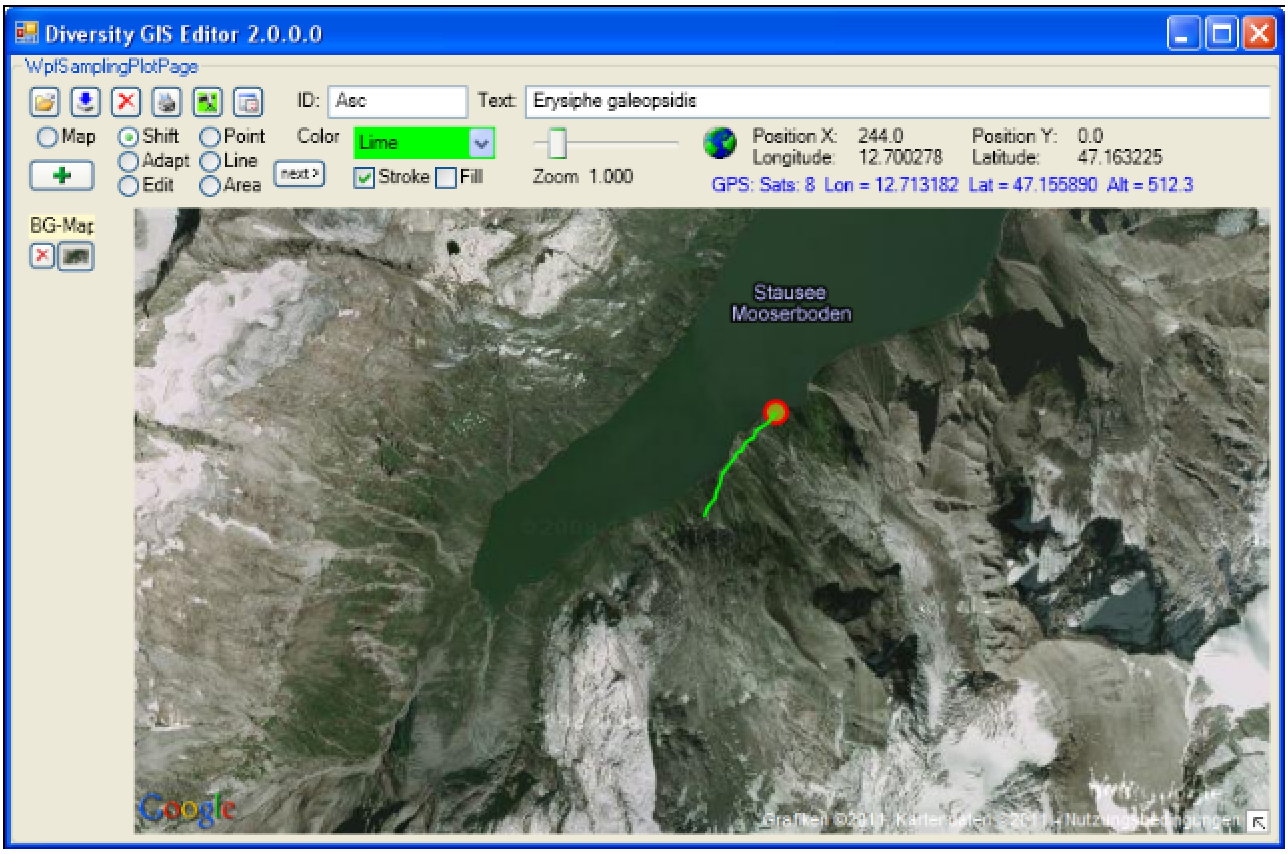
Chapter 2: GIS Editor Usage

Chapter 2.12: GPS Tracking

When pressing the GPS button in the Control Panel the hardware will be scanned for a GPS device. All available serial ports are opened and checked if they are delivering valid GPS data. This takes 2 seconds. Be sure that the correct baudrate for the GPS device has been set in the Settings menu (standard rate: 9600).

If no device is detected the button will be released. If a device has been found the button changes the color according to the numbers of satellites which have been fixed by the device: Red up to 3 satellites, yellow up to 5 and green if 6 satellites or more are available. The number of satellites, longitude, latitude and altitude delivered from the GPS device are displayed in the info line of the Control Panel beneath the status.

The current position will be shown by a GPS marker ○ if an appropriate background map has been loaded. If GPS Track in the Settings window is checked, the movement of the position will be drawn as a line string on the background map. The color and stroke thickness are similar to the last adjustment for lines. When switching off the GPS button again, the track will be added to the sample list automatically and could be saved for future documentation purposes.



Diversity GIS Editor 2.0.0.0

WpfSamplingPlotPage

ID: Asc

Text: Erysiphe galeopsidis

○ Map ● Shift ○ Point

○ Adapt ○ Line

○ Edit ○ Area

Color: Lime

☑ Stroke ☐ Fill

Zoom 1.000

Position X: 244.0 Position Y: 0.0

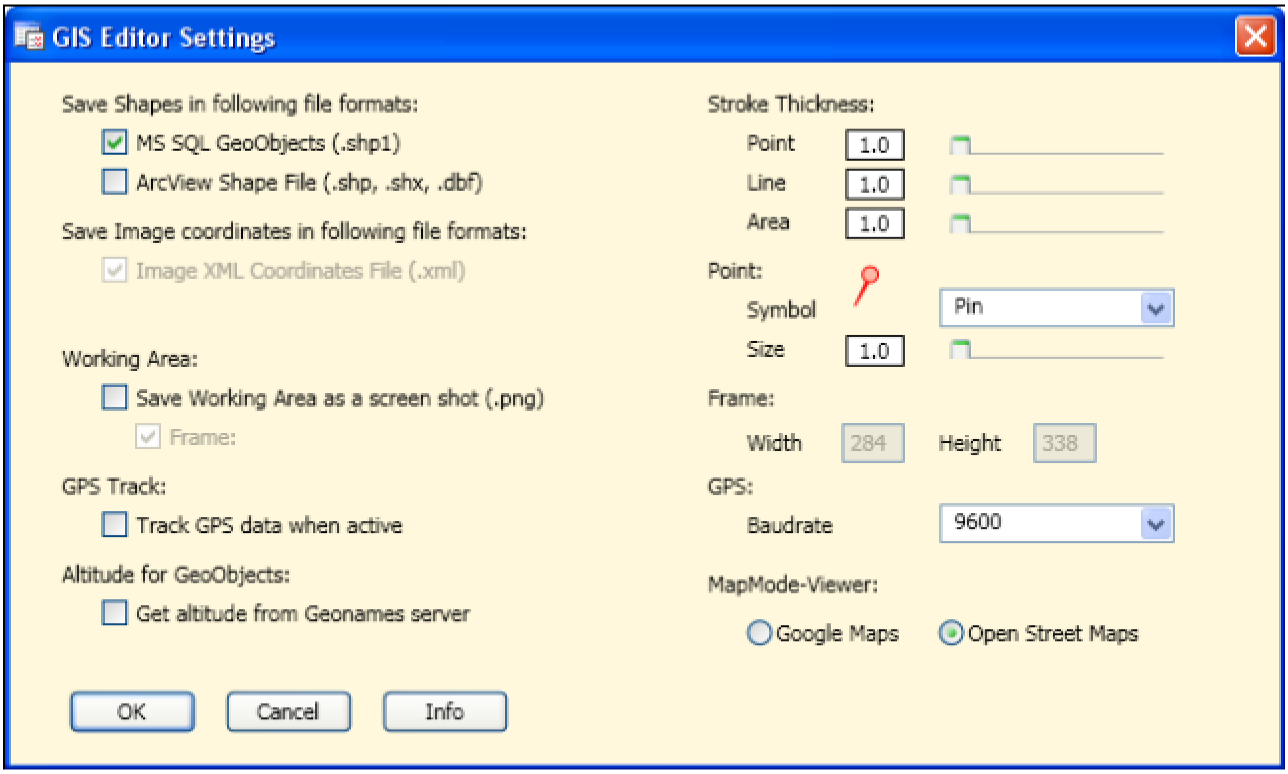
Longitude: 12.700278 Latitude: 47.163225

GPS: Sats: 8 Lon = 12.713182 Lat = 47.155890 Alt = 512.3

Chapter 2: GIS Editor Usage

Chapter 2.13: Settings

Pressing the Settings button in the Control Panel will open a dialog to adjust these GIS Editor settings which are not frequently changed:



GIS Editor Settings

Save Shapes in following file formats:
☑ MS SQL GeoObjects (.shp1)
☐ ArcView Shape File (.shp, .shx, .dbf)

Save Image coordinates in following file formats:
☑ Image XML Coordinates File (.xml)

Working Area:
☐ Save Working Area as a screen shot (.png)
☑ Frame:

GPS Track:
☐ Track GPS data when active

Altitude for GeoObjects:
☐ Get altitude from Geonames server

Stroke Thickness:
Point 1.0
Line 1.0
Area 1.0

Point:
Symbol Pin
Size 1.0

Frame:
Width 284 Height 338

GPS:
Baudrate 9600

MapMode-Viewer:
○ Google Maps ● Open Street Maps

Setting the file formats for saving objects

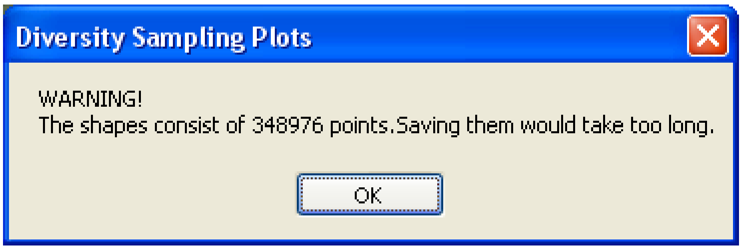
At the moment 2 formats for object files are supported:

- MS-SQL Geo Objects (.shp1)
- ArcView shape files (.shp, .shx, .dbf)

Microsoft SQL Geo Objects are part of a standard for storing geometry and geography data in an SQL database, as used by the Diversity modules. They are more or less a well defined text string containing the geometrical type (e.g. Polygon, Line, Point) and the geographical coordinates (longitude, latitude, optional altitude) of an object.
Together with the GIS Editor attributes (e.g. color, transparency) they are stored in a proprietary GIS Editor shape file in ASCII text format. This file can easily be read and changed using a text editor.

ArcView is a common Desktop GIS tool and saves its data in binary files. The GIS Editor can create ArcView compatible files to store the samples, which then may be read from ArcView GIS tools. 3 files are required for each type of shape: A data file with extension ".shp", an index file with extension ".shx" and a description file in dBase format with extension ".dbf".

The advantage of the first format is the transparency and readability of the data file, which is just one single text file. But storing huge samples is very time consuming. If the samples consist of more than 10,000 points, an error message is displayed and they are not saved in this format:



Diversity Sampling Plots

WARNING!
The shapes consist of 348976 points.Saving them would take too long.

Using the ArcView format makes the data files compatible with many applications. Huge samples can be stored much faster. But each type of sample requires a separate set of output files, because different types of objects within one file are not supported so far. So a sample list containing 10 objects will produce 30 data files (file name with an appended index, which is incremented for each sample). Furthermore the attributes like color, transparency and stroke thickness will not be saved.

Currently there is just one format supported for storing image coordinates. They are written into an XML file which is also used in DiversityMobile modules. Saving the coordinates in this format is required for the GIS Editor, so it cannot be disabled.

Saving the working area

Selecting this box and later on pressing the Save button will additionally scan the working area including all visible objects and save it as an image file under the name provided in the save file dialog, see Save Samples. This is useful for documentations.
Note: There are copyright restrictions on maps or aerial images which are created with the Google maps viewer. Please contact Google before using them for publications to grant a license, or use Open Street Maps captures, which could be used freely under the Creative Commons Attribution Share Alike license conditions.

When checking the "Frame" box just a rectangular part of the working area is saved. The pixel size of the frame has to be defined in the adjacent "Width" and "Height" fields. This is convenient if the resulting image should have well defined dimensions, e.g. fit the resolution of a smartphone display. This feature is only active when the Save Working Area box is checked. After closing the Settings window a rectangular frame of these dimensions is displayed on the working area which defines the part to be saved.

GPS Track

When checking this box the movement of the GPS marker on the background map will be tracked by a line string. After switching off the GPS button the line string will be added to the sample list automatically.

Altitude for geo objects

This box applies to MS-SQL Geo Objects only. If checked, the appropriate altitude of the object points (longitude, latitude) will be stored in the file, too. This is not recommended for sample objects with a lot of points or vertices, because for every point the Geonames server has to be contacted to request the associated altitude value. This could slow down the saving procedure immensely.

Setting the stroke thickness

The stroke thickness for area, line strings and point symbols can be set by using the appropriate slider. The value of the thickness is shown in the label box left of the slider. Double clicking the slider will reset the thickness to its default value 1.

Setting the Point symbol

The symbol for the points can be selected from the drop down menu. The symbol size can be set using the slider below the menu. The point symbol display will change accordingly.

Setting the GPS baudrate

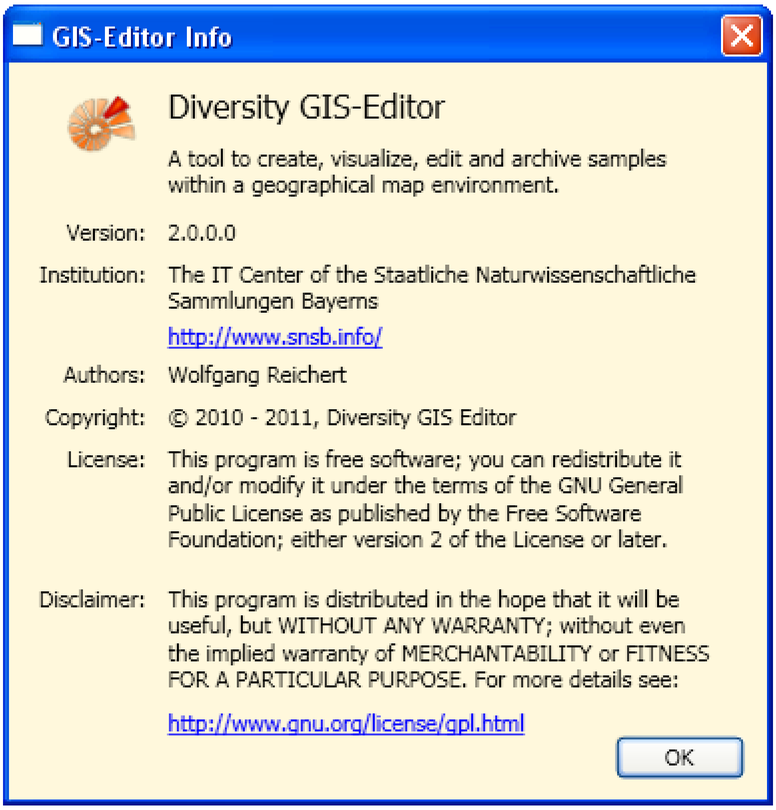
It is essential to set a suitable baudrate for a connected GPS device according to its specification. The rate can be selected from the list of the drop down menu. If no GPS device is available, Demo mode could be chosen to see the behaviour of the functionality.

Setting the Map Mode viewer

The radio buttons offer the choice of the viewer for creating a background map. Currently Google Maps and Open Street Maps are provided.

GIS Editor Info

Clicking the Info button will display a window containing GIS Editor version and license information.



Diversity GIS-Editor

A tool to create, visualize, edit and archive samples within a geographical map environment.

Version: 2.0.0.0

Institution: The IT Center of the Staatliche Naturwissenschaftliche Sammlungen Bayerns

http://www.snsb.info/

Authors: Wolfgang Reichert

Copyright: © 2010 - 2011, Diversity GIS Editor

License: This program is free software; you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation; either version 2 of the License or later.

Disclaimer: This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. For more details see:

http://www.gnu.org/license/gpl.html

Saving the settings

Finally pressing the OK Button will save the settings, pressing the Cancel button will discard them.

Access to the data

To get access to the data, you have to fulfil several requirements. In DiversityCollection, you must be a member of one of the user groups. You can only access data, which is listed in the projects you have access to. For external users data may be blocked by entries in the data witholding reasons or due to a data embargo.

Availability of data sets

The data of certain parts of the database can be blocked for remote access. If you want to prevent access for the whole dataset, enter your reason in the field **Withholding reason** in the header (see below).

Acc.No. M-0040397

Erysiphe aquilegiae var. ranunculi (Grev.) U. Braun

ID (Specimen / Event) 135548 / 211558

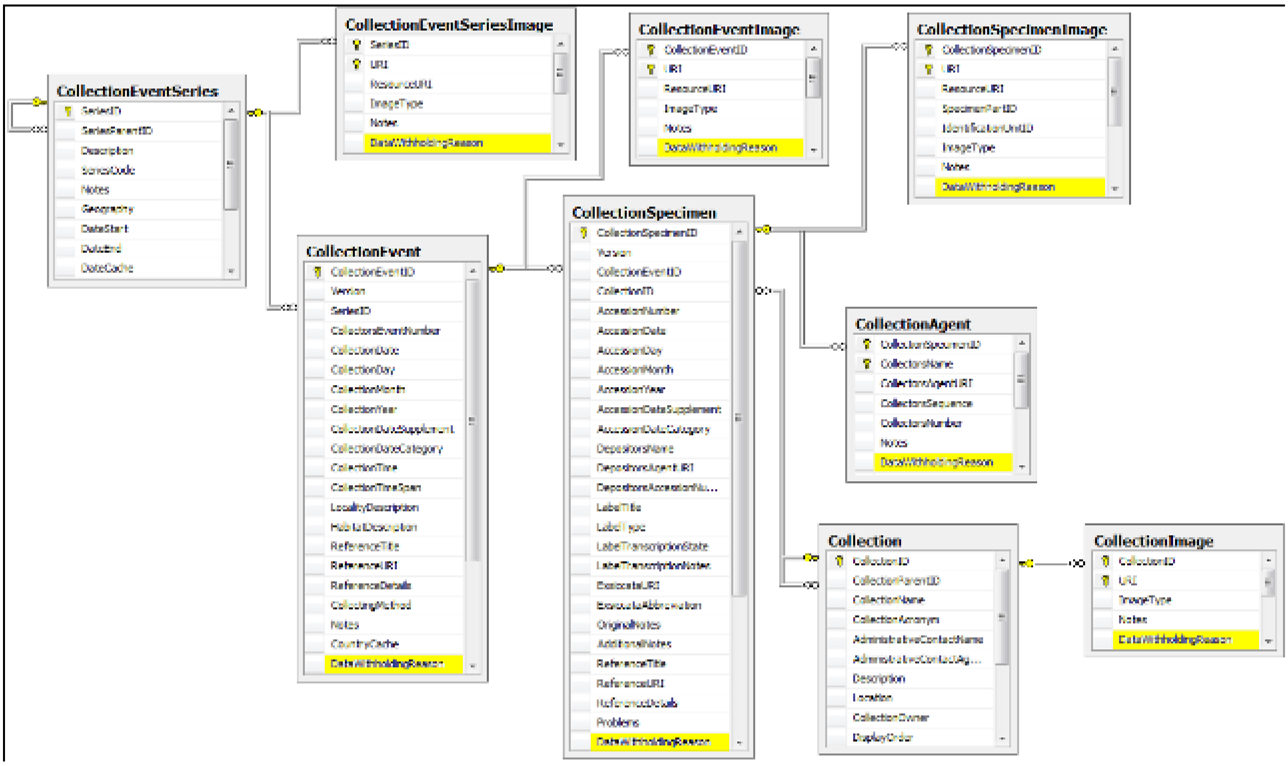
Version 3 / 1

Withhold. reason

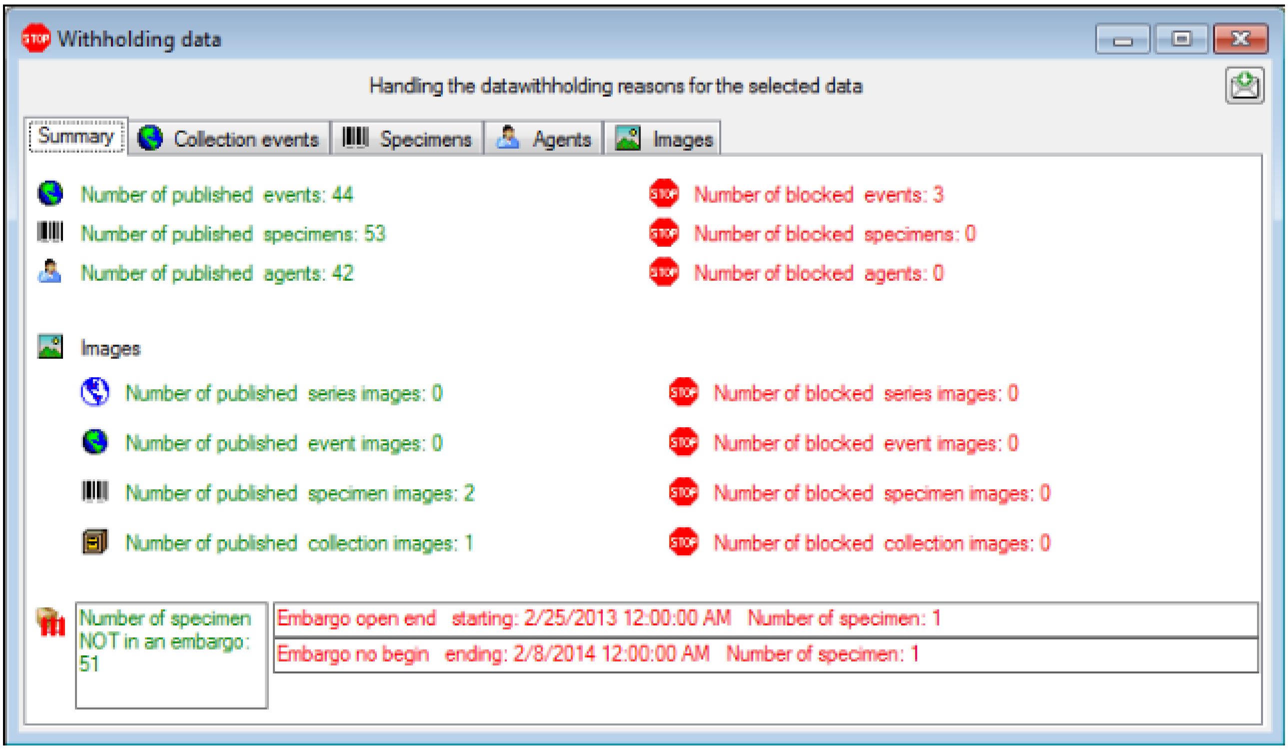
If you want to block only the access to the data of the collection event or the collector, choose them in the tree and enter your reason for withholding the data in the corresponding fields. The data will only be published, if these fields are empty.

Withhold.R.:

Within the database a user has only access to the data of those projects for which he has permission. If a data set belongs to a certain project, it is stored in the table CollectionProject. To prevent publication of the data it can be blocked for the whole data set (table CollectionSpecimen), for the locality and collection site information (table CollectionEvent) and for the collectors (table CollectionAgent) - see overview below - and for all image tables: CollectionSpecimenIma ge, CollectionSpecimenPart , CollectionEventImage , CollectionEventSer iesImage and CollectionImage.



To edit the withholding reasons for all specimen selected in the main window choose **Data - Export - Withhold data...** from the menu. A window will open as shown below, giving a summary of all withholding reasons set for the selected specimen and related data.



Number of published events: 44
Number of published specimens: 53
Number of published agents: 42

Number of blocked events: 3
Number of blocked specimens: 0
Number of blocked agents: 0

Images

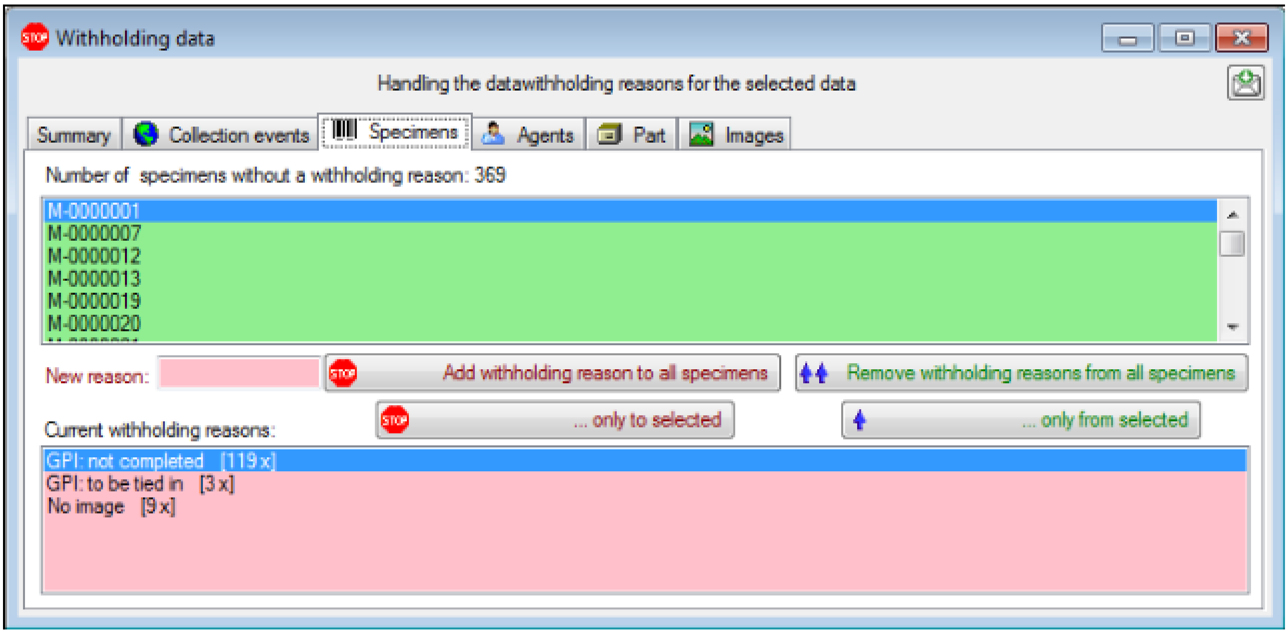
Number of published series images: 0
Number of published event images: 0
Number of published specimen images: 2
Number of published collection images: 1

Number of blocked series images: 0
Number of blocked event images: 0
Number of blocked specimen images: 0
Number of blocked collection images: 0

Number of specimen NOT in an embargo: 51

Embargo open end starting: 2/25/2013 12:00:00 AM Number of specimen: 1
Embargo no begin ending: 2/8/2014 12:00:00 AM Number of specimen: 1

To edit the withholding reasons for certain entries choose the corresponding page where the details are listed as shown below.



Number of specimens without a withholding reason: 369

M-0000001
M-0000007
M-0000012
M-0000013
M-0000019
M-0000020

GPI: not completed [119 x]
GPI: to be tied in [3 x]
No image [9 x]

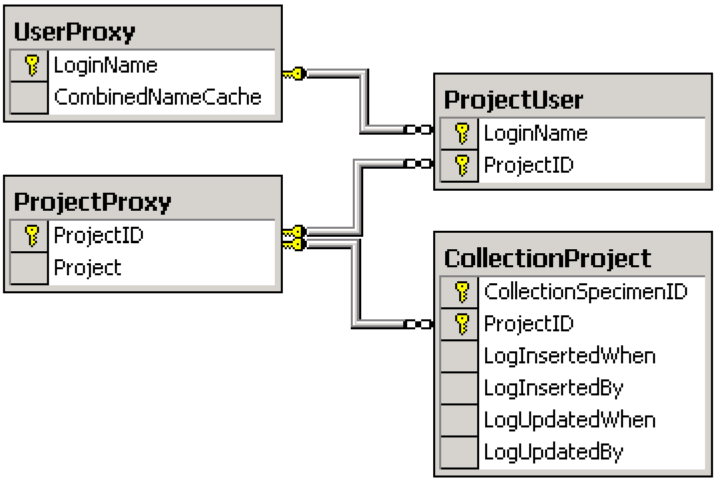
To block all data enter a new reason for withholding the data and click on the **Add withholding reason to all ...** button or the **... only to selected** button, if only the selected entries should be blocked. To remove the withholding reason from all data sets click on the **Remove withholding reasons for all ...** button or the **... only from selected** button, if only the selected entry should be published.

Data embargo

To mark data to be not published for a certain period you can define a data embargo and include the data in this data embargo.

Permissions for projects

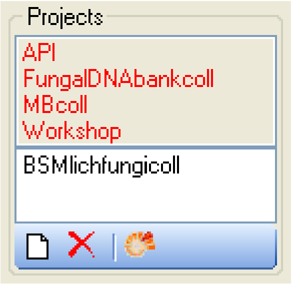
The user's access to the data within the database is stored in the tables shown below. The tables UserProxy and ProjectProxy are related to the Diversity Workbench modules DiversityUsers and DiversityProjects respectively. See User administration for further details.



Projects

Every CollectionSpecimen may be assigned to any number of projects. To assign a specimen to a project click on the 🗋 button. To remove it from a project select the project from the list and click on the ✕ button.

If there are projects, to which you have no access to, these will be listed in a separate list at the top as shown below.

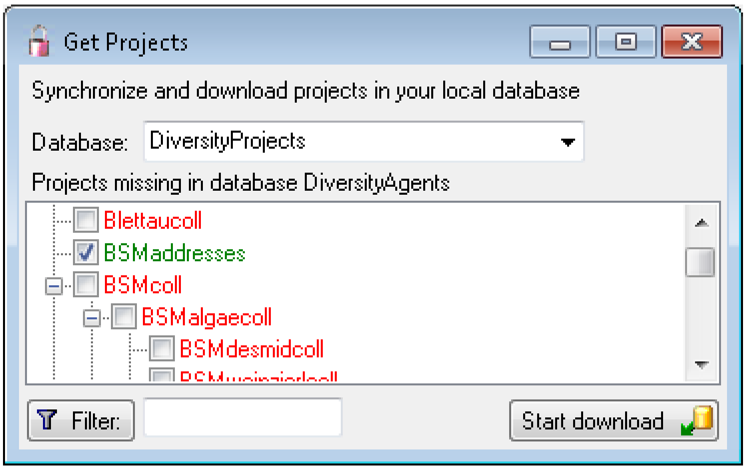


To transfer all selected specimen into an additional project choose **Data -> ➡ Transfer -> 🔒 To project...** from the menu. A window will open where you can select the project to which the specimen should be added.

To remove all selected specimen from an additional project choose **Data -> ✕ Remove from project...** from the menu. A window will open where you can select the project from which the specimen should be removed. The last project in which a specimen is placed can not be removed.

The data is stored in the table CollectionProject.

Details of the projects within the DiversityWorkbench are stored in the database DiversityProjects. To access further information on a project click on the button. To edit details in projects you require the application **DiversityProjects.exe** in your application directory and access to the database DiversityProjects. To synchronize the projects listed in DiversityProjects you may use the synchronize function in the user administration window as shown below. If DiversityProjects is not available, you may create a new project by clicking the 🔒 button. If DiversityProjects is available, use the synchronize function Synchronize with DiversityProjects .



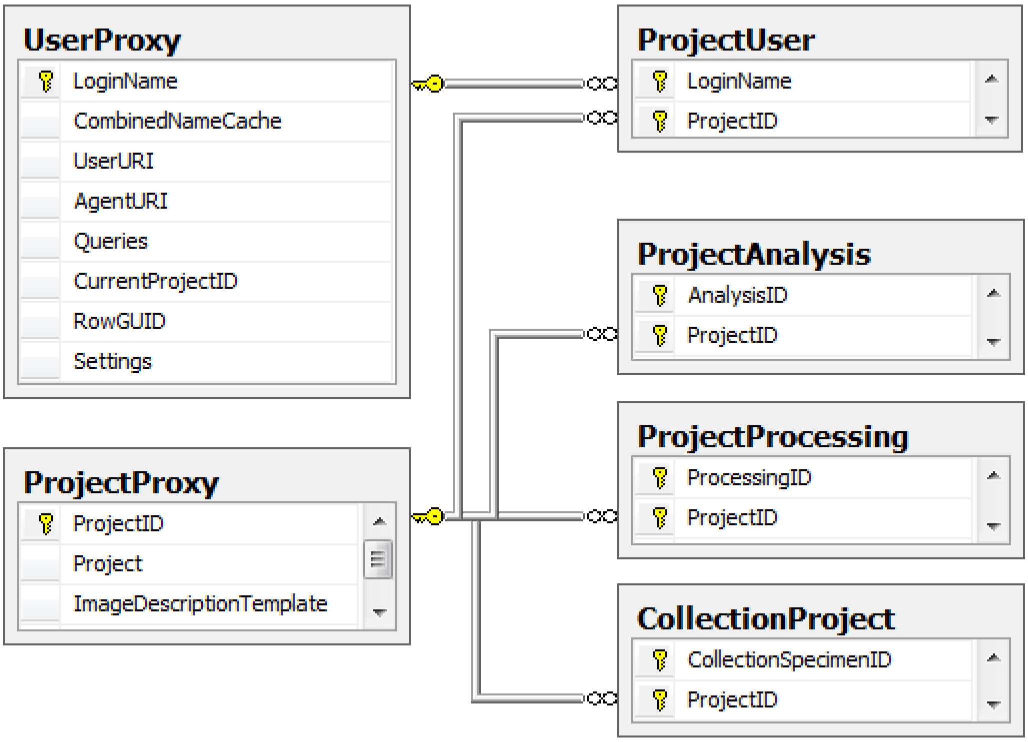
Synchronize and download projects in your local database

Database: DiversityProjects

Projects missing in database DiversityAgents

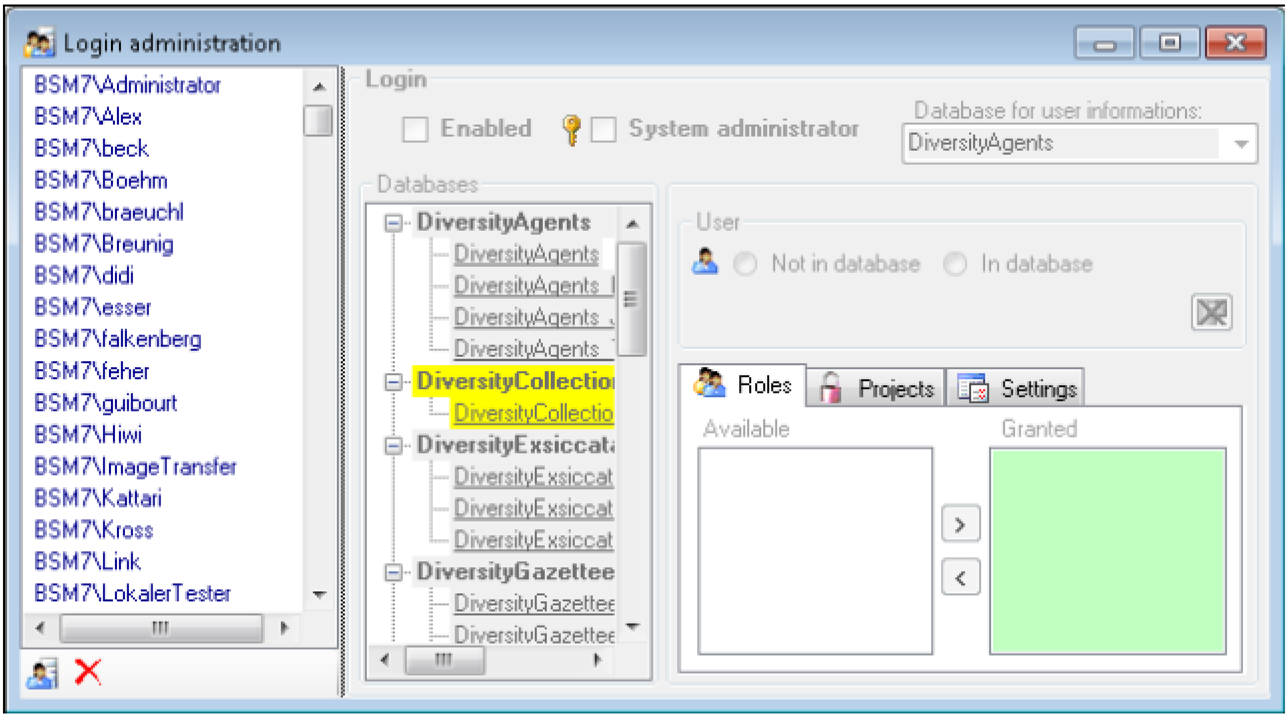
☐ Blettaucoll
☑ BSMaddresses
☐ BSMcoll
☐ BSMalgaecoll
☐ BSMdesmidcoll

The ER-chart below shows all tables with direct relations to the project tables. For more details see the sections Analysis, Processing and Image description.



Login administration

To administrate the logins on the database server, their permissions and roles respectively as well as access to projects choose **Administration** - **Logins** ... from the menu. A window will open as shown below.



BSM7\Administrator
BSM7\Alex
BSM7\beck
BSM7\Boehm
BSM7\braeuchl
BSM7\Breunig
BSM7\didi
BSM7\esser
BSM7\falkenberg
BSM7\feher
BSM7\guibourt
BSM7\Hiwi
BSM7\ImageTransfer
BSM7\Kattari
BSM7\Kross
BSM7\Link
BSM7\LokalerTester

☐ Enabled ☐ System administrator

Database for user informations: DiversityAgents

DiversityAgents
- DiversityAgents
- DiversityAgents_l
- DiversityAgents_
- DiversityAgents_

DiversityCollection
- DiversityCollectio

DiversityExsiccata
- DiversityExsiccat
- DiversityExsiccat
- DiversityExsiccat

DiversityGazettee
- DiversityGazettee
- DiversityGazettee

○ Not in database ○ In database

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.

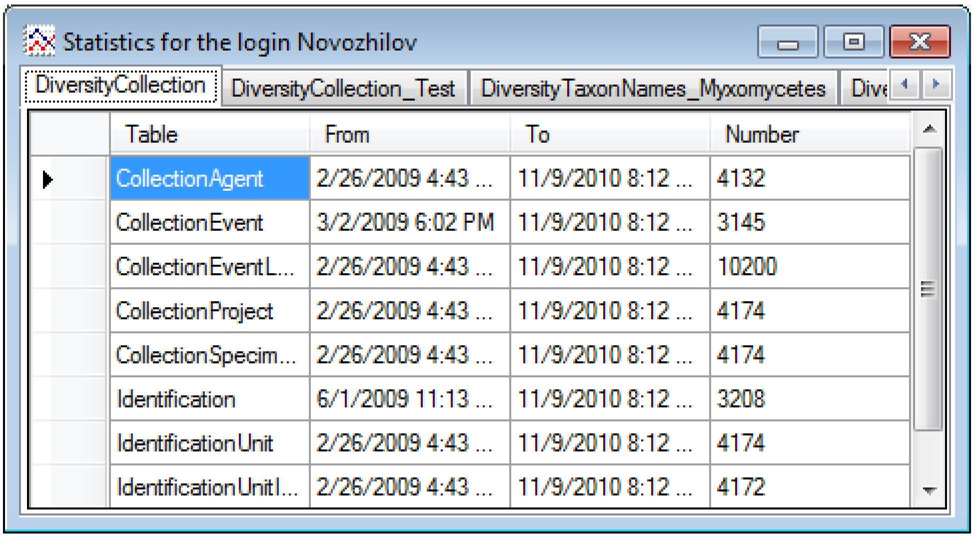
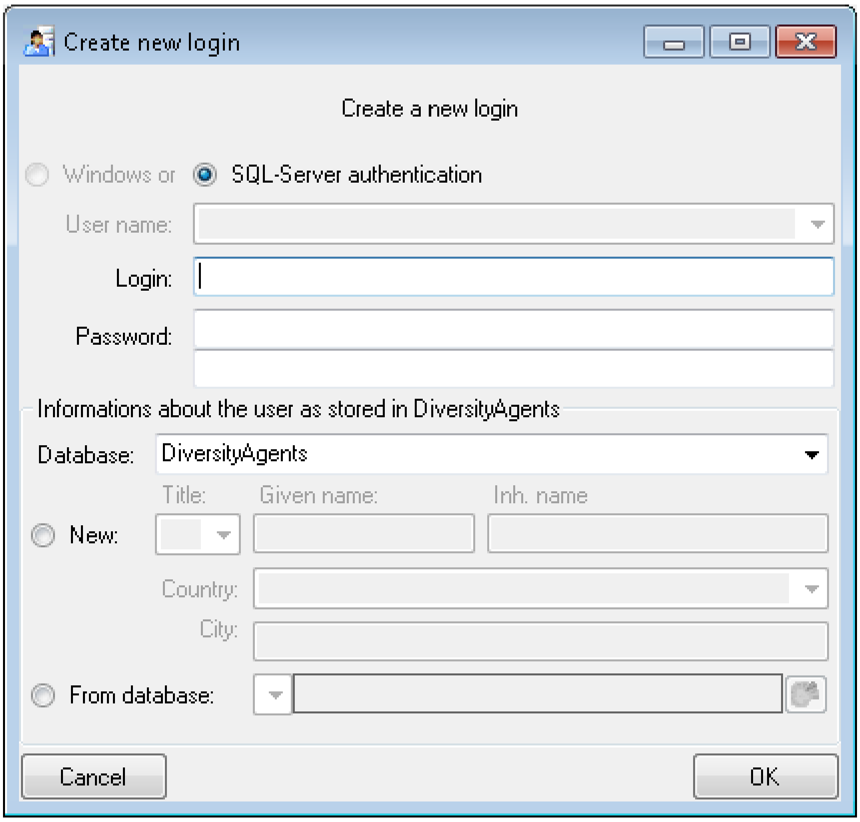


Table	From	To	Number
CollectionAgent	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4132
CollectionEvent	3/2/2009 6:02 PM	11/9/2010 8:12 ...	3145
CollectionEventL...	2/26/2009 4:43 ...	11/9/2010 8:12 ...	10200
CollectionProject	2/26/2009 4:43 ...	11/9/2010 8:12 ...	4174
CollectionSpecim...	2/26/2009 4:43 ...	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 create a new login click on the button. A window will open as shown below.



Create new login

Create a new login

○ Windows or ● SQL-Server authentication

User name:

Login:

Password:

Informations about the user as stored in DiversityAgents

Database: DiversityAgents

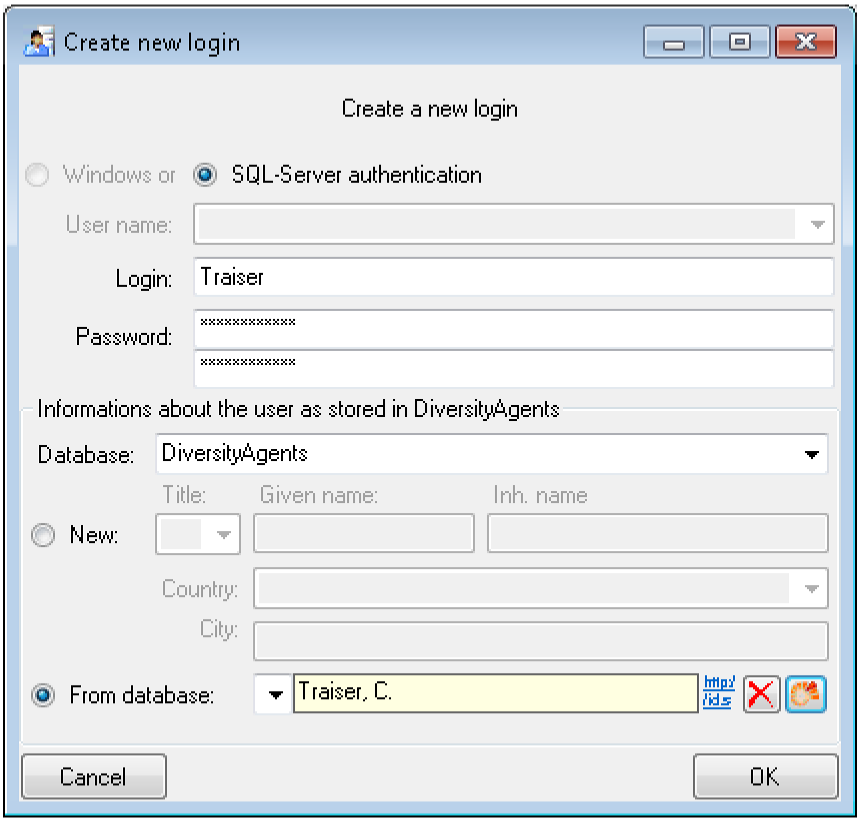
○ New: Title: Given name: Inh. name

Country:

City:

○ From database:

Here you can enter the name of the new login, the password and the information about the user which will be stored in a DiversityAgents database. You may 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).



Create new login

Create a new login

○ Windows or ● SQL-Server authentication

User name:

Login: Traiser

Password: ************
****

Informations about the user as stored in DiversityAgents

Database: DiversityAgents

○ New: Title: Given name: Inh. name

Country:

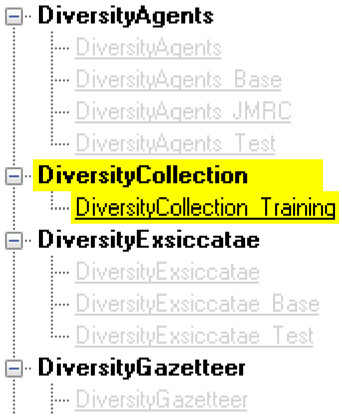
City:

● From database: Traiser, C.

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 (see below).


☐ **Enabled**

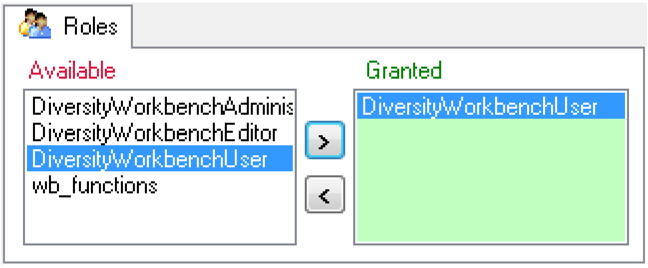
All databases on the server will be listed with the current database showing a yellow background. The databases where the login has no access will be listed in gray while the databases accessible for a login are black.


- **DiversityAgents**
  - DiversityAgents
  - DiversityAgents_Base
  - DiversityAgents_JMRC
  - DiversityAgents_Test
- **DiversityCollection**
  - DiversityCollection_Training
- **DiversityExsiccatae**
  - DiversityExsiccatae
  - DiversityExsiccatae_Base
  - DiversityExsiccatae_Test
- **DiversityGazetteer**
  - DiversityGazetteer

To allow the access to a database select the database from the list and choose database as shown below.


● Not in database ○ In database

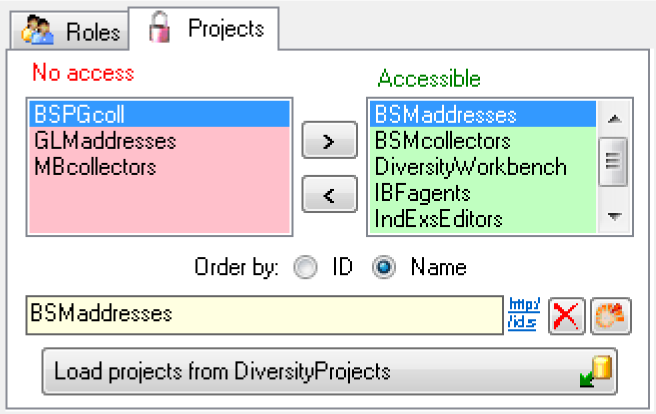
Use the **>** and **<** buttons to add or remove roles for the login in the database (see below).



Available
- DiversityWorkbenchAdminis
- DiversityWorkbenchEditor
- DiversityWorkbenchUser
- wb_functions

Granted
- DiversityWorkbenchUser

Depending on the database you can edit the list of projects accessible for a login (see below). Projects are related to the module DiversityProjects. To get additional information about a project select it in the the list and click on the button.



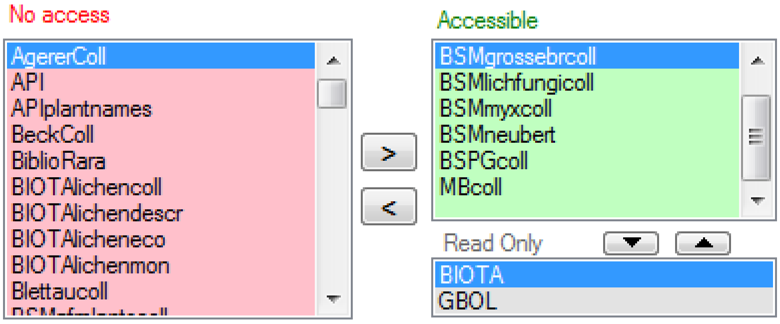
No access
- BSPGcoll
- GLMaddresses
- MBcollectors

Accessible
- BSMaddresses
- BSMcollectors
- DiversityWorkbench
- IBFagents
- IndExsEditors

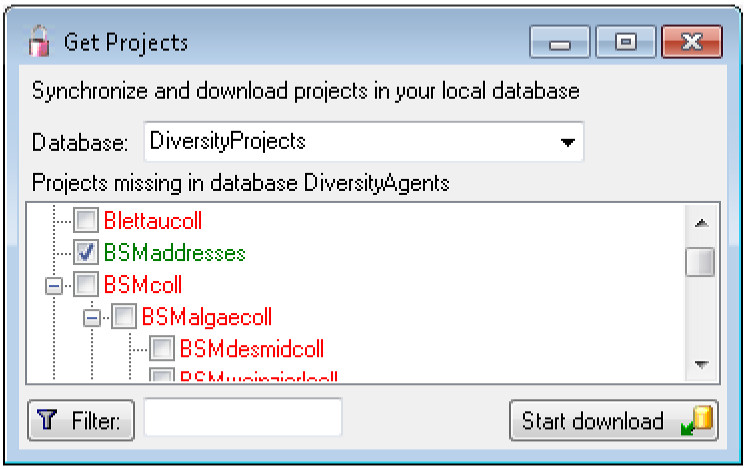
Order by: ○ ID ● Name

BSMaddresses

Starting with database version 02.05.35 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**.



To load additional projects click on the **Load projects** button. A window will open as shown below. 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.

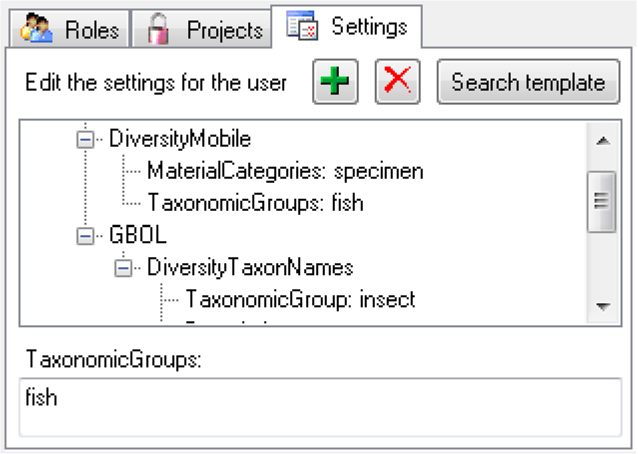


Synchronize and download projects in your local database

Database: DiversityProjects

Projects missing in database DiversityAgents

Depending on the database you can edit the settings of a login as shown below.



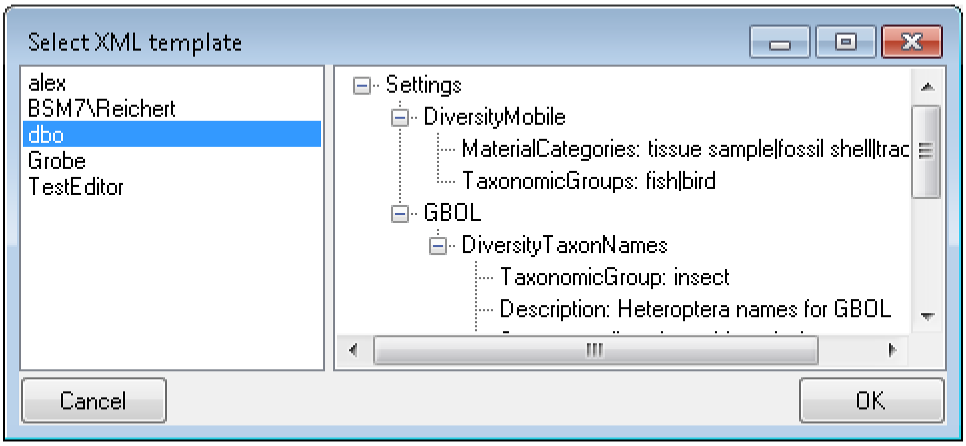
Edit the settings for the user

DiversityMobile
MaterialCategories: specimen
TaxonomicGroups: fish
GBOL
DiversityTaxonNames
TaxonomicGroup: insect

TaxonomicGroups:

fish

If you wish to use settings already defined for another login, click on the Search template button. A window (see below) will open where you can choose among the settings defined for logins in the database.



alex
BSM7\Reichert
dbo
Grobe
TestEditor

- Settings
  - DiversityMobile
    - MaterialCategories: tissue sample|fossil shell|trac
    - TaxonomicGroups: fish|bird
  - GBOL
    - DiversityTaxonNames
      - TaxonomicGroup: insect
      - Description: Heteroptera names for GBOL

Security

A user may be in 8 groups with diverse rights in the database. Here certain higher groups have all rights of lower groups in addition to special rights for the higher group, e.g. the group User may only read data of certain tables while Typist has the rights of User and additionally may edit the data in certain tables - see overview below.

Summarized overview of the group permissions

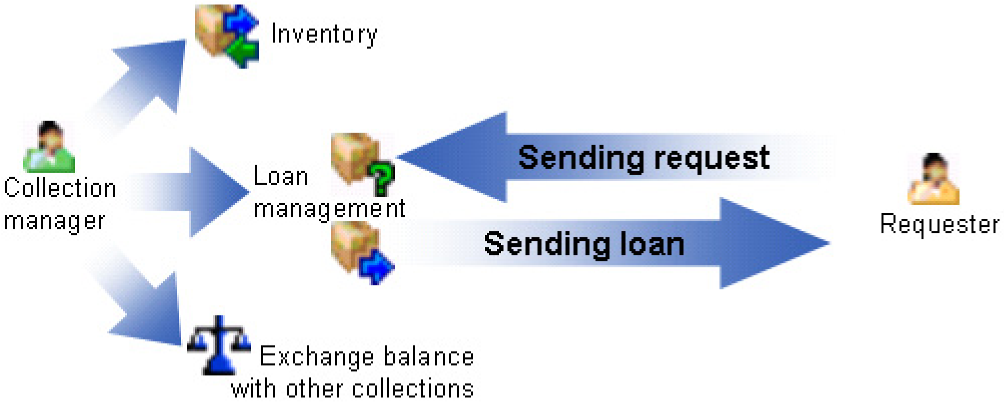
Role	**Permissions in addition to lower role and user group respectively**	**Included rights**
Administrator	Delete data, edit user permissions	DataManager
CollectionManager	Administration of collections, handling loans etc.	StorageManager
DataManager	Delete data, edit image descripton templates	Editor
Editor	Create new entries and delete details (not entire data sets)	Typist
Requester	Has the right to place requests for specimen	
StorageManager	Administration of stored parts, handling loans etc.	User
Typist	Edit data	User
User	See the data of the data tables, add annotations	

If you are an Administrator you may add a user to one of these groups.

Any user may have access to several projects.

Collection management

Collections are managed by collection managers (see **Administration -> Transaction management -> Collection managers ...** in the menu), who organize the transfer of specimen between collections and track the exchange balances. Any transfer of specimen is organized via transactions (see **Administration -> Transaction management -> Transaction ...** in the menu). To be able to place a request for specimen from a collection you must be in the group of requesters (see **Administration -> Transaction management -> Loan requesters ...** in the menu) for the requested collection and a collection manager for the requesting collection. An overview is given in the image below.

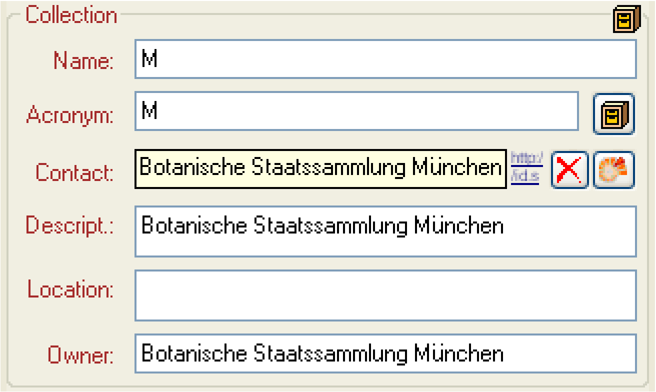


Collection

The organisms in a specimen can be stored in several collections. To see the place where a specimen or parts of it are stored use the lower tree and click on the icon to select the display according to the collections as shown below.

Botanische Staatssammlung München (M)
M-Fungi
Trichia persimilis P.Karst.
Trichia persimilis P.Karst.
Trichia persimilis P.Karst.
Trichia persimilis P.Karst.

In the tree shown above select the collection to display the data fields as shown below.



Collection
Name: M
Acronym: M
Contact: Botanische Staatssammlung München
Descript.: Botanische Staatssammlung München
Location:
Owner: Botanische Staatssammlung München

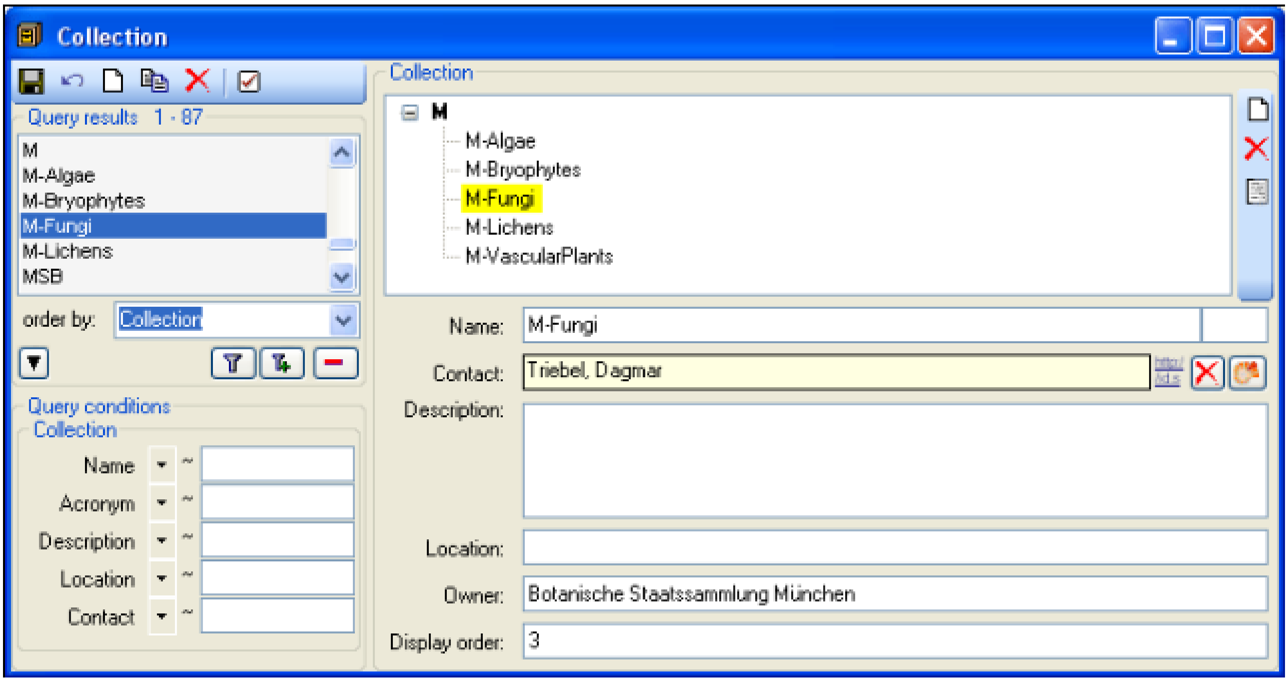
To be able to edit the details of a collection, you must be a collection manager of said collection. The restrictions for the access for editing the collections are defined in the CollectionManager section.

At the base of the fields you find the default collection, used for the creation of new specimen parts. Specimen parts that are not created as a part of another part will be placed in this collection. Use the button to edit this entry.

Default collection for new specimen parts
M - M-Algae - Diatom collection of F.J.Weinzierl - Dried vouchers - Box 2

Administration of the collections

If you need further information about a collection click on the button or choose **Administration - Collections...** from the menu to open the window for the collection administration (this menu entry is only available for collection managers). This will open a window (see below) where you can edit the collections used in your database for which you are a collection manager.



order by: Collection

Name: M-Fungi

Contact: Triebel, Dagmar

Description:

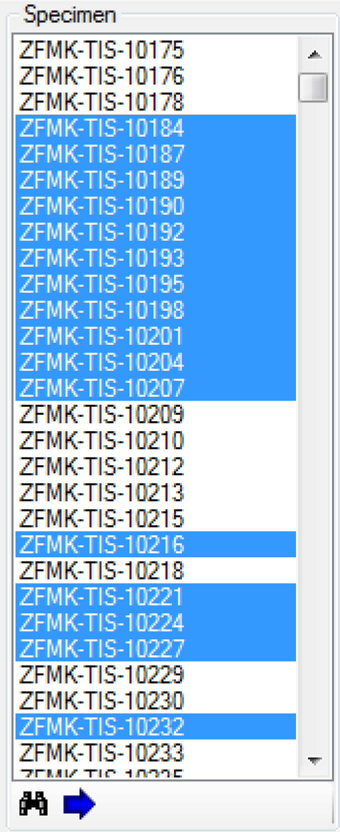
Location:

Owner: Botanische Staatssammlung München

Display order: 3

Specimen placed in the collections

The specimens stored in a selected collection are listed in the specimen list. You can hide / show this list using the ☒ / ☰ button. The specimen list will appear as shown below. Click on the collection in the tree view to fill the list and see the specimen that contain parts which are placed in the current collection. To transfer the parts of certain specimen from the current collection to another collection, choose them in the list and click on the ➡button. To change to a specimen from this list click on the 🔍button.



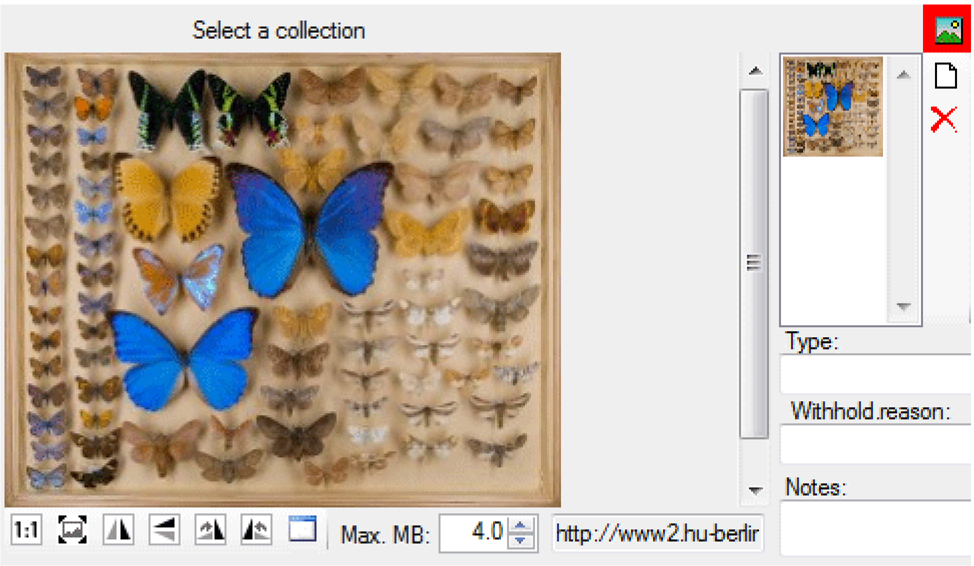
ZFMK-TIS-10175
ZFMK-TIS-10176
ZFMK-TIS-10178
ZFMK-TIS-10184
ZFMK-TIS-10187
ZFMK-TIS-10189
ZFMK-TIS-10190
ZFMK-TIS-10192
ZFMK-TIS-10193
ZFMK-TIS-10195
ZFMK-TIS-10198
ZFMK-TIS-10201
ZFMK-TIS-10204
ZFMK-TIS-10207
ZFMK-TIS-10209
ZFMK-TIS-10210
ZFMK-TIS-10212
ZFMK-TIS-10213
ZFMK-TIS-10215
ZFMK-TIS-10216
ZFMK-TIS-10218
ZFMK-TIS-10221
ZFMK-TIS-10224
ZFMK-TIS-10227
ZFMK-TIS-10229
ZFMK-TIS-10230
ZFMK-TIS-10232
ZFMK-TIS-10233

Creating new collections

To create a new collection use the button either above the Query results or the botton right of the hierarchy, where the new collection will be placed underneath the collection selected in the hierarchy. To copy a collection either use the button or the button. The latter will copy the collection including all child collections. To set the superior collection, use the button.

Images

To show the images related to a collection, click on the button. This will open the area for the images as shown below. Use the and buttons to add or delete images of your collection. For further details about handling images see chapter Images.

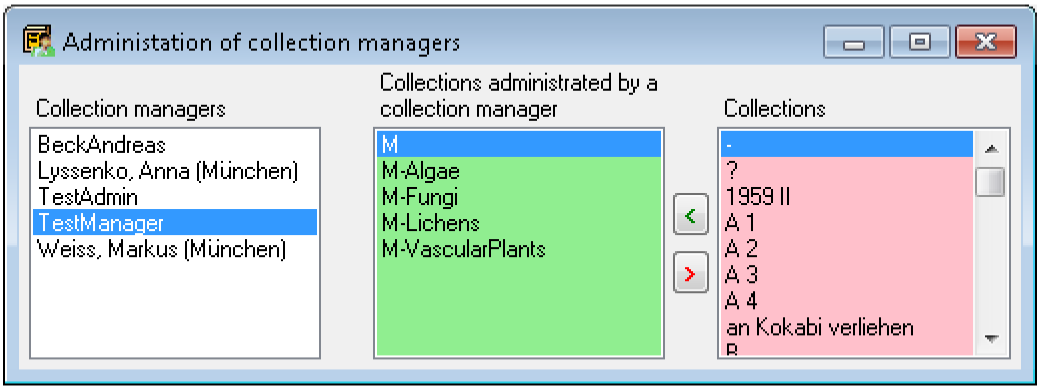


To view the history of a dataset, click on the button. A window with the history will open. For more details see chapter History.

For details about handling data see the Data section. Data of the collections is stored in the table Collection.

Collection manager

Collection managers are users with the right to edit the transactions for a collection, including loan, purchase, inventary etc. To administrate the collection managers you must be in the administrator group. Choose - **Administration** - **Collection managers** from the menu to open the editing window for the collection managers as shown below.

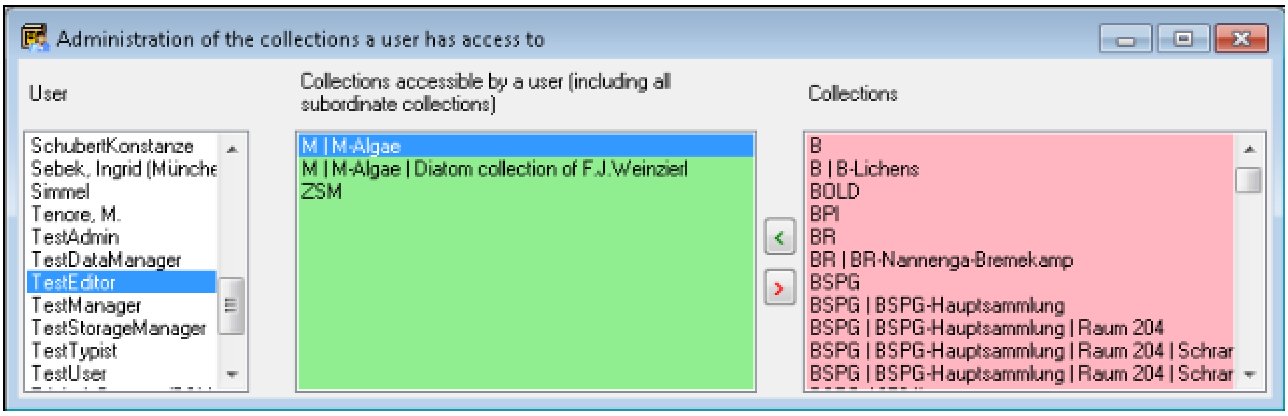


Use the < and > buttons to edit the list of the collections for which the selected collection manager can create and edit transactions.

For details about handling the collections see the Transaction section. Data of the collection managers is stored in the table CollectionManager.

Collection user

The access of users to collections can be restricted. To edit the collection list for a user choose - **Administration** - **Collection users ...** from the menu. A window will open, where you can add or remove collections a user has access to as shown below. The access includes all subordinate collections. This means adding a collection to the list a user has access to also grants the user access to the subcollections as defined in the hierachy of the collection. In the example shown below the second entry is not necessary as it is already included in the first entry.



SchubertKonstanze
Sebek, Ingrid (Münche
Simmel
Tenore, M.
TestAdmin
TestDataManager
TestEditor
TestManager
TestStorageManager
TestTypist
TestUser

M | M-Algae
M | M-Algae | Diatom collection of F.J.Weinzierl
ZSM

B
B | B-Lichens
BOLD
BPI
BR
BR | BR-Nannenga-Bremekamp
BSPG
BSPG | BSPG-Hauptsammlung
BSPG | BSPG-Hauptsammlung | Raum 204
BSPG | BSPG-Hauptsammlung | Raum 204 | Schrar
BSPG | BSPG-Hauptsammlung | Raum 204 | Schrar

Use the < and > buttons to edit the list of the collections for which the selected user has access to.

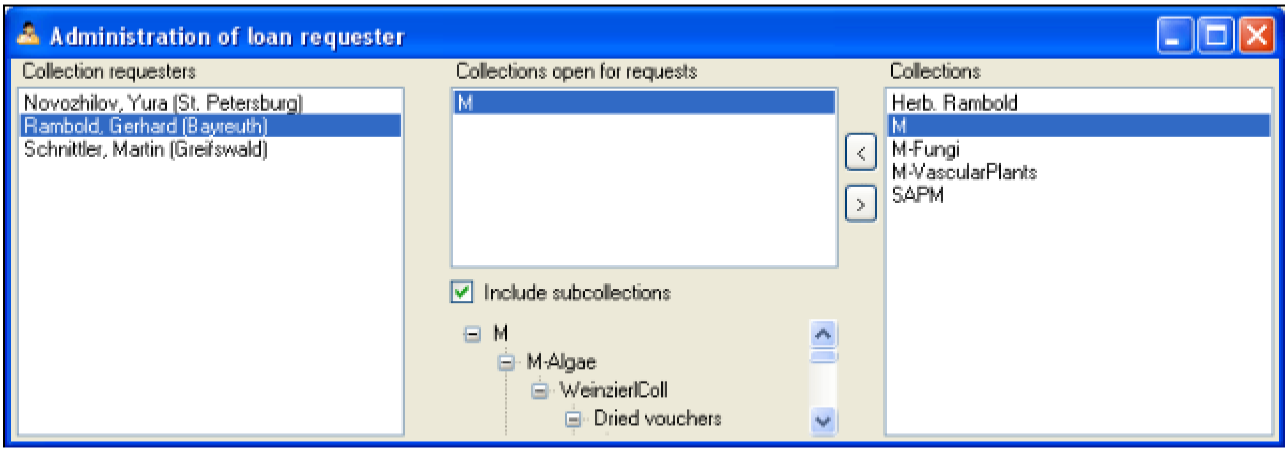
If a user has no collections in the list, all collections are available for this user.

A collection manager has access to the collections he is allowed to manage as well as those in the list as a collection user.

Data of the collections is stored in the table CollectionUser.

Collection requester

Collection requesters are users with the right to place requests for loans in other collections. To edit collection requesters you must be a collection manager for the requested collection. Choose - **Administration** - **Collection requesters** from the menu to open the editing window for collection requesters as shown below. The list on the left contains all users that are in the group Collection requesters. See UserAdministration for further details. Select a user in this list to edit the accessible collections for this requester.



Collection requesters:
Novozhilov, Yura (St. Petersburg)
Rambold, Gerhard (Bayreuth)
Schnittler, Martin (Greifswald)

Collections open for requests:
M

☑ Include subcollections

- M
  - M-Algae
    - WeinzierlColl
      - Dried vouchers

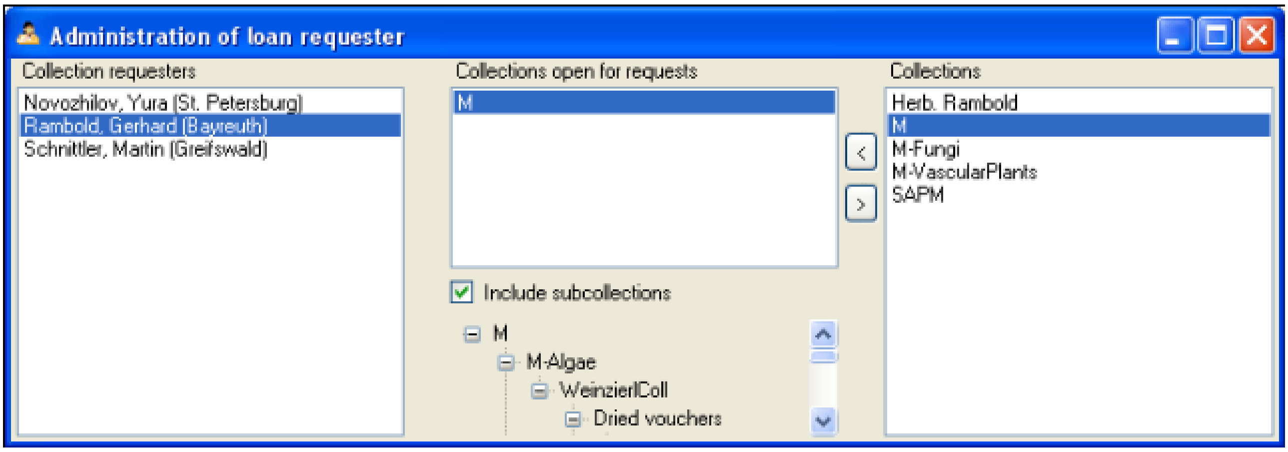
Collections:
Herb. Rambold
M
M-Fungi
M-VascularPlants
SAPM

Use the **<** and **>** buttons to edit the list of the collections for which the selected requester can place a request. If the option Include subcollections is choosen, the requester can send requests for all subcollections of a collection. Otherwise the requests can only be sent for the collections in the list. The subcollections are shown in the hierarchy below the list.

For details about handling the collections see the Transaction section. Data of the collection requesters is stored in the table CollectionRequester.

Transactions - Request

To enter a request for a loan you need to be in the user group or a DiversityCollectionRequester (see UserAdministration for further details). This is done by the CollectionManagers for their collections. To enable a user to place requests choose **Administration - Loan requesters** ... from the menu. A window will open as shown below.



Collection requesters:
Novozhilov, Yura (St. Petersburg)
Rambold, Gerhard (Bayreuth)
Schnittler, Martin (Greifswald)

Collections open for requests:
M

☑ Include subcollections

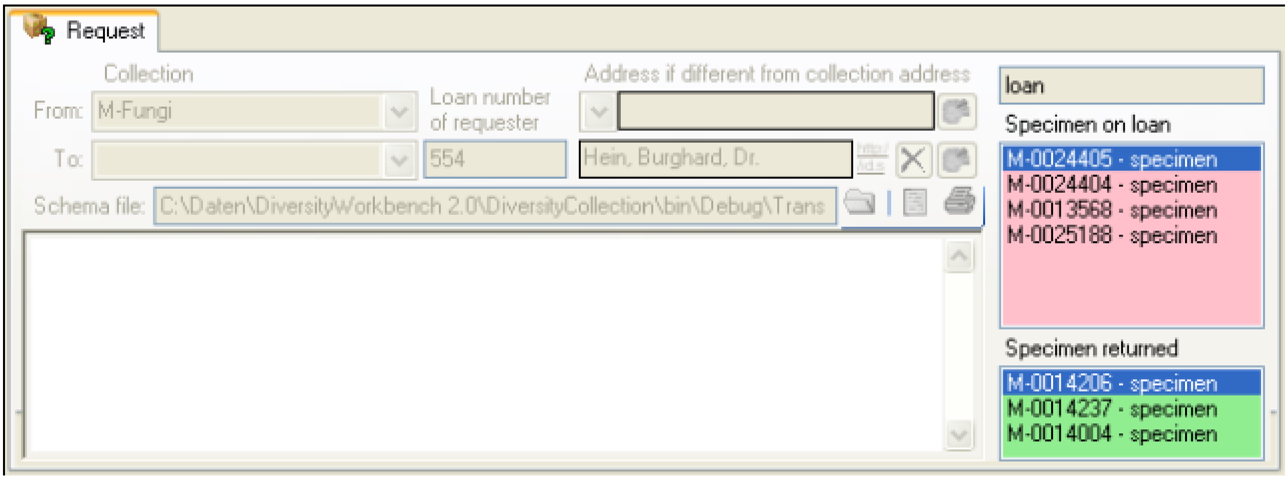
- M
  - M-Algae
    - WeinzierlColl
      - Dried vouchers

Collections:
Herb. Rambold
M
M-Fungi
M-VascularPlants
SAPM

As a CollectionManager you may give requesters access to the collections you manage. Click on the < or > buttons to add or remove collections from the list for which a user may place a request. If the option **Include subcollections** is choosen, a user is able to request specimens stored in subcollections of the administrating collection. To give you an overview of the subcollections the hierarchy of the collection is shown in the tree below the list.

If you are a CollectionManager and there are requests for your collections, the administration menu will contain a **Loan requests ...** entry. Choose it in order to open a window listing the requests for specimen in your collections.

If you have entered a request for specimen in a foreign collection, the administration menu will contain a **My requests...** entry. To inspect your request choose this entry from the menu to open a window as shown below. The window will show your requests and loans from foreign collections.



From: M-Fungi
To:
Loan number of requester: 554
Hein, Burghard, Dr.
Schema file: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Trans
loan

Specimen on loan:
M-0024405 - specimen
M-0024404 - specimen
M-0013568 - specimen
M-0025188 - specimen

Specimen returned:
M-0014206 - specimen
M-0014237 - specimen
M-0014004 - specimen

To enter a new request click on the button. Use the button to search for specimen in the collection and the button to remove unwanted specimen from your list.

Transactions

Prerequisites

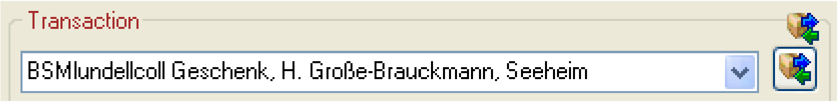
The transfer of a specimen between collections is handled with transactions. There are two prerequisites to use transactions in DiversityCollection. You are required to be in the user group or a CollectionManager (see UserAdministration) and the collections in which you have the right to handle transactions must have been assigned to you is shown in the CollectionManagers section.

Visibility of transactions

A specimen may be involved in diverse transactions between collections like loan, purchase, gift or exchange. The transactions are shown in the tree for the parts of a specimen and symbolized with a icon. For specimens which are still on loan a icon is shown while a returned loan is symbolized with a icon (see image below). A data embargo will be symbolized with a icon. If there are older accession numbers linked to a specimen involved in a transaction, these numbers can be documented together with the entry of the transaction of the respective part of the specimen.

Botanische Staatssammlung München (M)
M-Fungi
Arthrocladiella mougeotii
14.11.2007: Loan to B. Hein - 2007
Arthrocladiella mougeotii (Lév.) Vassilkov
28.03.2008: Loan to D. Nagel
Botanischer Garten und Botanisches Museum Berlin-Dahlem (B)
Arthrocladiella mougeotii (Lév.) Vassilkov
Exchange with B

If you are a CollectionManager, you may take a look at the details of a transaction. Select the specimen part in the tree and click on the button which will be shown in the details next to the name of the transaction. This will open the window for the transactions as described below.



Transaction
BSMlundellcoll Geschenk, H. Große-Brauckmann, Seeheim

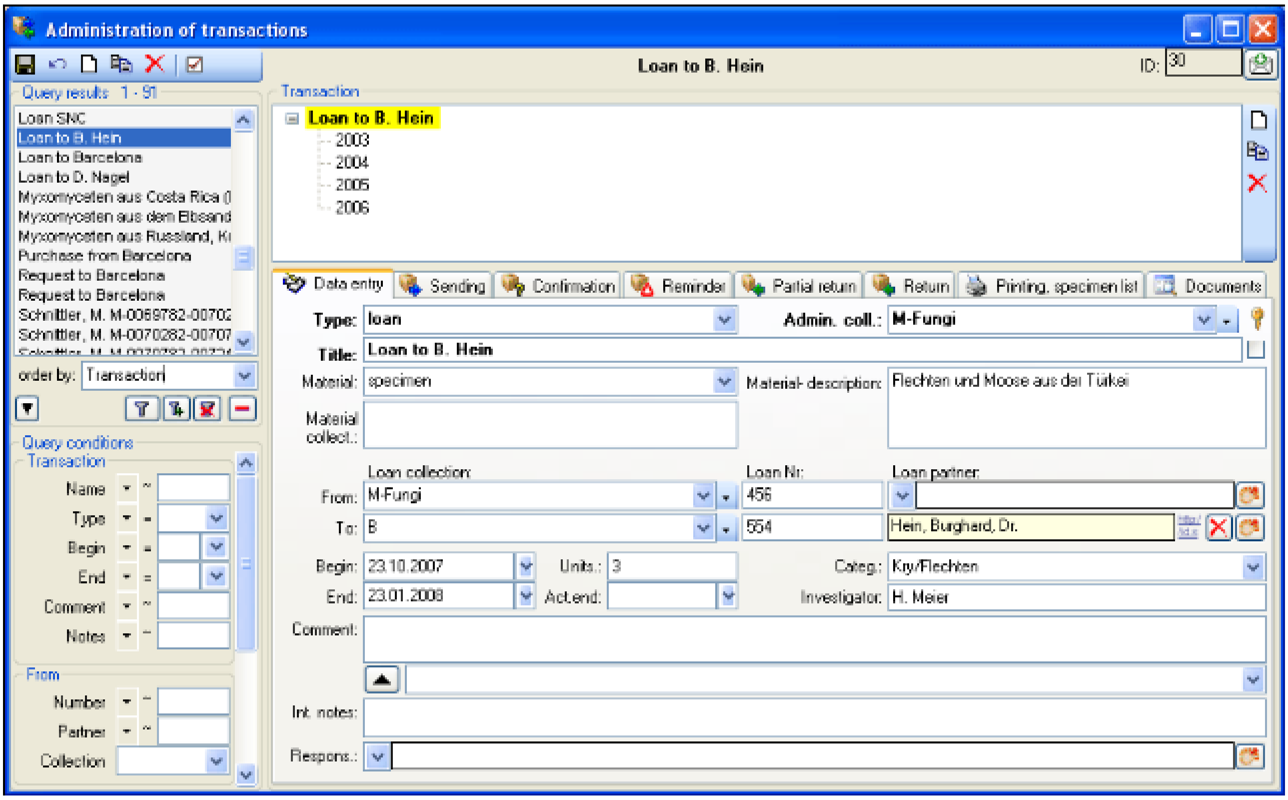
To edit the transactions choose **Administration - Transactions** from the menu. A window will open as shown below. In the tree at the top the relations between the transactions are shown. To create a transaction dependent on another transaction choose the superior transaction in the tree and click on the button in the panel right of the tree. With the button you may create a copy of a transaction. To delete a specimen from the list click on the button. To transfer all selected specimen in an existing transaction choose **Data -> Transfer -> To transaction...** from the menu and choose the transaction where the specimen with all their parts should be included. In two following dialogs you may restrict the transfered parts to a certain collection or material category. The data for the transactions is stored in the tables Transaction and CollectionSpeci menTransaction.

To view the history of a data set click on the button. A window with the history will open. For more details see the section History.

Data entry

On this page you may edit the data of a transaction. Every transaction is linked to an administrating collection (symbolized by the key) and can be edited exclusively by

CollectionManagers of this collection. To appoint managers choose **Administration - Managers** from the menu.



Query results:
- Loan SNC
- Loan to B. Hein
- Loan to Barcelona
- Loan to D. Nagel
- Myxomyceten aus Costa Rica (
- Myxomyceten aus dem Elbsand
- Myxomyceten aus Russland, K
- Purchase from Barcelona
- Request to Barcelona
- Request to Barcelona
- Schnittler, M. M-0069782-00702
- Schnittler, M. M-0070282-00707

order by: Transaction

Transaction:
- Loan to B. Hein
  - 2003
  - 2004
  - 2005
  - 2006

Type: loan
Admin. coll.: M-Fungi
Title: Loan to B. Hein
Material: specimen
Material- description: Flechten und Moose aus der Türkei
Loan collection: From: M-Fungi; Loan Nr: 456
Loan collection: To: B; Loan Nr: 554; Loan partner: Hein, Burghard, Dr.
Begin: 23.10.2007
Units.: 3
Categ.: Kry/Flechten
End: 23.01.2008
Investigator: H. Meier

The transactions can be organized in a hierarchy as shown in the image above, if e.g. you wish to keep together all loans to a certain institution. To create a transaction of an inferior transaction choose the superior transaction in the tree and click on the 🗋button in the panel at the right side of the tree. To create of copy of a transaction, use the ⧉button and the ✕ button to delete it.

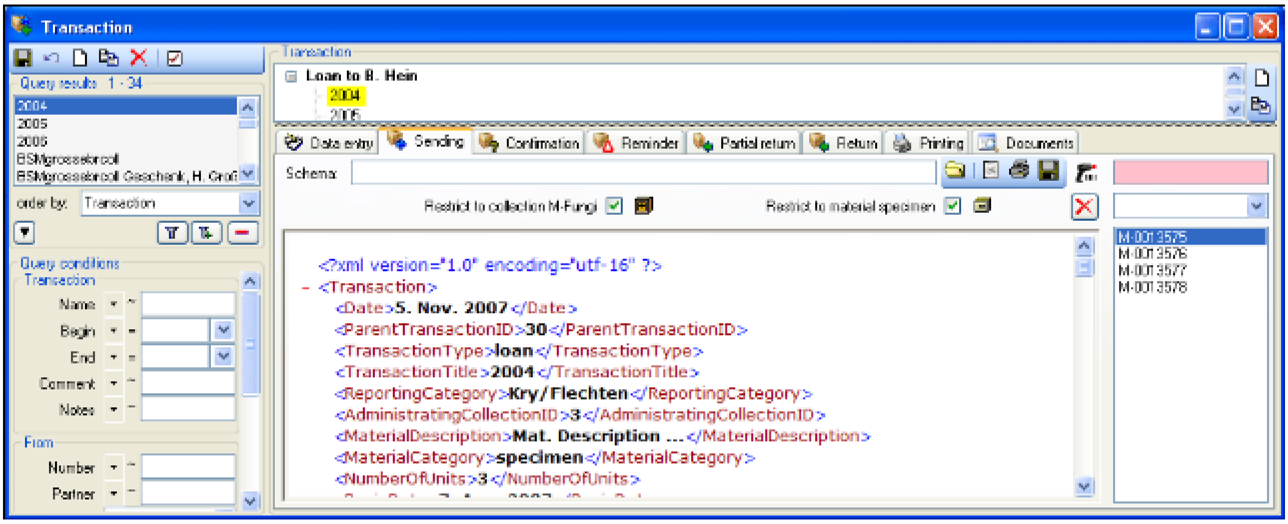
Depending on the type of the transaction additional tab pages will appear for creating documents.

Tabs	***Transaction types***							
Data entry	Loan	Borrow	Exchange	Gift	Purchase	Request	Inventory	Embargo
Sending	Loan	Borrow	Exchange	Gift	Purchase			
Confirmation	Loan	Borrow	Exchange	Gift	Purchase	Request		
Reminder	Loan	Borrow	Exchange	Gift	Purchase			
Partial return	Loan	Borrow						
Return	Loan	Borrow						
Printing	Loan	Borrow	Exchange	Gift	Purchase	Request	Inventory	

Documents	Loan	Borrow	Exchange	Gift	Purchase	Request	Inventory
Balance			Exchange				

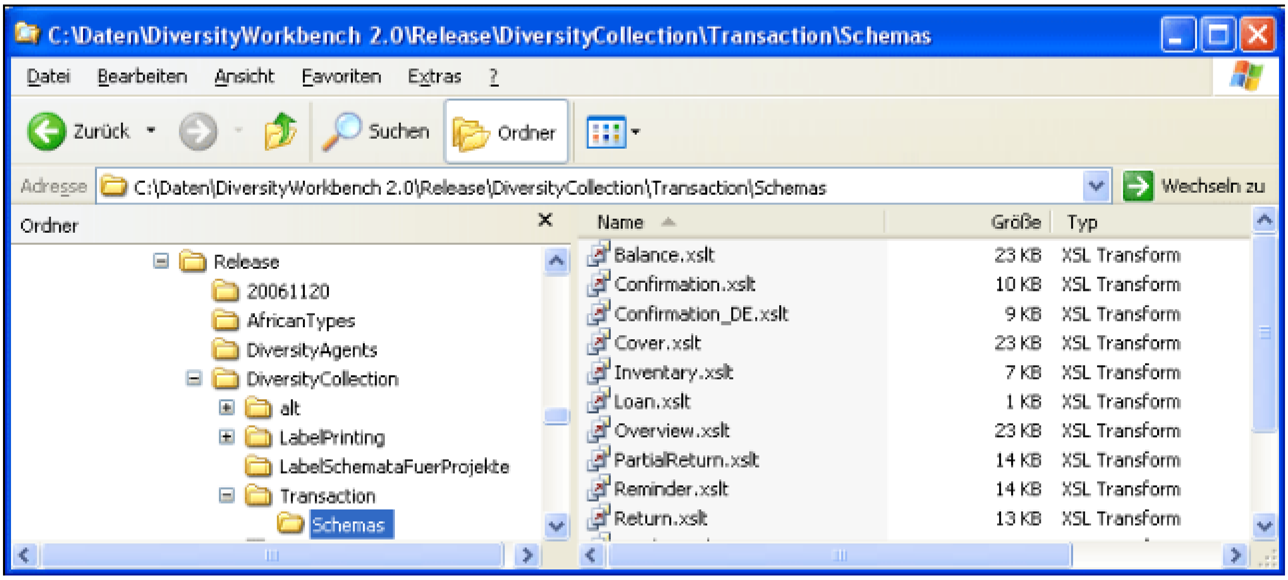
Common notes

On the tab pages for generating documents you need to specify a xml-schema for your document. Click on the 🗀 button to choose one of the predefined schemas or create your own. To edit the schema files (*.xslt) you may use a text editor or software like e.g. EditiX. If you do not specify a schema for your form (i.e. the field for the path of the schema is empty - see below), you will see the XML output created by the database as shown below.



```
  <?xml version="1.0" encoding="utf-16" ?>
- <Transaction>
    <Date>5. Nov. 2007</Date>
    <ParentTransactionID>30</ParentTransactionID>
    <TransactionType>loan</TransactionType>
    <TransactionTitle>2004</TransactionTitle>
    <ReportingCategory>Kry/Flechten</ReportingCategory>
    <AdministratingCollectionID>3</AdministratingCollectionID>
    <MaterialDescription>Mat. Description ...</MaterialDescription>
    <MaterialCategory>specimen</MaterialCategory>
    <NumberOfUnits>3</NumberOfUnits>
```

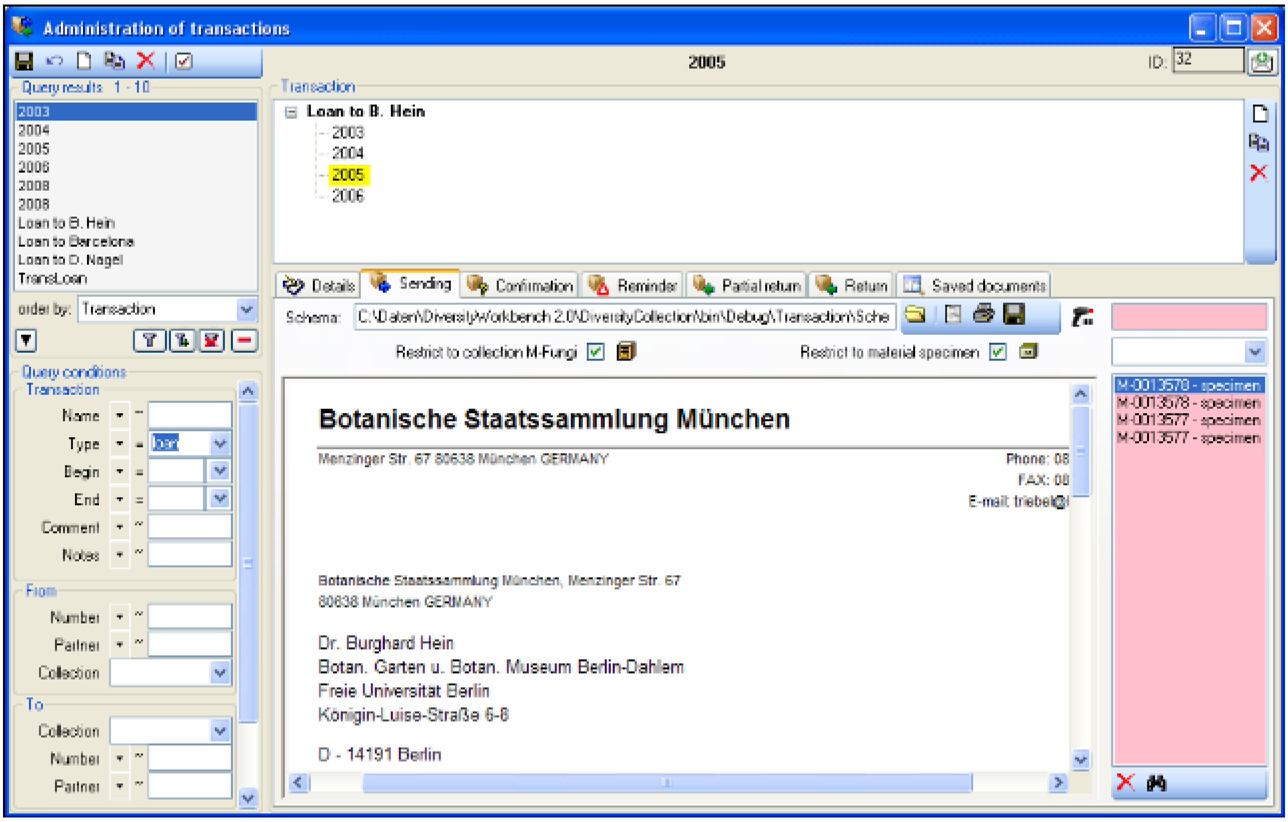
To choose a schema click on the 🗀 button and select a schema from the list. DiversityCollection contains several ready to use schemas in the folder **Transaction - Schemas**.



Adresse: C:\Daten\DiversityWorkbench 2.0\Release\DiversityCollection\Transaction\Schemas

Name	Größe	Typ
Balance.xslt	23 KB	XSL Transform
Confirmation.xslt	10 KB	XSL Transform
Confirmation_DE.xslt	9 KB	XSL Transform
Cover.xslt	23 KB	XSL Transform
Inventary.xslt	7 KB	XSL Transform
Loan.xslt	1 KB	XSL Transform
Overview.xslt	23 KB	XSL Transform
PartialReturn.xslt	14 KB	XSL Transform
Reminder.xslt	14 KB	XSL Transform
Return.xslt	13 KB	XSL Transform

Feel free to change these schemas according to your own needs (editors are available e.g. from http://www.altova.com/). Choose the schema you need and click on the 🗎 button to create a document. To print the document use the 🖶 button. To store the current document for later reference in Documents click on the 💾 button. An example for a document is shown below.



Type: loan

Schema: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Transaction\Sche

Restrict to collection M-Fungi ☑

Restrict to material specimen ☑

Botanische Staatssammlung München

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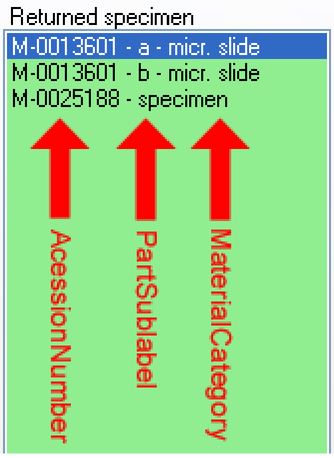
Botanische Staatssammlung München, Menzinger Str. 67
80638 München GERMANY

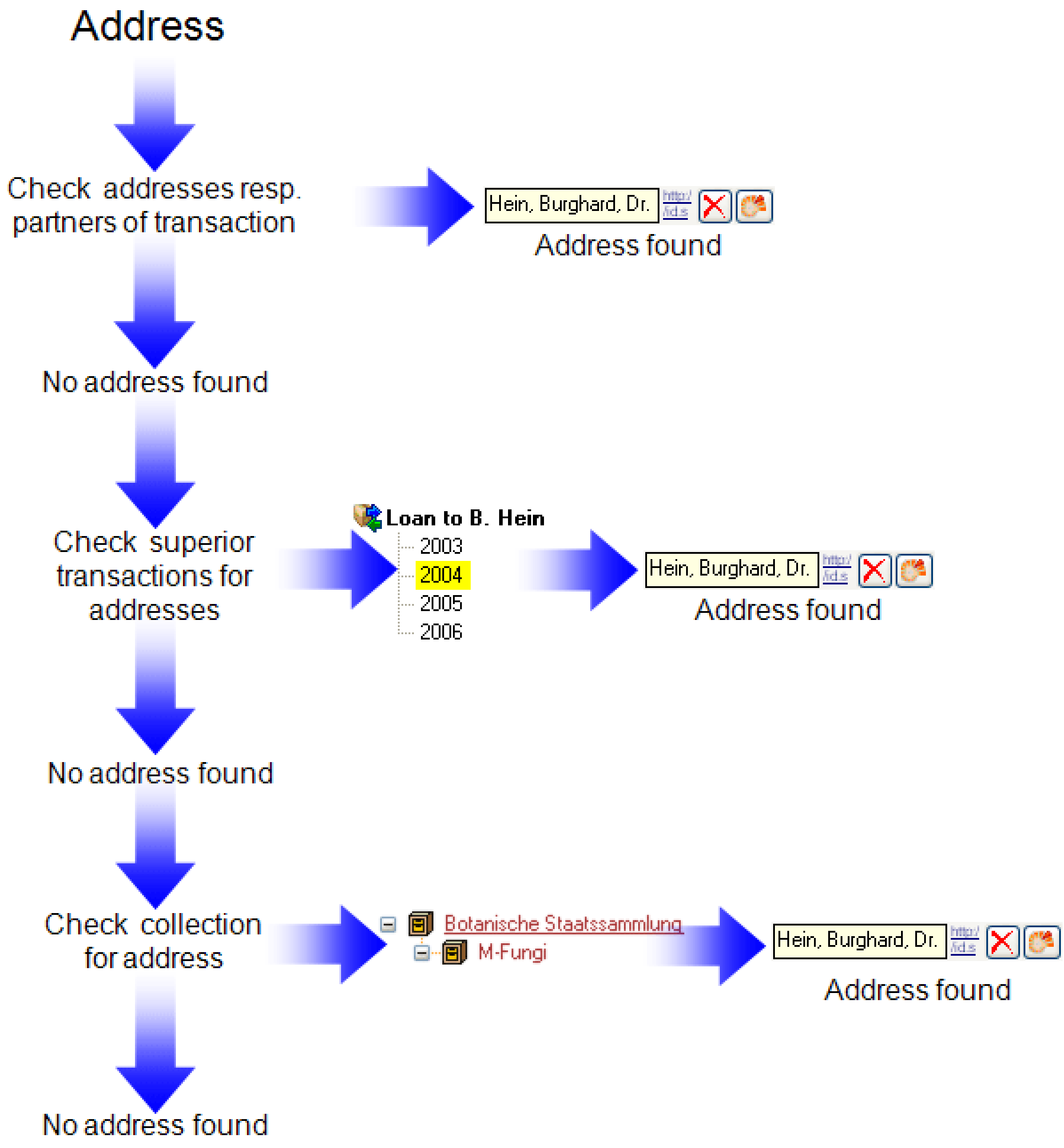
Dr. Burghard Hein
Botan. Garten u. Botan. Museum Berlin-Dahlem
Freie Universität Berlin
Königin-Luise-Straße 6-8

D - 14191 Berlin

The specimens will be listed with their accession number, an optional label of the part and the material category to ensure discrimination in case a specimen contains more than one part (see image below).


Returned specimen
M-0013601 - a - micr. slide
M-0013601 - b - micr. slide
M-0025188 - specimen

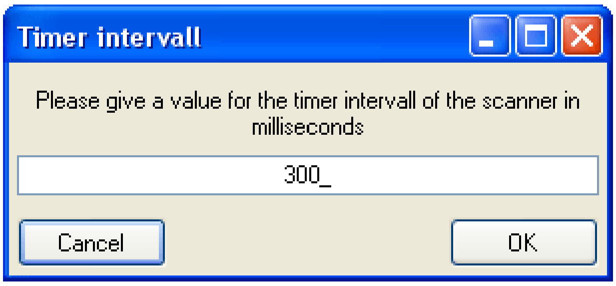
If a transaction entry has no address or transaction partner linked to an entry in the module DiversityAgents, where addresses are stored, the program will try to find an address in one of the superior transactions from the transaction partners found there. If no address exists in these transactions, the program will try to get an address from the collections. Therefore, a transaction partner linked to DiversityAgents is only necessary if either there are no addresses for the collections or you wish to use a different address. The search path as described is summarized in the image below.


Address
Check addresses resp. partners of transaction
Hein, Burghard, Dr.
Address found
No address found
Check superior transactions for addresses
Loan to B. Hein
2003
2004
2005
2006
Hein, Burghard, Dr.
Address found
No address found
Check collection for address
Botanische Staatssammlung
M-Fungi
Hein, Burghard, Dr.
Address found
No address found

Transactions - Sending

In the sending tab page of the transaction window you can create the covering note for a sent sample. To choose a schema click on the button and select a schema from the list. DiversityCollection contains several ready to use schemas in the folder **Transaction - Schemas**.

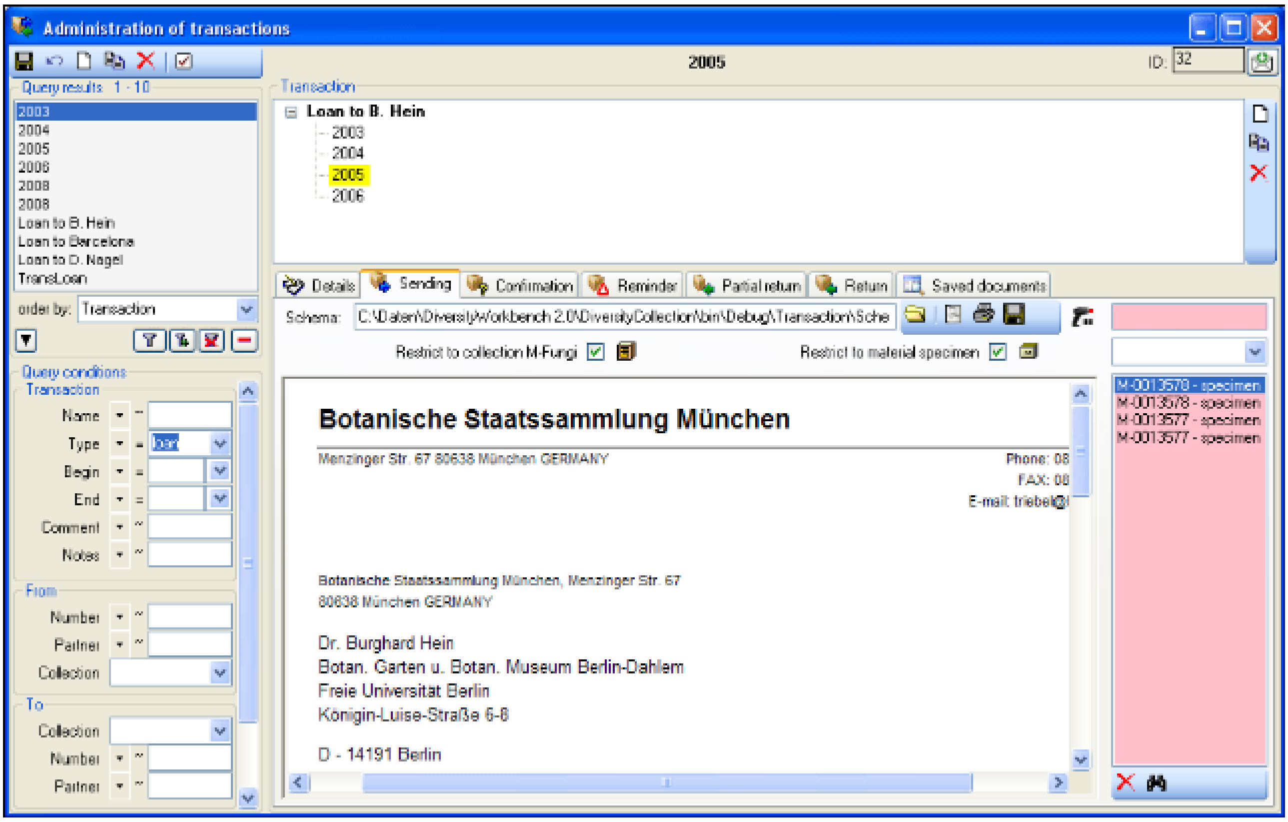
To add a specimen to the list, you can use a barcode scanner. The code detected by the scanner will be displayed in the field behind the symbol and entered in the list below. If no scanner or barcode is available, use the combobox underneath, enter the first letters of the accession number of the specimen and select your specimen from the drop down list. In case your scanner is reading only parts of the barcode try to adjust the timer intervall - click on the button to open a window as shown below.



Please give a value for the timer intervall of the scanner in milliseconds

300_

To restrict the selection of the specimens and parts of the specimens, you can check the **Restrict to collection** ... and **Restrict to material** ... options. To remove a specimen from the list, use the button under the specimen list. If you want to see the details of a specimen, choose it in the list and click on the button. Click on the button to create the document as shown below.



2005

ID: 32

2003
2004
2005
2006
2008
2008
Loan to B. Hein
Loan to Barcelona
Loan to D. Nagel
TransLoan

order by: Transaction

Type = loan

Transaction

Loan to B. Hein
- 2003
- 2004
- 2005
- 2006

Schema: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Transaction\Sche

Restrict to collection M-Fungi ☑

Restrict to material specimen ☑

M-0013578 - specimen
M-0013578 - specimen
M-0013577 - specimen
M-0013577 - specimen

Botanische Staatssammlung München

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Dr. Burghard Hein
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Transactions - Confirmation

On this page you may create an inquiry letter for a package sent, e.g. if a parcel was sent to a loan taker and no confirmation that the parcel reached its destination was returned so far.

With the 📂button choose the schema you need. Click on the 📄button to create a document. To print the document use the 🖨button. To store the current document for later reference in Documents click on the 💾button.

Schema: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Transaction\Schemas\Confirmation.xslt

Botanische Staatssammlung München **M**

Menzinger Str. 67 80638 München GERMANY

Phone: 089 17861 265
FAX: 089 17861 193
E-mail: office@bsm.mwn.de

Botanische Staatssammlung München, Menzinger Str. 67
80638 München GERMANY

Dr. Burghard Hein
Botan. Garten u. Botan. Museum Berlin-Dahlem
Freie Universität Berlin
Königin-Luise-Straße 6-8

D - 14191 Berlin

München, 13. Nov. 2007

The Botanische Staatssammlung München sent you as a loan the herbarium specimen(s) specified in the list attached.

Specimen
- M-0013570 - specimen
- M-0013571 - specimen
- M-0013572 - specimen
- M-0013573 - specimen
- M-0013574 - specimen
- M-0013575 - specimen
- M-0013576 - specimen

Transactions - Reminder

If a loan is due to return or a loan taker did not meet the deadline, you may create a prompt note here.

With the button choose the schema you need. Click on the button to create a document. To print the document use the button. To store the current document for later reference in Documents click on the button.

In the upper right list the missing specimen and at the lower right list the returned specimen are listed.

Schema: C:\Daten\DiversityWorkbench 2.0\Release\DiversityCollection\Transaction\Schemas\Reminder.xslt

Botanische Staatssammlung München M

Menzinger Str. 67 80638 München GERMANY

Phone: 089 17861 265
FAX: 089 17861 193
E-mail: office@bsm.mwn.de

Botanische Staatssammlung München, Menzinger Str. 67
80638 München GERMANY

Dr. Burghard Hein
Botan. Garten u. Botan. Museum Berlin-Dahlem
Freie Universität Berlin
Königin-Luise-Straße 6-8

D - 14191 Berlin

München, 14. Nov. 2007

The Botanische Staatssammlung München is acknowledging herewith the return (complete return) of the herbarium specimen(s) (7 fungi) sent on loan to your institution. The specimens arrived in good order.

Number of specimens returned:

1 as a total

Specimen on loan

- M-0013571 - specimen
- M-0013572 - specimen
- M-0013573 - specimen
- M-0013574 - specimen
- M-0013575 - specimen
- M-0013576 - specimen

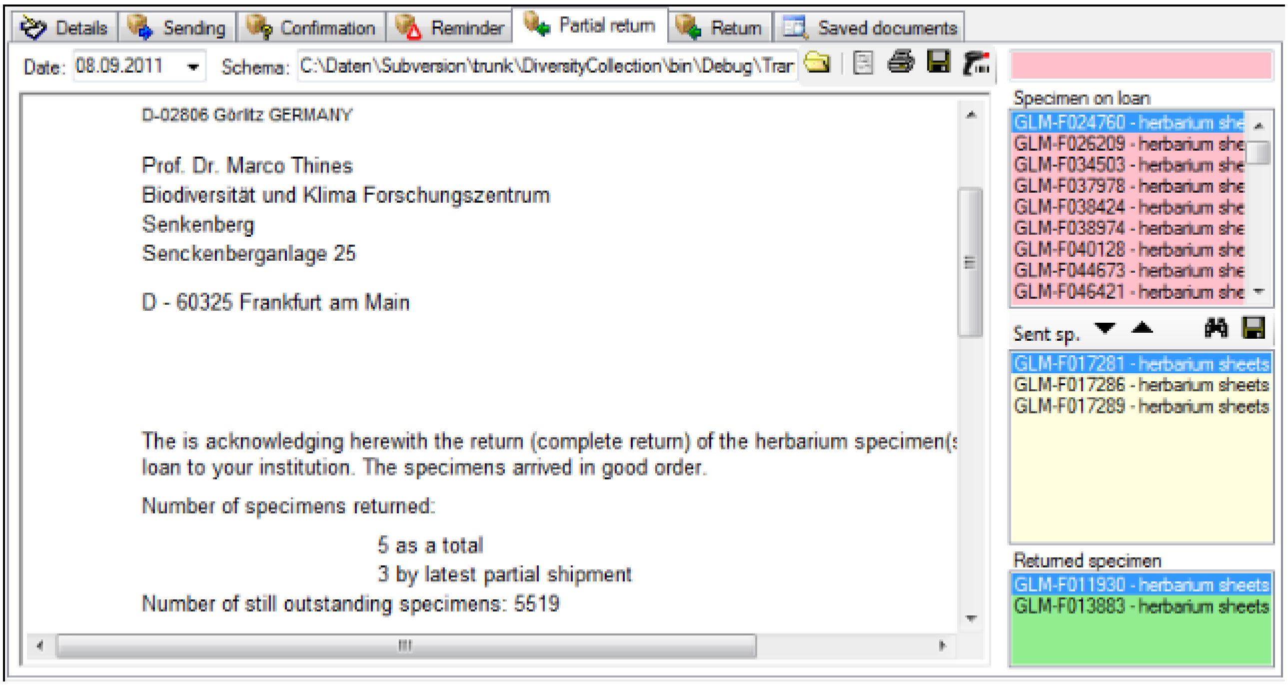
Returned specimen

- M-0013570 - specimen

Transactions - Partial Return

If parts of a loan were returned, create a letter of acknowledgment here.

With the button choose the schema you need. Click on the button to create a document. To print the document use the button. To store the current document for later reference in Documents click on the button.



Date: 08.09.2011

Schema: C:\Daten\Subversion\trunk\DiversityCollection\bin\Debug\Trar

D-02806 Görlitz GERMANY

Prof. Dr. Marco Thines
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D - 60325 Frankfurt am Main

The is acknowledging herewith the return (complete return) of the herbarium specimen(s
loan to your institution. The specimens arrived in good order.

Number of specimens returned:

5 as a total
3 by latest partial shipment

Number of still outstanding specimens: 5519

Specimen on loan

GLM-F024760 - herbarium she
GLM-F026209 - herbarium she
GLM-F034503 - herbarium she
GLM-F037978 - herbarium she
GLM-F038424 - herbarium she
GLM-F038974 - herbarium she
GLM-F040128 - herbarium she
GLM-F044673 - herbarium she
GLM-F046421 - herbarium she

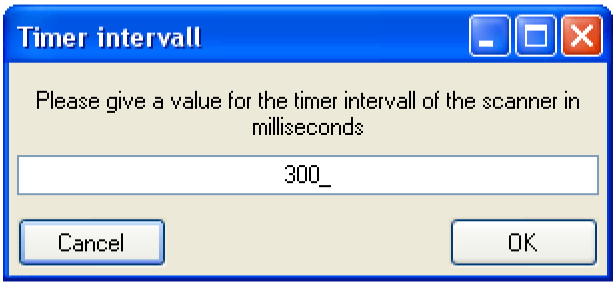
Sent sp.

GLM-F017281 - herbarium sheets
GLM-F017286 - herbarium sheets
GLM-F017289 - herbarium sheets

Returned specimen

GLM-F011930 - herbarium sheets
GLM-F013883 - herbarium sheets

You have two options to enter returned specimen. Use the ▲and ▼buttons respectively to move items between the lists or use a barcode scanner . Move the mouse cursor into the field for barcode detection and scan the barcode. The specimen will be automatically inserted into the list for the returned specimen. In case your scanner is reading only parts of the barcode try to ajust the timer intervall. Click on the button to open a window as shown below. Here you may set the interval to a value which is compatible with your scanner. If you wish to see the details of a specimen, choose it in the list and click on the button.

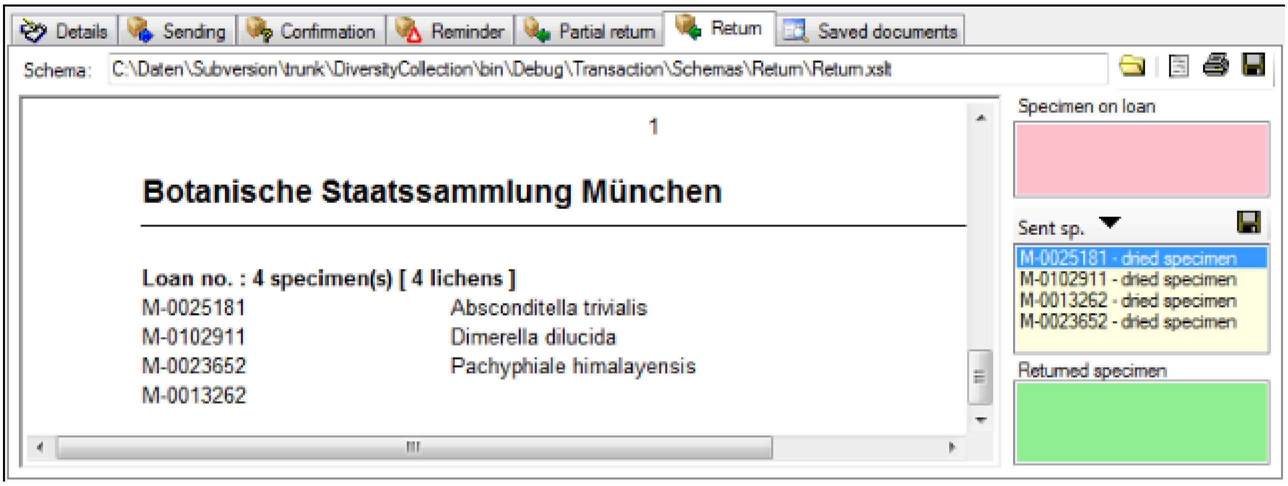


Please give a value for the timer intervall of the scanner in milliseconds

300_

Transactions - Return

If a loan is returned, you may create a letter of acknowledgment here. With the 🗁button choose the schema you need. If all specimen were returned, click on the ✓button. This will include all remaining specimen into the list of the returned specimens. With the date field you may define a different date as start, if e.g. you started to register the returned specimen several days earlier. Click on the 🗎button to create a document. To print the document use the 🖶button. To store the current document for later reference in Documents click on the 💾 button.



Schema: C:\Daten\Subversion\trunk\DiversityCollection\bin\Debug\Transaction\Schemas\Return\Return.xslt

1

Botanische Staatssammlung München

Loan no. : 4 specimen(s) [4 lichens]

M-0025181	Absconditella trivialis
M-0102911	Dimerella dilucida
M-0023652	Pachyphiale himalayensis
M-0013262	

M-0025181 - dried specimen
M-0102911 - dried specimen
M-0013262 - dried specimen
M-0023652 - dried specimen

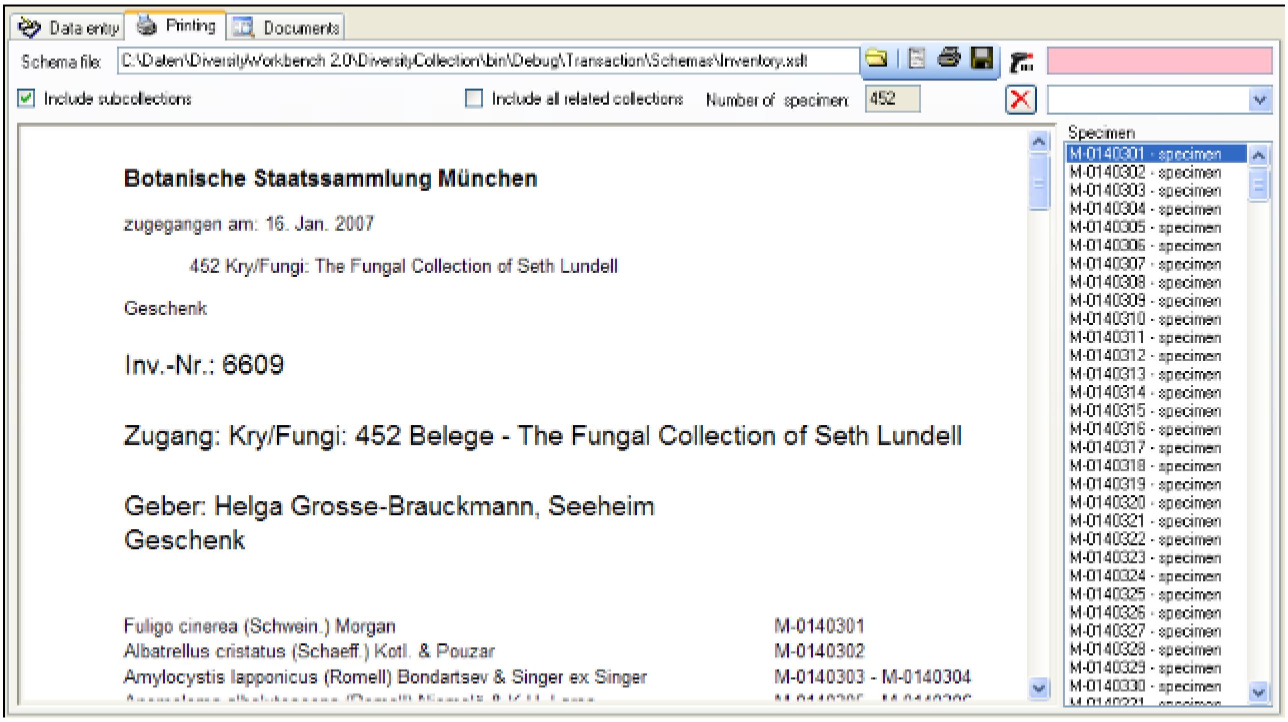
To transfer the items from the **Specimen on loan** list to the **Sent specimen** list click on the ▼button. After all documents are generated and saved, click on the 💾button above the **Sent specimen** list to enter the changes into the database.

Transactions - Printing / Inventory

In addition to special pages for creating letters along with a loan, this page provides the possibility to print cover letters, inventories etc. You may restrict the selected specimen to the current collection, include subcollections or all related collections - simply activate the corresponding checkboxes.

To add a specimen to the list you may either use the combobox or a barcode scanner. To use the barcode scanner move your mouse cursor into the pink field on the right of the scanner. In case your scanner is reading only parts of the barcode, try to adjust the timer intervall. Click on the button to open a window where you may set the timer intervall to a different value. To remove a specimen from the list select it and click on the button.

With the button choose the schema you need. Click on the button to create a preview of the document. To print the document use the button. To store the current document for later reference in Documents click on the button.



Schema file: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Transaction\Schemas\Inventory.xslt

☑ Include subcollections

☐ Include all related collections

Number of specimen: 452

Botanische Staatssammlung München

zugegangen am: 16. Jan. 2007

452 Kry/Fungi: The Fungal Collection of Seth Lundell

Geschenk

Inv.-Nr.: 6609

Zugang: Kry/Fungi: 452 Belege - The Fungal Collection of Seth Lundell

Geber: Helga Grosse-Brauckmann, Seeheim
Geschenk

Fuligo cinerea (Schwein.) Morgan	M-0140301
Albatrellus cristatus (Schaeff.) Kotl. & Pouzar	M-0140302
Amylocystis lapponicus (Romell) Bondartsev & Singer ex Singer	M-0140303 - M-0140304

Specimen
M-0140301 - specimen
M-0140302 - specimen
M-0140303 - specimen
M-0140304 - specimen
M-0140305 - specimen
M-0140306 - specimen
M-0140307 - specimen
M-0140308 - specimen
M-0140309 - specimen
M-0140310 - specimen
M-0140311 - specimen
M-0140312 - specimen
M-0140313 - specimen
M-0140314 - specimen
M-0140315 - specimen
M-0140316 - specimen
M-0140317 - specimen
M-0140318 - specimen
M-0140319 - specimen
M-0140320 - specimen
M-0140321 - specimen
M-0140322 - specimen
M-0140323 - specimen
M-0140324 - specimen
M-0140325 - specimen
M-0140326 - specimen
M-0140327 - specimen
M-0140328 - specimen
M-0140329 - specimen
M-0140330 - specimen

Transactions - Documents

This page stores all the documents created or received along with a transaction.

Botanische Staatssammlung München

zugegangen am: 16. Jan. 2007

452 Kry/Fungi: The Fungal Collection of Seth Lundell

Geschenk

Inv.-Nr.: 6609

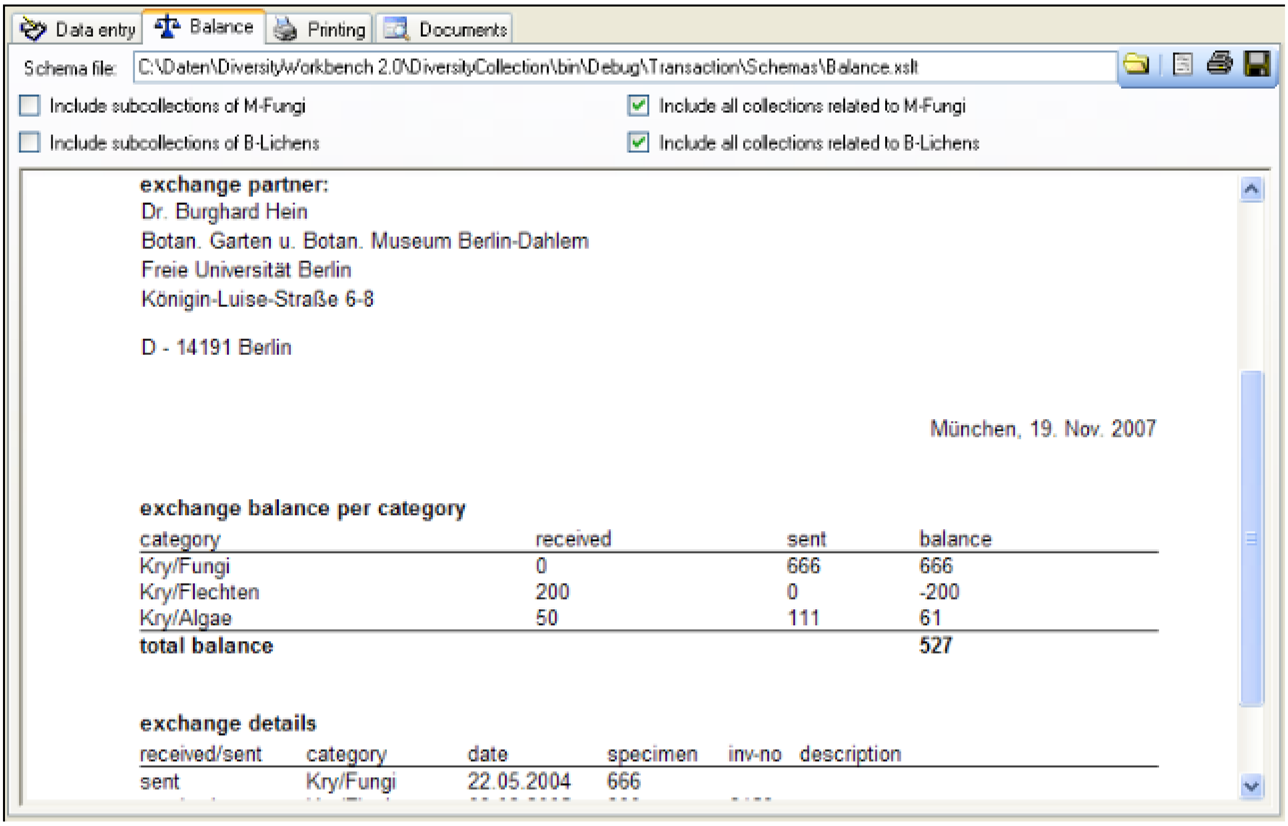
Zugang: Kry/Fungi: 452 Belege - The Fungal Collection of Seth Lundell

To add a document scan it and create a screeshot of said document. Then create a new entry (click on the button) and insert the screenshot with the Add image from document button. In the lower part you may enter any text related to the document.

Transactions - Balance ⚖

This is the balance for the exchange between two collections.

With the 📂button choose the schema you need. Click on the 📄button to create a document. To print the document use the 🖨button. To store the current document for later reference in Documents click on the 💾button. To include either the subcollections of any related collection or the collections of the current transaction select the corresponding checkboxes.



Schema file: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Transaction\Schemas\Balance.xslt

☐ Include subcollections of M-Fungi

☑ Include all collections related to M-Fungi

☐ Include subcollections of B-Lichens

☑ Include all collections related to B-Lichens

exchange partner:

Dr. Burghard Hein
Botan. Garten u. Botan. Museum Berlin-Dahlem
Freie Universität Berlin
Königin-Luise-Straße 6-8

D - 14191 Berlin

München, 19. Nov. 2007

exchange balance per category

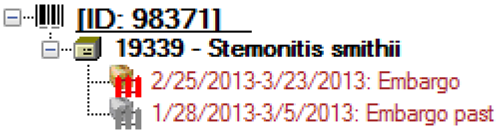
category	received	sent	balance
Kry/Fungi	0	666	666
Kry/Flechten	200	0	-200
Kry/Algae	50	111	61
total balance			**527**

exchange details

received/sent	category	date	specimen	inv-no	description
sent	Kry/Fungi	22.05.2004	666		

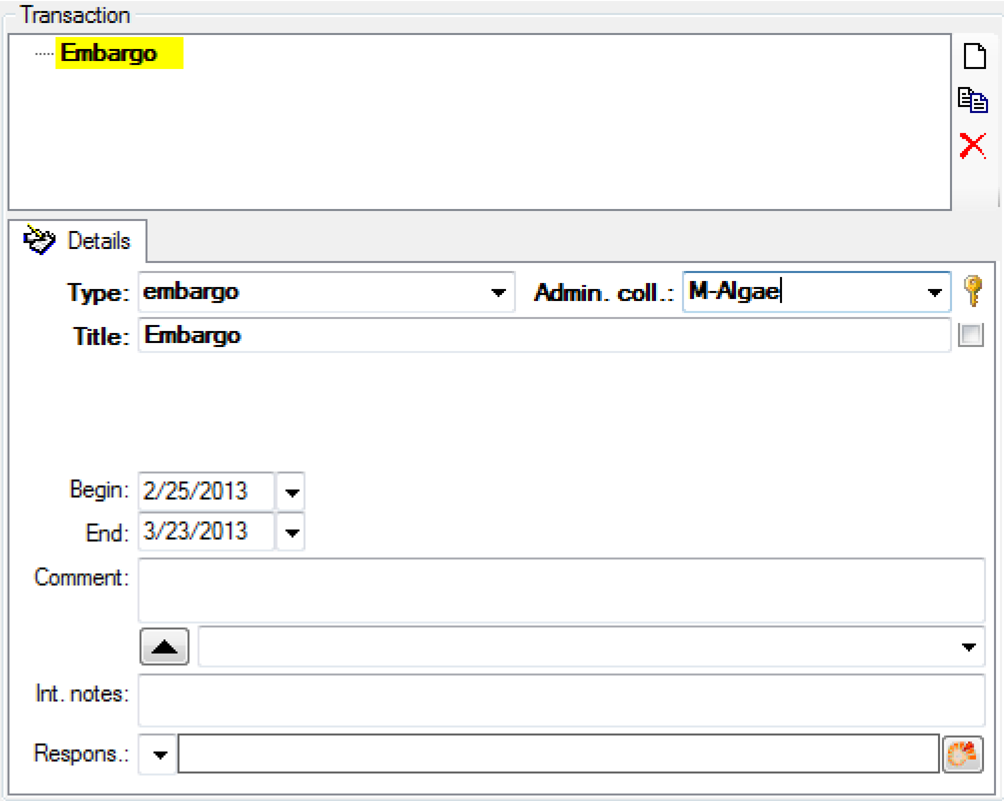
Transactions - Embargo

If specimens should not be published for a certain period, you are able to create a transaction of the type embargo and add parts of the specimen in question to this embargo. If a specimen is part of an embargo, it is shown as in the image below for current and past or future embargos .



[ID: 98371]
19339 - Stemonitis smithii
2/25/2013-3/23/2013: Embargo
1/28/2013-3/5/2013: Embargo past

To create an embargo choose **Administration -> Transaction management -> Transaction** from the menu, create a new transaction and choose the type embargo for the new transaction. The period of the embarge is defined by its **Begin**ning and **End** (see below).



Transaction
Embargo
Details
Type: embargo **Admin. coll.:** M-Algae
Title: Embargo
Begin: 2/25/2013
End: 3/23/2013
Comment:
Int. notes:
Respons.:

Maintenance

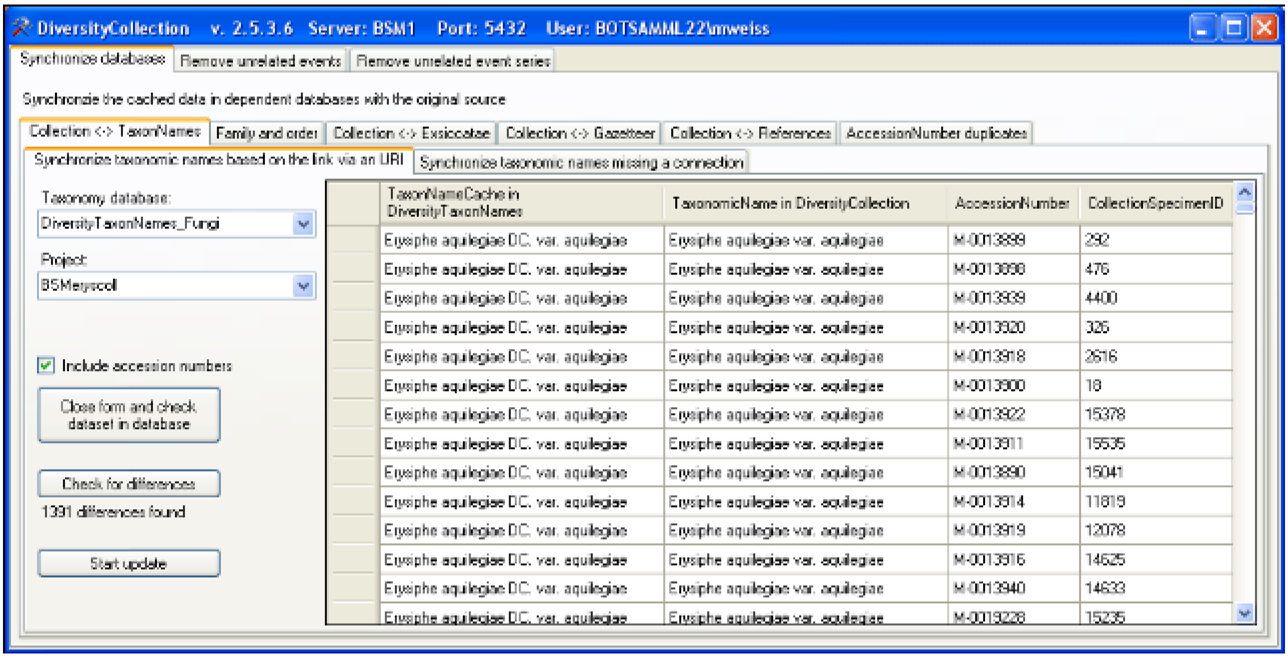
To open the maintenance form choose **Administration -> Maintenance ...** from the menu. With the maintenance functions you can update values cached from other modules or external webservices. DiversityCollection can be linked with several other modules of the DiversityWorkbench. If you link a data source to another module, the URI of the data set in the other module together with one or several cached values will be stored in DiversityCollection. 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, family and orders, people, exsiccatal series, geographical names and references. Further functions provided by maintenance are a search for duplicate accession numbers, the insert of updated taxonomic names, the removal of orphaned CollectionEventSeries and CollectionEvents, the search for additional geographical information based on WGS84 coordinates and the conversion of coordinate systems.

Maintenance - Taxonomic names

To synchronize the entries for the taxonomic names derived from the module DiversityTaxonNames choose **Administration -> Maintenance...** from the menu. A window will open as shown below. To synchronize the taxonomic names for entries linked to the module DiversityTaxonNames choose the tab **Collection <-> TaxonNames**. There are two ways to synchronize taxonomic names. You may either **Synchronize taxonomic names based on the link via an URI** 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.

Synchronize taxonomic names based on the link via an URI

The taxonomic names are stored in the field TaxonomicName in the table Identification. Select a taxonomic database and a project which should be synchronized. Start the query with a click on the Check for differences button.



DiversityCollection v. 2.5.3.6 Server: BSM1 Port: 5432 User: BOTSAMML22\mweiss

Synchronize the cached data in dependent databases with the original source

Taxonomy database: DiversityTaxonNames_Fungi

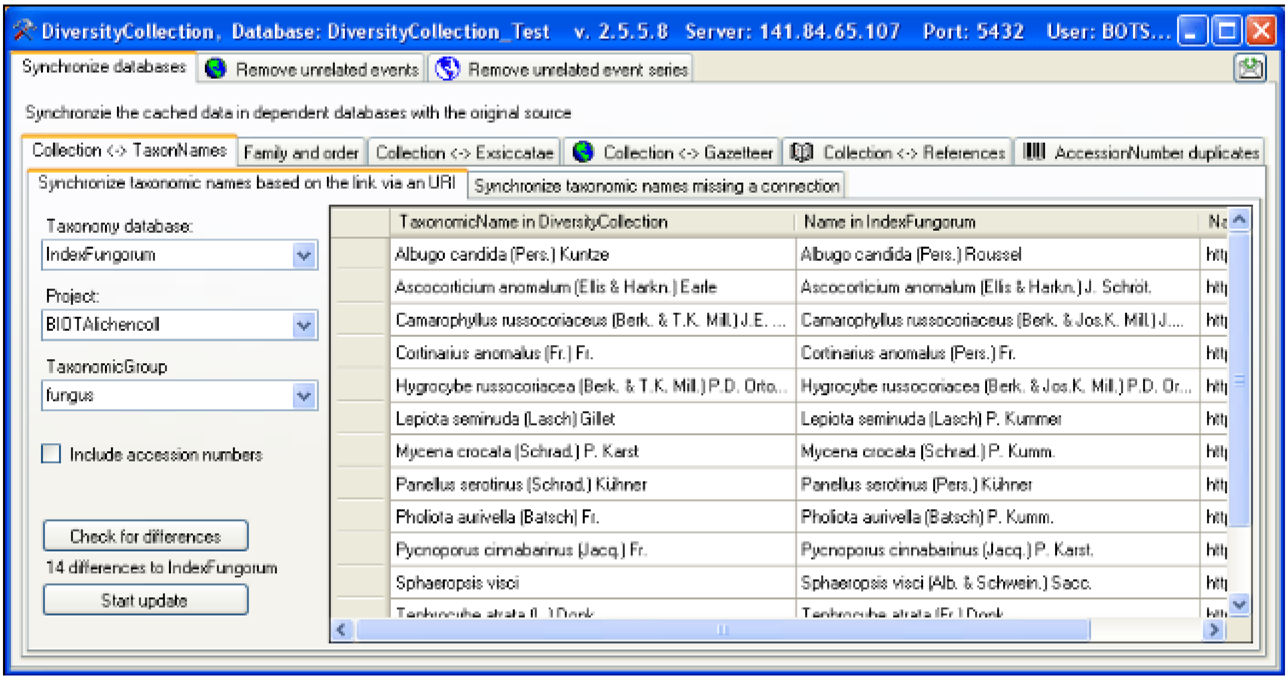
Project: BSMeyscoll

☑ Include accession numbers

1391 differences found

TaxonNameCache in DiversityTaxonNames	TaxonomicName in DiversityCollection	AccessionNumber	CollectionSpecimenID
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013899	292
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013898	476
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013939	4400
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013920	326
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013918	2616
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013900	18
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013922	15378
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013911	15535
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013890	15041
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013914	11819
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013919	12078
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013916	14625
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013940	14633
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0019228	15235

If you synchronize your data with a webservice as shown in the image below, you can specify the taxonomic group as well.



Taxonomy database: IndexFungorum

Project: BIOTAlichencoll

TaxonomicGroup: fungus

☐ Include accession numbers

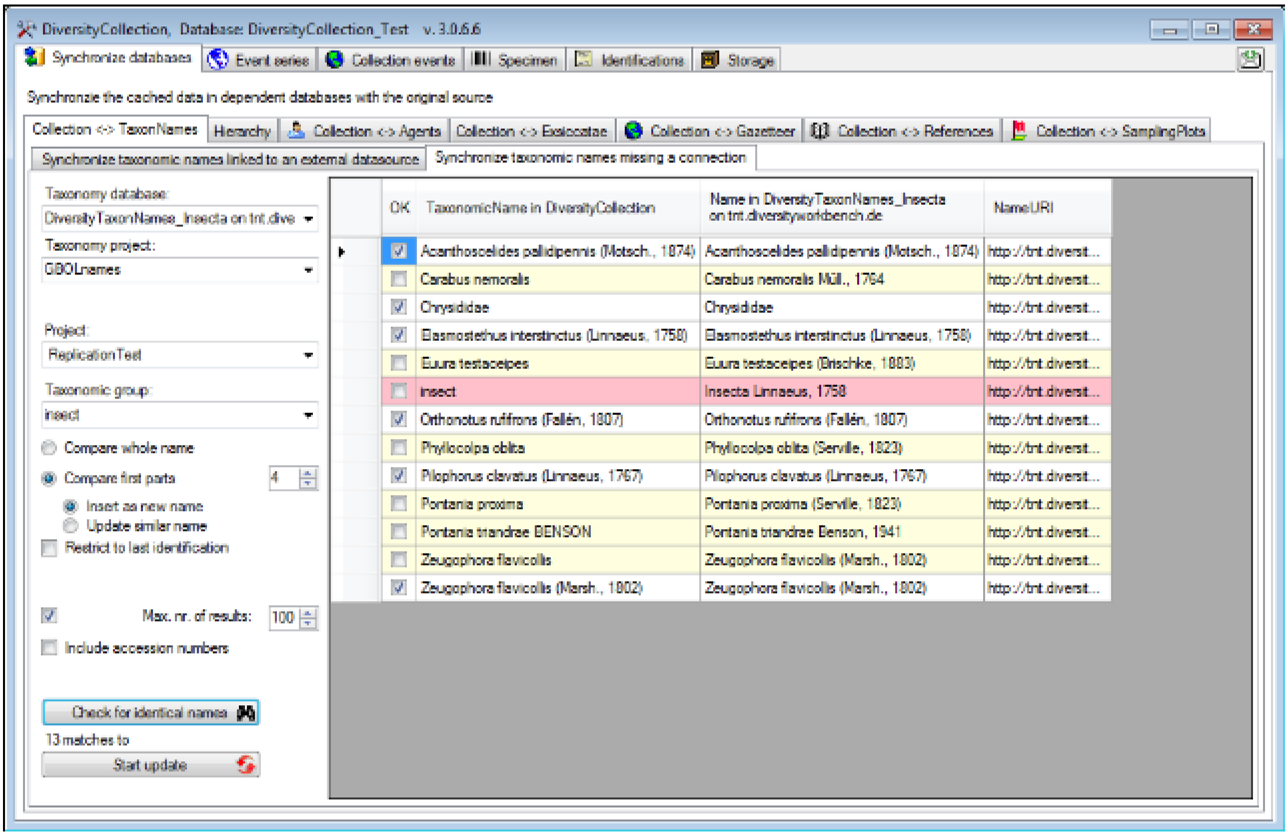
14 differences to IndexFungorum

TaxonomicName in DiversityCollection	Name in IndexFungorum	Na
Albugo candida (Pers.) Kuntze	Albugo candida (Pers.) Roussel	htt
Ascocorticium anomalum (Ellis & Harkn.) Earle	Ascocorticium anomalum (Ellis & Harkn.) J. Schröt.	htt
Camarophyllus russocoriaceus (Berk. & T.K. Mill.) J.E. ...	Camarophyllus russocoriaceus (Berk. & Jos.K. Mill.) J....	htt
Cortinarius anomalus (Fr.) Fr.	Cortinarius anomalus (Pers.) Fr.	htt
Hygrocybe russocoriacea (Berk. & T.K. Mill.) P.D. Orto...	Hygrocybe russocoriacea (Berk. & Jos.K. Mill.) P.D. Or...	htt
Lepiota seminuda (Lasch) Gillet	Lepiota seminuda (Lasch) P. Kummer	htt
Mycena crocata (Schrad.) P. Karst	Mycena crocata (Schrad.) P. Kumm.	htt
Panellus serotinus (Schrad.) Kühner	Panellus serotinus (Pers.) Kühner	htt
Pholiota aurivella (Batsch) Fr.	Pholiota aurivella (Batsch) P. Kumm.	htt
Pycnoporus cinnabarinus (Jacq.) Fr.	Pycnoporus cinnabarinus (Jacq.) P. Karst.	htt
Sphaeropsis visci	Sphaeropsis visci (Alb. & Schwein.) Sacc.	htt
Tephrocybe atrata (L.) Donk	Tephrocybe atrata (Fr.) Donk	htt

The form will list all differences found. To update the database click on the Start update button. If you wish to have a more detailed look on your data, you need to check the **Include accession number** checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

Synchronize taxonomic names missing a connection

Select a taxonomic database and a project within this database, a project in the collection database and a taxonomic group 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 collection database or import the name from the DiversityTaxonNames as a new identification (= **Insert as new name** - see options in the window depicted below). If you choose the option **Restrict to last identification**, the former idenfications of an organism will be ignored. 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.



Synchronize the cached data in dependent databases with the original source

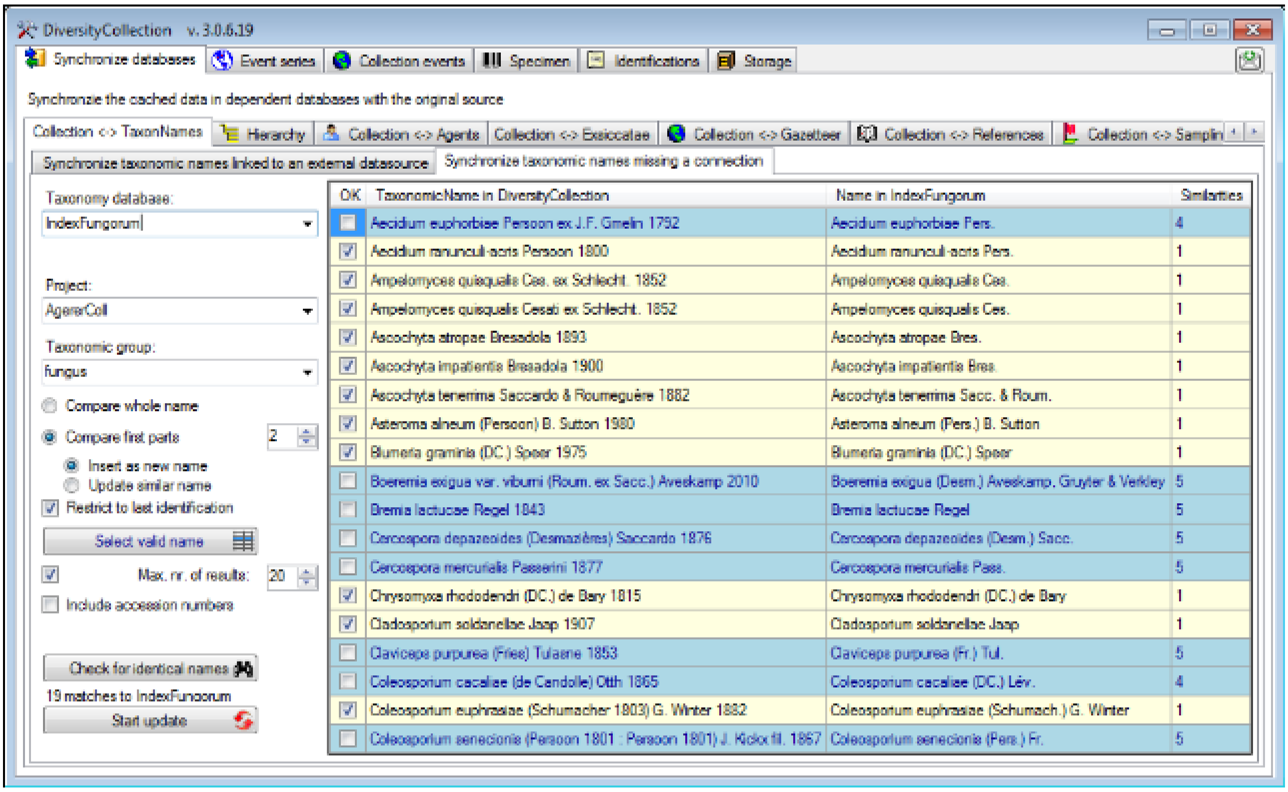
Taxonomy database: DiversityTaxonNames_Insecta on tnt.dive
Taxonomy project: GBOLnames
Project: ReplicationTest
Taxonomic group: insect
○ Compare whole name
● Compare first parts 4
● Insert as new name
○ Update similar name
☐ Restrict to last identification
☑ Max. nr. of results: 100
☐ Include accession numbers
13 matches to

OK	TaxonomicName in DiversityCollection	Name in DiversityTaxonNames_Insecta on tnt.diversityworkbench.de	NameURI
☑	Acanthoscelides pallidipennis (Motsch., 1874)	Acanthoscelides pallidipennis (Motsch., 1874)	http://tnt.diverst...
☐	Carabus nemoralis	Carabus nemoralis Müll., 1764	http://tnt.diverst...
☑	Chrysididae	Chrysididae	http://tnt.diverst...
☑	Elasmostethus interstinctus (Linnaeus, 1758)	Elasmostethus interstinctus (Linnaeus, 1758)	http://tnt.diverst...
☐	Euura testaceipes	Euura testaceipes (Brischke, 1883)	http://tnt.diverst...
☐	insect	Insecta Linnaeus, 1758	http://tnt.diverst...
☑	Orthonotus rufifrons (Fallén, 1807)	Orthonotus rufifrons (Fallén, 1807)	http://tnt.diverst...
☐	Phyllocolpa oblita	Phyllocolpa oblita (Serville, 1823)	http://tnt.diverst...
☑	Pilophorus clavatus (Linnaeus, 1767)	Pilophorus clavatus (Linnaeus, 1767)	http://tnt.diverst...
☐	Pontania proxima	Pontania proxima (Serville, 1823)	http://tnt.diverst...
☐	Pontania triandrae BENSON	Pontania triandrae Benson, 1941	http://tnt.diverst...
☐	Zeugophora flavicollis	Zeugophora flavicollis (Marsh., 1802)	http://tnt.diverst...
☑	Zeugophora flavicollis (Marsh., 1802)	Zeugophora flavicollis (Marsh., 1802)	http://tnt.diverst...

The form will list all matches found. To insert the links to the database click on the Start update button. If you wish to have a more detailed look on your data, you need to check the **Include accession number** checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

Synchronize taxonomic names missing a connection with Index Fungorum

To synchronize the taxonomic names with the webservice of Index Fungorum select IndexFungorum as **Taxonomy database**. You may either compare the entire name or the first parts of the name (see image below and description above). If the name in your data does not match the name in Index Fungorum perfectly, the name will be marked with a yellow background (see below).



Synchronize the cached data in dependent databases with the original source

Taxonomy database: IndexFungorum

Project: AgeraCol

Taxonomic group: fungus

○ Compare whole name

● Compare first parts 2

● Insert as new name

○ Update similar name

☑ Restrict to last identification

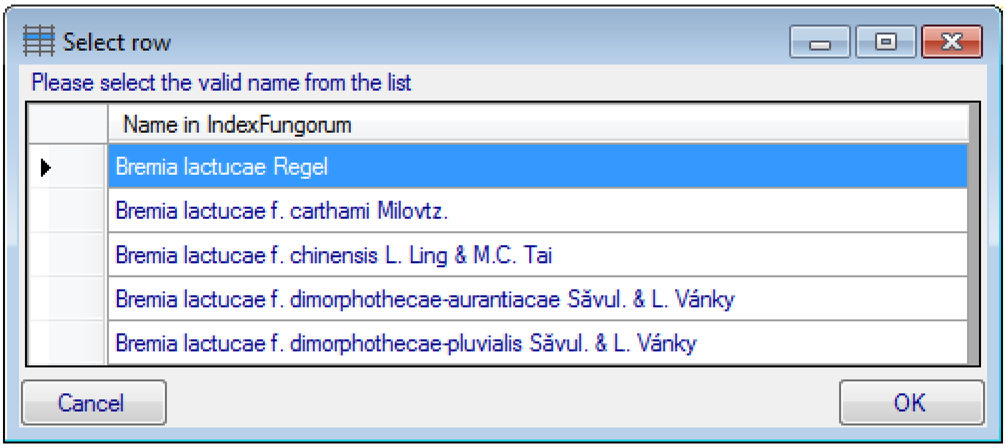
☑ Max. nr. of results: 20

☐ Include accession numbers

19 matches to IndexFungorum

OK	TaxonomicName in DiversityCollection	Name in IndexFungorum	Similarties
☐	Aecidium euphorbiae Persoon ex J.F. Gmelin 1792	Aecidium euphorbiae Pers.	4
☑	Aecidium ranunculi-acris Persoon 1800	Aecidium ranunculi-acris Pers.	1
☑	Ampelomyces quisqualis Ces. ex Schlecht. 1852	Ampelomyces quisqualis Ces.	1
☑	Ampelomyces quisqualis Cesati ex Schlecht. 1852	Ampelomyces quisqualis Ces.	1
☑	Ascochyta atropae Bresadola 1893	Ascochyta atropae Bres.	1
☑	Ascochyta impatientis Bresadola 1900	Ascochyta impatientis Bres.	1
☑	Ascochyta tenerrima Saccardo & Roumeguère 1882	Ascochyta tenerrima Sacc. & Roum.	1
☑	Asteroma alneum (Persoon) B. Sutton 1980	Asteroma alneum (Pers.) B. Sutton	1
☑	Blumeria graminis (DC.) Speer 1975	Blumeria graminis (DC.) Speer	1
☐	Boeremia exigua var. viburni (Roum. ex Sacc.) Aveskamp 2010	Boeremia exigua (Desm.) Aveskamp, Gruyter & Verkley	5
☐	Bremia lactucae Regel 1843	Bremia lactucae Regel	5
☐	Cercospora depazeoides (Desmazières) Saccardo 1876	Cercospora depazeoides (Desm.) Sacc.	5
☐	Cercospora mercurialis Passerini 1877	Cercospora mercurialis Pass.	5
☑	Chrysomyxa rhododendri (DC.) de Bary 1815	Chrysomyxa rhododendri (DC.) de Bary	1
☑	Cladosporium soldanellae Jaap 1907	Cladosporium soldanellae Jaap	1
☐	Claviceps purpurea (Fries) Tulasne 1853	Claviceps purpurea (Fr.) Tul.	5
☐	Coleosporium cacaliae (de Candolle) Otth 1865	Coleosporium cacaliae (DC.) Lév.	4
☑	Coleosporium euphrasiae (Schumacher 1803) G. Winter 1882	Coleosporium euphrasiae (Schumach.) G. Winter	1
☐	Coleosporium senecionis (Persoon 1801 : Persoon 1801) J. Kickx fil. 1867	Coleosporium senecionis (Pers.) Fr.	5

Names where several similar names were found will be marked with a blue background. To select one of the similar names click on the **Select valid name** button. A window will open as shown below listing all similar names found in Index Fungorum. Select one name and click OK to use it.



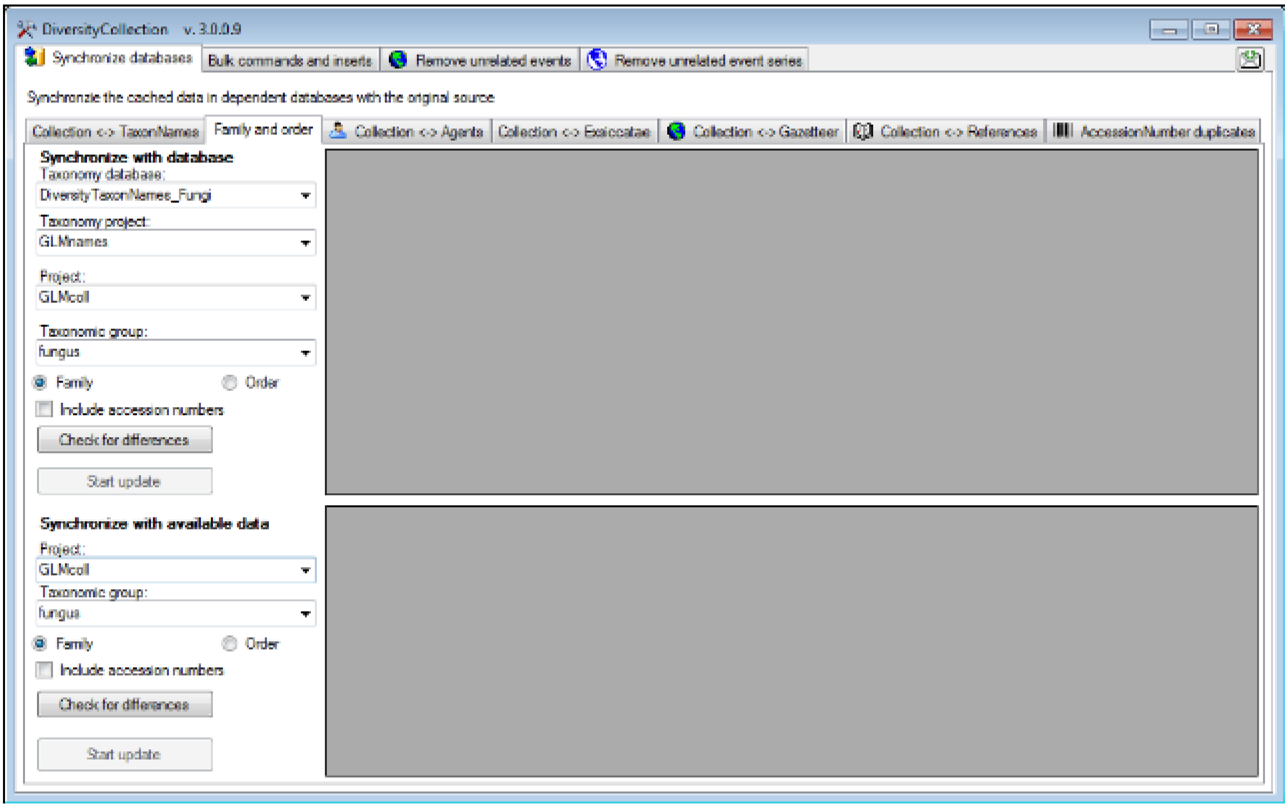
Please select the valid name from the list

Name in IndexFungorum
Bremia lactucae Regel
Bremia lactucae f. carthami Milovtz.
Bremia lactucae f. chinensis L. Ling & M.C. Tai
Bremia lactucae f. dimorphothecae-aurantiacae Săvul. & L. Vánky
Bremia lactucae f. dimorphothecae-pluvialis Săvul. & L. Vánky

Maintenance - Family and Order

To synchronize the entries for the family and order of taxa derived from the module DiversityTaxonNames choose **Administration -> Maintenance** from the menu. A window will open as shown below. To synchronize the higher taxonomic entries for entries linked to the module DiversityTaxonNames choose the tab **Family and order**. These entries are stored in the fields FamilyCache and OrderCache in the table IdentificationUnit.

In the upper part you may synchronize your data with the entries in taxonomic databases like DiversityTaxonNames_Fungi. Select a taxonomic database, a project and a taxonomic group, then choose whether you wish to synchronize the family or the order. If you wish to inspect single data sets you need to check the **Include accession number** checkbox. Then click on the Check for differences button to start the query.



Synchronize with database

Taxonomy database: DiversityTaxonNames_Fungi

Taxonomy project: GLMnames

Project: GLMcoll

Taxonomic group: fungus

● Family ○ Order

☐ Include accession numbers

Synchronize with available data

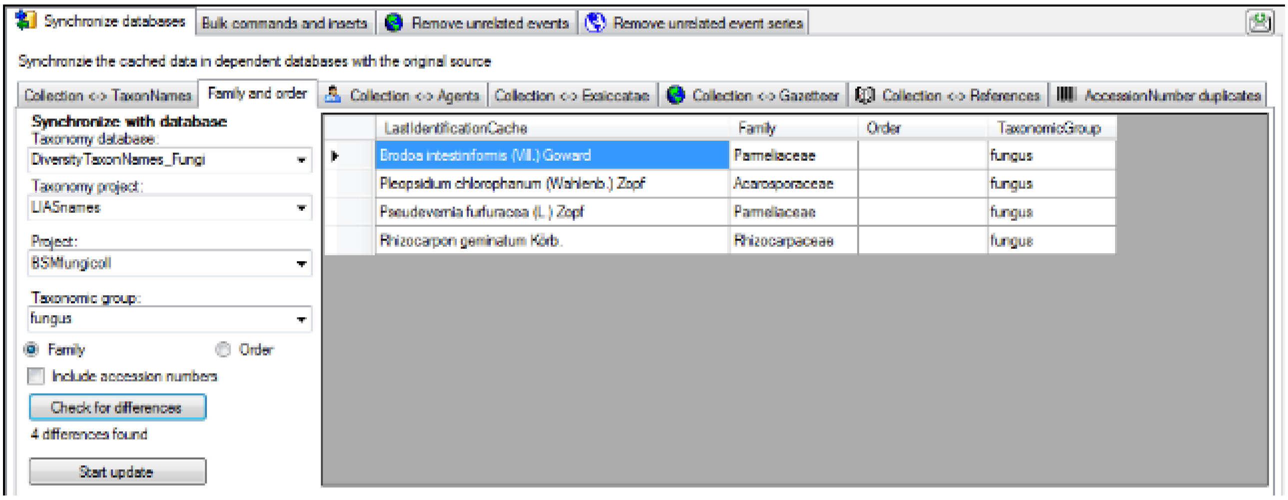
Project: GLMcoll

Taxonomic group: fungus

● Family ○ Order

☐ Include accession numbers

The form will list all differences found as shown below. To update the database click on the Start update button.

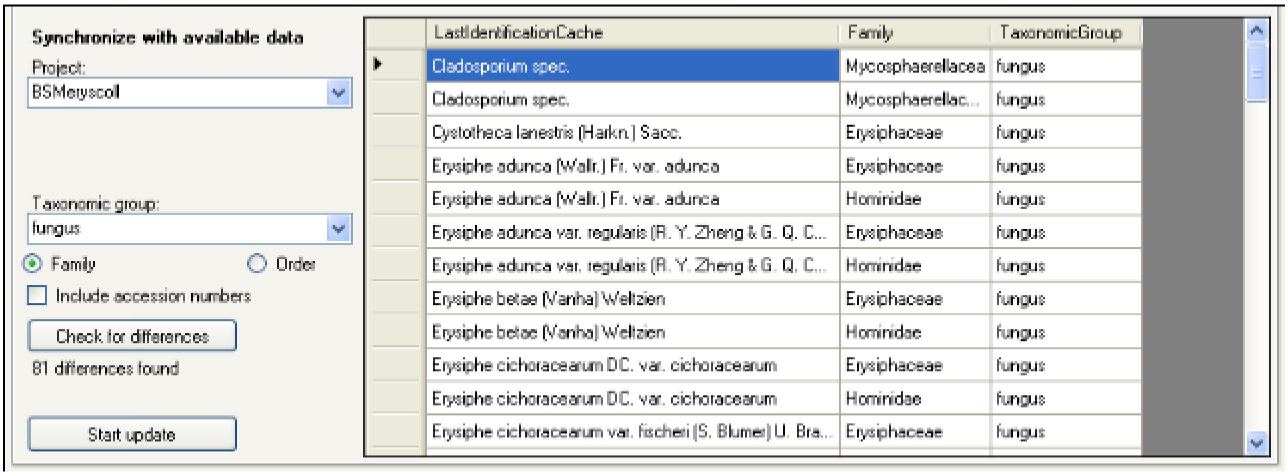


Synchronzie the cached data in dependent databases with the original source

Synchronize with database
Taxonomy database: DiversityTaxonNames_Fungi
Taxonomy project: UASnames
Project: BSMfungicoll
Taxonomic group: fungus
● Family ○ Order
☐ Include accession numbers
4 differences found

LastIdentificationCache	Family	Order	TaxonomicGroup
Brodoa intestiniformis (Vill.) Goward	Parmeliaceae		fungus
Pleopsidium chlorophanum (Wahlenb.) Zopf	Acarosporaceae		fungus
Pseudevernia furfuracea (L.) Zopf	Parmeliaceae		fungus
Rhizocarpon geminatum Körb.	Rhizocarpaceae		fungus

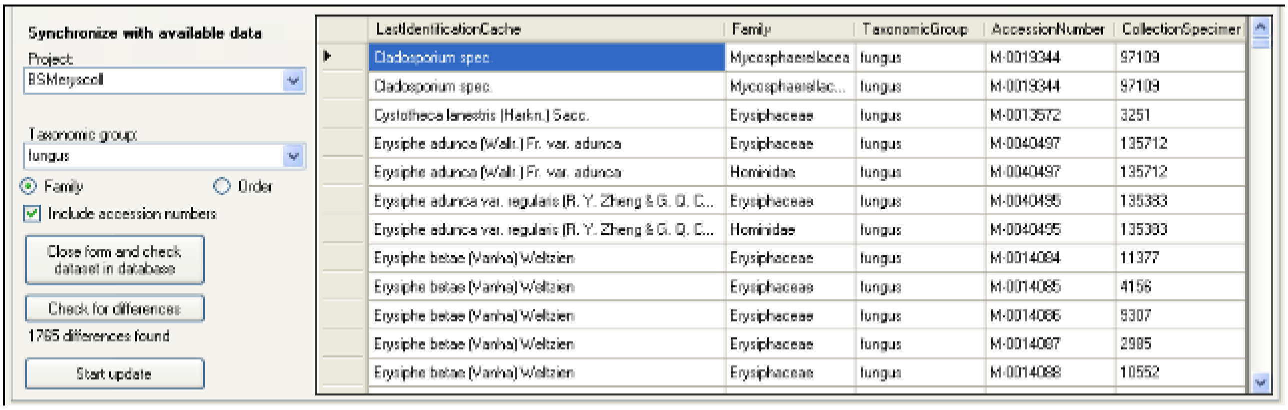
In the lower part you may synchronize your entries within the database. Choose a project, the taxonomic group and if you wish, the family or the order and click on the Check for differences button to start the query. To import the higher taxa to the data set click on the Start update button.



Synchronize with available data
Project: BSMeryscoll
Taxonomic group: fungus
● Family ○ Order
☐ Include accession numbers
81 differences found

LastIdentificationCache	Family	TaxonomicGroup
Cladosporium spec.	Mycosphaerellacea	fungus
Cladosporium spec.	Mycosphaerellac...	fungus
Cystotheca lanestris (Harkn.) Sacc.	Erysiphaceae	fungus
Erysiphe adunca (Wallr.) Fr. var. adunca	Erysiphaceae	fungus
Erysiphe adunca (Wallr.) Fr. var. adunca	Hominidae	fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. Q. C...	Erysiphaceae	fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. Q. C...	Hominidae	fungus
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus
Erysiphe betae (Vanha) Weltzien	Hominidae	fungus
Erysiphe cichoracearum DC. var. cichoracearum	Erysiphaceae	fungus
Erysiphe cichoracearum DC. var. cichoracearum	Hominidae	fungus
Erysiphe cichoracearum var. fischeri (S. Blumer) U. Bra...	Erysiphaceae	fungus

If you wish to have a more detailed look on your data, you need to check the **Include accession number** checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.



Synchronize with available data
Project: BSMeryscoll
Taxonomic group: fungus
● Family ○ Order
☑ Include accession numbers
1765 differences found

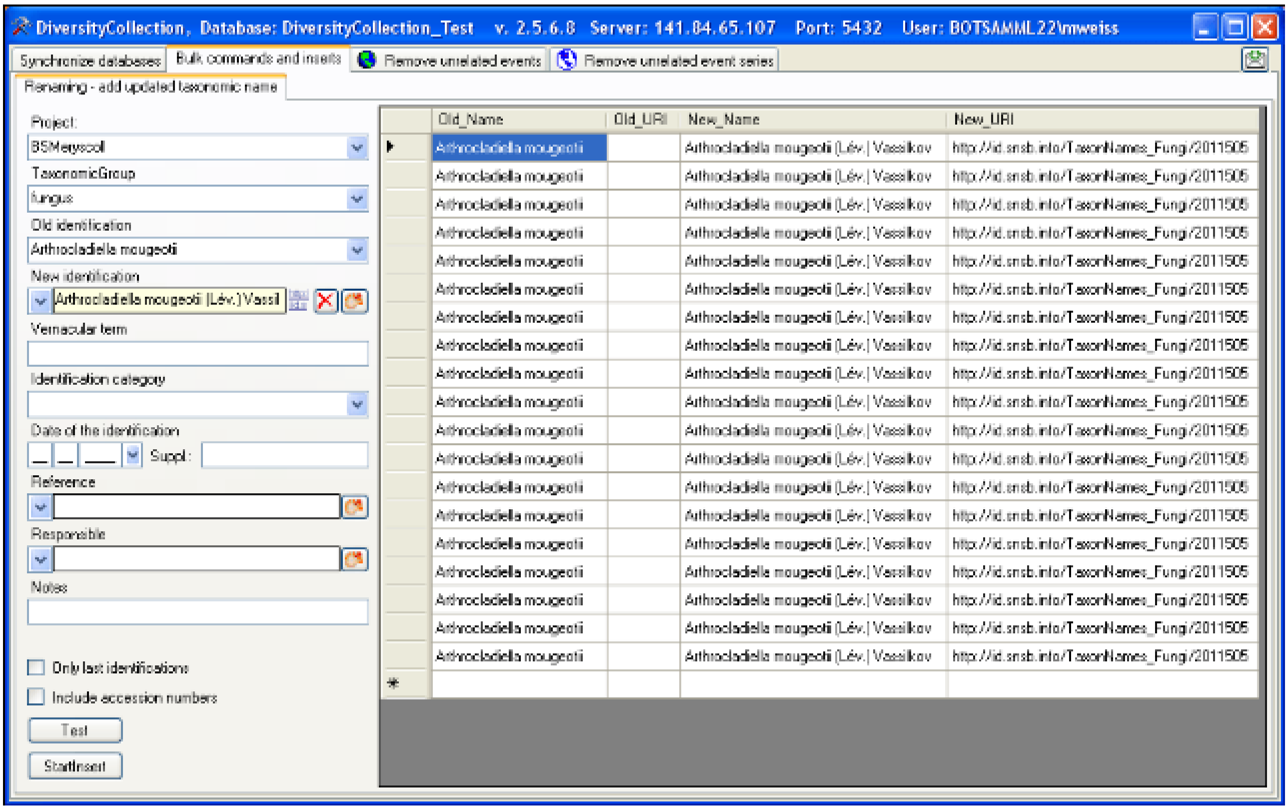
LastIdentificationCache	Family	TaxonomicGroup	AccessionNumber	CollectionSpecimen
Cladosporium spec.	Mycosphaerellacea	fungus	M-0019344	97109
Cladosporium spec.	Mycosphaerellac...	fungus	M-0019344	97109
Cystotheca lanestris (Harkn.) Sacc.	Erysiphaceae	fungus	M-0013572	3251
Erysiphe adunca (Wallr.) Fr. var. adunca	Erysiphaceae	fungus	M-0040497	135712
Erysiphe adunca (Wallr.) Fr. var. adunca	Hominidae	fungus	M-0040497	135712
Erysiphe adunca var. regularis (R. Y. Zheng & G. Q. C...	Erysiphaceae	fungus	M-0040495	135383
Erysiphe adunca var. regularis (R. Y. Zheng & G. Q. C...	Hominidae	fungus	M-0040495	135383
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus	M-0014084	11377
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus	M-0014085	4156
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus	M-0014086	9307
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus	M-0014087	2985
Erysiphe betae (Vanha) Weltzien	Erysiphaceae	fungus	M-0014088	10552

Maintenance - identifications

If you wish to add updated taxonomic names for specimen in the database, you can use the bulk insert function. Choose the project, the taxonomic group and the taxonomic name for which the new identification should be added. As shown in the window below you may enter additional information about this identification. By default the **[Only last identification]** option is checked to prevent you from searching in older identifications. If you uncheck this option, the program will search for any identification, irrespective whether it is the last or an older identification.

If you wish to check single data sets check the **[Include accession numbers]** option. A new button will appear which will enable you to close the window and turn to a specimen selected in the table.

To search for names click on the **[Test]** button. The found names will be listed in the table as shown below. To insert the new identification click the **[Start insert]** button.



Project: BSMeryscoll

TaxonomicGroup: fungus

Old identification: Arthrocladiella mougeotii

New identification: Arthrocladiella mougeotii (Lév.) Vassil

Vernacular term:

Identification category:

Date of the identification: __ __ ____ Suppl.:

Reference:

Responsible:

Notes:

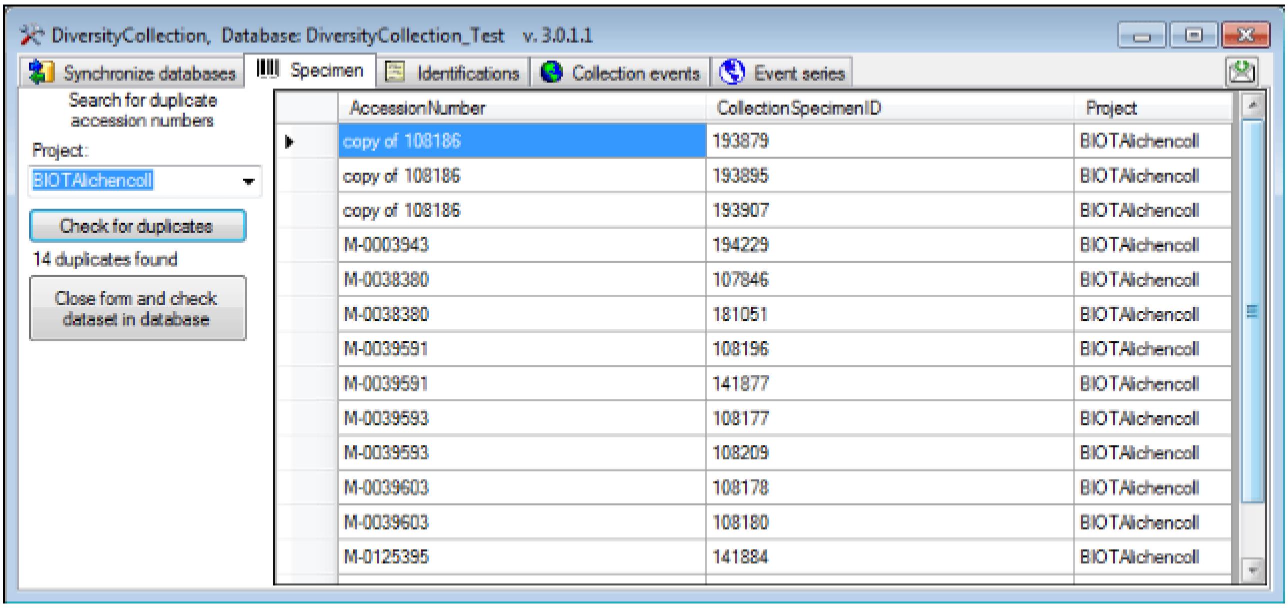
☐ Only last identifications

☐ Include accession numbers

Old_Name	Old_URI	New_Name	New_URI
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505
Arthrocladiella mougeotii		Arthrocladiella mougeotii (Lév.) Vassilkov	http://id.snsb.info/TaxonNames_Fungi/2011505

Maintenance - Accession number duplicates

The database will warn but not prevent you from entering an accession number several times e.g. via an import. To check for duplicate accession numbers choose **Administration -> Maintenance** from the menu. A window will open as shown below. On the tab page **Specimen** you may restrict the query to a project. To start the query simply click on the **Check for duplictes** button.



Project: BIOTAlichencoll

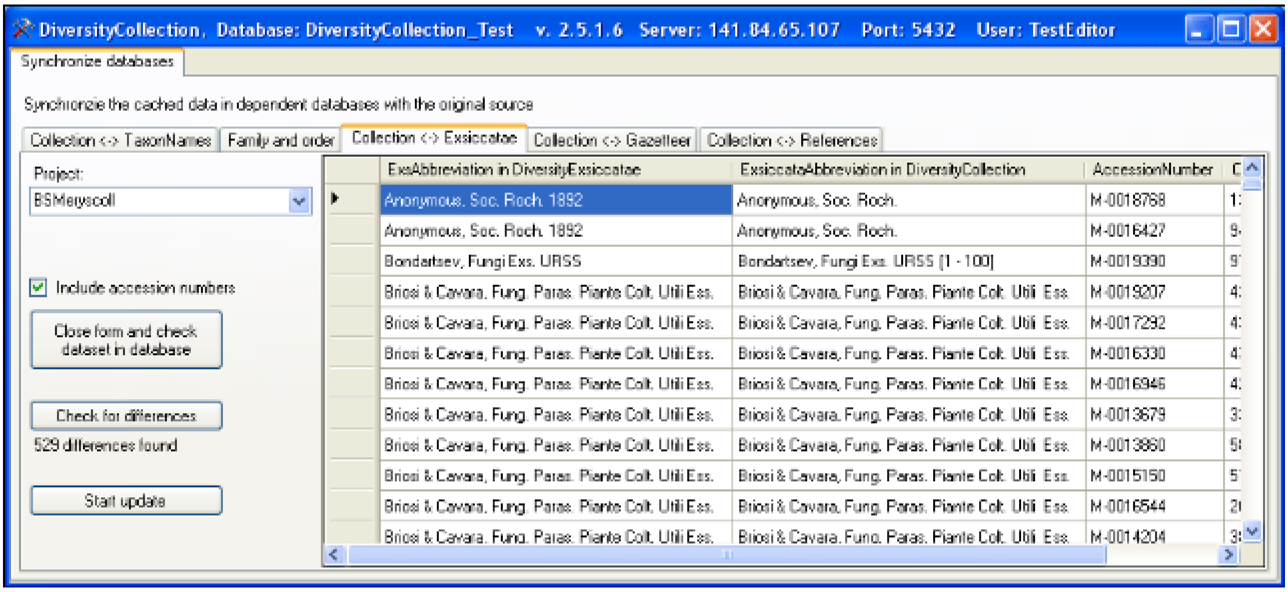
14 duplicates found

AccessionNumber	CollectionSpecimenID	Project
copy of 108186	193879	BIOTAlichencoll
copy of 108186	193895	BIOTAlichencoll
copy of 108186	193907	BIOTAlichencoll
M-0003943	194229	BIOTAlichencoll
M-0038380	107846	BIOTAlichencoll
M-0038380	181051	BIOTAlichencoll
M-0039591	108196	BIOTAlichencoll
M-0039591	141877	BIOTAlichencoll
M-0039593	108177	BIOTAlichencoll
M-0039593	108209	BIOTAlichencoll
M-0039603	108178	BIOTAlichencoll
M-0039603	108180	BIOTAlichencoll
M-0125395	141884	BIOTAlichencoll

The form will list all duplicates found as shown above. To switch to a data set in the database select it in the table and click on the Close form and check dataset in database button.

Maintenance - Exsiccatae

To synchronize the abbreviations of the exsiccatal series titles which are linked to the module DiversityExsiccatae choose **Administration -> Maintenance...** from the menu. A window will open as shown below. On the tab page **Collection <-> Exsiccatae** select the project for which the titles should be synchronized. The title is stored in the field ExsiccataAbbreviation in the table CollectionSpecimen. Select the project which should be synchronized and start the query by clicking on the Check for differences button.


DiversityCollection, Database: DiversityCollection_Test v. 2.5.1.6 Server: 141.84.65.107 Port: 5432 User: TestEditor

Synchronzie the cached data in dependent databases with the original source

Project: BSMeyscoll

☑ Include accession numbers

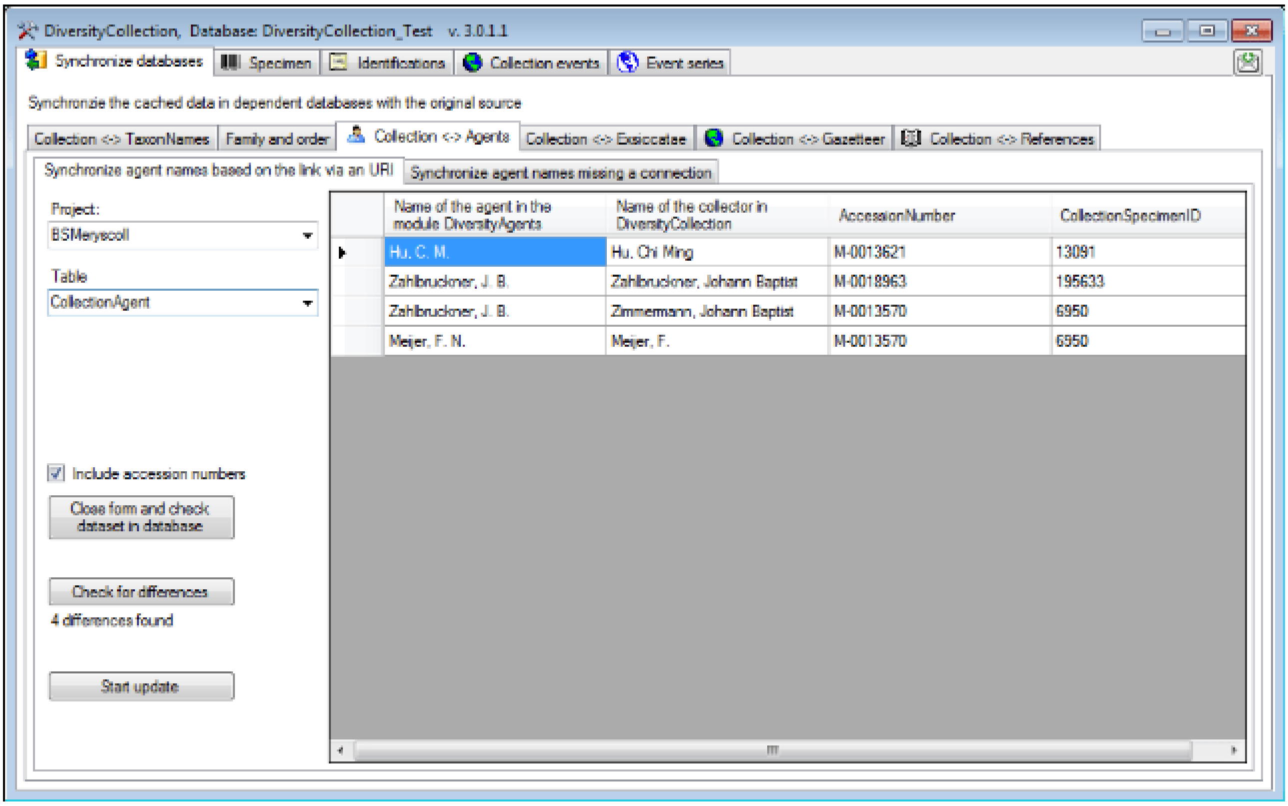
529 differences found

	ExsAbbreviation in DiversityExsiccatae	ExsiccataAbbreviation in DiversityCollection	AccessionNumber	C
▶	Anonymous, Soc. Roch. 1892	Anonymous, Soc. Roch.	M-0018768	1
	Anonymous, Soc. Roch. 1892	Anonymous, Soc. Roch.	M-0016427	9
	Bondartsev, Fungi Exs. URSS	Bondartsev, Fungi Exs. URSS [1 - 100]	M-0019390	9
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0019207	4
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0017292	4
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0016330	4
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0016946	4
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0013679	3
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0013860	5
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0015150	5
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0016544	2
	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	Briosi & Cavara, Fung. Paras. Piante Colt. Utili Ess.	M-0014204	3

The form will list all differences found. To update the database click on the Start update button. If you wish to have a more detailed look at your data, you need to check the "Include accession number" checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

Maintenance - Agents

To synchronize the names of collectors, determinators etc. which are linked to the module DiversityAgents choose **Administration -> Maintenance** from the menu. A window will open as shown below. On the tab page **Collection <-> Agents** select the project for which the agents should be synchronized. There are 9 tables which may contain links to DiversityAgents: Collection, CollectionAgent, CollectionEventLocalisation, CollectionEventProperty, CollectionSpecimen, CollectionSpecimenProcessing, Identification, IdentificationUnitAnalysis and Transaction. Choose one of these tables for the synchronization. Then start the query with a click on the Check for differences button. The type name is written as defined by the default display type in the module DiversityAgents - for more information please see the documentation on DiversityAgents.



Project: BSMerysecoll

Table: CollectionAgent

☑ Include accession numbers

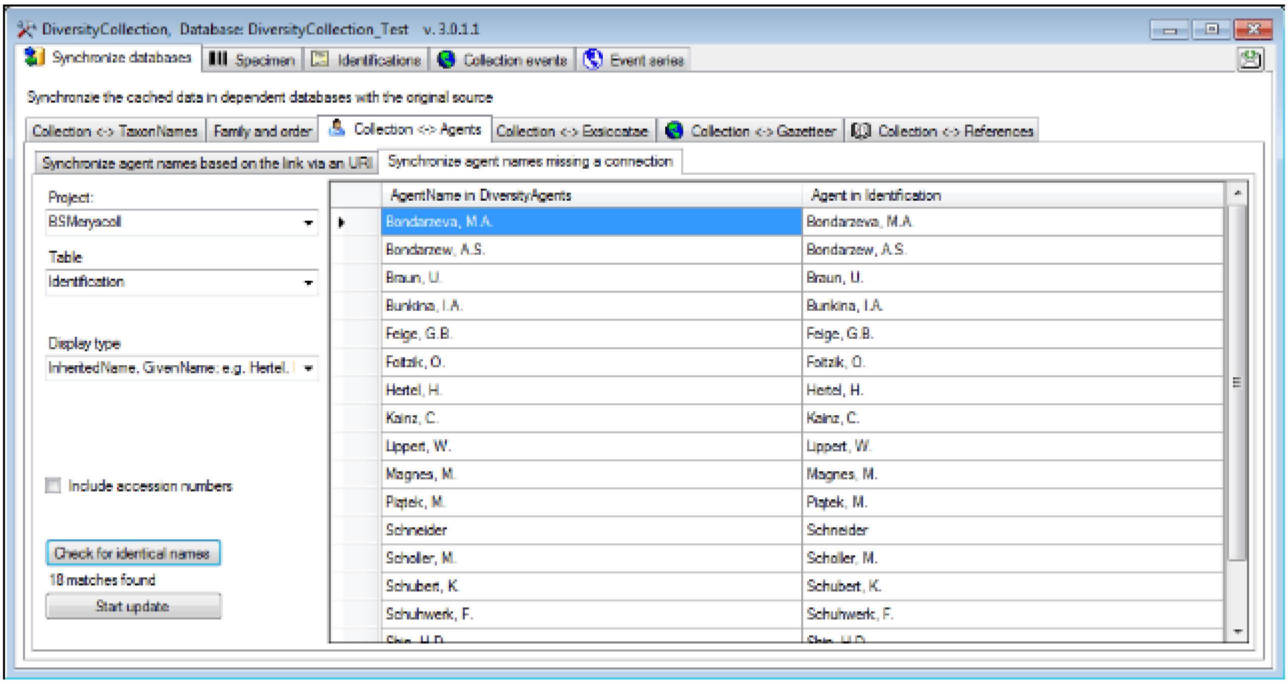
4 differences found

Name of the agent in the module DiversityAgents	Name of the collector in DiversityCollection	AccessionNumber	CollectionSpecimenID
Hu, C. M.	Hu, Chi Ming	M-0013621	13091
Zahlbruckner, J. B.	Zahlbruckner, Johann Baptist	M-0018963	195633
Zahlbruckner, J. B.	Zimmermann, Johann Baptist	M-0013570	6950
Meijer, F. N.	Meijer, F.	M-0013570	6950

The form will list all differences found. To update the database click on the Start update button. If you wish to have a more detailed look on one of the data sets in the list, you need to check the "Include accession number" checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

Search for possible links

You can either update the cached names for entries which are linked to DiversityAgents as described above or you can search for possible links based on the names as shown below. In addition to the options described above you may choose the display type for the query to find any possible match as names may be written like "Hertel, H.", "H. Hertel" etc.



Synchronzie the cached data in dependent databases with the original source

Project: BSMeryacoll

Table: Identification

Display type: InheritedName, GivenName: e.g. Hertel, I

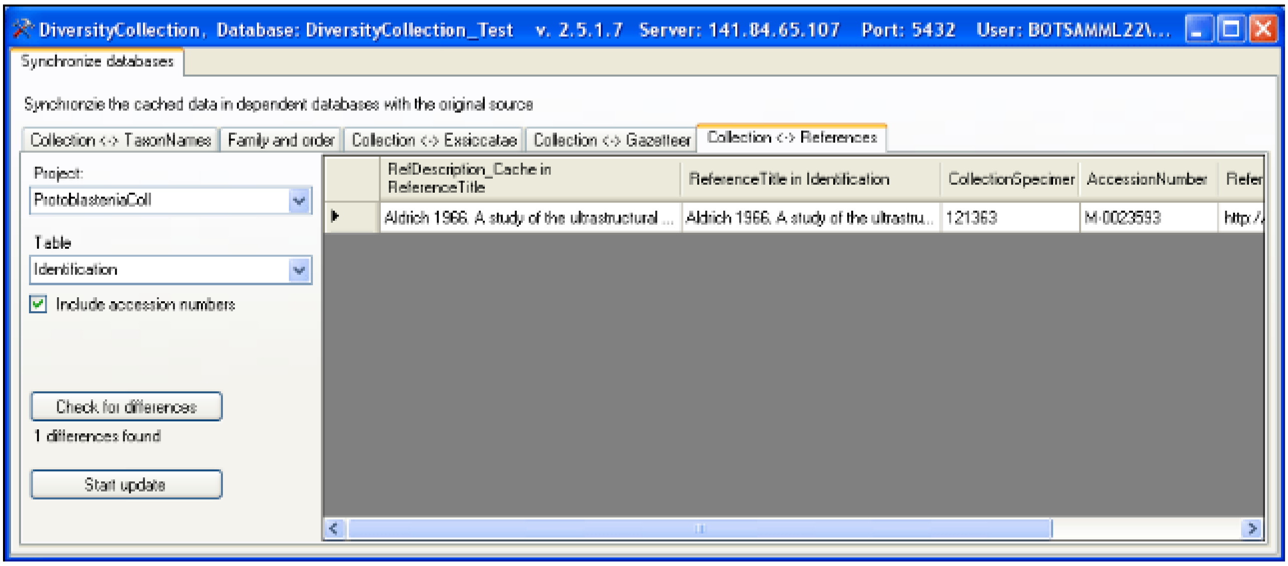
☐ Include accession numbers

18 matches found

AgentName in DiversityAgents	Agent in Identification
Bondarzeva, M.A.	Bondarzeva, M.A.
Bondarzew, A.S.	Bondarzew, A.S.
Braun, U.	Braun, U.
Bunkina, I.A.	Bunkina, I.A.
Feige, G.B.	Feige, G.B.
Foltzik, O.	Foltzik, O.
Hertel, H.	Hertel, H.
Kainz, C.	Kainz, C.
Lippert, W.	Lippert, W.
Magnes, M.	Magnes, M.
Piątek, M.	Piątek, M.
Schneider	Schneider
Scholler, M.	Scholler, M.
Schubert, K.	Schubert, K.
Schuhwerk, F.	Schuhwerk, F.

Maintenance - References

To synchronize the titles of the references which are linked to the module DiversityReferences choose **Administration -> Maintenance** from the menu. A window will open as shown below. On the tab page **Collection <-> References** select the project for which the reference titles should be synchronized. There are 3 tables which may contain links to DiversityReferences: CollectionEvent, CollectionSpecimen and Identification. Choose one of these tables for synchronization. Start the query with a click on the Check for differences button.


DiversityCollection, Database: DiversityCollection_Test v. 2.5.1.7 Server: 141.84.65.107 Port: 5432 User: BOTSAMML22\...

Synchronize databases

Synchronzie the cached data in dependent databases with the original source

Project: ProtoblasteniaColl

Table: Identification

☑ Include accession numbers

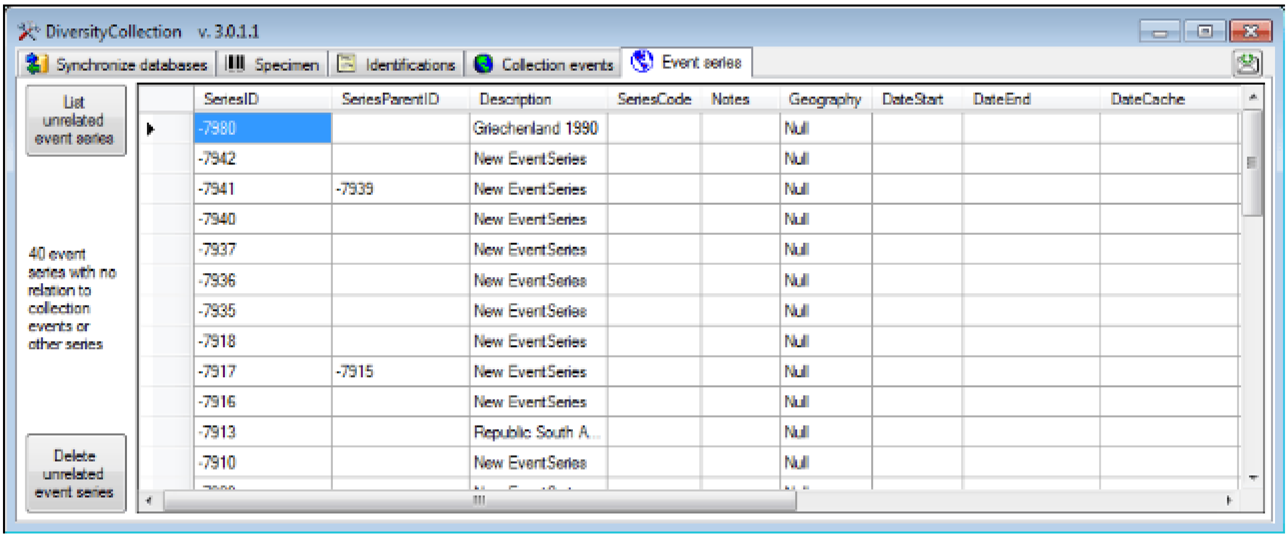
1 differences found

RefDescription_Cache in ReferenceTitle	ReferenceTitle in Identification	CollectionSpecimen	AccessionNumber	Refer
Aldrich 1966. A study of the ultrastructural ...	Aldrich 1966. A study of the ultrastru...	121363	M-0023593	http:/

The form will list all differences found. To update the database click on the Start update button. If you wish to have a more detailed look on one of the data sets in the list, you need to check the "Include accession number" checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

Maintenance - CollectionEventSeries

To delete CollectionEventSeries with no relation to CollectionEvents or other event series choose the tab page **Event series**. Click the **List unrelated event series** button to list these series and the **Delete unrelated event series** button to delete them.



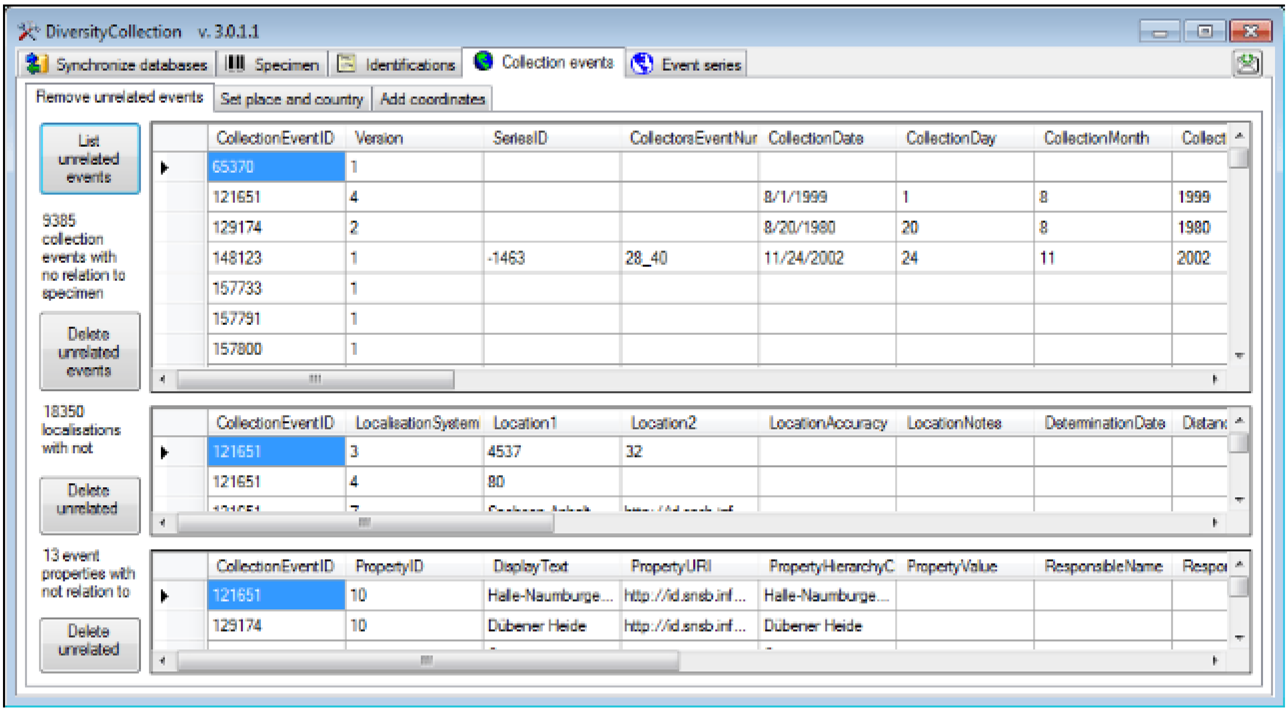
40 event series with no relation to collection events or other series

SeriesID	SeriesParentID	Description	SeriesCode	Notes	Geography	DateStart	DateEnd	DateCache
-7980		Griechenland 1990			Null			
-7942		New EventSeries			Null			
-7941	-7939	New EventSeries			Null			
-7940		New EventSeries			Null			
-7937		New EventSeries			Null			
-7936		New EventSeries			Null			
-7935		New EventSeries			Null			
-7918		New EventSeries			Null			
-7917	-7915	New EventSeries			Null			
-7916		New EventSeries			Null			
-7913		Republic South A...			Null			
-7910		New EventSeries			Null			

Maintenance - CollectionEvent

CollectionEvents - unrelated events

Provided you have the proper rights you can remove unlinked data sets in the tables CollectionEvent and CollectionEventSeries. To delete events which are not linked to any data in the database use the tab page **CollectionEvents** - **Remove unrelated events**. These unrelated data sets may e.g. be derived from specimens which were transferred to another CollectionEvent. Click on the **[List unrelated events]** button to list all events which are not related to a specimen. The found CollectionEvents will be listed in the upper part of the form. The lower part shows the localisations and the event properties related to these CollectionEvents. These must be deleted first before you can delete the events related to these data sets. Otherwise only the events with no relations to localisations or properties will be deleted.



9385 collection events with no relation to specimen

CollectionEventID	Version	SeriesID	CollectorsEventNur	CollectionDate	CollectionDay	CollectionMonth	Collect
65370	1						
121651	4			8/1/1999	1	8	1999
129174	2			8/20/1980	20	8	1980
148123	1	-1463	28_40	11/24/2002	24	11	2002
157733	1						
157791	1						
157800	1						

18350 localisations with not

CollectionEventID	LocalisationSystem	Location1	Location2	LocationAccuracy	LocationNotes	DeterminationDate	Distanc
121651	3	4537	32				
121651	4	80					

13 event properties with not relation to

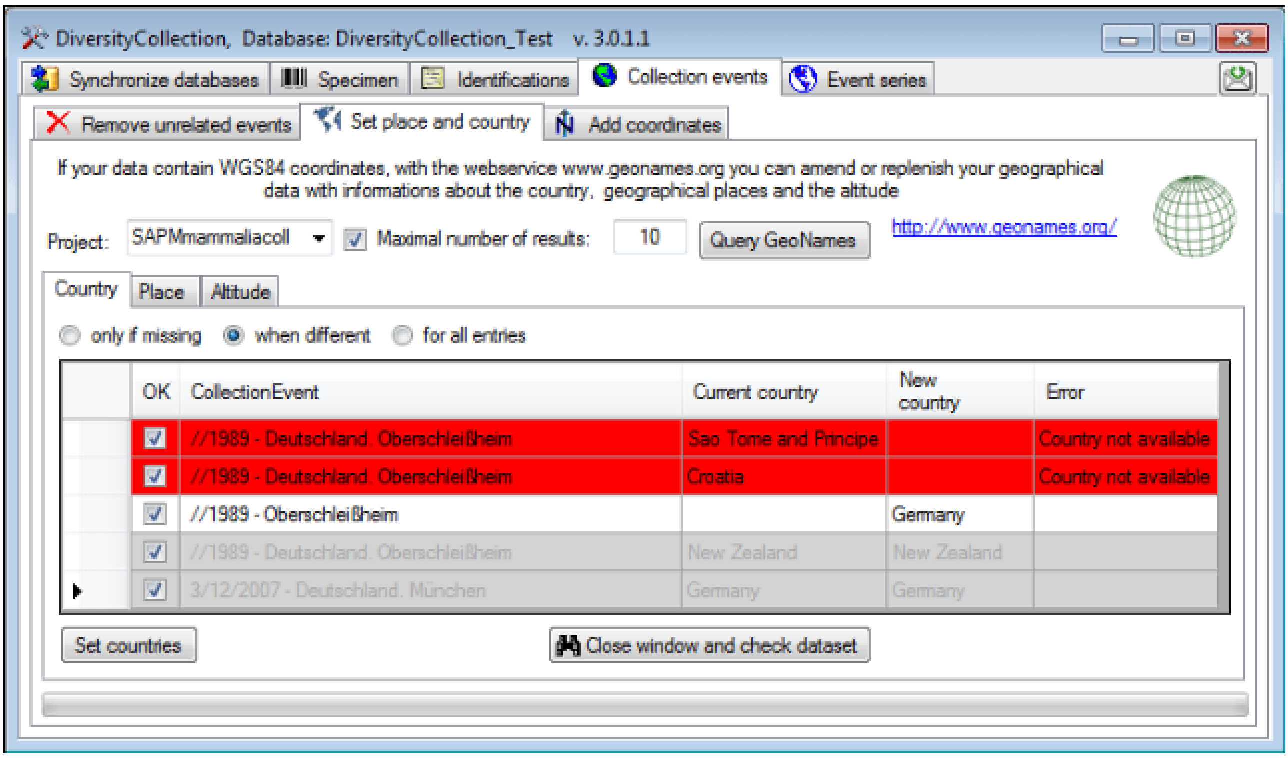
CollectionEventID	PropertyID	DisplayText	PropertyURI	PropertyHierarchyC	PropertyValue	ResponsibleName	Respo
121651	10	Halle-Naumburge...	http://id.snsb.inf...	Halle-Naumburge...			
129174	10	Dübener Heide	http://id.snsb.inf...	Dübener Heide			

Country, Place and Altitude via GeoNames

If your data sets contain WGS84 Coordinates, you can use the webservice www.geonames.org to insert or update the country, the place or the altitude of your collection sites. Choose the tab **Set place and country**, the project you wish to update and an optional upper limit of the data sets (recommended for slow connections). Click the **Query GeoNames** button to start the query. According to the selected option (only if missing / when different / for all entries) the retrieved data will be marked with colors as shown in the images below.

White	The data set will be inserted or changed
Red	An error occured
Grey	According to the selected option this data set will not be inserted or changed
Yellow	The data set has been deselected and will not be inserted or changed
Gree	The data set has been inserted or changed

n



If your data contain WGS84 coordinates, with the webservice www.geonames.org you can amend or replenish your geographical data with informations about the country, geographical places and the altitude

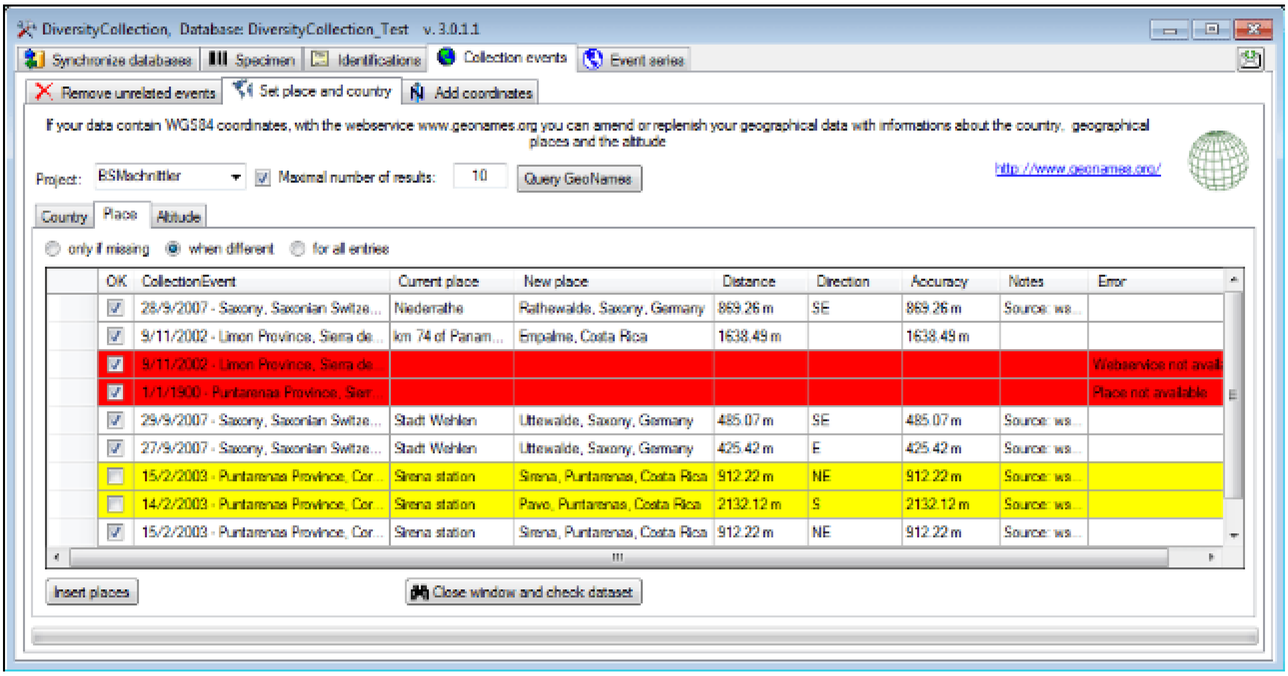
Project: SAPMmammaliacoll ☑ Maximal number of results: 10

○ only if missing ● when different ○ for all entries

OK	CollectionEvent	Current country	New country	Error
☑	//1989 - Deutschland, Oberschleißheim	Sao Tome and Principe		Country not available
☑	//1989 - Deutschland, Oberschleißheim	Croatia		Country not available
☑	//1989 - Oberschleißheim		Germany	
☑	//1989 - Deutschland, Oberschleißheim	New Zealand	New Zealand	
☑	3/12/2007 - Deutschland, München	Germany	Germany	

In the first column you can deselect a data set for the update. To inspect a single data set from the list select it and click on the **Close window and check data set** button. To update the data set click on the **Set countries** button.

As for countries, the places will be listed as shown below.



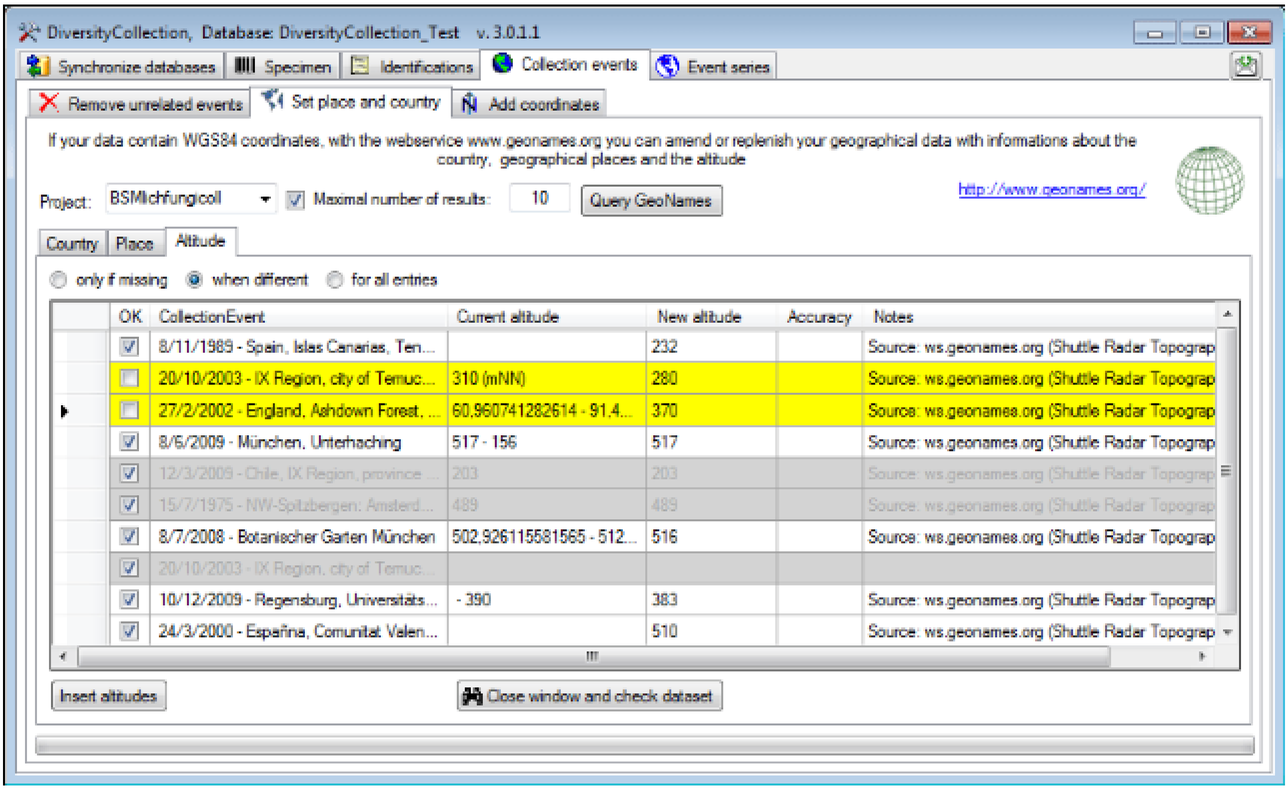
If your data contain WGS84 coordinates, with the webservice www.geonames.org you can amend or replenish your geographical data with informations about the country, geographical places and the altitude

Project: BSMachnitter ☑ Maximal number of results: 10

○ only if missing ● when different ○ for all entries

OK	CollectionEvent	Current place	New place	Distance	Direction	Accuracy	Notes	Error
☑	28/9/2007 - Saxony, Saxonian Switze...	Niederrathe	Rathewalde, Saxony, Germany	869.26 m	SE	869.26 m	Source: ws...	
☑	9/11/2002 - Limon Province, Sierra de...	km 74 of Panam...	Empalme, Costa Rica	1638.49 m		1638.49 m		
☑	9/11/2002 - Limon Province, Sierra de...							Webservice not avail
☑	1/1/1900 - Puntarenas Province, Sier...							Place not available
☑	29/9/2007 - Saxony, Saxonian Switze...	Stadt Wehlen	Uttewalde, Saxony, Germany	485.07 m	SE	485.07 m	Source: ws...	
☑	27/9/2007 - Saxony, Saxonian Switze...	Stadt Wehlen	Uttewalde, Saxony, Germany	425.42 m	E	425.42 m	Source: ws...	
☐	15/2/2003 - Puntarenas Province, Cor...	Sirena station	Sirena, Puntarenas, Costa Rica	912.22 m	NE	912.22 m	Source: ws...	
☐	14/2/2003 - Puntarenas Province, Cor...	Sirena station	Pavo, Puntarenas, Costa Rica	2132.12 m	S	2132.12 m	Source: ws...	
☑	15/2/2003 - Puntarenas Province, Cor...	Sirena station	Sirena, Puntarenas, Costa Rica	912.22 m	NE	912.22 m	Source: ws...	

To insert or update the selected data sets click the **Insert places** button.



If your data contain WGS84 coordinates, with the webservice www.geonames.org you can amend or replenish your geographical data with informations about the country, geographical places and the altitude

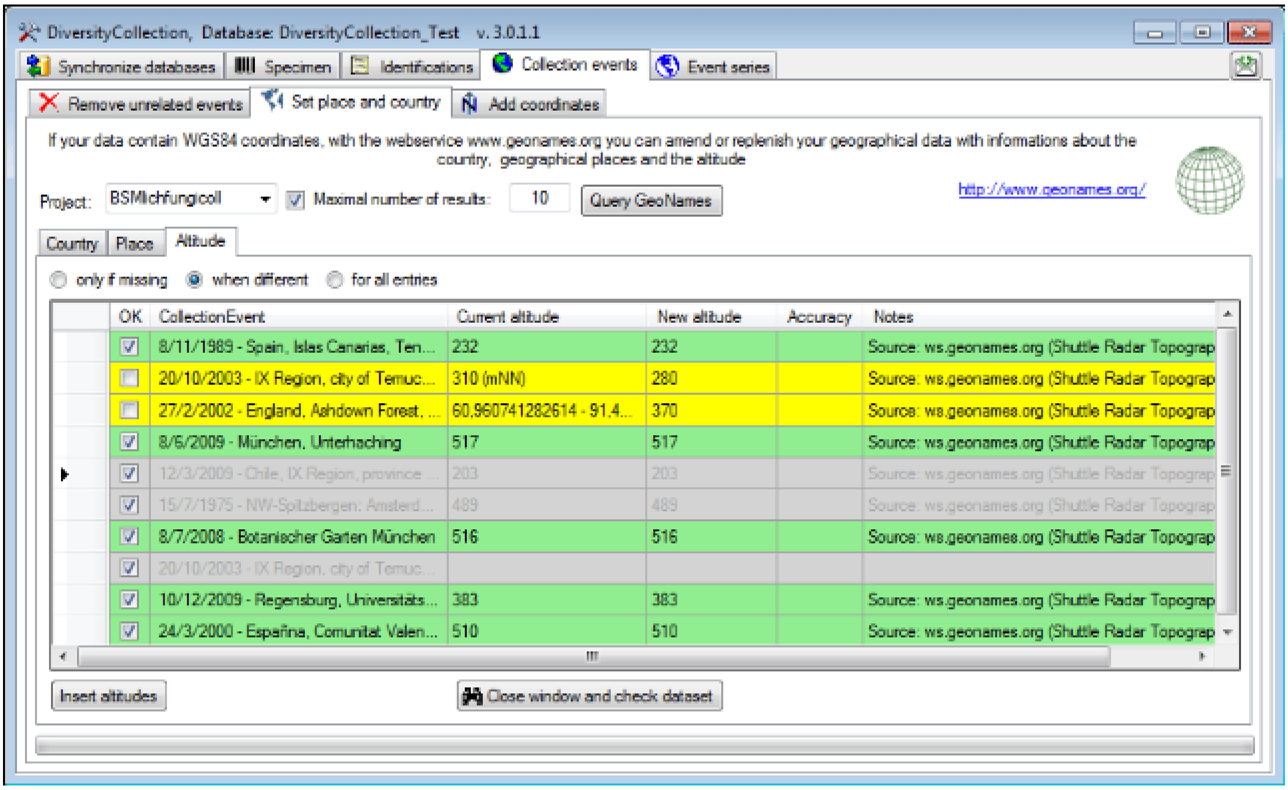
Project: BSMlchfungicoll

☑ Maximal number of results: 10

○ only if missing ● when different ○ for all entries

OK	CollectionEvent	Current altitude	New altitude	Accuracy	Notes
☑	8/11/1989 - Spain, Islas Canarias, Ten...		232		Source: ws.geonames.org (Shuttle Radar Topograp
☐	20/10/2003 - IX Region, city of Temuc...	310 (mNN)	280		Source: ws.geonames.org (Shuttle Radar Topograp
☐	27/2/2002 - England, Ashdown Forest, ...	60,960741282614 - 91.4...	370		Source: ws.geonames.org (Shuttle Radar Topograp
☑	8/6/2009 - München, Unterhaching	517 - 156	517		Source: ws.geonames.org (Shuttle Radar Topograp
☑	12/3/2009 - Chile, IX Region, province	203	203		Source: ws.geonames.org (Shuttle Radar Topograp
☑	15/7/1975 - NW-Spitzbergen: Amsterd...	489	489		Source: ws.geonames.org (Shuttle Radar Topograp
☑	8/7/2008 - Botanischer Garten München	502,926115581565 - 512...	516		Source: ws.geonames.org (Shuttle Radar Topograp
☑	20/10/2003 - IX Region, city of Temuc...				
☑	10/12/2009 - Regensburg, Universitäts...	- 390	383		Source: ws.geonames.org (Shuttle Radar Topograp
☑	24/3/2000 - España, Comunitat Valen...		510		Source: ws.geonames.org (Shuttle Radar Topograp

The image above shows the data for the altitude. After the update all updated data sets will be marked green (see below).



If your data contain WGS84 coordinates, with the webservice www.geonames.org you can amend or replenish your geographical data with informations about the country, geographical places and the altitude

Project: BSMlchfungicoll

☑ Maximal number of results: 10

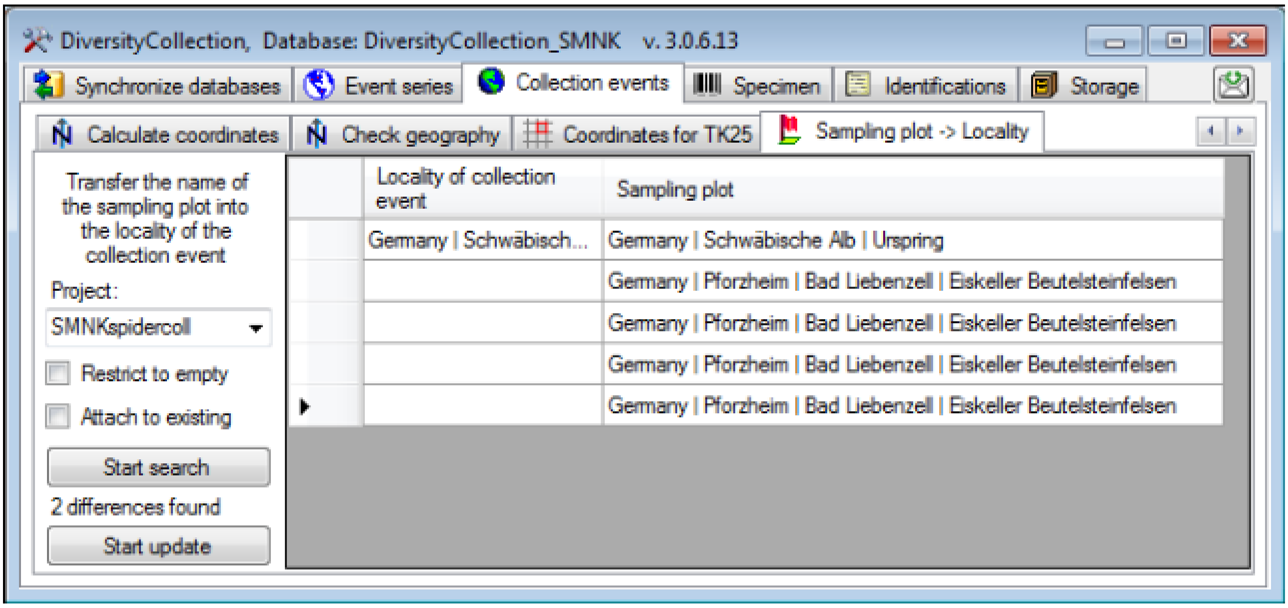
○ only if missing ● when different ○ for all entries

OK	CollectionEvent	Current altitude	New altitude	Accuracy	Notes
☑	8/11/1989 - Spain, Islas Canarias, Ten...	232	232		Source: ws.geonames.org (Shuttle Radar Topograp
☐	20/10/2003 - IX Region, city of Temuc...	310 (mNN)	280		Source: ws.geonames.org (Shuttle Radar Topograp
☐	27/2/2002 - England, Ashdown Forest, ...	60,960741282614 - 91.4...	370		Source: ws.geonames.org (Shuttle Radar Topograp
☑	8/6/2009 - München, Unterhaching	517	517		Source: ws.geonames.org (Shuttle Radar Topograp
☑	12/3/2009 - Chile, IX Region, province	203	203		Source: ws.geonames.org (Shuttle Radar Topograp
☑	15/7/1975 - NW-Spitzbergen: Amsterd...	489	489		Source: ws.geonames.org (Shuttle Radar Topograp
☑	8/7/2008 - Botanischer Garten München	516	516		Source: ws.geonames.org (Shuttle Radar Topograp
☑	20/10/2003 - IX Region, city of Temuc...				
☑	10/12/2009 - Regensburg, Universitäts...	383	383		Source: ws.geonames.org (Shuttle Radar Topograp
☑	24/3/2000 - España, Comunitat Valen...	510	510		Source: ws.geonames.org (Shuttle Radar Topograp

Sampling plots

If your data contains references to sampling plot coordinates, you can update the locality description according to the name of the sampling plot (see image below). Click on the **Start**

search button to find links to SamplingPlots where the locality description does not correspond to the name of the sampling plot. You can restrict the search to missing locality descriptions and attach the name of the sampling plot to the existing entry in the locality description. Use the **Start update** button to set the locality description according to your settings and the differences found.



Transfer the name of the sampling plot into the locality of the collection event

Project: SMNKspidercoll

☐ Restrict to empty

☐ Attach to existing

2 differences found

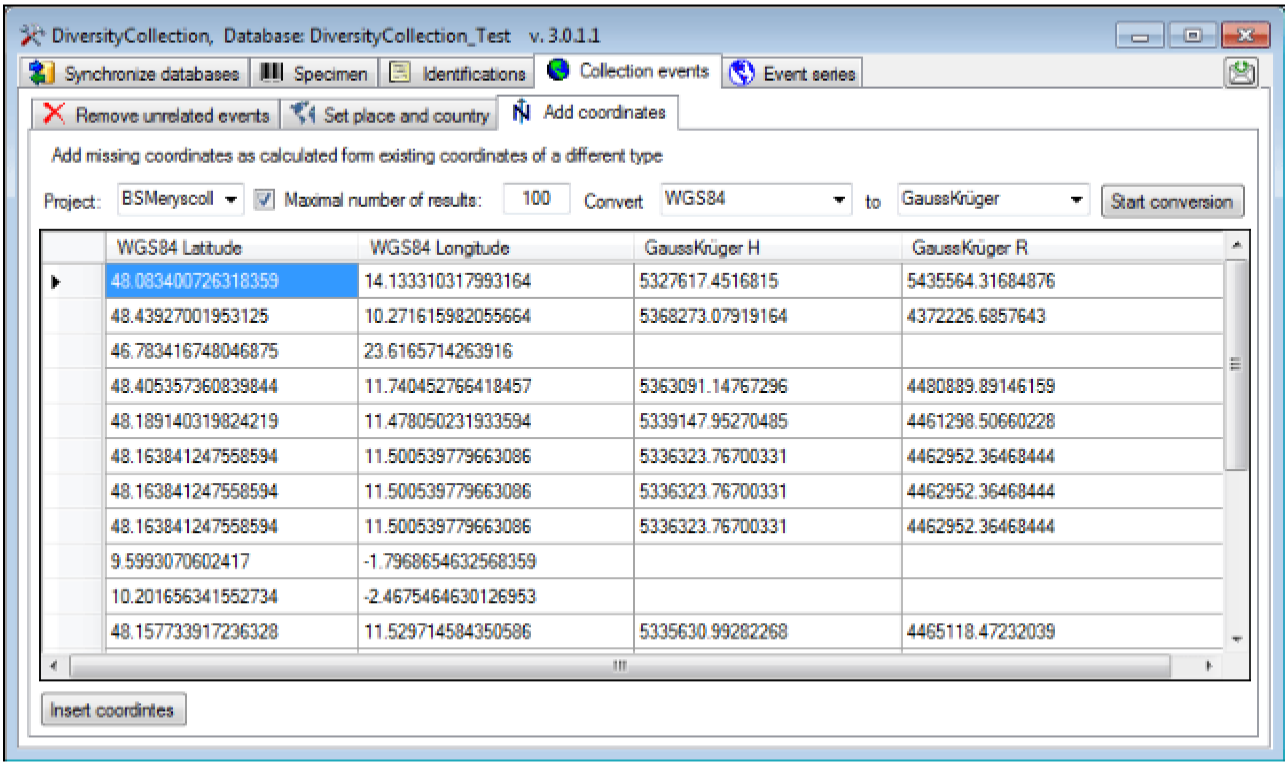
Locality of collection event	Sampling plot
Germany | Schwäbisch...	Germany | Schwäbische Alb | Urspring
	Germany | Pforzheim | Bad Liebenzell | Eiskeller Beutelsteinfelsen
	Germany | Pforzheim | Bad Liebenzell | Eiskeller Beutelsteinfelsen
	Germany | Pforzheim | Bad Liebenzell | Eiskeller Beutelsteinfelsen
	Germany | Pforzheim | Bad Liebenzell | Eiskeller Beutelsteinfelsen

If your data contains or needs coordinates, please see the corresponding chapter on adding and calculating coordinates.

Maintenance - Collection event coordinates

Add Coordinates

If your data contain coordinates you can add additional coordinates in a different system for those dataset, where entries of the additional coordinate system are missing. E.g. you can add WGS84 coordinates on the basis of Gauss Krueger coordinates. In the **Add coordinates** tab choose the project you want to update and an optional upper limit of the datasets. Then select the source coordinates and the coordinate system these should be converted into. Click on the **Start conversion** button to start the conversion. Where a conversion is not possible, the fields for the target system will be empty as shown below. Click the **Insert coordinates** button to insert the new coordinates into you datasets.



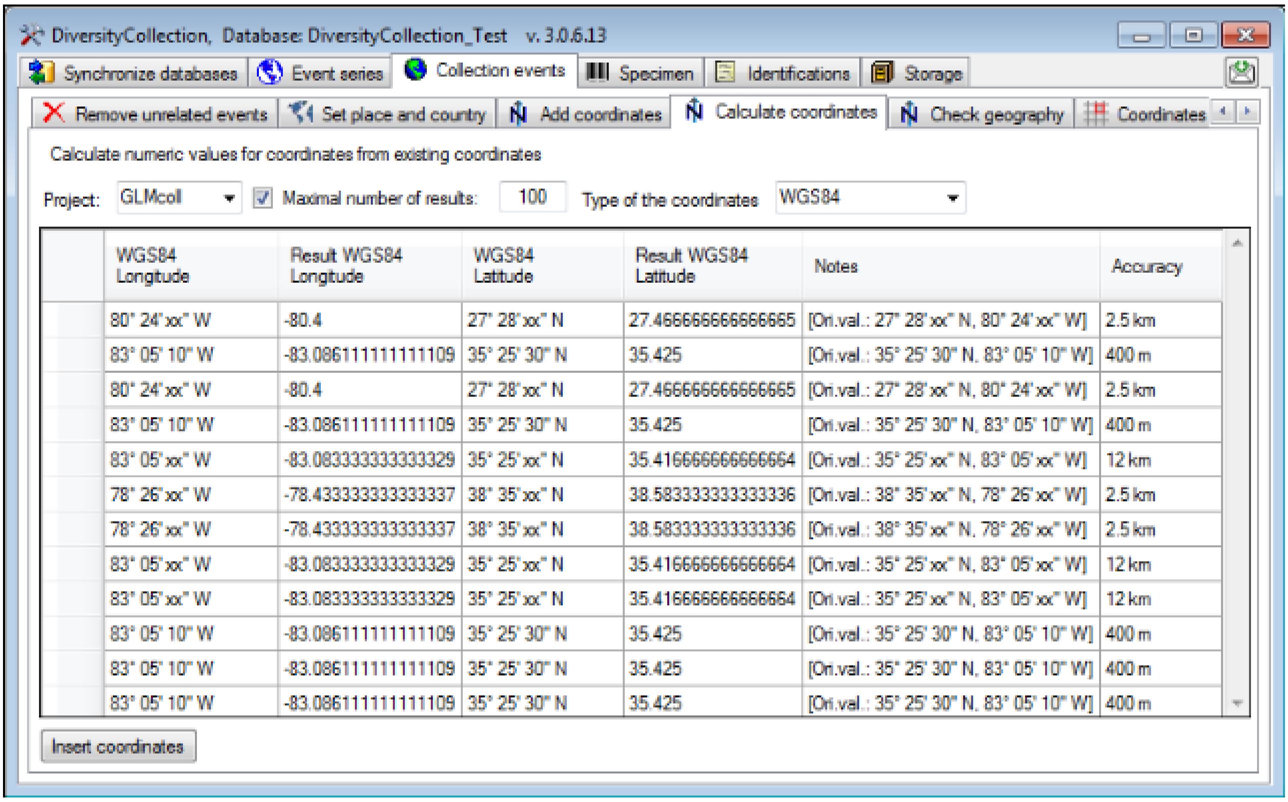
Add missing coordinates as calculated fom existing coordinates of a different type

Project: BSMeryscoll ☑ Maximal number of results: 100 Convert WGS84 to GaussKrüger

WGS84 Latitude	WGS84 Longitude	GaussKrüger H	GaussKrüger R
48.083400726318359	14.133310317993164	5327617.4516815	5435564.31684876
48.43927001953125	10.271615982055664	5368273.07919164	4372226.6857643
46.783416748046875	23.6165714263916		
48.405357360839844	11.740452766418457	5363091.14767296	4480889.89146159
48.189140319824219	11.478050231933594	5339147.95270485	4461298.50660228
48.163841247558594	11.500539779663086	5336323.76700331	4462952.36468444
48.163841247558594	11.500539779663086	5336323.76700331	4462952.36468444
48.163841247558594	11.500539779663086	5336323.76700331	4462952.36468444
9.5993070602417	-1.7968654632568359		
10.201656341552734	-2.4675464630126953		
48.157733917236328	11.529714584350586	5335630.99282268	4465118.47232039

Calculate Coordinates

If your data contain coordinates e.g. written as non numeric entries you can try to calculate numeric values from these entries(see below). Click the **Insert coordinates** button to insert the new coordinates into you datasets.



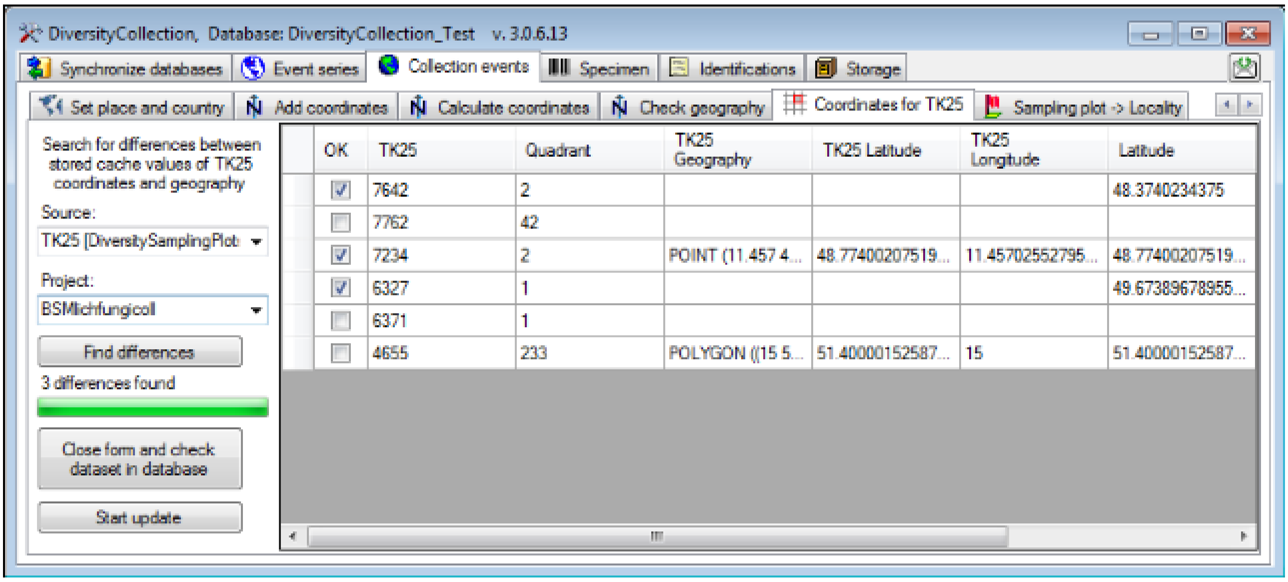
Calculate numeric values for coordinates from existing coordinates

Project: GLMcoll ☑ Maximal number of results: 100 Type of the coordinates WGS84

WGS84 Longitude	Result WGS84 Longitude	WGS84 Latitude	Result WGS84 Latitude	Notes	Accuracy
80° 24' xx" W	-80.4	27° 28' xx" N	27.4666666666666665	[Ori.val.: 27° 28' xx" N, 80° 24' xx" W]	2.5 km
83° 05' 10" W	-83.0861111111111109	35° 25' 30" N	35.425	[Ori.val.: 35° 25' 30" N, 83° 05' 10" W]	400 m
80° 24' xx" W	-80.4	27° 28' xx" N	27.4666666666666665	[Ori.val.: 27° 28' xx" N, 80° 24' xx" W]	2.5 km
83° 05' 10" W	-83.0861111111111109	35° 25' 30" N	35.425	[Ori.val.: 35° 25' 30" N, 83° 05' 10" W]	400 m
83° 05' xx" W	-83.0833333333333329	35° 25' xx" N	35.4166666666666664	[Ori.val.: 35° 25' xx" N, 83° 05' xx" W]	12 km
78° 26' xx" W	-78.4333333333333337	38° 35' xx" N	38.5833333333333336	[Ori.val.: 38° 35' xx" N, 78° 26' xx" W]	2.5 km
78° 26' xx" W	-78.4333333333333337	38° 35' xx" N	38.5833333333333336	[Ori.val.: 38° 35' xx" N, 78° 26' xx" W]	2.5 km
83° 05' xx" W	-83.0833333333333329	35° 25' xx" N	35.4166666666666664	[Ori.val.: 35° 25' xx" N, 83° 05' xx" W]	12 km
83° 05' xx" W	-83.0833333333333329	35° 25' xx" N	35.4166666666666664	[Ori.val.: 35° 25' xx" N, 83° 05' xx" W]	12 km
83° 05' 10" W	-83.0861111111111109	35° 25' 30" N	35.425	[Ori.val.: 35° 25' 30" N, 83° 05' 10" W]	400 m
83° 05' 10" W	-83.0861111111111109	35° 25' 30" N	35.425	[Ori.val.: 35° 25' 30" N, 83° 05' 10" W]	400 m
83° 05' 10" W	-83.0861111111111109	35° 25' 30" N	35.425	[Ori.val.: 35° 25' 30" N, 83° 05' 10" W]	400 m

Add Coordinates for TK25 entries

If your data contain TK25 (= MTB) entries you can add try to retrieve the coordinates and geography for these entries from data in the module DiversityGazetteer (see below). Choose a project and click on the **Find differences** button to search for coordinates. Click the **Start update** button to update the TK25 entries with the found coordinates.



Search for differences between stored cache values of TK25 coordinates and geography

Source: TK25 [DiversitySamplingPlot

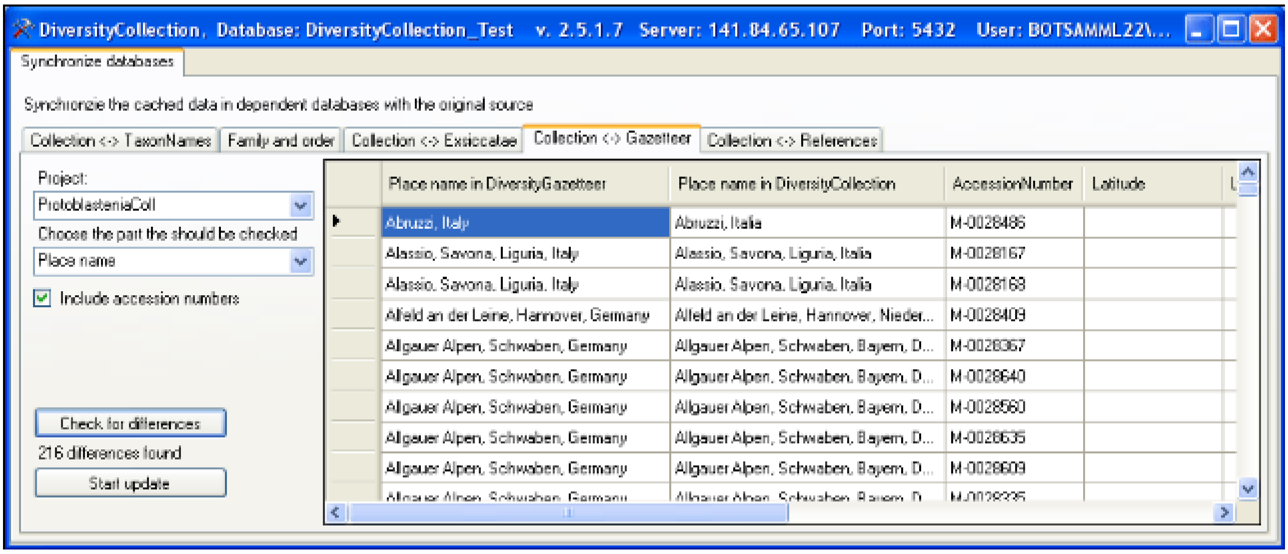
Project: BSMlichfungicoll

3 differences found

OK	TK25	Quadrant	TK25 Geography	TK25 Latitude	TK25 Longitude	Latitude
☑	7642	2				48.3740234375
☐	7762	42				
☑	7234	2	POINT (11.457 4...	48.77400207519...	11.45702552795...	48.77400207519...
☑	6327	1				49.67389678955...
☐	6371	1				
☐	4655	233	POLYGON ((15 5...	51.40000152587...	15	51.40000152587...

Maintenance - Gazetteer

To synchronize the entries derived from the module DiversityGazetteer choose **Administration -> Maintenance** from the menu. A window will open as shown below. On the tab page **Collection <-> Gazetteer** select the project for which the entries should be synchronized. There are 3 targets for the synchronization: Locality name stored in the field Location1 in table CollectionEventLo calisation, Country stored in the field CountryCache in the table CollectionEvent and the Coordinates stored in the fields AverageLatitudeCache and AverageLongitudeCache in the table CollectionEventLo calisation. Select one of these targets for synchronization. To start the query click on the Check for differences button.



Synchrorzie the cached data in dependent databases with the original source

Project: ProtoblasteniaColl

Choose the part the should be checked: Place name

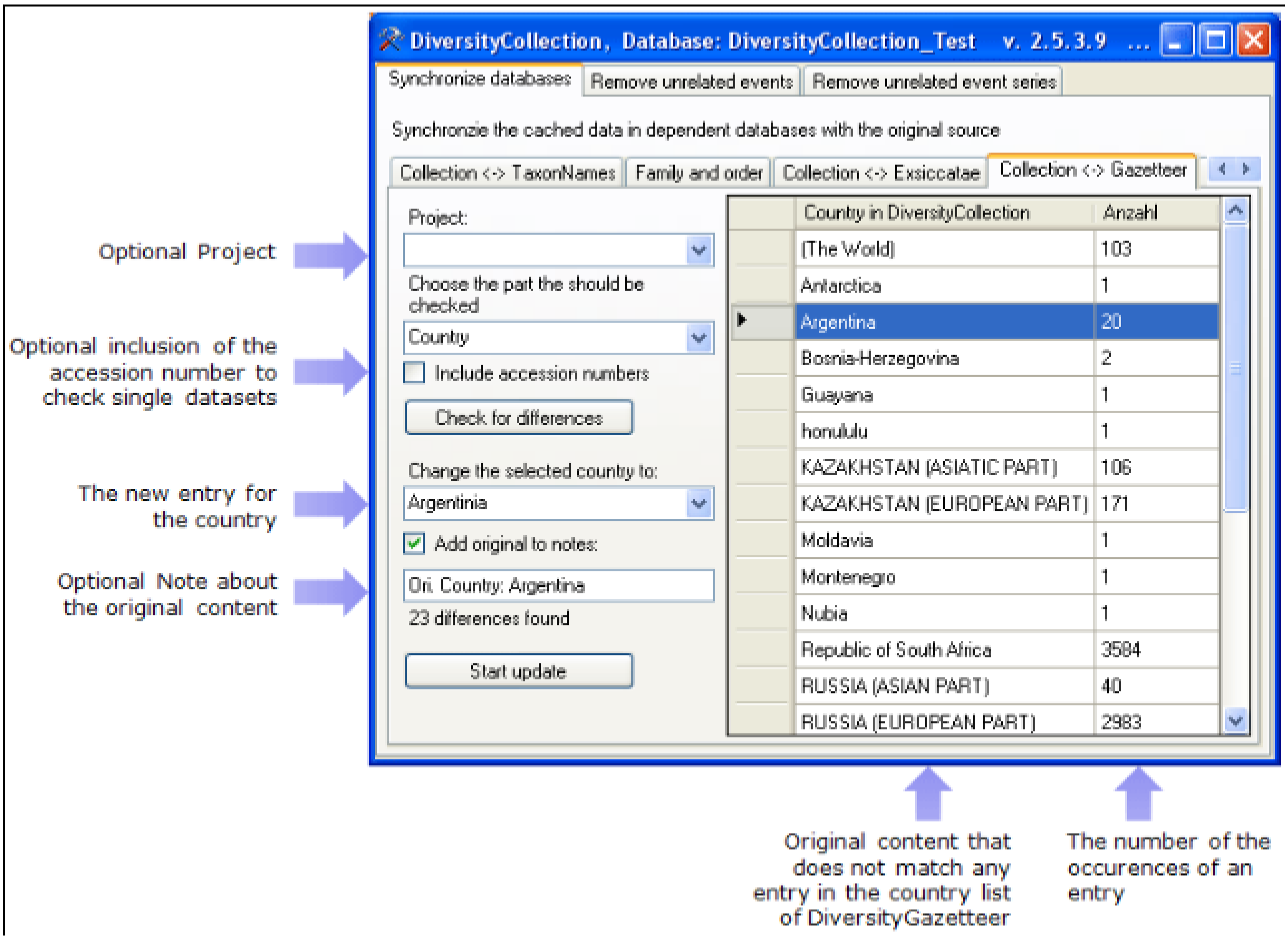
☑ Include accession numbers

216 differences found

Place name in DiversityGazetteer	Place name in DiversityCollection	AccessionNumber	Latitude
Abruzzi, Italy	Abruzzi, Italia	M-0028486	
Alassio, Savona, Liguria, Italy	Alassio, Savona, Liguria, Italia	M-0028167	
Alassio, Savona, Liguria, Italy	Alassio, Savona, Liguria, Italia	M-0028168	
Alfeld an der Leine, Hannover, Germany	Alfeld an der Leine, Hannover, Nieder...	M-0028409	
Algauer Alpen, Schwaben, Germany	Allgauer Alpen, Schwaben, Bayern, D...	M-0028367	
Algauer Alpen, Schwaben, Germany	Allgauer Alpen, Schwaben, Bayern, D...	M-0028640	
Algauer Alpen, Schwaben, Germany	Allgauer Alpen, Schwaben, Bayern, D...	M-0028560	
Algauer Alpen, Schwaben, Germany	Allgauer Alpen, Schwaben, Bayern, D...	M-0028635	
Algauer Alpen, Schwaben, Germany	Allgauer Alpen, Schwaben, Bayern, D...	M-0028609	

The form will list all differences found. To update the database click on the Start update button. If you wish to have a more detailed look on your data, you need to check the **Include accession number** checkbox before starting the query. A button Close form and check dataset in database will appear which will take you back to a single data set in the database.

To check for countries which do not match entries in DiversityGazetteer choose Country from the list as shown below.



Project:

Choose the part the should be checked: Country

☐ Include accession numbers

Change the selected country to: Argentinia

☑ Add original to notes: Ori. Country: Argentina

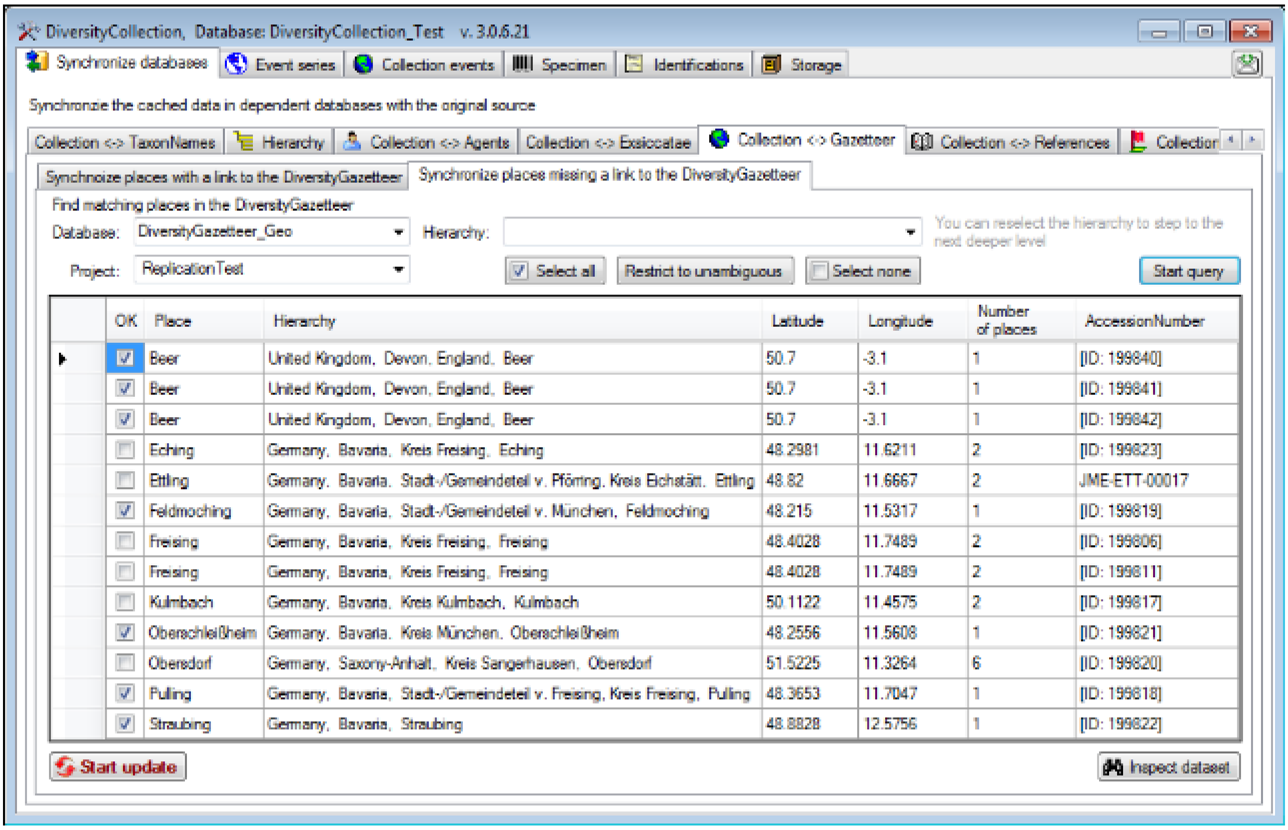
23 differences found

Country in DiversityCollection	Anzahl
[The World]	103
Antarctica	1
Argentina	20
Bosnia-Herzegovina	2
Guayana	1
honululu	1
KAZAKHSTAN (ASIATIC PART)	106
KAZAKHSTAN (EUROPEAN PART)	171
Moldavia	1
Montenegro	1
Nubia	1
Republic of South Africa	3584
RUSSIA (ASIAN PART)	40
RUSSIA (EUROPEAN PART)	2983

The image above summarizes the options for an update of the country. You may restrict your query to one of the projects you have access to. If you wish to check single data sets, check the **include accession numbers** option before you start the query. To keep the old entry in the Notes field check the **Add original to notes** option.

Maintenance - Gazetteer: Adding links

To set links to the DiversityGazetteer for places which are not linked so far choose the second tab under **Collection <-> Gazetteer** for synchroziation of places missing a connection to the DiversityGazetteer. Choose the database and the project and click on the **Start query** button. The results will be listed as shown below.



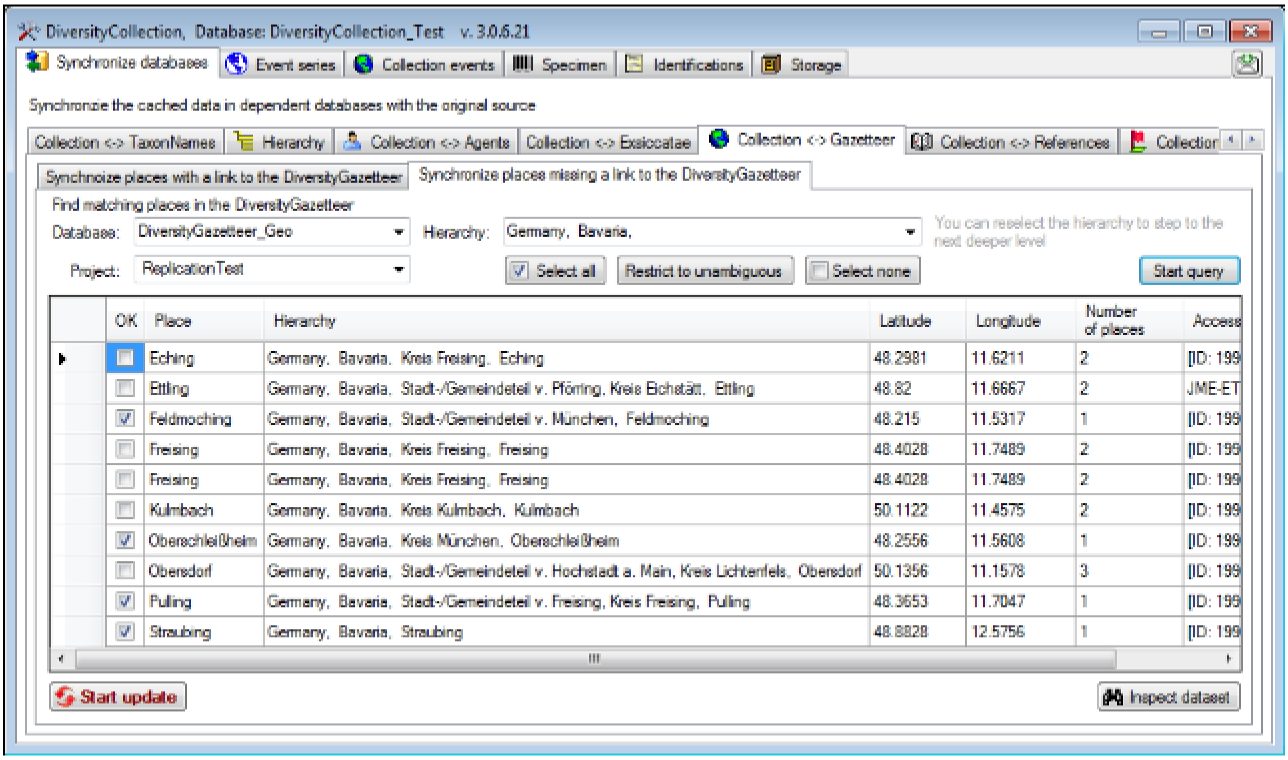
Database: DiversityGazetteer_Geo

Hierarchy:

Project: ReplicationTest

OK	Place	Hierarchy	Latitude	Longitude	Number of places	AccessionNumber
☑	Beer	United Kingdom, Devon, England, Beer	50.7	-3.1	1	[ID: 199840]
☑	Beer	United Kingdom, Devon, England, Beer	50.7	-3.1	1	[ID: 199841]
☑	Beer	United Kingdom, Devon, England, Beer	50.7	-3.1	1	[ID: 199842]
☐	Eching	Germany, Bavaria, Kreis Freising, Eching	48.2981	11.6211	2	[ID: 199823]
☐	Ettling	Germany, Bavaria, Stadt-/Gemeindeteil v. Pförring, Kreis Eichstätt, Ettling	48.82	11.6667	2	JME-ETT-00017
☑	Feldmoching	Germany, Bavaria, Stadt-/Gemeindeteil v. München, Feldmoching	48.215	11.5317	1	[ID: 199819]
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199806]
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199811]
☐	Kulmbach	Germany, Bavaria, Kreis Kulmbach, Kulmbach	50.1122	11.4575	2	[ID: 199817]
☑	Oberschleißheim	Germany, Bavaria, Kreis München, Oberschleißheim	48.2556	11.5608	1	[ID: 199821]
☐	Obersdorf	Germany, Saxony-Anhalt, Kreis Sangerhausen, Obersdorf	51.5225	11.3264	6	[ID: 199820]
☑	Pulling	Germany, Bavaria, Stadt-/Gemeindeteil v. Freising, Kreis Freising, Pulling	48.3653	11.7047	1	[ID: 199818]
☑	Straubing	Germany, Bavaria, Straubing	48.8828	12.5756	1	[ID: 199822]

As many places have identical names in different regions you may restrict the query to places within a certain hierarchy. In the example below this was done twice: First type e.g. Ger in the Hierarchy box and select Germany from the list. Then choose within the list to receive all levels within Germany - in this example Bavaria was chosen, restricting the query to places within Bavaria.



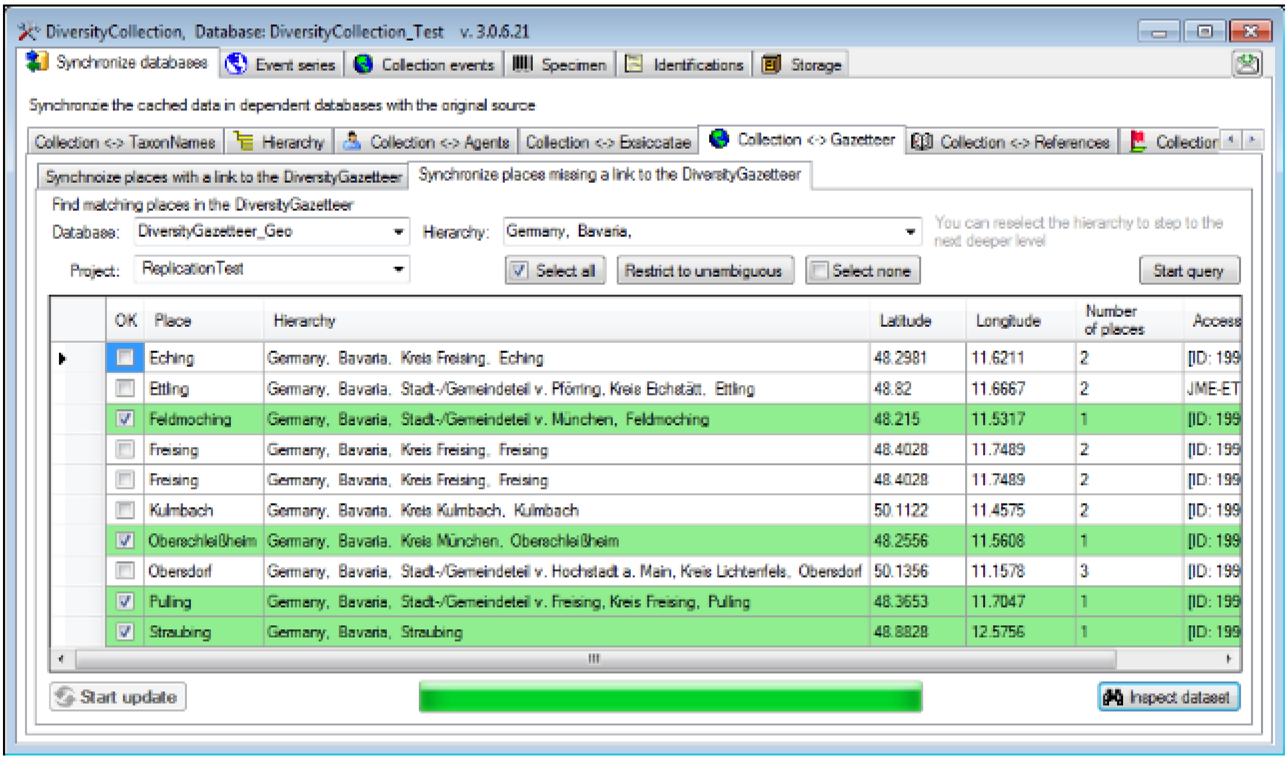
Database: DiversityGazetteer_Geo

Hierarchy: Germany, Bavaria,

Project: ReplicationTest

OK	Place	Hierarchy	Latitude	Longitude	Number of places	Access
☐	Eching	Germany, Bavaria, Kreis Freising, Eching	48.2981	11.6211	2	[ID: 199
☐	Ettling	Germany, Bavaria, Stadt-/Gemeindeteil v. Pförring, Kreis Eichstätt, Ettling	48.82	11.6667	2	JME-ET
☑	Feldmoching	Germany, Bavaria, Stadt-/Gemeindeteil v. München, Feldmoching	48.215	11.5317	1	[ID: 199
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199
☐	Kulmbach	Germany, Bavaria, Kreis Kulmbach, Kulmbach	50.1122	11.4575	2	[ID: 199
☑	Oberschleißheim	Germany, Bavaria, Kreis München, Oberschleißheim	48.2556	11.5608	1	[ID: 199
☐	Obersdorf	Germany, Bavaria, Stadt-/Gemeindeteil v. Hochstadt a. Main, Kreis Lichtenfels, Obersdorf	50.1356	11.1578	3	[ID: 199
☑	Pulling	Germany, Bavaria, Stadt-/Gemeindeteil v. Freising, Kreis Freising, Pulling	48.3653	11.7047	1	[ID: 199
☑	Straubing	Germany, Bavaria, Straubing	48.8828	12.5756	1	[ID: 199

The unambigous results will be selected by default (see image above). The number of identical names found in the gazetteer is listed in the column **Number of places**. Ambigous names will not be selected by default, you may, however, include them in the update, if matches for the name were found. To inspect a single data set to evaluate the found place select it in the list and click on the **Inspect data set** button. This will open a window showing the entire data set. Finally, click on the **Start update** button to enter the results in the database (see below).



Database: DiversityGazetteer_Geo

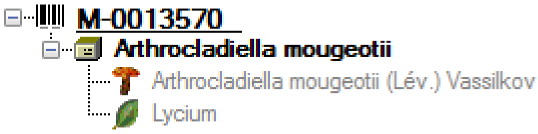
Hierarchy: Germany, Bavaria,

Project: ReplicationTest

OK	Place	Hierarchy	Latitude	Longitude	Number of places	Access
☐	Eching	Germany, Bavaria, Kreis Freising, Eching	48.2981	11.6211	2	[ID: 199
☐	Ettling	Germany, Bavaria, Stadt-/Gemeindeteil v. Pförring, Kreis Eichstätt, Ettling	48.82	11.6667	2	JME-ET
☑	Feldmoching	Germany, Bavaria, Stadt-/Gemeindeteil v. München, Feldmoching	48.215	11.5317	1	[ID: 199
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199
☐	Freising	Germany, Bavaria, Kreis Freising, Freising	48.4028	11.7489	2	[ID: 199
☐	Kulmbach	Germany, Bavaria, Kreis Kulmbach, Kulmbach	50.1122	11.4575	2	[ID: 199
☑	Oberschleißheim	Germany, Bavaria, Kreis München, Oberschleißheim	48.2556	11.5608	1	[ID: 199
☐	Obersdorf	Germany, Bavaria, Stadt-/Gemeindeteil v. Hochstadt a. Main, Kreis Lichtenfels, Obersdorf	50.1356	11.1578	3	[ID: 199
☑	Pulling	Germany, Bavaria, Stadt-/Gemeindeteil v. Freising, Kreis Freising, Pulling	48.3653	11.7047	1	[ID: 199
☑	Straubing	Germany, Bavaria, Straubing	48.8828	12.5756	1	[ID: 199

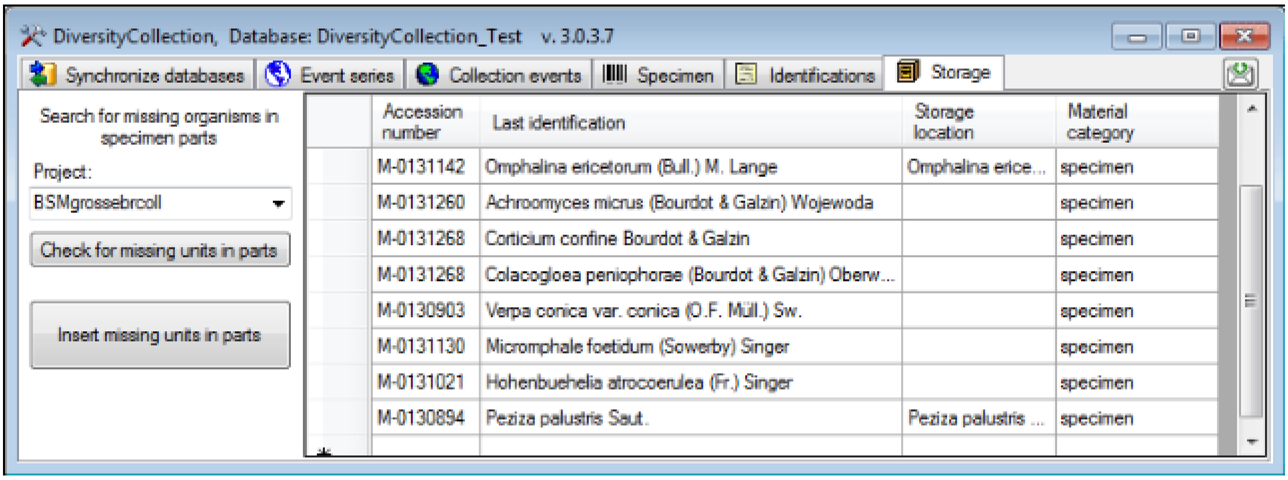
Maintenance - Insert missing organisms in specimen parts

To print a label for your samples you need to specify which of the organisms in the specimen should be shown on the label. If for any reason the organisms where not included into the parts as shown in the image below, you may do this belated for all data sets for a selected project.



M-0013570
  Arthrocladiella mougeotii
    Arthrocladiella mougeotii (Lév.) Vassilkov
    Lycium

Select the print tab as well as the project and click on the **[Check for missing units in parts]** button. The missing entries will be listed as shown below. To insert them click on the corresponding button.



Project: BSMgrossebrcoll

Accession number	Last identification	Storage location	Material category
M-0131142	Omphalina ericetorum (Bull.) M. Lange	Omphalina erice...	specimen
M-0131260	Achroomyces micrus (Bourdot & Galzin) Wojewoda		specimen
M-0131268	Corticium confine Bourdot & Galzin		specimen
M-0131268	Colacogloea peniophorae (Bourdot & Galzin) Oberw...		specimen
M-0130903	Verpa conica var. conica (O.F. Müll.) Sw.		specimen
M-0131130	Micromphale foetidum (Sowerby) Singer		specimen
M-0131021	Hohenbuehelia atrocoerulea (Fr.) Singer		specimen
M-0130894	Peziza palustris Saut.	Peziza palustris ...	specimen

Import

There are several import mechanisms:

Import wizard for tab separated lists: Import data from foreign sources and attach further data to data sets in the database.

Import of specimen scans: Import image data, where the accession number is a part of the file name. Image data can be imported together with default information to the entire batch.

Import and reimport of tab-separated lists: Import data from foreign sources and reimport after external editing.

Export

There are several export mechanisms:

Export of tab-separated lists: Export data in a tab separated format for external analysis or editing.

Export from Grid-Mode using the export function.

ABCD: Export data as XML according to ABCD schema 2.06.

JSTOR: Export data as XML according to format of JSTOR and the Global Plant Initiative respectively.

BIB: Export data as files according to format of the Botanischer Informationsknoten Bayern.

Naturgucker: Export data as files according to format of the Naturgucker initiative.

Generation of **labels**.

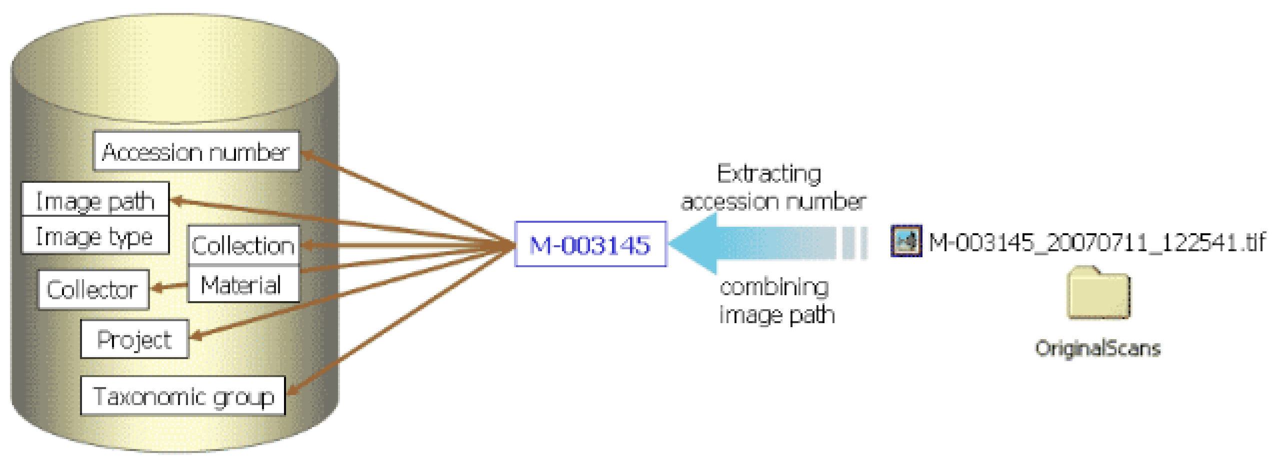
Generation of **inventary lists**.

Replication with a local database

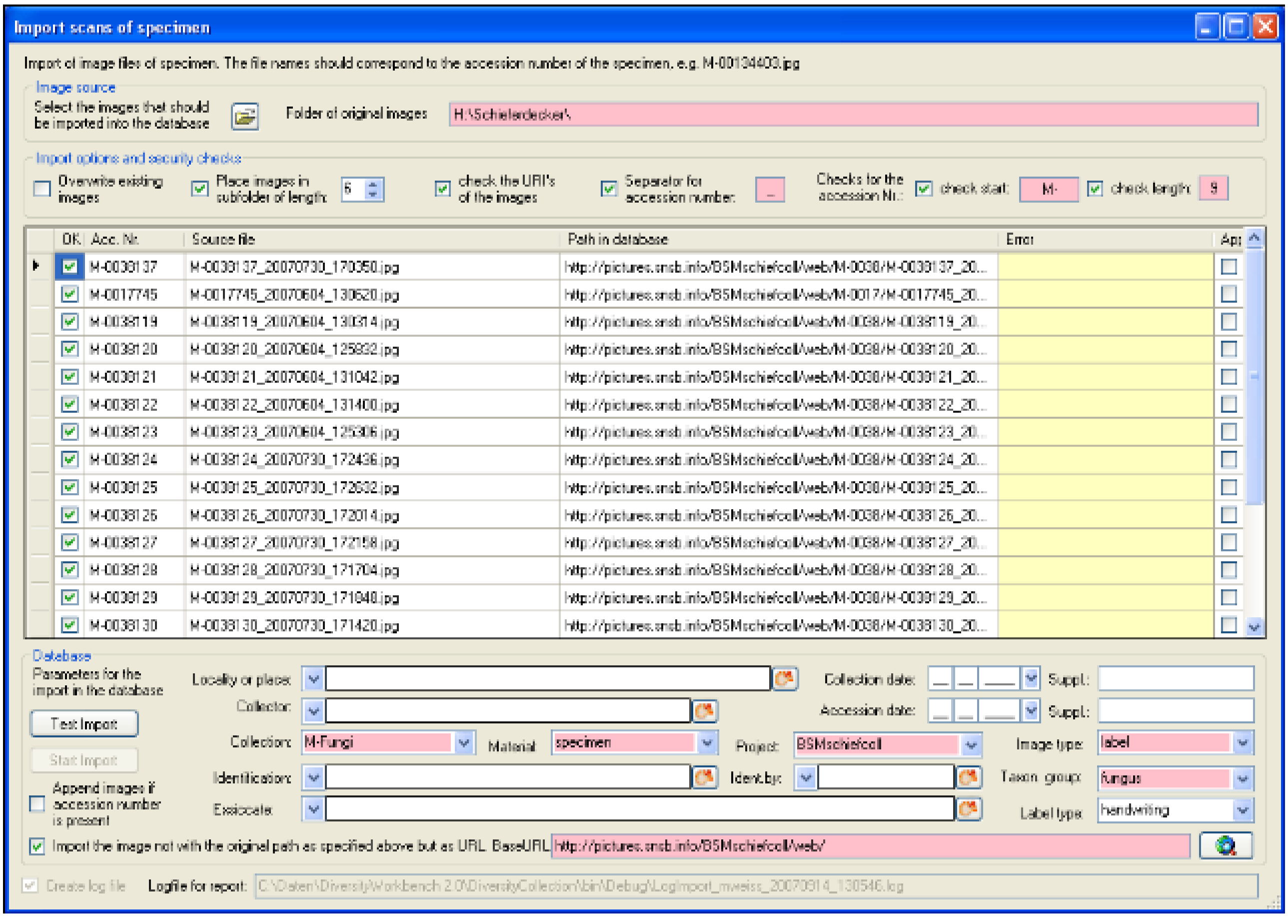
An overview of some options for the im- and export of data is shown in the image below. The export and reimport of tab-separated list allows external editing of the data in e.g. spread sheet programs

Import specimen scans

With this import routine you can import new data sets along with new images into the database. To achieve this the image files should be named corresponding to the accession numbers of the data sets which should be imported (e.g. M-003145 in the example below) and an optional trailing identifier (e.g. _20070711_122541 in the example below. The image below shows an overview of the entire import process.



To import images like scanned labels from specimens choose **Data - Import - Specimen scans...** from the menu. A window for the import of images will be opened (see below).



Import of image files of specimen. The file names should correspond to the accession number of the specimen, e.g. M-00134403.jpg

Image source

Select the images that should be imported into the database

Folder of original images: H:\Schieferdecker\

Import options and security checks

☐ Overwrite existing images

☑ Place images in subfolder of length: 6

☑ check the URI's of the images

☑ Separator for accession number: _

Checks for the accession Nr.: ☑ check start: M- ☑ check length: 9

OK	Acc. Nr.	Source file	Path in database	Error	Ap
☑	M-0038137	M-0038137_20070730_170350.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038137_20...		☐
☑	M-0017745	M-0017745_20070604_130620.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0017/M-0017745_20...		☐
☑	M-0038119	M-0038119_20070604_130314.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038119_20...		☐
☑	M-0038120	M-0038120_20070604_125832.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038120_20...		☐
☑	M-0038121	M-0038121_20070604_131042.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038121_20...		☐
☑	M-0038122	M-0038122_20070604_131400.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038122_20...		☐
☑	M-0038123	M-0038123_20070604_125306.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038123_20...		☐
☑	M-0038124	M-0038124_20070730_172436.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038124_20...		☐
☑	M-0038125	M-0038125_20070730_172632.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038125_20...		☐
☑	M-0038126	M-0038126_20070730_172014.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038126_20...		☐
☑	M-0038127	M-0038127_20070730_172158.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038127_20...		☐
☑	M-0038128	M-0038128_20070730_171704.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038128_20...		☐
☑	M-0038129	M-0038129_20070730_171048.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038129_20...		☐
☑	M-0038130	M-0038130_20070730_171420.jpg	http://pictures.snsb.info/BSMschiefcoll/web/M-0038/M-0038130_20...		☐

Database

Parameters for the import in the database

Locality or place:

Collector:

Collection: M-Fungi

Material: specimen

Project: BSMschiefcoll

Identification:

Ident.by:

Exsiccata:

Collection date: __ __ ____ Suppl.:

Accession date: __ __ ____ Suppl.:

Image type: label

Taxon group: fungus

Label type: handwriting

☐ Append images if accession number is present

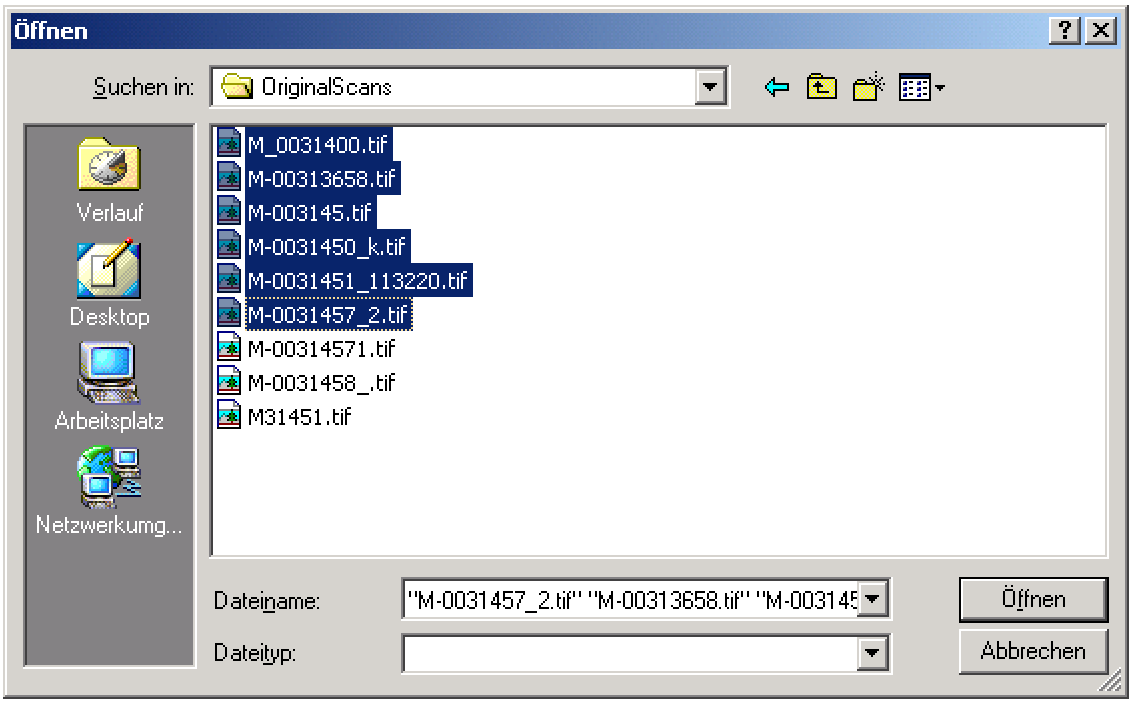
☑ Import the image not with the original path as specified above but as URL. BaseURL: http://pictures.snsb.info/BSMschiefcoll/web/

☑ Create log file Logfile for report: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\LogImport_mweiss_20070914_130546.log

The fields marked with red are mandatory.

Image source

To select the images you wish to import in the database click on the button. A dialog will open where you can select the images you wish to import into your database.



Dateiname: "M-0031457_2.tif" "M-00313658.tif" "M-00314

Select the files and close the window to enter the selection of the images in the list in the form.

Import options and security checks

If you wish to replace data sets for images already in the database, check the **Overwrite existing images** checkbox. If the images are located in a subfolder wich is named according to the first characters of the accession number, check the **Place images in subfolder of length** checkbox and specify the length of the name of the folder. If you wish to check the URIs of the images, check the corresponding checkbox. The data sets will then only be imported if the images are available on the web. If the filename next to the accession number contains a trailing identifier, it must be separated by a unique character. Check the corresponding box and enter the separating character. If you wish to assess whether the accession numbers are correct, you can check the start and the length of the accession number by checking the appropriate checkboxes.

Image list

The list shows the image files selected for the import. To test if all files satisfy the specified checks, click on the **Test import** button. If the file name passed all checks, the OK field for the image will be checked after the test. Otherwise an explanation for not passing the checks will be shown in the Error column.

The first column of the list shows the accession number extracted from the file name. The second column shows the file name of the original image file and the path written in the database. These paths may differ from the original, if you select the option for setting a different **BaseURL**. If a data set for an image already exists in the database and you selected the **Append images** option, the checkbox **Append** at the right end of the table will be checked.

Database

You can set several mandatory and optional values to be written in the database for all imported data. The fields marked with red are mandatory. These are the collections in which the specimens are located: the material categories of the specimens, the project, the content type of the scans (e.g. label) and the taxonomic group of the main organism in the specimens. If you wish to refer to a web source for the labels instead of a local file, you need to provide the base URL as well. Optional fields are a place according to the DiversityGazetteer and the date of the gathering event, the collector, the accession date, an identification, an exsiccatal series and the type of the label. For explanation of the buttons see module related entries .

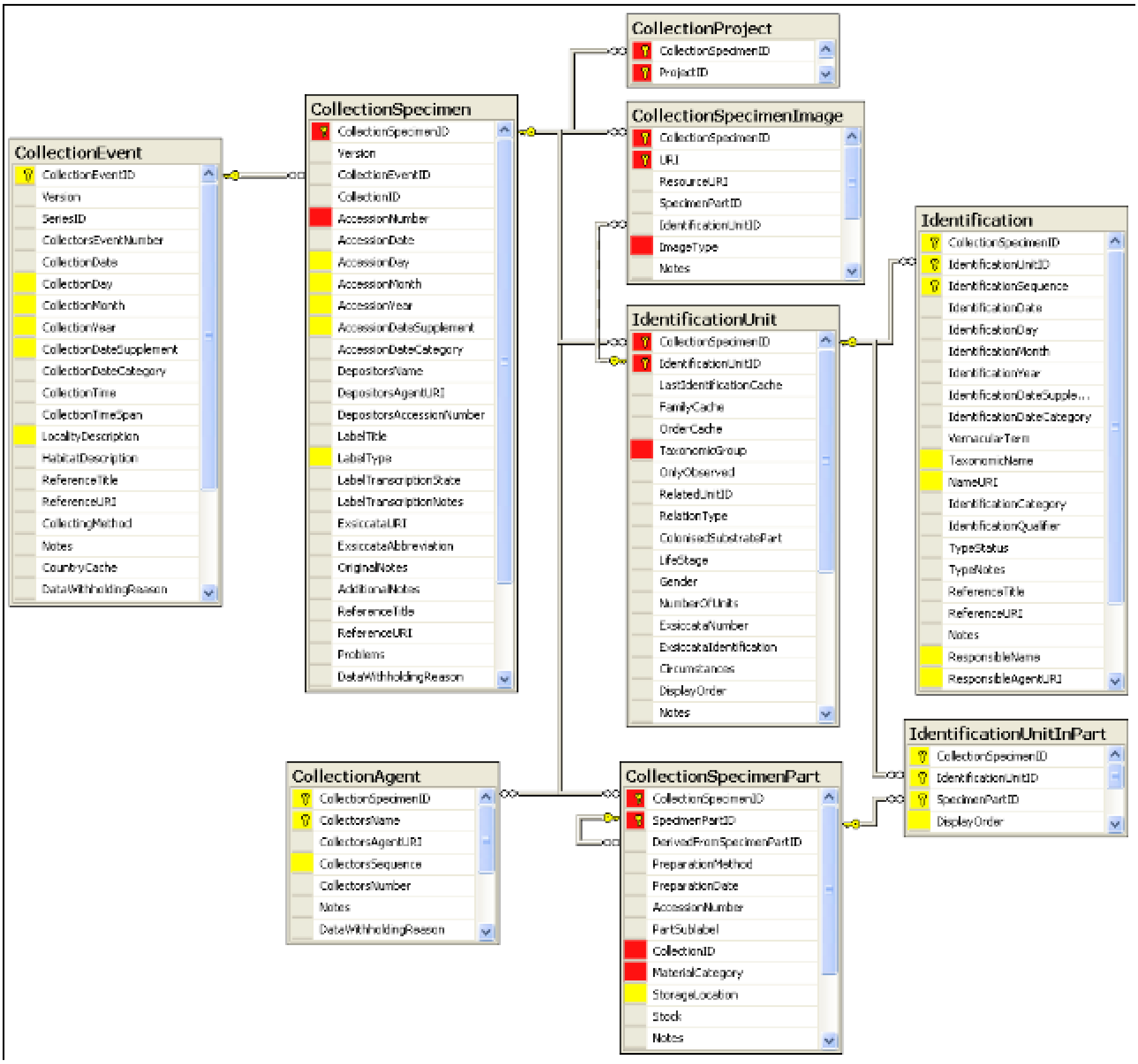
To test the import and whether the images are present in the database click on the Test Import button. If everything is fine click on the Start Import button to start the import.

Logfile: To log the list of imported images and any errors during the import check the Create log file checkbox. This will create a log file with your name, the date and time of the import in the directory where the image files are located.

The program will check whether an accession number is already present in the database. It will only import the data, if the option **Append images if accession number is present** is checked. Otherwise this data will not be imported.

If the images will be provided by a webserver, check the appropriate checkbox and specify the folder or click on the 🔍 button to search for the website.

In the overview below the mandatory fields are marked with red, the optional fields with yellow.


CollectionProject
CollectionSpecimenID
ProjectID
CollectionSpecimenImage
CollectionSpecimenID
URI
ResourceURI
SpecimenPartID
IdentificationUnitID
ImageType
Notes
CollectionEvent
CollectionEventID
Version
SeriesID
CollectorsEventNumber
CollectionDate
CollectionDay
CollectionMonth
CollectionYear
CollectionDateSupplement
CollectionDateCategory
CollectionTime
CollectionTimeSpan
LocalityDescription
HabitatDescription
ReferenceTitle
ReferenceURI
CollectingMethod
Notes
CountryCache
DataWithholdingReason
CollectionSpecimen
CollectionSpecimenID
Version
CollectionEventID
CollectionID
AccessionNumber
AccessionDate
AccessionDay
AccessionMonth
AccessionYear
AccessionDateSupplement
AccessionDateCategory
DepositorsName
DepositorsAgentURI
DepositorsAccessionNumber
LabelTitle
LabelType
LabelTranscriptionState
LabelTranscriptionNotes
ExsiccataURI
ExsiccataAbbreviation
OriginalNotes
AdditionalNotes
ReferenceTitle
ReferenceURI
Problems
DataWithholdingReason
IdentificationUnit
CollectionSpecimenID
IdentificationUnitID
LastIdentificationCache
FamilyCache
OrderCache
TaxonomicGroup
OnlyObserved
RelatedUnitID
RelationType
ColonisedSubstratePart
LifeStage
Gender
NumberOfUnits
ExsiccataNumber
ExsiccataIdentification
Circumstances
DisplayOrder
Notes
Identification
CollectionSpecimenID
IdentificationUnitID
IdentificationSequence
IdentificationDate
IdentificationDay
IdentificationMonth
IdentificationYear
IdentificationDateSupple...
IdentificationDateCategory
VernacularTerm
TaxonomicName
NameURI
IdentificationCategory
IdentificationQualifier
TypeStatus
TypeNotes
ReferenceTitle
ReferenceURI
Notes
ResponsibleName
ResponsibleAgentURI
IdentificationUnitInPart
CollectionSpecimenID
IdentificationUnitID
SpecimenPartID
DisplayOrder
CollectionAgent
CollectionSpecimenID
CollectorsName
CollectorsAgentURI
CollectorsSequence
CollectorsNumber
Notes
DataWithholdingReason
CollectionSpecimenPart
CollectionSpecimenID
SpecimenPartID
DerivedFromSpecimenPartID
PreparationMethod
PreparationDate
AccessionNumber
PartSublabel
CollectionID
MaterialCategory
StorageLocation
Stock
Notes

Import tab-separated lists

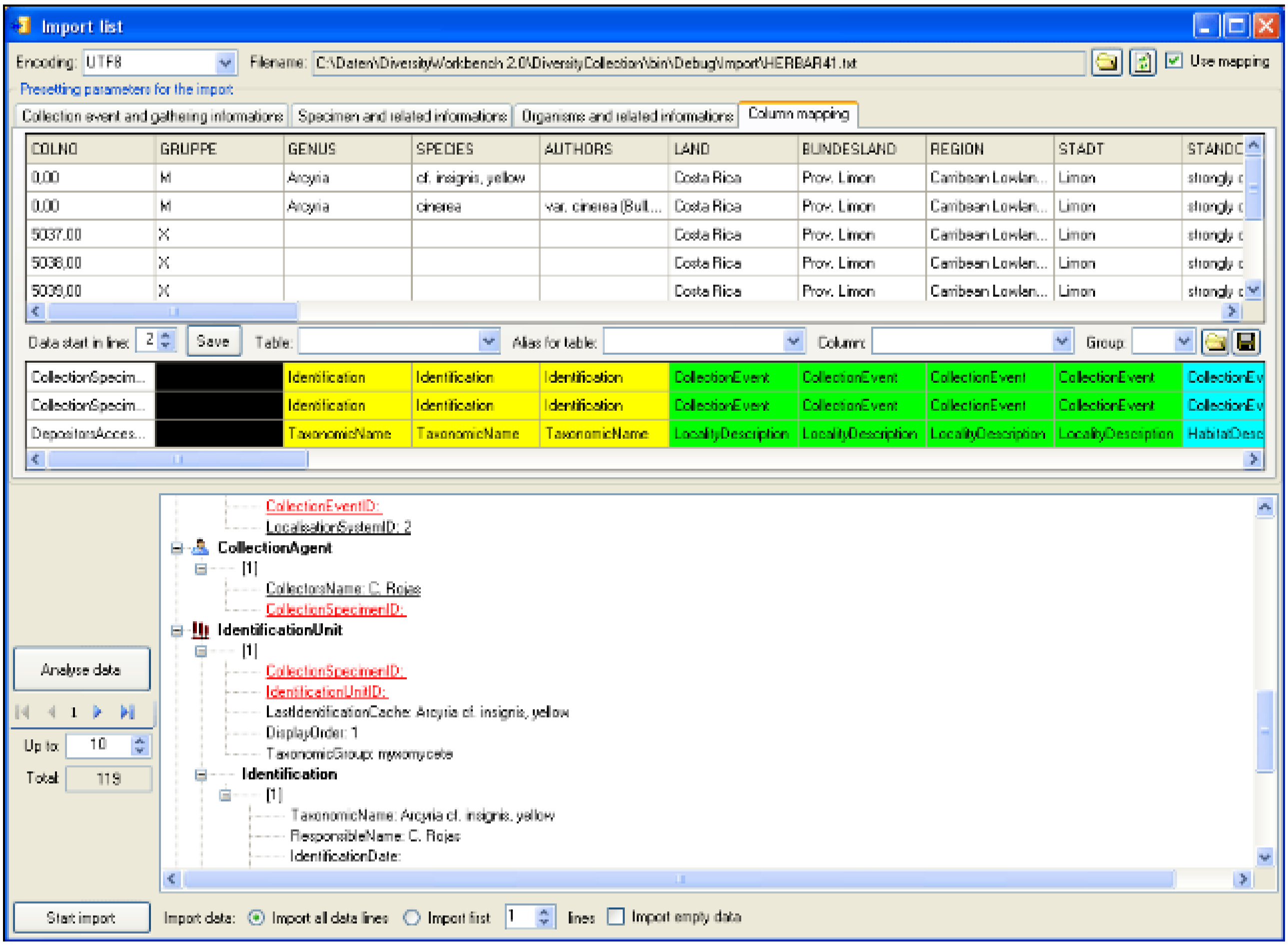
With this import routine you can import data as tab-separated lists into the database. Choose **Data -> Import -> Import list...** from the menu to open the window for import. In the window click on the 📂button to select the file with the data you wish to import. Use the proper **[encoding]** to ensure that all special characters will be transferred correctly. If you change the encoding after opening the file, click on the 🔄button to reload the file with the new encoding.

The content of the file will be shown in the upper part of the **[Column mapping]** tab page. Use **[Data start in line]** to set the area for the import. Preceeding lines will be ignored and depicted with a gray background as shown below. Every column in your file must be either ignored or mapped to a column in the database. The lower part of the mapping section shows your mapping while the upper part contains the first lines of your file. You can either use a prepared column mapping or create a new one. To import a previous column mapping click on the 📂 button and choose one of the XML-files.

Column mapping

For a column which should not be imported choose the black color from the group as shown for the second column in the image below. These columns will be ignored for the analysis and the import. For all other columns choose the **[Table]** and the **[Column]** your data corresponds to. If you wish to import two different data sets in the same table, you need to change the **[Alias for table]** to a unique value for this data set.

If some columns should be transferred into one field, you have to choose a group for these columns as shown below for columns 3 to 5, 6 to 9, ... Simply choose a color from the group combobox other than white or black to choose a group. To save the current mapping click on the 💾button.



Encoding: UTF8

Filename: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Import\HERBAR41.txt

☑ Use mapping

COLNO	GRUPPE	GENUS	SPECIES	AUTHORS	LAND	BUNDESLAND	REGION	STADT	STANDC
0,00	M	Arcyria	cf. insignis, yellow		Costa Rica	Prov. Limon	Caribean Lowlan...	Limon	strongly c
0,00	M	Arcyria	cinerea	var. cinerea (Bull....	Costa Rica	Prov. Limon	Caribean Lowlan...	Limon	strongly c
5037,00	X				Costa Rica	Prov. Limon	Caribean Lowlan...	Limon	strongly c
5038,00	X				Costa Rica	Prov. Limon	Caribean Lowlan...	Limon	strongly c
5039,00	X				Costa Rica	Prov. Limon	Caribean Lowlan...	Limon	strongly c

Data start in line: 2

CollectionSpecim...		Identification	Identification	Identification	CollectionEvent	CollectionEvent	CollectionEvent	CollectionEvent	CollectionEv
CollectionSpecim...		Identification	Identification	Identification	CollectionEvent	CollectionEvent	CollectionEvent	CollectionEvent	CollectionEv
DepositorsAcces...		TaxonomicName	TaxonomicName	TaxonomicName	LocalityDescription	LocalityDescription	LocalityDescription	LocalityDescription	HabitatDesc

```
      CollectionEventID:
      LocalisationSystemID: 2
CollectionAgent
   [1]
      CollectorsName: C. Rojas
      CollectionSpecimenID:
IdentificationUnit
   [1]
      CollectionSpecimenID:
      IdentificationUnitID:
      LastIdentificationCache: Arcyria cf. insignis, yellow
      DisplayOrder: 1
      TaxonomicGroup: myxomycete
   Identification
      [1]
         TaxonomicName: Arcyria cf. insignis, yellow
         ResponsibleName: C. Rojas
         IdentificationDate:
```

1

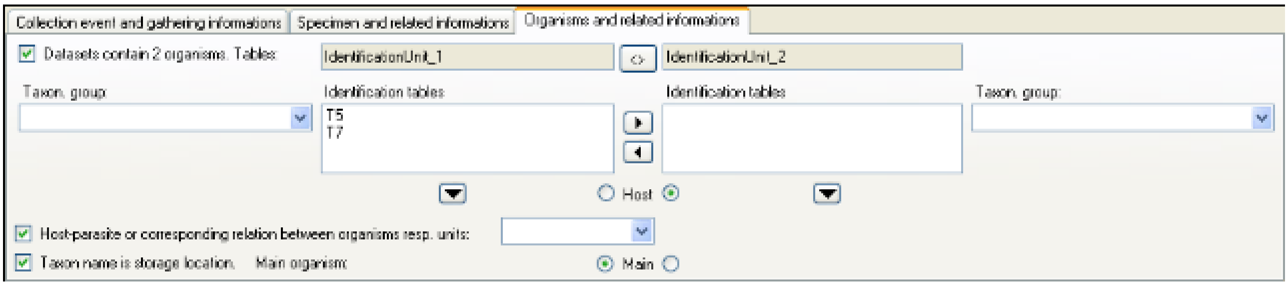
Up to: 10

Total: 119

Import data: ● Import all data lines ○ Import first 1 lines ☐ Import empty data

To analyse the data in the file click on the **[Analyse]** button. During the analysis the program may ask you to give additional information like the taxonomic groups of the imported organisms. In the upper part of the window you may add information to be imported together with your data from the file. The available options depend on the structure of your data.

The image below shows the tab page where you can define the relations between two organisms. This might be necessary if e.g. your data contains information on parasites and hosts. The data tables which are related to an identification are listed with their aliases in the lists for the identification tables. Use the ▶ and ◀ buttons to move them between the lists. Use the ▼ buttons to change the sequence within a list. With the **[Host]** option ○ Host ● you define the host and the **[Main]** option defines which organism will be chosen as the first to be printed e.g. on a label.



☑ Datasets contain 2 organisms. Tables: IdentificationUnit_1 IdentificationUnit_2

Taxon. group:

Identification tables: T5, T7

Identification tables:

Taxon. group:

○ Host ●

☑ Host-parasite or corresponding relation between organisms resp. units:

☑ Taxon name is storage location. Main organism: ● Main ○

By default one CollectionEvent will be created for each data set.

● Separate collection events

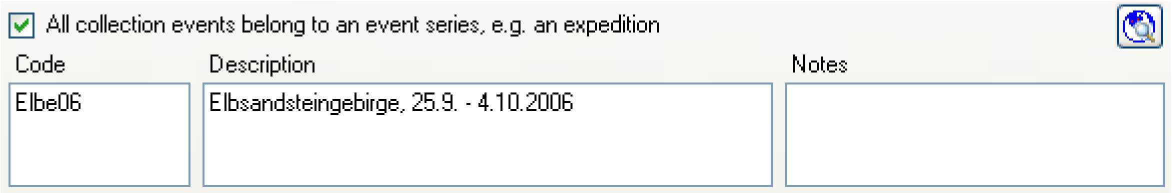
- Collection event
  - Collection specimen
- Collection event
  - Collection specimen

If the events should be joined following the entries in the file, you can choose the second option as shown below. The import will create a new event, if there were any changes made to the data related to the CollectionEvent, like the description of the locality, the altitude, the coordinates etc.

● Group collection events

- Collection event
  - Collection specimen
  - Collection specimen

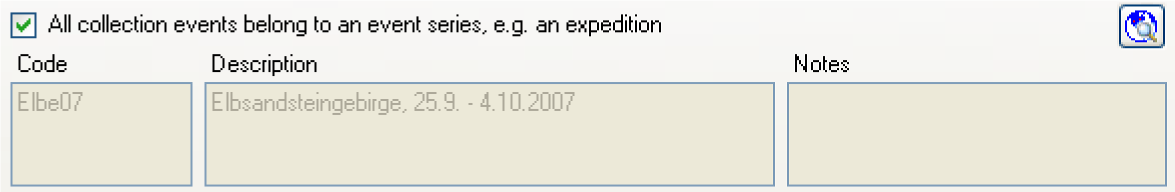
If all the data sets belong to one EventSeries e.g. to one expedition, you can choose the option as shown below and enter the code and description of the EventSeries in the corresponding fields.



☑ All collection events belong to an event series, e.g. an expedition

Code	Description	Notes
Elbe06	Elbsandsteingebirge, 25.9. - 4.10.2006	

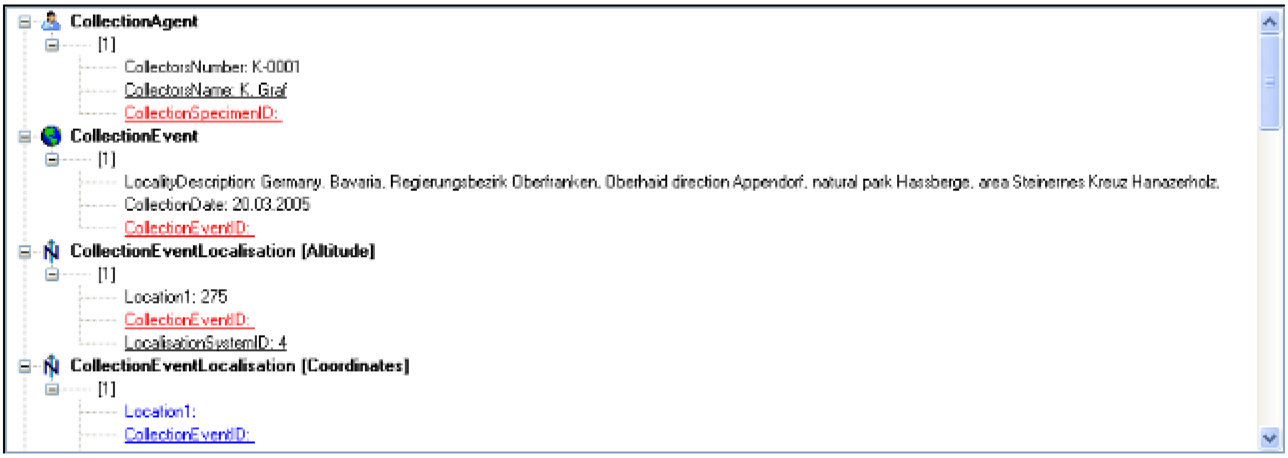
If you wish to use an existing EventSeries, click on the button and select a series from the form. The code and description of the selected series will be shown as in the image below.



☑ All collection events belong to an event series, e.g. an expedition

Code	Description	Notes
Elbe07	Elbsandsteingebirge, 25.9. - 4.10.2007	

After your data was successfully analysed, the window will show you the result as shown in the image below. During the analysis the program will add missing tables and columns necessary for the import. The first data set will be shown in the form. If you wish to check more data sets, set the number of the last position you wish to check and click on the **[Analyse]** button. The data is arranged according to the tables in the database in which they will be imported. The underlined fields belong to the primary keys of the respective tables and are red, if missing. These missing values will be generated during the import. If a data set contains no values and will therefore not be imported into the database, the columns will be shown in blue. To import these entries anyway choose the **[import empty values]** option. To browse through the data sets in the preview use the |◀ ◀ 2 ▶ ▶| buttons.



- **CollectionAgent**
  - [1]
    - CollectorsNumber: K-0001
    - CollectorsName: K. Graf
    - CollectionSpecimenID:
- **CollectionEvent**
  - [1]
    - LocalityDescription: Germany, Bavaria, Regierungsbezirk Oberfranken, Oberhaid direction Appendorf, natural park Hassberge, area Steinernes Kreuz Hanazerholz.
    - CollectionDate: 20.03.2005
    - CollectionEventID:
- **CollectionEventLocalisation [Altitude]**
  - [1]
    - Location1: 275
    - CollectionEventID:
    - LocalisationSystemID: 4
- **CollectionEventLocalisation [Coordinates]**
  - [1]
    - Location1:
    - CollectionEventID:

To import the data click on the **[Start import]** button. If you wish to import only part of the data e.g. for a test, choose the **[Import first ... lines]** option.

Export

There are several options to export your data. You can either export data of the entire database or the content of the data sets listed in the specimen list.

Export data of the whole database

Export of the content of the entire database is possible either as a backup on the database server or as export as csv files. See the Backup chapter for more details.

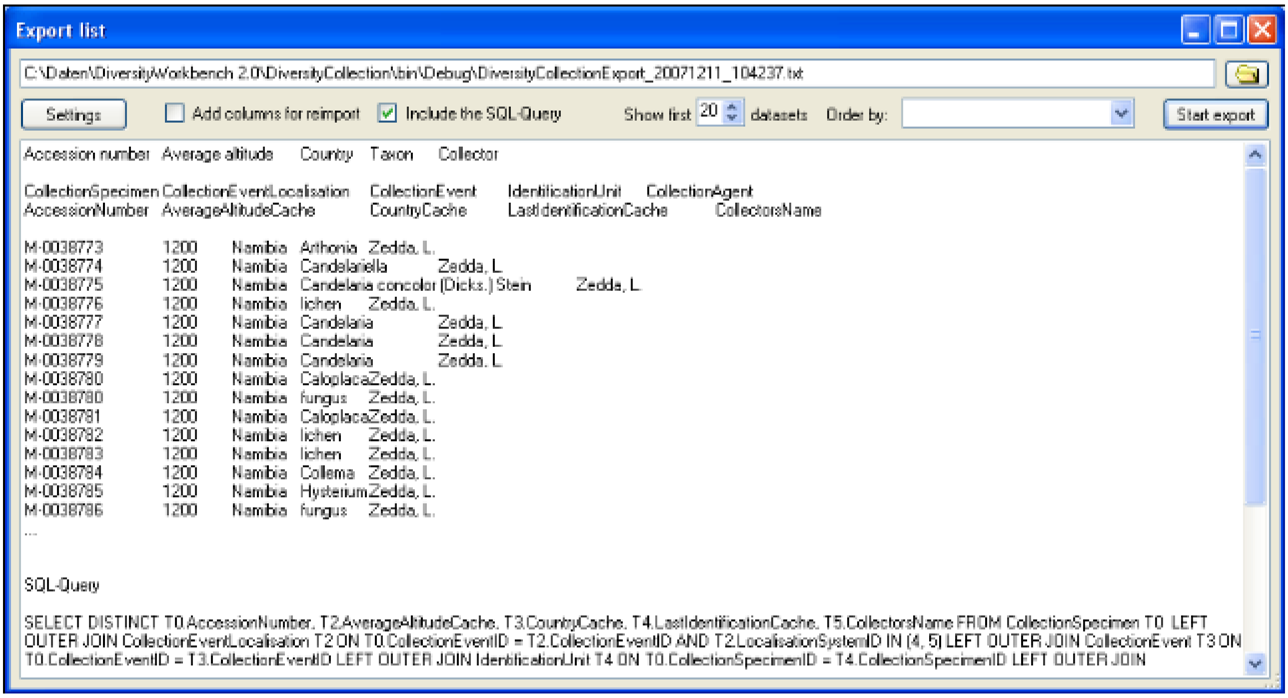
Export data of selected specimen

For the export of selected specimen there are several options. If you want to define the content and format which should be exported, use the List export. An export which can be configurated my also be executed using the export functions of the grid views for Specimen, Organisms , Parts and CollectionEvents.

Predefined export formats are available as XML for the ABCD (see www.tdwg.org) and the GPI/JSTOR standard as well as text files for the BIB (see www.bayernflora.de) and Naturgucker (see www.naturgucker.net) portals.

Export data as tab-separated lists

You can export the content of the datasets listed in the specimen list into a tab-separated list. Choose **Data - Export - Export list...** from the menu. A window as shown below will open. To change the preset path of the export file use the button.



C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\DiversityCollectionExport_20071211_104237.txt

☐ Add columns for reimport

☑ Include the SQL-Query

Show first 20 datasets

```
Accession number  Average altitude     Country   Taxon     Collector

CollectionSpecimen CollectionEventLocalisation    CollectionEvent      IdentificationUnit     CollectionAgent
AccessionNumber   AverageAltitudeCache            CountryCache         LastIdentificationCache        CollectorsName

M-0038773       1200     Namibia   Arthonia   Zedda, L.
M-0038774       1200     Namibia   Candelariella        Zedda, L.
M-0038775       1200     Namibia   Candelaria concolor (Dicks.) Stein        Zedda, L.
M-0038776       1200     Namibia   lichen     Zedda, L.
M-0038777       1200     Namibia   Candelaria           Zedda, L.
M-0038778       1200     Namibia   Candelaria           Zedda, L.
M-0038779       1200     Namibia   Candelaria           Zedda, L.
M-0038780       1200     Namibia   CaloplacaZedda, L.
M-0038780       1200     Namibia   fungus     Zedda, L.
M-0038781       1200     Namibia   CaloplacaZedda, L.
M-0038782       1200     Namibia   lichen     Zedda, L.
M-0038783       1200     Namibia   lichen     Zedda, L.
M-0038784       1200     Namibia   Collema    Zedda, L.
M-0038785       1200     Namibia   HysteriumZedda, L.
M-0038786       1200     Namibia   fungus     Zedda, L.
...


SQL-Query

SELECT DISTINCT T0.AccessionNumber, T2.AverageAltitudeCache, T3.CountryCache, T4.LastIdentificationCache, T5.CollectorsName FROM CollectionSpecimen T0  LEFT
OUTER JOIN CollectionEventLocalisation T2 ON T0.CollectionEventID = T2.CollectionEventID AND T2.LocalisationSystemID IN (4, 5) LEFT OUTER JOIN CollectionEvent T3 ON
T0.CollectionEventID = T3.CollectionEventID LEFT OUTER JOIN IdentificationUnit T4 ON T0.CollectionSpecimenID = T4.CollectionSpecimenID LEFT OUTER JOIN
```

To start the export click on the **[Start export]** button. A file will be created in your application directory, containing the exported data. A preview of the data is shown in the lower part of the form. If you check the **include columns for reimport** option, the header will contain an additional line for table names which you can use for reimporting the data. If you check the **include the SQL-Query** option, the Text of the command for selecting the datasets will be attached at the end of your report. The form will show the first lines as set in the Show first ... datasets (range: 1 - 99) as a preview. During the first export, the list for the fields for sorting the results **[Order by:]** will be filled. So if you need sorted results just restart the export after selecting the field after the first export.

To choose the fields you want to see in the export click on the Settings button. A window will open as shown below, where you can choose the fields you want to export.

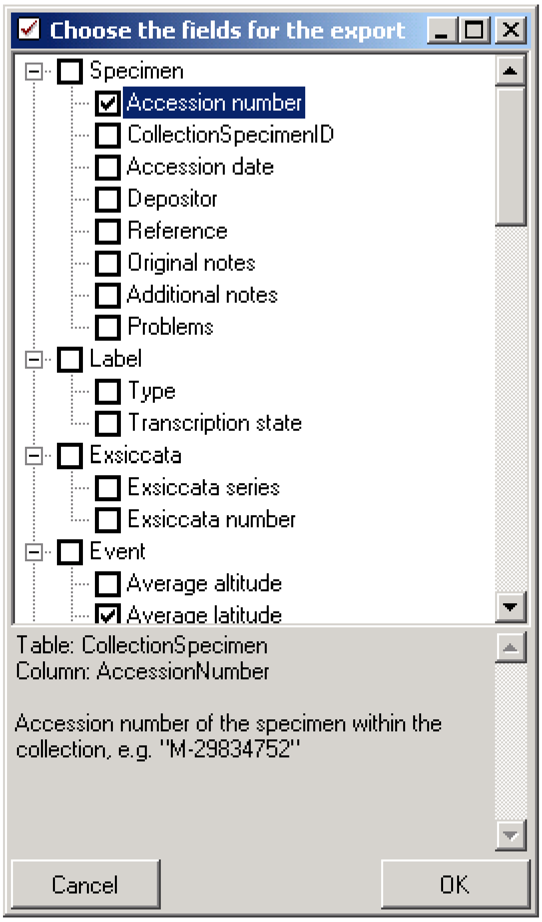


Table: CollectionSpecimen
Column: AccessionNumber

Accession number of the specimen within the collection, e.g. "M-29834752"

Please keep in mind, that only the datasets listed in the **specimen list** of the main form will be exported. If for example you set the maximal number for the specimen list to 100, only these datasets will be exported, even if the number of datasets related to your query will be more than 100.

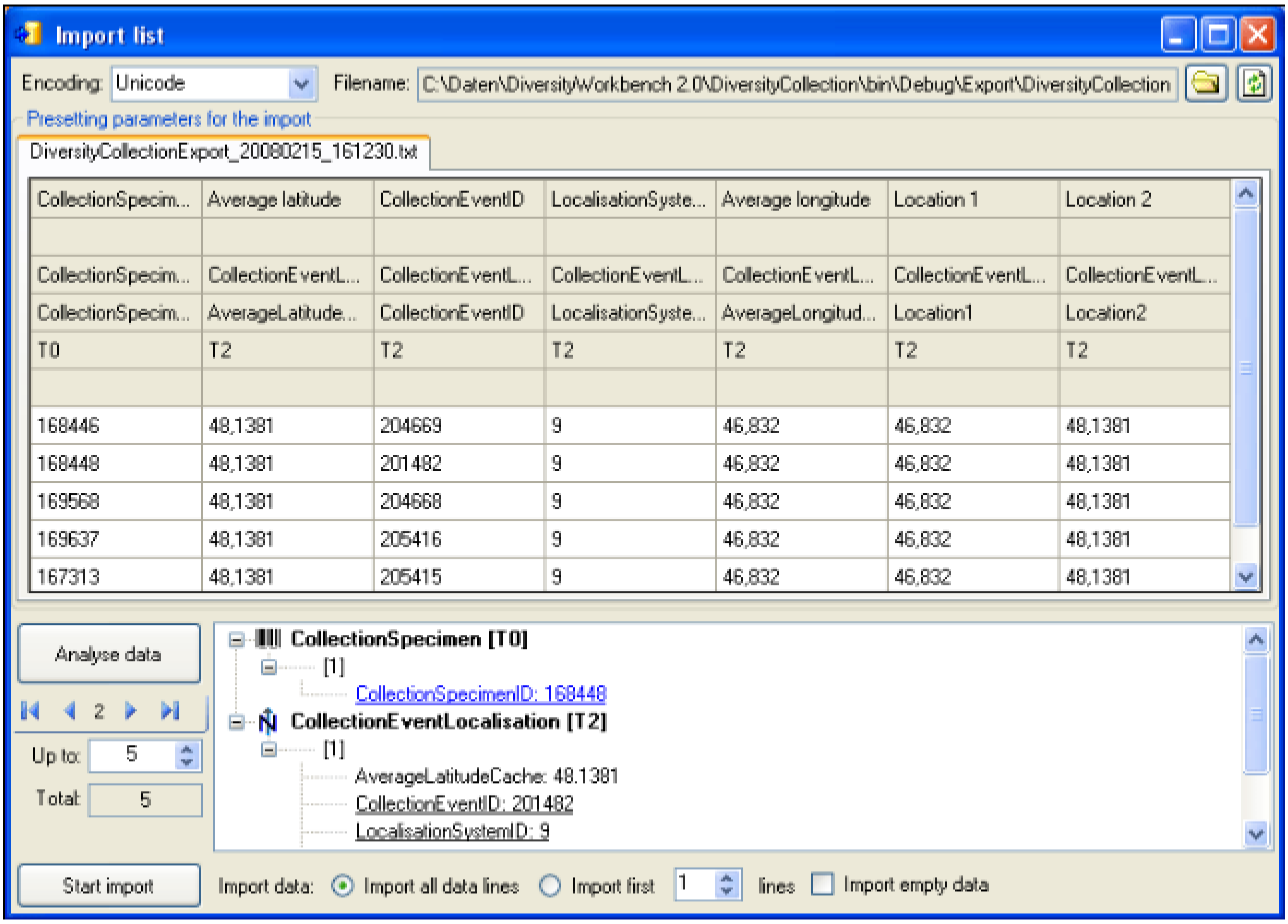
Please be aware, that you will get "**cross joins**" between the data in your database as in the example shown below. If for example you start an export containing taxa and collectors and you have 3 taxa and 2 collectors in a dataset this will result in 6 lines in the export: every taxon combined with every collector (3 x 2 = 6). To evaluate the data you have to group the results accordingly. The first line in the file corresponds to the description as shown in the form above for the selection of the export fields. The second line shows the tables and the third line the column within the database. The following lines contain the data. If you want to avoid these cross joins and need only one line for each dataset, please use the export funktion of the **grid mode**.

Accession number	**Taxon**	**Collector**
CollectionSpecimen	**IdentificationUnit**	**CollectionAgen**
AccessionNumber	**LastIdentificationCache**	**CollectorsNam**
M-0013579	Arthrocladiella mougeotii (Lev.) Vassilkov	Sandu, C.
M-0013579	Arthrocladiella mougeotii (Lev.) Vassilkov	Savulescu, T.
M-0013579	Blumeria graminis (DC.) Speer	Sandu, C.
M-0013579	Blumeria graminis (DC.) Speer	Savulescu, T.
M-0013579	Lycium barbarum	Sandu, C.
M-0013579	Lycium barbarum	Savulescu, T.

Reimport tab-separated lists

With this import routine you are able to reimport data in tab-separated lists which have been exported from the database. Choose **Data -> Import -> Reimport list...** from the menu to open the window for the reimport. To reimport data it must have been exported using the option **[add columns for reimport]** to ensure correct header lines in your file. As the client provides no possibility to change data on the basis of lists, you may export the respective data to a tab-separated list, change your values and reimport the data.

In the window click on the button to select the file with the data you wish to import. Use the proper **[encoding]** to ensure that all special characters will be transferred correctly. If you change the encoding after opening the file, click on the button to reload the file with the new encoding. The content of the file will be visible as shown below. For a reimport the data will always start in line 7, indicated by a gray background of the header lines.



Encoding: Unicode
Filename: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\Export\DiversityCollection

DiversityCollectionExport_20080215_161230.txt

CollectionSpecim...	Average latitude	CollectionEventID	LocalisationSyste...	Average longitude	Location 1	Location 2
CollectionSpecim...	CollectionEventL...	CollectionEventL...	CollectionEventL...	CollectionEventL...	CollectionEventL...	CollectionEventL...
CollectionSpecim...	AverageLatitude...	CollectionEventID	LocalisationSyste...	AverageLongitud...	Location1	Location2
T0	T2	T2	T2	T2	T2	T2
168446	48,1381	204669	9	46,832	46,832	48,1381
168448	48,1381	201482	9	46,832	46,832	48,1381
169568	48,1381	204668	9	46,832	46,832	48,1381
169637	48,1381	205416	9	46,832	46,832	48,1381
167313	48,1381	205415	9	46,832	46,832	48,1381

CollectionSpecimen [T0]
  [1]
    CollectionSpecimenID: 168448
CollectionEventLocalisation [T2]
  [1]
    AverageLatitudeCache: 48.1381
    CollectionEventID: 201482
    LocalisationSystemID: 9

|◀ ◀ 2 ▶ ▶|
Up to: 5
Total: 5

Import data: ● Import all data lines ○ Import first 1 lines ☐ Import empty data

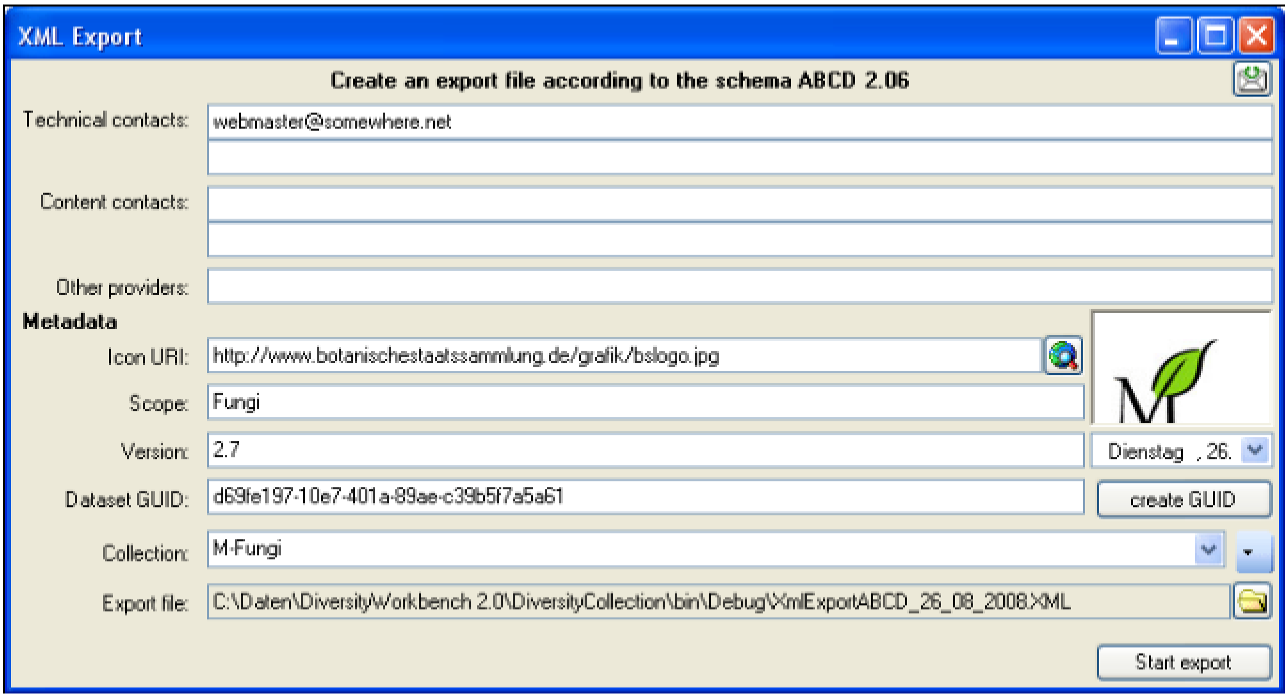
To analyse the data in the file click on the **[Analyse]** button. After a successful analysis, the window will show you the result as shown in the image below. The first data set will be shown in the form. If you wish to check more data sets, set the number of the last position you wish to check and click on the **[Analyse]** button. The data is presented according to the tables in the database where they will be inserted. Underlined columns belong to the primary key of the respective tables and are red, if missing. These missing values will be generated during the import. If a data set contains no values and will therefore not be imported into the database or updated, the colums will be shown in blue. To import these entries anyway choose the **[import empty values]** option. To browse through the data sets in the preview use the |◀ ◀ 2 ▶ ▶| buttons.

To import your data click on the **[Start import]** button. If you wish to import only a part of the data, e.g. for a test, choose the **[Import first ... lines]** option.

Export ABCD

In the current version only the main data from DiversityCollection will be exported to ABCD.

To export the data of the specimen selected in the specimen list following the [ABCD schema 2.06]() choose **Data -> Export -> XML (ABCD Schema)...** from the menu. A window will open where you can set some additional parameters defined in ABCD and [BioCASE]() respectively as shown below.



Technical contacts: webmaster@somewhere.net

Content contacts:

Other providers:

Metadata

Icon URI: http://www.botanischestaatssammlung.de/grafik/bslogo.jpg

Scope: Fungi

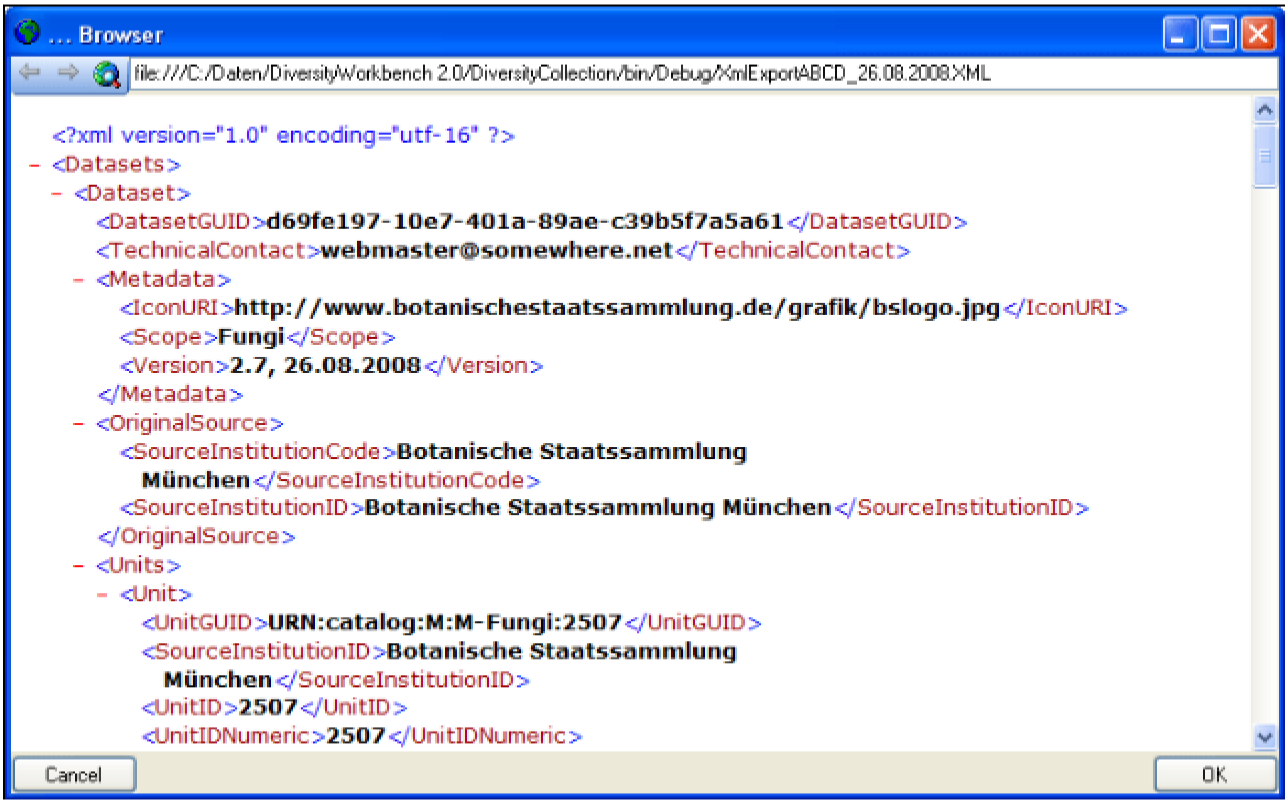
Version: 2.7 Dienstag , 26.

Dataset GUID: d69fe197-10e7-401a-89ae-c39b5f7a5a61

Collection: M-Fungi

Export file: C:\Daten\DiversityWorkbench 2.0\DiversityCollection\bin\Debug\XmlExportABCD_26_08_2008.XML

To start the export click on the **Start export** button. The data will be exported into a file in your application directory. Click on the 📂button to inspect the exported data (see below).

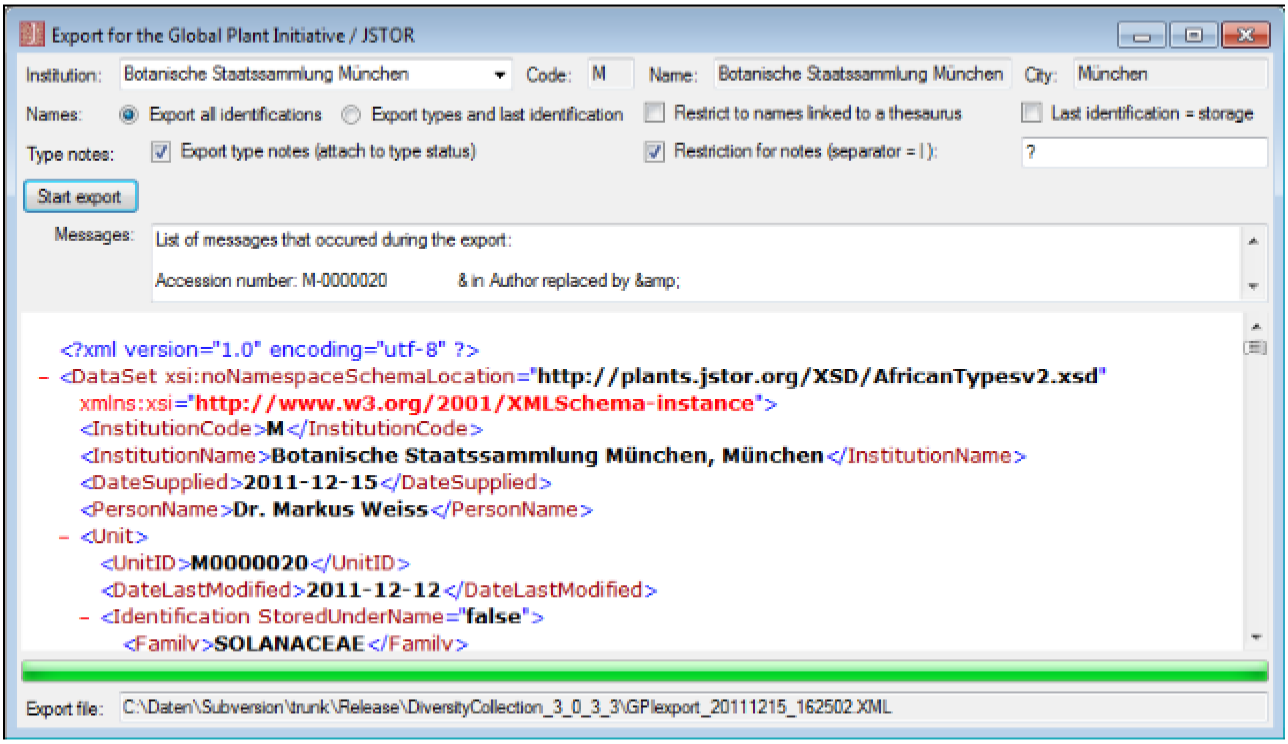


file:///C:/Daten/DiversityWorkbench 2.0/DiversityCollection/bin/Debug/XmlExportABCD_26.08.2008.XML

```
  <?xml version="1.0" encoding="utf-16" ?>
- <Datasets>
  - <Dataset>
      <DatasetGUID>d69fe197-10e7-401a-89ae-c39b5f7a5a61</DatasetGUID>
      <TechnicalContact>webmaster@somewhere.net</TechnicalContact>
    - <Metadata>
        <IconURI>http://www.botanischestaatssammlung.de/grafik/bslogo.jpg</IconURI>
        <Scope>Fungi</Scope>
        <Version>2.7, 26.08.2008</Version>
      </Metadata>
    - <OriginalSource>
        <SourceInstitutionCode>Botanische Staatssammlung
          München</SourceInstitutionCode>
        <SourceInstitutionID>Botanische Staatssammlung München</SourceInstitutionID>
      </OriginalSource>
    - <Units>
      - <Unit>
          <UnitGUID>URN:catalog:M:M-Fungi:2507</UnitGUID>
          <SourceInstitutionID>Botanische Staatssammlung
            München</SourceInstitutionID>
          <UnitID>2507</UnitID>
          <UnitIDNumeric>2507</UnitIDNumeric>
```

Export for the Global Plant Initiative / JSTOR

To export the data of the specimen selected in the specimen list according to the Global Plant Initiative / JSTOR choose **Data -> Export -> XML -> GPI / JSTOR ...** from the menu. A window will open where you can set some additional options for the export (see below). The data sets will be exported according to the JSTOR Plant Science Handbook (June 2011).



Institution: Botanische Staatssammlung München
Code: M
Name: Botanische Staatssammlung München
City: München
Names: ● Export all identifications ○ Export types and last identification ☐ Restrict to names linked to a thesaurus ☐ Last identification = storage
Type notes: ☑ Export type notes (attach to type status) ☑ Restriction for notes (separator = |): ?

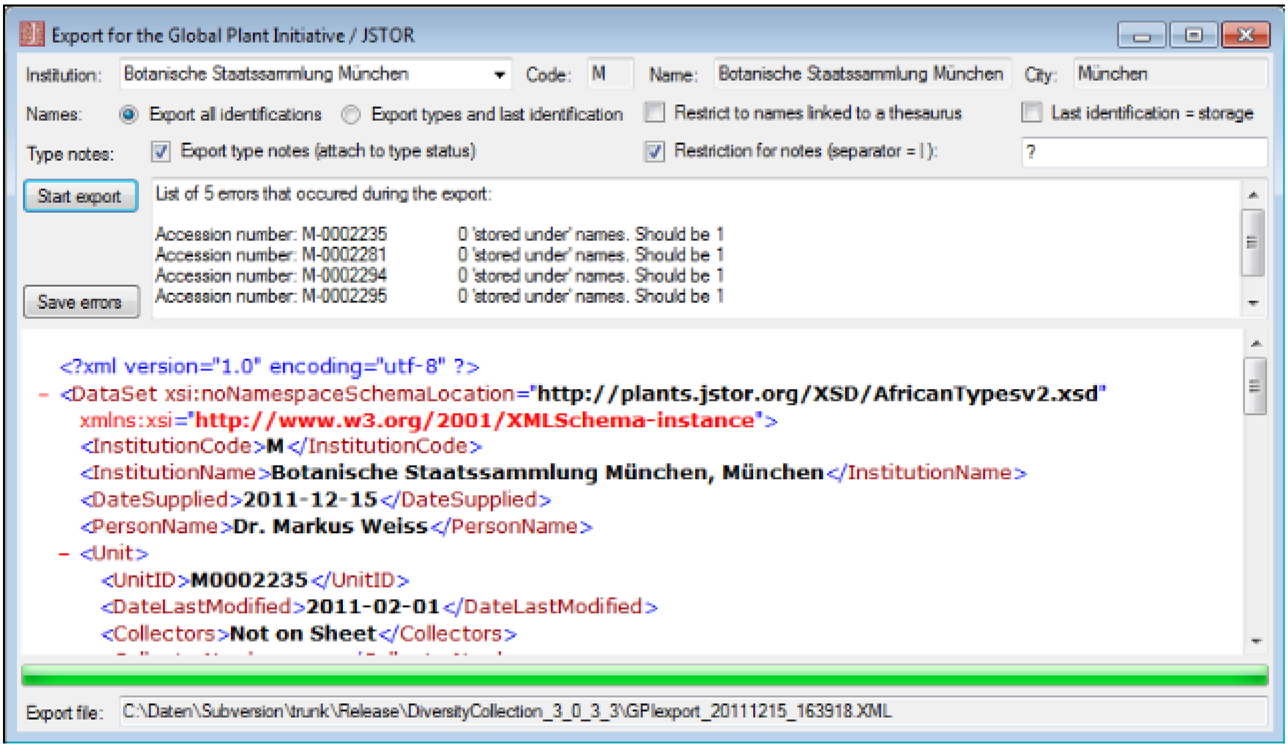
Messages: List of messages that occured during the export:

Accession number: M-0000020 & in Author replaced by &

```
  <?xml version="1.0" encoding="utf-8" ?>
- <DataSet xsi:noNamespaceSchemaLocation="http://plants.jstor.org/XSD/AfricanTypesv2.xsd"
    xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance">
    <InstitutionCode>M</InstitutionCode>
    <InstitutionName>Botanische Staatssammlung München, München</InstitutionName>
    <DateSupplied>2011-12-15</DateSupplied>
    <PersonName>Dr. Markus Weiss</PersonName>
  - <Unit>
      <UnitID>M0000020</UnitID>
      <DateLastModified>2011-12-12</DateLastModified>
    - <Identification StoredUnderName="false">
        <Family>SOLANACEAE</Family>
```

Export file: C:\Daten\Subversion\trunk\Release\DiversityCollection_3_0_3_3\GPIexport_20111215_162502.XML

If the data does not fulfill the critera of the Global Plant Initiative / JSTOR, the errors will be listed as shown below. You have to fix these errors in your data to create a valid export file. To start the export click on the **Start export** button. The data will be exported into a file in your application directory. Click on the button to inspect the exported data (see below).



Institution: Botanische Staatssammlung München Code: M Name: Botanische Staatssammlung München City: München

Names: ● Export all identifications ○ Export types and last identification ☐ Restrict to names linked to a thesaurus ☐ Last identification = storage

Type notes: ☑ Export type notes (attach to type status) ☑ Restriction for notes (separator = |): ?

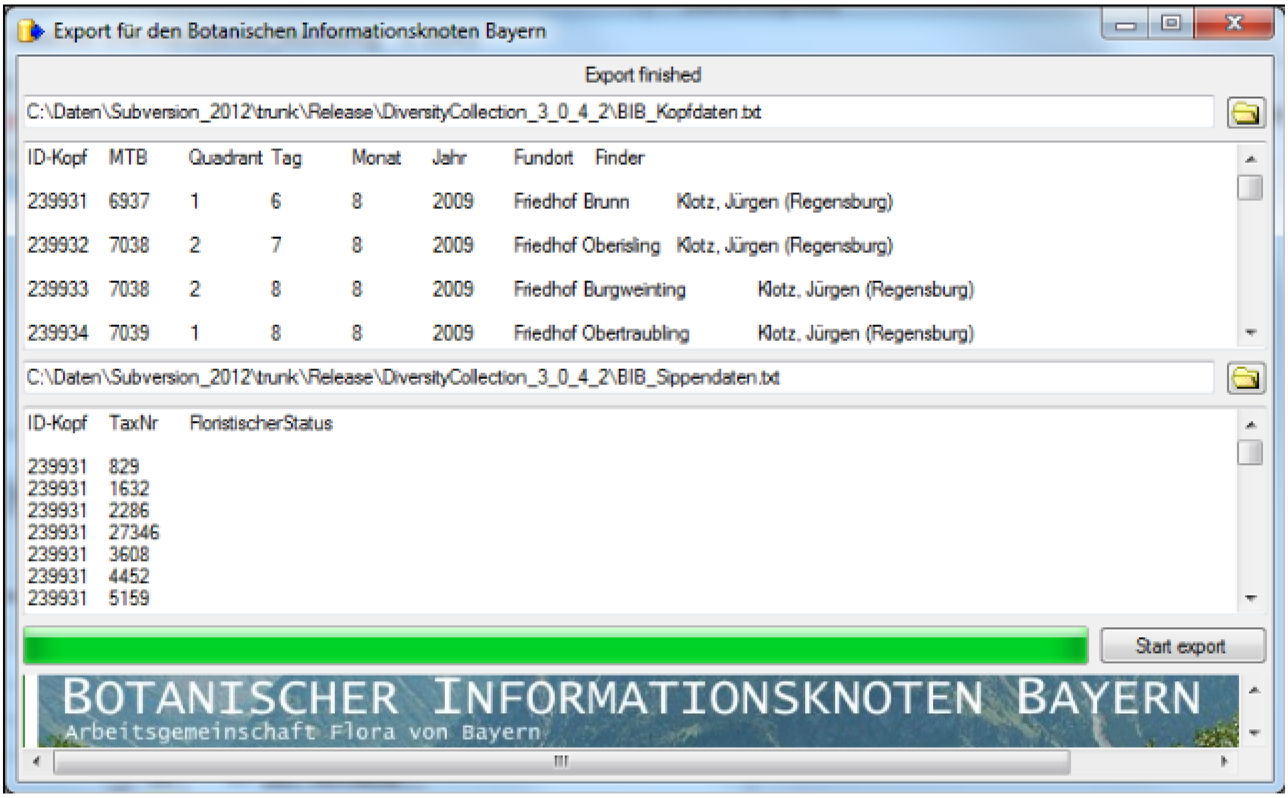
```
List of 5 errors that occured during the export:

Accession number: M-0002235          0 'stored under' names. Should be 1
Accession number: M-0002281          0 'stored under' names. Should be 1
Accession number: M-0002294          0 'stored under' names. Should be 1
Accession number: M-0002295          0 'stored under' names. Should be 1
```

```
  <?xml version="1.0" encoding="utf-8" ?>
- <DataSet xsi:noNamespaceSchemaLocation="http://plants.jstor.org/XSD/AfricanTypesv2.xsd"
   xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance">
   <InstitutionCode>M</InstitutionCode>
   <InstitutionName>Botanische Staatssammlung München, München</InstitutionName>
   <DateSupplied>2011-12-15</DateSupplied>
   <PersonName>Dr. Markus Weiss</PersonName>
 - <Unit>
     <UnitID>M0002235</UnitID>
     <DateLastModified>2011-02-01</DateLastModified>
     <Collectors>Not on Sheet</Collectors>
```

Export file: C:\Daten\Subversion\trunk\Release\DiversityCollection_3_0_3_3\GPIexport_20111215_163918.XML

Export for the Botanischer Informationsknoten Bayern (BIB)

To export the data of the specimen selected in the specimen list according to the Botanischer Informationsknoten Bayern choose **Data -> Export -> Floristic lists -> BIB ...** from the menu. A window will open as shown below. The data sets will be exported in 2 files according to the format of BIB.



Export finished

C:\Daten\Subversion_2012\trunk\Release\DiversityCollection_3_0_4_2\BIB_Kopfdaten.txt

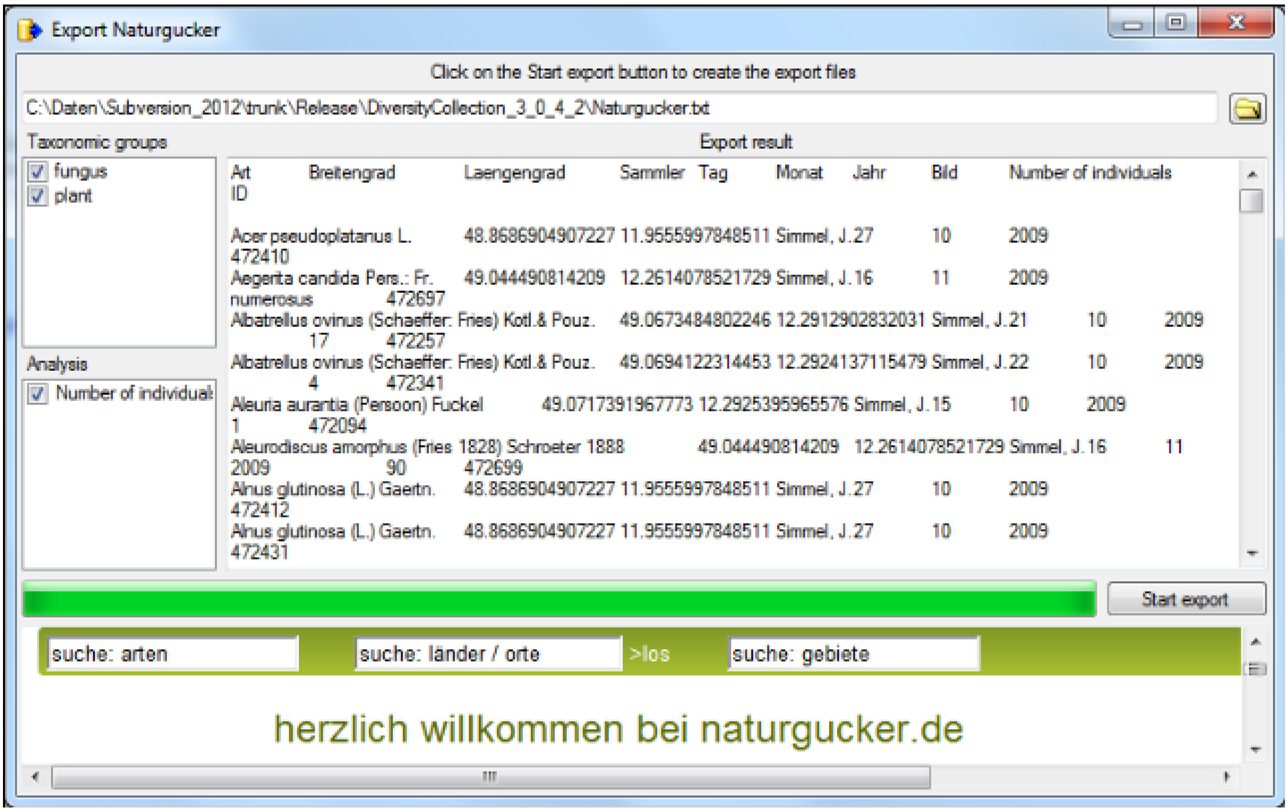
```
ID-Kopf  MTB   Quadrant Tag  Monat  Jahr  Fundort    Finder
239931   6937  1        6    8      2009  Friedhof Brunn        Klotz, Jürgen (Regensburg)
239932   7038  2        7    8      2009  Friedhof Oberisling   Klotz, Jürgen (Regensburg)
239933   7038  2        8    8      2009  Friedhof Burgweinting          Klotz, Jürgen (Regensburg)
239934   7039  1        8    8      2009  Friedhof Obertraubling         Klotz, Jürgen (Regensburg)
```

C:\Daten\Subversion_2012\trunk\Release\DiversityCollection_3_0_4_2\BIB_Sippendaten.txt

```
ID-Kopf  TaxNr  FloristischerStatus

239931   829
239931   1632
239931   2286
239931   27346
239931   3608
239931   4452
239931   5159
```

Export for naturgucker

To export the data of the specimen selected in the specimen list according to naturgucker choose **Data -> Export -> Floristic lists -> Naturgucker ...** from the menu. A window will open as shown below. The data sets will be exported in a file according to the format of Naturgucker. In the form you can choose among the taxonomic groups and analysis provided in the selected data.



C:\Daten\Subversion_2012\trunk\Release\DiversityCollection_3_0_4_2\Naturgucker.txt

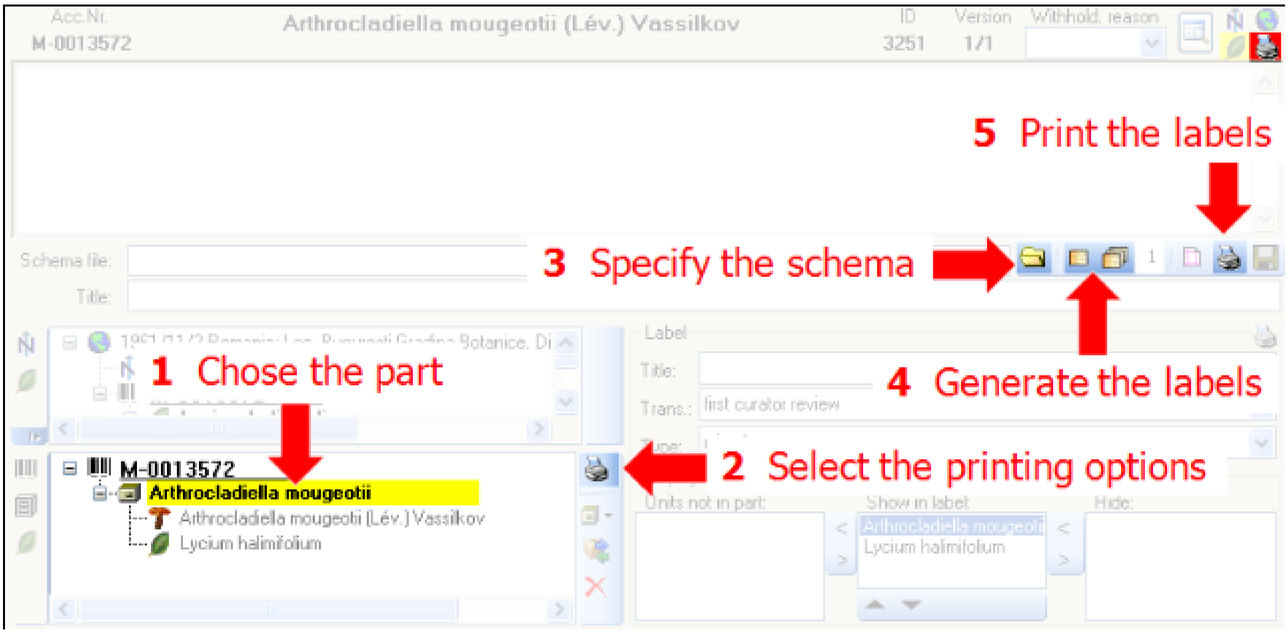
☑ fungus
☑ plant

☑ Number of individuals

```
Art	Breitengrad	Laengengrad	Sammler	Tag	Monat	Jahr	Bild	Number of individuals
ID

Acer pseudoplatanus L.	48.8686904907227 11.9555997848511 Simmel, J.27	10	2009
472410
Aegerita candida Pers.: Fr.	49.044490814209	12.2614078521729 Simmel, J.16	11	2009
numerosus	472697
Albatrellus ovinus (Schaeffer: Fries) Kotl.& Pouz.	49.0673484802246 12.2912902832031 Simmel, J.21	10	2009
	17	472257
Albatrellus ovinus (Schaeffer: Fries) Kotl.& Pouz.	49.0694122314453 12.2924137115479 Simmel, J.22	10	2009
	4	472341
Aleuria aurantia (Persoon) Fuckel	49.0717391967773 12.2925395965576 Simmel, J.15	10	2009
1	472094
Aleurodiscus amorphus (Fries 1828) Schroeter 1888	49.044490814209	12.2614078521729 Simmel, J.16	11
2009	90	472699
Alnus glutinosa (L.) Gaertn.	48.8686904907227 11.9555997848511 Simmel, J.27	10	2009
472412
Alnus glutinosa (L.) Gaertn.	48.8686904907227 11.9555997848511 Simmel, J.27	10	2009
472431
```

Label

If there is only one part in your specimen, click on the printer symbol in the button to switch to the printing mode. If your specimen contains more than one part, choose the part of the specimen for which the label should be generated and click on the button in the right panel. The image area will switch to the label view and in the data area the details related to the label will be accessible. The sequence is shown in the image below.



1 Chose the part

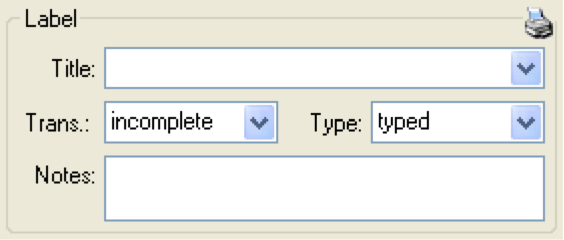
2 Select the printing options

3 Specify the schema

4 Generate the labels

5 Print the labels

Additional information about a label is entered in the label section (see image below). The data is stored in the table [CollectionSpecimen](#).&nb sp;


Label

Title:

Trans.: incomplete

Type: typed

Notes:

The organisms of a specimen are printed on a label according to the [display order](#).

To print a label for a specimen you have to select a schema file. There are default schema files available in the folder **LabelPrinting/Schemas** in your application directory. Click on the button to open the directory. You will find several prepared schema files among which you can choose or change them to your own needs or create new ones respectively. The schema file **LabelTemplates.xslt** provides templates for the other schema files. You may give a title for the print in the field Title. From the Collection and MaterialCategory available for the selected specimen choose one from the list (**Coll./Mat.**). To generate the label for the current specimen click on the button. To generate labels for all specimens in your query click on the button. If you need duplicates of your labels change the number in the duplicates box 3 to the desired value. You can print 1 - 99 duplicates of one label. If there are more than 20 specimens in the list, you receive a warning whether you really wish to create all these labels as this could be somewhat time consuming. The labels are generated as

XML files with XSLT-schema files, transformed to HTML-files and depicted in a browser. To print the label click on the 🖨 button.

Botanische Staatssammlung München Nr. M-0013663

***Blumeria graminis* (DC.) Speer**

LATVIA. Lettland, Prov. Vidzeme, Kr. Riga: Ogre auf dem Felde.
On *Triticum sativum* .
1936/ 7/ 19 leg.: Smarods, J.
det.: Smarods, J.

M-0013663

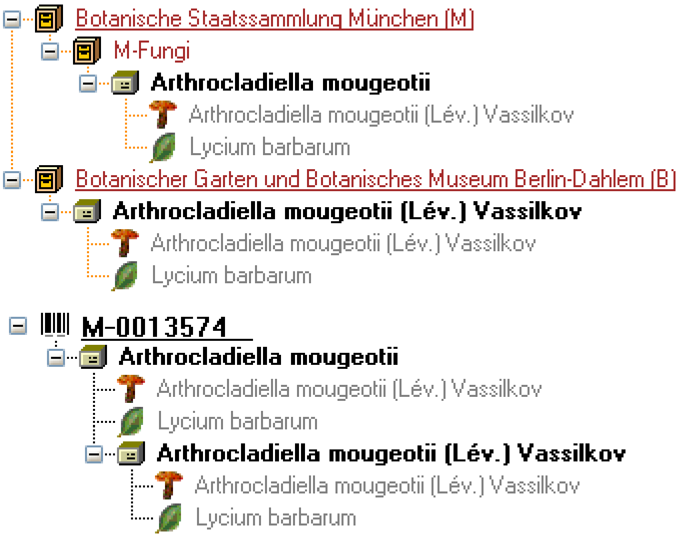
Schema file: Label.xslt

Title:

☐ Regard stock for duplicates

Restrict to collection: M-Fungi ☐ Restrict to material: specimen ☐

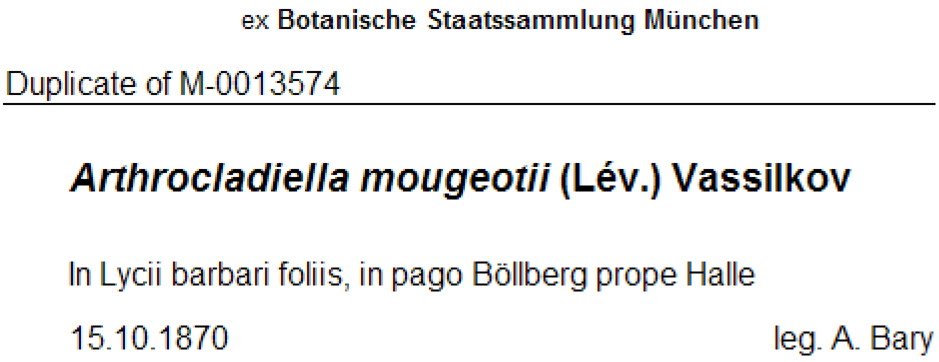
If you wish to print labels for duplicates which are stored in a different collection, the duplicate should be a child of the original specimen as shown in the example below.



- Botanische Staatssammlung München (M)
  - M-Fungi
    - **Arthrocladiella mougeotii**
      - Arthrocladiella mougeotii (Lév.) Vassilkov
      - Lycium barbarum
- Botanischer Garten und Botanisches Museum Berlin-Dahlem (B)
  - **Arthrocladiella mougeotii (Lév.) Vassilkov**
    - Arthrocladiella mougeotii (Lév.) Vassilkov
    - Lycium barbarum

- **M-0013574**
  - **Arthrocladiella mougeotii**
    - Arthrocladiella mougeotii (Lév.) Vassilkov
    - Lycium barbarum
    - **Arthrocladiella mougeotii (Lév.) Vassilkov**
      - Arthrocladiella mougeotii (Lév.) Vassilkov
      - Lycium barbarum

Depending on the schema you use, the label will be marked as duplicat and contain a reference to the original specimen (see below).



ex **Botanische Staatssammlung München**

Duplicate of M-0013574

***Arthrocladiella mougeotii* (Lév.) Vassilkov**

In Lycii barbari foliis, in pago Böllberg prope Halle

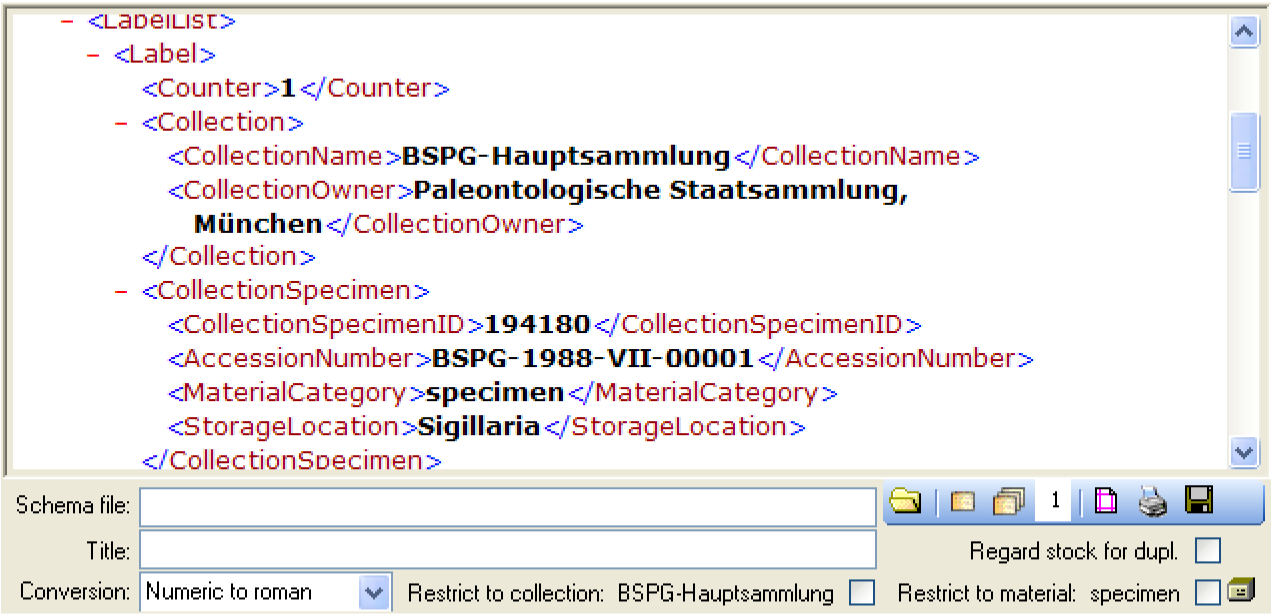
15.10.1870 leg. A. Bary

If you wish to save the generated files for later printing, click on the 💾 button to do so. Note that the program will by default create a file **Label.xml** and in case a schema file is specified a file **Label.htm** in the **LabelPrinting** directory which will be overwritten every time you generate a new label. Thus, you need to save the file under a different name or in a different directory to prevent the program to erase this data.

If you use **Code 39** for your labels and wish to print the barcodes on the labels, you need the font code39.ttf , which is included in the DiversityCollection package. Place this font in the folder where your fonts are stored (e.g.: C:\WINNT\Fonts). If the font is not available, the Barcode will appear as the accession number between two '*' signs.

If you wish to print labels for all the specimens in the specimen list, you can restrict these to the collection and the material category of the current specimen part (see image above).

If you do not select a schema file, i.e. the textbox **Schema file:** is empty, you will see the generated XML-file as shown in the image below. The XML file is the base for all label types you wish to generate. To create your own labels simply design your own XSLT-schema file. See e.g. http://www.w3.org/TR/xslt for further information about schema files.



```
- <LabelList>
  - <Label>
      <Counter>1</Counter>
    - <Collection>
        <CollectionName>BSPG-Hauptsammlung</CollectionName>
        <CollectionOwner>Paleontologische Staatsammlung,
          München</CollectionOwner>
      </Collection>
    - <CollectionSpecimen>
        <CollectionSpecimenID>194180</CollectionSpecimenID>
        <AccessionNumber>BSPG-1988-VII-00001</AccessionNumber>
        <MaterialCategory>specimen</MaterialCategory>
        <StorageLocation>Sigillaria</StorageLocation>
      </CollectionSpecimen>
```

Schema file:

Title:

Regard stock for dupl. ☐

Conversion: Numeric to roman

Restrict to collection: BSPG-Hauptsammlung ☐

Restrict to material: specimen ☐

If you wish to reformat the accession number, you may choose among the options provided by the program, e.g. conversion of arabic to roman numbers (BSPG-1988-007-00001 -> BSPG-1988-VII-00001). Select the format from the combobox **[Conversion]** shown above.

Replication

If you wish to work with your data on a local database (called *subscriber*), e.g. on your labtop, not linked to a database on a central server (called *publisher*) and these data should be synchronized with the data in the database on the server, you may use the replication function of DiversityCollection. To install the database on your local computer see the installation section.

To use the replication function you require the roles **Replicator** or **Administrator**.

Add Publisher

To define a publishing database choose **Data -> Replication -> Add Publisher** from the menu. A window will open where you choose the *publisher*. After the *publisher* is set, you may transfer data between your local database (*subscriber*) and the *publisher*. This function is only available for administrators.

Remove Publisher

To remove a publisher from the list choose **Data -> Replication -> [Publisher] -> Remove** from the menu (where [Publisher] is the name of the publishing database on the publishing server). This function is only available for administrators.

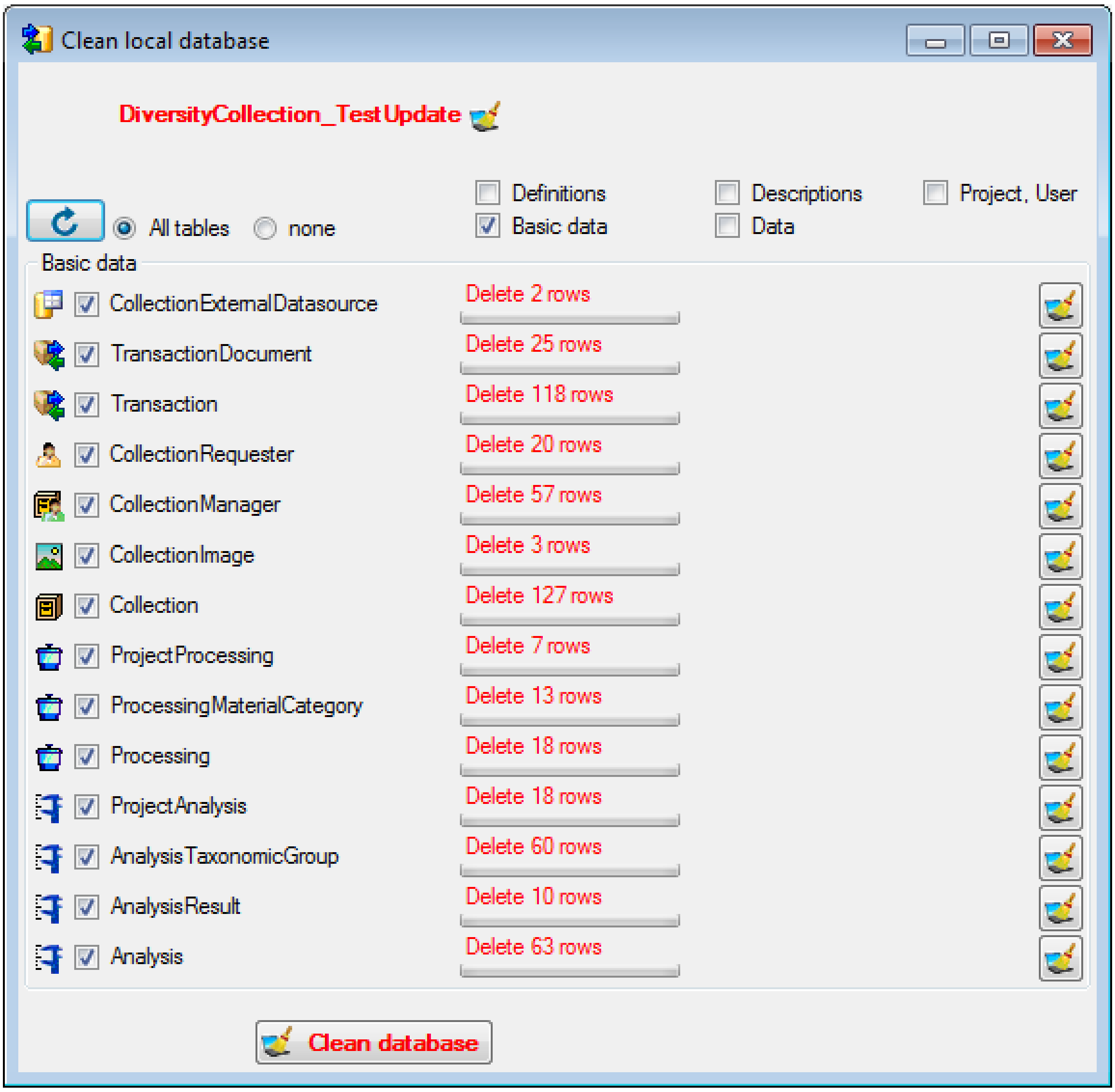
Clean database

Initially you may wish to remove all previous data from your local database (*subscriber*). Choose **Data -> Replication -> Clean database ...** from the menu. A window will open as shown below where you may choose the ranges which should be cleared:

- Definitions = the basic definitions within the database, e.g. the available taxonomic groups.
- Descriptions = the descriptions and their translations of the tables and columns of the database.

- Project, User = the available projects and users.
- Basic data = basic data like the collection.
- Data = the specimen, organisms etc.

Choose the data ranges you wish to clear and click on the button. All tables which contain data will be listed as shown below.



DiversityCollection_TestUpdate

● All tables ○ none

☐ Definitions ☐ Descriptions ☐ Project, User
☑ Basic data ☐ Data

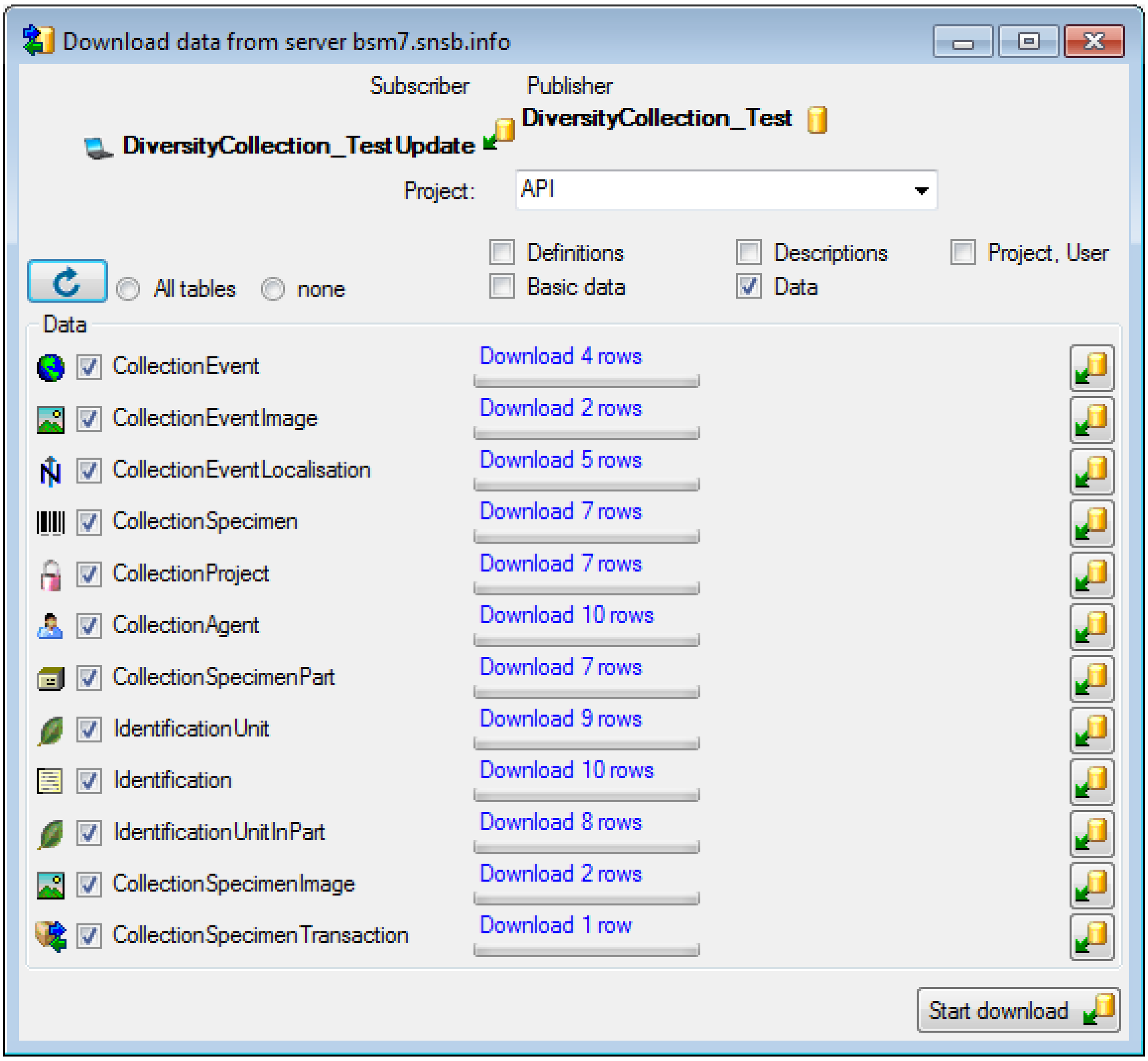
Basic data

☑ CollectionExternalDatasource	Delete 2 rows
☑ TransactionDocument	Delete 25 rows
☑ Transaction	Delete 118 rows
☑ CollectionRequester	Delete 20 rows
☑ CollectionManager	Delete 57 rows
☑ CollectionImage	Delete 3 rows
☑ Collection	Delete 127 rows
☑ ProjectProcessing	Delete 7 rows
☑ ProcessingMaterialCategory	Delete 13 rows
☑ Processing	Delete 18 rows
☑ ProjectAnalysis	Delete 18 rows
☑ AnalysisTaxonomicGroup	Delete 60 rows
☑ AnalysisResult	Delete 10 rows
☑ Analysis	Delete 63 rows

Choose the tables which should be cleared and click on the **Clean database** button. Please keep in mind that you can not delete data from a table as long as there is data in a relateted table depending on the data you wish to delete. The sequence of the tables is organized to avoid these problems.

Download

To download data from the *publisher* choose **Data -> Replication -> [Publisher] -> Download** from the menu (where [Publisher] is the name of the publishing database on the publishing server). A form will open as shown below. Choose the project of the data and the data ranges (see above) which you wish to download. Click on the button to list the tables containing data. To start the download click on the **Start download** button.


Download data from server bsm7.snsb.info

Subscriber: DiversityCollection_TestUpdate

Publisher: DiversityCollection_Test

Project: API

○ All tables ○ none

☐ Definitions ☐ Descriptions ☐ Project, User

☐ Basic data ☑ Data

Data

☑ CollectionEvent	Download 4 rows
☑ CollectionEventImage	Download 2 rows
☑ CollectionEventLocalisation	Download 5 rows
☑ CollectionSpecimen	Download 7 rows
☑ CollectionProject	Download 7 rows
☑ CollectionAgent	Download 10 rows
☑ CollectionSpecimenPart	Download 7 rows
☑ IdentificationUnit	Download 9 rows
☑ Identification	Download 10 rows
☑ IdentificationUnitInPart	Download 8 rows
☑ CollectionSpecimenImage	Download 2 rows
☑ CollectionSpecimenTransaction	Download 1 row

Merge

To merge data from your local *subscriber* database with the *publisher* you must first choose a project. Choose **Data -> Replication -> [Publisher] -> Merge** from the menu (where [Publisher] is the name of the publishing database on the publishing server). As with the download, choose the data ranges and click on the ↻ button. To start the upload click on the **Start merge** button.

Upload

To transfer data from your local *subscriber* database to the *publisher* you must first choose a project. Choose **Data -> Replication -> [Publisher] -> Upload** from the menu (where [Publisher] is the name of the publishing database on the publishing server). As with the download, choose the data ranges and click on the ↻ button. To start the upload click on the **Start upload** button.

Conflict

If the transfer of data was successfull, the numbers of the transfered data will be shown as below.


☐ IdentificationUnit

1 row transfered

Updated: 0
Inserted: 1

Conflicts: 0
Errors: 0

During the download or upload a conflict may occur, if the data has been edited in both databases. This will be indicated as shown below.

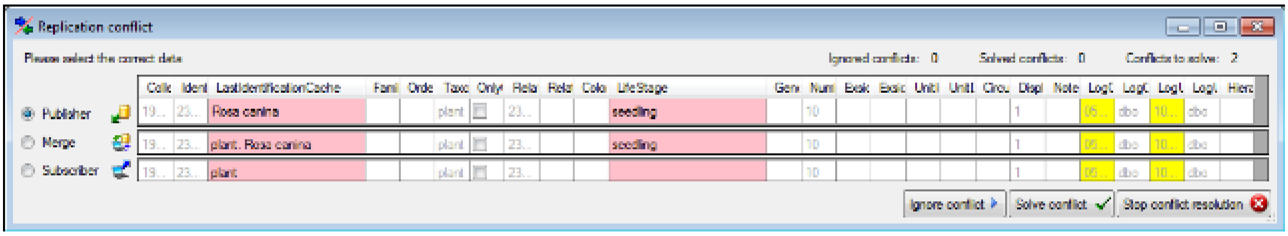

☐ IdentificationUnit

0 rows transfered

Updated: 0
Inserted: 0

Conflicts: 2
Errors: 0

Click on the button to open a window as shown below where you can choose between the two versions of the data as found in the *publisher* and the *subscriber* database.


Replication conflict

Please select the correct data

Ignored conflicts: 0 Solved conflicts: 0 Conflicts to solve: 2

	Colle	Ident	LastIdentificationCache	Fami	Orde	Taxo	Only	Rela	Rela	Colo	LifeStage	Gen	Num	Exsic	Exsic	Unit	Unit	Circu	Displ	Note	LogC	LogC	LogU	LogU	Hier
● Publisher	19...	23...	Rosa canina			plant	☐	23...			seedling		10						1		05...	dbo	10...	dbo	
○ Merge	19...	23...	plant. Rosa canina			plant	☐	23...			seedling		10						1		05...	dbo	10...	dbo	
○ Subscriber	19...	23...	plant			plant	☐	23...					10						1		05...	dbo	10...	dbo	

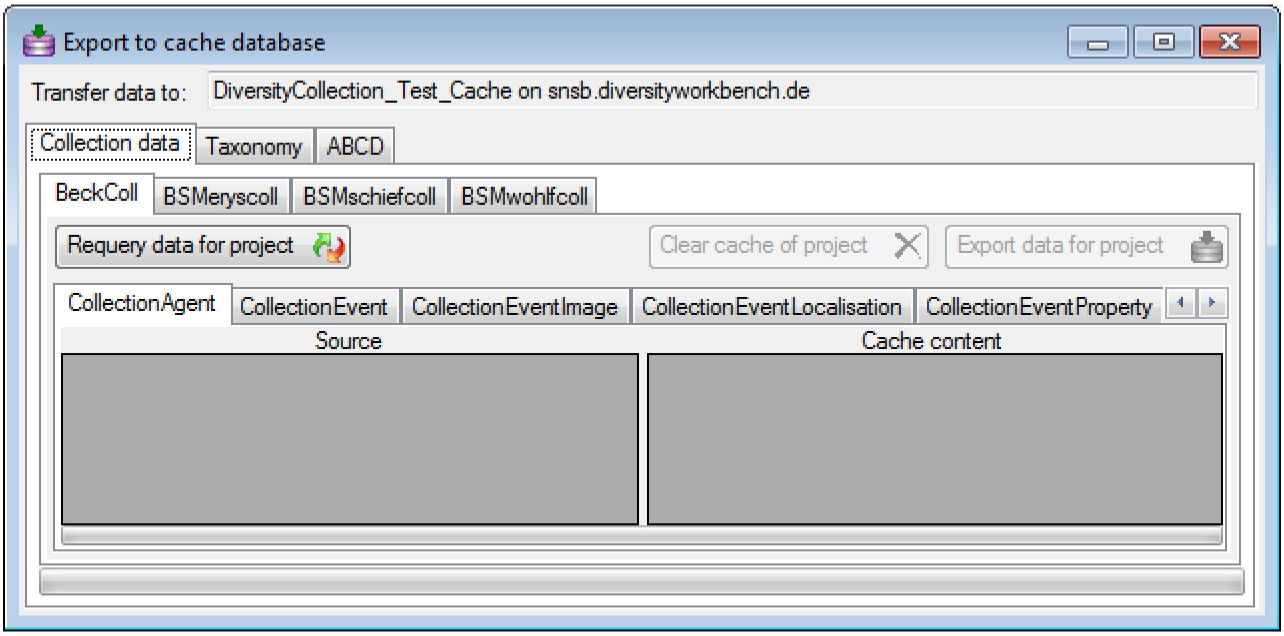
The conflicting columns are marked red. For text values the program will create a combination of both values (see above) in a merged version of the data. Choose the prefered version of the data and click **Solve conflict** ✓button. If you can not solve a conflict, use the **Ignore conflict** ▸or **Stop conflict resolution** ⊗buttons respectively.

Report

At the end of each transfer a report will be created with a summary for every table which has been included.

Export into the cache databases

To export data into the cache databases, choose **Data -> Export -> Cache database** from the menu. If several cache databases are available, select one of them in the window that will open. After a cache database has been selected a window will open as shown below.



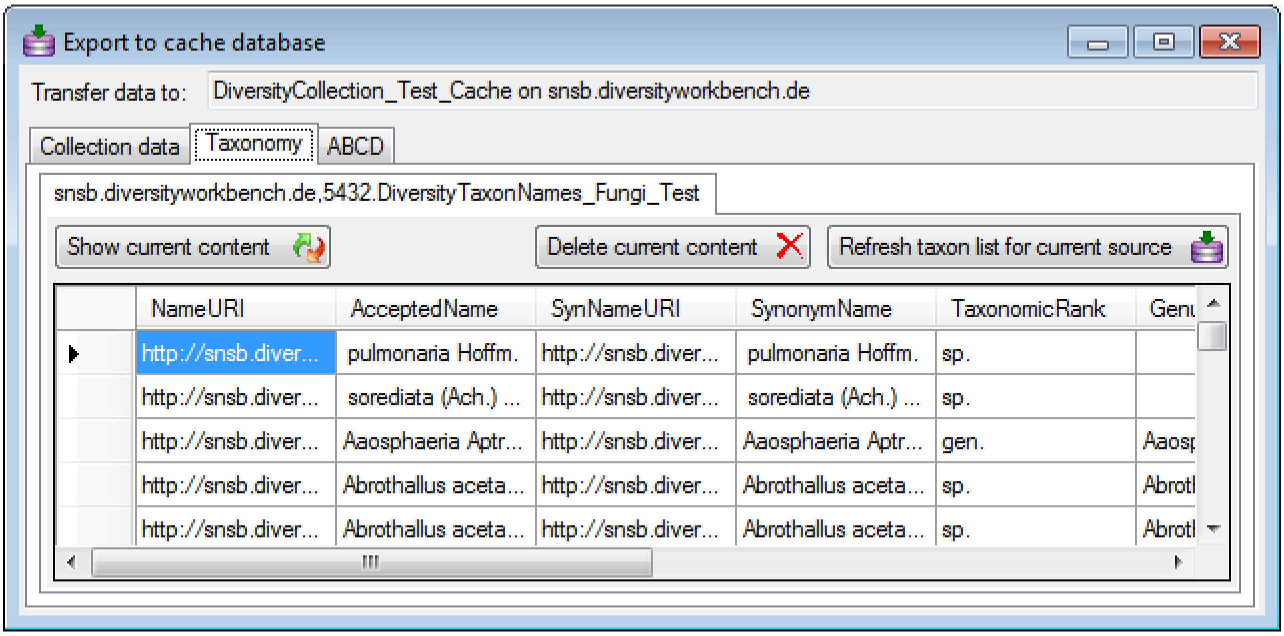
Transfer data to: DiversityCollection_Test_Cache on snsb.diversityworkbench.de

Collection data

Every project that has been selected for transfer into the cache database will be visible in the Collection data tab with its own page. To display the data available in the source and the cache database click on the **Requery data for project** button. For every table containing data for the selected project a page will show the current content within the source and the cache database. To export the data click on the **Export data for project** button. In the cache database this will delete the current data of the project and import the data as availble in the source. If for any reason the data of the project should be removed from the cache database click on the **Clear cache of project** button. If no cache database has been defined so far, use the button to create a new cache database. You will be asked for the server, the port used by the server, the directory of the database files, the name of the new cache database and finally the name of the projects database where the metadata of the projects transfered into the cache database are stored.

Taxonomy

All sources for taxa defined for the cache database (see chapter on Configuration) will be listed with one page in the **Taxonomy** tab (see image below). To transfer the current content of the taxonomy sources, use the **Refresh taxon list for current source** button. To transfer the taxonomic data delete a once created cache database by using the button.

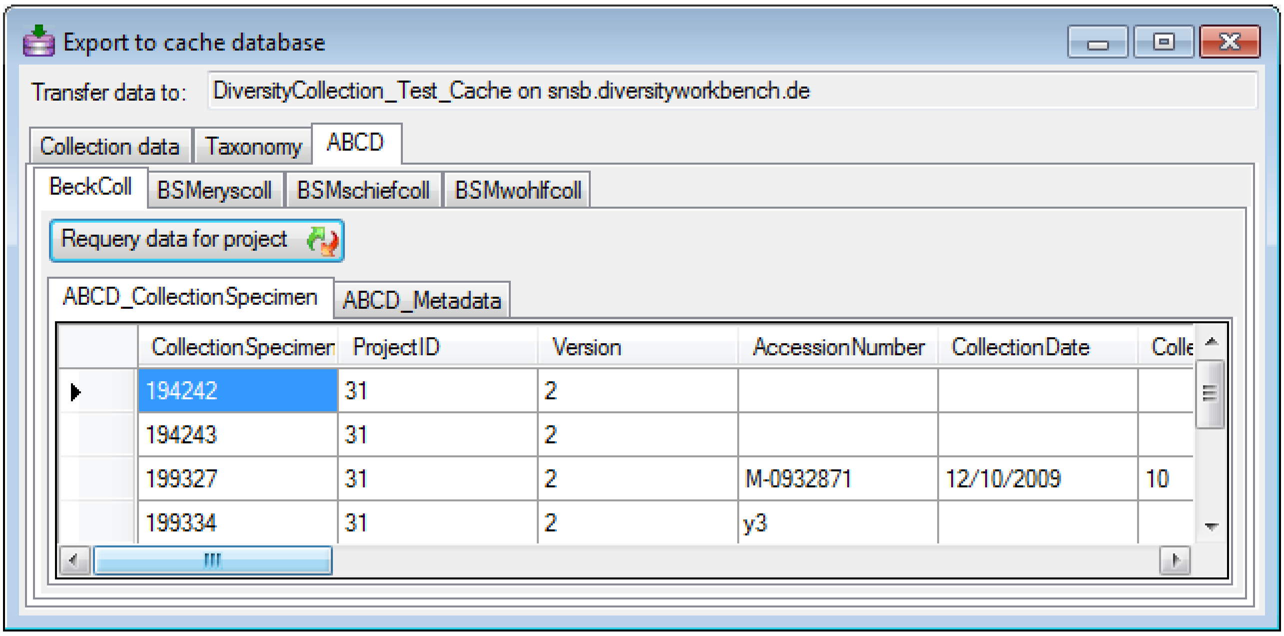


Transfer data to: DiversityCollection_Test_Cache on snsb.diversityworkbench.de

NameURI	AcceptedName	SynNameURI	SynonymName	TaxonomicRank	Genu
http://snsb.diver...	pulmonaria Hoffm.	http://snsb.diver...	pulmonaria Hoffm.	sp.	
http://snsb.diver...	sorediata (Ach.) ...	http://snsb.diver...	sorediata (Ach.) ...	sp.	
http://snsb.diver...	Aaosphaeria Aptr...	http://snsb.diver...	Aaosphaeria Aptr...	gen.	Aaosp
http://snsb.diver...	Abrothallus aceta...	http://snsb.diver...	Abrothallus aceta...	sp.	Abrotl
http://snsb.diver...	Abrothallus aceta...	http://snsb.diver...	Abrothallus aceta...	sp.	Abrotl

Interface

Together with the updates of the cache database, interfaces will be defined e.g. for ABCD (see below). To display the data of a project formated for the interface click on the Requery data for project button.



Transfer data to: DiversityCollection_Test_Cache on snsb.diversityworkbench.de

CollectionSpecimer	ProjectID	Version	AccessionNumber	CollectionDate	Colle
194242	31	2			
194243	31	2			
199327	31	2	M-0932871	12/10/2009	10
199334	31	2	y3		

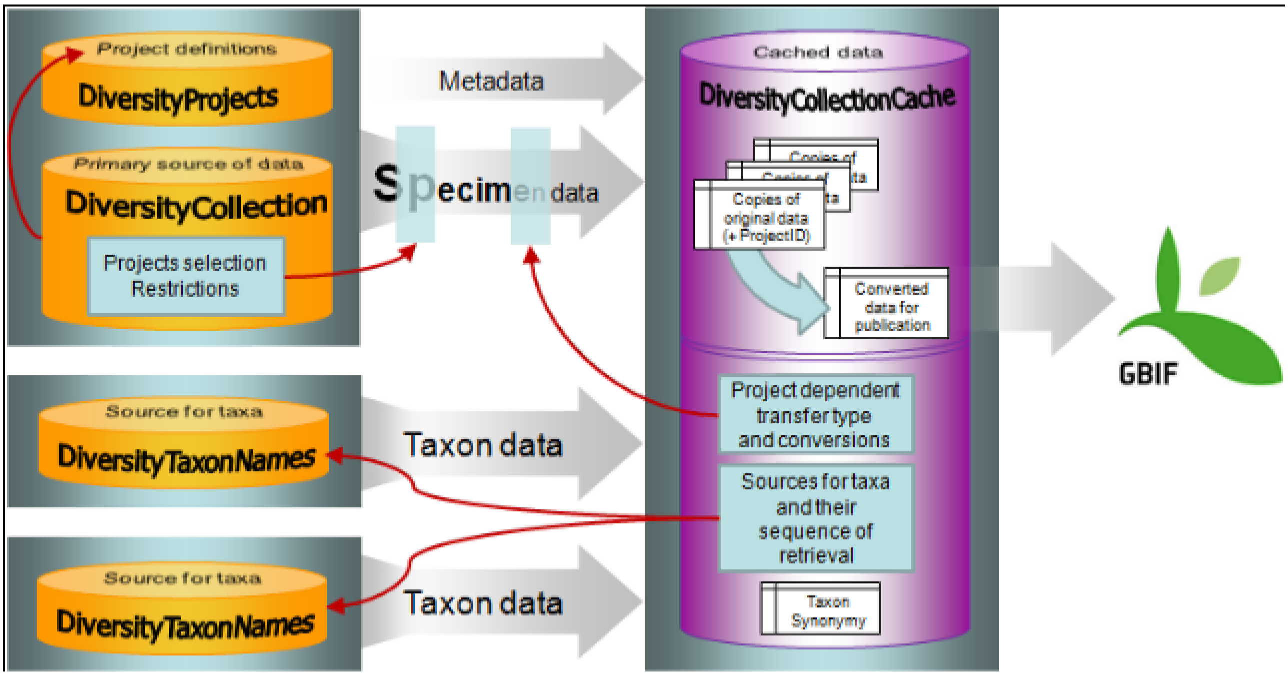
Configuratation of the cache databases

The cache databases for DiversityCollection are designed as sources for preformated data for publication in e.g. public user portals like GBIF. There may be several cache databases which can be located on several servers. The restrictions of the published data are defined in the main database via projects, data withholding and embargos. The publication of the data is allways related to a project, defined in DiversityProjects, holding the metadata that will be transfered into the cache database. Therefore every dataset copied from the source into the cache database contains a reference to the project (ProjectID). The publication of the data includes several steps:

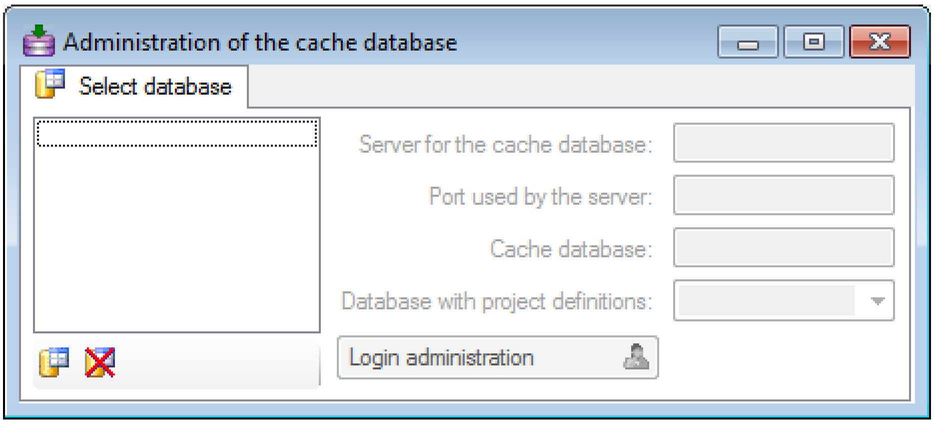
- Setting of restrictions within the original data with data withholding and embargos
- Selection of the project
- Transfer of the data into the cache database
- Conversion of the data into the format required by the portal

In Addition to the data transfered from DiversityCollection, the data for the taxonomy has to be transfered from the relevant sources. The links to these sources and the project dependent retrieval are stored in the cache database.

The image below gives an overview for the process described above.



To configure your cache databases, choose **Administration -> Cache database** from the menu. A window will open as shown below.



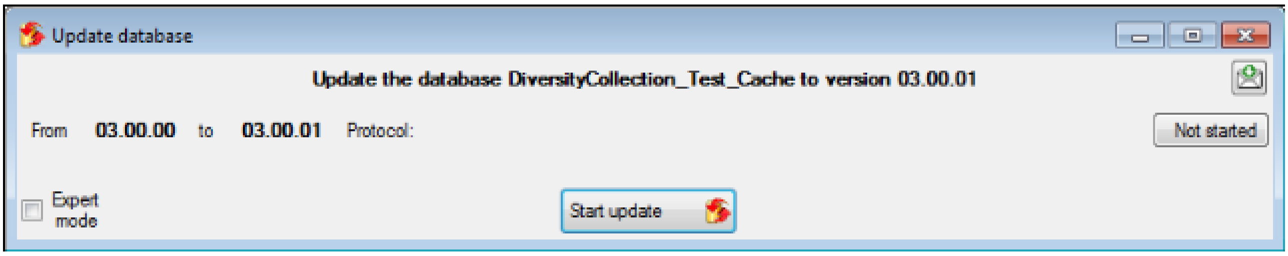
Creation of a cache database

If no cache database has been defined so far, use the button to create a new cache database. You have to be a System administrator to be able to create a cache database. You will be asked for the server, the port used by the server, the directory of the database files, the name of the new cache database and finally the name of the projects database where the metadata of the projects transfered into the cache database are stored.

To delete a once created cache database, use the button.

Updates of the cache database

After the new cache database has been created or if you select an outdated cache database, a button **Update database** will appear, instructing you to run updates for the cache database. Click on the button to open a window as shown below.



Update the database DiversityCollection_Test_Cache to version 03.00.01

From 03.00.00 to 03.00.01 Protocol:

All update scripts for the database will be listed. Click on the **Start update** button to update the database to the current version.

Login administration

To handle the data for the cache database a user needs access to the data on the source database, the cache database, the project database and the taxon databases. To administrate the users that can transfer data into the cache database use the button **Login administration**. For details see the chapter Login administration.

Configuration, Projects

Data transfer to the cache database is linked to projects . To add a project of which the data should be transfered into the cache database click on the ✚ button. For every project that should be transferred you have several options for configuration:

- Restriction of transfered taxonomic groups
- Restriction of transfered material categories
- Restriction of transfered localisations
    - Restriction of the precision of the coordinates
- Restriction of transfered images

Data types handle the data for the cache database. A user needs access to the data in the source database, the cache database, the project database and the taxon databases. To administrate the users who can transfer data into the cache database, use the button **Login administration**. For details see the chapter Login administration.

Restriction of Taxonomic groups, Material categories, Localisation systems or Images

To restrict the Taxonomic groups, Material catagories, Localisation systems or Images that are transferred to the cache database choose the corresponding options and select those that should be transferred into the cache database in the tab pages that are added.

Coordinate precision

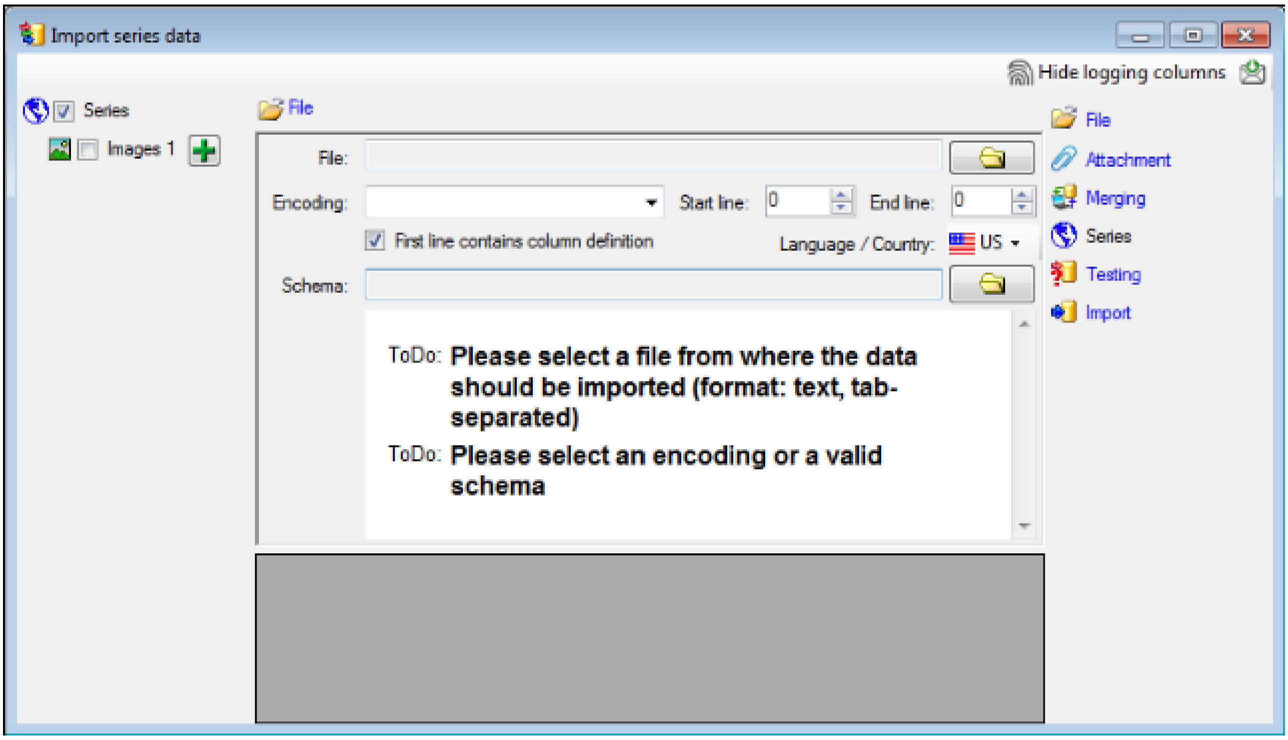
To reduce the precision of the coordinates of the localisation systems transferred to the cache database you can check the corresponding option and determine the number of digits after the decimal point.

Taxonomy

The collection data may be linked to sources holding taxonomic information (DiversityTaxonNames). To provide this information add all sources used in your collection data and transfer the corresponding data into the cache database. The data in the taxonomic sources are organized by projects, thus, you need to provide the sequence of the projects that should be imported into the cache database for every source. A name will be imported only once. This means that the name with synonymy to the first imported project will be imported, all following data with this name will be ignored.

Import wizard for tab separated lists

With this import routine, you can import data from text files (as tab-separated lists) into the database. Choose **Data -> Import -> Wizard** and then the type of data that should be imported, e.g. **import Series ...** from the menu. 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.

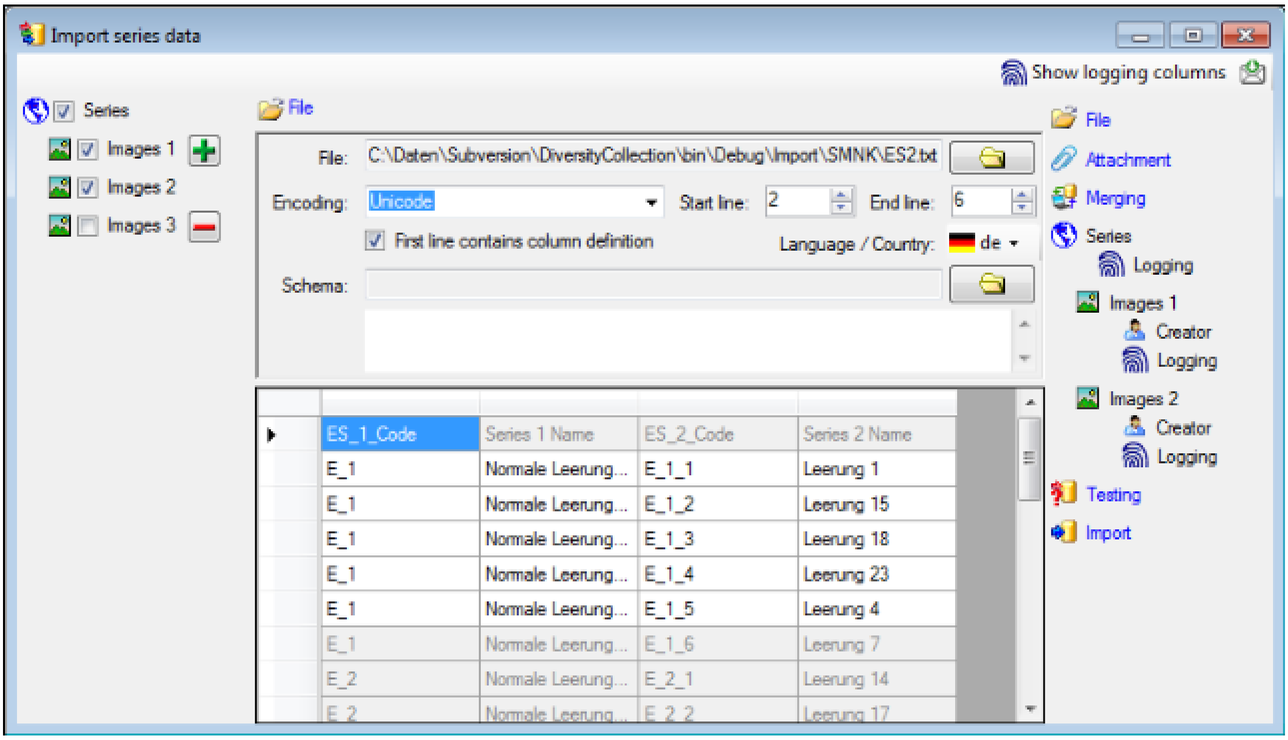


ToDo: Please select a file from where the data should be imported (format: text, tab-separated)

ToDo: Please select an encoding or a valid schema

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. Than 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 where notations differ between countries (e.g. 31.4.2013 - 4.31.2013), 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.



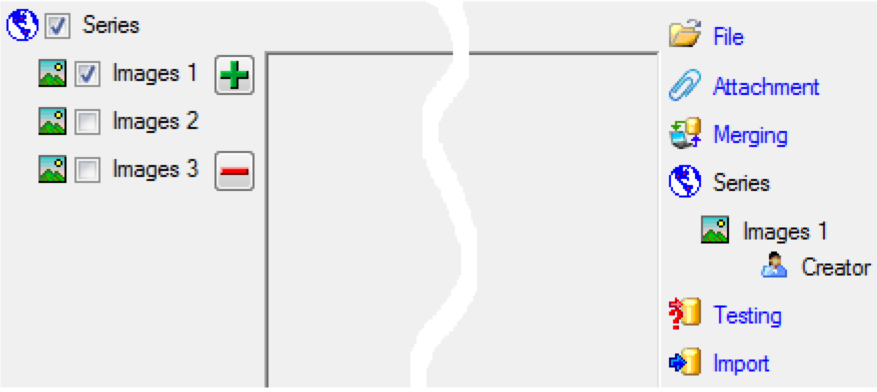
File: C:\Daten\Subversion\DiversityCollection\bin\Debug\Import\SMNK\ES2.txt
Encoding: Unicode
Start line: 2
End line: 6
☑ First line contains column definition
Language / Country: de
Schema:

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
E_1	Normale Leerung...	E_1_6	Leerung 7
E_2	Normale Leerung...	E_2_1	Leerung 14
E_2	Normale Leerung...	E_2_2	Leerung 17

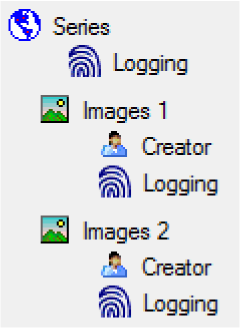
Choosing the data ranges

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 informations of logging columns like who created and changed the data, click on button in the header line. This will include a 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.



- Series
  - Logging
  - Images 1
    - Creator
    - Logging
  - Images 2
    - Creator
    - Logging

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 SeriesCode in the table Series in the example below.

● Import as new data

Series

○ SeriesCode

If you select a column for attachment, this column will be marked with a blue backgroud (see below and chapter **Table data**).

Merging data

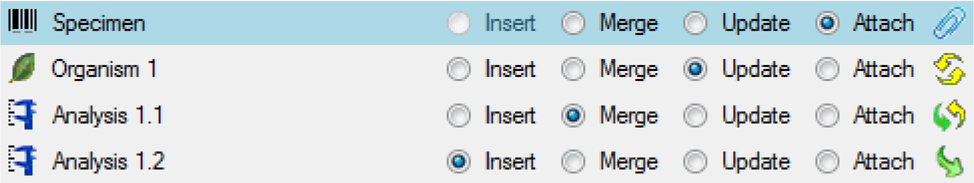
You can either import your data as new data or **Merge** them wih data in the database. Select the import step **Merge** from the list. For every table you can choose between **Insert**, **Merge**, **Update** and **Attach** (see below).

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.

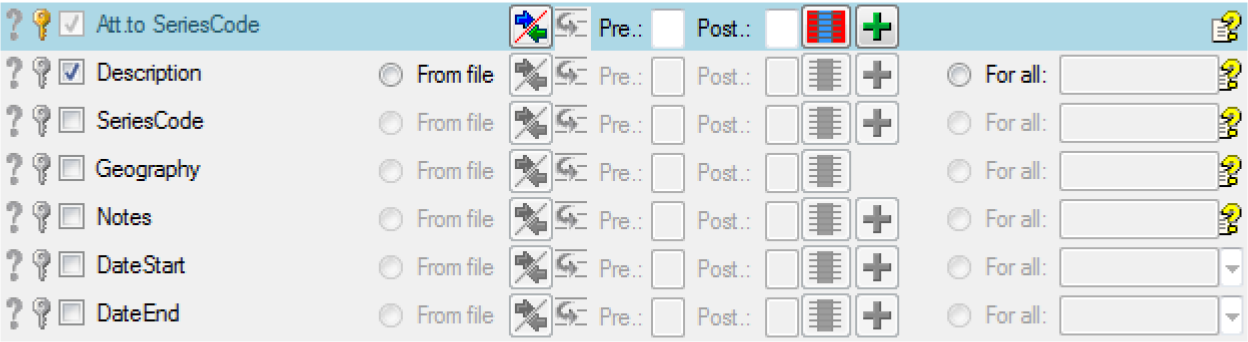
The **Attach** option will compare the data from the file with those in the database according to the **Key columns**. The found data will not be changed, but used as a reference data in depending tables.



Specimen	○ Insert	○ Merge	○ Update	● Attach
Organism 1	○ Insert	○ Merge	● Update	○ Attach
Analysis 1.1	○ Insert	● Merge	○ Update	○ Attach
Analysis 1.2	● 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. All columns available for importing data will be listed in the central part of the window. In the example shown below, the first column is used to attach the new data to data in the database.



☑ Att.to SeriesCode		Pre.:	Post.:	
☑ Description	○ From file	Pre.:	Post.:	○ For all:
☐ SeriesCode	○ From file	Pre.:	Post.:	○ For all:
☐ Geography	○ From file	Pre.:	Post.:	○ For all:
☐ Notes	○ From file	Pre.:	Post.:	○ For all:
☐ DateStart	○ From file	Pre.:	Post.:	○ For all: ▼
☐ DateEnd	○ From file	Pre.:	Post.:	○ For all: ▼

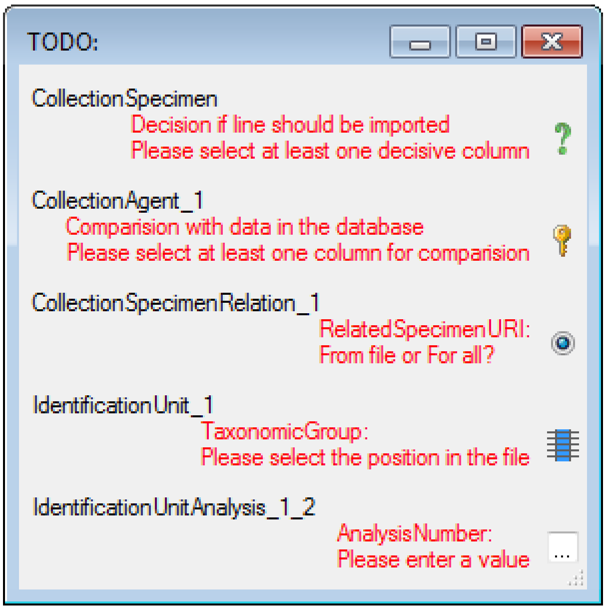
A reminder in the header line will show you what actions are still needed to import the data into the table:

- 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

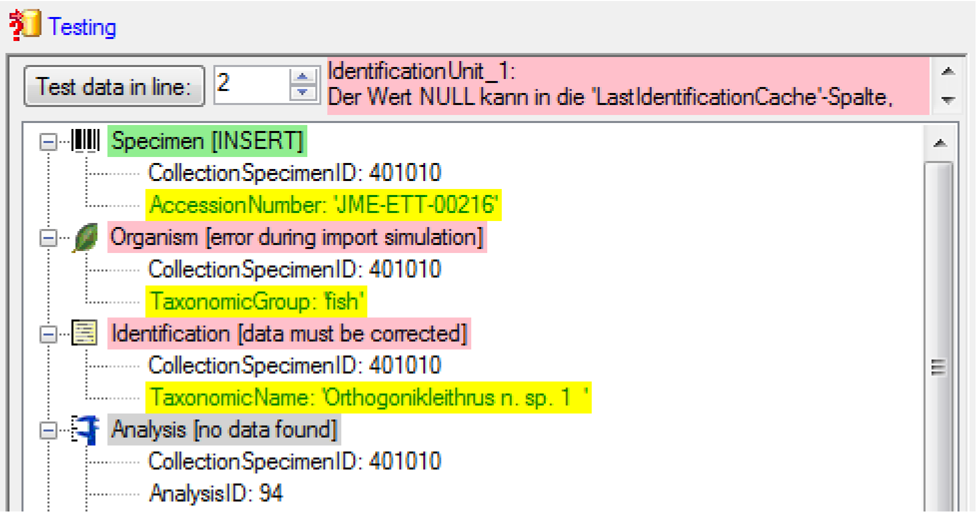
CollectionAgent_1
Comparision with data in the database
Please select at least one column for comparision

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.

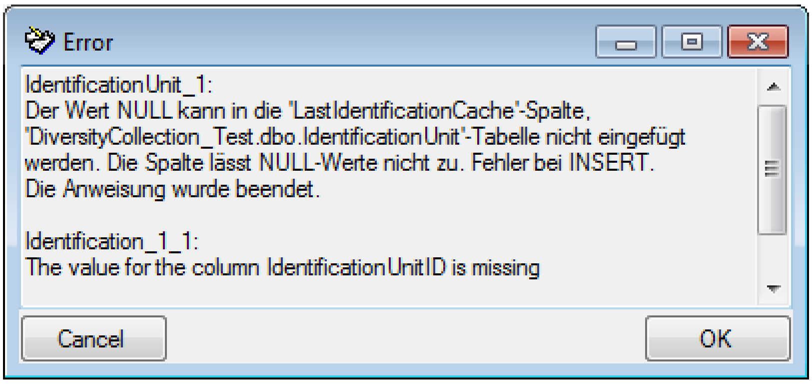


2

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.

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
CollectionSpecimenID
AccessionNumber

IdentificationUnit_1 (IdentificationUnit)
Parent: CollectionSpecimen
Merge handling: **Merge**

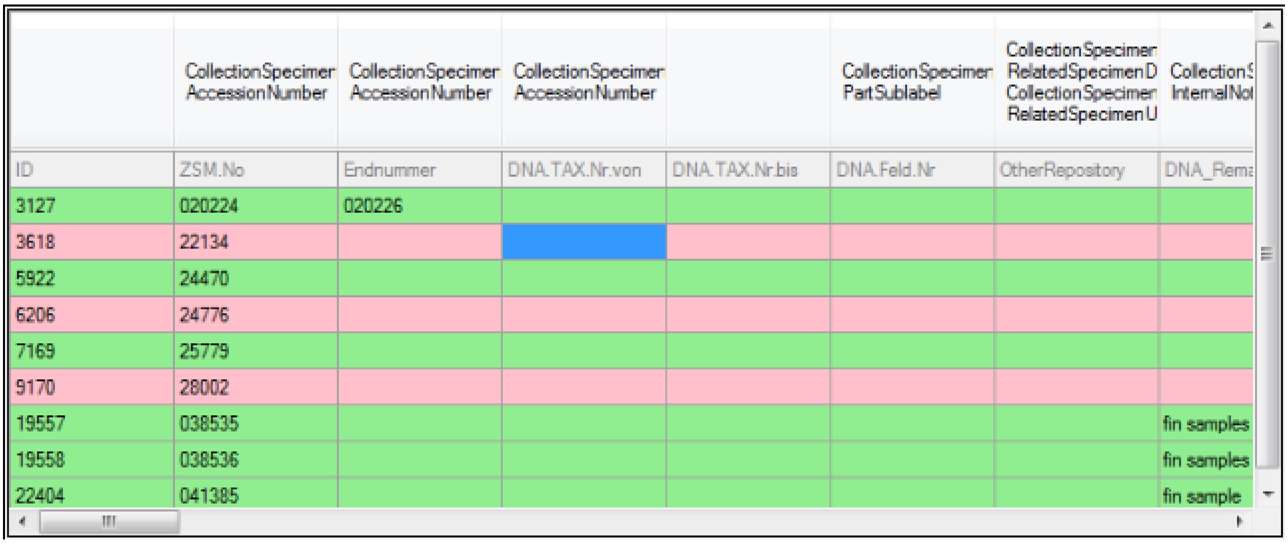
Column in table	?	Key	Copy	Pre	Post	File pos.	Transformations	Value	Source
CollectionSpecimenID									Database
IdentificationUnitID									Database
LastIdentificationCache		?				2			File
+						3			File
+						4			File
+						5			File
TaxonomicGroup	?							fish	Interface

IdentificationUnitAnalysis_1_1 (IdentificationUnitAnalysis)
Parent: IdentificationUnit_1
Merge handling: **Update**

Column in table	?	Key	Copy	Pre	Post	File pos.	Transformations	Value	Source
CollectionSpecimenID									Database
IdentificationUnitID									Database

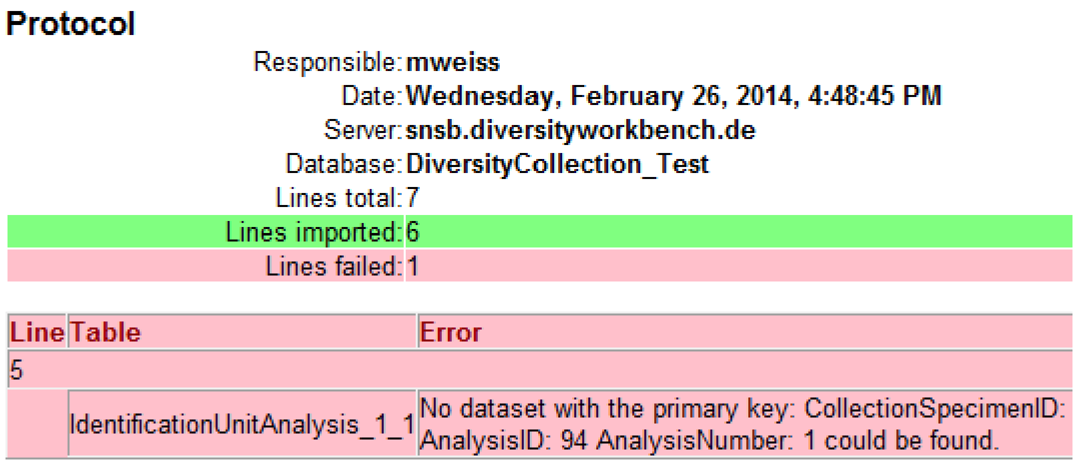
AnalysisID								94	Interface	
AnalysisNumber								1	Interface	
AnalysisResult	?	?				39			File	

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	CollectionS 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).

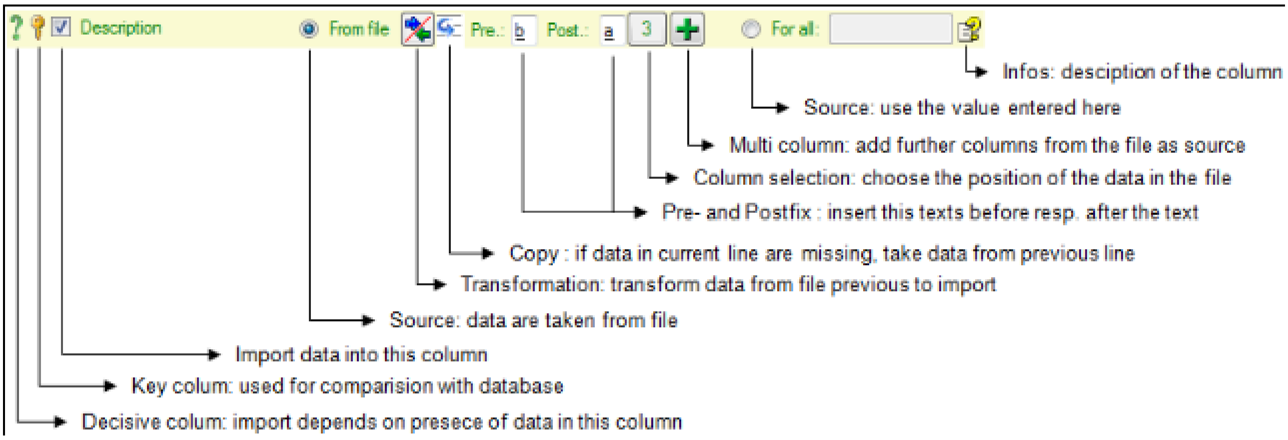


Protocol

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.

Import wizard - Columns



Infos: desciption 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 colum: used for comparision with database

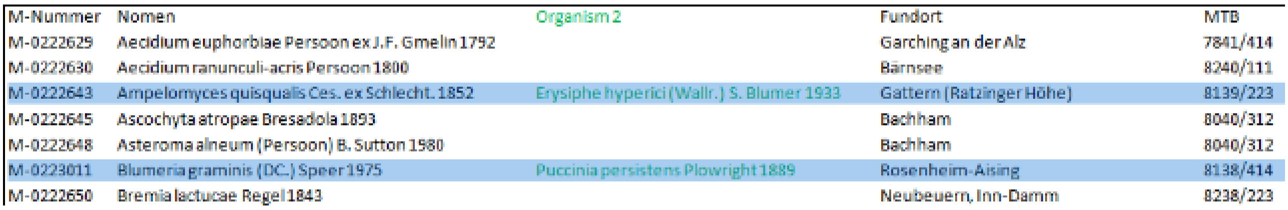
Decisive colum: import depends on presece of data in this column

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.



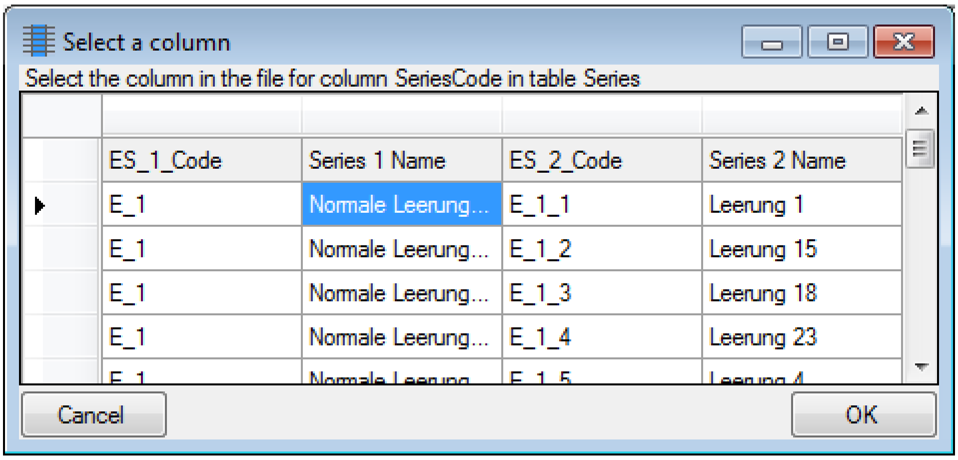
M-Nummer	Nomen	Organism 2	Fundort	MTB
M-0222629	Aecidium euphorbiae Persoon ex J.F. Gmelin 1792		Garching an der Alz	7841/414
M-0222630	Aecidium ranunculi-acris Persoon 1800		Bärnsee	8240/111
M-0222643	Ampelomyces quisqualis Ces. ex Schlecht. 1852	Erysiphe hyperici (Wallr.) S. Blumer 1933	Gattern (Ratzinger 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,

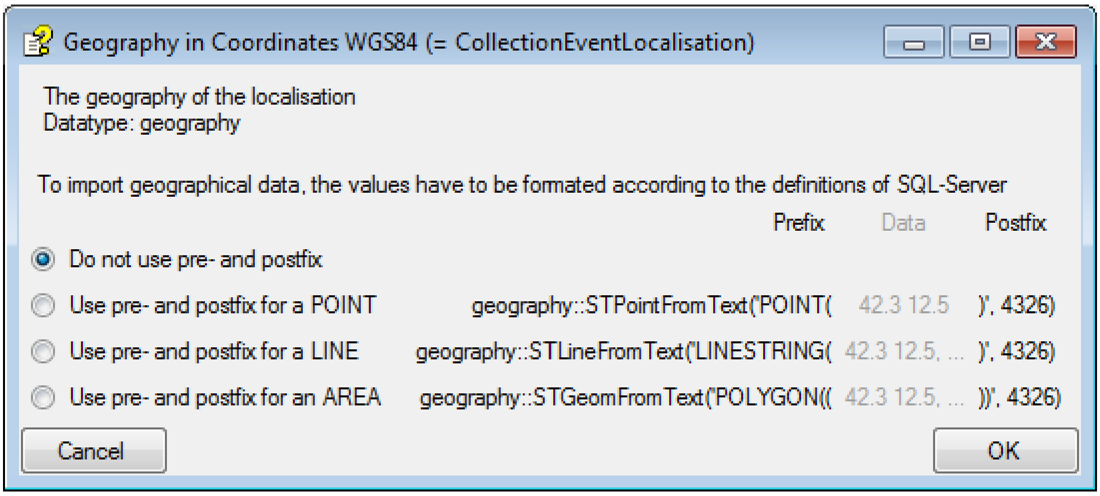
13.07.2003	48,2460	12,4567	Carex	firma
				acuta
	48,3453	12,8997		vaginata
			Festuca	ovina
				gigantea
14.07.2003	48,5669	11,9698	Carex	flacca
				acuta
15.07.2003	48,4520	11,2385	Festuca	rubra

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. 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)

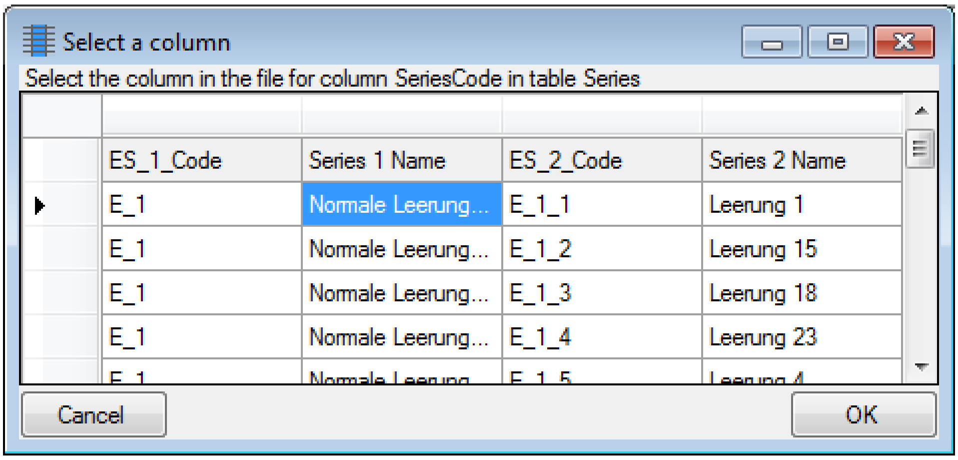
The geography of the localisation
Datatype: geography

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.



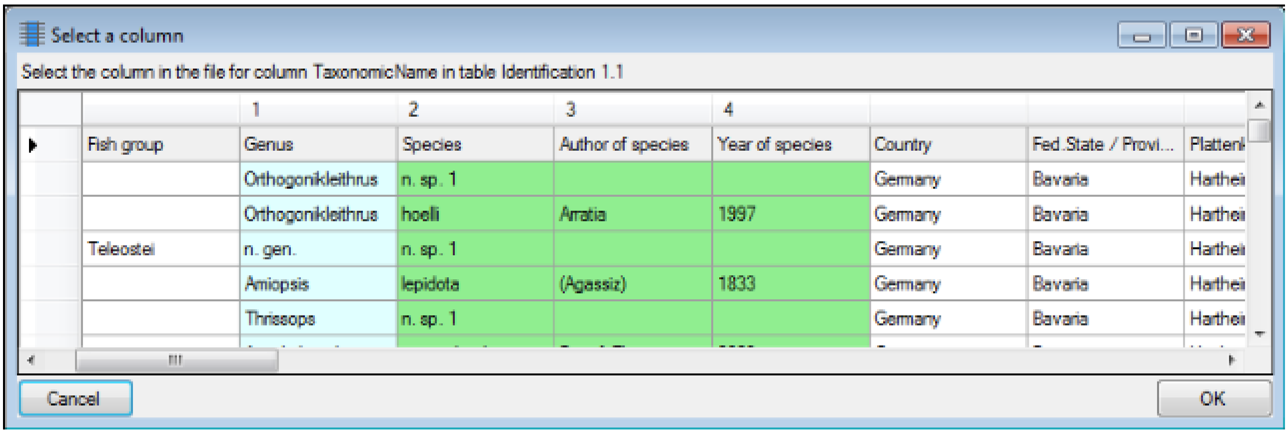
Select a column

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 +

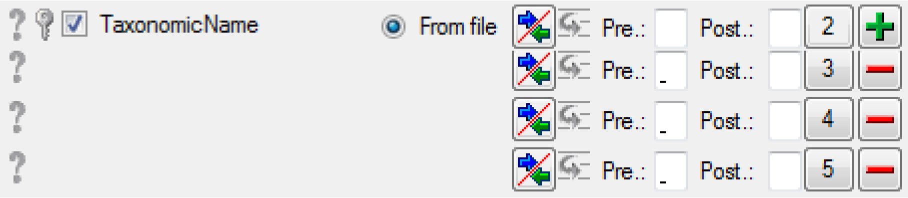
The content of a column can be composed from the content of several columns in the file. To add additional file columns, click on the + button. A window as shown below will pop up, showing you the column selected so far, where the sequence is indicated in the header line. The first colum is marked with 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...	Plattenk
	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

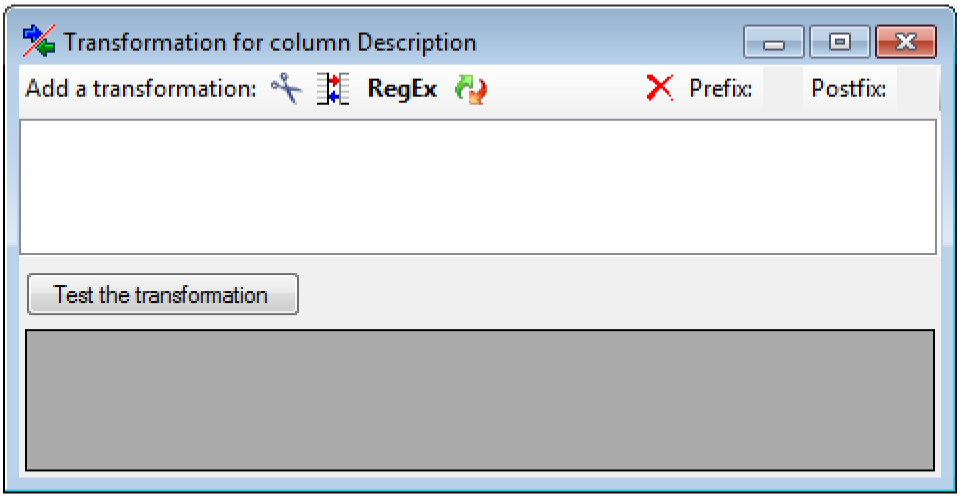
Pre.: _ Post.: 5

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

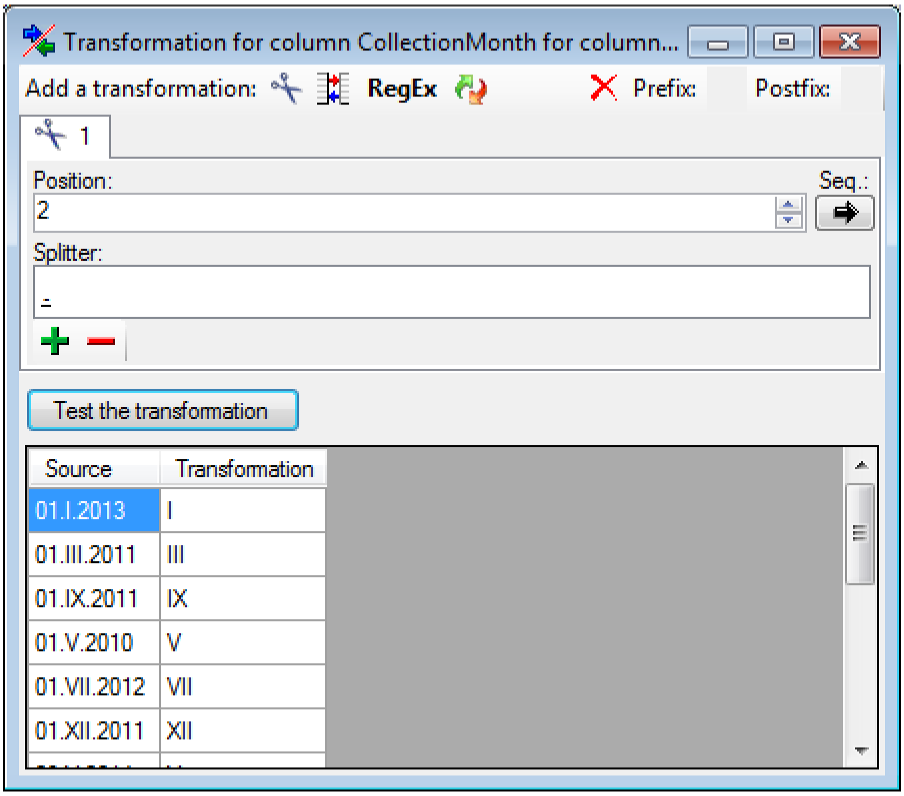
The data imported may be transformed e.g. to adapt them to a format demanded by the database. Click on the button to open a window as shown below.



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.



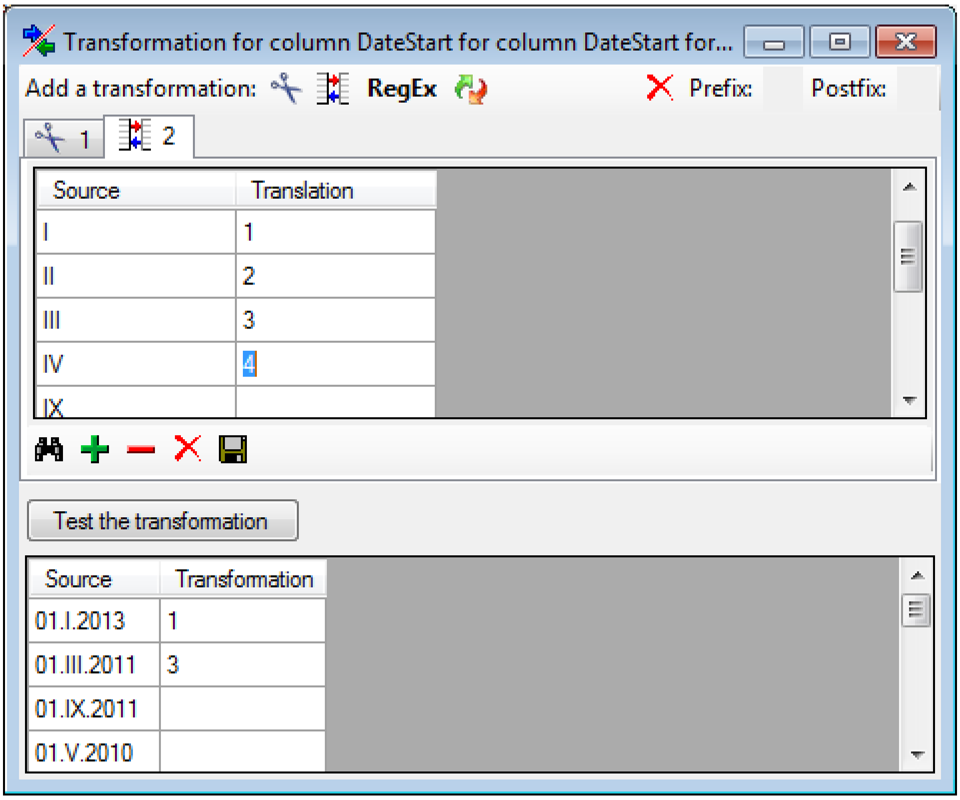
Position: 2

Splitter: .

Source	Transfomation
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.

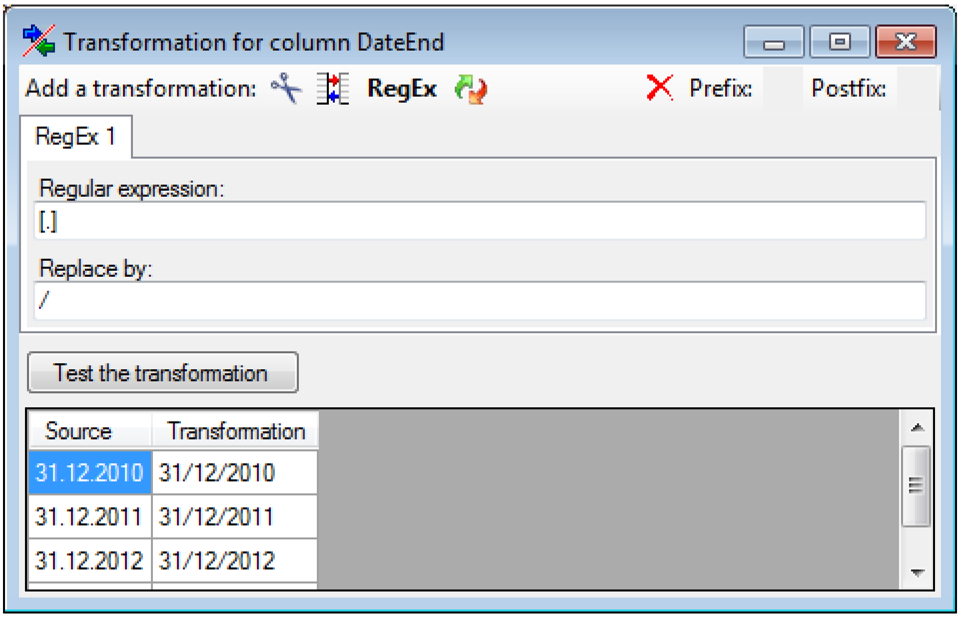


Source	Translation
I	1
II	2
III	3
IV	4
IX	

Source	Transformation
01.I.2013	1
01.III.2011	3
01.IX.2011	
01.V.2010	

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.



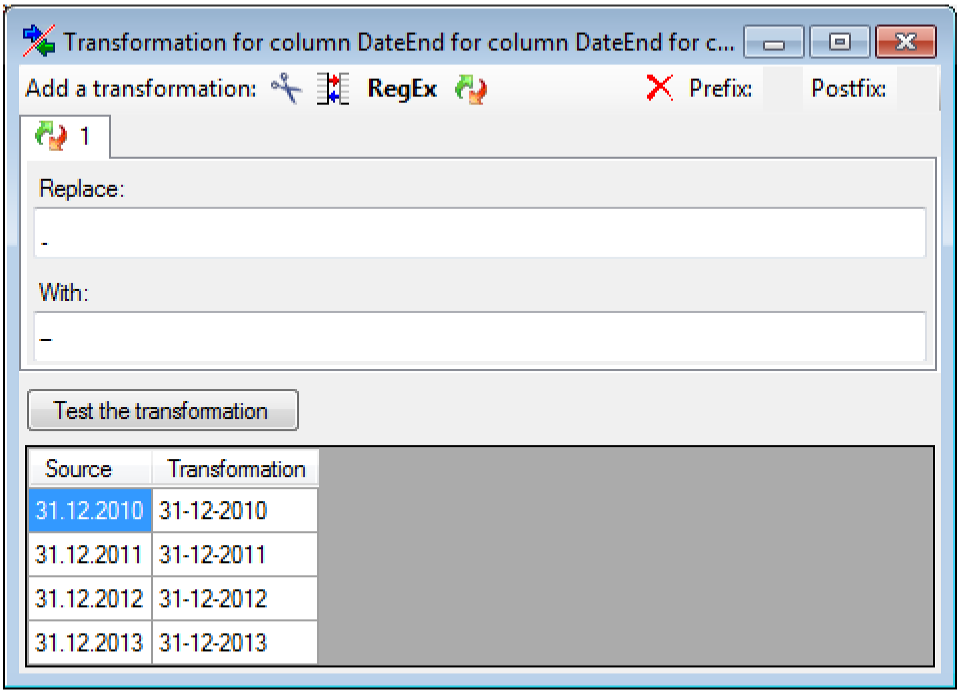
Regular expression:
[.]

Replace by:
/

Source	Transformation
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 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.



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

-

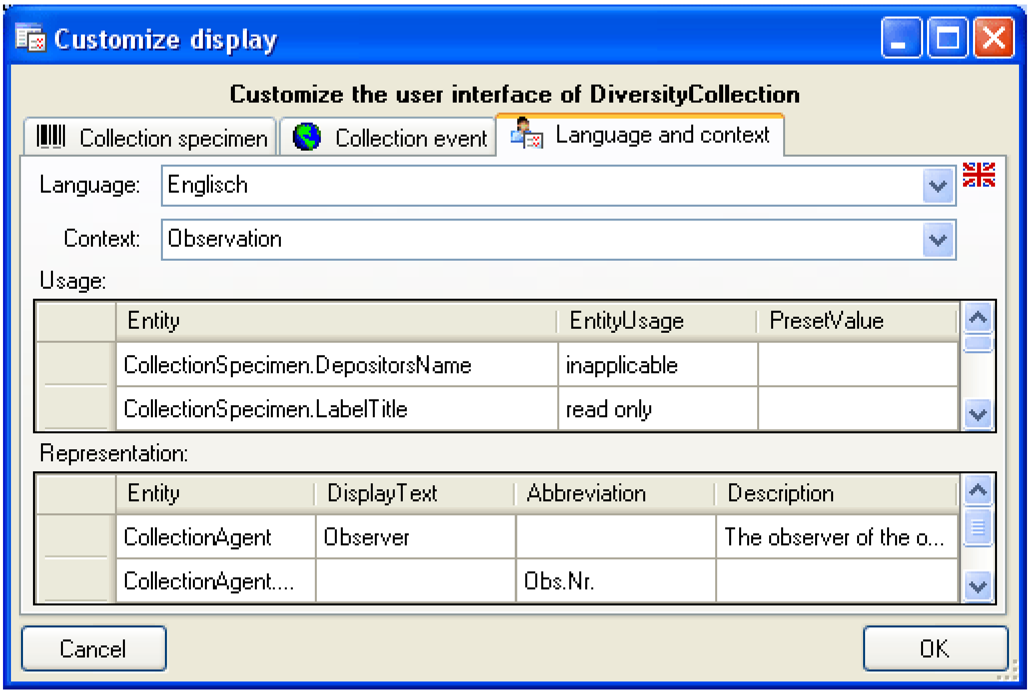
Customization of the application

DiversityCollection provides several ways to adapt the forms to your needs. There are special adaptations for the main window and for the grid view. General adaptations are performed with the context.

Entities, contexts, usage and languages

DiversityCollection may be used in diverse contexts like collection management, observations or field mapping. To ensure that a user working in a certain area will see the descriptions corresponding to his domain the DiversityWorkbench provides the possibility to define corresponding contexts.

To set the context and the language for the program choose **Administration - Customize display ...** from the menu. A window will open as shown below where you may select the language and the context which should be used. By default the language will be set according to the settings of your operating system, however, you may change it here. The default language within DiversityCollection is english. If you select a certain context, the tables in the lower part of the form will show you the special setting within this context. These settings are edited as described below.



Language: Englisch

Context: Observation

Usage:

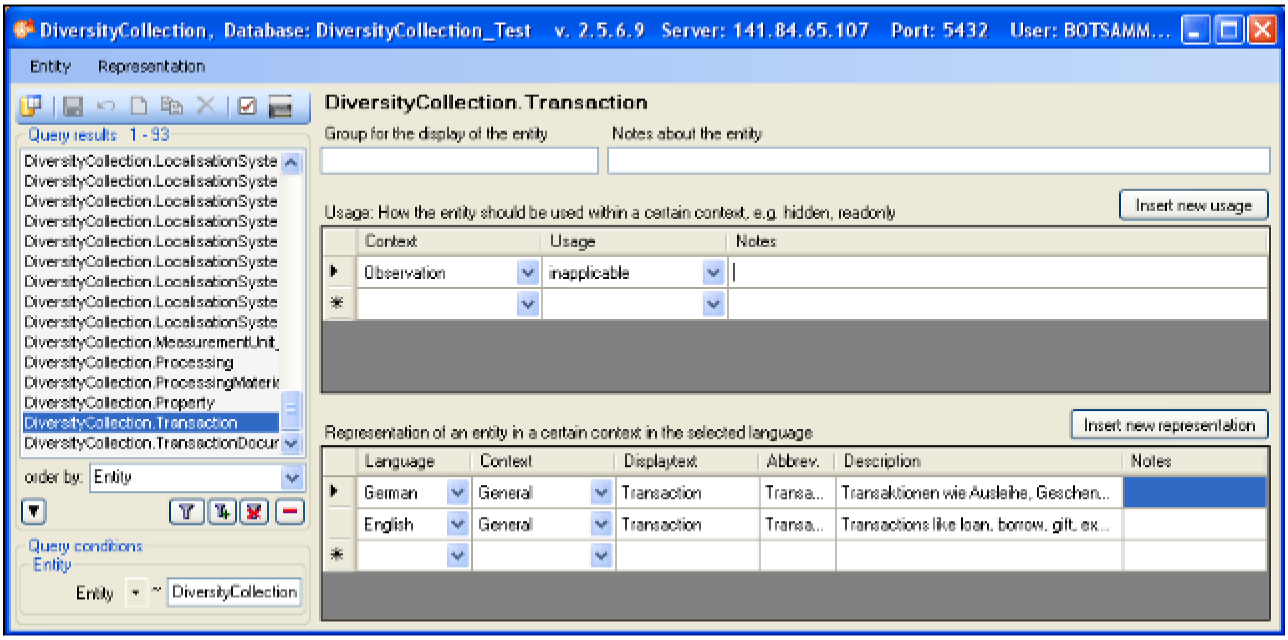
	Entity	EntityUsage	PresetValue
	CollectionSpecimen.DepositorsName	inapplicable	
	CollectionSpecimen.LabelTitle	read only	

Representation:

	Entity	DisplayText	Abbreviation	Description
	CollectionAgent	Observer		The observer of the o...
	CollectionAgent....		Obs.Nr.	

For the documentation of the tables used for the storage of the entity related data please see the section Entity tables.

To edit the entities choose **Administration - Application description ...** from the menu. A window will open as shown below where you may edit the entities defined for the programm.



DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.LocalisationSyste
DiversityCollection.MeasurementUnit_
DiversityCollection.Processing
DiversityCollection.ProcessingMateri
DiversityCollection.Property
DiversityCollection.Transaction
DiversityCollection.TransactionDocur

order by: Entity

Entity ~ DiversityCollection

DiversityCollection.Transaction

Group for the display of the entity

Notes about the entity

Usage: How the entity should be used within a certain context, e.g. hidden, readonly

Context	Usage	Notes
Observation	inapplicable	

Representation of an entity in a certain context in the selected language

Language	Context	Displaytext	Abbrev.	Description	Notes
German	General	Transaction	Transa...	Transaktionen wie Ausleihe, Geschen...	
English	General	Transaction	Transa...	Transactions like loan, borrow, gift, ex...	

Group for the display of the entity

If in a user interface certain entities should be displayed in a group, enter the name of the group here.

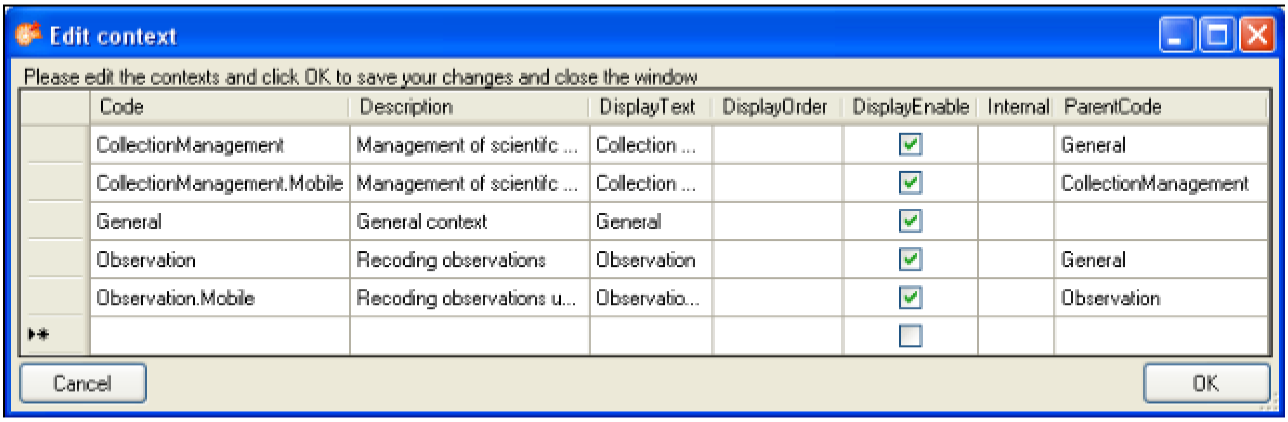
Usage

If nothing is defined for the usage of an entity, it will be handeled according to the rights of the user. In certain context an entity may be set to e.g. read only, inapplicable or not used. In case of the later two possiblities the entity will not appear in the interface of the program. For example, transaction management (e.g. loan) will not be handled with a mobile device, thus the corresponding entities will be set to "not used". Use the **[Insert new usage]** button to insert a new usage for an entity. To edit the possible usages choose **Administration - Usage ...** from the menu.

- inapplicable: An entity which may not be applied in a certain context will not be shown in a user interface, e.g. the depositors accession number in the context observation.
- preset: An entity will have a preset value, e.g. 'determination' for the identification category in the context observation.
- read only: An entity may not be changed.
- hidden: An entity should be hidden from the user interface.

Context

The default context is General. Thus, in the beginning you will find all representations within this context. Within the representation, when a certain context is missing, the program will search for a representation in the parent context until a represention is found. To edit the context choose **Administration - Context ...** from the menu. A window will open as shown below where you may edit the context.



Please edit the contexts and click OK to save your changes and close the window

	Code	Description	DisplayText	DisplayOrder	DisplayEnable	Internal	ParentCode
	CollectionManagement	Management of scientifc ...	Collection ...		☑		General
	CollectionManagement.Mobile	Management of scientifc ...	Collection ...		☑		CollectionManagement
	General	General context	General		☑		
	Observation	Recoding observations	Observation		☑		General
	Observation.Mobile	Recoding observations u...	Observatio...		☑		Observation
▸*					☐		

Representation

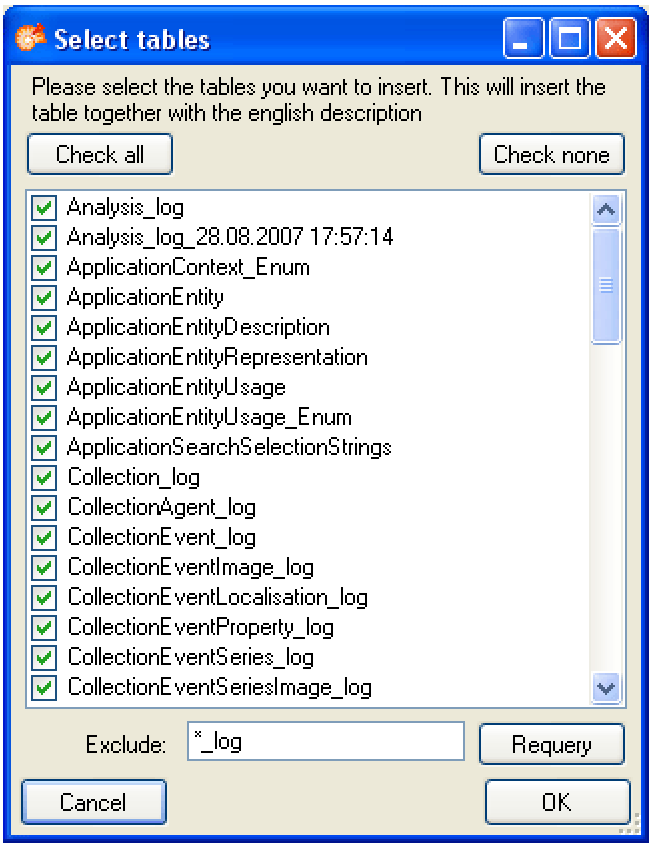
An entity may have differing representations in different contexts. For example a CollectionEvent may corrrespond to an observation or gathering in other contexts. Use the Entity and Representation menu to fill in missing entries. If an only if entity should receive a different title or description in the user interface, enter the values in the table. If nothing is defined in a certain context, the program will walk up the tree defined with the parent code (see the image above) to find available values for the title or description of the entity. The highest entry in the hierarchy is the context General with the language english. If you define deviating values for the display text, the abbreviation or the description, you must at least enter values in the highest entry (General, english) as a default value for all other entities.

Language

The default language used in DiversityCollection is english. Thus, in the beginning you will find all descriptions etc. in english. All representations may be defined for any language. Use the Representation menu to automatically fill in missing entries of a language. If there are changes in the original description of tables or columns in the database, choose **Representation - Update descriptions according to database** from the menu to import the updated descriptions for the english version and context "General".

Entity

To insert missing entities use the Entity menu. To insert all missing tables of a database choose **Entity - Insert all missing tables ...** from the menu. A window will open listing the missing tables. Use the **[Exclude: ...]** field and **[Requery]** button to remove certain tables from the list, e.g. if you do not wish to define entities for log tables, enter *_log and then click **[Requery]**. You may repeat this until the list contains only tables you wish to use.

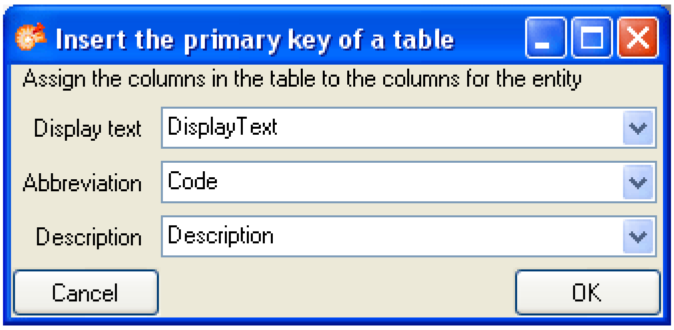


Please select the tables you want to insert. This will insert the table together with the english description

- ☑ Analysis_log
- ☑ Analysis_log_28.08.2007 17:57:14
- ☑ ApplicationContext_Enum
- ☑ ApplicationEntity
- ☑ ApplicationEntityDescription
- ☑ ApplicationEntityRepresentation
- ☑ ApplicationEntityUsage
- ☑ ApplicationEntityUsage_Enum
- ☑ ApplicationSearchSelectionStrings
- ☑ Collection_log
- ☑ CollectionAgent_log
- ☑ CollectionEvent_log
- ☑ CollectionEventImage_log
- ☑ CollectionEventLocalisation_log
- ☑ CollectionEventProperty_log
- ☑ CollectionEventSeries_log
- ☑ CollectionEventSeriesImage_log

Exclude: *_log

You find corresponding functions for single tables and for entries in a table. The later function is restricted to tables with a primary key with one column. A window will open where you map the columns, provided for the entity documentation to columns in the table, of which you wish to import the entries (see image below).



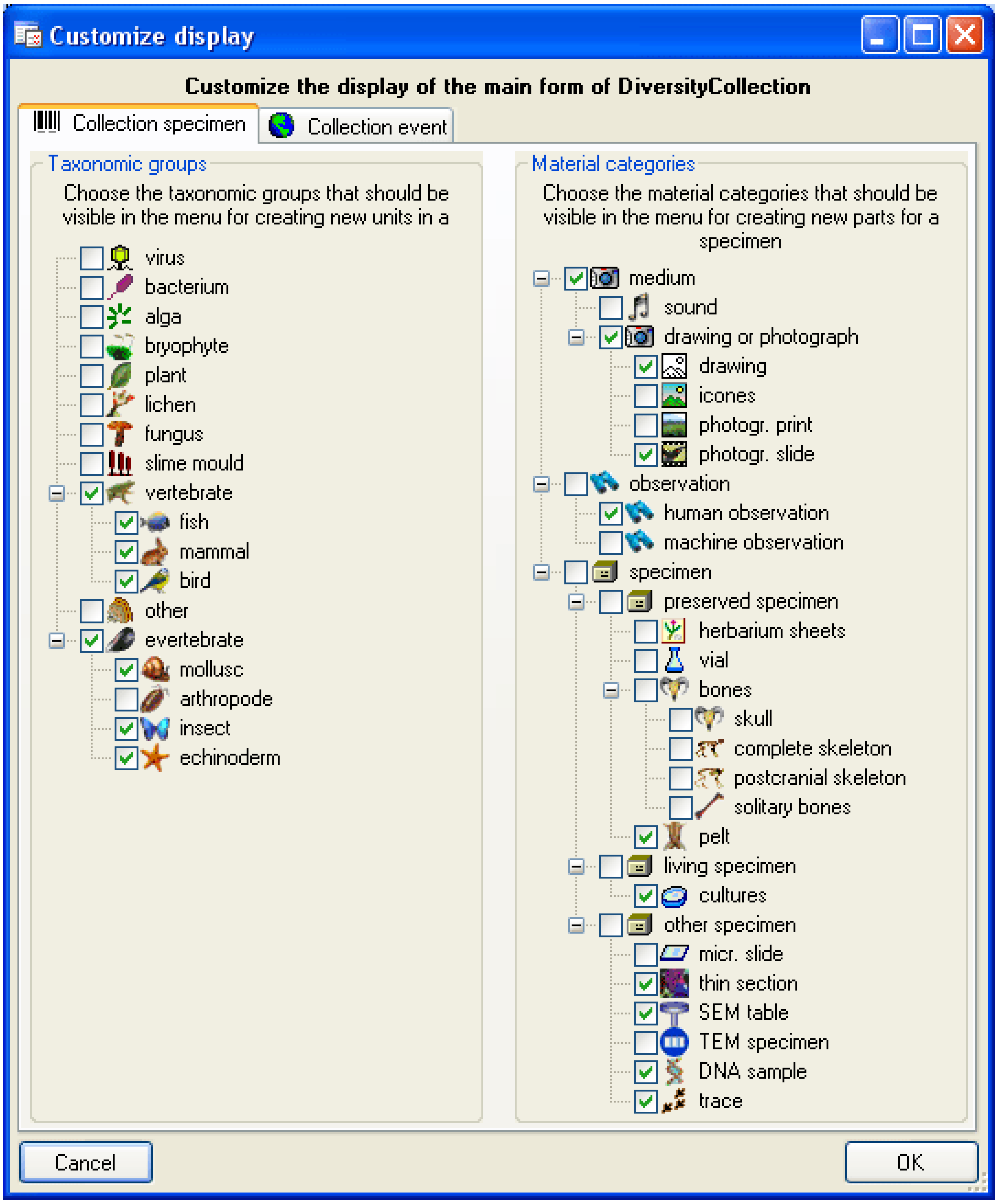
Assign the columns in the table to the columns for the entity

Display text: DisplayText
Abbreviation: Code
Description: Description

This may be necessary, if e.g. certain entries in a table should not be used in a certain context or if you wish to translate the contents into another language.

Customize the main form

The main window can be customised in several parts. To change the visible parts in the main window select **Administration - Customize display ...** from the menu. A window (see below) will open where you can select the groups which should be displayed. In the first tab you can change the visibility for the taxonomic groups and material categories.



Taxonomic groups

Choose the taxonomic groups that should be visible in the menu for creating new units in a

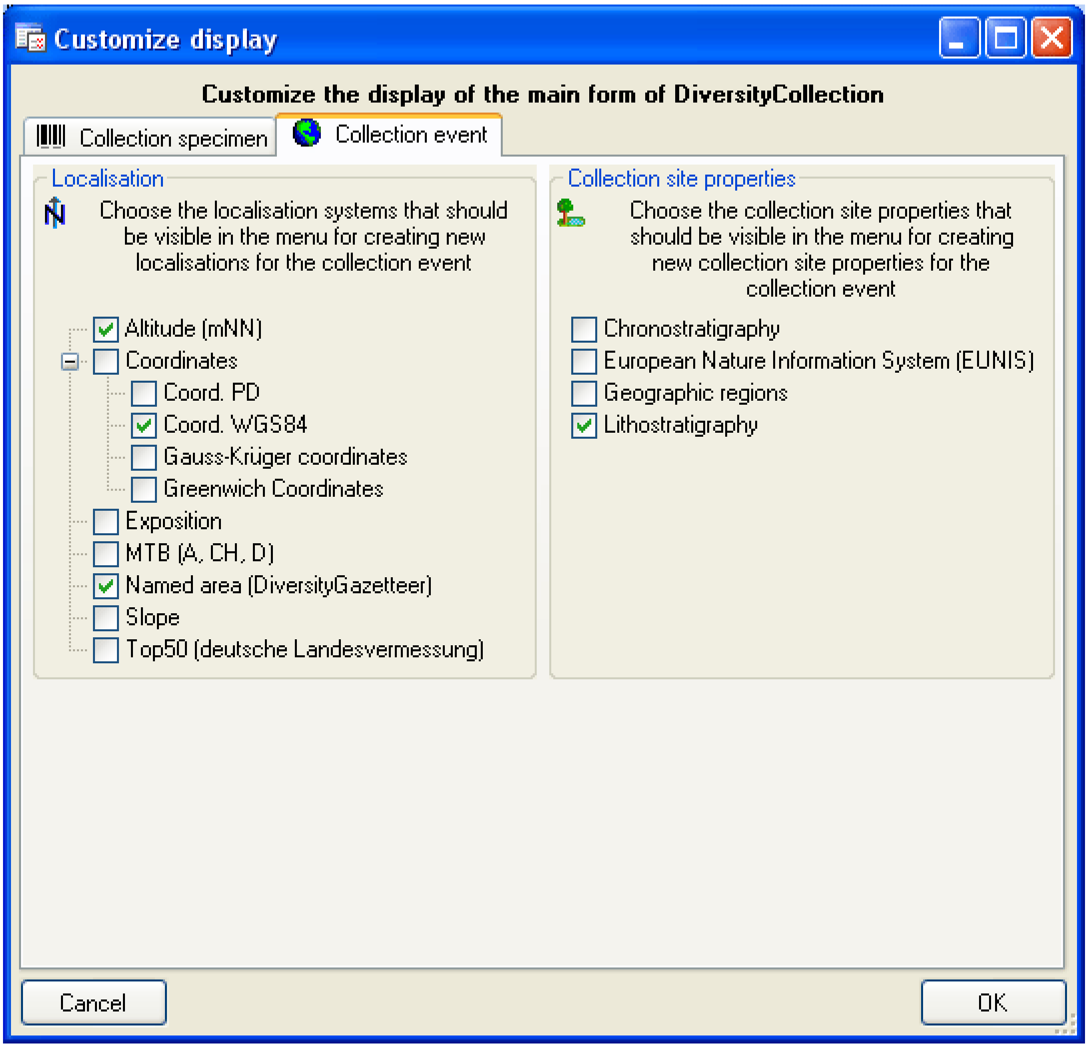
- ☐ virus
- ☐ bacterium
- ☐ alga
- ☐ bryophyte
- ☐ plant
- ☐ lichen
- ☐ fungus
- ☐ slime mould
- ☑ vertebrate
  - ☑ fish
  - ☑ mammal
  - ☑ bird
- ☐ other
- ☑ evertebrate
  - ☑ mollusc
  - ☐ arthropode
  - ☑ insect
  - ☑ echinoderm

Material categories

Choose the material categories that should be visible in the menu for creating new parts for a specimen

- ☑ medium
  - ☐ sound
  - ☑ drawing or photograph
    - ☑ drawing
    - ☐ icones
    - ☐ photogr. print
    - ☑ photogr. slide
- ☐ observation
  - ☑ human observation
  - ☐ machine observation
- ☐ specimen
  - ☐ preserved specimen
    - ☐ herbarium sheets
    - ☐ vial
    - ☐ bones
      - ☐ skull
      - ☐ complete skeleton
      - ☐ postcranial skeleton
      - ☐ solitary bones
    - ☑ pelt
  - ☐ living specimen
    - ☑ cultures
  - ☐ other specimen
    - ☐ micr. slide
    - ☑ thin section
    - ☑ SEM table
    - ☐ TEM specimen
    - ☑ DNA sample
    - ☑ trace

In the second tab (see below) you can set the visibility of the localisation systems and collection site properties. These are listed in the drop down menus for adding items to a collection event.



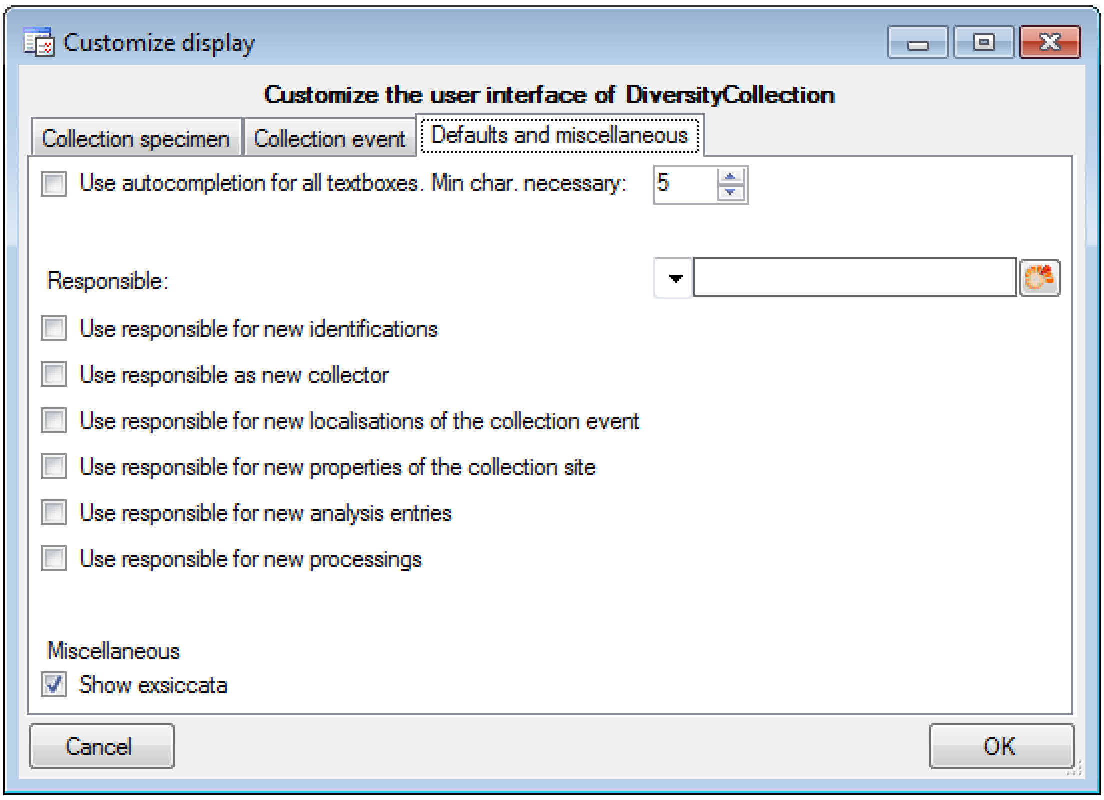
Choose the localisation systems that should be visible in the menu for creating new localisations for the collection event

- ☑ Altitude (mNN)
- ☐ Coordinates
  - ☐ Coord. PD
  - ☑ Coord. WGS84
  - ☐ Gauss-Krüger coordinates
  - ☐ Greenwich Coordinates
- ☐ Exposition
- ☐ MTB (A, CH, D)
- ☑ Named area (DiversityGazetteer)
- ☐ Slope
- ☐ Top50 (deutsche Landesvermessung)

Choose the collection site properties that should be visible in the menu for creating new collection site properties for the collection event

- ☐ Chronostratigraphy
- ☐ European Nature Information System (EUNIS)
- ☐ Geographic regions
- ☑ Lithostratigraphy

In the third tab (see below) you can add the name of responsible persons for several entries and show/hide the controls for the exsiccata.



Customize the user interface of DiversityCollection

☐ Use autocompletion for all textboxes. Min char. necessary: 5

Responsible:

☐ Use responsible for new identifications

☐ Use responsible as new collector

☐ Use responsible for new localisations of the collection event

☐ Use responsible for new properties of the collection site

☐ Use responsible for new analysis entries

☐ Use responsible for new processings

Miscellaneous

☑ Show exsiccata

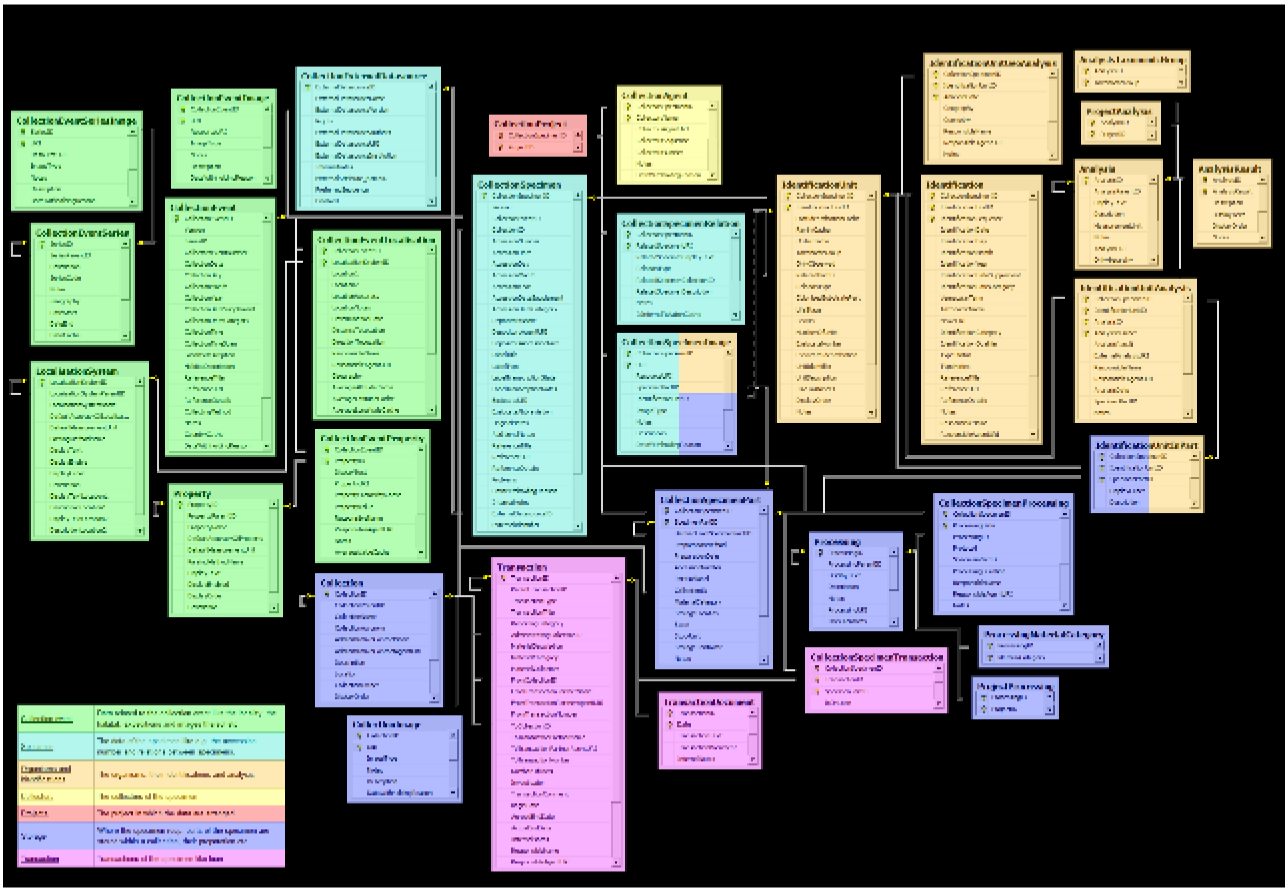
Database

The database for DiversityCollection is based on Microsoft SQL-Server 2005.

Organisation of the data

The main tables of the database are CollectionEvent corresponding to the event of the collection and CollectionSpecimen holding the specimens collected. Connected to these tables you find tables for additional information.

The image below shows the main tables of the database.



The diagram shows the tables of the database marked according to their logical groups. In the center the table CollectionSpecimen holds specimen data e.g. the accession number. On the left you find the tables containing collection event data and on the right tables related to the organisms and their identifications. Further logical groups are collectors, projects, storage and transaction.

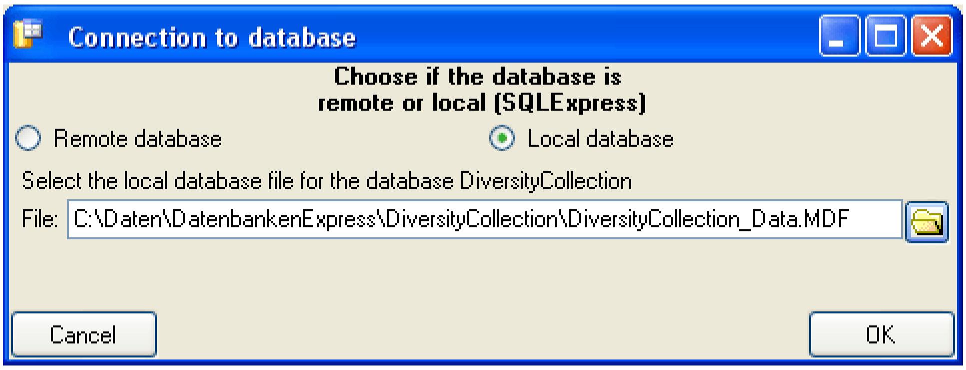
Further details: tables , application tables, access.

Installation of the database

DiversityCollection uses Microsoft SQL-Server 2008 as database engine. If you do not have a database server with DiversityCollection already available, you need to install the database engine first. Downlo ad the free version of Microsoft SQL Server Express 2008 (e.g. SQLEXPRADV_x86_DEU.exe) from http://www.microsoft.com/downloads/. Start the program and follow the instructions for the installation.

Download the database files DiversityCollection_Data.MDF and DiversityCollection_log.LDF from http://www.diversityworkbench.net/Portal/ provided as a zip archive (DiversitCollection.zip) and copy them into your database directory.

If you plan to use the database on your local computer (SQL Server Express), start the program DiversityCollection.exe and in the main window click on the button or choose **Connection -> Database ...** from the menu. A window will open as shown below. Here choose the option **Local database** and select the database file in your directory.



Choose if the database is remote or local (SQLExpress)

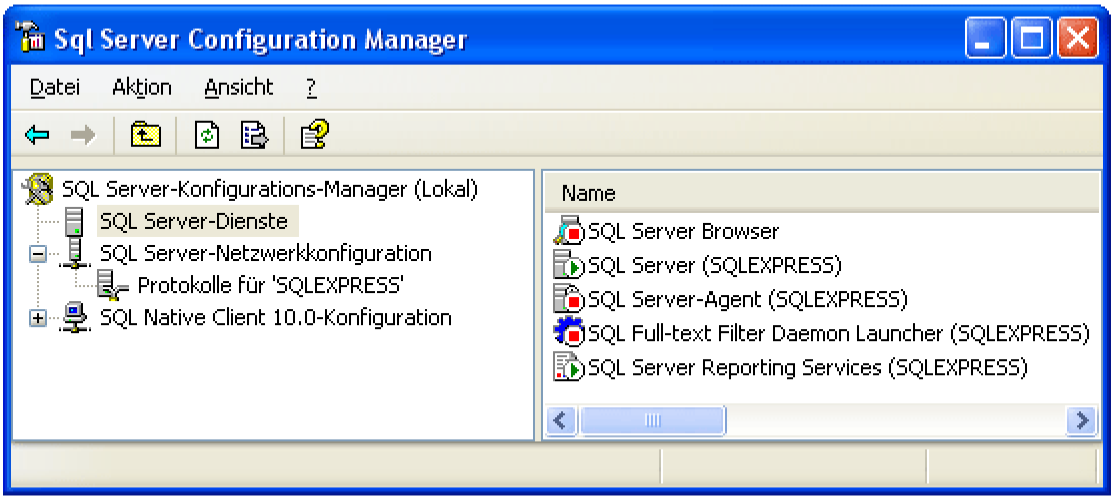
○ Remote database ● Local database

Select the local database file for the database DiversityCollection

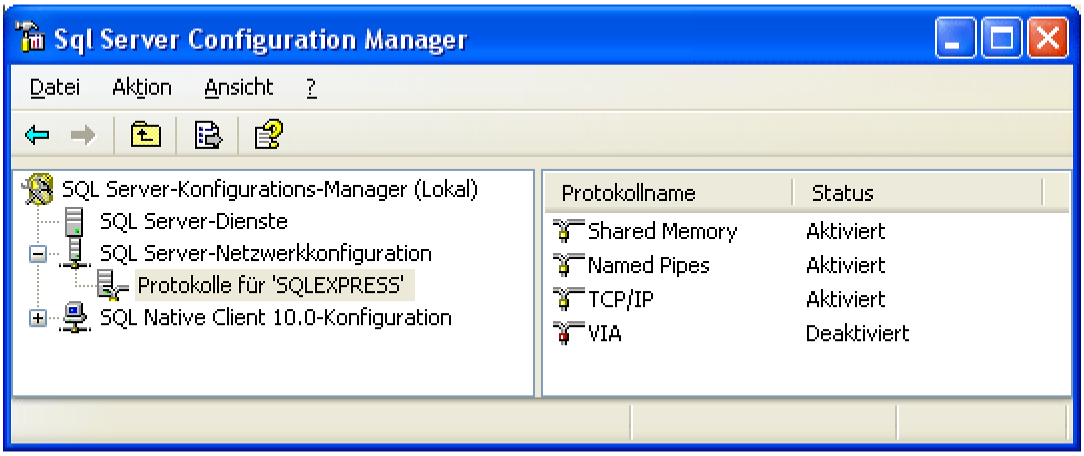
File: C:\Daten\DatenbankenExpress\DiversityCollection\DiversityCollection_Data.MDF

Server configuration

To configure your server for remote access launch the **SQL Server Configuration Manager** (see image below).

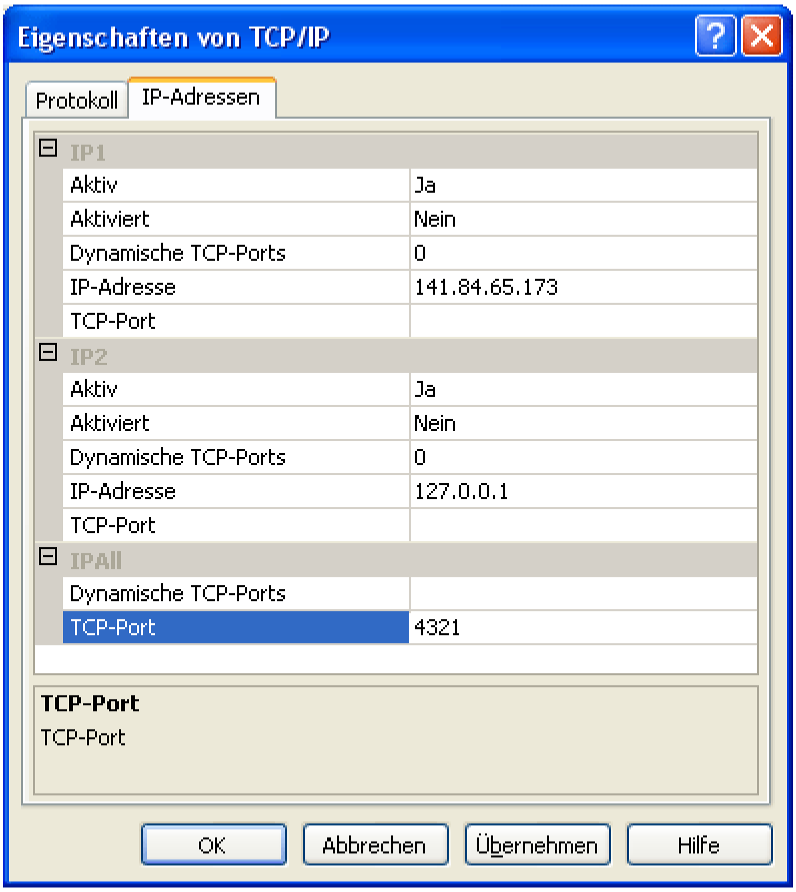


Then click on the "**Protocols** for SQLEXPRESS" node. Right click on "**TCP/IP**" in the list of Protocols and choose "enable" for TCP/IP.



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.

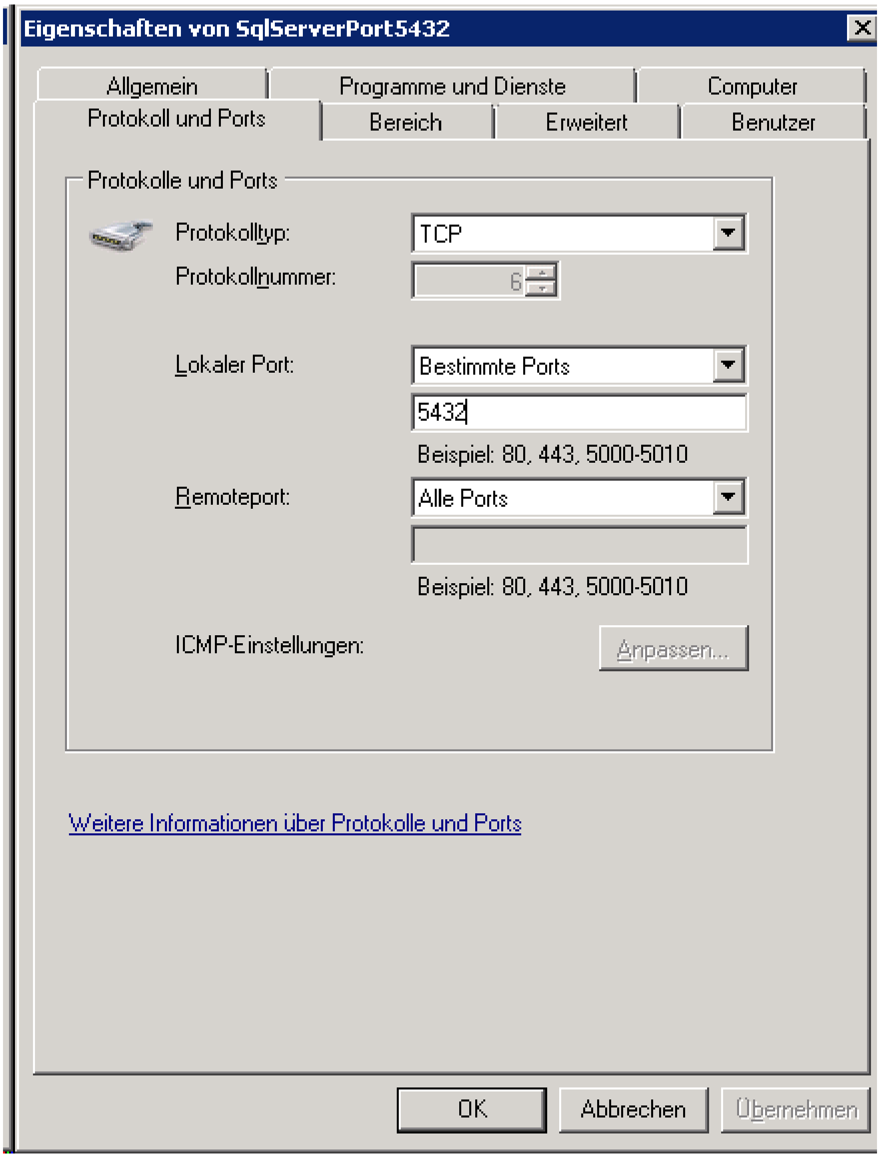


IP1	
Aktiv	Ja
Aktiviert	Nein
Dynamische TCP-Ports	0
IP-Adresse	141.84.65.173
TCP-Port	
IP2	
Aktiv	Ja
Aktiviert	Nein
Dynamische TCP-Ports	0
IP-Adresse	127.0.0.1
TCP-Port	
IPAll	
Dynamische TCP-Ports	
TCP-Port	4321

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. "4321" as shown above. You have to restart the SQL Server Express service before you can connect to your database.

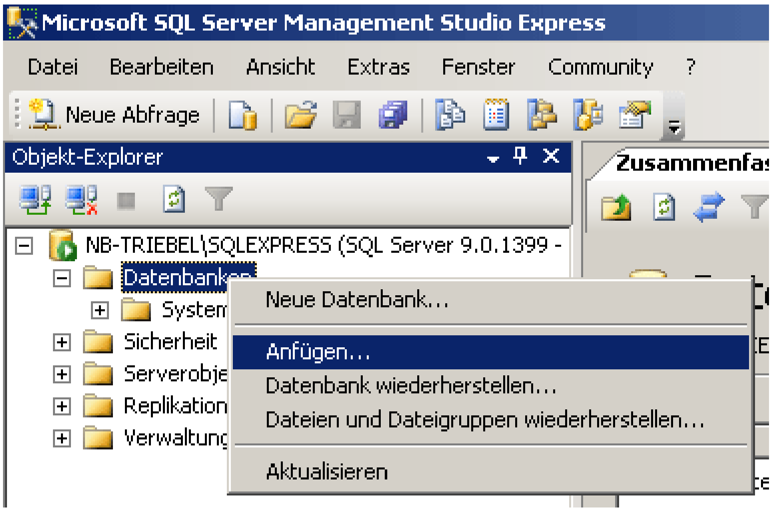
If you use a database on a server, make sure that the firewall of the server allows access via the port you set for the connection (see below).



Eigenschaften von SqlServerPort5432

Protokolltyp: TCP
Protokollnummer: 6
Lokaler Port: Bestimmte Ports
5432
Beispiel: 80, 443, 5000-5010
Remoteport: Alle Ports
Beispiel: 80, 443, 5000-5010
ICMP-Einstellungen:

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 DiversityCollection_Data.MDF from your database directory and attach it to the database engine.



After the installation make sure to get the latest updates from http://windowsupdate.microsoft.com/.

Database configuration

To configure your database use the client as described in Database configuration.

Configuration of the database

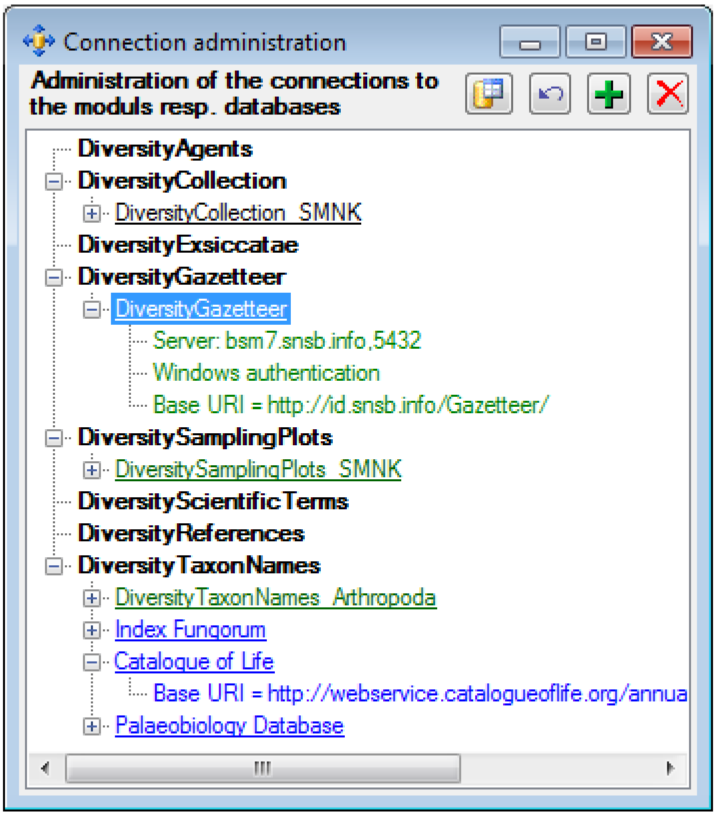
To configure your database choose **Administration -> Database -> Rename database** to change the name of the database according to your requirements. During this renaming all processes in the database will be terminated (you will get a warning if processes from other hosts are active).

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 provide an identifier for your database, e.g. http://xy.diversityworkbench.de/Collection/ .

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 data sets from other modules linked to data in the database would otherwise point to outdated addresses.

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 (see below) will open where you can edit said connections.



Administration of the connections to the moduls resp. databases

- **DiversityAgents**
- **DiversityCollection**
  - DiversityCollection_SMNK
- **DiversityExsiccatae**
- **DiversityGazetteer**
  - DiversityGazetteer
    - Server: bsm7.snsb.info,5432
    - Windows authentication
    - Base URI = http://id.snsb.info/Gazetteer/
- **DiversitySamplingPlots**
  - DiversitySamplingPlots_SMNK
- **DiversityScientificTerms**
- **DiversityReferences**
- **DiversityTaxonNames**
  - DiversityTaxonNames_Arthropoda
  - Index Fungorum
  - Catalogue of Life
    - Base URI = http://webservice.catalogueoflife.org/annua
  - Palaeobiology Database

To edit a connection select it in the tree and click on the button. 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. Webservices like Index Fungorum will be displayed in blue.

Database - access

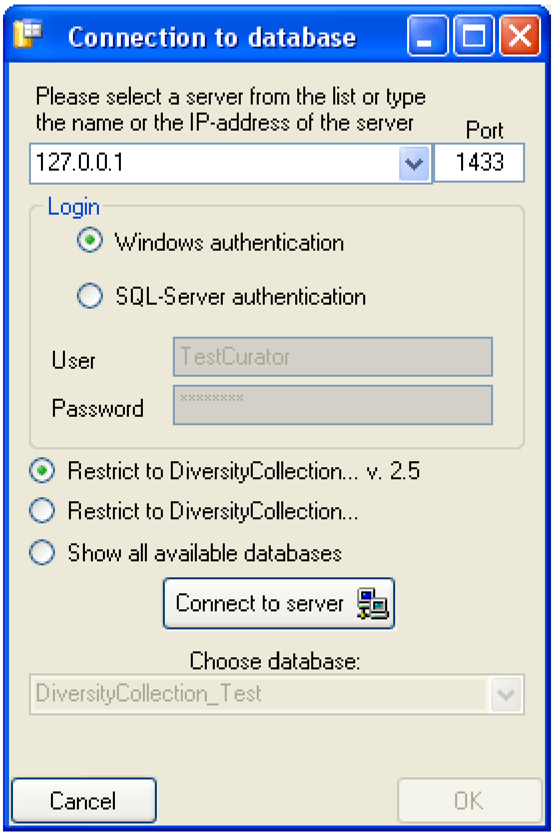
The database engine for DiversityCollection is Microsoft SQL-Server 2005.

When you are connected to a database it is indicated by the icon of the connection button in the upper left corner. When you are not connected the following icon will be shown. 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 central server or remote computer, start the program DiversityCollection.exe. In the main window click on the button or choose **Connection -> Database ...** from the menu. A window will open as shown below. Here choose the option **Remote database** and 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 as well as to select the authentication mode. You can either choose Windows authentication (see left image below) or SQL-Server authentication (see middle image below).



Connection to database

Please select a server from the list or type the name or the IP-address of the server

Port

127.0.0.1 1433

Login

● Windows authentication

○ SQL-Server authentication

User TestCurator

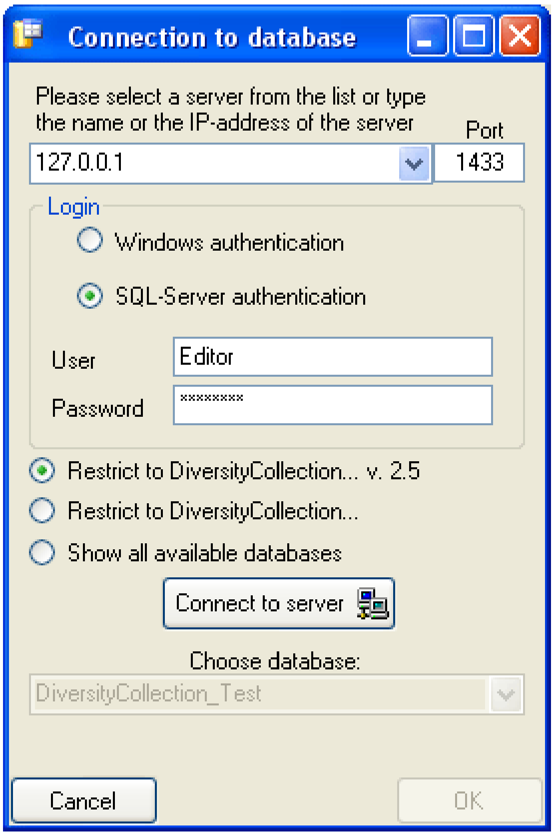
Password ********

● Restrict to DiversityCollection... v. 2.5

○ Restrict to DiversityCollection...

○ Show all available databases

Choose database: DiversityCollection_Test



Connection to database

Please select a server from the list or type the name or the IP-address of the server

Port

127.0.0.1 1433

Login

○ Windows authentication

● SQL-Server authentication

User Editor

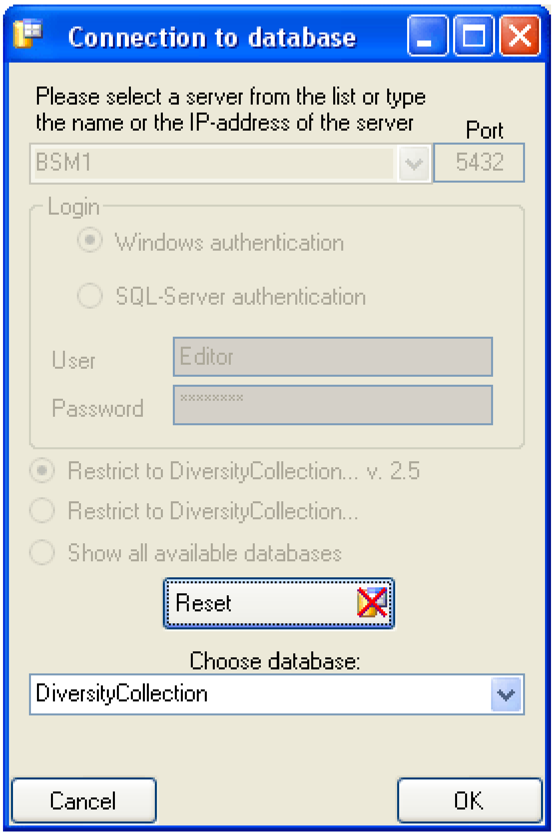
Password ********

● Restrict to DiversityCollection... v. 2.5

○ Restrict to DiversityCollection...

○ Show all available databases

Choose database: DiversityCollection_Test



Connection to database

Please select a server from the list or type the name or the IP-address of the server

Port 5432

BSM1

Login

● Windows authentication

○ SQL-Server authentication

User Editor

Password ********

● Restrict to DiversityCollection... v. 2.5

○ Restrict to DiversityCollection...

○ Show all available databases

Choose database: DiversityCollection

The standard port number for SQL-Server is 1433 and will be set as a default. If the database server is configured using a different port, you must enter its number in the field Port. Click on the Connect to server button to connect to the server. If the connection information is valid, you can choose a database from the server in the combo box at the base of the window (see right image above). To restart the connecting process click on the Reset button.

Module connections

The program will automatically try to establish a connection to Diversity Workbench databases and webservices. For further details see the Connections section.

Index

- IdentificationUnitInPart
- LocalisationSystem
- Processing
- ProcessingMaterialCategory
- ProjectAnalysis
- ProjectProcessing
- Property
- Transaction
- TransactionDocument

Table Analysis

Analysis types used within the database

Column	Data type	Description
AnalysisID	int	ID of the analysis (Primary key)
AnalysisParentID	int	Analysis ID of the parent analysis if it belongs to a certain type documented in this table
DisplayText	nvarchar (50)	Name of the analysis as e.g. shown in user interface
Description	nvarchar (MAX)	Description of the analysis
MeasurementUnit	nvarchar (50)	The measurement unit used for the analysis, e.g. mm, µmol, kg
Notes	nvarchar (MAX)	Notes concerning this analysis
AnalysisURI	varchar (255)	URI referring to an external documentation of the analysis
OnlyHierarchy	bit	If the entry is only used for the hierarchical arrangement of the entries *Default value: (0)*
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*

LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table <u>AnalysisResult</u>

Value lists for analysis types with predefined values, e.g. "0, 1, 2, 3, ..." for Red list category. Includes description etc. for the values in the list.

Column	Data type	Description
<u>AnalysisID</u>	int	ID of the analysis (Primary key)
<u>AnalysisResult</u>	nvarchar (255)	The categorized value of the analysis
Description	nvarchar (500)	Description of enumerated object, displayed in the user interface
DisplayText	nvarchar (50)	Short abbreviated description of the object, displayed in the user interface
DisplayOrder	smallint	The order in which the entries are displayed. The order may be changed at any time, but all values must be unique.
Notes	nvarchar (500)	Internal development notes about usage, definition, etc. of an enumerated object
LogInsertedBy	nvarchar (50)	Name of user who first entered (typed or imported) the data. *Default value: user_name()*
LogInsertedWhen	smalldatetime	Date and time when the data were first entered (typed or imported) into this database. *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of user who last updated the data. *Default value: user_name()*
LogUpdatedWhen	smalldatetime	Date and time when the data were last updated. *Default value: getdate()*

Table <u>AnalysisTaxonomicGroup</u>

The types of analysis that are available for a taxonomic group

Column	Data type	Description

AnalysisID	int	Analysis ID, foreign key of table Analysis.
TaxonomicGroup	nvarchar (50)	Taxonomic group the organism identified by this unit belongs to. Groups listed in table CollTaxonomicGroup_Enum (= foreign key)
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table Annotation

Annotations to datasets in the database

Column	Data type	Description
AnnotationID	int	ID of the annotation (Primary key)
ReferencedAnnotationID	int	If an annotation refers to another annotation, the ID of the referred annotation
AnnotationType	nvarchar (50)	The type of the annotation as defined in AnnotationType_Enum, e.g. Reference
Title	nvarchar (50)	Title of the annotation
Annotation	nvarchar (MAX)	The annotation entered by the user
URI	varchar (255)	The complete URI address of a resource related to the annotation. May be link to a module, e.g. for the annotation type reference
ReferenceDisplayText	nvarchar (500)	The title of the reference. If the entry is linked to an external module like DiversityReferences, the cached display text of the referenced dataset
ReferenceURI	varchar (255)	If the entry is linked to an external module like DiversityReferences, the link to the referenced dataset
SourceDisplayText	nvarchar (500)	The name of the source. If the entry is linked to an external module like DiversityAgents, the cached

		display text of the referenced dataset
SourceURI	varchar (255)	If the entry is linked to an external module like DiversityAgents, the link to the referenced dataset
IsInternal	bit	If an annotation is restricted to authorized users of the database
ReferencedID	int	The ID of the dataset in the table the annotation refers to
ReferencedTable	nvarchar (500)	The name of the table the annotation refers to
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	RowGUID - Annotation *Default value: newsequentialid()*

Table Collection

The collections where the specimen are stored

Column	Data type	Description
CollectionID	int	Unique reference ID for the collection (= Primary key)
CollectionParentID	int	For a subcollection within another collection: CollectionID of the collection to which the subcollection belongs. Empty for an independent collection
CollectionName	nvarchar (255)	Name of the collection (e. g. 'Herbarium Kew') or subcollection (e. g. 'cone collection', 'alcohol preservations'). This text should be kept relatively short, use Description for additional information
CollectionAcronym	nvarchar (10)	A unique code for the Collection, e.g. the herbarium code from Index Herbariorum

AdministrativeContactName	nvarchar (500)	The name of the person or organisation responsible for this collection
AdministrativeContactAgentURI	varchar (255)	The URI of the person or organisation responsible for the Collection e.g. as provided by the module DiversityAgents
Description	nvarchar (MAX)	A short description of the collection
Location	nvarchar (255)	Optionally location of the collection, e.g. the number within a file system or a description of the room(s) housing the (sub)collection
CollectionOwner	nvarchar (255)	The owner of the collection as e.g. printed on a label, should be given if CollectionParentID is null
DisplayOrder	smallint	The order in which the entries are displayed. The order may be changed at any time, but all values must be unique.
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionAgent

The collector(s) of collection specimens

Column	Data type	Description
CollectionSpecimenID	int	Refers to ID of CollectionEvent (= Foreign key and part of primary key)
CollectorsName	nvarchar (255)	Name of the Collector
CollectorsAgentURI	varchar (255)	The URI of the Agent, e.g. as stored within the module DiversityAgents
CollectorsSequence	datetime	The order of collectors in a team. Automatically set by the database system

		Default value: getdate()
CollectorsNumber	nvarchar (50)	Number assigned to a specimen or a batch of specimens by the collector during the collection event (= 'field number')
Notes	nvarchar (MAX)	Notes about the collector, e.g. if the name is uncertain
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionEvent

The collection event where the specimen was collected

Column	Data type	Description
CollectionEventID	int	Unique ID for the collection event (= Primary key)
Version	int	The version of the dataset. Automatically set by the system. *Default value: (1)*
SeriesID	int	The ID of the related expedition. Relates to the PK of the table CollectionExpedition (Foreign key).
CollectorsEventNumber	nvarchar (50)	Number assigned to a collection event by the collector (= 'field number')
CollectionDate	datetime	The date of the event calulated from the entries in CollectionDay, -Month and -Year.
CollectionDay	tinyint	The day of the date of the event or when the collection event started

CollectionMonth	tinyint	The month of the date of the event or when the collection event started
CollectionYear	smallint	The year of the date of the event or when the collection event started
CollectionDateSupplement	nvarchar (100)	Verbal or additional collection date information, e.g. 'end of summer 1985', 'first quarter', '1888-1892'. The end date if the collection event comprises a period. The time of the event if necessary.
CollectionDateCategory	nvarchar (50)	Category of the date of the identification e.g. "system", "estimated" (= foreign key, see in table CollEventDateCategory_Enum)
CollectionTime	varchar (50)	The time of the event or when the collection event started
CollectionTimeSpan	varchar (50)	The time span e.g. in seconds of the collection event
LocalityDescription	nvarchar (MAX)	Locality description of the locality, exactly as written on the original label (i.e. without corrections during data entry)
HabitatDescription	nvarchar (MAX)	Geo-ecological description of the locality, exactly as written on the original label (i.e. without corrections during data entry)
ReferenceTitle	nvarchar (255)	The title of the publication where the collection event was published. Note this is only a cached value where ReferenceURI is present
ReferenceURI	varchar (255)	URI (e.g. LSID) of the source publication where the collection event is published, may e.g. refer to the module DiversityReferences
ReferenceDetails	nvarchar (50)	The exact location within the reference, e.g. pages, plates
CollectingMethod	nvarchar (MAX)	Description of the method used for collecting the samples, e.g. traps, moist chambers, drag net
Notes	nvarchar (MAX)	Notes about the collection event
CountryCache	nvarchar (50)	The country where the collection event took place. Cached value derived from an entry in CollectionGeography

DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionEventImage

The images showing the site of the collection event

Column	**Data type**	**Description**
CollectionEventID	int	Unique ID for the collection event (= Primary key)
URI	varchar (255)	The complete URI address of the image. This is only a cached value if ResourceID is available referring to the module DiversityResources
ResourceURI	varchar (255)	The URI of the resource (e.g. see module DiversityResources)
ImageType	nvarchar (50)	Type of the image, e.g. map
Notes	nvarchar (MAX)	Notes to this image concerning the collection event
Description	xml (MAX)	Description of the image
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*

RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table **CollectionEventLocalisation**

The geographic localisation of a collection event

Column	Data type	Description
CollectionEventID	int	Refers to the ID of CollectionEvent (= Foreign key and part of primary key)
LocalisationSystemID	int	Refers to the ID of LocalisationSystem (= Foreign key and part of primary key)
Location1	nvarchar (255)	Either a named location selected from a thesaurus (e. g. 'Germany, Bavaria, Kleindingharting') or altitude range or other values (e. g. 100-200 m)
Location2	nvarchar (255)	Corresponding value to Location1 e.g. ID or URI of gazetteer or thesaurus
LocationAccuracy	nvarchar (50)	The accuracy of the determination of this locality
LocationNotes	nvarchar (MAX)	Notes on the location
DeterminationDate	smalldatetime	Date of the determination of the geographical localisation
DistanceToLocation	varchar (50)	Distance from the specified place to the real location of the collection event (m)
DirectionToLocation	varchar (50)	Direction from the specified place to the real location of the collection event (Degrees rel. to north)
ResponsibleName	nvarchar (255)	The name of the agent (person or organization) responsible for this entry. *Default value: [dbo].[CurrentUserName]()*
ResponsibleAgentURI	varchar (255)	URI of the person or organisation responsible for the data (see e.g. module DiversityAgents)
Geography	geography	The geography of the localisation
AverageAltitudeCache	float	Calculated altitude as parsed from the location fields
AverageLatitudeCache	float	Calculated latitude as parsed from the location fields
AverageLongitudeCache	float	Calculated longitude as parsed

		from the location fields
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*
RecordingMethod	nvarchar (500)	The method or device used for the recording of the localisation

Table CollectionEventProperty

A property of a collection site, e.g. exposition, slope, vegetation. May refer to Diversity Workbench module DiversityScientificTerms

Column	Data type	Description
CollectionEventID	int	Refers to the ID of CollectionEvent (= Foreign key and part of primary key)
PropertyID	int	The ID of the descriptor of the collection event, foreign key, see table Descriptor
DisplayText	nvarchar (255)	The text for the property as shown e.g. in a user interface
PropertyURI	varchar (255)	URI referring to an external datasource e.g. DiversityTerminology
PropertyHierarchyCache	nvarchar (MAX)	A cached text of the complete name of the descriptor including superior categories if present
PropertyValue	nvarchar (255)	The value of a captured feature e.g. temperature, pH, vegetation etc. If there is a range this is the lower or first value
ResponsibleName	nvarchar (255)	The name of the agent (person or organization) responsible for this entry.
ResponsibleAgentURI	varchar (255)	URI of the person or organisation responsible for the data (see e.g. module DiversityAgents)

Notes	nvarchar (MAX)	Notes about the property of the colletion site.
AverageValueCache	float	For numeric values - a cached average value according to the
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionEventSeries

The series whithin which collection events take place

Column	Data type	Description
SeriesID	int	Primary key. The ID for this expedition (= Primary key)
SeriesParentID	int	The ID of the superior expedition
Description	nvarchar (MAX)	The description of the expedition as it will be printed on e.g. the label
SeriesCode	nvarchar (50)	The user defined code for an expedition
Notes	nvarchar (MAX)	Notes about this expedition
Geography	geography	The geography of the collection event series
DateStart	datetime	The date and time when the collection event series started
DateEnd	datetime	The date and time when the collection event series ended
DateCache	datetime	The first date of the depending events, used for sorting the expeditions [controlled by the database]
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this

		dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionEventSeriesImage

The images showing the sites of a collection event series, e.g. an expedition or sampling plot

Column	**Data type**	**Description**
SeriesID	int	Unique ID for the collection event series (= Foreign key and part of primary key)
URI	varchar (255)	The complete URI address of the image. This is only a cached value if ResourceID is available referring to the module DiversityResources
ResourceURI	varchar (255)	The URI of the resource (e.g. see module DiversityResources)
ImageType	nvarchar (50)	Type of the image, e.g. map
Notes	nvarchar (MAX)	Notes to this image concerning the collection event
Description	xml (MAX)	Description of the image
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionExternalDatasource

CollectionExternalDatasource document the sources of the names.

Column	Data type	Description
ExternalDatasourceID	int	An ID to identify an external data collection of collection specimen (primary key, the ID has no meaning outside of the DiversityWorkbench system)
ExternalDatasourceName	nvarchar (255)	The name of the data collection that has been integrated or can be linked to for further analysis
ExternalDatasourceVersion	nvarchar (255)	The version of this data collection (either official version number, or dates when the collection was integrated)
Rights	nvarchar (500)	A description of copyright agreements or permission to use data from the external database
ExternalDatasourceAuthors	nvarchar (200)	The persons or institutions responsible for the external database
ExternalDatasourceURI	nvarchar (300)	The URI of the database provider resp. the external database
ExternalDatasourceInstitution	nvarchar (300)	The institution responsible for the external database
InternalNotes	nvarchar (1500)	Additional notes concerning this data collection
ExternalAttribute_NameID	nvarchar (255)	The table and field name in the external data collection to which CollectionExternalID refers
PreferredSequence	tinyint	For selection in e.g. picklists: of several equal names only the name from the source with the lowest preferred sequence will be provided.
Disabled	bit	If this source should be disabled for selection of names e.g. in picklists
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionImage

The images showing the collection

Column	Data type	Description
CollectionID	int	Refers to the ID of Collection (= Foreign key and part of primary key)
URI	varchar (255)	The complete URI address of the image.
ImageType	nvarchar (50)	Type of the image, e.g. label
Notes	nvarchar (MAX)	Notes about the collection image
Description	xml (MAX)	Description of the image
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogInsertedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogInsertedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	RowGUID - CollectionImage *Default value: newsequentialid()*

Table CollectionProject

The projects within which the collection specimen were placed

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*

LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimen

The data directly attributed to the collection specimen

Column	Data type	Description
CollectionSpecimenID	int	Unique reference ID for the collection specimen record (primary key)
Version	int	The version of the dataset *Default value: (1)*
CollectionEventID	int	Refers to the ID of CollectionEvent (= Foreign key and part of primary key)
CollectionID	int	ID of the Collection as stored in table Collection (= foreign key, see table Collection)
AccessionNumber	nvarchar (50)	Accession number of the specimen within the collection, e.g. "M-29834752"
AccessionDate	datetime	The date of the accession calculated from the entries in AccessionDay, -Month and -Year
AccessionDay	tinyint	The day of the date when the specimen was acquired in the collection
AccessionMonth	tinyint	The month of the date when the specimen was acquired in the collection
AccessionYear	smallint	The year of the date when the specimen was acquired in the collection
AccessionDateSupplement	nvarchar (255)	Verbal or additional accession date information, e.g. 'end of summer 1985', 'first quarter', '1888-1892'
AccessionDateCategory	nvarchar (50)	Category of the date of the identification e.g. "system", "estimated" (= foreign key, see in table xColl_DateCategory_Enum)
DepositorsName	nvarchar (255)	The name of the depositor(s) (person or organization responsible for deposition). Where entire collections are deposited, this should also

		contain the collection name (e.g. 'Herbarium P. Döbbler')
DepositorsAgentURI	varchar (255)	The URI of the depositor(s) (person or organization responsible for deposition)
DepositorsAccessionNumber	nvarchar (50)	Accession number of the specimen within the previous or original collection, e.g. 'D-23948'
LabelTitle	nvarchar (255)	The title of the label e.g. for printing labels.
LabelType	nvarchar (50)	Printed, typewritten, typewritten with handwriting added, entirely in handwriting, etc.
LabelTranscriptionState	nvarchar (50)	The state of the transcription of a label into the database: 'Not started', 'incomplete', 'complete'
LabelTranscriptionNotes	nvarchar (255)	User defined notes concerning the transcription of the label into the database
ExsiccataURI	varchar (255)	If specimen is an exsiccata: The URI of the Exsiccata series, e.g. as stored within the DiversityExsiccata module
ExsiccataAbbreviation	nvarchar (255)	If specimen is an exsiccata: Standard abbreviation of the exsiccata (not necessarily a unique identifier; editors or publication places may change over time)
OriginalNotes	nvarchar (MAX)	Notes found on the label of the specimen, by the original collector or from a later revision
AdditionalNotes	nvarchar (MAX)	Additional notes made by the editor of the specimen record, e. g. 'doubtful identification/locality'
ReferenceTitle	nvarchar (255)	The title of the publication where the specimen was published. Note this is only a cached value where ReferenceURI is present
ReferenceURI	varchar (255)	URI (e.g. LSID) of reference where specimen is published, e.g. referring to the module DiversityReferences
ReferenceDetails	nvarchar (50)	The exact location within the reference, e.g. pages, plates
Problems	nvarchar (255)	Description of a problem that occurred during data editing. Typically these entries should

		be deleted after help has been obtained. Do not enter scientific problems here; use AdditionalNotes for such permanent problems!
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
InternalNotes	nvarchar (MAX)	Internal notes that should not be published e.g. on websites
ExternalDatasourceID	int	An ID to identify an external data collection of collection specimen (primary key, the ID has no meaning outside of the DiversityWorkbench system)
ExternalIdentifier	nvarchar (100)	The identifier of the external specimen as defined in the external datasource
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimenImage

The images of a collection specimen or of an identification unit within this specimen

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
URI	varchar (255)	The complete URI address of the image. This is only a cached value if ResourceID is available referring to the module DiversityResources
ResourceURI	varchar (255)	The URI of the image, e.g. as stored in the module DiversityResources.
SpecimenPartID	int	Optional: If the dataset is not related to a part of a specimen, the ID of a related

		part (= foreign key)
IdentificationUnitID	int	If image refers to only on out of several identification units for a specimen, refers to the ID of an IdentificationUnit for a CollectionSpecimen (= foreign key)
ImageType	nvarchar (50)	Type of the image, e.g. photograph
Notes	nvarchar (MAX)	Notes about the specimen image
Description	xml (MAX)	Description of the image
DataWithholdingReason	nvarchar (255)	If the dataset is withhold, the reason for withholding the data, otherwise null
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimenPart

Parts of a collection specimen. Includes a possible hierarchy of the parts

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
SpecimenPartID	int	ID of the collection specimen part (= part of Primary key).
DerivedFromSpecimenPartID	int	SpecimenPartID of the specimen from which the current specimen is derived from
PreparationMethod	nvarchar (MAX)	The method used for the preparation of the part of the specimen, e.g. the inoculation method for cultures
PreparationDate	datetime	The date and time when the part was preparated e.g when it was separated from the source object

AccessionNumber	nvarchar (50)	Accession number of the part of the specimen within the collection if it is different from the accession number of the specimen as stored in the table CollectionSpecimen, e.g. "M-29834752"
PartSublabel	nvarchar (50)	The label for a part of a specimen, e.g. if duplicats of a specimen have a separate number
CollectionID	int	ID of the Collection as stored in table Collection (= foreign key, see table Collection)
MaterialCategory	nvarchar (50)	Material category of specimen. Examples: 'herbarium sheets', 'drawings', 'microscopic slides' etc. (= foreign key, see table CollMaterialCategory_Enum) *Default value: N'specimen'*
StorageLocation	nvarchar (255)	A code identifying the place where the specimen is stored within the collection. Frequently the accepted scientific name is used as storage location code.
Stock	float	Number of stock units if the specimen is stored in separated units e.g. several boxes or vessels (max. 255)
StockUnit	nvarchar (50)	If empty the stock is given as a count, else it contains the unit in which stock is expressed, e.g. µl, ml, kg etc.
StorageContainer	nvarchar (500)	The container in which the part is stored
Notes	nvarchar (MAX)	Notes concerning the storage of the sample
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimenProcessing

The processing that was applied to a collection specimen

Column	Data type	Description
CollectionSpecimenID	int	Refers to ID of CollectionSpecimen (= Foreign key and part of primary key)
ProcessingDate	datetime	Date and time of the start of the processing *Default value: getdate()*
ProcessingID	int	ID of the processing. Refers to ProcessingID in table Processing (foreign key) *Default value: (1)*
Protocoll	nvarchar (100)	The label of the processing protocoll
SpecimenPartID	int	Optional: If the dataset is related to a part of a specimen, the ID of a related part (= foreign key, see table CollectionSpecimenPart)
ProcessingDuration	varchar (50)	The duration of the processing including the unit (e.g. 5 min) or the end of the processing starting at the processingDate (e.g. 23.05.2008)
ResponsibleName	nvarchar (255)	Name of the person or institution responsible for the determination *Default value: [dbo].[CurrentUserName]()*
ResponsibleAgentURI	varchar (255)	URI of the person or institution responsible for the determination (= foreign key) as stored in the module DiversityAgents.
Notes	nvarchar (MAX)	Notes about the processing
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimenRelation

The relations of a collection specimen to other collection specimen

Column	Data type	Description
CollectionSpecimenID	int	Unique reference ID for the collection specimen record (primary key)
RelatedSpecimenURI	varchar (255)	URI of the related specimen
RelatedSpecimenDisplayText	varchar (255)	The name of a related specimen as shown e.g. in a user interface
RelationType	nvarchar (50)	Type of the relation between the specimen (= foreign key, see table CollRelationType_Enum)
RelatedSpecimenCollectionID	int	ID of the Collection as stored in table Collection (= foreign key, see table Collection)
RelatedSpecimenDescription	nvarchar (MAX)	Description of the related specimen
Notes	nvarchar (MAX)	Notes on the relation to the specimen
IsInternalRelationCache	bit	If the relation represents a connection between specimen in this database *Default value: (1)*
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table CollectionSpecimenTransaction

The transactions in which a specimen was involved

Column	Data type	Description
CollectionSpecimenID	int	Refers to ID of CollectionSpecimen (= Foreign

		key and part of primary key)
TransactionID	int	Unique ID for the transaction (= Foreign key and part of primary key)
SpecimenPartID	int	Optional: If the dataset is related to a part of a specimen, the ID of a related part (= foreign key, see table CollectionSpecimenPart)
IsOnLoan	bit	True if a specimen is on loan
LogInsertedBy	nvarchar (50)	Name of user who first entered (typed or imported) the data. *Default value: user_name()*
LogInsertedWhen	smalldatetime	Date and time when the data were first entered (typed or imported) into this database. *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of user who last updated the data. *Default value: user_name()*
LogUpdatedWhen	smalldatetime	Date and time when the data were last updated. *Default value: getdate()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table Identification

The identifications of the organisms within a specimen

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
IdentificationUnitID	int	Refers to the ID of IdentficationUnit (= foreign key and part of primary key)
IdentificationSequence	smallint	The sequence of the identifications. The last identification (having the highest sequence) is regarded as valid *Default value: (1)*
IdentificationDate	datetime	The date of the identification calculated from the entries in IdentificationDay, -Month and -Year
IdentificationDay	tinyint	The day of the identification event
IdentificationMonth	tinyint	The month of the

		identification event
IdentificationYear	smallint	The year of the identification event. The year may be empty if only the day or month are known.
IdentificationDateSupplement	nvarchar (255)	Verbal or additional identification date information, e.g. 'end of summer 1985', 'first quarter', '1888-1892'
IdentificationDateCategory	nvarchar (50)	Category of the date of the identification e.g. "system", "estimated" (= foreign key, see in table CollDateCategory_Enum)
VernacularTerm	nvarchar (255)	Name or term other than a taxonomic (= scientific) name, e.g. 'pine', 'limestone', 'conifer', 'hardwood'
TaxonomicName	nvarchar (255)	Valid name of the species (including the taxonomic author where available). Example: 'Rosa canina L.'
NameURI	varchar (255)	The URI of the taxonomic name, e.g. as provided by the module DiversityTaxonNames.
IdentificationCategory	nvarchar (50)	Category of the identification e.g. 'determination', 'confirmation', 'absence' (= foreign key, see table CollIdentificationCategory_Enum)
IdentificationQualifier	nvarchar (50)	Qualification of the identification e.g. "cf."," aff.", "sp. nov." (= foreign key, see table CollIdentificationQualifier_Enum)
TypeStatus	nvarchar (50)	If identification unit is type of a taxonomic name: holotype, syntype, etc. (= foreign key, see table CollTypeStatus_Enum)
TypeNotes	nvarchar (MAX)	Notes concerning the typification of this specimen
ReferenceTitle	nvarchar (255)	Publications or authoritative opinions of scientist used during the identification process. Example: enter 'Schmeil-Fitschen 1995' if this field flora was used.
ReferenceURI	varchar (255)	The URI of the reference e.g. as provided by the module DiversityReferences
ReferenceDetails	nvarchar (50)	The exact location within the reference, e.g. pages, plates

Notes	nvarchar (MAX)	User defined notes, e.g. the reason for a re-determination / change of the name, etc.
ResponsibleName	nvarchar (255)	Name of the person or institution responsible for the determination *Default value: [dbo].[CurrentUserName]()*
ResponsibleAgentURI	varchar (255)	URI of the person or institution responsible for the determination (= foreign key) as stored in the module DiversityAgents.
LogCreatedWhen	datetime	Date and time when the dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Login of the user who created the dataset *Default value: user_name()*
LogUpdatedWhen	datetime	Date and time when the dataset was changed *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Login of the user who changed the dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table IdentificationUnit

Organism that is present in or on a collection specimen

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
IdentificationUnitID	int	ID of the identification unit (= part of Primary key). Usually one of possibly several organisms present on the collection specimen. Example: parasite with hyperparasite on plant leaf = 3 units,
LastIdentificationCache	nvarchar (255)	The last identification as entered in table Identification
FamilyCache	nvarchar (255)	A cached value of the family of the taxon of the last identification. Can be set by the editor if NameURI in table Identification is NULL, otherwise set by the system.
OrderCache	nvarchar (255)	A cached value of the order

		of the taxon of the last identification. Can be set by the editor if NameURI in table Identification is NULL, otherwise set by the system.
TaxonomicGroup	nvarchar (50)	Taxonomic group the organism identified by this unit belongs to. Groups listed in table CollTaxonomicGroup_Enum (= foreign key)
OnlyObserved	bit	True if the organism was only observed rather than collected. It is therefore not present on the preserved specimen. Example: Tree under which the collected mycorrhizal fungus grew. *Default value: (0)*
RelatedUnitID	int	The IdentificationUnitID of the organism or substrate, on which this organism is growing (= foreign key)
RelationType	nvarchar (50)	The relation of an unit to its substrate, e.g. parasitism, symbiosis etc. as stored in CollRelationType_Enum (= foreign key)
ColonisedSubstratePart	nvarchar (255)	If a substrate association exists: part of the substrate that is affected in the interaction (e.g. 'leaves' if a fungus is growing on the leaves of an infected plant)
LifeStage	nvarchar (255)	Examples: 'II, III' for spore generations of rusts or 'seed', 'seedling' etc. for higher plants
Gender	nvarchar (50)	The gender of the identification unit, e.g. 'male'
NumberOfUnits	smallint	The number of units of this identification unit, e.g. 400 beetle in a bottle
ExsiccataNumber	nvarchar (50)	If specimen is an exsiccata: Number of current specimen within the exsiccata series
ExsiccataIdentification	smallint	Refers to the IdentificationSequence in Identification (= foreign key). The name under which the collection specimen resp. this unit is published within an exsiccata.
UnitIdentifier	nvarchar (50)	An identifier for the identification of the unit e.g. a number painted on a tree within an experimental plot

UnitDescription	nvarchar (50)	Description of the unit, esp. if not the an organism but parts or remnants of it were present or observed, e.g. a nest of an insect or a song of a bird
Circumstances	nvarchar (50)	Circumstances of the occurence of the organism
DisplayOrder	smallint	The sequence in which the units within this specimen will appear on e.g. a label where the first unit may be printed in the header and others in the text below. 0 means the unit should not appear on a label. *Default value: (1)*
Notes	nvarchar (MAX)	Further information on the identification unit or interaction, e. g. infection symptoms like 'producing galls'
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table IdentificationUnitAnalysis

The analysis values taken from an identification unit

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
IdentificationUnitID	int	Refers to the ID of IdentficationUnit (= foreign key and part of primary key)
AnalysisID	int	Analysis ID, foreign key of table Analysis.
AnalysisNumber	nvarchar (50)	Number of the analysis
AnalysisResult	nvarchar (MAX)	The result of the analysis
ExternalAnalysisURI	varchar (255)	An URI for an analysis as defined in an external datasoure

ResponsibleName	nvarchar (255)	Name of the person or institution responsible for the determination *Default value: [dbo].[CurrentUserName]()*
ResponsibleAgentURI	varchar (255)	URI of the person or institution responsible for the determination (= foreign key) as stored in the module DiversityAgents.
AnalysisDate	nvarchar (50)	The date of the analysis
SpecimenPartID	int	ID of the part of a specimen (optional, Foreign key) if the analysis was done with a part of the specimen (see table CollectionSpecimenPart).
Notes	nvarchar (MAX)	Notes concerning this analysis
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table IdentificationUnitGeoAnalysis

The geographical position or region of an organism at a certain time

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
IdentificationUnitID	int	Refers to the ID of IdentficationUnit (= foreign key and part of primary key)
AnalysisDate	datetime	The date of the analysis
Geography	geography	The geography of the identification unit according to WGS84, e.g. a point (latitide, longitude and altitude)
Geometry	geometry (MAX)	The geometry of the identifiction unit, e.g. an area
ResponsibleName	nvarchar (255)	Name of the person or institution responsible for the

		determination
ResponsibleAgentURI	varchar (255)	URI of the person or institution responsible for the determination (= foreign key) as stored in the module DiversityAgents.
Notes	nvarchar (MAX)	Notes concerning this analysis
LogCreatedWhen	datetime	The time when this dataset was created
LogCreatedBy	nvarchar (50)	Who created this dataset
LogUpdatedWhen	datetime	The last time when this dataset was updated
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table IdentificationUnitInPart

The list of the organisms that are found in a part of the specimen

Column	Data type	Description
CollectionSpecimenID	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
IdentificationUnitID	int	ID of the identification unit (= part of Primary key). Usually one of possibly several organisms present on the collection specimen. Example: parasite with hyperparasite on plant leaf = 3 units,
SpecimenPartID	int	ID of the part of a specimen (optional, Foreign key) if the identification unit is located on a part of the specimen (see table CollectionSpecimenPart).
DisplayOrder	smallint	The sequence in which the units within this part will appear on e.g. a label where the first unit may be printed in the header and others in the text below. 0 means the unit should not appear on a label. *Default value: (1)*
Description	nvarchar (500)	A description of the unit, esp. if not a whole unit but e.g. parts of it are stored in the collection, e.g. a nest of a bird
LogInsertedBy	nvarchar (50)	Name of user who first

		entered (typed or imported) the data. *Default value: user_name()*
LogInsertedWhen	smalldatetime	Date and time when the data were first entered (typed or imported) into this database. *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of user who last updated the data. *Default value: user_name()*
LogUpdatedWhen	smalldatetime	Date and time when the data were last updated. *Default value: getdate()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table LocalisationSystem

The geographic localisation systems, e.g. coordinates

Column	**Data type**	**Description**
LocalisationSystemID	int	Unique ID for the localisation system (= Primary key)
LocalisationSystemParentID	int	LocalisationSystemID of the superior LocalisationSystem
LocalisationSystemName	nvarchar (100)	Name of the system used for the determination of the place of the collection, e. g. Gauss-Krüger, MTB, GIS
DefaultAccuracyOfLocalisation	nvarchar (50)	The default for the accuracy of values that can be reached with this method
DefaultMeasurementUnit	nvarchar (50)	The default measurement unit for the localisation system, e.g. m, geograpic coordinates
ParsingMethodName	nvarchar (50)	Internal value, specifying a programming method used for parsing text in fields Location1/Location2 in table CollectionLocalisation
DisplayText	nvarchar (50)	Short abbreviated description of the localisation system as displayed in the user interface
DisplayEnable	bit	Specifies if this item is enabled to be used within the database. LocalisationSystems can be disabled to avoid seeing them, but to keep the definition for the future.
DisplayOrder	smallint	The order in which the entries are displayed. The order may

		be changed at any time, but all values must be unique.
Description	nvarchar (255)	Description of the localisation method
DisplayTextLocation1	nvarchar (50)	Short abbreviated description of the attribute Location1 in the table CollectionGeography as displayed in the user interface
DescriptionLocation1	nvarchar (255)	Description of the attribute Location1 in the table CollectionGeography as displayed in the user interface
DisplayTextLocation2	nvarchar (50)	Short abbreviated description of the attribute Location2 in the table CollectionGeography as displayed in the user interface
DescriptionLocation2	nvarchar (255)	Description of the attribute Location2 in the table CollectionGeography as displayed in the user interface
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table Processing

The processings of the specimen

Column	Data type	Description
ProcessingID	int	ID of the processing (Primary key)
ProcessingParentID	int	The ID of the superior type of the processing
DisplayText	nvarchar (50)	The display text of the processing as shown e.g. in a user interface
Description	nvarchar (MAX)	Description of the processing
Notes	nvarchar (MAX)	Notes about the processing
ProcessingURI	varchar (255)	An URI for a processing as defined in an external datasource
OnlyHierarchy	bit	If the entry is only used for the hierarchical arrangement of the entries *Default value: (0)*
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*

LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table <u>ProcessingMaterialCategory</u>

The processings that are possible for a certain material category

Column	Data type	Description
<u>ProcessingID</u>	int	ID of the processing. Refers to ProcessingID in table Processing (foreign key) *Default value: (1)*
<u>MaterialCategory</u>	nvarchar (50)	Material category of specimen. Examples: 'herbarium sheets', 'drawings', 'microscopic slides' etc. *Default value: N'specimen'*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table <u>ProjectAnalysis</u>

The types of the analysis that are available for a project

Column	Data type	Description
<u>AnalysisID</u>	int	ID of the analysis (Primary key)
<u>ProjectID</u>	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this

		dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table **ProjectProcessing**

The types of processing available within a project

Column	Data type	Description
ProcessingID	int	ID of the Processing (Primary key)
ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table **Property**

The list of the properties that can be specified for the collection site

Column	Data type	Description
PropertyID	int	Unique ID for the localisation system (= Primary key)
PropertyParentID	int	LocalisationSystemID of the superior LocalisationSystem
PropertyName	nvarchar (100)	Name of the system used for the determination of the place of the collection, e. g. Gauss-Krüger, MTB, GIS
DefaultAccuracyOfProperty	nvarchar (50)	The default for the accuracy of values that can be reached

		with this method
DefaultMeasurementUnit	nvarchar (50)	The default measurement unit for the characterisation system, e.g. pH
ParsingMethodName	nvarchar (50)	Internal value, specifying a programming method used for parsing text in fields Location1/Location2 in table CollectionLocalisation
DisplayText	nvarchar (50)	Short abbreviated description of the localisation system as displayed in the user interface
DisplayEnabled	bit	Specifies if this item is enabled to be used within the database. LocalisationSystems can be disabled to avoid seeing them, but to keep the definition for the future.
DisplayOrder	smallint	The order in which the entries are displayed. The order may be changed at any time, but all values must be unique.
Description	nvarchar (255)	Description of the localisation method
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table Transaction

Transactions like loan, borrow, gift, exchange etc. of specimen if they are e.g. permanently or temporary transfered from one collection to another

Column	Data type	Description
TransactionID	int	Unique ID for the transaction (= Primary key)
ParentTransactionID	int	The ID of a preceeding transaction of a superior transaction if transactions are organized in a hierarchy
TransactionType	nvarchar (50)	Type of the transaction e.g. gift in or out, exchange in or out, purchase in or out *Default value: N'exchange'*
TransactionTitle	nvarchar (200)	The title of the transaction as e.g. shown in an user interface
ReportingCategory	nvarchar (50)	A group defined for the transaction, e. g. a taxonomic group as used for exchange balancing
AdministratingCollectionID	int	ID of the collection thas is

		responsible for the administration of the transaction.
MaterialDescription	nvarchar (MAX)	ID of the project to which the transaction belongs (Projects are defined in DiversityProjects) *Default value: ''*
MaterialCategory	nvarchar (50)	Material category of specimen. Examples: 'herbarium sheets', 'drawings', 'microscopic slides' etc. *Default value: N'specimen'*
MaterialCollectors	nvarchar (MAX)	The collectors of the material
FromCollectionID	int	The ID of the collection from which the specimen were transfered, e.g. the donating collection of a gift
FromTransactionPartnerName	nvarchar (255)	Name of the person or institution from which the specimen were transfered, e.g. the donator of a gift
FromTransactionPartnerAgentURI	varchar (255)	The URI of the transaction partner (see e.g. module DiversityAgents)
FromTransactionNumber	nvarchar (50)	Number or code by which a transaction may be recorded by the administration of the source of the specimen, e.g. the donating collection of a gift
ToCollectionID	int	The ID of the collection to which the specimen were transfered, e.g. the receiver of a gift
ToTransactionPartnerName	nvarchar (255)	Name of the person or institution to which the specimen were transfered, e.g. the receiver of a gift
ToTransactionPartnerAgentURI	varchar (255)	The URI of the transaction partner (see e.g. module DiversityAgents)
ToTransactionNumber	nvarchar (50)	Number or code by which a transaction may be recorded by the administration of the destination of the specimen, e.g. the receiving collection of a gift
NumberOfUnits	smallint	The number of units that were (initially) included in the transaction
Investigator	nvarchar (50)	The investigator for whose study a transacted material was sent

TransactionComment	nvarchar (MAX)	Comments about the exchanged material addressed to the transaction partner
BeginDate	datetime	Date when the transaction started
AgreedEndDate	datetime	End of the transaction period, e.g. if the time for borrowing the specimen is restricted
ActualEndDate	datetime	Actual end of the transaction when e.g. the borrowed specimen were returned to the owner
InternalNotes	nvarchar (MAX)	Internal notes about this transaction, not to be published e.g. on a web page
ResponsibleName	nvarchar (255)	The person responsible for this transaction
ResponsibleAgentURI	varchar (255)	The URI of the person, team or organisation responsible for the data (see e.g. module DiversityAgents)
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table TransactionDocument

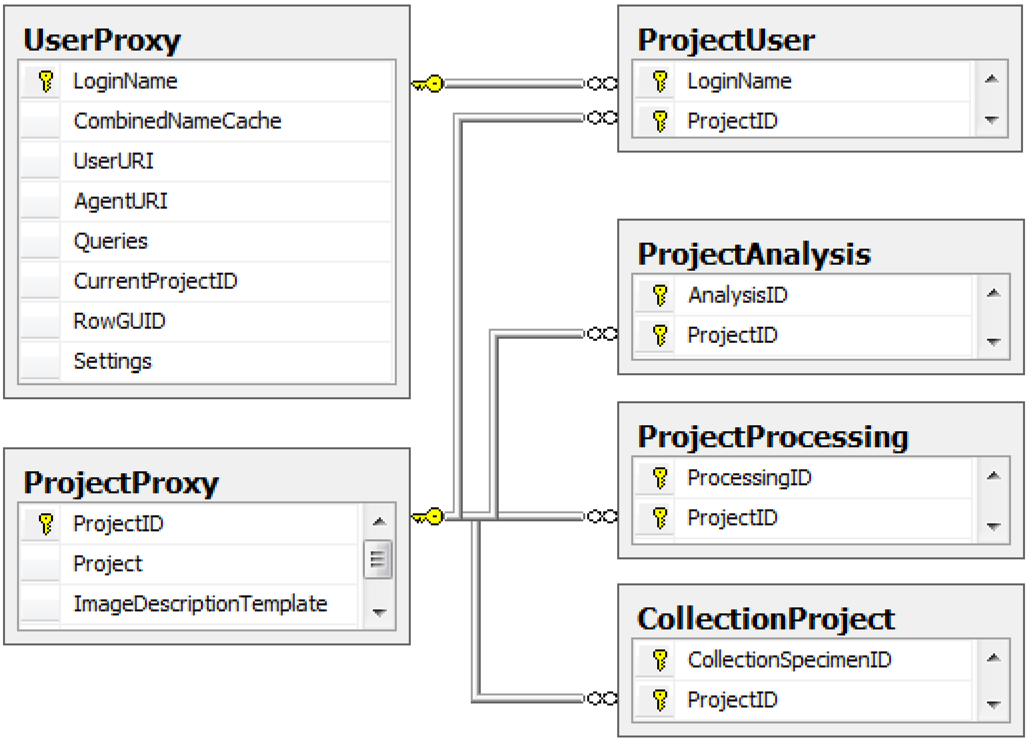
The history of transactions resp. the documents connected to the transactions

Column	Data type	Description
TransactionID	int	Unique ID for the Transaction, refers to table Transaction (= Part of primary key and foreign key)
Date	datetime	The date of the event of a transaction
TransactionText	nvarchar (MAX)	The text of a transaction document
TransactionDocument	image (2147483647)	A scanned document connected to this transaction

		event
InternalNotes	nvarchar (MAX)	Internal notes about this transaction event
LogCreatedWhen	datetime	The time when this dataset was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Who created this dataset *Default value: user_name()*
LogUpdatedWhen	datetime	The last time when this dataset was updated *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Database - Project related tables

Information concerning the projects and related tables are stored in the tables shown in the diagram below.



Index

- CollectionProject
- ProjectAnalysis
- ProjectProcessing
- ProjectProxy
- ProjectUser
- UserProxy

Table CollectionProject

The projects which the collection specimen were placed in

Column	Data type	Description
CollectionSpecimenID	int	ID of the CollectionSpecimen (= Foreign key and part of primary key)

ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table ProjectAnalysis

The types of the analysis that are available for a project

Column	Data type	Description
AnalysisID	int	ID of the analysis (Primary key)
ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table ProjectProcessing

The types of processing available within a project

Column	Data type	Description
ProcessingID	int	ID of the processing (Primary key)
ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

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)	Name or title of the project as shown in a user interface (Projects are defined in DiversityProjects)
ImageDescriptionTemplate	xml (MAX)	Template for the description of images
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table **ProjectUser**

The projects a user can access

Column	Data type	Description
LoginName	nvarchar (50)	Login name of the user to access DivesityWorkbench, Microsoft domains, etc..

ProjectID	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table UserProxy

The user as stored in the module DiversityUsers

Column	Data type	Description
LoginName	nvarchar (50)	Login name of the user to access DivesityWorkbench, Microsoft domains, etc..
CombinedNameCache	nvarchar (255)	Short name of the user, e.g. P. Smith *Default value: NULL*
UserURI	varchar (255)	URI of the user in a remote module, e.g. refering to UserInfo.UserID in database DiversityUsers
AgentURI	varchar (255)	AgentURI - UserProxy
Queries	xml (MAX)	Queries created by the user
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Database - Entity tables

Information concerning the entities are stored in the tables shown in the diagram below.

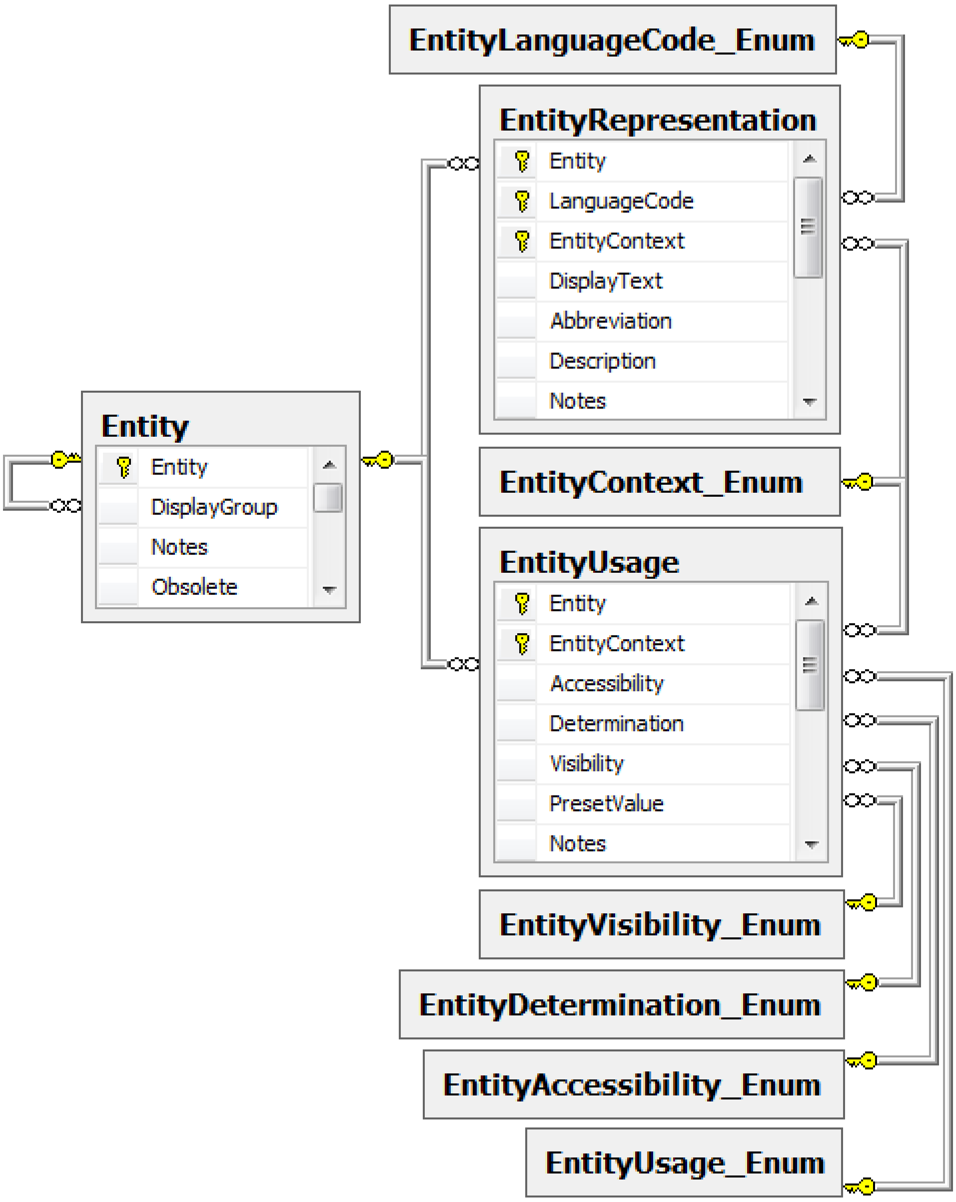


Table **Entity**

The entities in an application e.g. the tables and columns in a database

Column	Data type	Description
Entity	varchar (500)	Name of the entity, e.g. Table.Column.Content within the database or a unique string for e.g. a message within the DiversityWorkbench (e.g. "DiversityWorkbench.Message.Connection.NoAccess"), primary key
DisplayGroup	nvarchar (50)	Name of the group, if DiversityWorkbench entities should be displayed in a group.
Notes	nvarchar (MAX)	Notes about the entity
Obsolete	bit	True if an entity is obsolete. Obsolete entities may be

		kept to ensure compatibility with older modules
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table EntityRepresentation

The description of the entity in a certain context in different languages

Column	Data type	Description
Entity	varchar (500)	Name of the entity. Foreign key, relates to table Entity
LanguageCode	nvarchar (50)	ISO 639: 2-letter codes for the language of the content
EntityContext	nvarchar (50)	Context for the representation, e.g. "Exchange with ABCD", "collection management" or "observation" as defined in table EntityContext_Enum
DisplayText	nvarchar (50)	Text for the entity as shown e.g. in a user interface
Abbreviation	nvarchar (20)	Abbreviation for the entity as shown e.g. in a user interface
Description	nvarchar (MAX)	Description of the entity
Notes	nvarchar (MAX)	Notes about the representation of the entity
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

Table **EntityUsage**

The usage of an entity in a certain context, e.g. hidden, read only

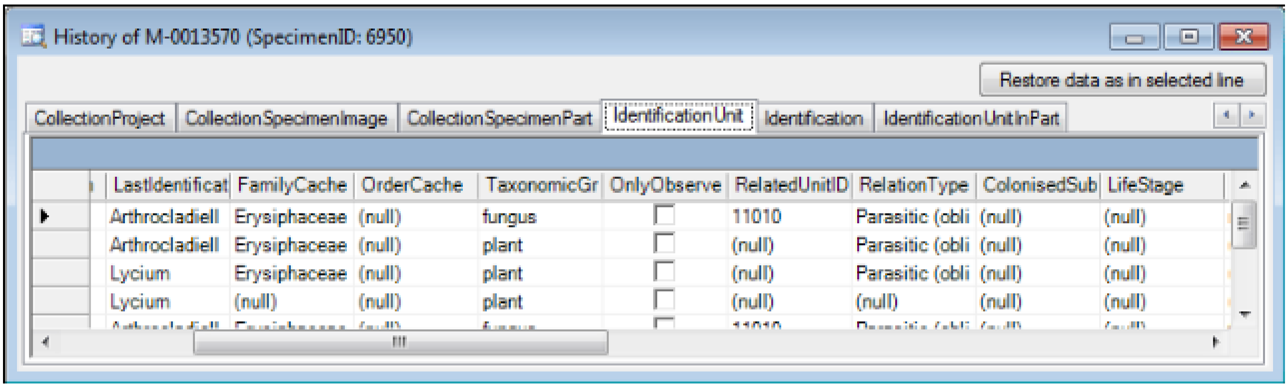
Column	Data type	Description
Entity	varchar (500)	Name of the entity. Foreign key, relates to table Entity
EntityContext	nvarchar (50)	Context for the representation, e.g. "Exchange with ABCD", "collection management" or "observation" as defined in table EntityContext_Enum
Accessibility	nvarchar (50)	Whether the access to an entity is resticted to e.g. read only or can be edited without restrictions
Determination	nvarchar (50)	Whether a value is determined e.g. by the system or the user
Visibility	nvarchar (50)	Whether the entity is visible or hidden from e.g. a user interface
PresetValue	nvarchar (500)	Whether a value resp. SQL statement for the value is preset, e.g. 'determination' for identifications when using a mobile device during an expedition
Notes	nvarchar (MAX)	Notes about the usage of the entity
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*
RowGUID	uniqueidentifier	- *Default value: newsequentialid()*

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. The database DiversityCollection handles 2 different histories - one for the CollectionSpecimen and one for the CollectionEvent. The version shown in the header of the main window refers to these histories . The first number refers to the version of the specimen. If an event was defined a second number is shown, referring to the version of the CollectionEvent e.g. **5** 3 means version **5** of the specimen and version 3 of the CollectionEvent.

Specimen	Event	Version
199354	224429	**5** 3

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.



LastIdentificat	FamilyCache	OrderCache	TaxonomicGr	OnlyObserve	RelatedUnitID	RelationType	ColonisedSub	LifeStage
Arthrocladiell	Erysiphaceae	(null)	fungus	☐	11010	Parasitic (obli	(null)	(null)
Arthrocladiell	Erysiphaceae	(null)	plant	☐	(null)	Parasitic (obli	(null)	(null)
Lycium	Erysiphaceae	(null)	plant	☐	(null)	Parasitic (obli	(null)	(null)
Lycium	(null)	(null)	plant	☐	(null)	(null)	(null)	(null)

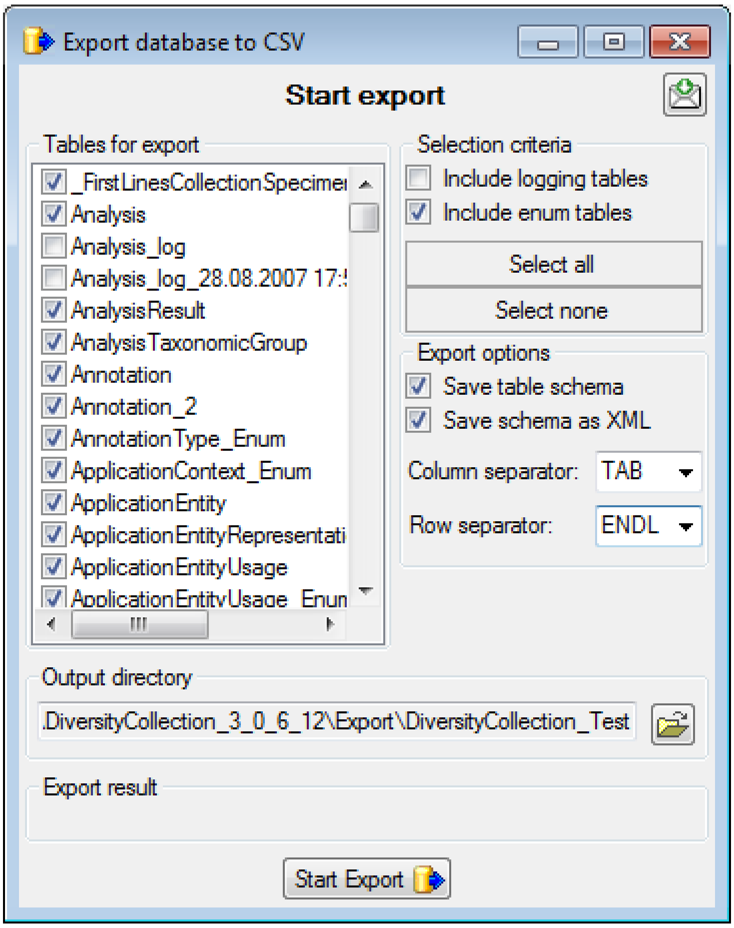
The version will be set automatically. If a data set is changed the version will be increased if the last changes were done by a different user or the last change is more than 24 hours ago (for further details see topic Logging).

Backup

If you want to create a backup of your database, there are 2 options. You may either export the data as csv files to your local computer or you may create a backup on the server.

Export data as csv

To export your data as csv files to your local computer, choose **Data -> Export -> CSV(bcp) ...** from the menu. A window will open as shown below, where you can select the tables that should be exported. Click on the Start Export button to export your data. If you choose the option as shown below 2 files will be created for every table. The first file (*.csv) contains the data while the second file (*.xml) contains the structure of the table.



Tables for export:
- ☑ _FirstLinesCollectionSpecimen
- ☑ Analysis
- ☐ Analysis_log
- ☐ Analysis_log_28.08.2007 17:
- ☑ AnalysisResult
- ☑ AnalysisTaxonomicGroup
- ☑ Annotation
- ☑ Annotation_2
- ☑ AnnotationType_Enum
- ☑ ApplicationContext_Enum
- ☑ ApplicationEntity
- ☑ ApplicationEntityRepresentati
- ☑ ApplicationEntityUsage
- ☑ ApplicationEntityUsage_Enum

Selection criteria:
- ☐ Include logging tables
- ☑ Include enum tables

Export options:
- ☑ Save table schema
- ☑ Save schema as XML

Column separator: TAB

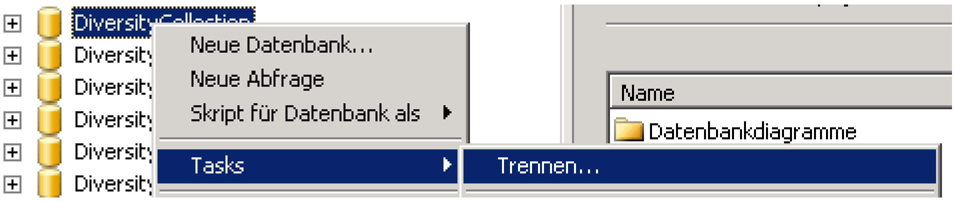
Row separator: ENDL

Output directory: DiversityCollection_3_0_6_12\Export\DiversityCollection_Test

Create backup on the server

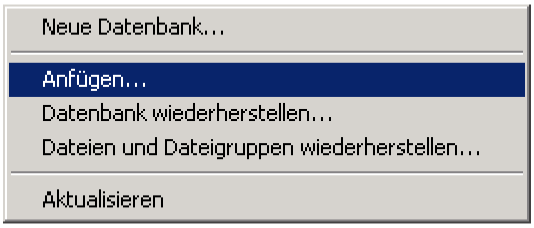
To create a backup of your database on the server, choose **Data -> Backup database** from the menu. This will create a SQL-Server backup on the server where the database is located. Ensure that there is enough space on the server.

Another option is to create a direct copy of the database files on the server. For this you have to use the functions provided by SQL-Server. However, you need administration rights for the database you want to create a backup of. Open the Enterprise Manager for SQL-Server, choose the database and detach it from the server as shown in the image below.



After detaching the database, you can save a copy of the ..._Data.MDF file to keep it as a backup.

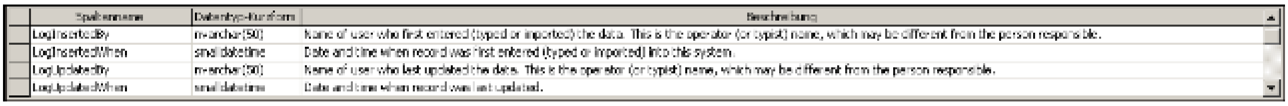
After storing the backup you have to re-attach the database.



A dialog will appear where you have to select the original database file in your directory.

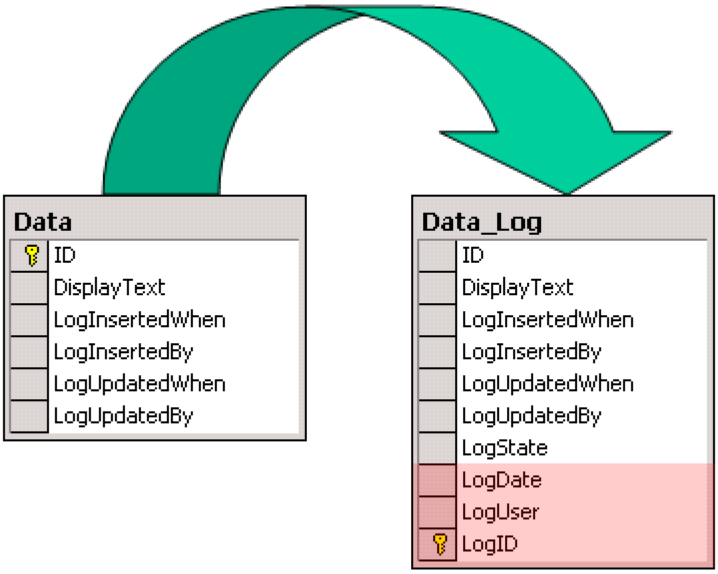
Logging

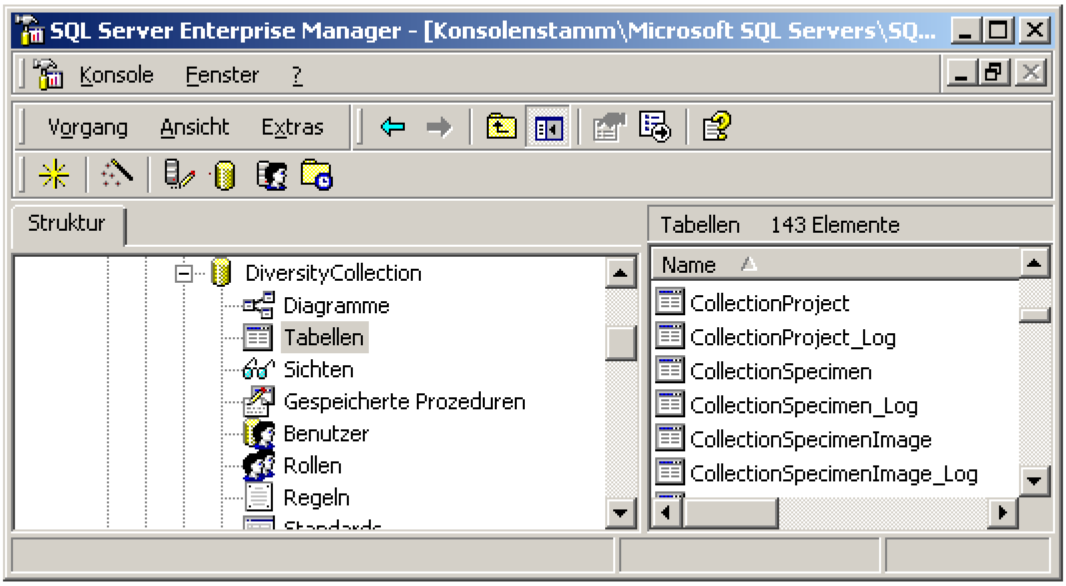
Changes within the database will be documented for each data set together with the time and the responsible user in the columns shown in the image below.



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 orignial data set will be stored in this logging table together with information about by whom and when changes were made last.





Version of data sets

The **Version** of a data set consists of two parts, e.g. 3 / 1 as shown in the header of the specimen in the main form. The first number refers to the version of the data set as stored in table CollectionSpecimen. The second number refers to the version as stored in table CollectionEvent. Both versions will be set to a higher number if the data in the tables themselves or in dependent tables are changed. Thus, if a new identification is inserted in the table Identification the specimen number of the version will increase from 3 to 4 resulting in a version 4 / 1 for the whole data set. The changes in the version will only occur if the last changes in the data were more than **24 hours** ago or a **different user** is changing the data. This ensures that a user can change several parts in a data set within 24 hours and the version will only be increased by 1.

Acc.No. M-0040397

Erysiphe aquilegiae var. ranunculi (Grev.) U. Braun

ID (Specimen / Event) 135548 / 211558

Version 3 / 1

The data is stored in the tables CollectionSpecimen and CollectionEvent.

Database - Application tables

Information concerning the predefined queries for users are stored in the table shown in the diagram below.

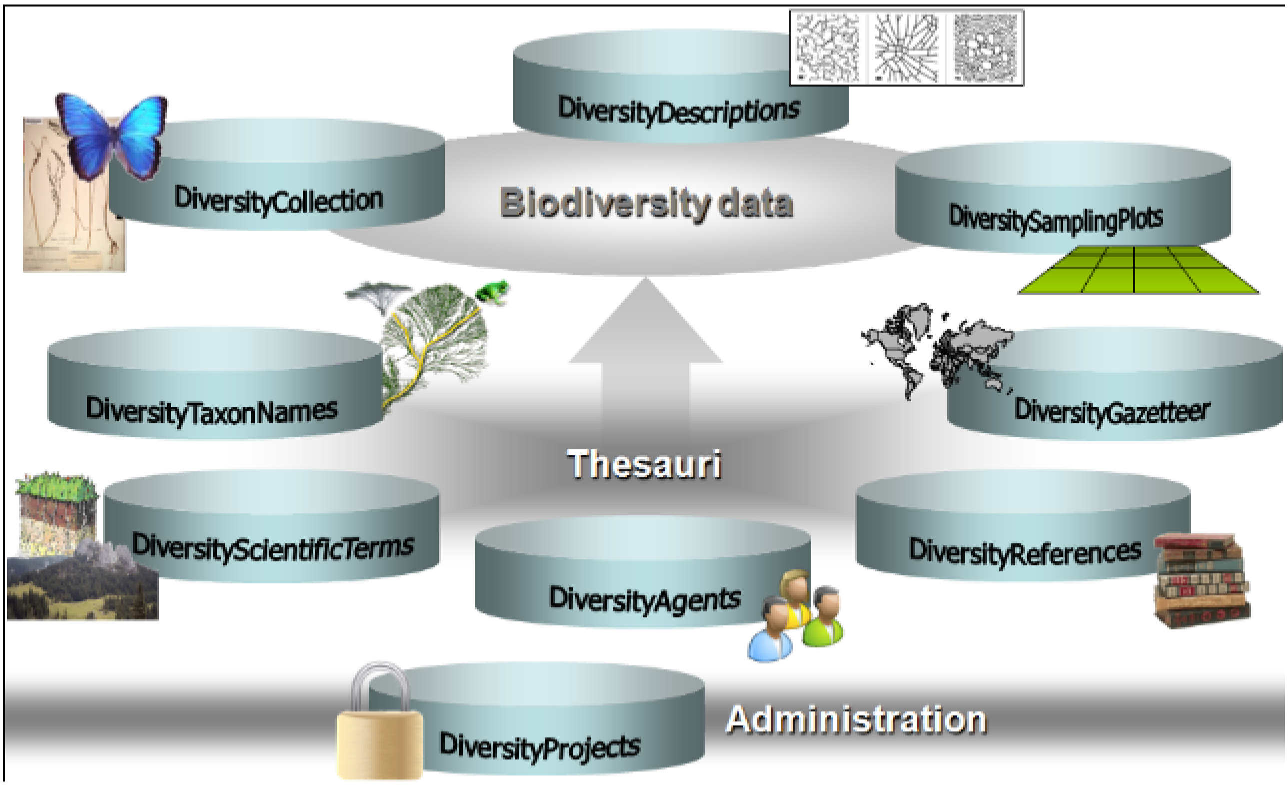
Table ApplicationSearchSelectionStrings

Selection strings for customized queries for users

Column	Data type	Description
UserName	varchar (50)	Name of the user who created this SQL string *Default value: user_name()*
SQLStringIdentifier	varchar (50)	Identifier for the selection string as shown in a user interface
ItemTable	varchar (50)	Main table from which the data sets should be selected *Default value: 'TaxonName'*
SQLString	varchar (MAX)	SQL string for selecting data sets from the database
Description	nvarchar (MAX)	Description of the results set and the purpose of the query
LogCreatedWhen	datetime	Point in time when this data set was created *Default value: getdate()*
LogCreatedBy	nvarchar (50)	Name of the creator of this data set *Default value: user_name()*
LogUpdatedWhen	datetime	Point in time when this data set was updated last *Default value: getdate()*
LogUpdatedBy	nvarchar (50)	Name of the person to update this data set last *Default value: user_name()*

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. DiversityCollection can link data to the modules DiversityExsiccatae, DiversityGazetteer, DiversityScientificTerms, DiversityTaxonNames, DiversityAgents and DiversityReferences as illustrated in the image below.



The modules communicate with each other to provide their services for the other modules.

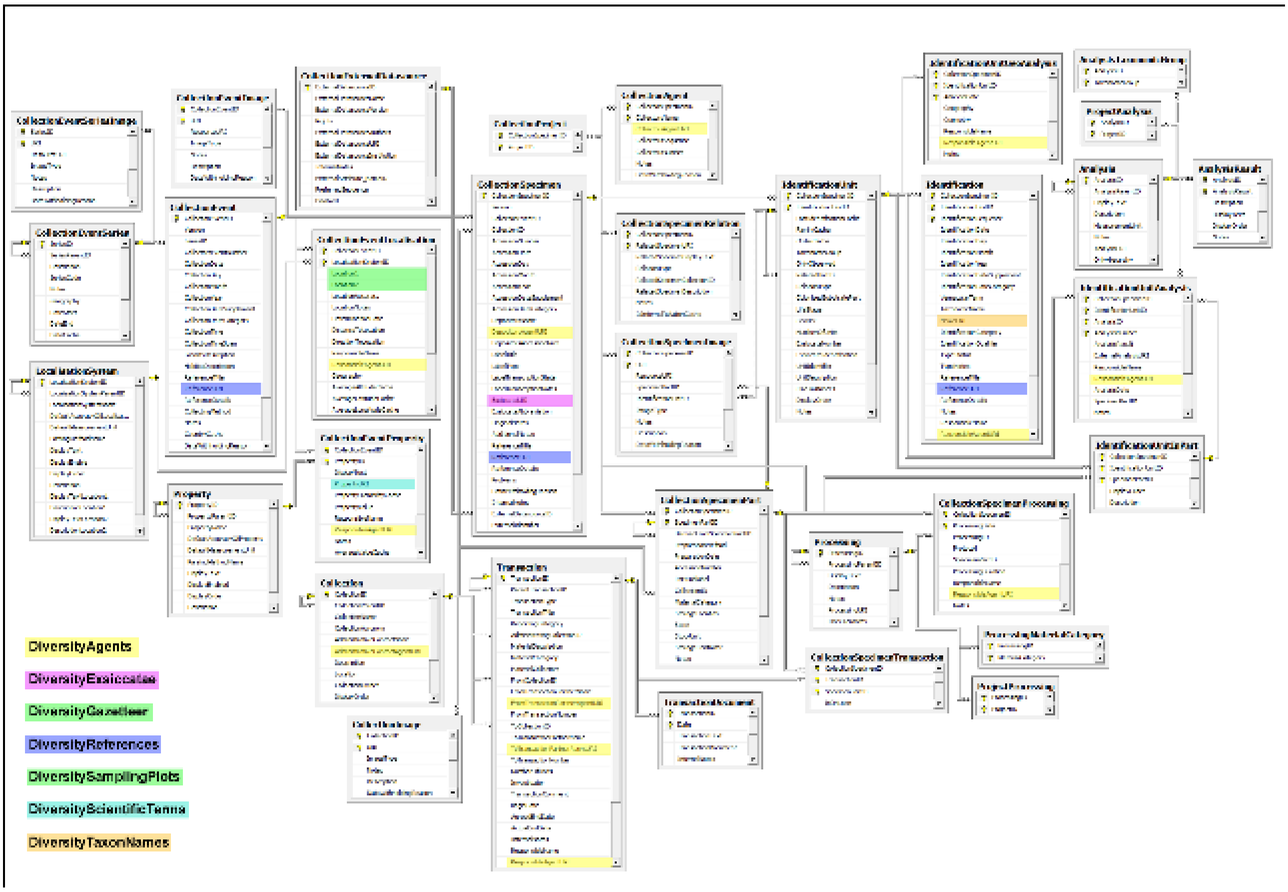
Modules

The DiversityWorkbench 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. their addresses
DiversityCollection	Administration of the scientific collections and specimens within these collections
DiversityExsiccatae	Administration of exsiccatal series
DiversityGazetteer	A data collection to enable the linking of geographical records with the Getty Thesaurus of Geographical Names (TGN), the Germ geographical names
DiversityScientificTerms	Data collections of scientific terms from foreign sources like vegetation, stratigraphy, soil science etc.
DiversityReferences	Administration of references
DiversityTaxonNames	Administration of taxonomic names, their synonyms and hier archical position

Each module provides services for the other modules. To use the service of a module you require access to the database of the module and optionally the module application placed in your application directory.

In the figure shown below the connections to other modules within DiversityCollection are indicated.


CollectionEventSeriesImage
CollectionEventImage
CollectionExternalDatasource
CollectionProject
CollectionAgent
IdentificationUnitGeoAnalysis
AnalysisTaxonomicGroup
ProjectAnalysis
Analysis
AnalysisResult
CollectionEventSeries
CollectionEvent
CollectionEventLocalisation
CollectionSpecimen
CollectionSpecimenRelation
IdentificationUnit
Identification
IdentificationUnitAnalysis
LocalisationSystem
CollectionSpecimenImage
CollectionEventProperty
Property
IdentificationUnitInPart
CollectionSpecimenPart
CollectionSpecimenProcessing
Processing
Collection
Transaction
ProcessingMaterialCategory
CollectionSpecimenTransaction
CollectionImage
TransactionDocument
ProjectProcessing
DiversityAgents
DiversityExsiccatae
DiversityGazetteer
DiversityReferences
DiversitySamplingPlots
DiversityScientificTerms
DiversityTaxonNames

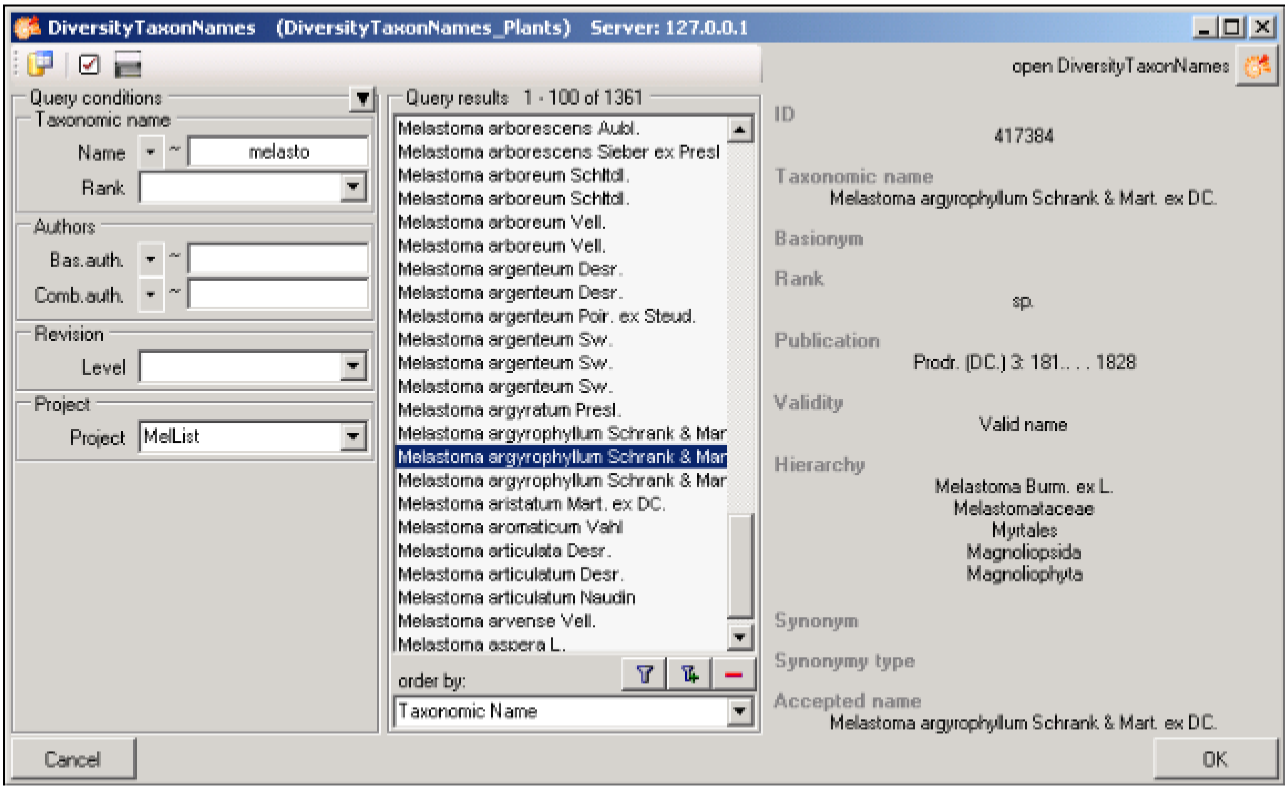
Module related entry

The DiversityWorkbench 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 3 states of this interface:

1 - the value is only set in the local database with no connection to the remote module

Tax.name: Melastoma argyrophyllum Schrank & Mart. ex DC.

In this state you may either type the value or select it from the values which 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 wish 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_Plants) Server: 127.0.0.1

open DiversityTaxonNames

Query conditions

Taxonomic name

Name ~ melasto

Rank

Authors

Bas.auth. ~

Comb.auth. ~

Revision

Level

Project

Project: MelList

Query results 1 - 100 of 1361

- Melastoma arborescens Aubl.
- Melastoma arborescens Sieber ex Presl
- Melastoma arboreum Schltdl.
- Melastoma arboreum Schltdl.
- Melastoma arboreum Vell.
- Melastoma arboreum Vell.
- Melastoma argenteum Desr.
- Melastoma argenteum Desr.
- Melastoma argenteum Poir. ex Steud.
- Melastoma argenteum Sw.
- Melastoma argenteum Sw.
- Melastoma argenteum Sw.
- Melastoma argyratum Presl.
- Melastoma argyrophyllum Schrank & Mar
- Melastoma argyrophyllum Schrank & Mar
- Melastoma argyrophyllum Schrank & Mar
- Melastoma aristatum Mart. ex DC.
- Melastoma aromaticum Vahl
- Melastoma articulata Desr.
- Melastoma articulatum Desr.
- Melastoma articulatum Naudin
- Melastoma arvense Vell.
- Melastoma aspera L.

order by: Taxonomic Name

ID: 417384

Taxonomic name: Melastoma argyrophyllum Schrank & Mart. ex DC.

Basionym

Rank: sp.

Publication: Prodr. (DC.) 3: 181... 1828

Validity: Valid name

Hierarchy:
Melastoma Burm. ex L.
Melastomataceae
Myrtales
Magnoliopsida
Magnoliophyta

Synonym

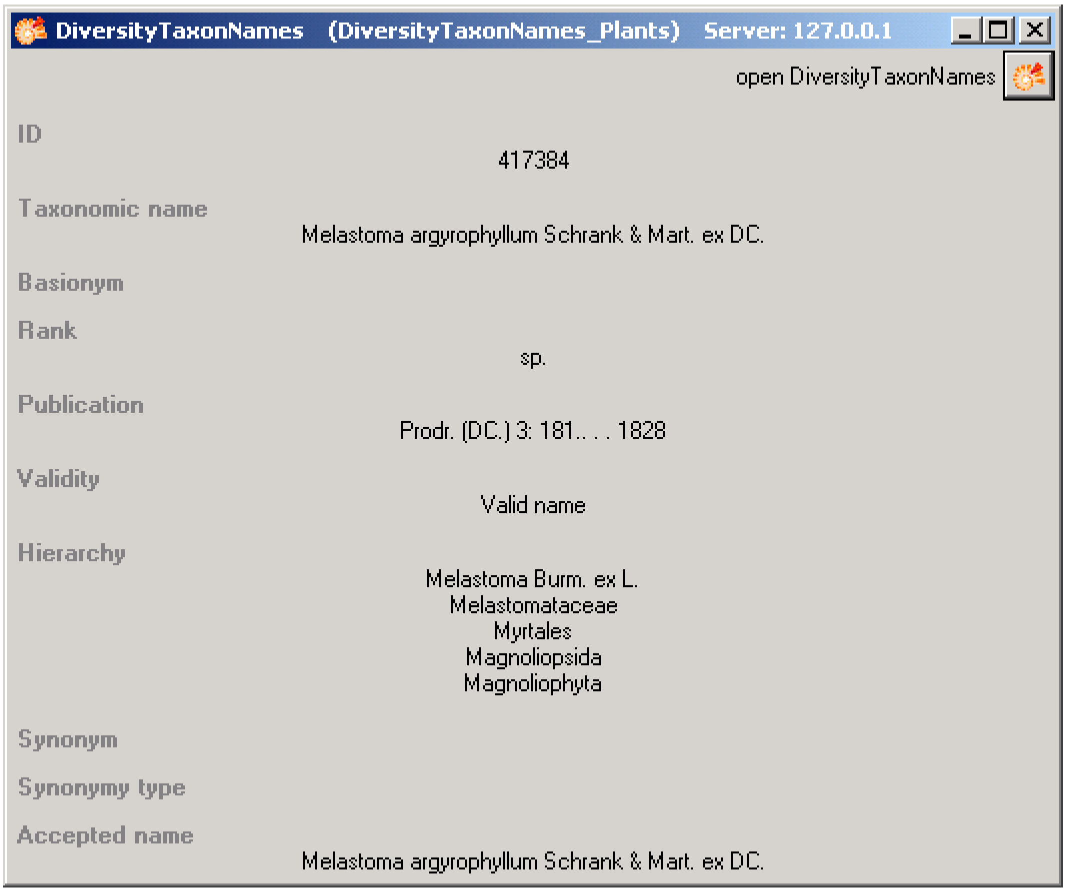
Synonymy type

Accepted name: Melastoma argyrophyllum Schrank & Mart. ex DC.

2 - the value is related to the remote module

Tax.name: Melastoma argyrophyllum Schrank & Mart. ex DC.

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 require further information on the value, click on the button. This will open a form showing an overview of the related value.



ID
417384

Taxonomic name
Melastoma argyrophyllum Schrank & Mart. ex DC.

Basionym

Rank
sp.

Publication
Prodr. (DC.) 3: 181.. . . 1828

Validity
Valid name

Hierarchy
Melastoma Burm. ex L.
Melastomataceae
Myrtales
Magnoliopsida
Magnoliophyta

Synonym

Synonymy type

Accepted name
Melastoma argyrophyllum Schrank & Mart. ex DC.

If the client application of the module is available, you may inspect the details of the entry. To start the client application of the remote module simply click on the button.

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 DiversityWorkbench, a window will open where you are able to choose from either DiversityWorkbench modules or external Webservices. See Webservice for further details

Reference

Details about References are stored in the module DiversityReferences. You may choose one of the entries in this module from the picklist. To directly change to DiversityReferences click on .

For access to the references from other modules you require the application **DiversityReferences.exe** in your application directory. To use the application DiversityReferences.exe you require access to the database DiversityReferences. For more information see the DiversityWorkbench Portal.

Webservice - foreign sources

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 Index Fungorum. To establish a connection to an external webservice click on the button. A window will open where you may choose from either DiversityWorkbench modules or external Webservices. The provided webservices currently are:

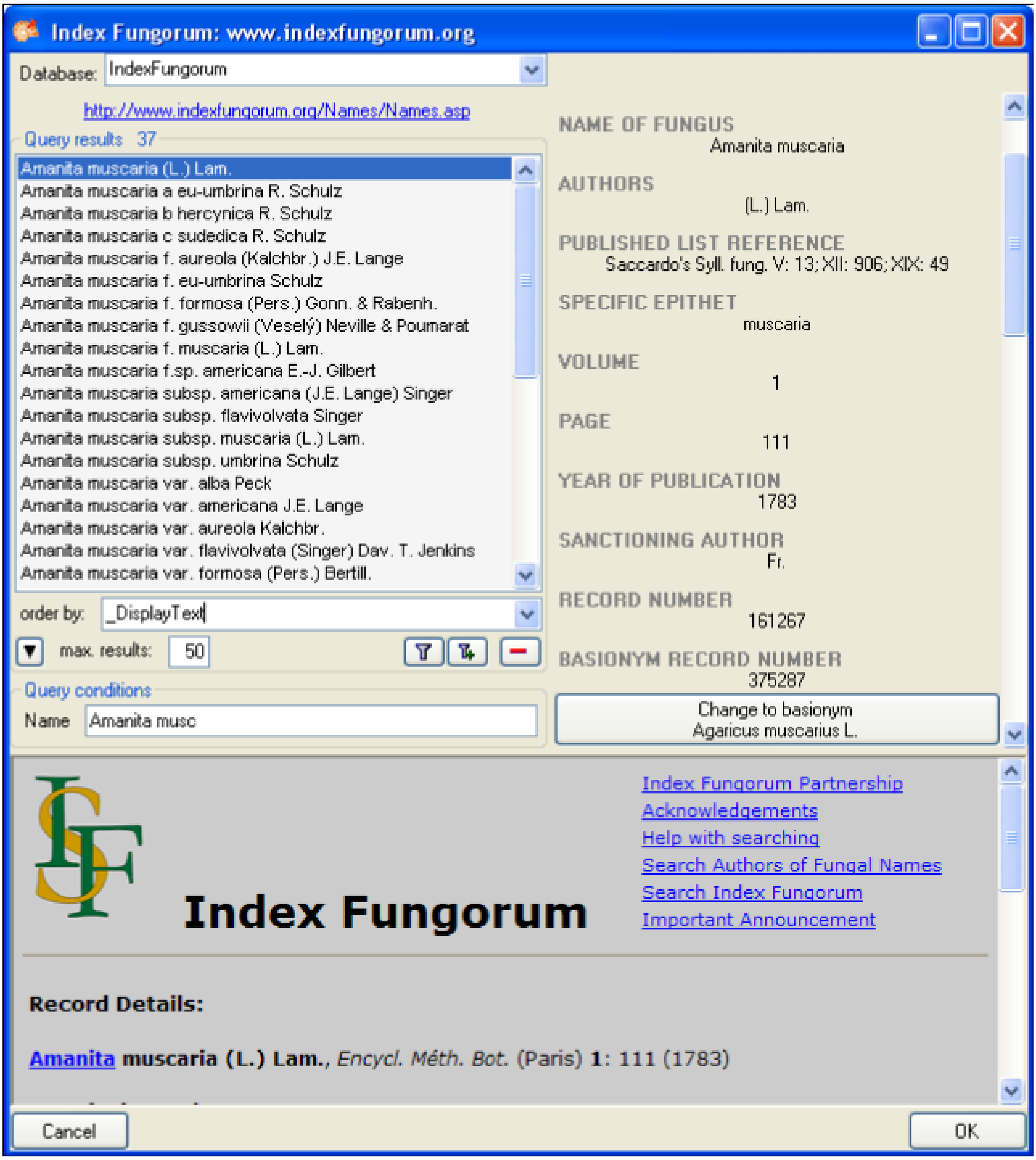
Index Fungorum

The Palaeontology Database

The Catalogue of Life

Index Fungorum - 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 Index Fungorum. To establish a connection to this webservice, click on the button. A window will open where you may choose Index Fungorum from the database list (see below).



Index Fungorum: www.indexfungorum.org

Database: IndexFungorum

http://www.indexfungorum.org/Names/Names.asp

Query results 37

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. eu-umbrina Schulz
Amanita muscaria f. formosa (Pers.) Gonn. & Rabenh.
Amanita muscaria f. gussowii (Veselý) Neville & Poumarat
Amanita muscaria f. muscaria (L.) Lam.
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 Schulz
Amanita muscaria var. alba Peck
Amanita muscaria var. americana J.E. Lange
Amanita muscaria var. aureola Kalchbr.
Amanita muscaria var. flavivolvata (Singer) Dav. T. Jenkins
Amanita muscaria var. formosa (Pers.) Bertill.

order by: _DisplayText

max. results: 50

Query conditions

Name: Amanita musc

NAME OF FUNGUS: Amanita muscaria

AUTHORS: (L.) Lam.

PUBLISHED LIST REFERENCE: Saccardo's Syll. fung. V: 13; XII: 906; XIX: 49

SPECIFIC EPITHET: muscaria

VOLUME: 1

PAGE: 111

YEAR OF PUBLICATION: 1783

SANCTIONING AUTHOR: Fr.

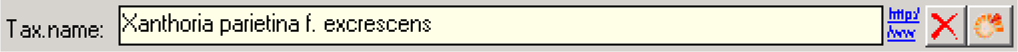
RECORD NUMBER: 161267

BASIONYM RECORD NUMBER: 375287

Record Details:

Amanita muscaria (L.) Lam., *Encycl. Méth. Bot.* (Paris) 1: 111 (1783)

Enter the query restriction for the name in the **Name** field in Query conditions. The maximum number of records you receive may be set in the max. results field max. results: 50 (choose a low number, if you have a slow connection to the internet). 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. 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 wish to change to one of these related data sets from 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.



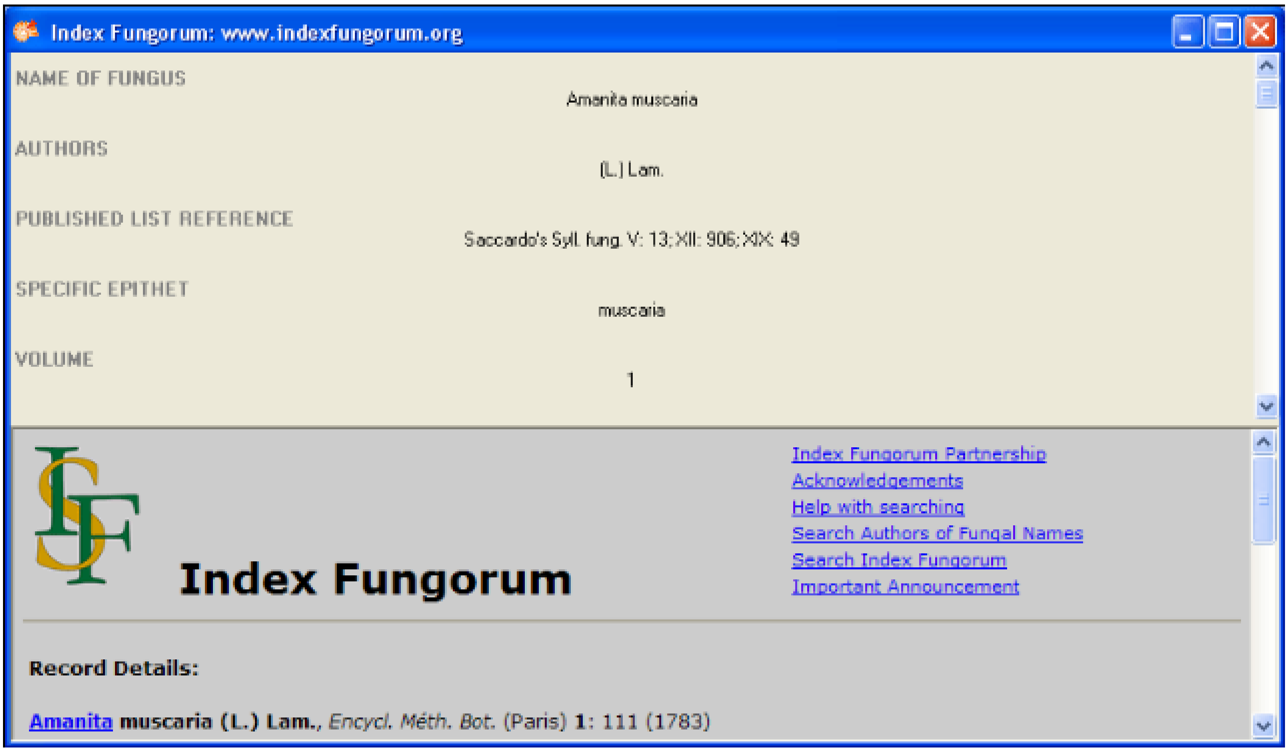
Tax.name: Xanthoria parietina f. excrescens

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 Xanthoria parietina f. excrescens

http://www.indexfungorum.org/IXFWebService/Fungus.asmx/NameByKeyRDF?NameLsid=416173

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.



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
VOLUME	1

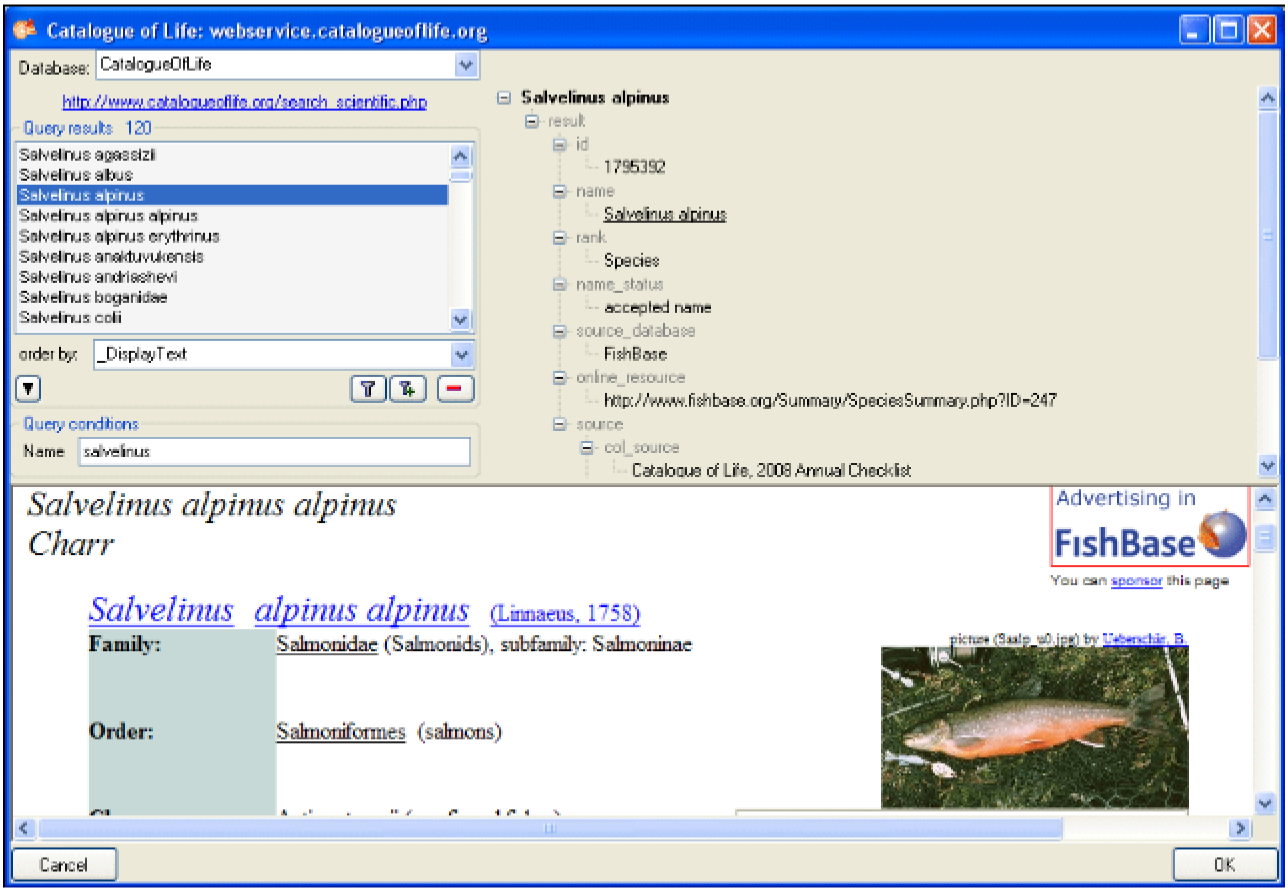
Record Details:

Amanita muscaria (L.) Lam., *Encycl. Méth. Bot.* (Paris) **1**: 111 (1783)

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.

Catalogue of Life - webservice

DiversityWorkbench provides the possibility to link your data to an external webservice. The webservice provided by the Catalogue of Life is possible through the module DiversityTaxonNames. To establish a connection to this external webservice click on the button. A window will open where you may choose this webservice (see below).



Catalogue of Life: webservice.catalogueoflife.org

Database: CatalogueOfLife

http://www.catalogueoflife.org/search_scientific.php

Query results 120

Salvelinus agassizii
Salvelinus albus
Salvelinus alpinus
Salvelinus alpinus alpinus
Salvelinus alpinus erythrinus
Salvelinus anaktuvukensis
Salvelinus andriashevi
Salvelinus boganidae
Salvelinus colii

order by: _DisplayText

Query conditions

Name: salvelinus

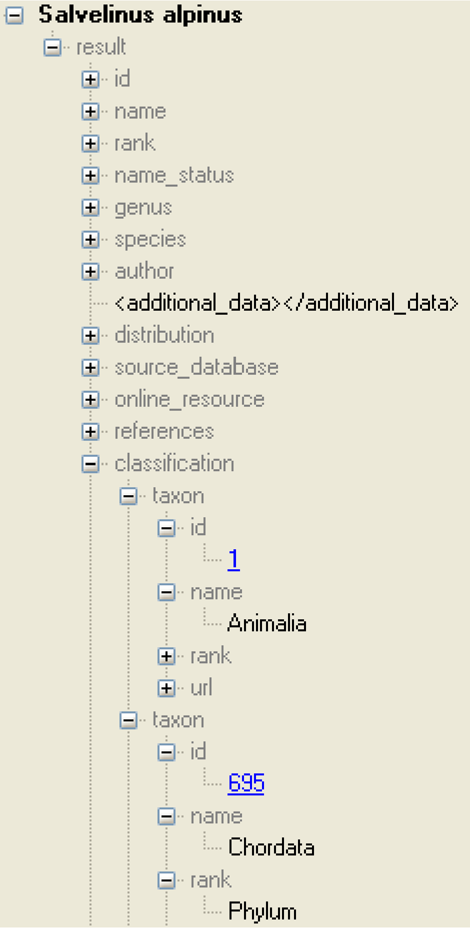
```
Salvelinus alpinus
  result
    id
      1795392
    name
      Salvelinus alpinus
    rank
      Species
    name_status
      accepted name
    source_database
      FishBase
    online_resource
      http://www.fishbase.org/Summary/SpeciesSummary.php?ID=247
    source
      col_source
        Catalogue of Life, 2008 Annual Checklist
```

Salvelinus alpinus alpinus
Charr

Salvelinus alpinus alpinus (Linnaeus, 1758)

Family:	Salmonidae (Salmonids), subfamily: Salmoninae
Order:	Salmoniformes (salmons)

In the field **Name** in Query conditions enter your 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.

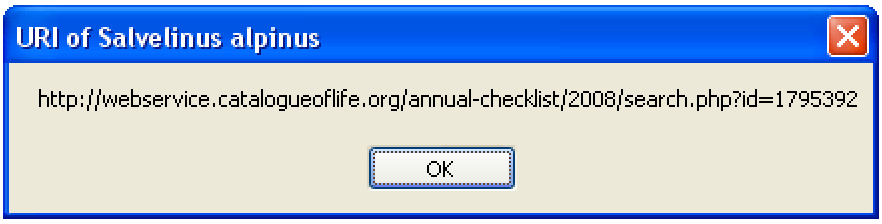


```
⊟ Salvelinus alpinus
  ⊟ result
    ⊞ id
    ⊞ name
    ⊞ rank
    ⊞ name_status
    ⊞ genus
    ⊞ species
    ⊞ author
      <additional_data></additional_data>
    ⊞ distribution
    ⊞ source_database
    ⊞ online_resource
    ⊞ references
    ⊟ classification
      ⊟ taxon
        ⊟ id
            1
        ⊟ name
            Animalia
        ⊞ rank
        ⊞ url
      ⊟ taxon
        ⊟ id
            695
        ⊟ name
            Chordata
        ⊟ rank
            Phylum
```

For higher taxa and 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 - in the example above ID: 695 . To include 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.

Tax.name: Salvelinus alpinus

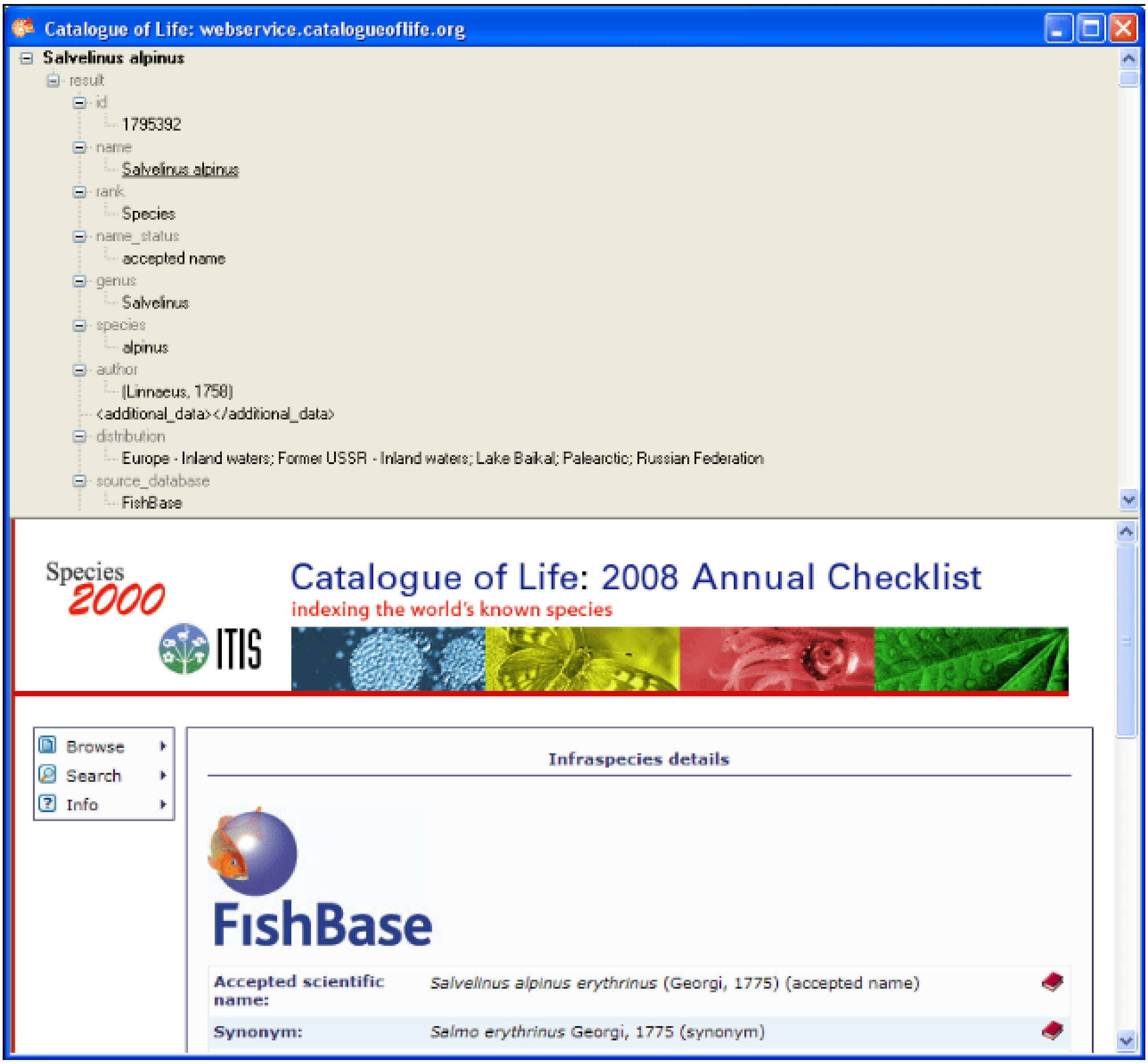
If you double-click on the link area, a window will open providing you with the retrieval information of the webservice.



URI of Salvelinus alpinus

http://webservice.catalogueoflife.org/annual-checklist/2008/search.php?id=1795392

To receive the information related to an entry as provided by the webservice click on the button. A window will open as shown below where information on the webservice is listed in the upper part. If available, additional information provided on a corresponding website will be shown in the lower part.



```
⊟ Salvelinus alpinus
   ⊟ result
      ⊟ id
         1795392
      ⊟ name
         Salvelinus alpinus
      ⊟ rank
         Species
      ⊟ name_status
         accepted name
      ⊟ genus
         Salvelinus
      ⊟ species
         alpinus
      ⊟ author
         (Linnaeus, 1758)
      <additional_data></additional_data>
      ⊟ distribution
         Europe - Inland waters; Former USSR - Inland waters; Lake Baikal; Palearctic; Russian Federation
      ⊟ source_database
         FishBase
```

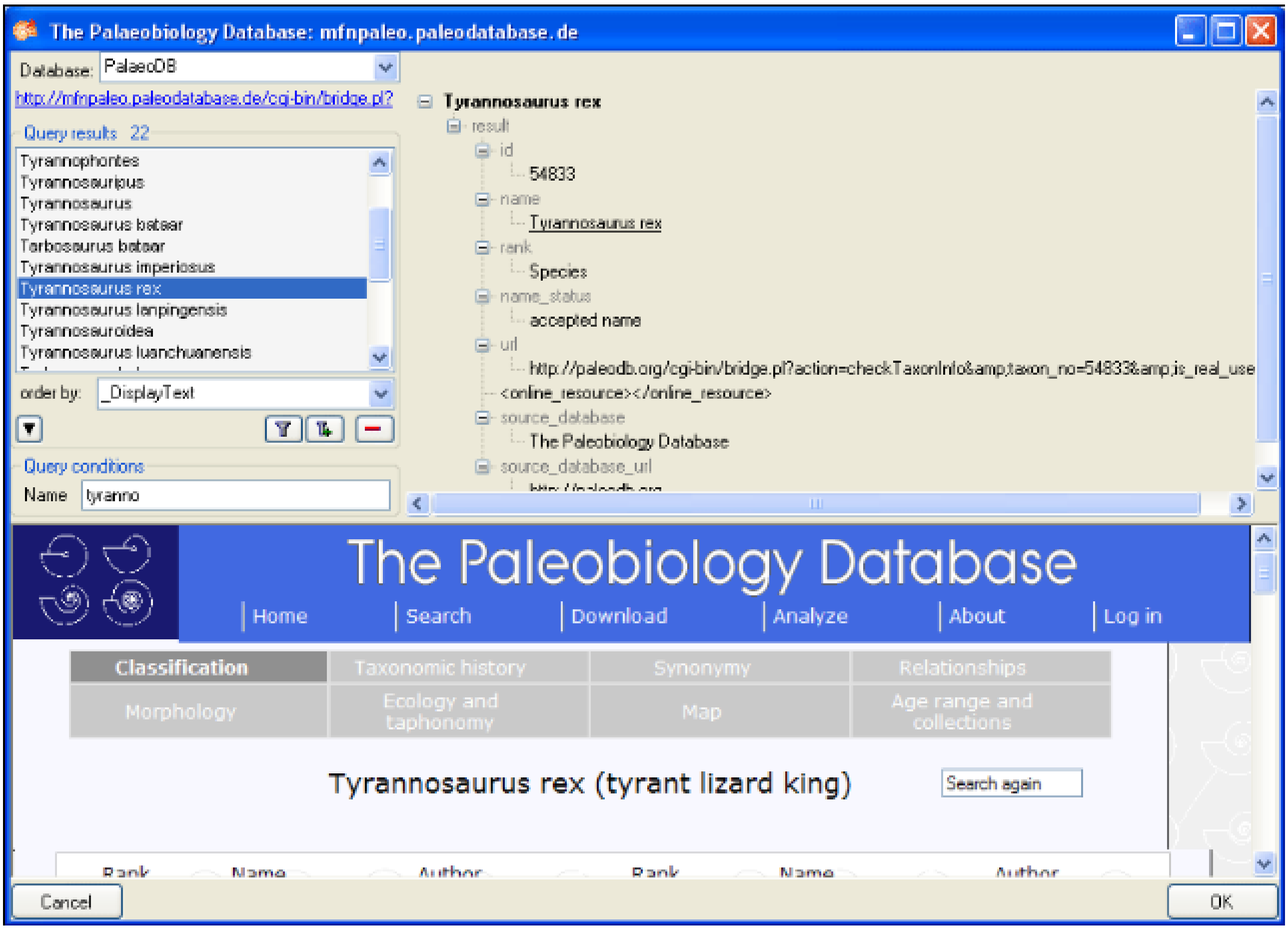
Infraspecies details

Accepted scientific name:	*Salvelinus alpinus erythrinus* (Georgi, 1775) (accepted name)
Synonym:	*Salmo erythrinus* Georgi, 1775 (synonym)

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

DiversityWorkbench provides the possibility to link your data to an external webservice. The webservice provided by the [Palaeontology Database]() is possible through the module DiversityTaxonNames. To establish a connection to this external webservice click on the button. A window will open where you may choose this webservice (see below).



The Palaeobiology Database: mfnpaleo.paleodatabase.de

Database: PalaeoDB

http://mfnpaleo.paleodatabase.de/cgi-bin/bridge.pl?

Query results 22

- Tyrannophontes
- Tyrannosauripus
- Tyrannosaurus
- Tyrannosaurus bataar
- Tarbosaurus bataar
- Tyrannosaurus imperiosus
- Tyrannosaurus rex
- Tyrannosaurus lanpingensis
- Tyrannosauroidea
- Tyrannosaurus luanchuanensis

order by: _DisplayText

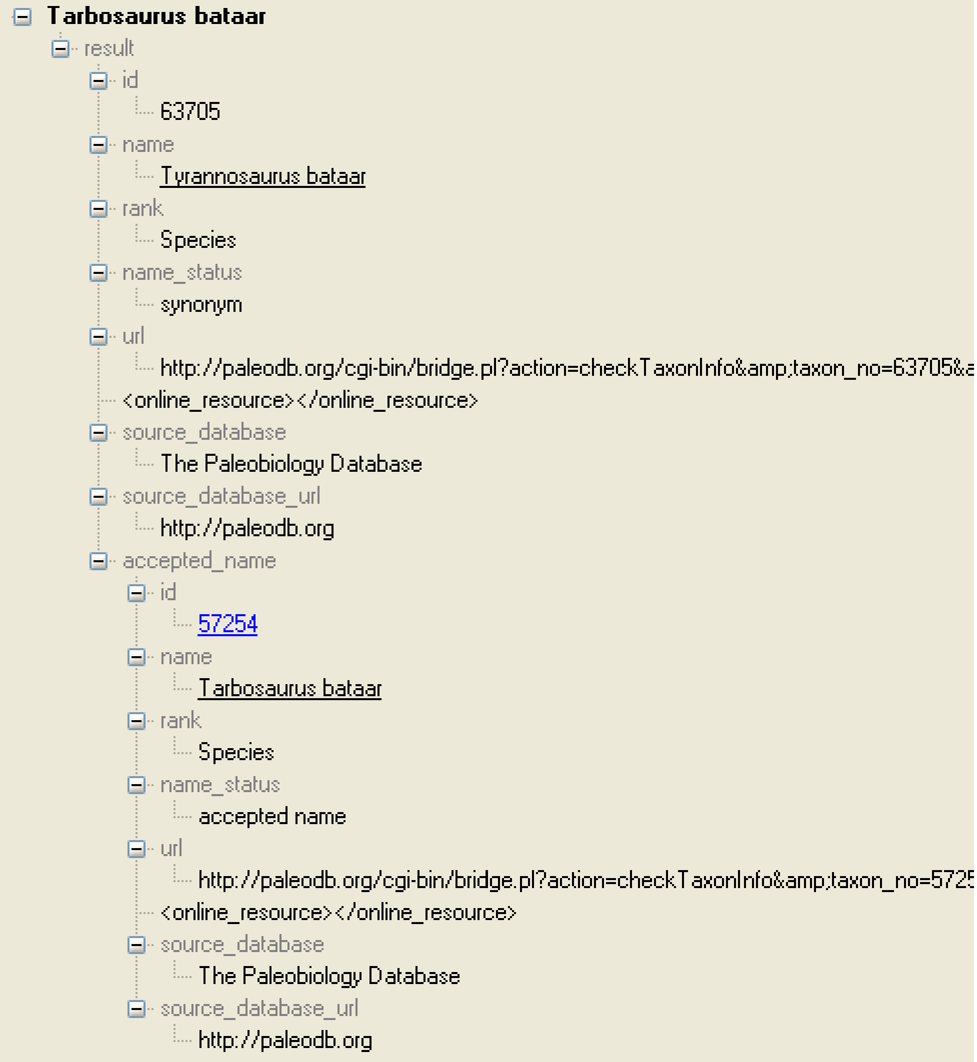
Query conditions

Name: tyranno

```
⊟ Tyrannosaurus rex
  ⊟ result
    ⊟ id
        54833
    ⊟ name
        Tyrannosaurus rex
    ⊟ rank
        Species
    ⊟ name_status
        accepted name
    ⊟ url
        http://paleodb.org/cgi-bin/bridge.pl?action=checkTaxonInfo&amp;taxon_no=54833&amp;is_real_use
      <online_resource></online_resource>
    ⊟ source_database
        The Paleobiology Database
    ⊟ source_database_url
```

Tyrannosaurus rex (tyrant lizard king)

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.



```
Tarbosaurus bataar
  result
    id
      63705
    name
      Tyrannosaurus bataar
    rank
      Species
    name_status
      synonym
    url
      http://paleodb.org/cgi-bin/bridge.pl?action=checkTaxonInfo&amp;taxon_no=63705&a
    <online_resource></online_resource>
    source_database
      The Paleobiology Database
    source_database_url
      http://paleodb.org
    accepted_name
      id
        57254
      name
        Tarbosaurus bataar
      rank
        Species
      name_status
        accepted name
      url
        http://paleodb.org/cgi-bin/bridge.pl?action=checkTaxonInfo&amp;taxon_no=5725
      <online_resource></online_resource>
      source_database
        The Paleobiology Database
      source_database_url
        http://paleodb.org
```

For synonyms the accepted name will be shown as well as shown above. To change to the accepted name click on the linked entry of the ID - in the example above ID: 57254. To include 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.

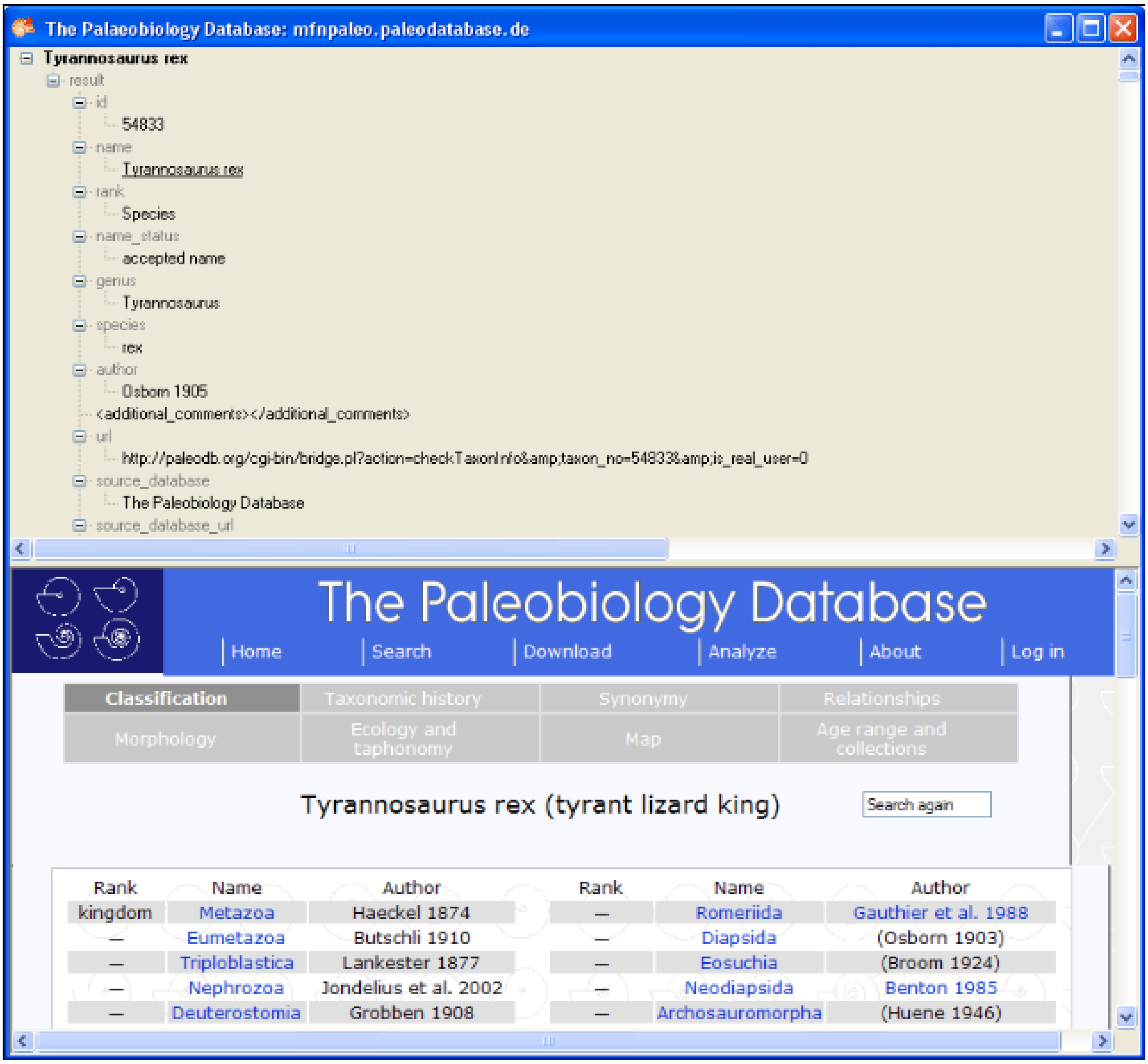
Tax.name: Tarbosaurus bataar

If you double-click on the link area, a window will open providing you with the retrieval information of the webservice.

URI of Tarbosaurus bataar

http://mfnpaleo.paleodatabase.de/cgi-bin/bridge.pl?action=getTaxonomyXML&id=57254

To receive the information related to an entry as provided by the webservice click on the button. A window will open as shown below where information on the webservice is listed in the upper part. If available, additional information provided on a corresponding website will be shown in the lower part.



```
Tyrannosaurus rex
  result
    id
      54833
    name
      Tyrannosaurus rex
    rank
      Species
    name_status
      accepted name
    genus
      Tyrannosaurus
    species
      rex
    author
      Osborn 1905
    <additional_comments></additional_comments>
    url
      http://paleodb.org/cgi-bin/bridge.pl?action=checkTaxonInfo&amp;taxon_no=54833&amp;is_real_user=0
    source_database
      The Paleobiology Database
    source_database_url
```

Tyrannosaurus rex (tyrant lizard king)

Rank	Name	Author	Rank	Name	Author
kingdom	Metazoa	Haeckel 1874	—	Romeriida	Gauthier et al. 1988
—	Eumetazoa	Butschli 1910	—	Diapsida	(Osborn 1903)
—	Triploblastica	Lankester 1877	—	Eosuchia	(Broom 1924)
—	Nephrozoa	Jondelius et al. 2002	—	Neodiapsida	Benton 1985
—	Deuterostomia	Grobben 1908	—	Archosauromorpha	(Huene 1946)

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.