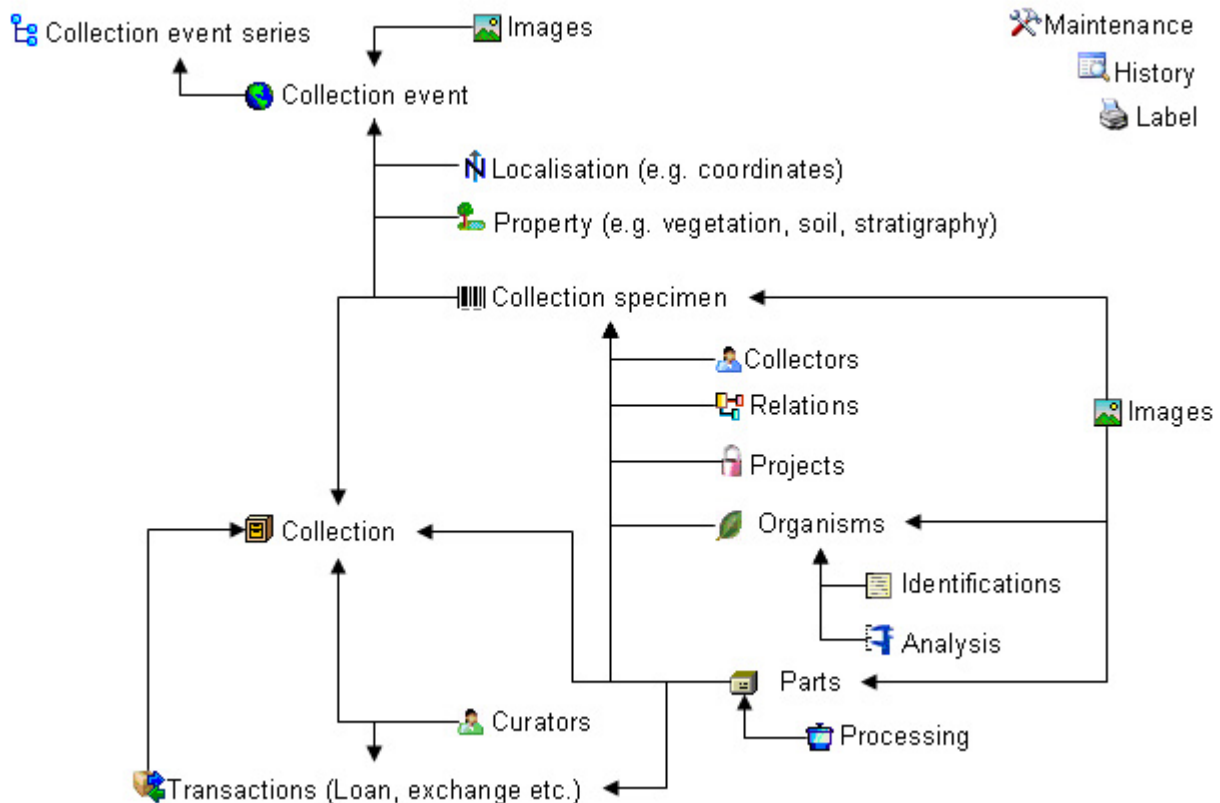























DiversityCollection

DiversityCollection (Version 2) is part of the database framework [Diversity Workbench](#). 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 [Diversity Workbench](#). DiversityCollection might also be used as a stand-alone application.

The image below gives you an overview of the main parts, relations and functions of DiversityCollection

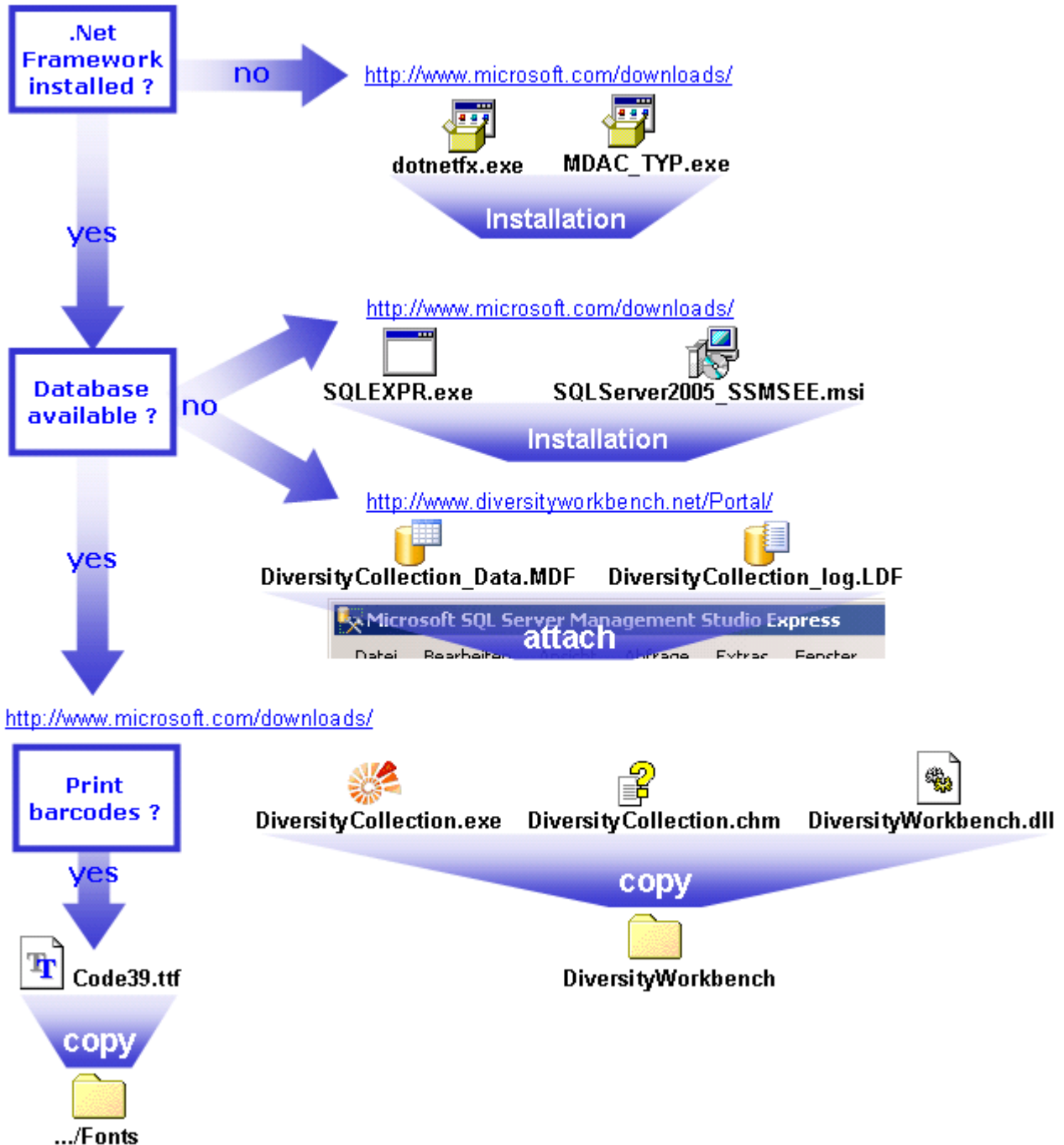


The image below gives an overview for some typical data depicted in DiversityCollection together with the symbols used throughout the program. A typical specimen  may have been collected at a collection event  during an expedition . The site of the collection event may be localized  and characterized . 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 curator  sent some of the samples  to another collection. The samples were collected as part of a project . Certain parts were cultivated , analysed  and processed . The organisms on specimen were identified  several times. Images  were taken for the event series, the collection event, the collection specimen as well as organisms and part of this specimen.

Installation


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


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




Database

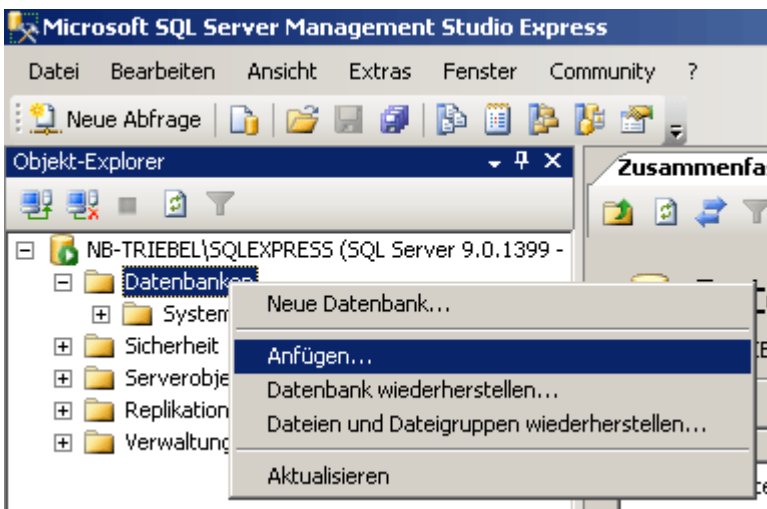
DiversityCollection uses Microsoft SQL-Server 2005 as database engine. If you do not have a database server with DiversityCollection already available, you have to install the database engine first. Download the free version of Microsoft SQL Server Express

(SQLEXPRESS.exe  resp. the version of your preferred language, e.g. SQLEXPRESS_DE.exe) and

Microsoft SQL Server Management Studio Express (SQLServer2005_SSMSEE.msi ) 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/> and copy them into your database directory. You have to attach the database to the database engine using the Microsoft SQL Server Management Studio Express. In the **Object-Explorer** select databases and choose attach from the context menu as shown below.




A form will open where you can choose the file DiversityCollection_Data.MDF and attach it to the database engine.

Client




The client is based on the .Net framework from Microsoft. If not already present, you have to install the following components first:

Microsoft .NET Framework Version 2.0. Download (dotnetfx.exe ) , start the program and follow the installation instructions.

Microsoft Data Access Components (MDAC) 2.8. Download (MDAC_TYP.exe ) , start the program and follow the installation instructions.

(see <http://www.microsoft.com/downloads/> for the latest versions)

Download the files for DiversityCollection from <http://www.diversityworkbench.net/Portal/>



Copy all files (DiversityCollection.exe , DiversityCollection.chm , DiversityWorkbench.dll ) into your DiversityWorkbench directory. To print barcodes of the font Code 39(Code39.ttf ) must be copied to the folder C:\WINNT\Fonts.

After the installation make shure to get the latest updates from <http://v4.windowsupdate.microsoft.com/>.


Menu

Overview of the menu in DiversityCollection



Connection

-  **Database** Choose one of the databases available on the server. Only those databases will be listed to which the user has access permission
-  **Transfer previous settings** Transfer the settings of a previous version
- Quit** Quit the application and stop all processes started by the application












Query

- Show query** Show or hide the query list
- Predefined queries** Under this menu entry all predefined queries will be listed
-  **Scan mode** Change to the scan mode to open the dataset of a specimen by scanning the barcode



Data

-  **Import**
 - Specimen scans ...** Import scans of specimen labels
 - Import list ...** Import tab-separated lists
-  **Export**
 - Export list ...** Export a tabulator separated file with the data of the specimen
 - XML ...** Export data as a XML-file according to ABCD


Administration

-  **Analysis ...** Administration of the analysis methods used for the specimens
-  **Collections ...** Administration used for the collections
-  **Maintenance ...** Maintenance of database entries especially if connected to other modules
-  **Material categories ...** Administration of the material categories that should be visible when creating a new part for a specimen
-  **Processing ...** Administration of the processing procedures applied in the collection
-  **Queries ...** Creating and editing predefined queries
-  **Taxonomic groups ...** Administration of the taxonomic groups that should be visible for creating a new identification unit
-  **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
-  **User ...** Administration of the user and their permissions in the database.
-  **Curators ...** Administration of the curators, responsible for the administration of the transactions

Help

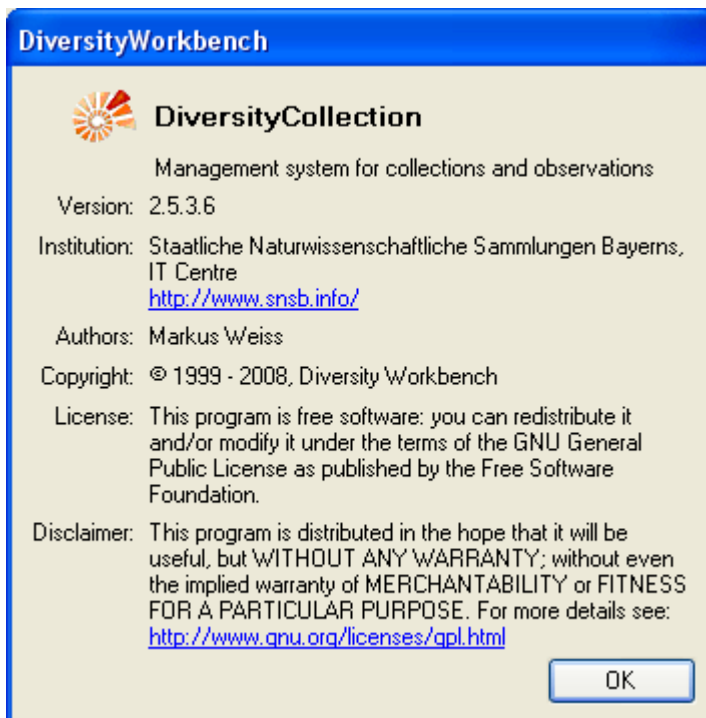
-  **Manual** Opens the online manual
- Info** Show the version and corresponding information
-  **Feedback ...** Opens a form for sending feedback

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 to any topic in the application DiversityCollection and open this manual, just click on the field you need information about and press F1.

Version

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



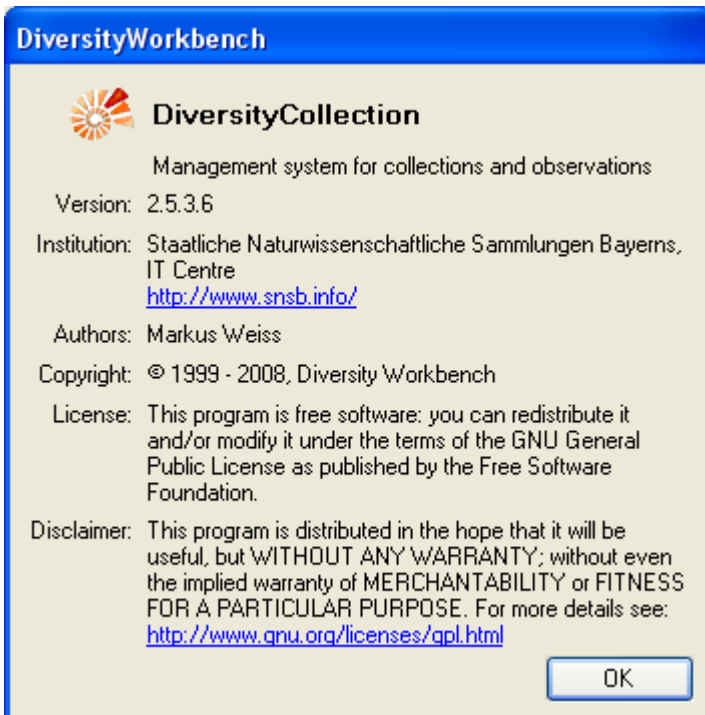
The current version in the example above is 2.5.3.6

License

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

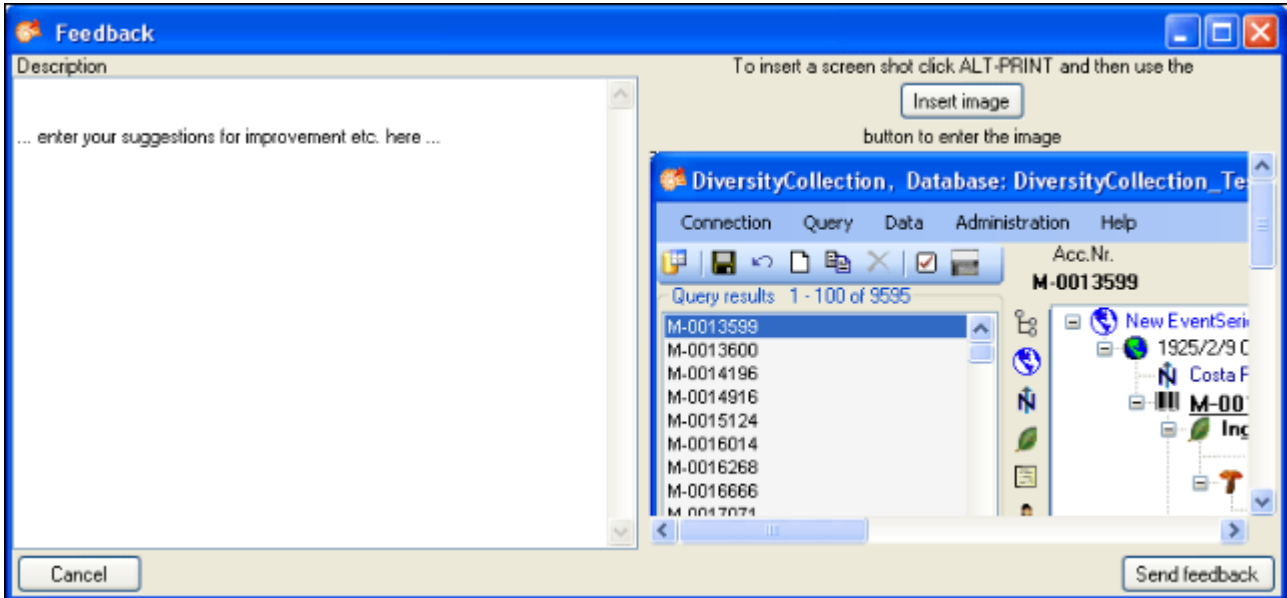



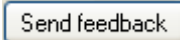
The client software is free software: you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation.

The client software 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. See the [GNU General Public License \(GPL\)](#) for more details.

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 form as shown below.



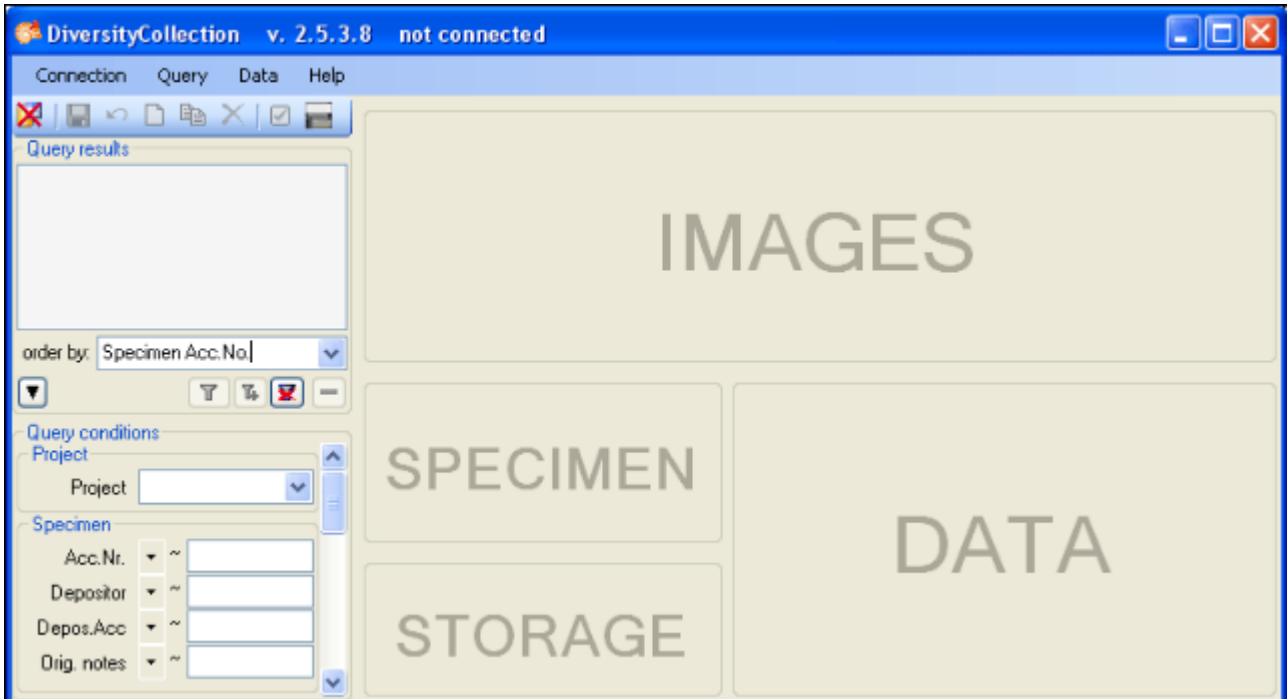
Click on the  button to insert the screen shot and give a comment about your problem. Then click on the  button to send your feedback to the administrator.


Error logging

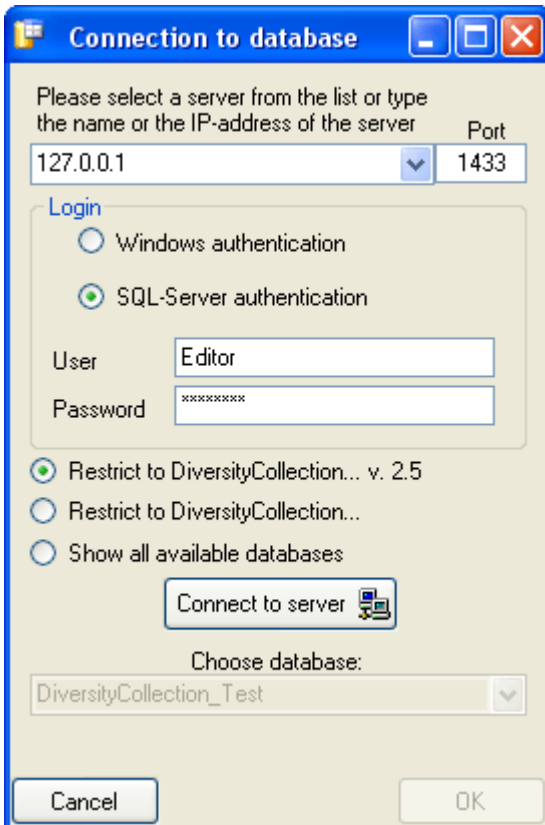
If any error messages show up through working with the application you can find further details concerning the part of the application where the error occurred and the parameters involved in the file DiversityCollectionError.log located in your application directory.


Tutorial - first steps

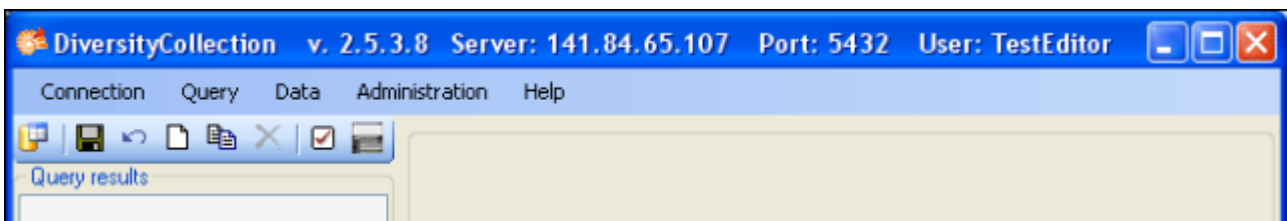
This tutorial will guide you through the first basic steps to enter a single dataset in DiversityCollection. After the [installation](#), make sure, you have [access](#) to the database. To start the program, double click on the DiversityCollection.exe in the directory where you copied the files of DiversityCollection. The main form will open.



If you open this form for the first time, you have to connect to the database. Click on the  button or choose **Connection -> Database...** from the menu. A form will open where you can enter your account information and choose the database (see image below, for further informations see [database access](#)).




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. In addition the header of the form shows your current login informations (see below).



This tutorial is continued in the sections listed below.

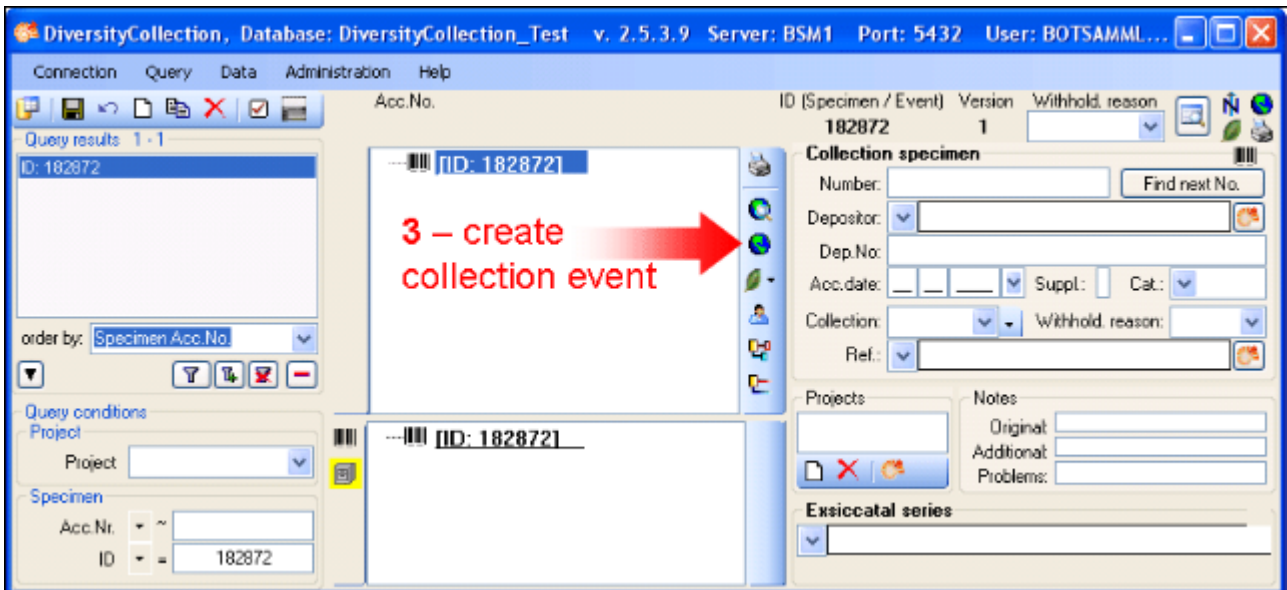
- section [Collection event](#)
- section [Collection specimen](#)
- section [Collection specimen relations](#)
- section [Organisms and identifications](#)
- section [Specimen parts and storage](#)

Tutorial - collection event


To enter a new dataset, click on the  [button](#) in the upper left panel (see point **1** in image below). In case there are accession numbers in the database, the software will ask whether you want to take the next free number. Finally you will find a new entry in the [specimenlist](#) on the left and the trees for the [specimen](#) (see point **2** in image below) and the [storage](#) as shown below.



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. This will open the fields where you can enter the details for the specimen in the area right from the tree.




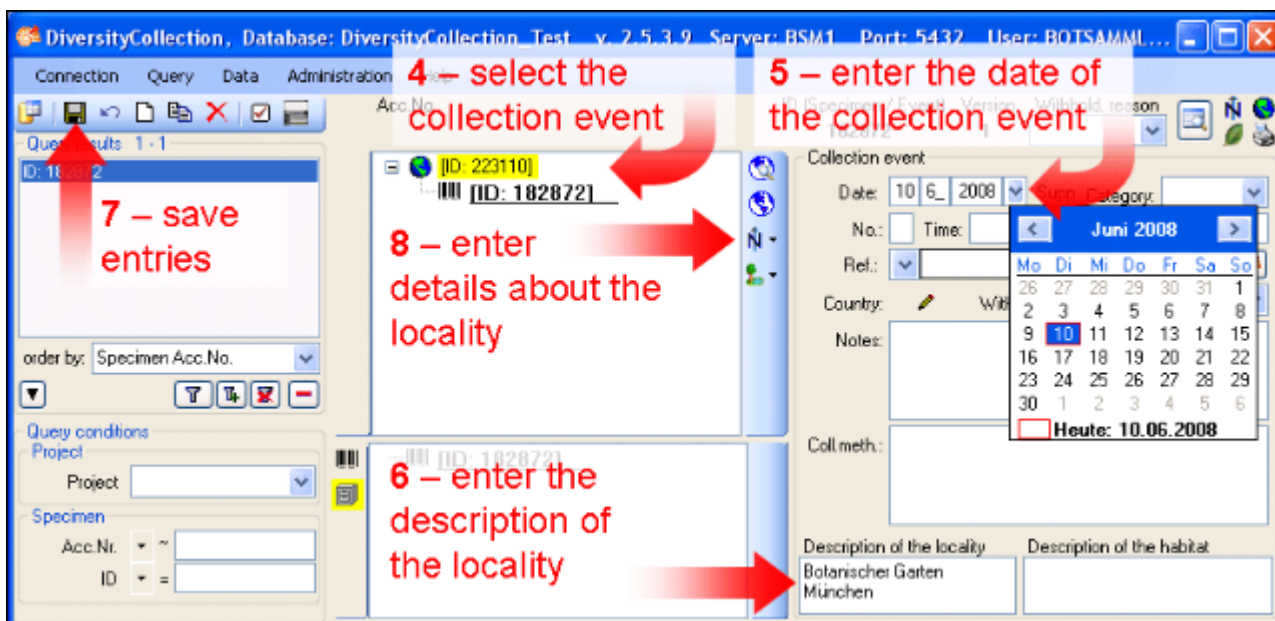
In the panel in the middle of the form, several buttons will appear where you can enter additional informations to this specimen. To enter information about the [collection event](#)


(when and where the specimen was collected) click on the  button (see point 3 in image above). This will add an entry for the collection event in the upper tree as shown below. Select this entry in the tree (see point 4 in image below), to open the fields for the collection event. To see the projected contents of any data field, simply place your mouse in the field. A explanation will appear like for the field **Description of the locality**:

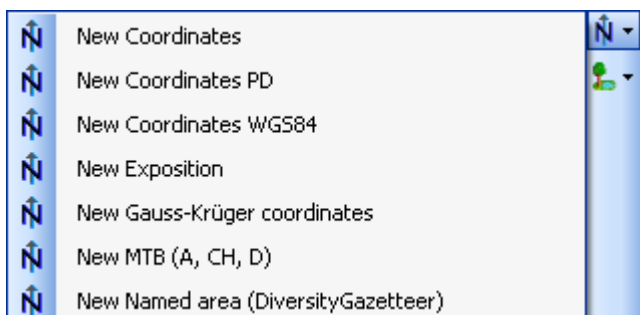
Locality description of the locality, exactly as written on the original label (i.e. without corrections during data entry)

See the [event](#) part for further details.

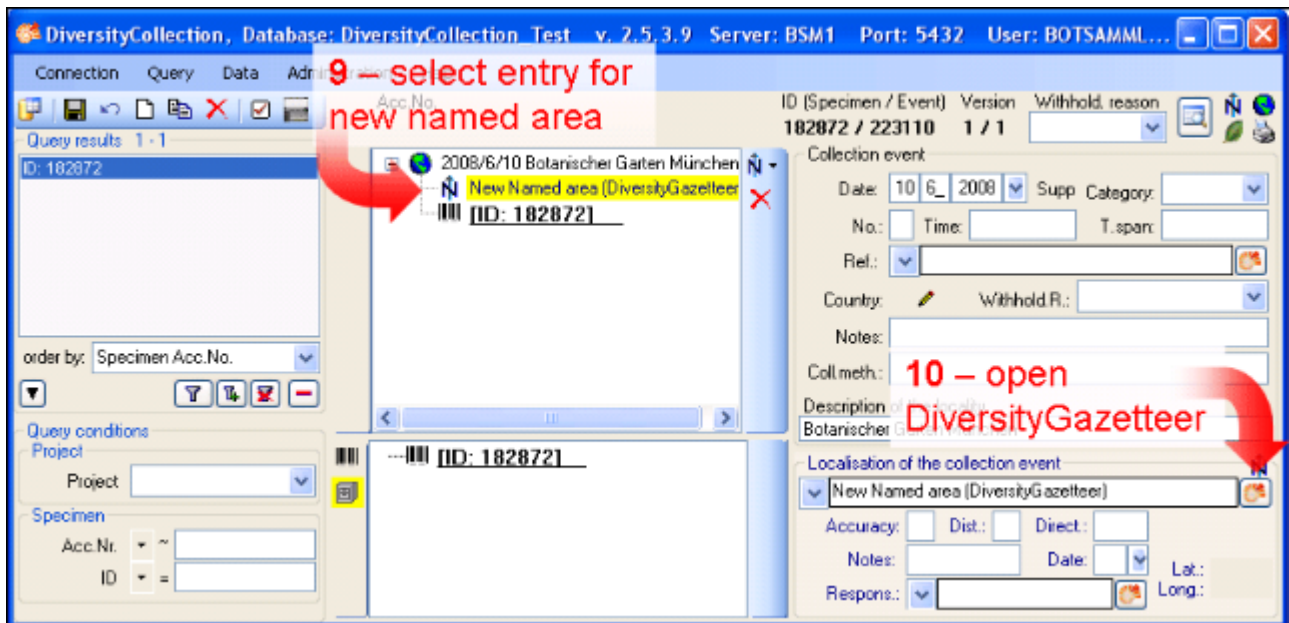
Then enter the date (see point 5 in image below) of the collection event. If you click on the drop down button as shown in the image below, a calendar will open where you can select the date. Then enter the description of the locality (see point 6 in image below). To store the data entered so far, click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





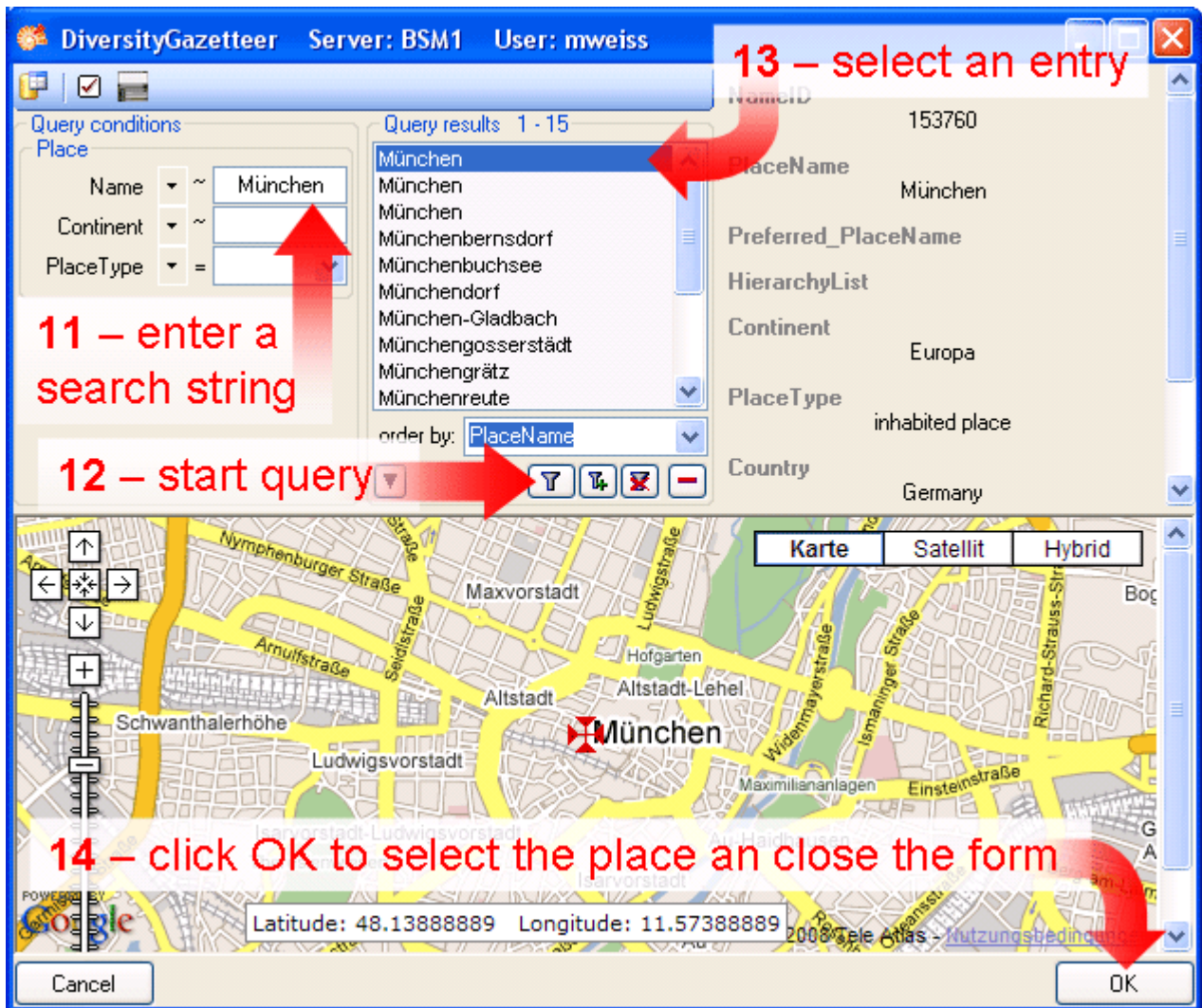
To enter coordinates, named places etc. click on the  button (see point 8 in image above) and select an option from the list.



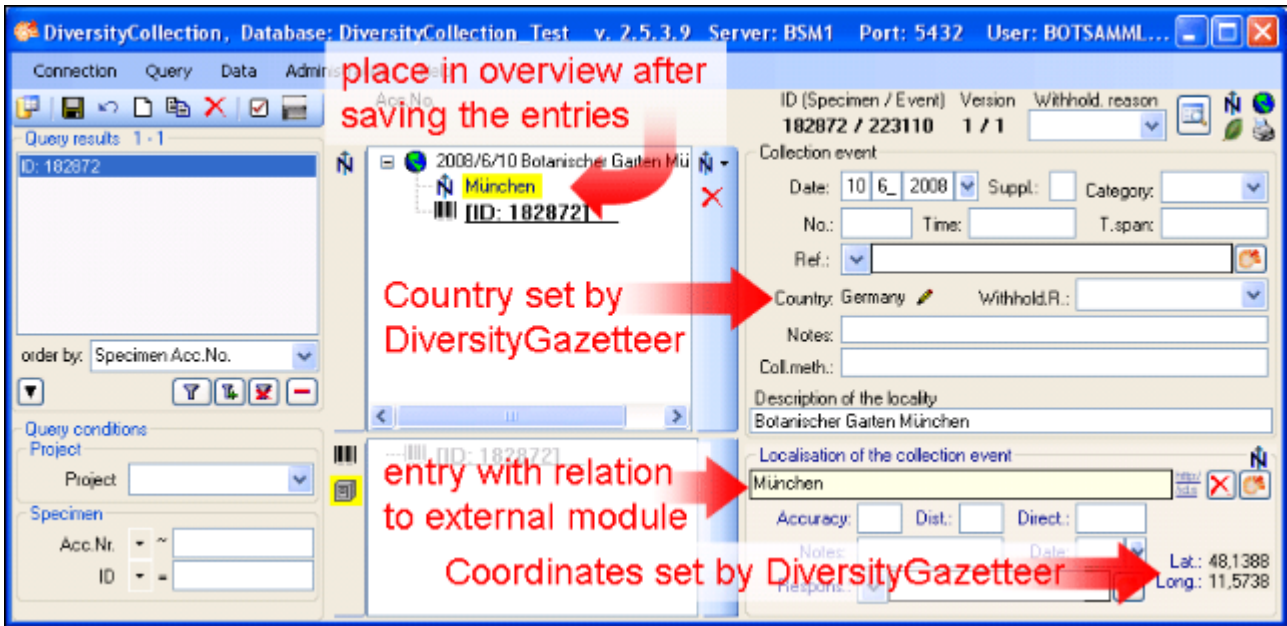
To enter a name of the place using the DiversityGazetteer, choose **New Named area (DiversityGazetteer)** from the list. In the overview tree in the middle of the form an entry will be inserted as shown below. Select it to open the detail fields for this entry (see point 9 in image below).



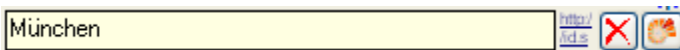
To open the connection to the DiversityGazetteer, click on the  button (see point **10** in image above). A window as shown below will open. Enter a search string for e.g. the city you want to find (see point **11** in image below) and start the query with a click on the  button (see point **12** in image below).



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 from the list and the base will show a map corresponding to the coordinates connected to this entry. After selecting the correct entry (see point **13** in image above) click on the OK button to return to the main form (see point **14** 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.

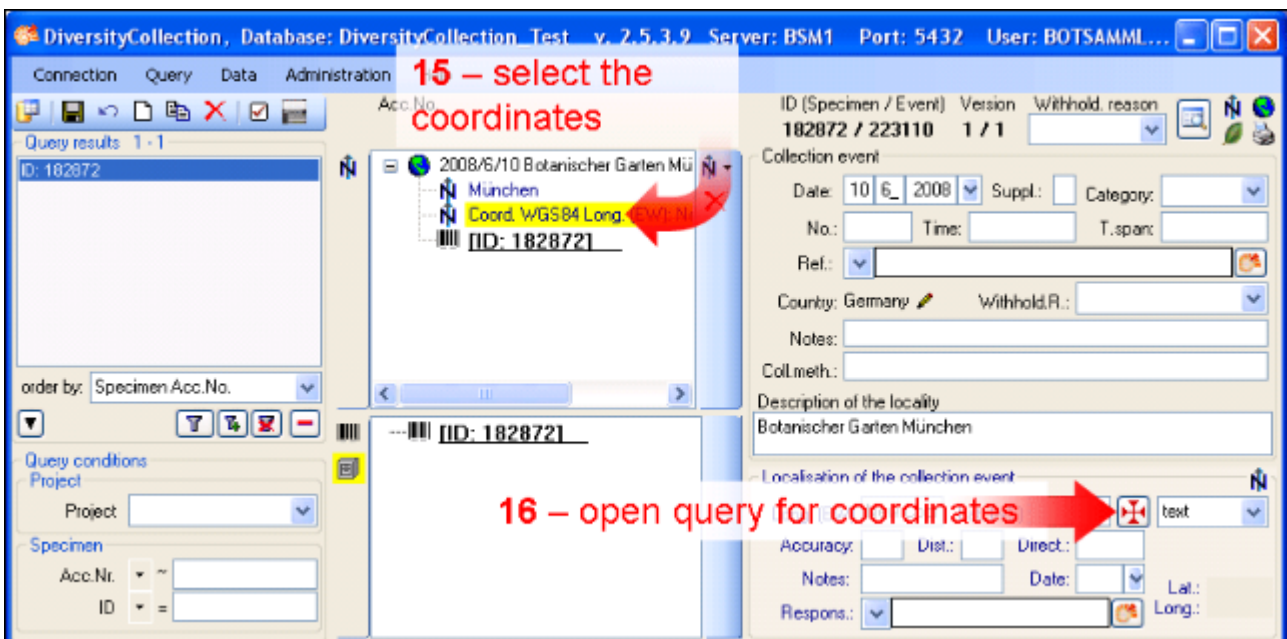



The area where you entered the name now changed to a locked state and will prevent you from changing the entry (see image below). Next to the field with the place you find the link to the external module. Double-click it for more details.

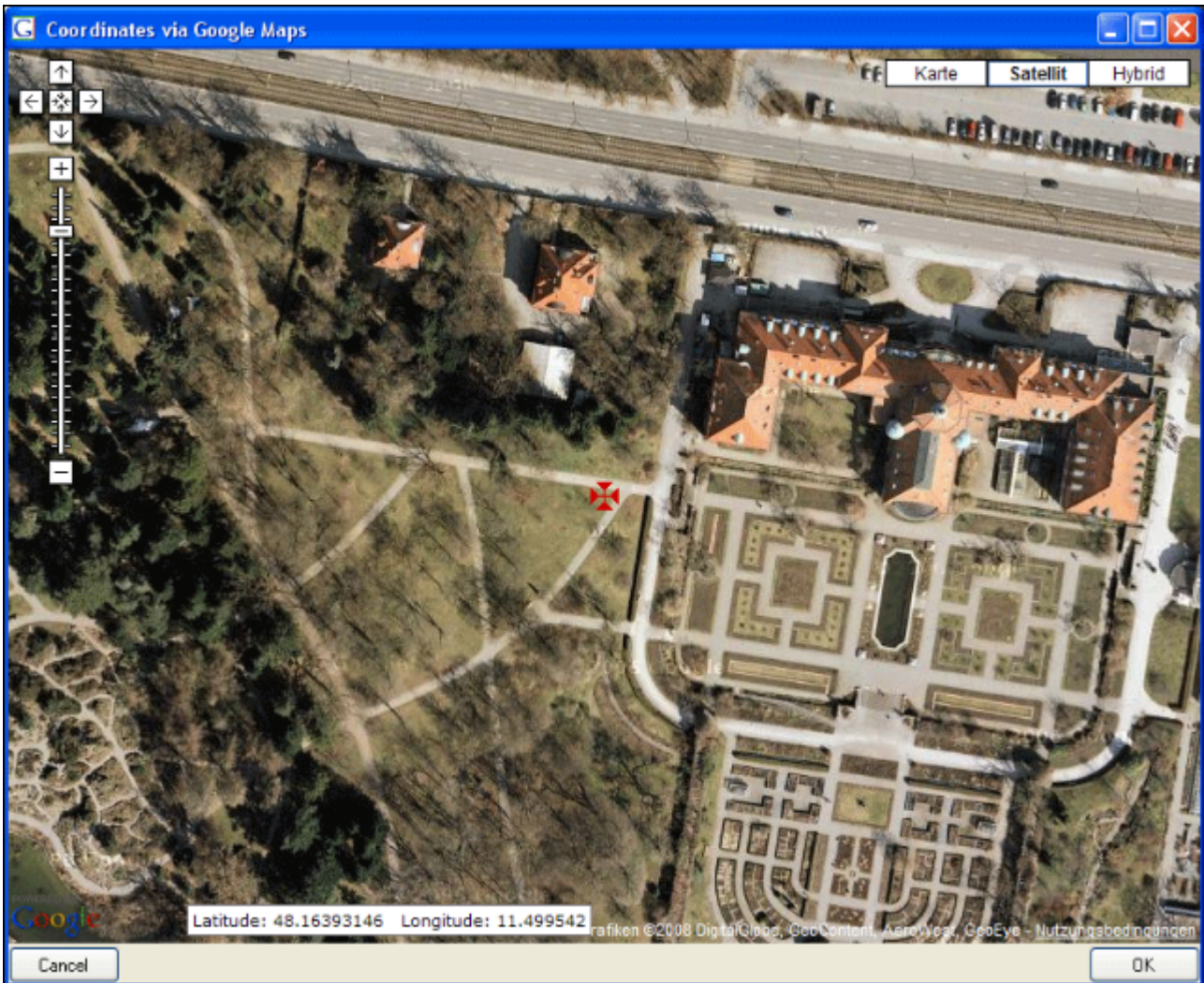


If you want to remove the connection to the external module click on the **X** button. This will keep all entries (country, place, coordinates) but remove the connection to DiversityGazetteer.

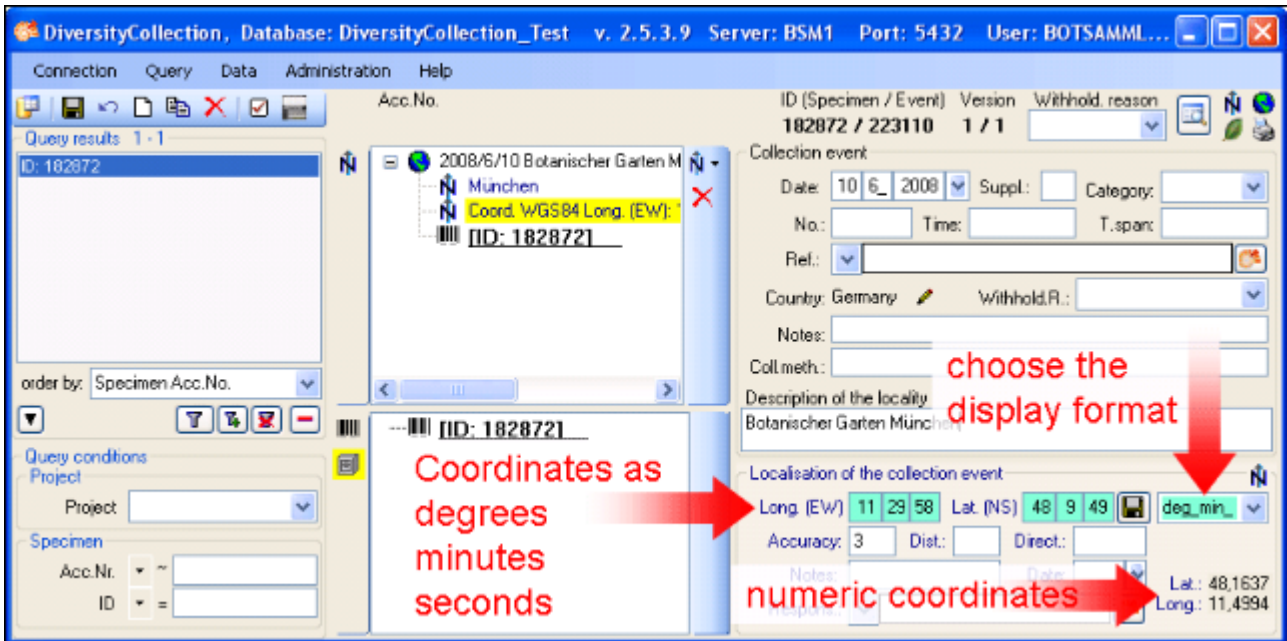
Now lets add the exact coordinates for the locality with the assistance of Google Maps. Click on the **N** button (see point **8** above) and choose **New Coordinates WGS84** (Google Maps uses WGS84). This will add a new entry in the overview. Select it (see point **15** in the image below) to open the details for this entry. Here click on the **X** button (see point **16** in image below).



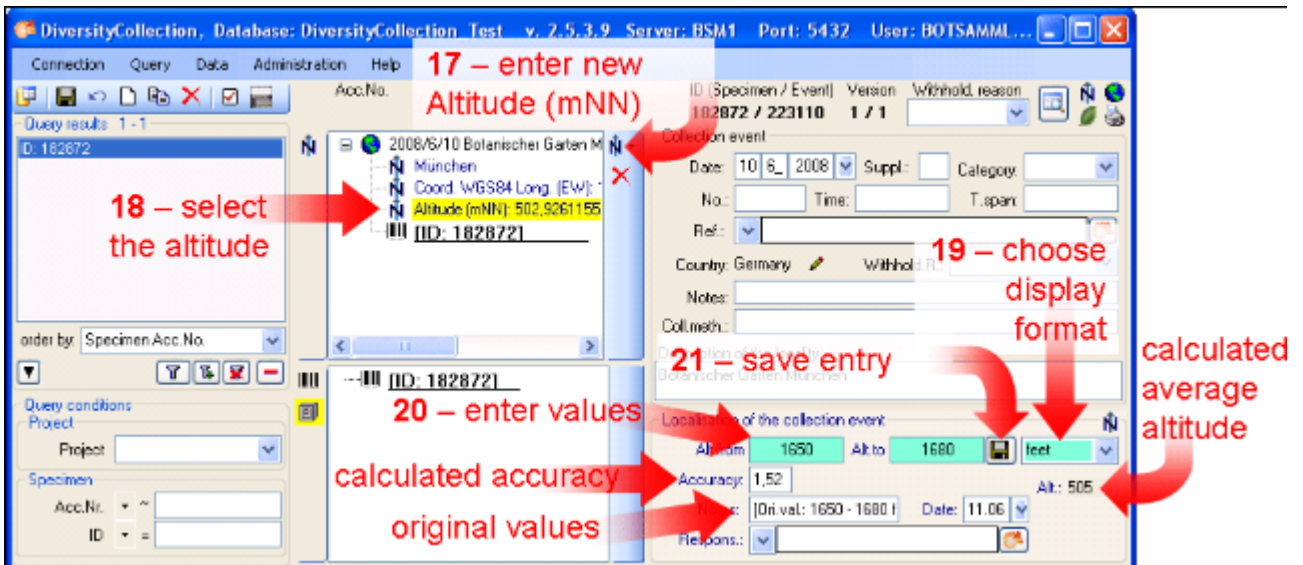
A window as shown below will open where you can set the coordinates simply by dragging the map with your mouse. The coordinates correspond to the center of the map, symbolized with the . Click on the OK button to store the coordinates.



In the main form as shown below the coordinates will be stored at two positions - see image below. In the upper area, you can set the values and choose a different format for display as shown here the more familiar form with degrees, minutes and seconds. You change the values and click on the button, to change the original entry. In parallel the numeric values are stored in fields that can not be edited by the user (see below).



As a last information about the locality, we enter the altitude. Click on the **N** button (see point **8** above) and choose **New Altitude (mNN)** (see point **17** in the image below). Then select the new entry in the overview to open the datafields (see point **18** in the image below). Lets suppose, you have only feet values available - so change the display format to feet (see point **19** in the image below). Enter your values (see point **20** in the image below) and click on the **Save** button (see point **21** in the image below) to save your entries. Now your values are converted to meter, the internal format of DiversityCollection. The program calculates an average value for the altitude and an 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.

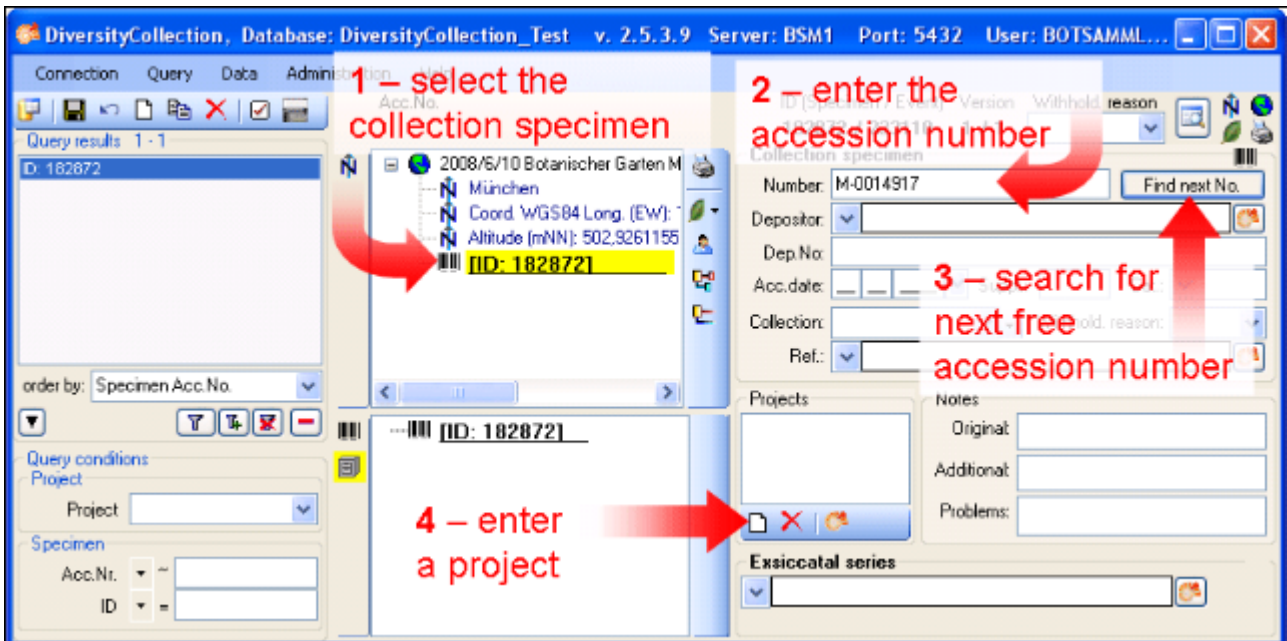


Next we turn to the collection specimen and set the accession number in the first section listed below.

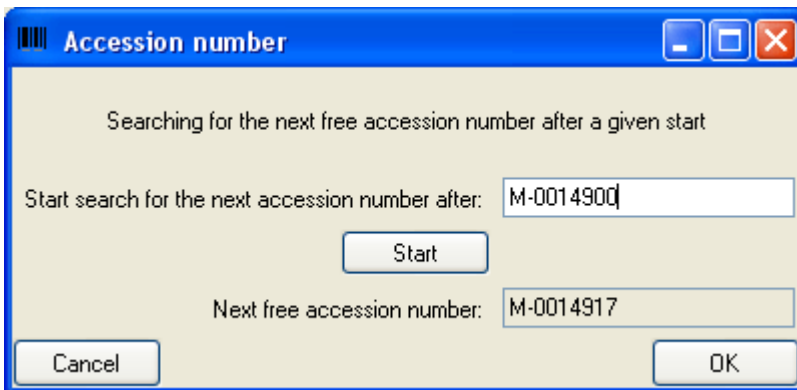
- section [Collection specimen](#)
- section [Organisms and identifications](#)
- section [Specimen parts and storage](#)

Tutorial - collection specimen


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

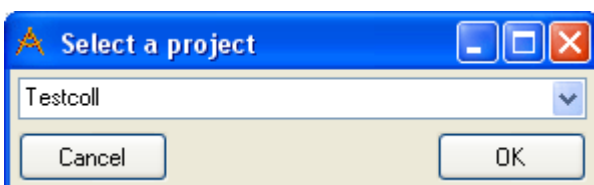


To search for the next free accession number, click on the corresponding button as shown above (see point **3** in image above). A window as shown below will open. Start the search for a free accession number. If the query ended successful, click **OK** to take the new accession number in your dataset.





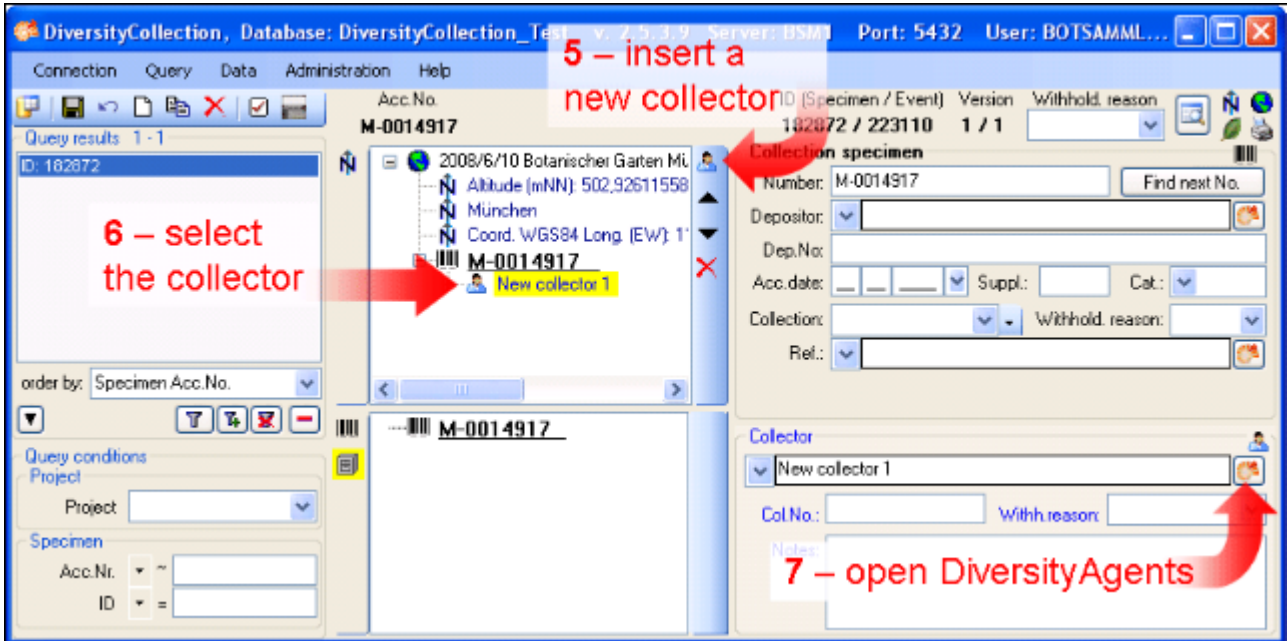
Project


To restrict the access to your dataset, add it to a project (click on the  button - see point **4** in image above). A dialog will open where you can 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.

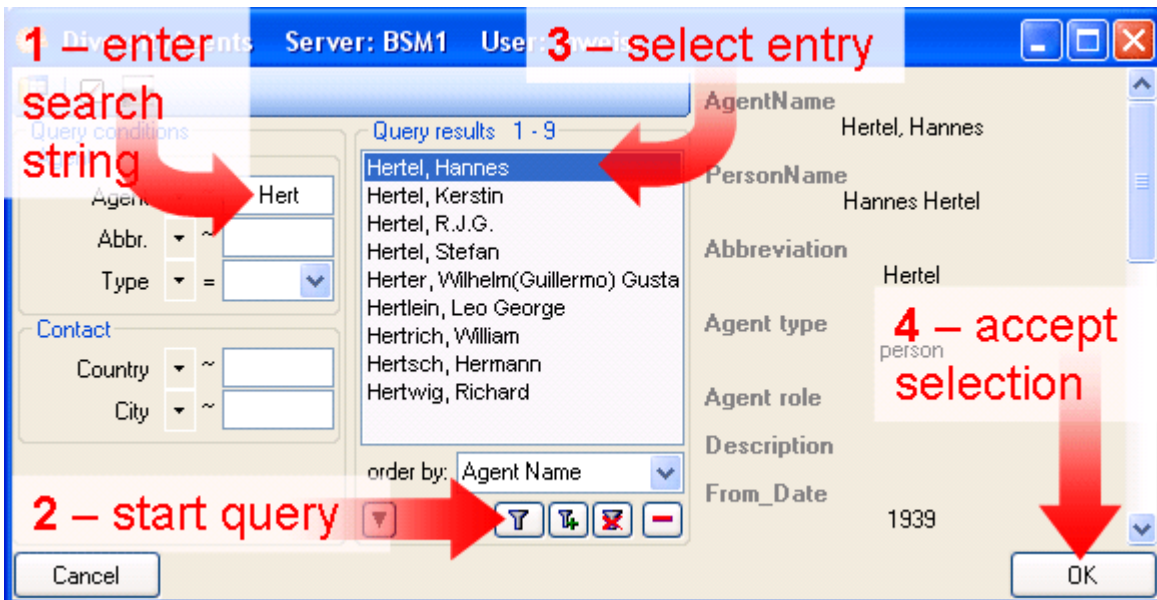


Collectors

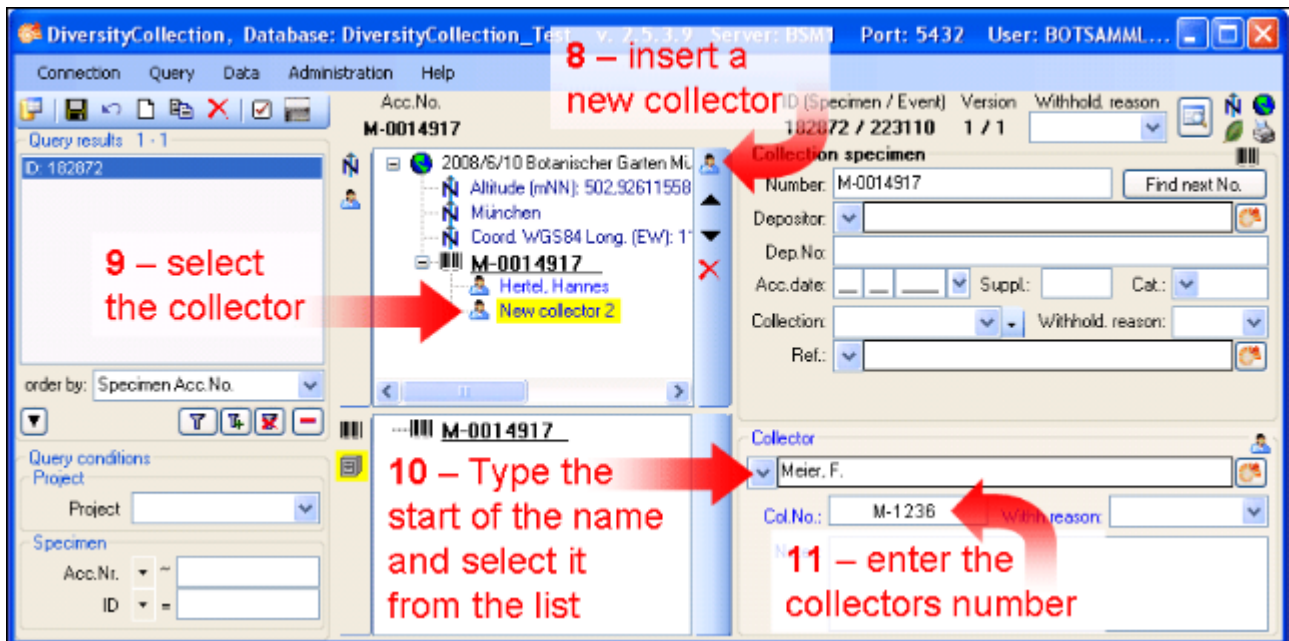
Now we will add the collectors of the specimen. In the overview, select the specimen (see point 1 above) then click on the  button to insert a new collector (see point 5 in image below). Select the collector in the overview (see point 6 in image below). Now we use the module DiversityAgents to search for a certain person. Click on the  button to open the interface to the module (see point 7 in image below).



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).



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. Insert the next collector (see point 8 in image below), select it (see point 9 in image below), type the start of the name in the field for the name and click on the drop down button (see point 10 in image below) to select a name from the list of collectors already stored in the database. Finally enter the field number of this collector (see point 11 in image below).



This tutorial is continued in the sections listed below:

- section [Collection specimen relations](#)
- section [Organisms and identifications](#)
- section [Specimen parts and storage](#)

Tutorial - relations between specimen

There are two types of relations possible:

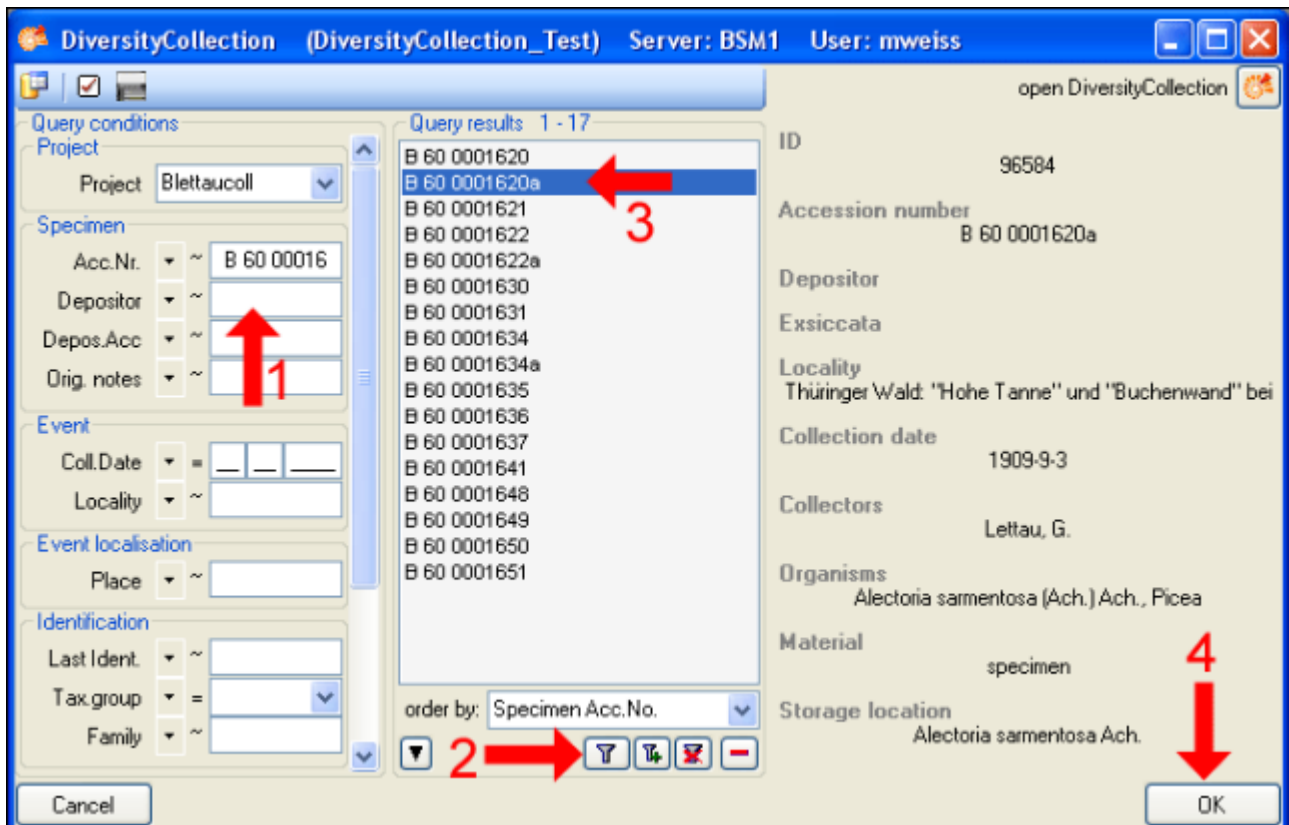
1. relation to a specimen within DiversityCollection
2. relation to a specimen not administrated in the local database.

1. Internal relations

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

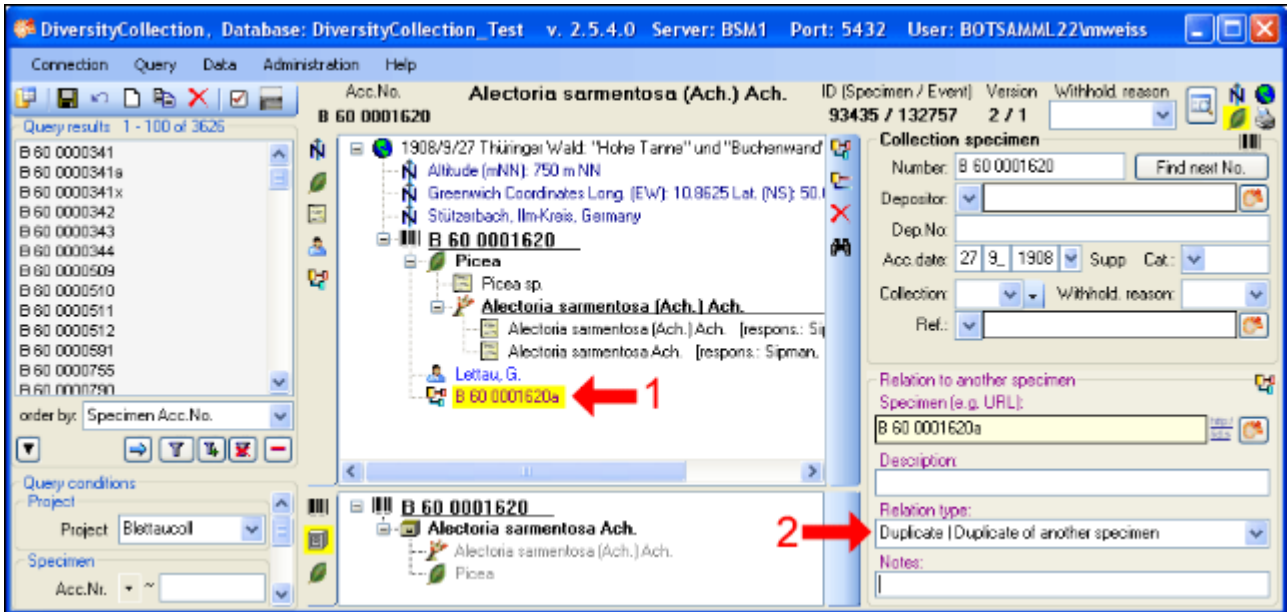


A form will open where you can search for the related specimen. In the form enter your restrictions (see point 1 in image below), start the query (see point 2 in image below), select the related specimen from the result list (see point 3 in image below) and click OK (see point 4 in image below) to insert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



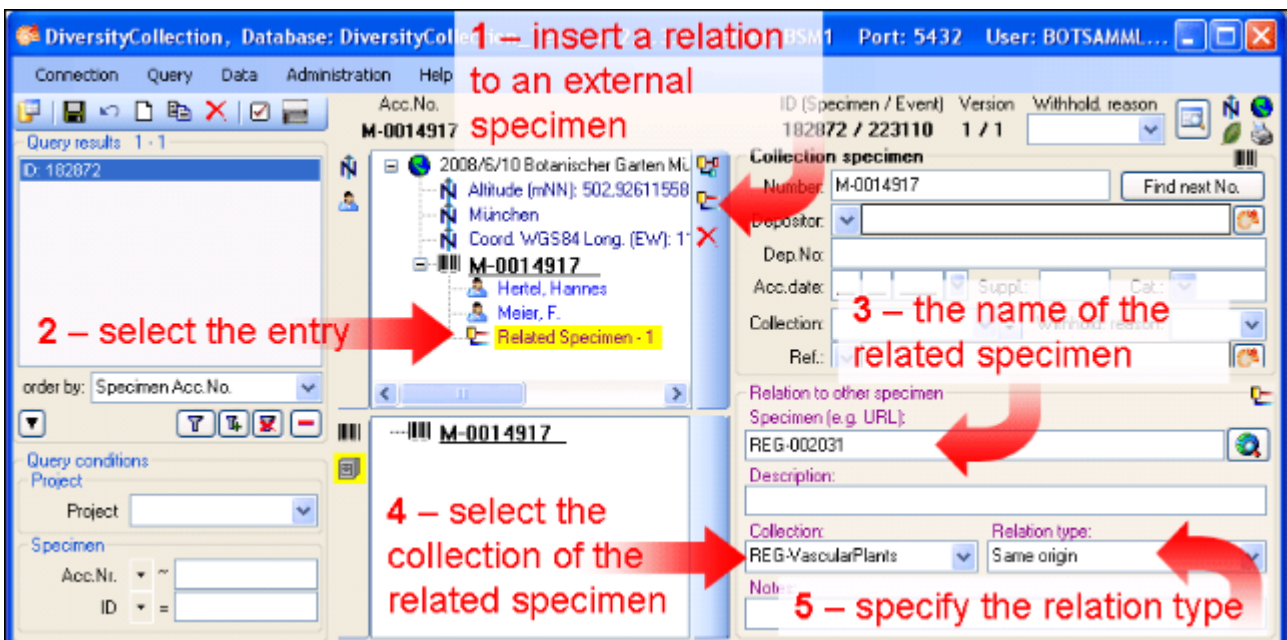
In the form select the entry for the relation (see point 1 in image below) to display the fields

for the details. Then enter the type of the relation (see point 2 in image below).



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).

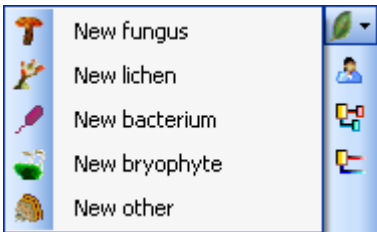


If there is a dataset for the collection available you can select it from the list (see point 4 in image above). Otherwise you first have to add this collection to the list. If you have the permissions to edit the collections choose Administration -> Collections from the menu to add a collection. See the section [collection](#) for details.

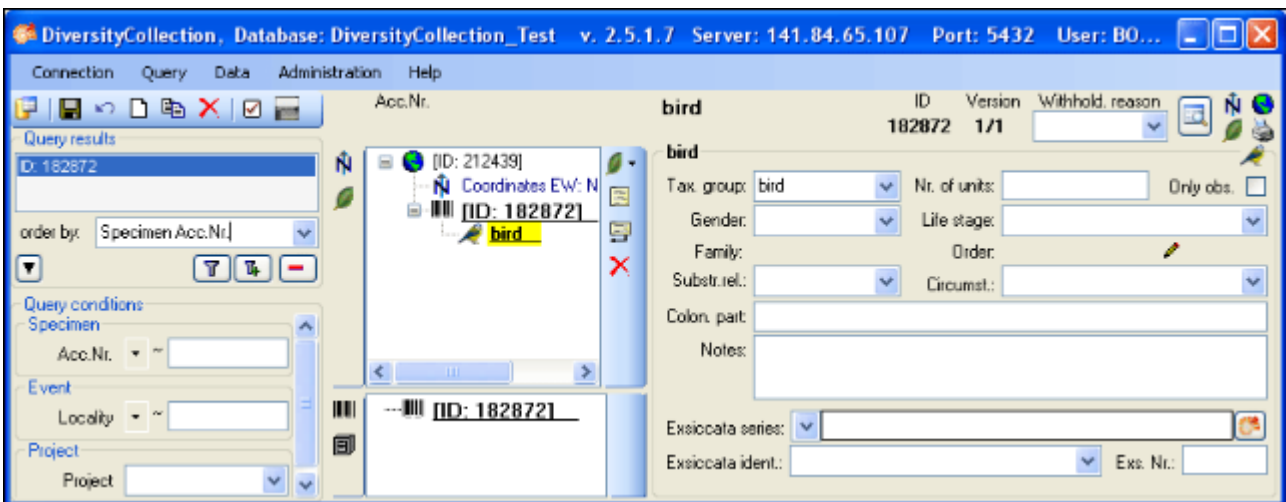
For further informations about the relations turn to the section [relation](#).


Tutorial - organisms and identifications

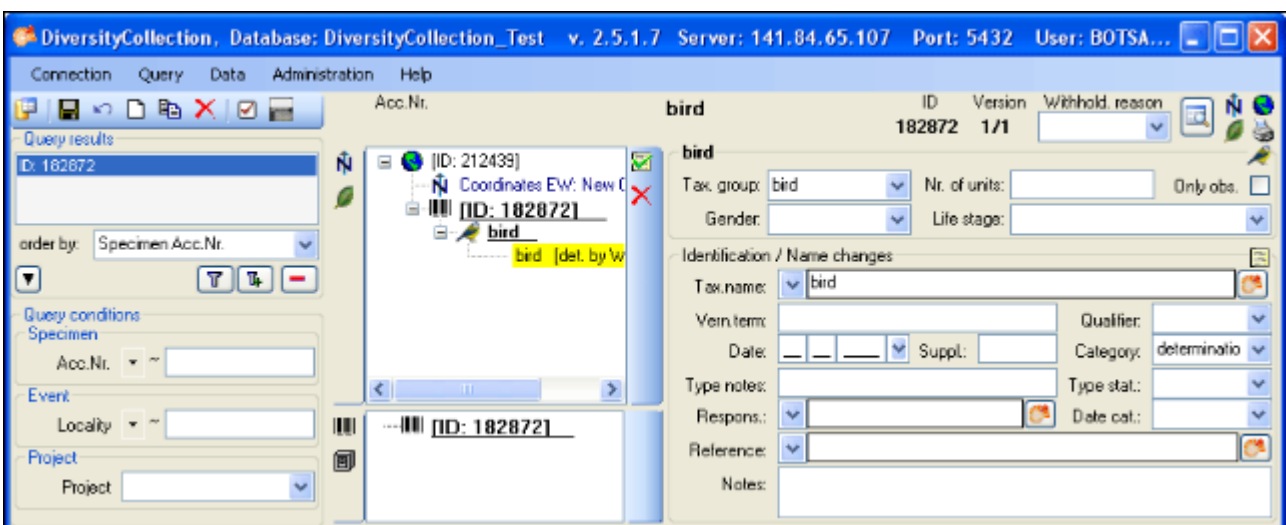
To enter the [organism](#), choose the specimen entry in the tree. Then select the organism from the  list.



This will enter an entry for the organism underneath the entry of the specimen as shown below. To enter details for this organism, select the entry in the tree.



To enter an [identification](#), click on the  button. This will insert a dataset for the identification of the organism underneath the organism as shown below. Select this entry to enter the details of the identification.



As a last step, enter the data connected with the [storage](#) of the specimen. In the bottom tree, select the entry for the specimen and then select a material category from the list. This will enter a dataset for a specimen part underneath the specimen as shown below. Select this entry to edit the data for the collection, the storage location etc.

DiversityCollection, Database: DiversityCollection_Test v. 2.5.1.7 Server: 141.84.65.107 Port: 5432 User: BOTSA...

Connection Query Data Administration Help

Acc.Nr. **bird** ID Version Withhold_reason
182872 1/1

Query results
D: 182872

order by: Specimen Acc.Nr.

Query conditions
Specimen
Acc.Nr. ~
Event
Locality ~
Project
Project

(ID: 212439)
Coordinates EW: New
(ID: 182872)
bird
bird

(ID: 182872)
bird
bird

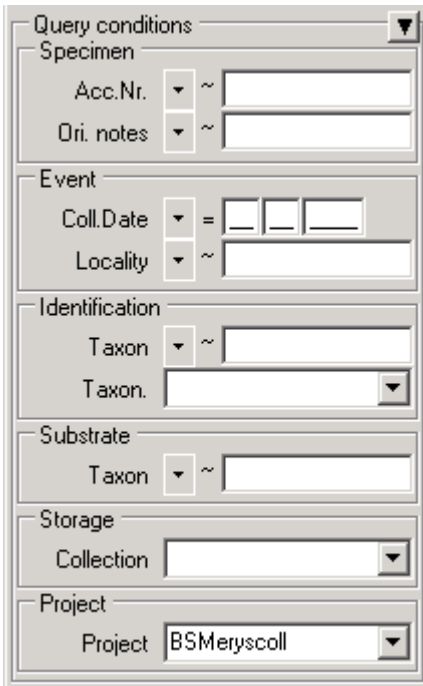
Specimen part
Acc.Nr.: Part:
Collection: SAPM Date:
Preparat.:
Stor. loc.: bird
Mat. cat.: specimen Stock:
Notes:

Display order
Units not in part: Show in label: Hide:

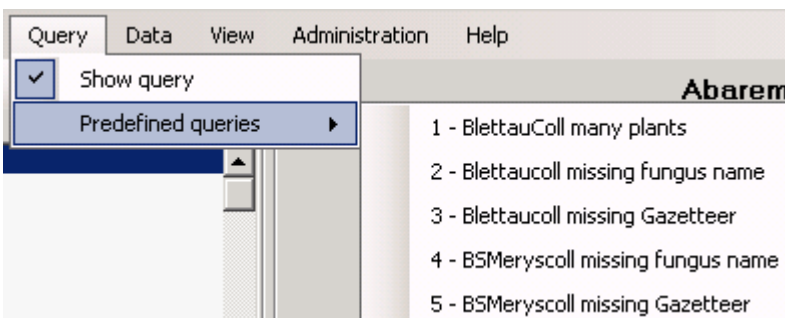
< bird >

Queries - Overview

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

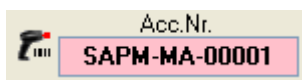


With the [user defined](#) queries, you can define any query condition.



The [predefined queries](#) are defined

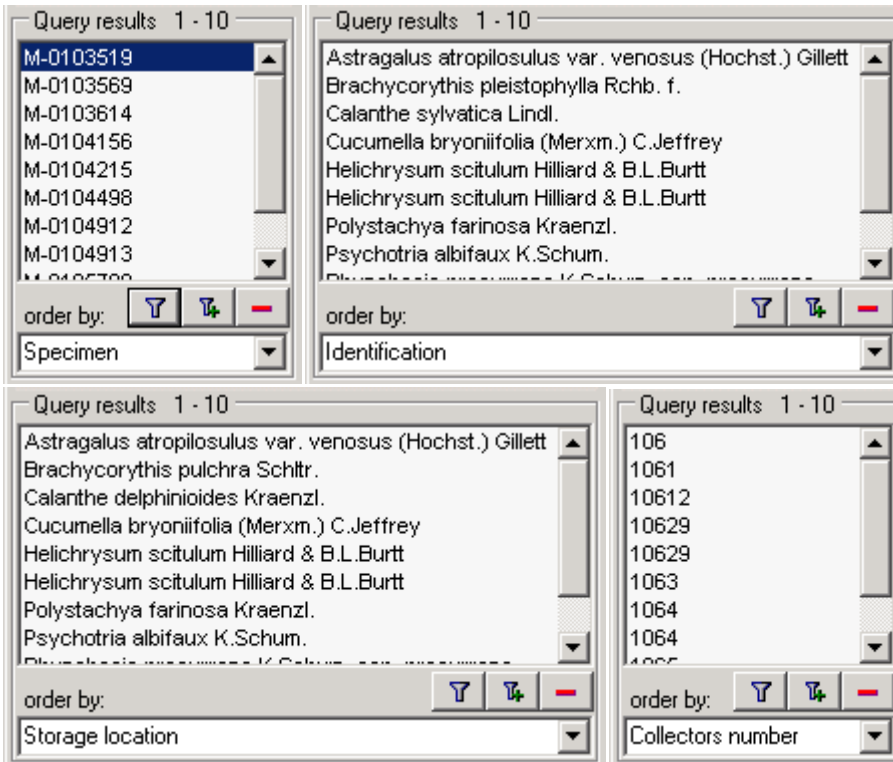
by the system administrator and are accessible via the menu.



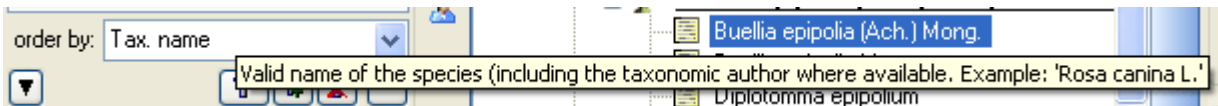
With the scan mode you can use a barcode scanner to search for a specimen

Result list

The result list displays the specimens found in a [query](#).

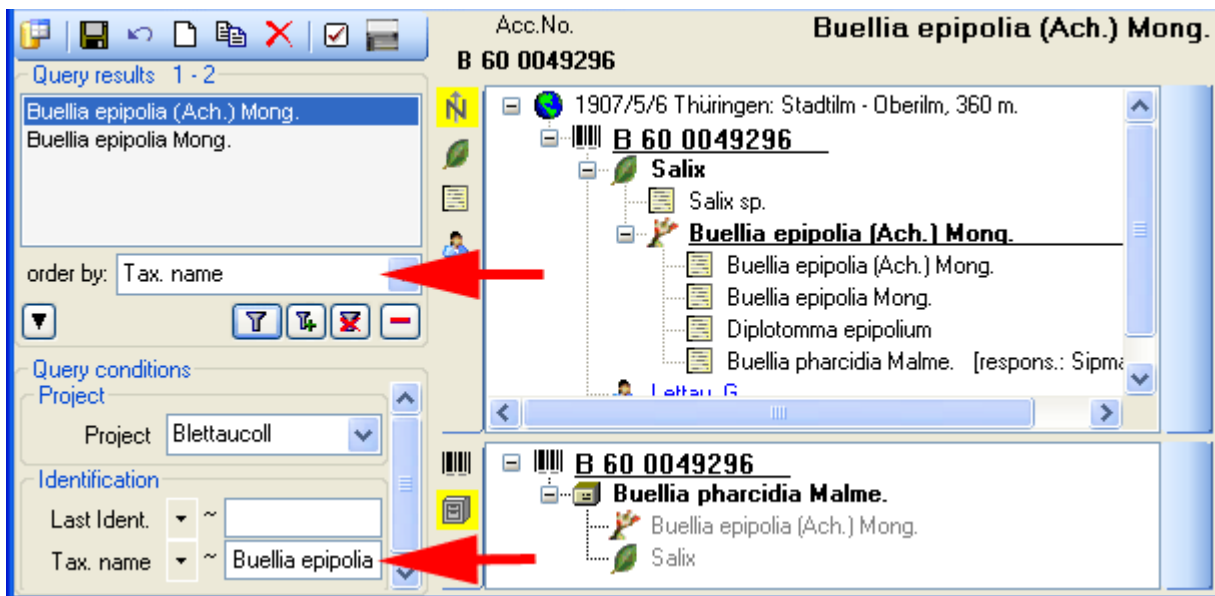


The specimens can for example be shown with their accession number, their identifications or their storage location etc. as shown in the images above. To get further informations about the chosen field, just place the mouse in the field. A text box will appear with the description of the field (see below).

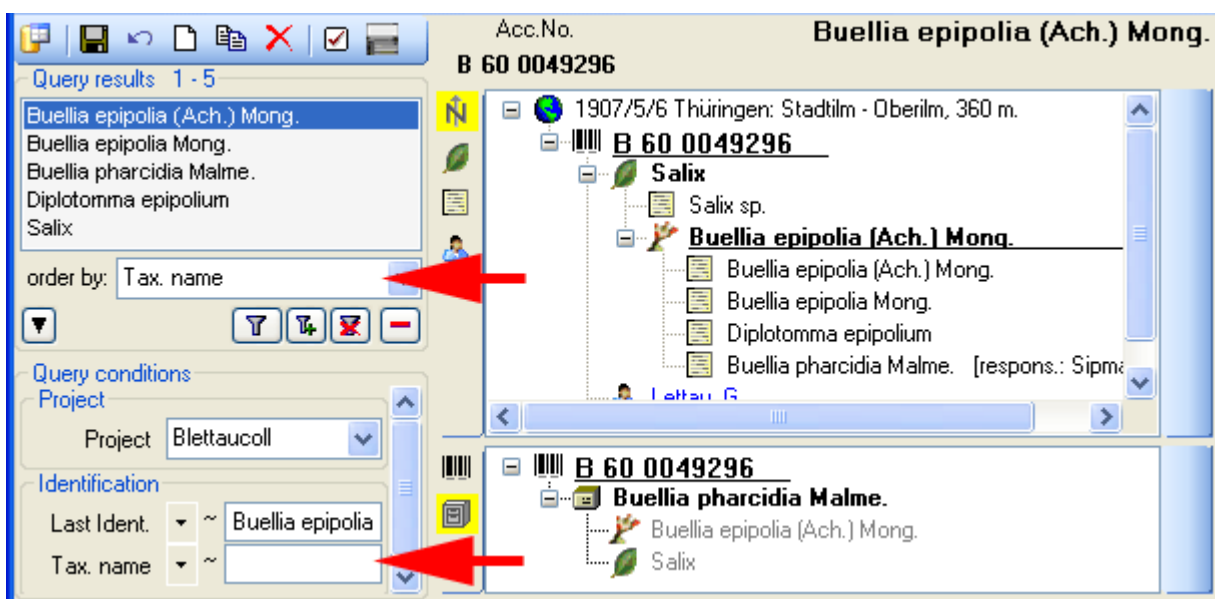






You can restrict the maximal number of specimens together with the [query options](#) (click on the button), for example if you have a slow connection to the database. As a default the maximal number is set to 100. If the number of datasets according to your query is higher than the maximal value set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

To 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 where used for restricting the query and the display (**Tax. name**). Here the Query results will be restricted to this field.



In the second example a different field for the restriction was chosen (**Last ident. <> Tax. name**). The query result in consequence will list all entries found in the field **Tax. name** from the datasets where an entry matches the restriction (see below).



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 maximal number of returned items you can browse the next items with the  button. If you want to remove entries from the selected list, choose them in the list and click on the  button. This will not delete the data from the database, but remove them from your query result.

Here some examples you can 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

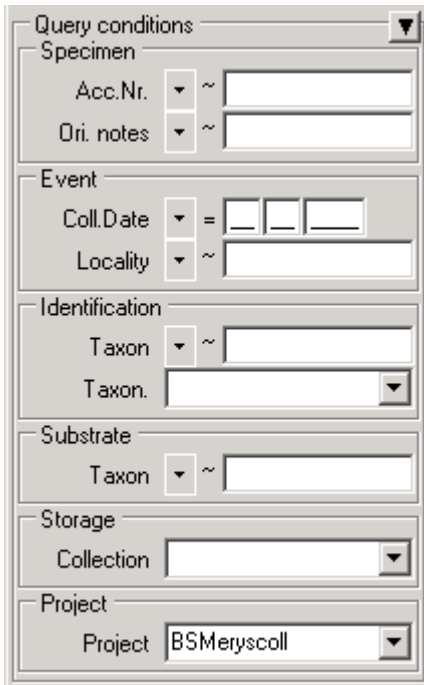
there can be several units in one specimen several entries for one specimen may appear in the list.







[Storage location](#): The storage location of every part of a specimen stored in the collections is shown in the list. As 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 can have several collectors each with 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 form beneath the list of the items. You can change this arrangement using the  /  button to place the query options on the left side of the item list.



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. If the list of items is longer than your maximal number of returned items you can browse the next items with the  button. To move back to the previous block of items click on the  button. If you want to remove entries from the selected list, choose them and click on the  button. This will not delete the data from the database, but remove them from your query result.

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

Operator	Meaning	Example
Text		
~	search for an entry like ...	Pinus s[iy]lvestris % (you can use wildcards)
=	search for an entry exactly equal to ...	Pinus silvestris L.
≠	search for an entry not like ...	Pinus s[iy]lvestris % (you can use wildcards)

∅	search for an entry where a value is missing ...	
-	search for an entry between ... and ...	2000 - 2005
Numeric		
=	search for an entry exactly equal to ...	2006
<	search for an entry lower than ...	2006
>	search for an entry bigger than ...	2006
-	search for an entry between ... and ...	2000 - 2005



∅ search for an entry where a value is missing ...

Date		
=	search for an entry exactly equal to ...	20.3.2006
<	search for an entry lower than ...	20.3.2006
>	search for an entry bigger than ...	20.3.2006

Hierarchy		
=	search for an entry exactly equal to ...	M-Fungi
≠	search for an entry that is not equal to ...	M-Fungi


∅ search for missing entry ... M-Fungi

Δ search including childs in a hierarchy ... M-Fungi

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


To change the displayed fields for searching specimens click on the  button to change the [query options](#).

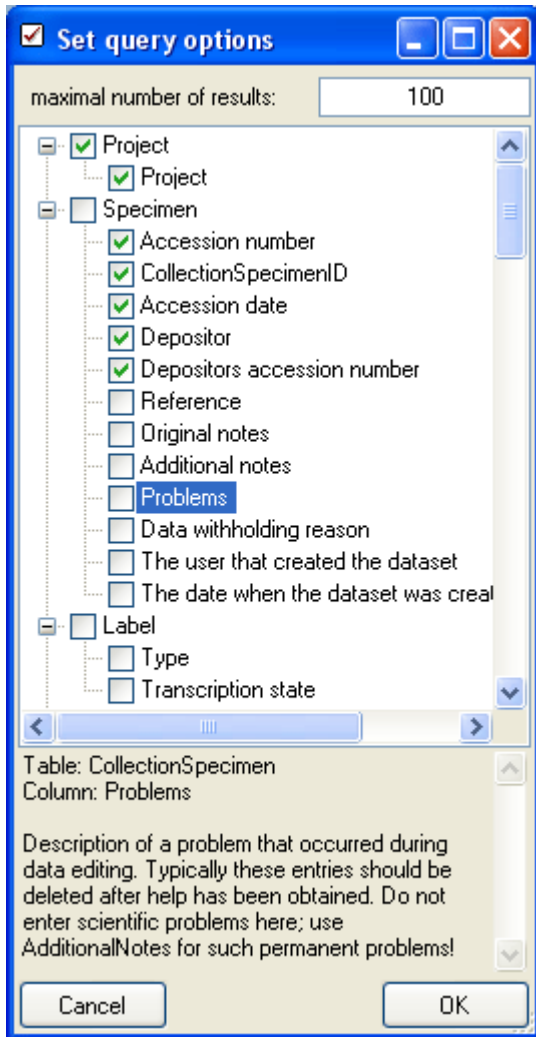
Scan mode

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 then be accessible for the entry with 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. Then scan the barcode and the program will start the search for the specimen in the database.

Query options

The maximal number of items shown in a query result can be set in the form for the query options. The default value is set to 100. If you have a fast connection to your database or need to see more or less results, you may change this value to any number you like.

To change the displayed search fields click on the  button. This opens a form where you can select and deselect the fields shown for searching specimens. You might also change the maximum number of items that will be shown in the result list.



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.

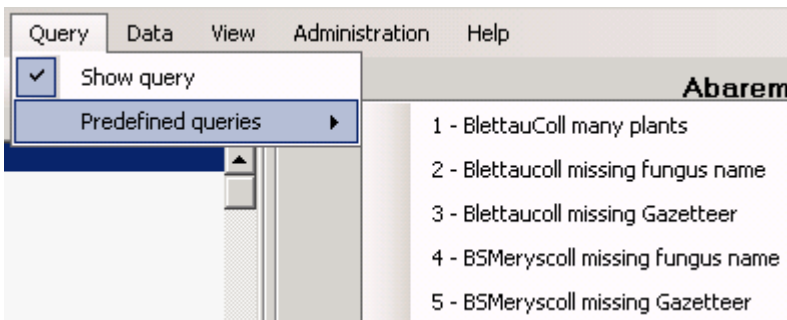
_ a single character, e.g. Pinus s_**_**lvestris will find Pinus **sy**lvestris and Pinus **si**lvestris etc.

[] 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.

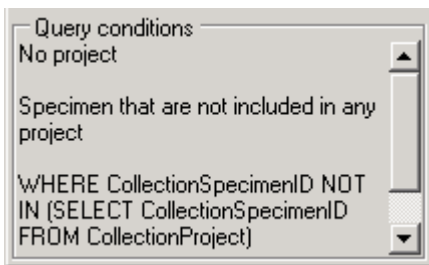
[^] any character not in a given range like **[^abcde]** or **[^a-e]**, e.g. Pinus s**[^i]**lvestris will find Pinus sylvestris but not Pinus silvestris.

Predefined queries

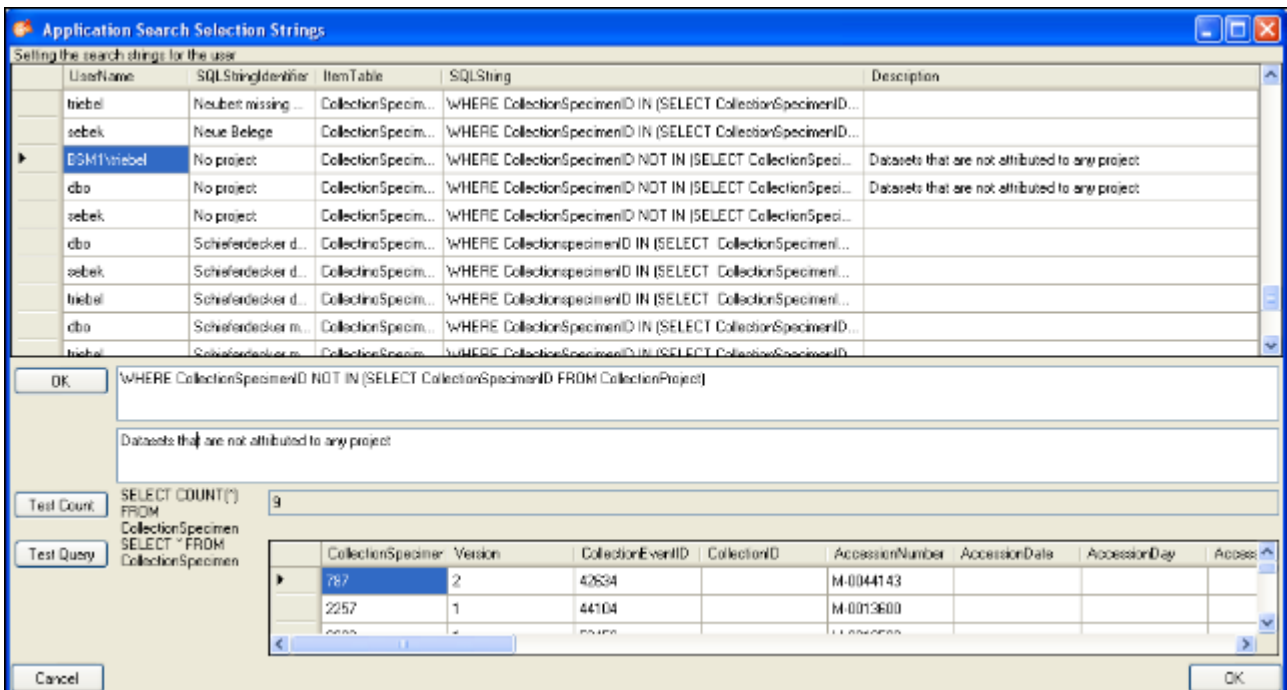
Besides setting queries for specimens via the query options you can define separate predefined user-specific queries. These are listed under the menu topic **Query - Predefined queries**.



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 that restricts the selection of the datasets (= WHERE-clause of the SQL-statement).



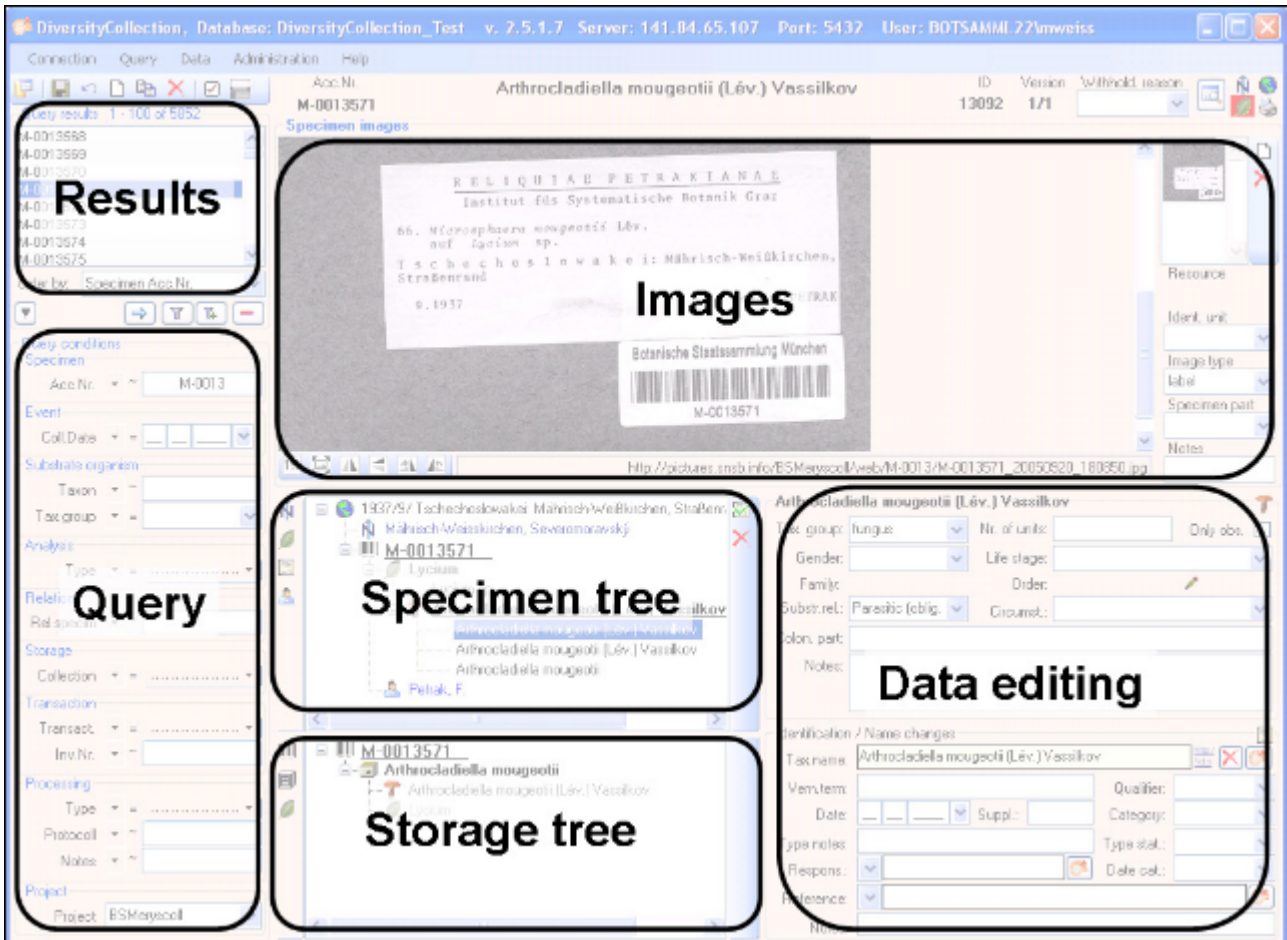
If you are an administrator you can create new queries for users. To create a predefined query choose **Administration - Queries...** from the menu. A form as shown below will open, where you can create, edit and test your queries.






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. So 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 form of the DiversityCollection client contains two main areas. At the left you find the query and the results of this query. In the right part the data of the dataset selected in the result list is shown. The upper part of the data area shows the 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 are shown in the data editing part.

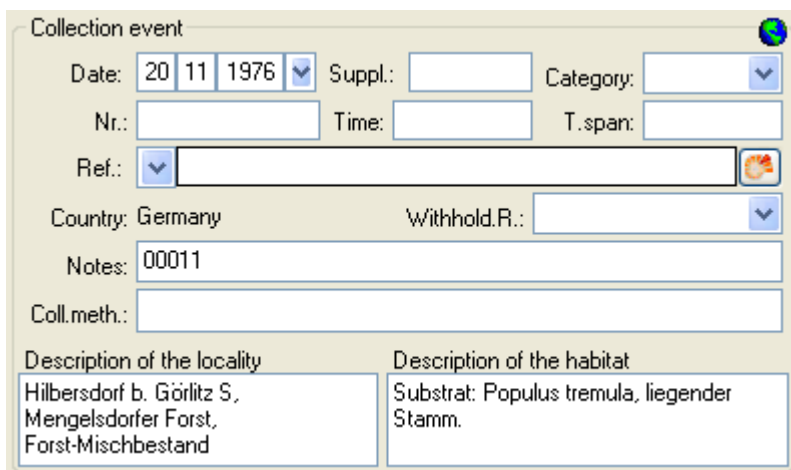



Collection event

Specimens stored in a collection are gathered during a collection event. This collection event keeps information about the geographic locality, the habitat, the collection date etc. During an collection event, several specimens may have been collected. If a specimen is not assigned to a collection event, you can assign the specimens to an existing event with a click on the  button. To create a new event for a specimen click on the  button. If you assign the specimen to an existing event, a form will open as shown below where you can search for the events already included in the database. Choose an event and click OK to assign the specimen to this event. In the tree view, the collection event is symbolized with an  icon as shown below.




To edit the data of the collection event, 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 timespan.





Collection event		
Date: 20 11 1976	Suppl.: <input type="text"/>	Category: <input type="text"/>
Nr.: <input type="text"/>	Time: <input type="text"/>	T.span: <input type="text"/>
Ref.: <input type="text"/>		
Country: Germany	Withhold.R.: <input type="text"/>	<input type="text"/>
Notes: 00011	<input type="text"/>	
Coll.meth.: <input type="text"/>	<input type="text"/>	
Description of the locality	Description of the habitat	
Hilbersdorf b. Görlitz S, Mengelsdorfer Forst, Forst-Mischbestand	Substrat: Populus tremula, liegender Stamm.	

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

If other specimens were collected during the same collection event, this will be visible if you show the whole hierarchy of the event series. To do this click on the  button in the panel on the left of the tree. See [event series](#) for further details. Here you can move a specimen to another event by drag and drop.

Data are stored in the table [CollectionEvent](#).

Collection event series

If you need a hierarchical order of your collection events respectively to organise your collection events e.g. to document expeditions, you can do this with a [collection event series](#). For a better differentiation between events and [collection event series](#) you have a [blue text](#) in the hierarchy and the editing part and a different icon . A collection event series can contain other collection event series and collection events. Information about the geographic locality, properties of the collection site, the date of collecting etc. are stored in the [collection event](#). To show or hide the collection event series you have two options. In the panel of the right of the tree the  button will show the superior event series of the current collection event as shown below.





The  button will show the whole hierarchy of the event series as shown below.





To edit the data of an event series, select it in the tree to display the fields with the details as shown below.





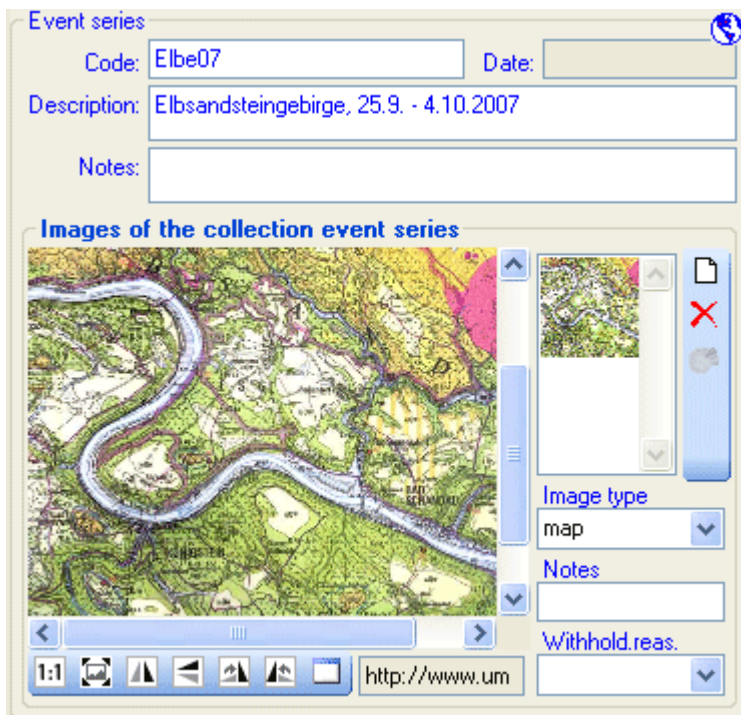
To insert a new collection event series click on the  button. If there are no collection event series so far, the collection event will be placed within the new collection event series. If there are collection event series present, the new collection event series will be placed below the selected collection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








To move an item within the hierarchy, just drag it with the mouse to whatever position it should be placed. Keep in mind, that specimens can only be placed in collection events and collection events only in collection event series.


If you want to delete a collection event series or an collection event, remove all depending collection event series, events and specimen and click on the  button. A specimen can not

be deleted here. If you want to remove a collection event from a collection event series, click on the  button to open the form for selecting a collection event series. Then select nothing but simply click OK to remove the link to the collection event series.

The images for a collection event series are shown below the data of the collection event series as shown below. To add images to a collection event series, click on the  button, to remove an image use the  button.





To zoom a sector of the image, just drag 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  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.

If you want to change to another specimen listed in the collection event series select it in the hierarchy and click on the  button.








The current specimen together with the event and all superior collection event series will be **highlighted**.

The data about the collection event series are stored in the table [CollectionEventSeries](#).

Event images


The specimens stored in a collection are gathered during a [collection event](#). To insert an image related to a collection event click on the  button. If you want to delete an image, click on the  button.




To zoom a sector of the image, just drag 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  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.

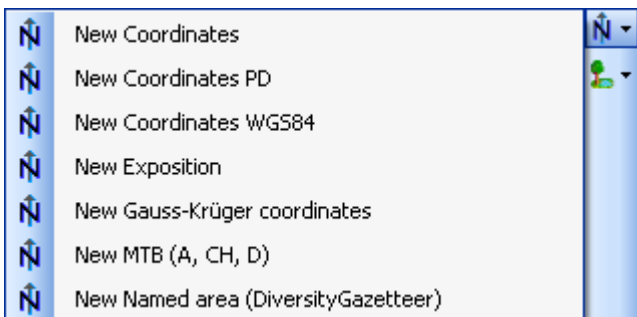
Data are stored in the table [CollectionEventImage](#).

Geography

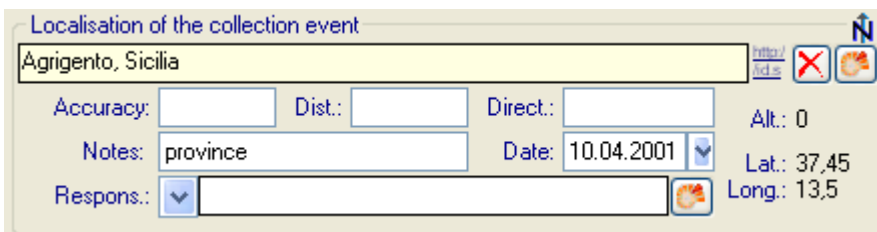
As additional information to the description of the locality you can use several localisation systems, e.g. georeferencing. These entries are marked with an  icon in the tree as shown below.





To add a new entry choose the localisation system from the drop down list as shown below. If a localisation should be removed, select it from the list and click on the  button.

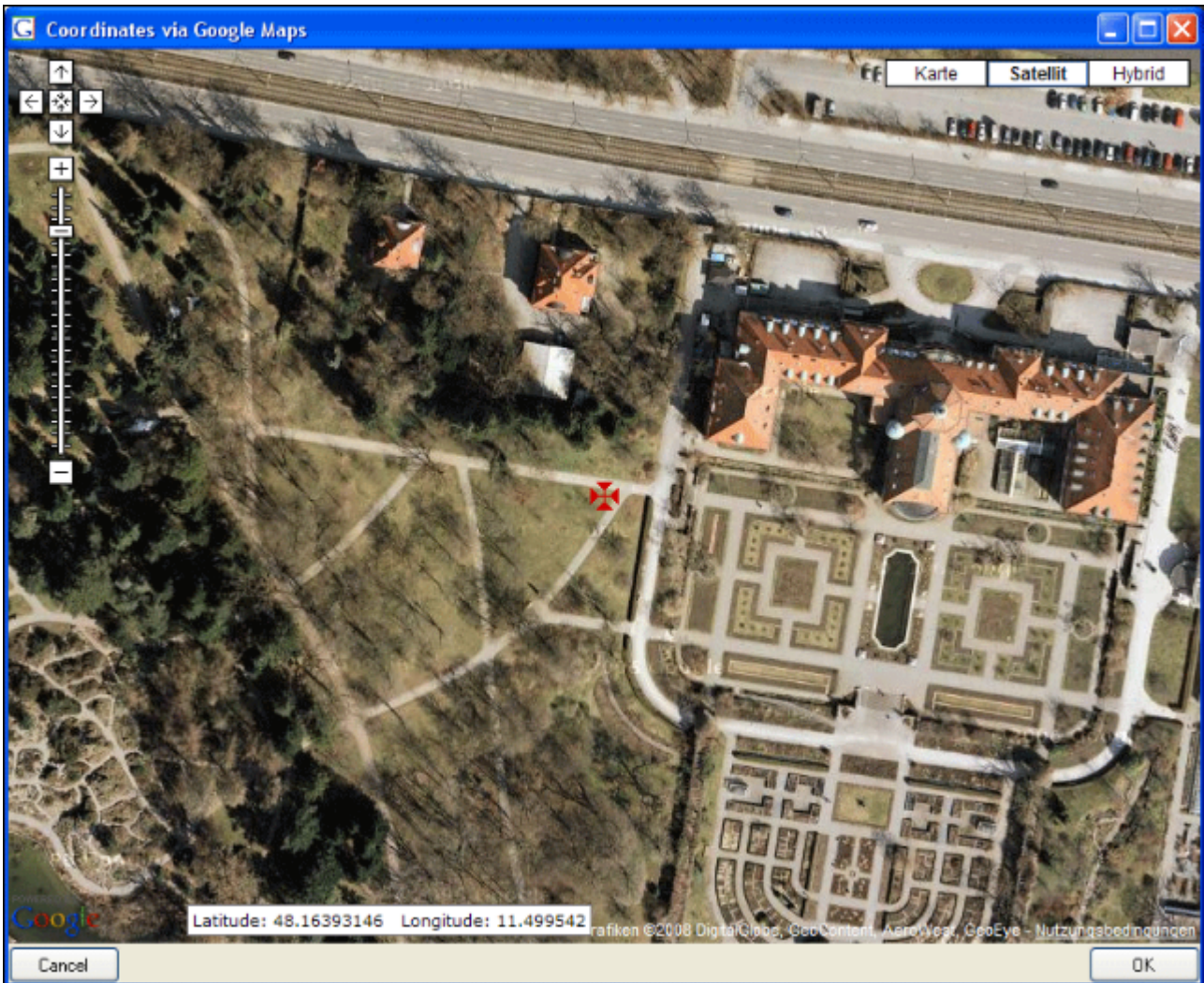



To edit the details of an entry, select in the list to open the fields in the form on the right. The localisation system DiversityGazetteer is linked to the module DiversityGazetteer within the Diversity Workbench, providing information on geographical names as shown below.



If the localisation system contains coordinates (Coordinates, Coordinates PD, Coordinates WGS84), a button  will appear, that will provide you with the possibility to set the


coordinates via Google Maps. Just click on the  button, and a window will open where you will see the 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. So you may use an entry for a named area (DiversityGazetteer) as a approximate localisation and than additional coordinates as the more accurate localisation.




If you start with existing geographic coordinates 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 bottom of the map. To take these coordinates in your data, just click OK.

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


The values for any localisation system are stored in two text fields. You can enter your values as simple text. This may prevent any calculations with your values. So you should prefer to enter your values according to the measurement units available. Whatever antique measurement units like feet or Fahrenheit may exist, within the Diversity Workbench measurement data are stored in units according to the [Système international d'unités \(SI\)](#). For those who still need to use these 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)	<input type="text" value="18"/>	<input type="text" value="36"/>	<input type="text" value="1,6111111"/>	Lat. (NS)	<input type="text" value="-31"/>	<input type="text" value="16"/>	<input type="text" value="34,8888888"/>		deg_min_sec <input type="text" value=""/>
------------	---------------------------------	---------------------------------	--	-----------	----------------------------------	---------------------------------	---	---	---

You can then edit the values and click on the  button to take the changed values in your data. The system will calculate the corresponding value for storage in the database together with the default accuracy. 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.

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 Alt. to  Available units: meter and feet.

Exp. from to  Available units: Orientation (N, NE, ...) and degree rel. to North.

Slope from to  Available units: degree and percent.




The accuracy resp. uncertainty 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) resp. degrees for angles.

The data for the geography are stored in the table [CollectionEventLocalisation](#).

Maps of the collection event

If there are coordinates available for your collection site of your locality using




To use this service, you need access to the internet. Click on the  button in the control to show the maps. Click on the  button to see the location of your event or if the event is part of a series the  button to see all locations of the event series. The site can be displayed either as a satellite image



or a geographical map. If you click on one of the needles marking the locations of the events, a window will show you the description of the event.



To generate a map you need coordinates stored in the table [CollectionEventLocalisation](#).

To show a distribution map as shown below of all the specimens found in your query, use the  button. This functionality is limited in the number of specimens that can be depicted, so it may be necessary to restrict your query.

Acc.Nr. **Erysiphe aquilegiae var. ranunculi (Grev.) R. Y.**
M-0014011

Query results 1 - 24

- Delphinium x cultorum Voss.
- Delphinium x cultorum Voss.
- Erysiphe aquilegiae var. ranunculi (Grev.) R. Y. Zher
- Erysiphe aquilegiae var. ranunculi (Grev.) R. Y. Zher
- Erysiphe aquilegiae var. ranunculi (Grev.) R. Y. Zher
- Erysiphe aquilegiae var. ranunculi (Grev.) R. Y. Zher

order by: Identification

Query conditions

Event

Country ~ Germany



Identification

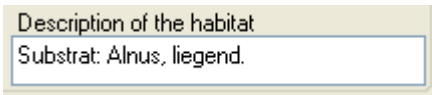
Taxon ~ Erysiphe aquilegiae var. ranunculi



Substrate organism

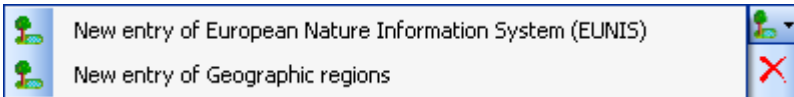
Taxon ~ Delphinium

Habitats and properties of the collection site

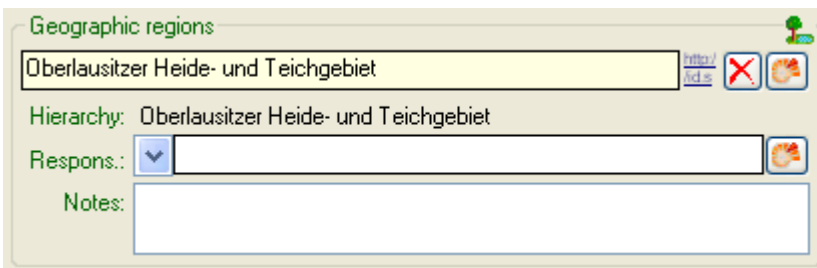
For the description of the habitat select the collection event  or an existing collection site property . The description is entered in the section **Description of the habitat**.





To enter a new property of the collection site, select the collection event  or an existing collection site property  and then choose the type of the property you want to enter.






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.



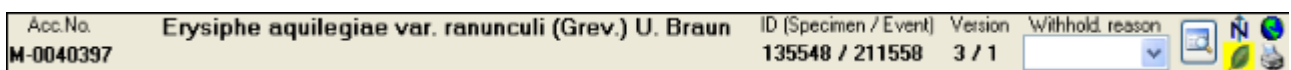
To delete entries use the  button. You can enter a value by either typing the name of the collection site property or by selection from the module DiversityScientificTerms. To search for properties from this module click on the  button. As responsible user the name of the current user will be inserted.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


The data concerning the habitats are 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 are 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 form shows some important parameters for the specimen selected. On the left side the **accession number** is shown. In the center you find the last [identification](#) of the main [identification unit](#) 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 **Versions** for the specimen and the collection event. For details about the version of a dataset see the [version](#) topic. The [availability](#) of a specimen can be changed by entering an appropriate reason in the field **Withholding reason**.



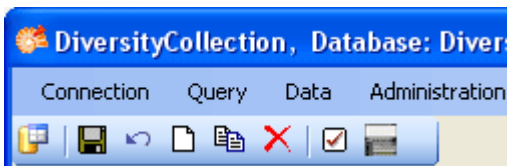
To inspect the history of a specimen click on the  button. For further details see the [history](#) section.

With the   buttons you can control the upper part of the form with the maps , the images for the collection event  and the specimen  as well as the label print . The buttons with the corresponding sector visible in the form are depicted with a red  background. If there are images available and they are hidden, the background will turn to yellow .


The data are stored in the table [CollectionSpecimen](#).


Data


The controls to handle datasets in the database are located in the left upper part of the form as shown in the image below. A step-by-step introduction for the creation of new datasets is provided in the [tutorial](#).

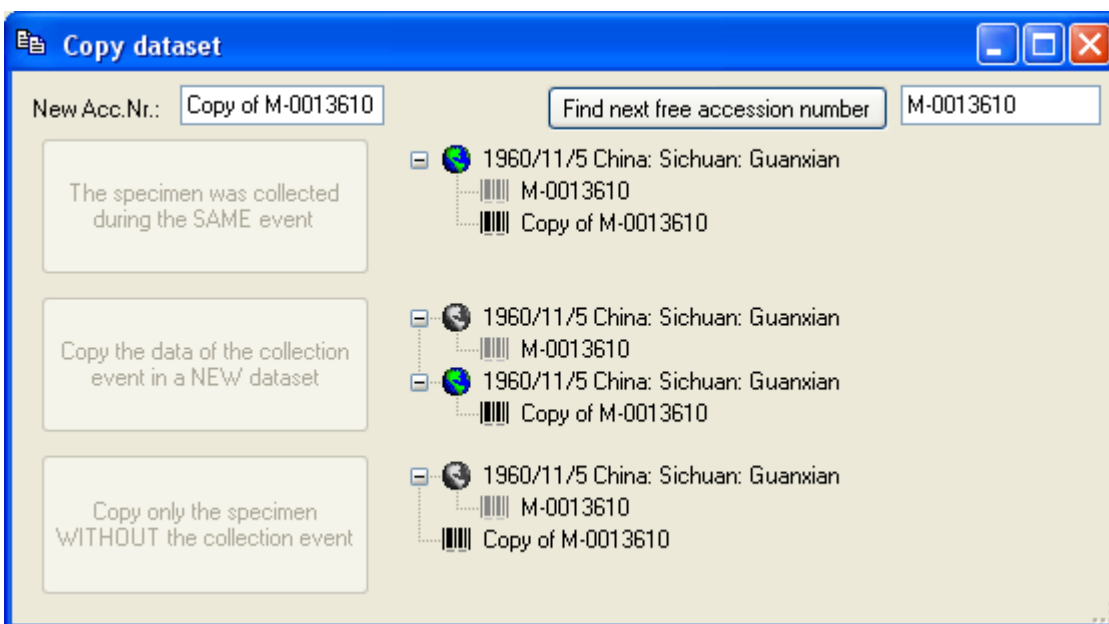


To **save** the changes in a dataset click on the  button. If you select another dataset from the result list, the current changes will be saved automatically.

To **undo** the changes in a dataset click on the  button. This will recover the original data unless the changes had been saved or changes were done in certain tables or hierarchies where the data must be stored to display the hierarchy.

To create a **new** entry in the database, click on the  button below the search result listbox. This will create a new record of a specimen and show it in the result list.

To **copy** the data of a specimen record, choose it from the list and click on the button . If the specimen you want to copy is linked to a collection event, a form will open and provide you with several possibilities for the copy as shown below.

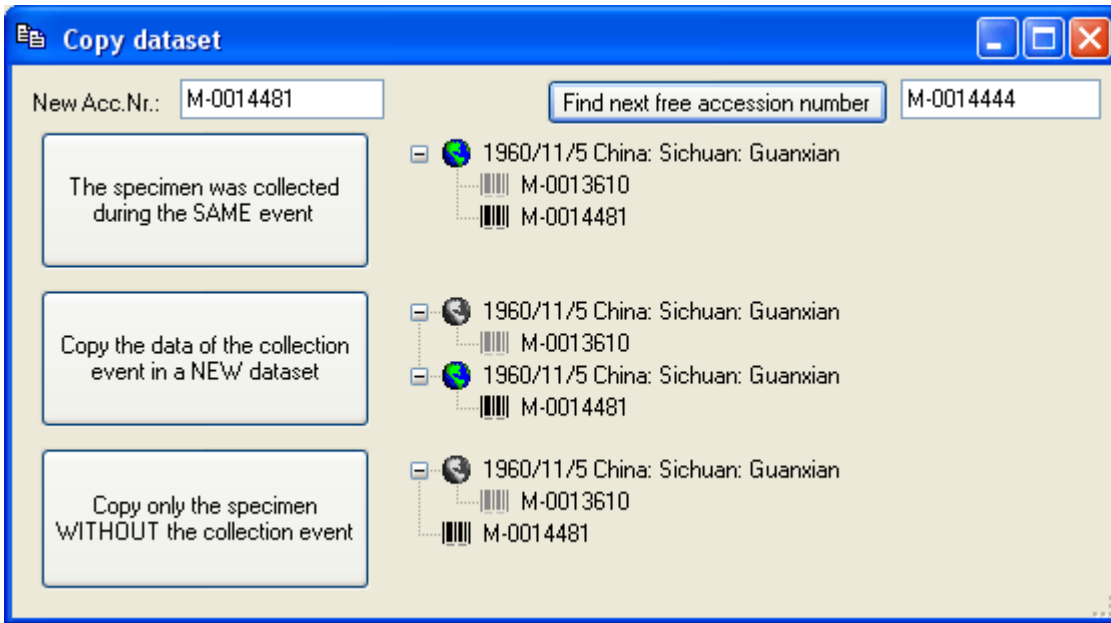


The field for the new accession number contains a string like Copy of If you change this the accession number to a value that is already present in the database you will be warned as shown below.



Use the **[Find next free accession number for:]** button to search for the next free number

for the accession number shown in the second field. If the program finds a free number, it will be used as shown below.

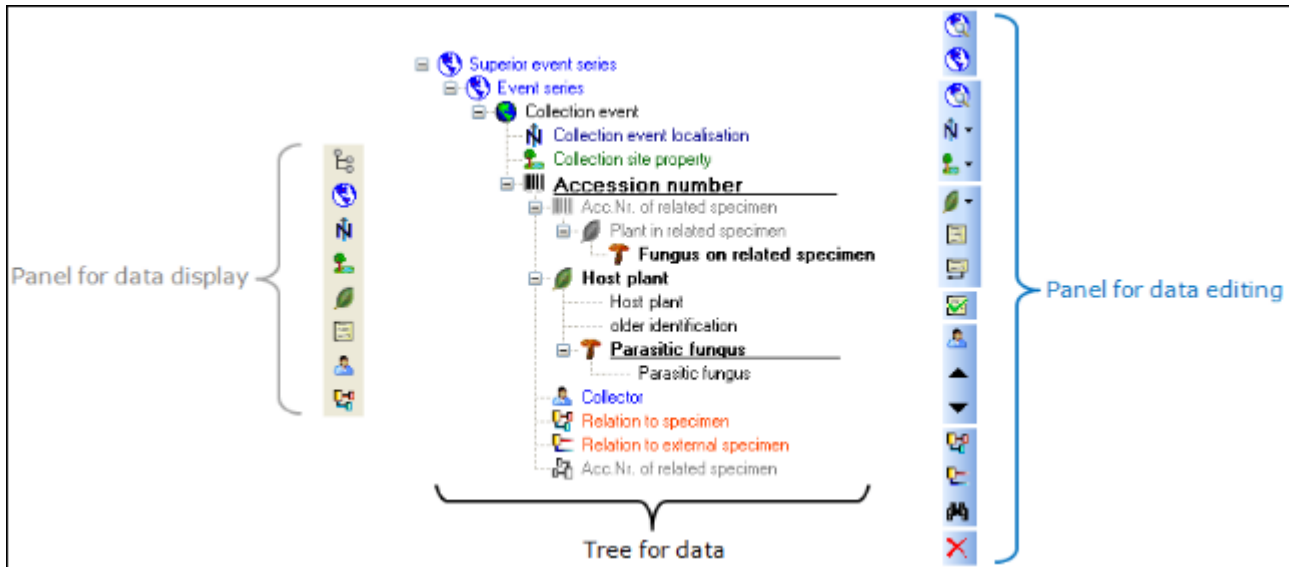


The first option will take the new dataset in the same collection event as the original data, so no new data for a collection event will be generated. The second option will create a copy of the original data for the collection event and connect the copy of the specimen record with the new event. The last option will only copy the specimen data and establish no connection to any collection event.

To **delete** a dataset click on the button .

Tree for the specimen

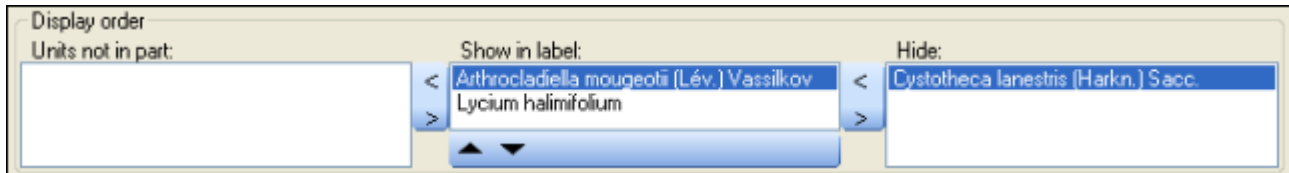
The upper tree in the form provides an overview for all the data linked with the specimen. With the buttons in the left panel you can hide or show certain nodes in the tree. So if for example you do not want to see the collectors, just click on the 👤 button and they will be hidden in the tree. The button will change to a grey version 🙋 and the background will turn to yellow to show that there are hidden data of the collectors. The first two buttons (🌐, 🗺️) are visible if the collection event is part of a collection event series. They switch between two display modes for the event series. If you click on the 🌐 button only the superior event series will be shown. To show the whole hierarchy of the event series, click on the 🗺️ button.



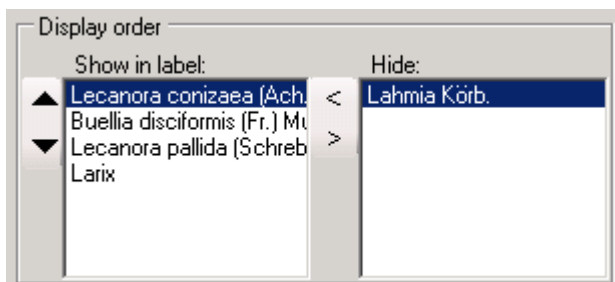
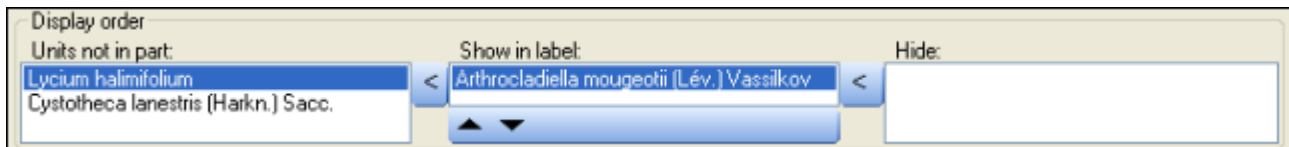
The panel on the right side of the tree is for editing the data, like for example the 👤 button will insert a new collector. For further details see the special sections.

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 that will be shown on a label. The first unit can not be transferred to the hide list.

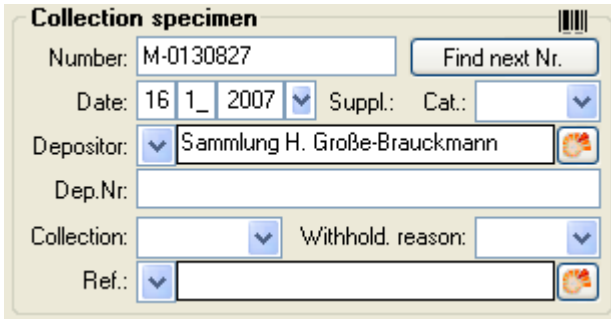


In addition to the display order you can specify whether an organism is present in a selected part of a specimen.



Accession

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

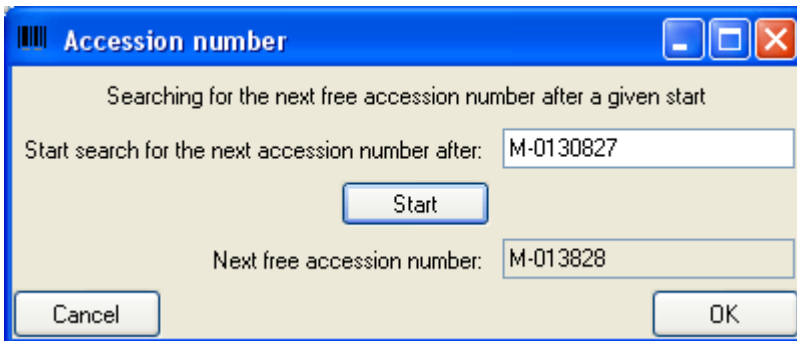


The screenshot shows a form titled "Collection specimen" with the following fields and controls:

- Number: M-0130827 (text input) and Find next Nr. (button)
- Date: 16 1_ 2007 (date picker) and Suppl.: Cat.: (dropdown)
- Depositor: Sammlung H. Große-Brauckmann (dropdown) and a small icon button
- Dep.Nr.: (text input)
- Collection: (dropdown) and Withhold. reason: (dropdown)
- Ref.: (dropdown) and a small icon button

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








The screenshot shows a dialog box titled "Accession number" with the following content:

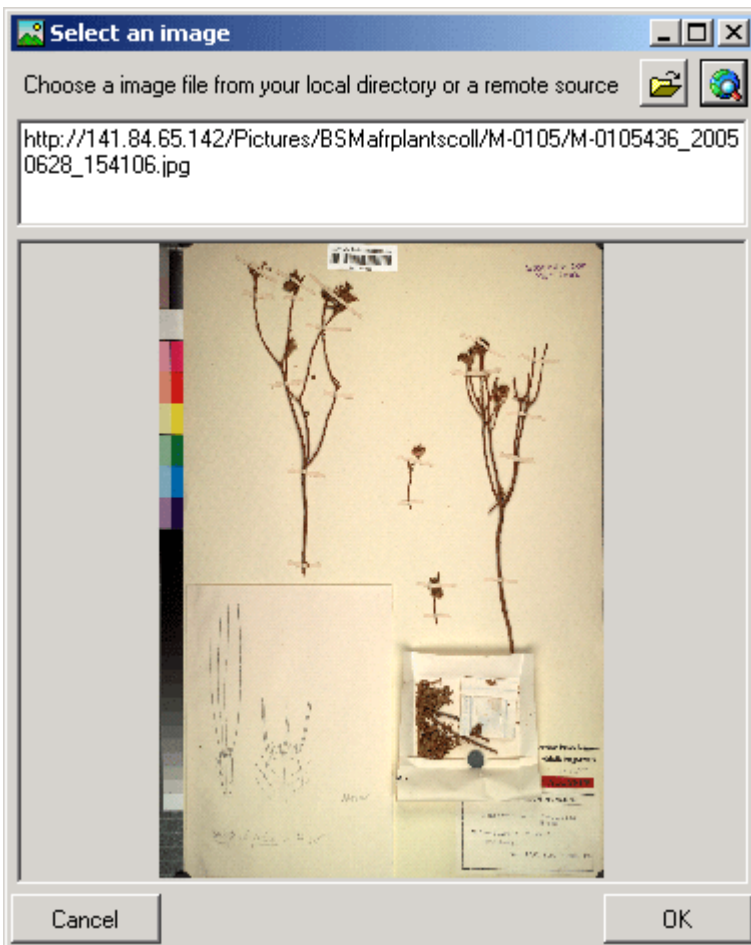
- Searching for the next free accession number after a given start
- Start search for the next accession number after: M-0130827 (text input)
- Start (button)
- Next free accession number: M-013828 (text input)
- Cancel (button) and OK (button)


The system will try to find the next free number on the basis of the accession numbers available in the database. Click OK to use the number for the specimen.

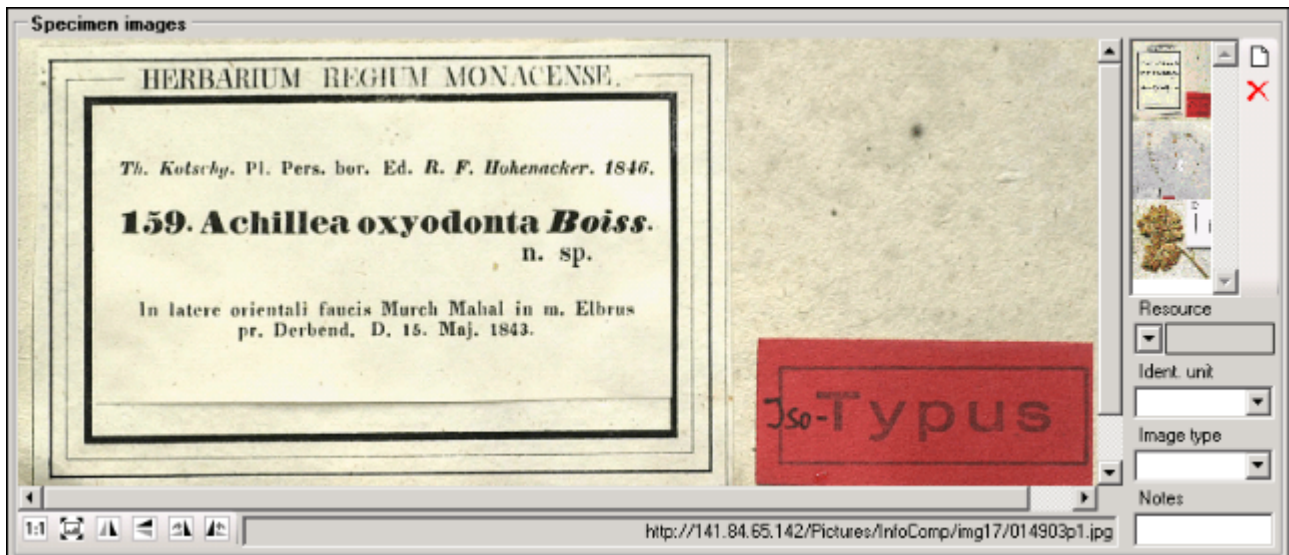
Data concerning the accession and deposition are stored in the table [CollectionSpecimen](#).








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 local with its path or as a reference to the module DiversityResources within the Diversity Workbench. To enter 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 in your local directories or on the  button to search for a web address. The selected image will be shown in the preview.





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

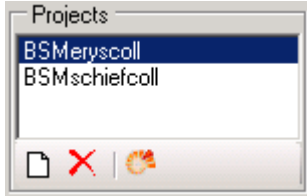


To zoom a sector of the image, just drag the mouse over the image. A red square will indicate the zoomed area. To set the size of the image to the original resolution click on the  button. To adapt the size of the image to the available space in the form click on the  button. To change the orientation 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.

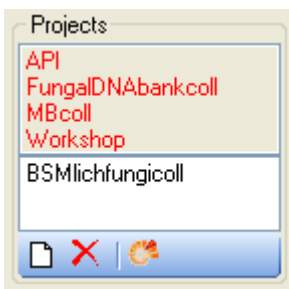
Data are stored in the table [CollectionSpecimenImage](#).

Projects

Every collection specimen can 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.





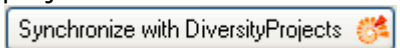
If there are projects, to which you have no access to, these will be listed in a separate list at the top as shown below.



Data are stored in the table [CollectionProject](#).

Details upon the projects within the Diversity Workbench are stored in the database

DiversityProjects. To open a project to see further information upon a project click on the  button. To edit details in the projects you need the application **DiversityProjects.exe** in your application directory and access to the database DiversityProjects. To synchronize the projects listed in DiversityProjects you can use the synchronize functionality in the [user administration](#) form as shown below. If DiversityProjects is not available you can create a new project with the  button. If DiversityProjects is available, use the synchronize functionality



User administration

Synchronise with DiversityUsers

Weiss, Markus

User accounts available in the database

- dbuser
- guest

User accounts with access to projects

- dbo
- fwweiss

Permissions of user

Projects that are available for a user

- BIOTAlchemicoll

Roles of the user

- db_owner
- DiversityCollectionAdministrator

Synchronise with DiversityProjects

Project that are not available for a user

- APIplantnames
- Bleitaucoll
- B5Maltplantscoll
- B5Mcompcoll
- B5Meryscoll
- B5Mlichfungicoll
- B5Mmicrofexscoll
- B5Mrysmaincoll
- B5Mneubert
- B5Mschiefcoll
- B5Mschnitler
- B5Mwahlfcoll
- GLMcoll
- HALLcoll
- HOHaltplantscoll
- MELxnames
- MSBaltplantscoll
- MSBcompcoll
- REGaltplantscoll

Role permissions

	name	permission_name	state_desc
▶	AgentID	EXECUTE	GRANT
	AgentIDPresent	EXECUTE	GRANT
	AgentOneString	SELECT	GRANT
	Analysis	INSERT	GRANT
	Analysis	SELECT	GRANT
	Analysis	UPDATE	GRANT
	Analysis_log	INSERT	GRANT
	ApplicationSearc...	SELECT	GRANT
	ApplicationSearc...	SELECT	GRANT
	CollCharacterTyp...	SELECT	GRANT
	Collection	INSERT	GRANT

Roles available in the database

- AfricanTypes
- db_accessadmin
- db_backupoperator
- db_datareader
- db_datawriter
- db_ddladmin
- db_denydatareader
- db_denydatawriter
- db_owner
- db_securityadmin
- DiversityCollectionAdministrator
- DiversityCollectionEditor
- DiversityCollectionUser

Role members

- AfricanTypes
- DiversityCollectionAdministrator

Notes and problems

To enter notes or problems connected with the specimen select it in the hierarchy. The data form will then 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 that 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!

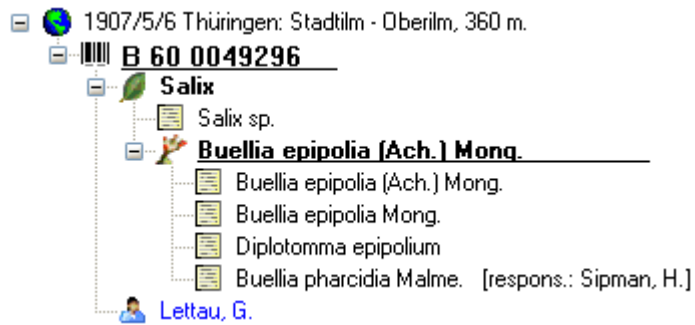


The image shows a screenshot of a web-based data entry form. The form is titled "Notes" and is contained within a light-colored rectangular box. It features three distinct input fields, each with a label to its left and a corresponding text area to its right. The first field is labeled "Original:" and is the top-most text area. The second field is labeled "Additional:" and is the middle text area. The third field is labeled "Problems:" and is the bottom-most text area. All three text areas are currently empty.

The data are stored in the table [CollectionSpecimen](#).

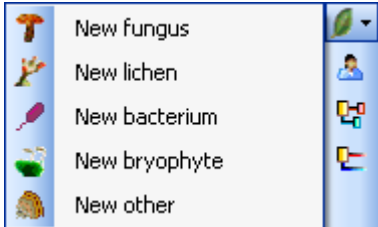
Organisms and identifications

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

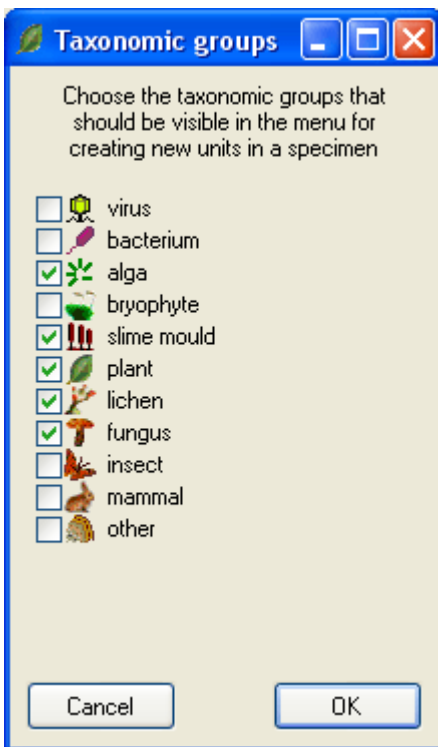



Identification unit

The items or organisms in one collection specimen are regarded as identification units. One specimen can contain several identification units, 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 - Taxonomic groups ... from the menu. A form as shown below will open where you can select the groups that should be shown.




The organisms of the specimen are shown in the tree. To edit the relations between the organisms just do this by 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.




To enter details about one of the organisms like the e.g. the gender or the life stage, select it in the tree. Then the fields for the details of this organism are shown in the right area of the

form as shown below.

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 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 that 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 background 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 and 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.




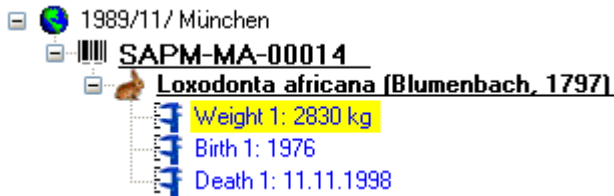
For details about [exsiccatal series](#) and [analysis](#) see the related topics. You can sort your identification units e.g. for display on a label with the [display order](#). Each identification unit






can have several [identifications](#).

The data for the organisms are stored in the table [IdentificationUnit](#).

Analysis

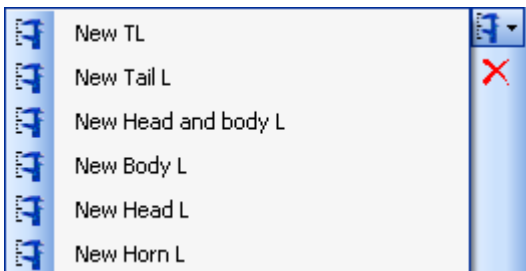
The organisms in a specimen can be analysed by analysis types defined in the database. In the tree the analysis entries are symbolized with an  as shown below. Only the types of analysis that were assigned to the group of the organism can be selected. An analysis always refers to an organism and may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





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 analysis entries will be shown as above. If you click a second time on the  button it will change to the hierarchy mode  and the entries will be shown as in the tree below. The last state  will hide the entries.



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.

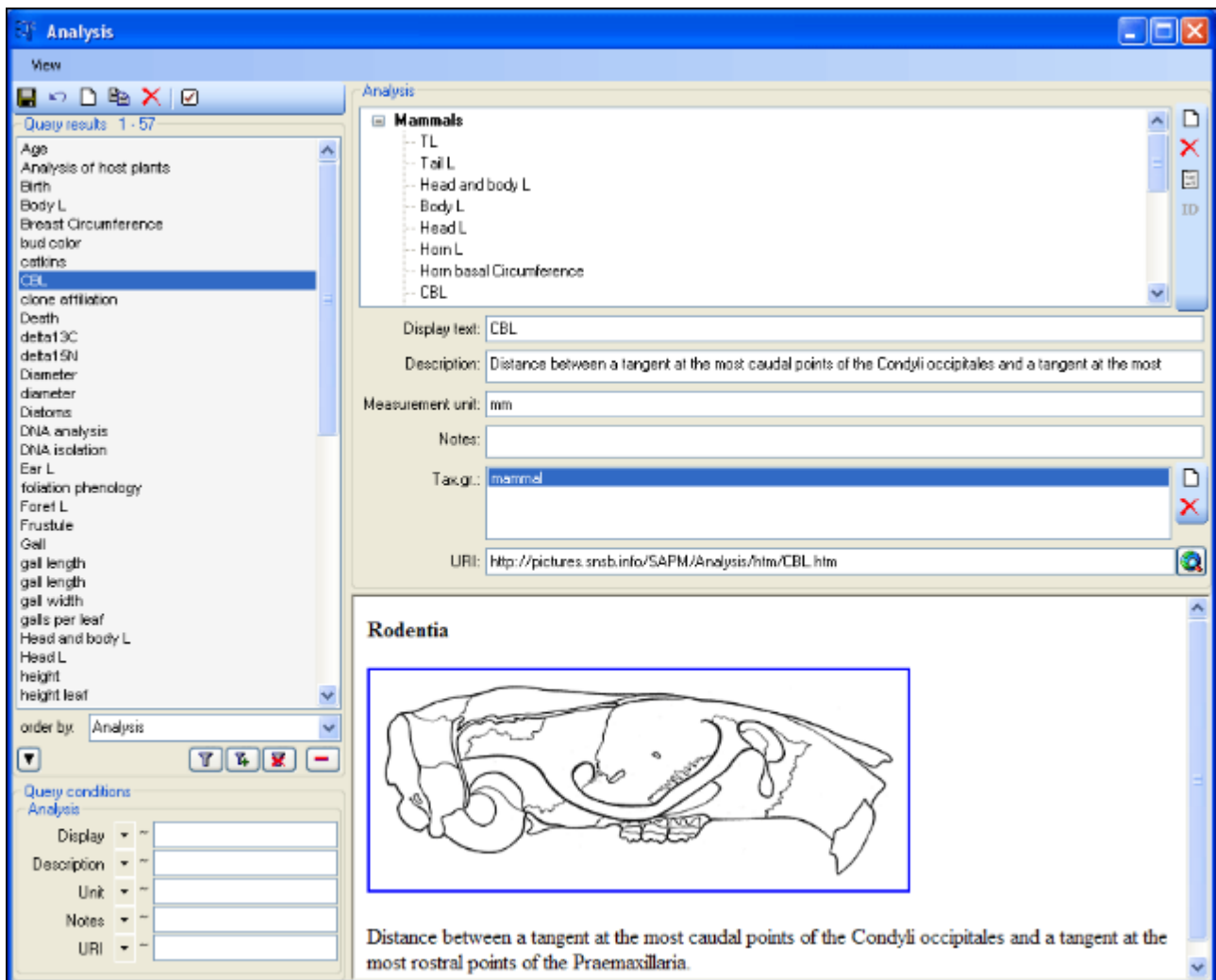


To delete an analysis, select it in the tree and use the  button in the panel on the left. To edit the details of an analysis, select it in the tree to enter the fields as shown below. To enter or inspect an URI given for a single analysis, click on the  button.

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





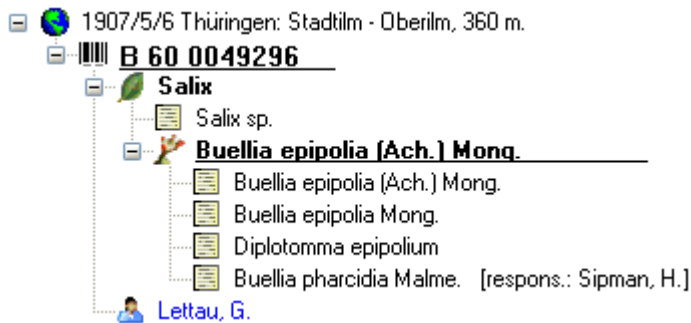
For the import and export of data it is sometimes necessary to know the ID's of the analysis types. To see the ID's, click on the **ID** button. Then the ID's will be shown as in the image below.




- ☐ **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. Edit the list of taxonomic groups that can use a certain analysis using the  and  button. For details about handling the data see the [data](#) section. If you want to or inspect an URI given for an analysis type, click on the  button. In the window below the URL related to the analysis can be shown.


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.




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 a identification, choose it in the tree and then click on the  button. 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 then can enter the details in the form opening on the right side of the tree as shown below.

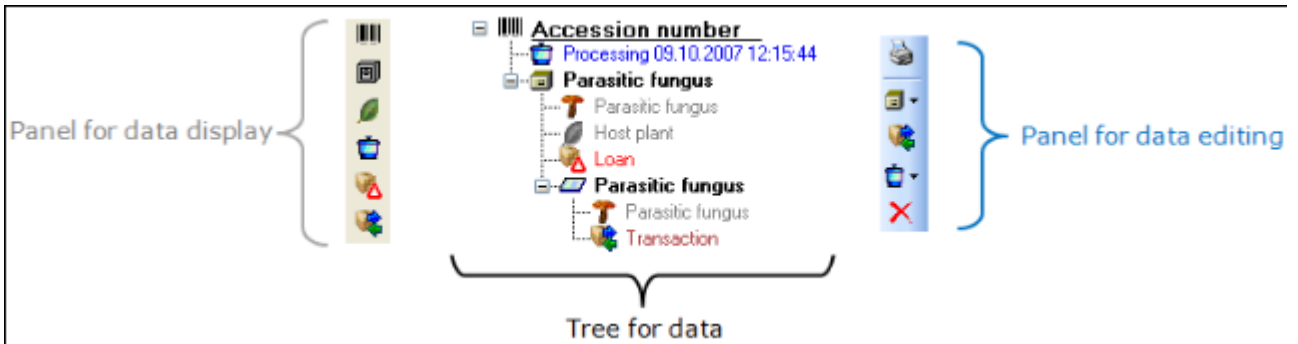
The taxonomic name of an organism can be selected from either the names already available in DiversityCollection or from the module DiversityTaxonNames. To choose from the local names type the beginning of the name and click on the drop down button  to get a list of the available names. You can use [wildcards](#)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


To select a name from an external database for taxonomic names, click on the  button. A [form](#) will open where you can search for a taxonomic name.

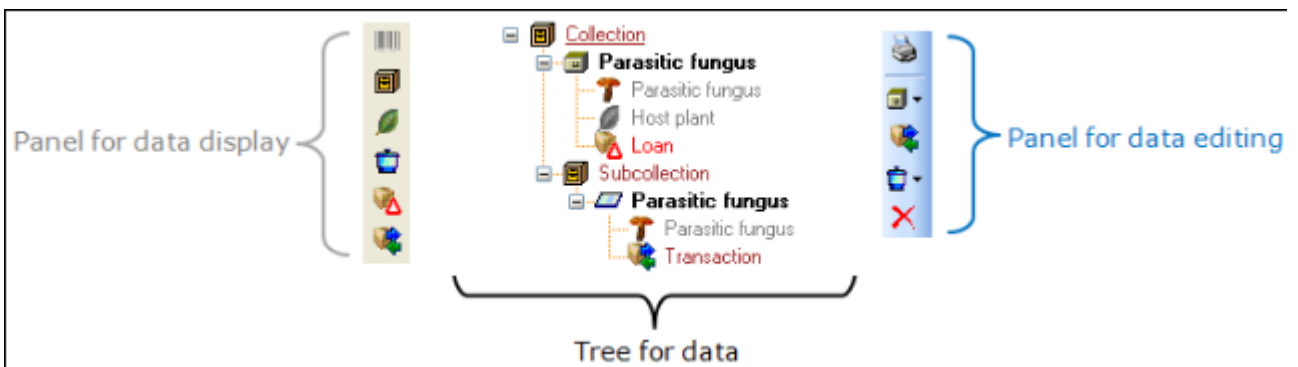
In the database the data for the identification are stored in table [Identification](#).



Storage and trees for the parts of the specimen


In the tree at the base of the form 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).

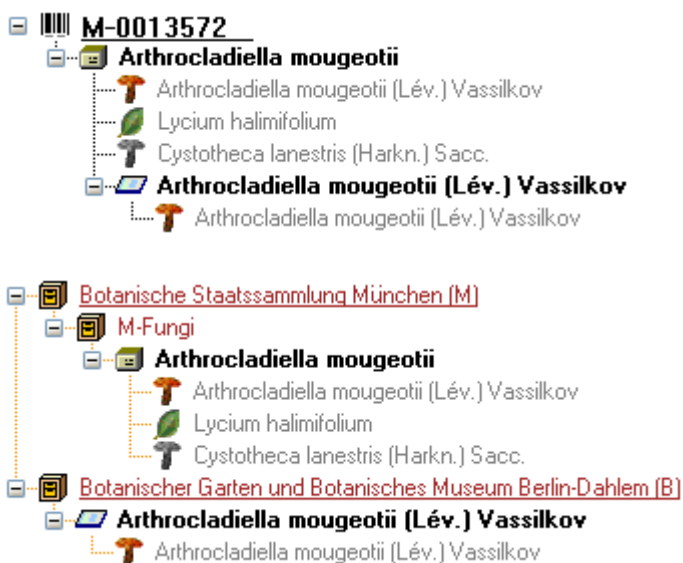


With the buttons in the left panel you can hide or show certain nodes in the tree. So if for example you do not want to see the processings, just click on the  button and they will be hidden in the tree. The button will change to a grey version  and the background will turn to yellow, to show you that there are hidden data of the processings.

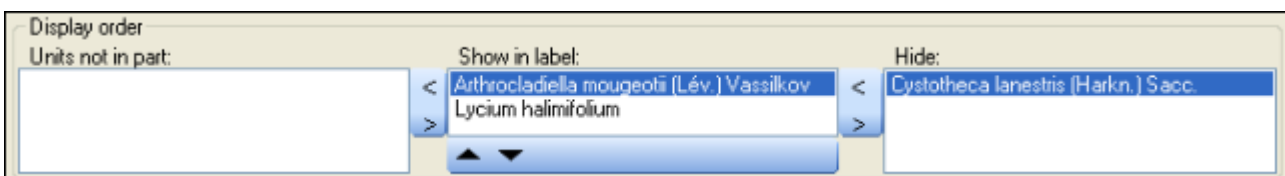
The panel on the right of the tree is for editing the data, like for example the  button will insert a new transaction. For further details see the sections [Transaction](#) and [Processing](#) .




Parts of the specimen

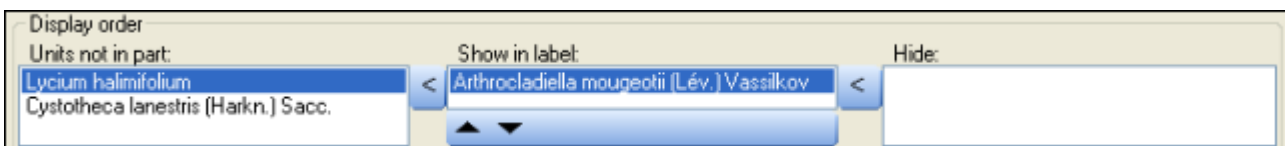
A specimen can contain several parts which may be stored in several collections. These parts may represent different material categories, e.g. herbarium sheets, microscopic slides etc. The parts are shown in the part tree under the main tree. This tree depicts the parts either in accordance to their 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 where 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. 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 a child of the old part. You can later edit these relations by drag & drop. If you want to create a copy of a part, use the  button in the panel right of the tree.



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






In the example above, all organisms are present in the specimen, but the fungus *Cystotheca lanestrus* was chosen to not appear on the label and transferred to the **Hide** list. This is symbolized by a grey icon  in the tree. The slide, symbolized by the  icon, was created from the sample, so 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. So 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).



To move the organisms between the lists use the > and < buttons. In the list **Show in label** you can 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 that will be 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.








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 enter the **storage location** you can 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 specimens are shown with their dependence upon each other, but where they are located with the collections. To get information about a collection just select it in the tree. If you have the necessary rights, you can use the  button to open for the administration of the collections. This form is as well accessible under the menu entry **Administration - Collections...**

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




Here some examples:

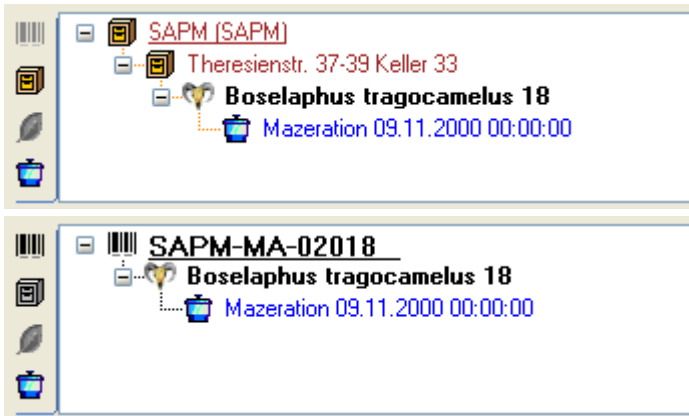
-  bones: bones or skeleton from vertebrates
-  cultures: living cultures of organisms
-  drawing: original line or color drawing
-  herbarium sheets: capsules or sheets as stored in a botanical collection
-  icones: icones, images etc. stored in a botanical collection
-  micr. slide: glass plate with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

Specimens can be included in a [transaction](#) and every stored part of a specimen can be treated with several [processings](#).

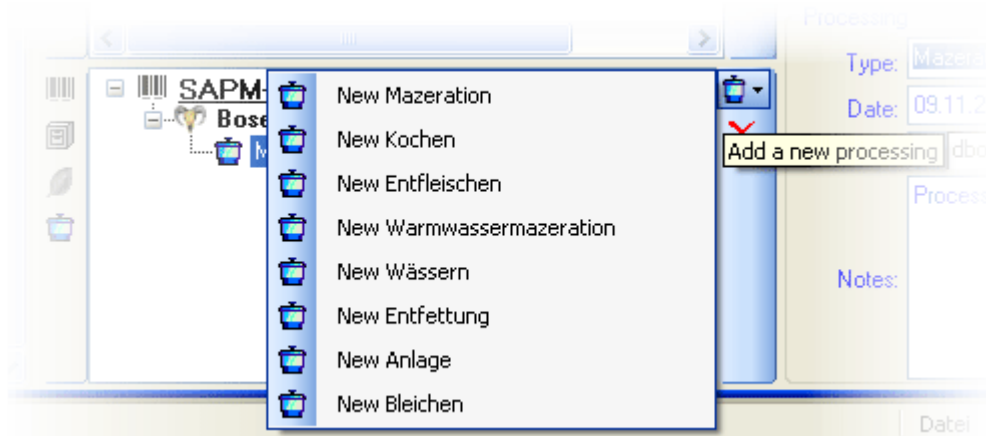
Data are stored in the table [CollectionSpecimenPart](#).


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 this will be indicated by the icon in the tool bar. You can hide  or show  the processings in the hierarchy with a click on the icon. The images below show a processing in either the collection or the specimen tree for the parts.

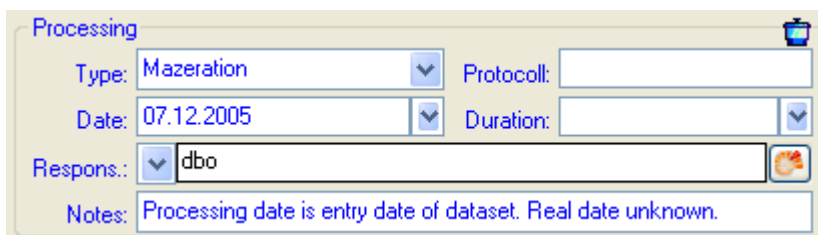


You can enter a new processing for either the whole specimen or a part of the specimen. To do this select the specimen or a part in the hierarchy and then choose a processing from the list as shown below.

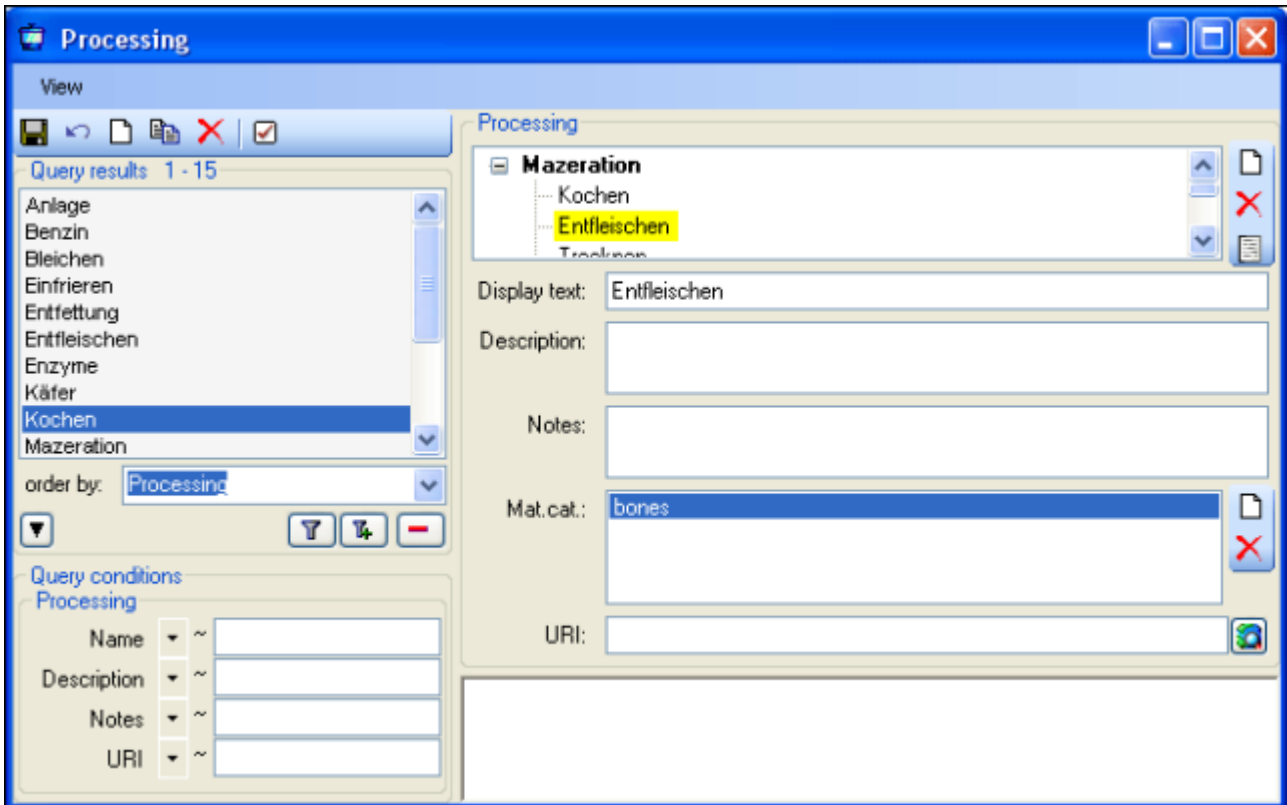





To delete a processing select it and click on the  button. To edit the data for a processing select it in the hierarchy. The form will show you the fields related to the processing as shown below.

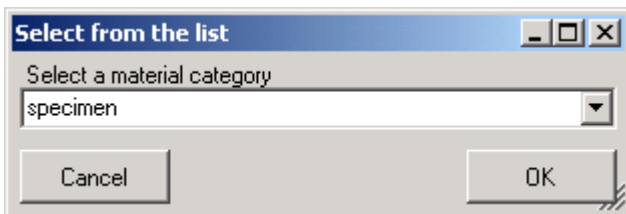
In the form select the type of your processing from the list.



If you have the proper rights you can edit the processing types under the menu entry **Administration - Processing...**



In this form 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 that should be connected to the selected processing, click on the  button in the panel right of the material categories. A form will open and you have to select the material category that should be connected with the processing (see below).




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 datasets, click on the **ID** button. Then the ID's will be shown as in the image below.

```

Mazeration [5]
├── Kochen [6]
├── Entfleischen [8]
└── Trocknen [9]
  
```


The data of the processing are stored in the table [CollectionSpecimenProcessing](#).

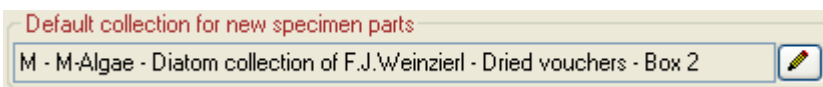
Collection


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.

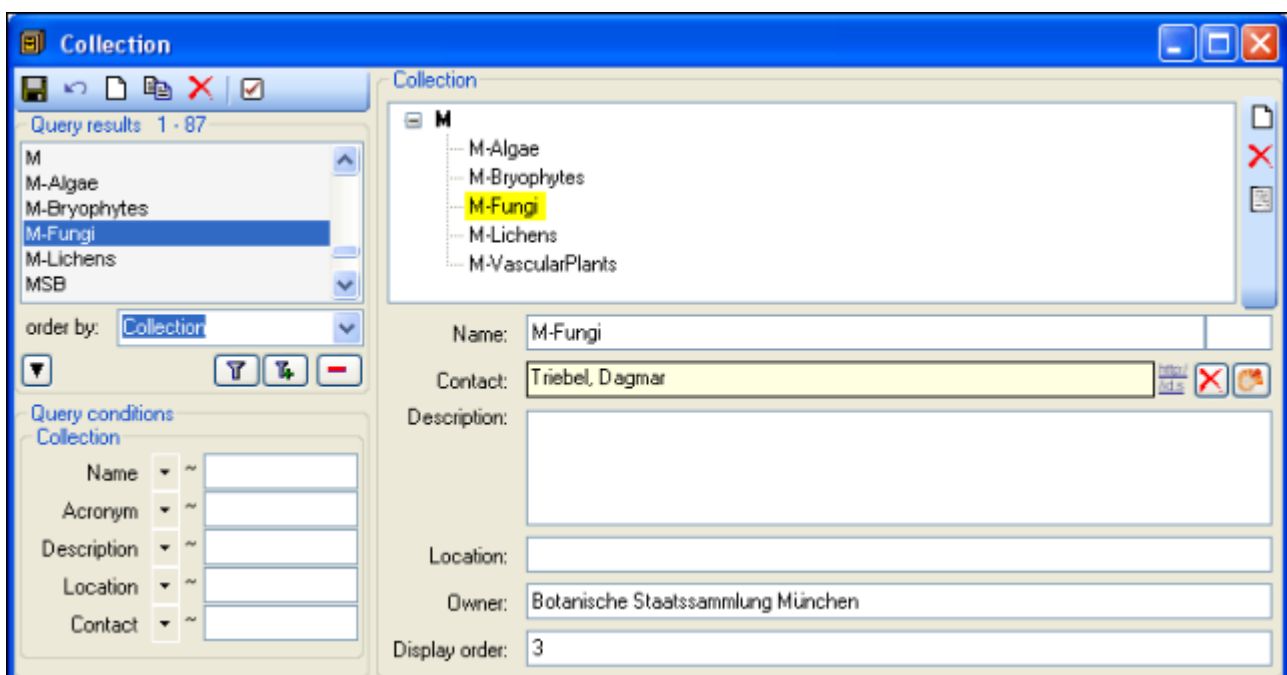





To edit the details of a collection, select it in the tree to display the datafields.

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.




If you need further information about a collection click on the  icons. To open the form for the collection administration choose **Administration - Collections...** from the menu (this menu entry is only available for administrators). This will open a form as shown below where as an administrator you can edit the collections used in your database.

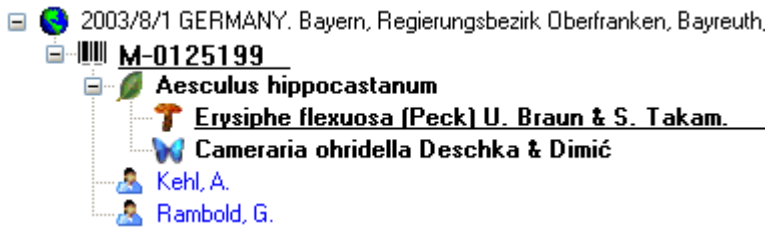




The specimens stored in a selected collection are listed in the specimen list. You can hide / show this list using the  /  button. To change to a specimen from this list click on the  button.

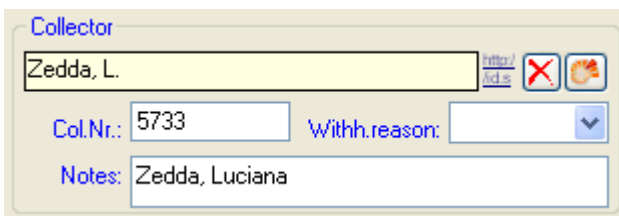
For details about handling the data see the [data](#) section. Data of the collections are stored in the table [Collection](#).




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.



To hide or show the collectors in the tree use the  icon in the left panel. 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. To enter details for a collector, select it in the tree. In the right part of the form the fields for the details will then displayed (see below).








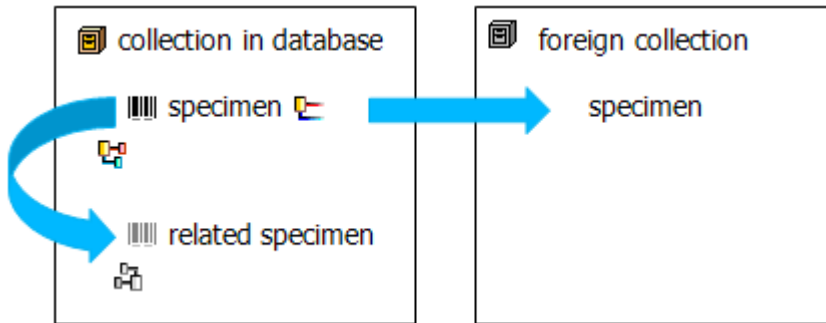
If a collector should refer to a dataset in the module DiversityAgents click on the  button. In the. The sequence of the collectors (e.g. for print on a label) as shown in the tree can be changed by with the  and  buttons in the panel on the right of the tree.

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](#).



Relation

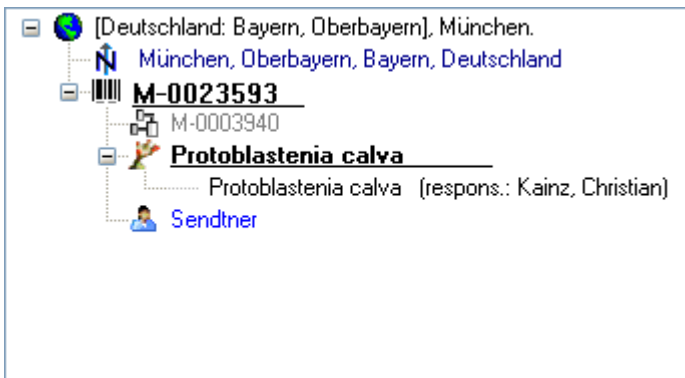
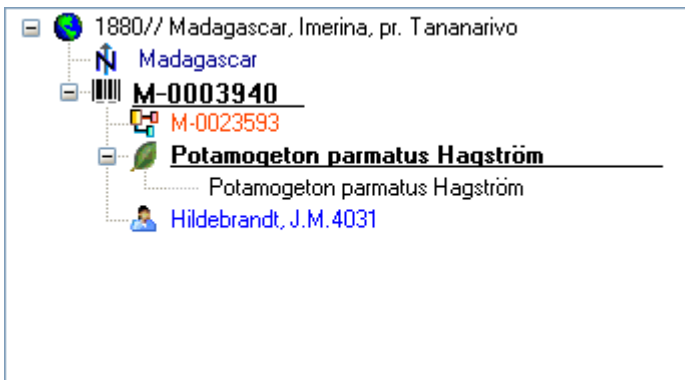
Each specimen may have relations to other specimens. This can be documented by adding relations to these specimens. To add a relation select the specimen in the tree (symbolized by the barcode ). Then you can either add a relation to a local specimen using the  button or a relation to a remote specimen 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 can search for the related specimen.

Select the related specimen from the query result list and click OK to close the form 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.



With internal relations you can navigate to the related specimens using the  button.

External relation


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




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 form the details of the dataset will be shown (see below).

Relation to other specimen 

Specimen (e.g. URL):
 

Description:

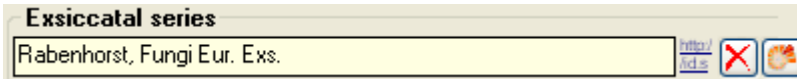
Collection:  Relation type: 

Notes:

The data are stored in the table [CollectionSpecimenRelation](#).

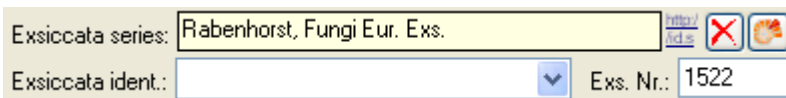
Exsiccatae

A [specimen](#) may be part of an exsiccatal series. These series are administrated in the Diversity Workbench module DiversityExsiccatae. To enter the exsiccatal series select the specimen or the organism resp. identification unit in the tree. With the specimen the exsiccatal series is shown at the base of the data form as shown below.



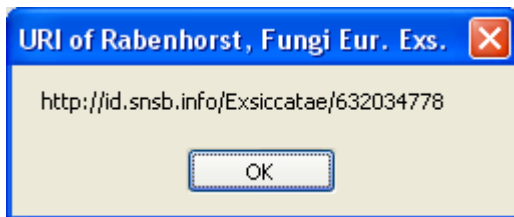
The screenshot shows a data form with a field titled "Exsiccatal series". The field contains the text "Rabenhorst, Fungi Eur. Exs.". To the right of the text input are three icons: a small "info" icon, a red "X" icon, and a globe icon.

As there may be several organisms with separate exsiccatal numbers in one specimen the numbers are handled together with the identification units. Select the concerned organism to enter data in the form as shown below.



The screenshot shows two fields in a data form. The first field is labeled "Exsiccata series:" and contains the text "Rabenhorst, Fungi Eur. Exs.". To its right are the same three icons as in the previous screenshot. The second field is labeled "Exsiccata ident:" and contains a dropdown menu with a blue arrow pointing down. To the right of this field is a text input field labeled "Exs. Nr.:" containing the number "1522".

You can either type the name of the exsiccatal series or choose one from the [module](#) DiversityExsiccatae. If you click on the [info](#) Link a form will open showing the link to the entry as derived from the module.



The screenshot shows a dialog box with a blue title bar that reads "URI of Rabenhorst, Fungi Eur. Exs." and a red "X" icon in the top right corner. The main area of the dialog box contains the text "http://id.snsb.info/Exsiccatae/632034778". At the bottom center of the dialog box is an "OK" button.

The data about the exsiccatal series are stored in the table [CollectionSpecimen](#), the data about the number and the taxon are stored in the table [IdentificationUnit](#).

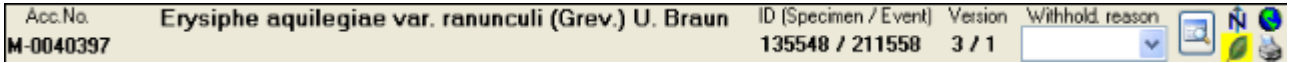
Access to the data

To get access to the data, you have to take several hurdles. In DiversityCollection, you must be a member of one of the [user groups](#). You have only access to those data, that are listed in the [projects](#) you have access to. For external users, data may be blocked by entries in the [data withholding reasons](#).

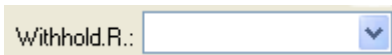


Availability of datasets

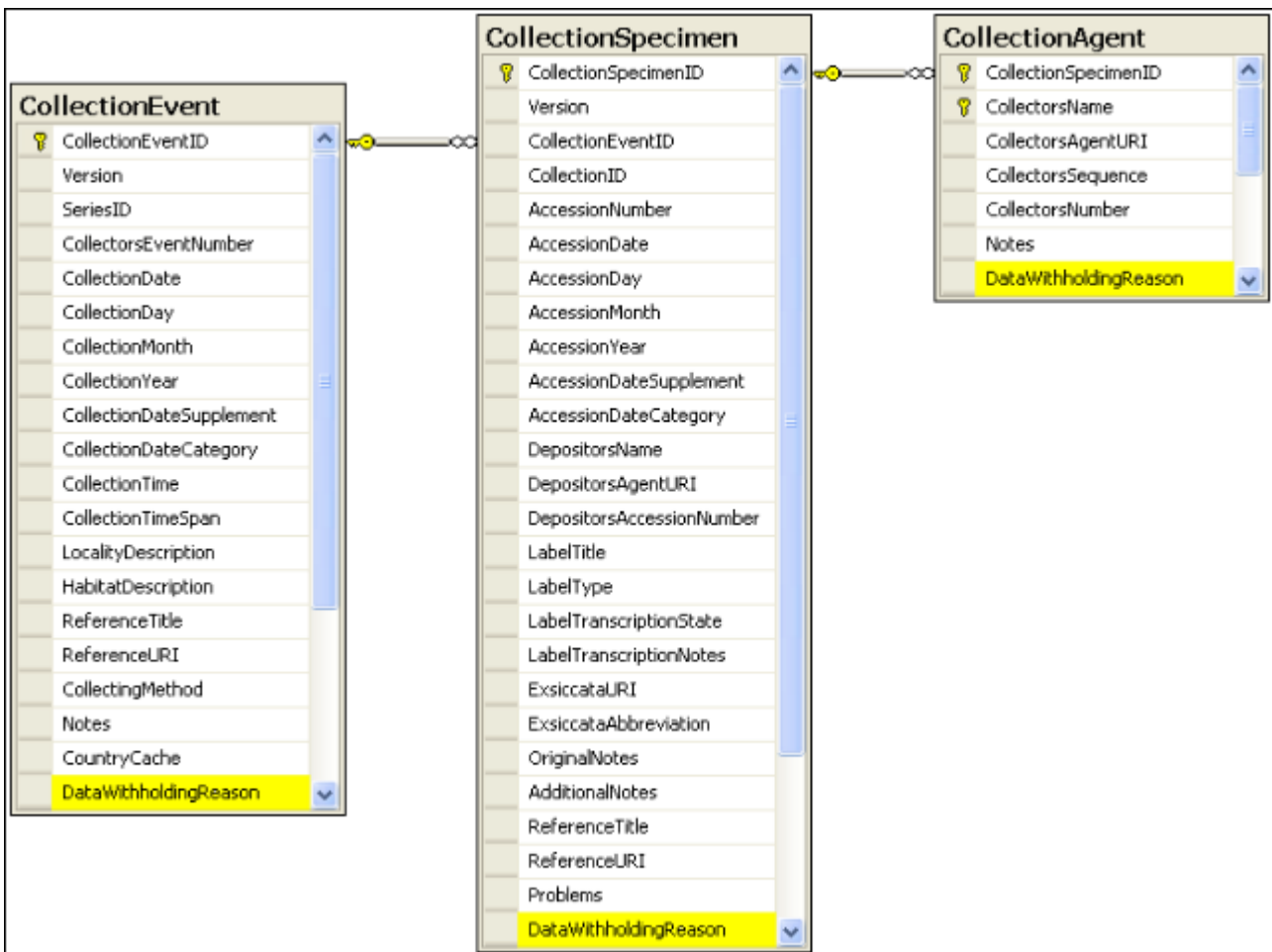
The data of certain parts of the database can be blocked for remote access. If you want to prevent access for the whole dataset, enter your reason in the field **Withholding reason** in the header (see below).



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.

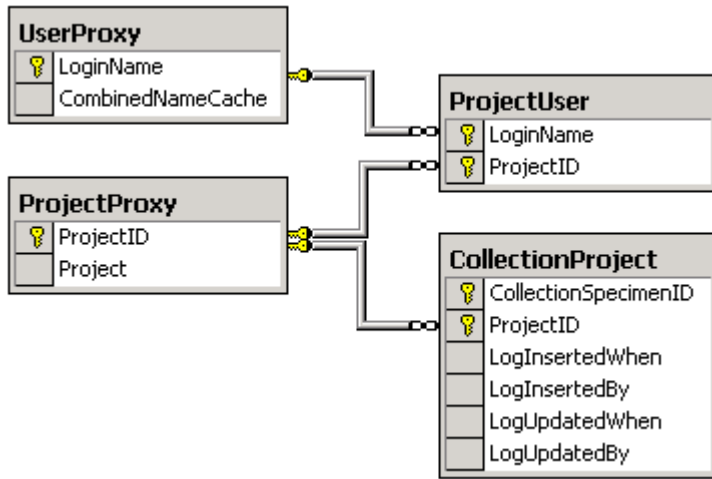


Within the database a user has only access to the data of those projects for which he has the permission. If a dataset belongs to a certain project, this is stored in the table [CollectionProject](#). To prevent a publication of the data these can be blocked for the whole dataset (table [CollectionSpecimen](#)), for the [locality and collection](#) site informations (table [CollectionEvent](#)) and for the [collectors](#) (table [CollectionAgent](#)) - see overview below.





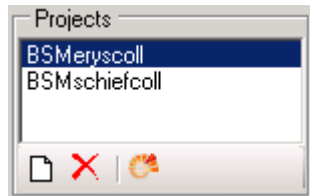
Permissions for projects

The access for the user to the data within the database are stored in the tables shown below. The tables [UserProxy](#) and [ProjectProxy](#) are related to the Diversity Workbench modules [DiversityUsers](#) and [DiversityProjects](#) respectively.

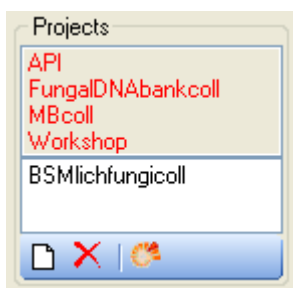


Projects



Every collection specimen can 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.

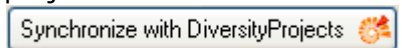


If there are projects, to which you have no access to, these will be listed in a separate list at the top as shown below.



Data are stored in the table [CollectionProject](#).

Details upon the projects within the Diversity Workbench are stored in the database DiversityProjects. To open a project to see further information upon a project click on the  button. To edit details in the projects you need the application **DiversityProjects.exe** in your application directory and access to the database DiversityProjects. To synchronize the projects listed in DiversityProjects you can use the synchronize functionality in the [user administration](#) form as shown below. If DiversityProjects is not available you can create a new project with the  button. If DiversityProjects is available, use the synchronize functionality



User administration

Synchronise with DiversityUsers

Weiss, Markus

User accounts available in the database

- dbuser
- guest

User accounts with access to projects

- dbo
- fwweiss

Permissions of user

Projects that are available for a user

- BIOTAlchemicoll

Roles of the user

- db_owner
- DiversityCollectionAdministrator

Synchronise with DiversityProjects

Project that are not available for a user

- APIplantnames
- Bleitaucoll
- B5Maltplantscoll
- B5Mcompcoll
- B5Meryscoll
- B5Mlichfungicoll
- B5Mmicrofexscoll
- B5Mrysmaincoll
- B5Mneubert
- B5Mschiefcoll
- B5Mschnitler
- B5Mwahlfcoll
- GLMcoll
- HALLcoll
- HOHaltplantscoll
- MELnames
- MSBaltplantscoll
- MSBcompcoll
- REGaltplantscoll

Role permissions

	name	permission_name	state_desc
▶	AgentID	EXECUTE	GRANT
	AgentIDPresent	EXECUTE	GRANT
	AgentOneString	SELECT	GRANT
	Analysis	INSERT	GRANT
	Analysis	SELECT	GRANT
	Analysis	UPDATE	GRANT
	Analysis_log	INSERT	GRANT
	ApplicationSearc...	SELECT	GRANT
	ApplicationSearc...	SELECT	GRANT
	CollCharacterTyp...	SELECT	GRANT
	Collection	INSERT	GRANT





Roles available in the database









- AfricanTypes
- db_accessadmin
- db_backupoperator
- db_datareader
- db_datawriter
- db_ddladmin
- db_denydatareader
- db_denydatawriter
- db_owner
- db_securityadmin
- DiversityCollectionAdministrator
- DiversityCollectionEditor
- DiversityCollectionUser

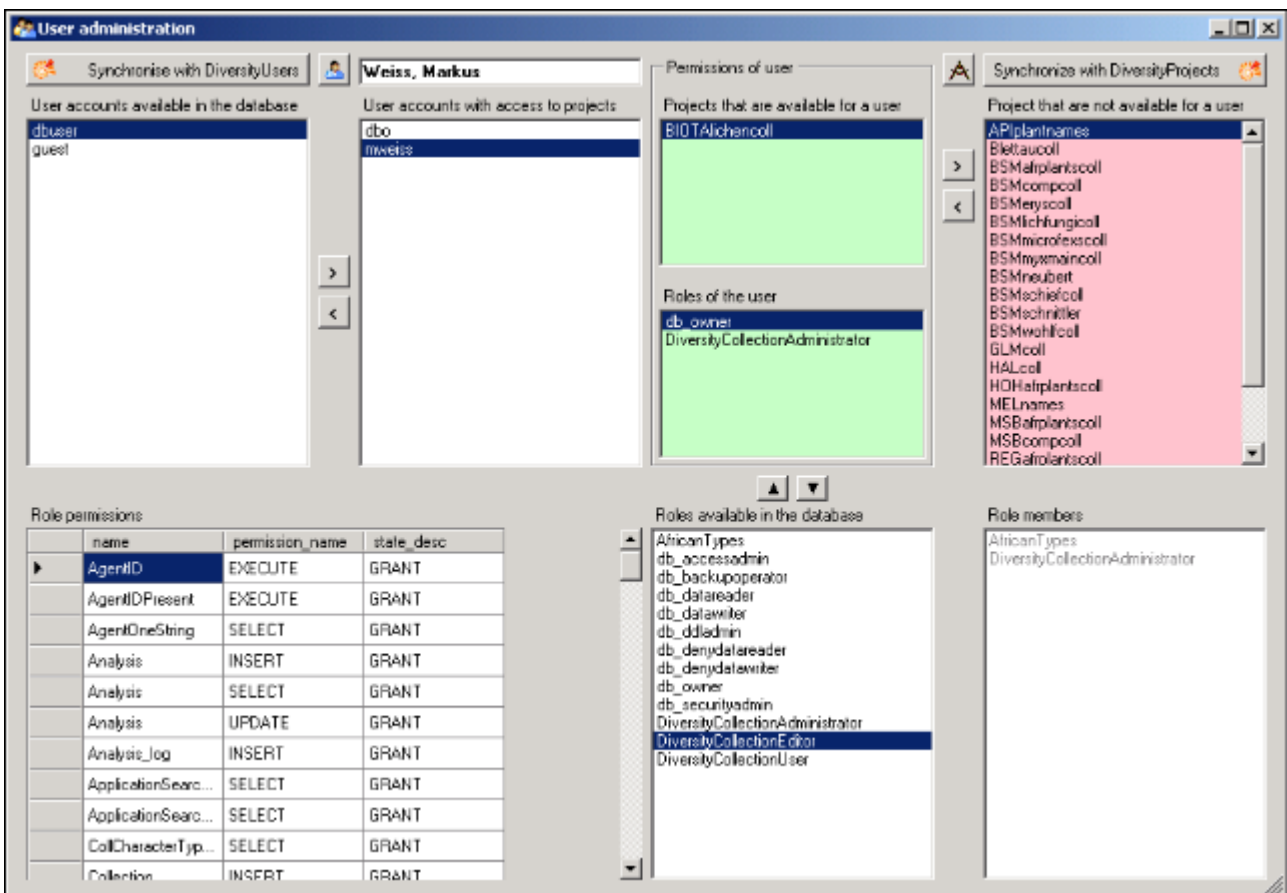
Role members

- AfricanTypes
- DiversityCollectionAdministrator

User administration

The permissions of users in the database are set via user groups resp. roles in the database and the access to the projects. To set the permissions choose **Administration - User ...** from the menu. A form will open where you can change the permissions of the user. The first list shows the user accounts that are available in the database but have no access to any of the projects. To synchronize this list with the Diversity Workbench module DiversityUsers click on the  button. To create a new SQL-Server User, click on the  button. To create a new Windows user with access to the database resp. allow an existing user the access to the database use the Microsoft SQL Server Management Studio (see the [installation](#) section for further details). To permit access to a project click on the  button. To remove a user from this list use the  button.

The area **Permission of user** shows the projects a user has access to and the roles of the user within the database. To move users between the lists **Projects that are available for a user** and **Projects that are not available for a user** use the  and  buttons. To create a new project click on the  button. If you use the Diversity Workbench module DiversityProjects, you can create a new project there and use the synchronize button . To change the roles of a user use the  and  buttons. Underneath the project list for a user you find the list of the **Roles of the user**. This list can be changed by using the  and  buttons. Underneath the roles list you find the list with the roles available in the database. On the left side of this list the permissions of the selected role are listed and on the right side the members of this role.



The screenshot shows the 'User administration' window with the following sections:

- User accounts available in the database:** dbuser, guest
- User accounts with access to projects:** dbo, mxvelis
- Projects that are available for a user:** BIOTAlchemcoll
- Roles of the user:** db_owner, DiversityCollectionAdministrator
- Project that are not available for a user:** APIplantnames, Blettaucoll, BSMaltplantscoll, BSMcompcoll, BSMeryscoll, BSMlichfungicoll, BSMmicrofexscoll, BSMmyxmaincoll, BSMnesubert, BSMschiefcoll, BSMschmittler, BSMwohlficoll, GLMcoll, HALcoll, HOHaltplantcoll, MELnames, MSBaltplantscoll, MSBcompcoll, REGafrolantscoll
- Role permissions table:**

name	permission_name	state_desc
AgentID	EXECUTE	GRANT
AgentIDPresent	EXECUTE	GRANT
AgentOneString	SELECT	GRANT
Analysis	INSERT	GRANT
Analysis	SELECT	GRANT
Analysis	UPDATE	GRANT
Analysis_log	INSERT	GRANT
ApplicationSearc...	SELECT	GRANT
ApplicationSearc...	SELECT	GRANT
CollCharacterTyp...	SELECT	GRANT
Collection	INSERT	GRANT
- Roles available in the database:** AfricanTypes, db_accessadmin, db_backupoperator, db_datareader, db_datawriter, db_ddladmin, db_denydatareader, db_denydatawriter, db_owner, db_securityadmin, DiversityCollectionAdministrator, DiversityCollectionEditor, DiversityCollectionUser
- Role members:** AfricanTypes, DiversityCollectionAdministrator

The permissions of the roles are shown in the lower left part of the form.

The role **DiversityCollectionUser** can see the data within the permitted projects, but can not change anything.

The role **DiversityCollectionTypist** can edit a part of the user defined data.






The role **DiversityCollectionEditor** can change the user defined parts of the data.

The role **DiversityCollectionCurator** has the same rights as the group DiversityCollectionEditor and in addition can handle transactions, i.e. shipments of specimen between collections.

The role **DiversityCollectionAdministrator** can delete data, edit the contents of internal tables, change user permissions etc.

Security

A user can be in 5 groups with diverse rights in the database where the higher groups have all rights of lower groups in addition to special rights for this group, e.g. DiversityCollectionUser can only read the data of certain tables while DiversityCollectionTypist has the rights of DiversityCollectionUser and additionally can edit the data in certain tables - see overview below.

-  DiversityCollectionAdministrator
-  DiversityCollectionCurator
-  DiversityCollectionEditor
-  DiversityCollectionTypist
-  DiversityCollectionUser

Summarized overview of the permissions of the groups

Group	Permissions in addition to lower group
Administrator	Delete data, edit user permissions
Curator	Create and edit transactions (e.g. loans)
Editor	Create new entries and delete details (not whole datasets)
Typist	Edit data
User	See the data of the data tables






If you are an Administrator you can add a user to one of these [groups](#)

Any user may have access to several [projects](#).

Transactions




Prerequisites

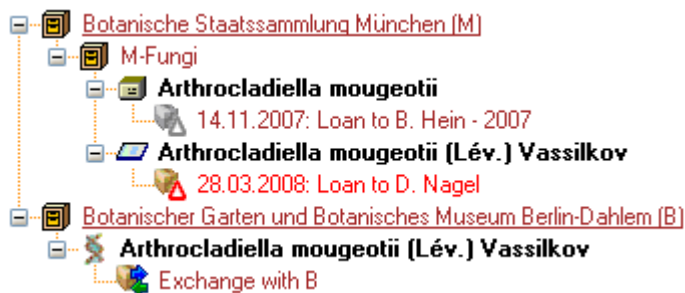
The transfer of a specimen between collections is handled with transactions. There are two prerequisites to use transactions in DiversityCollection. You must be in the group DiversityCollectionCurator (see [user administration](#)).


-  DiversityCollectionAdministrator
-  DiversityCollectionCurator
-  DiversityCollectionEditor
-  DiversityCollectionTypist
-  DiversityCollectionUser




and the collections you have the right to handle transactions for must have been assigned to you as shown in the [curators](#) 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 an  icon. For specimens that are still on loan an  icon as shown while a returned loan is symbolized with an  icon (see image below).

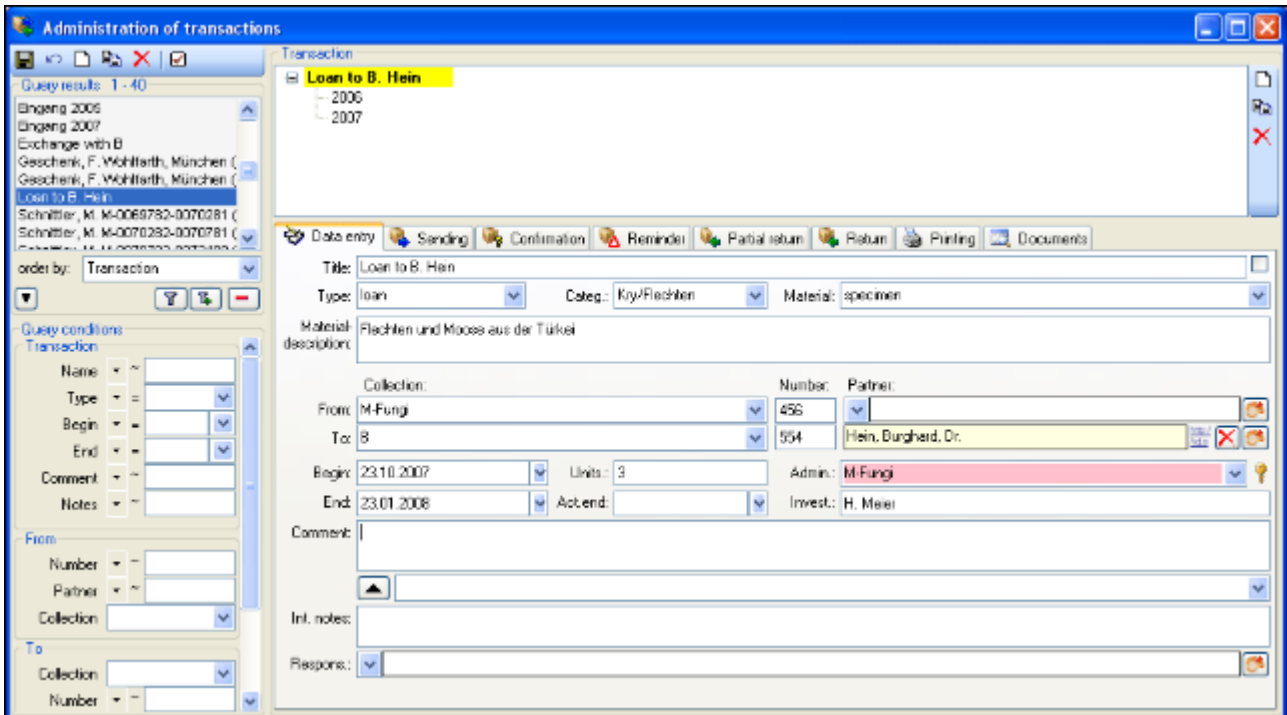


If you are a curator you can take a look at the details of a transaction. Select the specimen part in the tree and then click on the  button that will be shown in the details next to the name of the transaction. This will open the form for the transactions as described below.

To edit the transactions choose **Administration - Transactions** from the menu. A form 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 from the tree. With the  button you can create a copy of a transaction. To delete a specimen from the list click on the  button. The data for the transactions are stored in the tables [Transaction](#) and [CollectionSpecimenTransaction](#).

Data entry

On this page you can edit the data of a transaction. If a transaction is linked to an administrating collection (symbolized by the key ) , it can be edited exclusively by [curators](#) of this collection. To appoint curators choose **Administration - Curators** from the menu.




Depending on the type of the transaction additional tab pages will appear for creating documents.

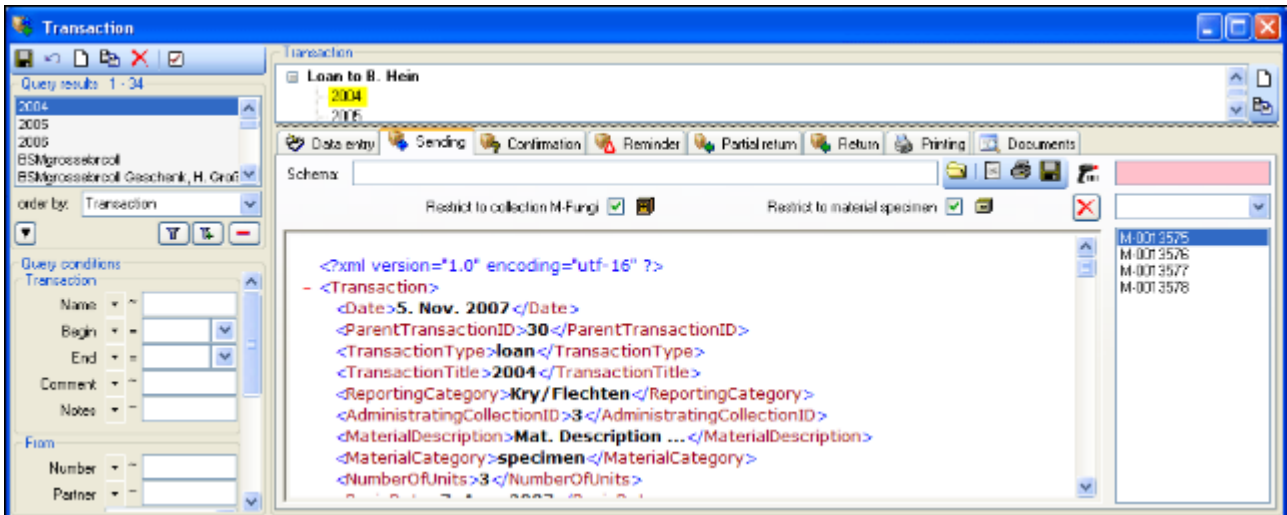
Transaction type


Tab pages

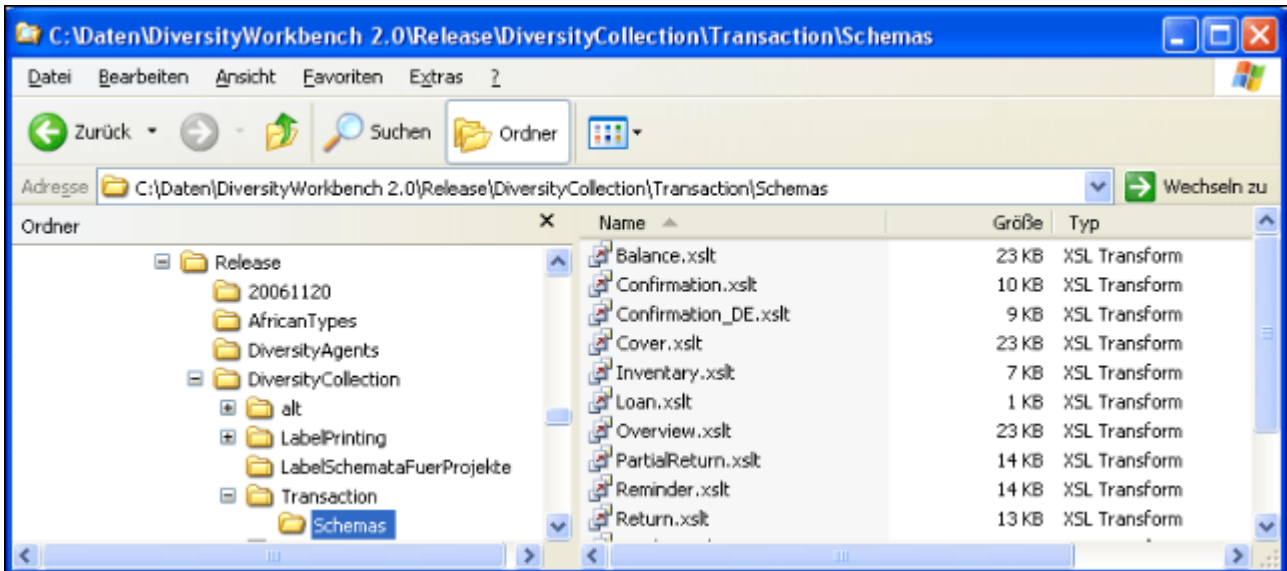
Sending	Loan	Borrow	Exchange	Gift	Purchase	
Confirmation	Loan	Borrow	Exchange	Gift	Purchase	Request
Reminder	Loan	Borrow	Exchange	Gift	Purchase	
Partial return	Loan	Borrow				
Return	Loan	Borrow				
Printing	Loan	Borrow	Exchange	Gift	Purchase	Request
Documents	Loan	Borrow	Exchange	Gift	Purchase	Request
Balance			Exchange			




Common notes

On the tab pages for generating documents you have to specify a xml-schema for your document - click on the  button to choose one of the predefined schemas or create your own schema. If you do not specify a schema for your form you will see the XML output created by the database as shown below.





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**.

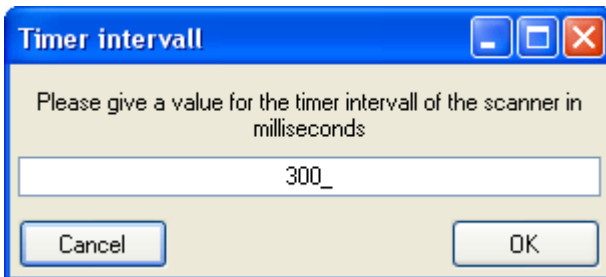


Feel free to change these schemas to your own needs. Choose the schema you need and then click on the  button to create a document. To print the document, use the  button. To store the current document in the documents for later reference click on the  button.



Transactions - Sending

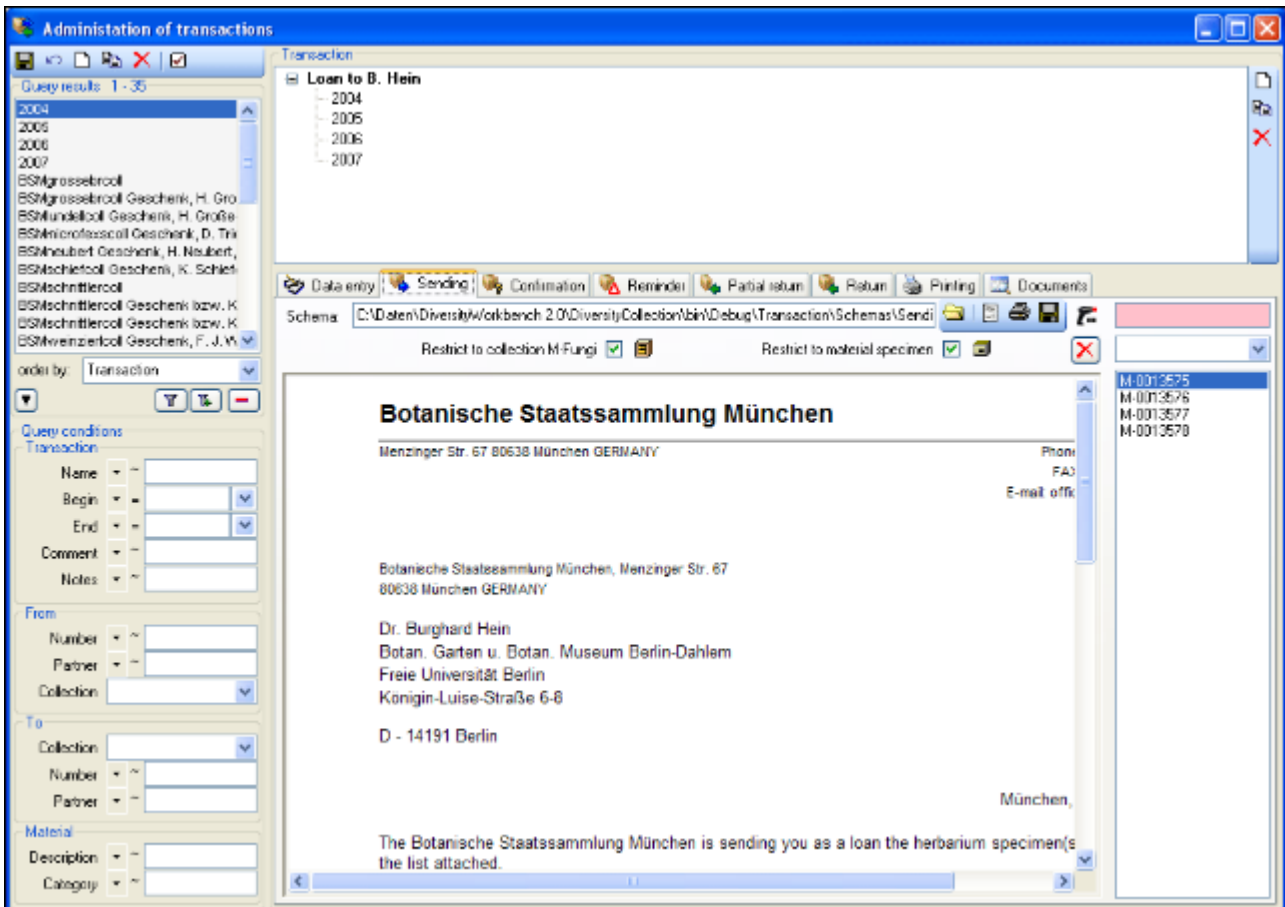
In the sending tab page of the transaction form you can create the covering note for a sent sample. To choose a schema click on the  button and select a schema from the list. DiversityCollection contains several ready to use schemas in the folder **Transaction - Schemas**.

To add a specimen to the list, you can either use the combobox or a barcode scanner. In case your scanner is reading only parts of the barcode try to adjust the timer interval - click on the  button to open a form as shown below.



A dialog box titled "Timer intervall" with a blue header and standard window controls. The text inside says "Please give a value for the timer interval of the scanner in milliseconds". Below the text is a text input field containing "300_". At the bottom are "Cancel" and "OK" buttons.





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. Click on the  button to create the document as shown below.



The "Administration of transactions" window shows a transaction form for "Loan to B. Hein" covering the years 2004-2007. The "Sending" tab is active, showing a schema path: "C:\Daten\Diversity\Workbench 2.0\DiversityCollection\bin\Debug\Transaction\Schemas\Sendi". Two checkboxes are checked: "Restrict to collection M-Fungi" and "Restrict to material specimen". The main area displays a covering note for "Botanische Staatssammlung München" with contact information for Dr. Burghard Hein at the Freie Universität Berlin. A list of material IDs (M-0013575 to M-0013578) is visible on the right.

Transactions - Confirmation

On this page you can 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 in the documents for later reference click on the  button.



Schema: C:\Daten\Diversity\Workbench 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@bam.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 resp. a loan taker did not meet the deadline, you can 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 in the documents for later reference click on the  button.

The at the upper right the missing specimen and at the lower right the returned specimen are listed.



Botanische Staatssammlung München **M**
Menzinger Str. 67 80638 München GERMANY
Phone: 089 17861 265
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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

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

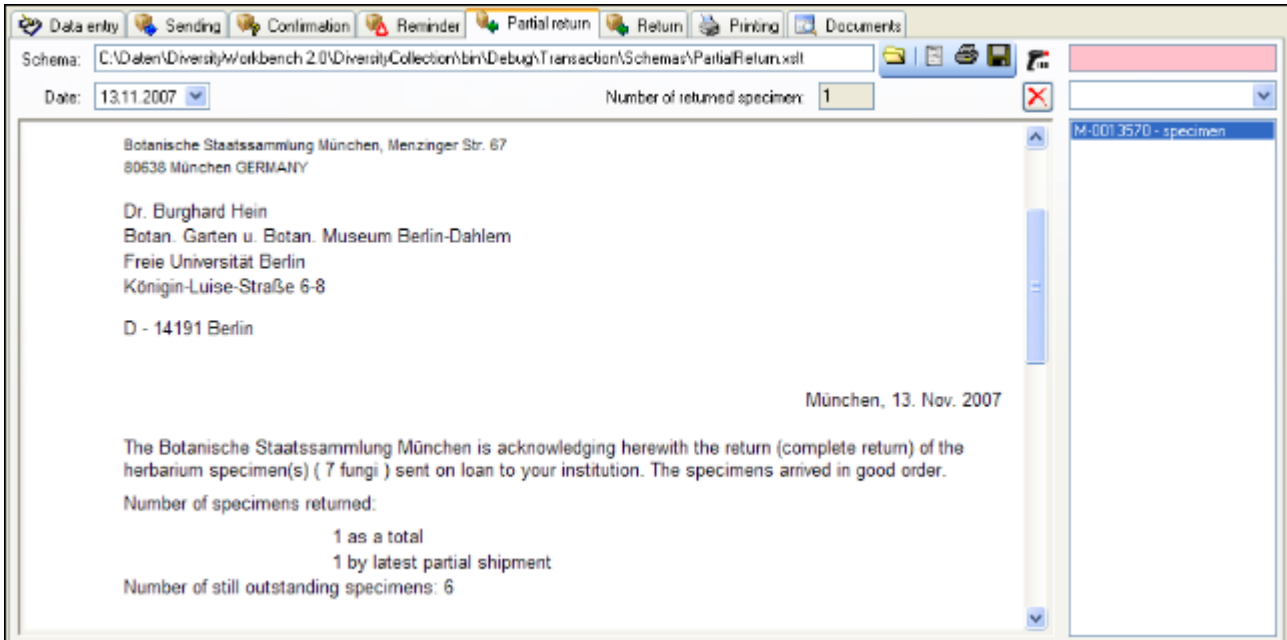
Specimen on loan
M-0013571 - specimen
M-0013572 - specimen
M-0013573 - specimen
M-0013574 - specimen
M-0013575 - specimen
M-0013576 - specimen

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 in the documents for later reference click on the  button.



Schema: C:\Daten\Diversity\Workbench 2.0\Diversity\Collection\bin\Debug\Transaction\Schemas\PartialReturn.xml

Date: 13.11.2007 Number of returned specimen: 1

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 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:

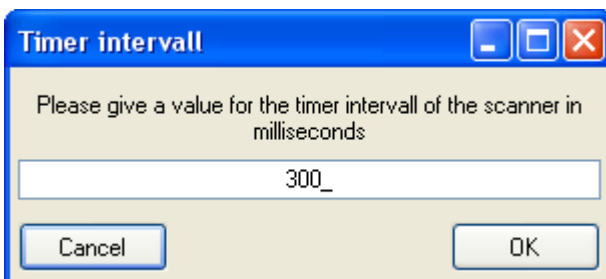
1 as a total
1 by latest partial shipment

Number of still outstanding specimens: 6

M-001.3570 - specimen

You have two option to enter returned specimen.

You may either use a barcode scanner  - move the mouse cursor into the field for the barcode detection, then scan the barcode. The specimen will be automatically inserted into the list. In case your scanner is reading only parts of the barcode try to ajust the timer intervall - click on the  button to open a form as shown below. Here you can set the interval to a value that is compatible to your scanner.



Timer intervall

Please give a value for the timer intervall of the scanner in milliseconds






300_

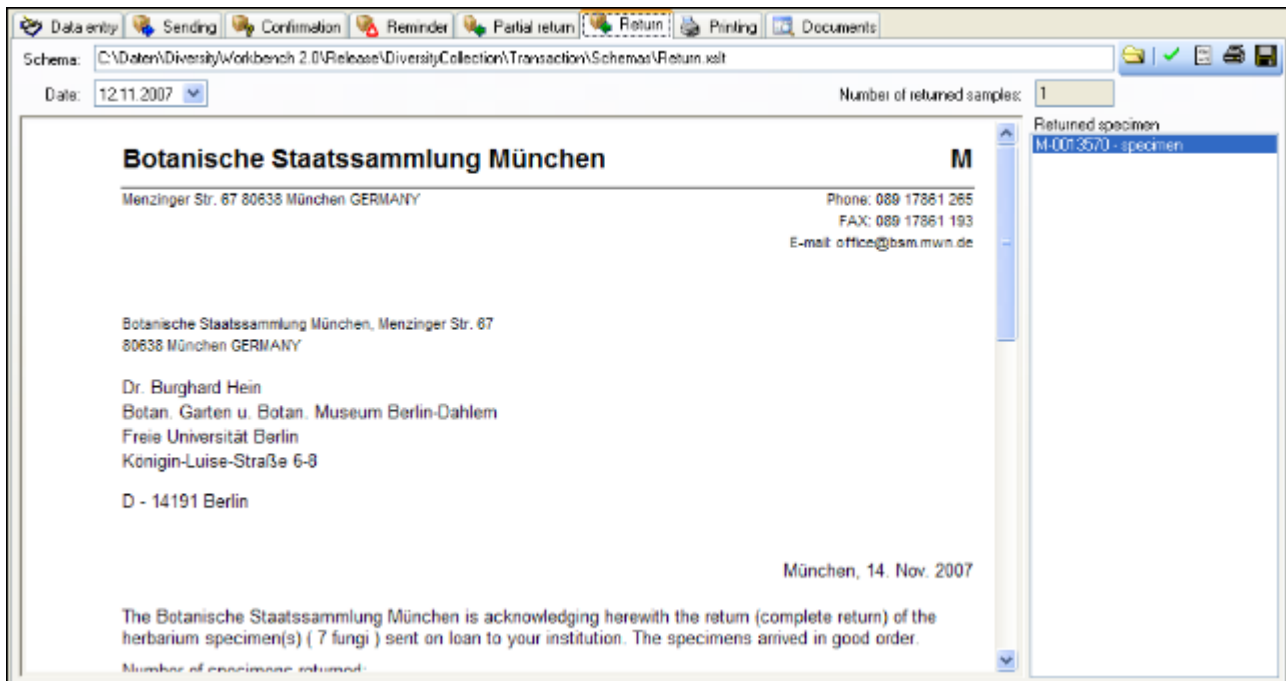
Cancel OK

If you lack a scanner or you do not use barcodes, use the drop down box to select the specimen from the list.

To remove a specimen from the list use the  button.

Transactions - Return



If a loan is returned, create a letter of acknowledgment here. With the  button, choose the schema you need. If all specimen were returned, click on the  button. This take all remaining specimen into the list of the returned specimens. With the date field you can define a different date as the start if e.g. you starting to register the returned specimen some days before. Click on the  button to create a document. To print the document, use the  button. To store the current document in the documents for later reference click on the  button.








The screenshot shows a software window with a menu bar containing: Data entry, Sending, Confirmation, Reminder, Partial return, Return, Printing, and Documents. Below the menu bar, there are fields for 'Schema:' (C:\Data\Diversity\Workbench 2.0\Release\DiversityCollection\Transaction\Schema\Return.xsl) and 'Date:' (12.11.2007). A 'Number of returned samples:' field is set to 1. The main content area displays a letter template for 'Botanische Staatssammlung München' (M). The letter includes the institution's address (Menzinger Str. 67, 80638 München, GERMANY), contact information (Phone: 089 17861 265, FAX: 089 17861 193, E-mail: office@bsm.mwn.de), and the recipient's address (Dr. Burghard Hein, Botan. Garten u. Botan. Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, D - 14191 Berlin). The date is 'München, 14. Nov. 2007'. The body of the letter states: '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.' A field for 'Number of specimens returned:' is visible at the bottom. On the right side, there is a 'Returned specimen' list with one entry: 'M-0013570 - specimen'.

Transactions - Printing / Inventory

Besides the special pages for creating letters along with a loan this page provides the possibility to print cover letters, inventories and the like. You can restrict the selected specimen to the current collection, include the subcollections or all related collections - just activate the corresponding checkboxes.

To add a specimen to the list, you can either use the combobox or a barcode scanner. To use the barcode scanner, move your mouse cursor into the pink field right from 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 form where you can set the timer intervall to a different value. To remove specimen form the list, select it and then click on the .

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 in the documents for later reference click on the .



Schema file: C:\Daten\Divesity\Workbench 2.0\DivesityCollection\bin\Debug\Transaction\Schemas\Inventory.xml

Include subcollections Include all related collections Number of specimen: 452

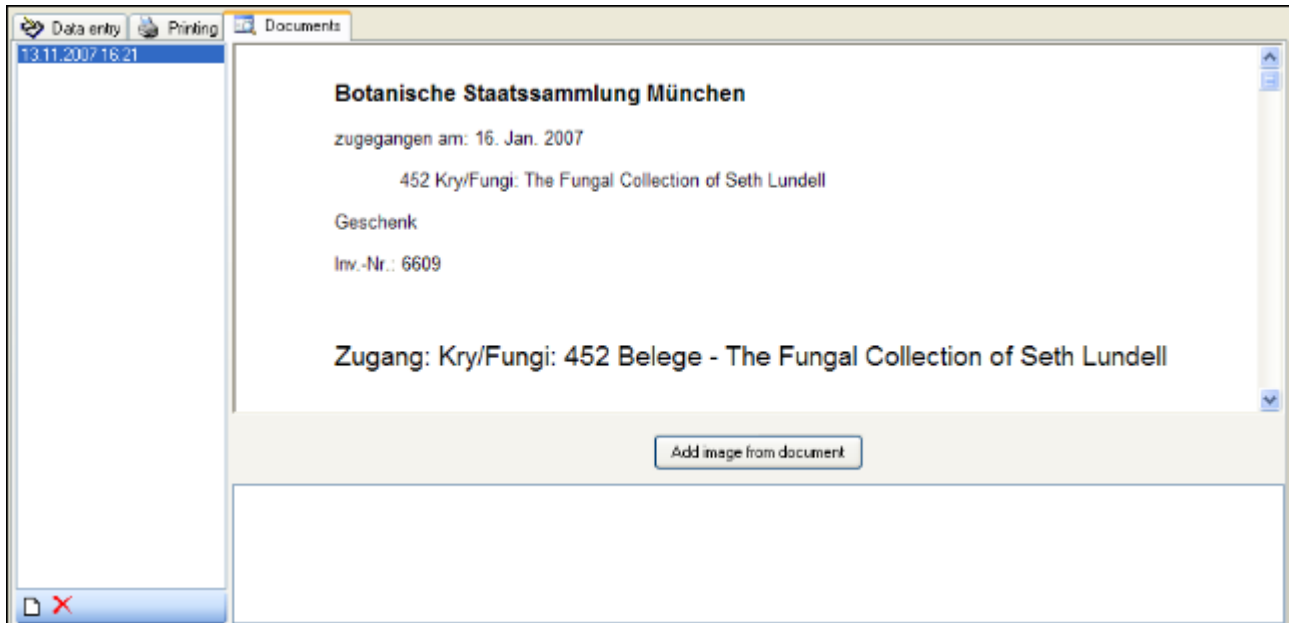
Botanische Staatssammlung München
zugegangen am: 16. Jan. 2007
452 Kry/Fungi: The Fungal Collection of Seth Lundell
Geschenk
Inv.-Nr.: 6609
Zugang: Kry/Fungi: 452 Belege - The Fungal Collection of Seth Lundell
Geber: Helga Grosse-Brauckmann, Seeheim
Geschenk

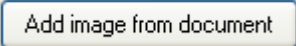
Fuligo cinerea (Schwein.) Morgan M-0140301
Albatrellus cristatus (Schaeff.) Kotl. & Pouzar M-0140302
Amylocystis lapponicus (Romell) Bondartsev & Singer ex Singer M-0140303 - M-0140304
Ascomyces albicollis (Cesati) Moresb. & K. H. Lam M-0140305 - M-0140306

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
M-0140331 - specimen

Transactions - Documents





This page stores all the documents created or received along with a transaction.

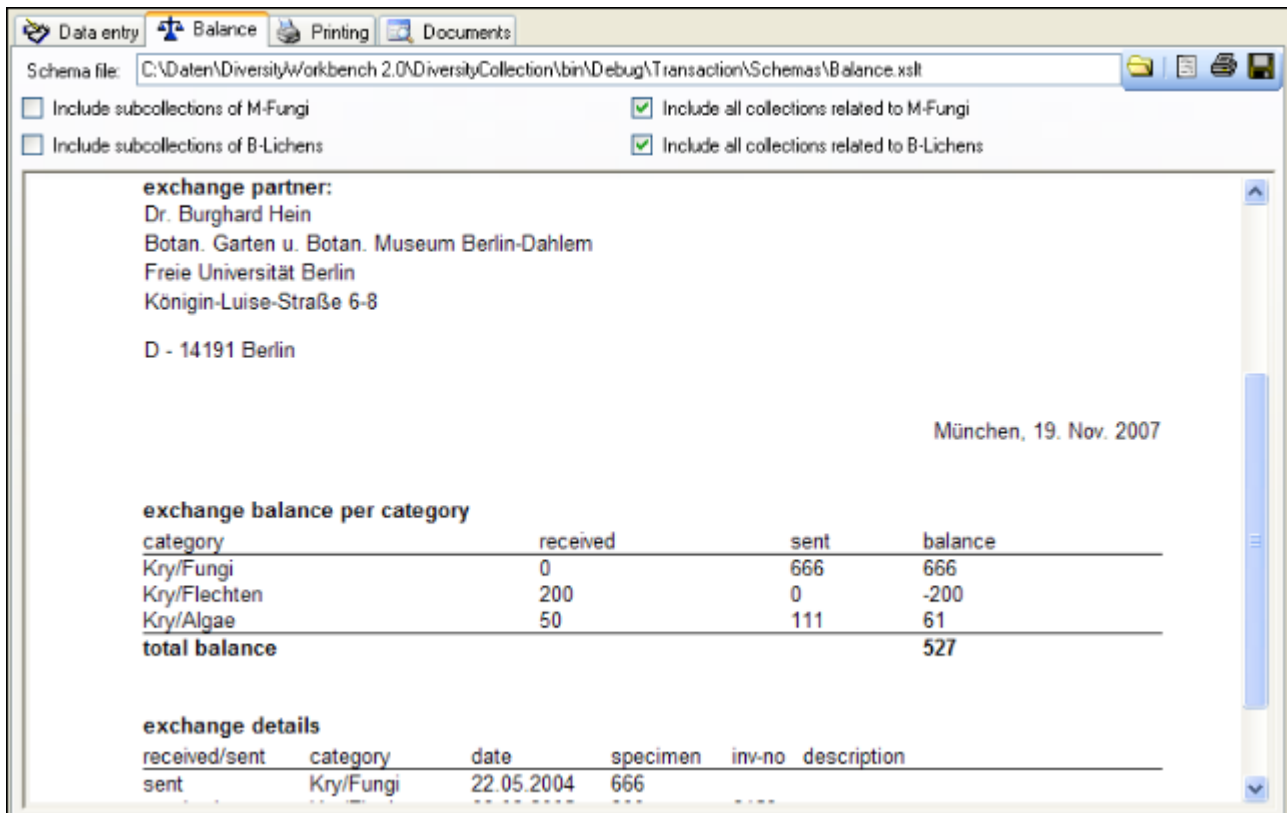


To add a document, create a screenshot of this document, then create a new entry (click on the button) and insert the screenshot with the  button. In the lower part you can enter any text related to the document.

Transactions - Balance

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 in the documents for later reference click on the  button. To include either the subcollections of any related collections to the collections of the current transaction select the corresponding checkboxes.



The screenshot shows a software window with a menu bar containing 'Data entry', 'Balance', 'Printing', and 'Documents'. The 'Balance' menu is active. Below the menu bar, there is a 'Schema file' field with the path 'C:\Daten\Diversity\Workbench 2.0\DiversityCollection\bin\Debug\Transaction\Schemas\Balance.xslt'. There are four checkboxes: 'Include subcollections of M-Fungi' (unchecked), 'Include all collections related to M-Fungi' (checked), 'Include subcollections of B-Lichens' (unchecked), and 'Include all collections related to B-Lichens' (checked).

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		

Maintenance

DiversityCollection can be linked several other modules within the Diversity Workbench. If you link a datasource to another module, the URI of the dataset in the other module together with several cached values will be stored in DiversityCollection. Along with changes in the other modules these cached values may differ from the original values. To get the actual values you can set these with the maintenance function within DiversityCollection.

toChoose Administration -> from the menu. A form as shown below will open. To transfer the higher taxonomic entries choose the tab Family and order. The upper part will synchronize the entries with taxonomic databases like DiversityTaxonNames_Fungi. Select a taxonomic database, a project and a taxonomic group, then choose if you want to synchronize the Family or th order. If you want to take a look at the single datasets you have to check the "Include accession number" checkbox. Than start the query with a click on the

Check for differences

button.

The screenshot shows a web application window titled "DiversityCollection, Database: DiversityCollection_Test v. 2.3.5.0 Server: 141.84.65.107 Port: 5432 User: BOTSAMP108\mweiss". The main content area is titled "Synchronize databases" and contains the instruction "Synchronize the cached data in dependent databases with the original source". There are four tabs: "Collection <-> TaxonNames", "Family and order", "Collection <-> Exsiccatae", and "Collection <-> Gazetteer". The "Family and order" tab is selected. Under "Synchronize with database", there are dropdown menus for "Taxonomy database" (set to "DiversityTaxonNames_Fungi"), "Project" (set to "BSMeyerscoll"), and "Taxonomic group" (set to "fungus"). There are radio buttons for "Family" (selected) and "Order", and a checkbox for "Include accession numbers" which is unchecked. Below these are "Check for differences" and "Start update" buttons. A second section, "Synchronize with available data", has a "Project" dropdown set to "BSMeyerscoll" and an unchecked "Include accession numbers" checkbox, also with "Check for differences" and "Start update" buttons. The right side of the form is a large greyed-out area.

The form will list all differences found as shown below. To update the database click on the

Start update

button.

Collection <-> TaxonNames Family and order | Collection <-> Exsiccateae | Collection <-> Gazetteer | Collection <-> References

Synchronize with database
 Taxonomy database:
 DiversityTaxonNames_Fungi

Project:
 BSMeyscoll

Taxonomic group:
 fungus

Family Order
 Include accession numbers

Check for differences
 233 differences found

Start update

LastIdentificationCache	Family	Order	TaxonomicGroup
Anthrocladia mougeoti (Lév.) Vassilkov	Erysiphaceae		fungus
Blumeria graminis (DC.) Speer	Erysiphaceae		fungus
Brasiliomyces trina (Harkn.) R. Y. Zheng	Erysiphaceae		fungus
Cystotheca lanestris (Harkn.) Sacc.	Erysiphaceae		fungus
Cystotheca wrightii Berk. & M. A. Curtis	Erysiphaceae		fungus
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae		fungus
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae		fungus
Erysiphe adunca (Walk.) Fr.	Erysiphaceae		fungus
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae		fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. ...	Erysiphaceae		fungus
Erysiphe aggregata (Peck) Farl.	Erysiphaceae		fungus
Erysiphe alphitoides (Giffon & Maubl.) U. Braun & ...	Erysiphaceae		fungus
Erysiphe aquilegiae DC.	Erysiphaceae		fungus
Erysiphe aquilegiae var. aquilegiae	Erysiphaceae		fungus
Erysiphe aquilegiae var. ranunculii (Grev.) R. Y. Z...	Erysiphaceae		fungus

In the lower part you can synchronize your entries within the database. Choose a project and click on the **Check for differences** button to start the query. To transfer the higher taxa to the found dataset click on the **Start update** button.

Synchronize with available data
 Project:
 BSMeyscoll

Include accession numbers

Check for differences
 97 differences found

Start update

LastIdentificationCache	Family	Order	TaxonomicGroup
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae	Erysiphales	fungus
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. ...	Erysiphaceae	Erysiphales	fungus
Erysiphe aggregata (Peck) Farl.	Erysiphaceae	Erysiphales	fungus
Erysiphe alphitoides (Giffon & Maubl.) U. Braun & ...	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae DC.	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae var. aquilegiae	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae var. ranunculii (Grev.) R. Y. Z...	Erysiphaceae	Erysiphales	fungus
Erysiphe artemisiae Grev.	Erysiphaceae	Erysiphales	fungus

If you want to have a more detailed look on you data you have to check the "Include accession number" checkbox before starting the Query. A button **Close form and check dataset in database** will appear that will take you back to a single dataset in the database.

Synchronize with available data
 Project:
 BSMeyscoll

Include accession numbers

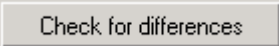
Close form and check dataset in database

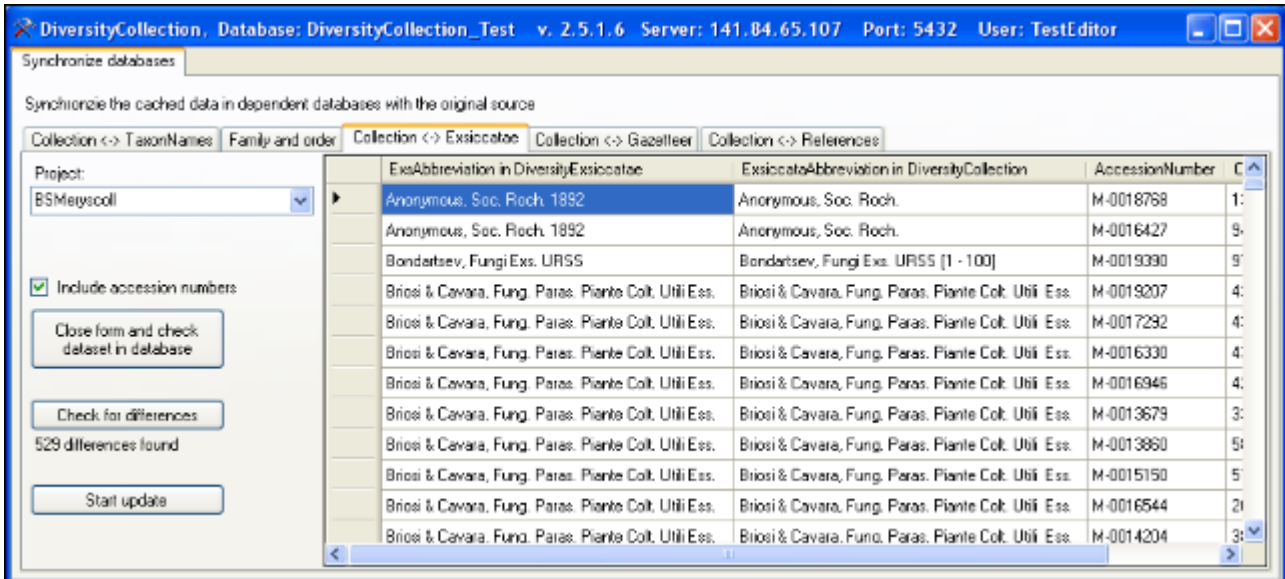
Check for differences
 2208 differences found

Start update

LastIdentificationCache	Family	Order	TaxonomicGroup	AccessionN
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae	Erysiphales	fungus	M-0019406
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus	M-0013772
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus	M-0013771
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019304
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019395
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019394
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019303
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019328
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus	M-0019297
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus	M-0123959

Maintenance - Exsiccatae

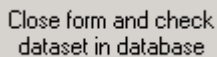
To synchronize the abbreviations titles of the titles of the exsiccatal series that are linked to the module DiversityExsiccatae choose **Administration -> Maintenance** from the menu. A form as shown below will open. On the tab page **Collection <-> Exsiccatae** select the project for which the titles should be synchronized. The title is stored in the field ExsiccataAbbreviation in the table CollectionSpecimen. Select the project that should be synchronized. Then start the query with a click on the  button.



The form will list all differences found. To update the database click on the

 button.

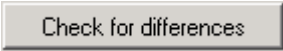
If you want to have a more detailed look on you data you have to check the "Include accession number" checkbox before starting the Query. A button

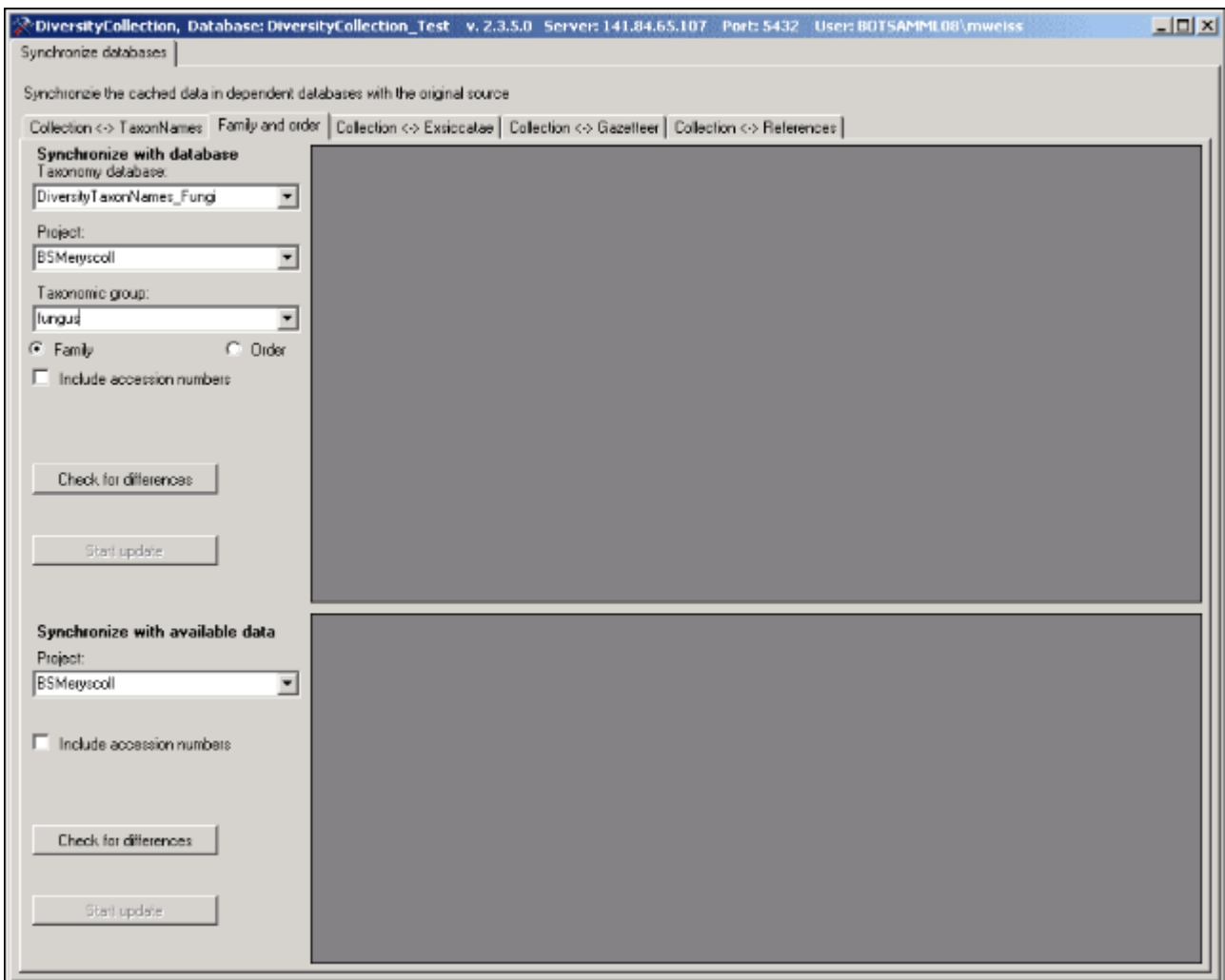


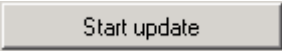
will appear that will take you back to a single dataset in the database.

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 form as shown below will open. To synchronize the higher taxonomic entries for entries linked to the module DiversityTaxonNames choose the tab **Family and order**. These are stored in the fields FamilyCache and OrderCache in the table IdentificationUnit .

In the upper part will synchronize the entries with taxonomic databases like DiversityTaxonNames_Fungi. Select a taxonomic database, a project and a taxonomic group, then choose if you want to synchronize the Family or the order. If you want to take a look at the single datasets you have to check the "Include accession number" checkbox. Then start the query with a click on the  button.



The form will list all differences found as shown below. To update the database click on the  button.

Collection <-> TaxonNames Family and order | Collection <-> Exsiccateae | Collection <-> Gazetteer | Collection <-> References

Synchronize with database
 Taxonomy database:
 DiversityTaxonNames_Fungi

Project:
 BSMeyscoll

Taxonomic group:
 fungus

Family Order
 Include accession numbers

Check for differences
 233 differences found

Start update

LastIdentificationCache	Family	Order	TaxonomicGroup
Anthrocladia mougeoti (Lév.) Vassilkov	Erysiphaceae		fungus
Blumeria graminis (DC.) Speer	Erysiphaceae		fungus
Brasiomyces trina (Harkn.) R. Y. Zheng	Erysiphaceae		fungus
Cystotheca lanestris (Harkn.) Sacc.	Erysiphaceae		fungus
Cystotheca wrightii Berk. & M. A. Curtis	Erysiphaceae		fungus
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae		fungus
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae		fungus
Erysiphe adunca (Walk.) Fr.	Erysiphaceae		fungus
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae		fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. ...	Erysiphaceae		fungus
Erysiphe aggregata (Peck) Farl.	Erysiphaceae		fungus
Erysiphe alphitoides (Griffon & Maubl.) U. Braun & ...	Erysiphaceae		fungus
Erysiphe aquilegiae DC.	Erysiphaceae		fungus
Erysiphe aquilegiae var. aquilegiae	Erysiphaceae		fungus
Erysiphe aquilegiae var. ranunculii (Grev.) R. Y. Z...	Erysiphaceae		fungus

In the lower part you can synchronize your entries within the database. Choose a project and click on the **Check for differences** button to start the query. To transfer the higher taxa to the found dataset click on the **Start update** button.

Synchronize with available data
 Project:
 BSMeyscoll

Include accession numbers

Check for differences
 97 differences found

Start update

LastIdentificationCache	Family	Order	TaxonomicGroup
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae	Erysiphales	fungus
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus
Erysiphe adunca var. regularis (R. Y. Zheng & G. ...	Erysiphaceae	Erysiphales	fungus
Erysiphe aggregata (Peck) Farl.	Erysiphaceae	Erysiphales	fungus
Erysiphe alphitoides (Griffon & Maubl.) U. Braun & ...	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae DC.	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae var. aquilegiae	Erysiphaceae	Erysiphales	fungus
Erysiphe aquilegiae var. ranunculii (Grev.) R. Y. Z...	Erysiphaceae	Erysiphales	fungus
Erysiphe artemisiae Grev.	Erysiphaceae	Erysiphales	fungus

If you want to have a more detailed look on you data you have to check the "Include accession number" checkbox before starting the Query. A button **Close form and check dataset in database** will appear that will take you back to a single dataset in the database.

Synchronize with available data
 Project:
 BSMeyscoll

Include accession numbers

Close form and check dataset in database

Check for differences
 2208 differences found

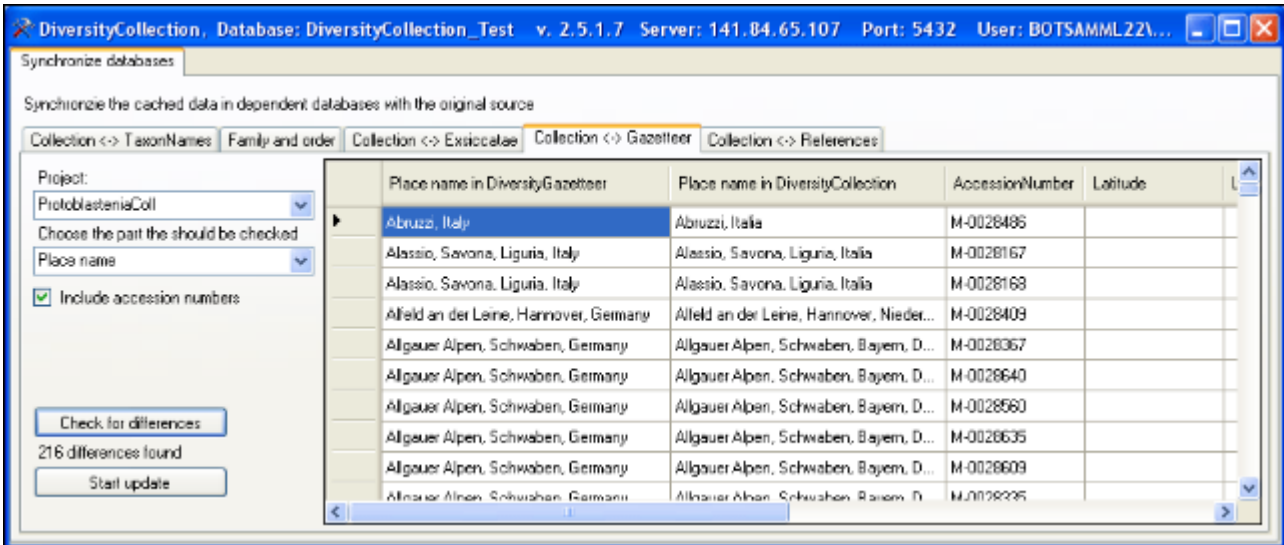
Start update

LastIdentificationCache	Family	Order	TaxonomicGroup	AccessionN
Erysiphe abbreviata (Peck) U. Braun & S. Takam.	Erysiphaceae	Erysiphales	fungus	M-0019406
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus	M-0013772
Erysiphe acalyphae (F. L. Tai) R. Y. Zheng & G. Q...	Erysiphaceae	Erysiphales	fungus	M-0013771
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019304
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019395
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019394
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019303
Erysiphe adunca (Walk.) Fr.	Erysiphaceae	Erysiphales	fungus	M-0019328
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus	M-0019297
Erysiphe adunca (Walk.) Fr. var. adunca	Erysiphaceae	Erysiphales	fungus	M-0123959

Maintenance - Gazetteer

To synchronize the entries derived from the module DiversityGazetteer choose **Administration -> Maintenance** from the menu. A form as shown below will open. On the tab page **Collection <-> Gazetteer** select the project for which the entries should be synchronized. There are 3 targets for the synchronization: Place name in the field Location1 in table CollectionEventLocalisation, Country stored in the field CountryCache in the table CollectionEvent and the Coordinates stored in the fields AverageLatitudeCache and AverageLongitudeCache in the table CollectionEventLocalisation. Select one of these targets

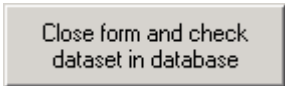
for the synchronization. Then start the query with a click on the



The form will list all differences found. To update the database click on the



button. If you want to have a more detailed look on you data you have to check the "Include accession number" checkbox before starting the Query. A button



will appear that will take you back to a single dataset in the database.

To check for countries that do not match entries in DiversityGazetteer choose Country from the list as shown below.

The screenshot shows the 'DiversityCollection, Database: DiversityCollection_Test v. 2.5.3.9' window. The interface includes a 'Synchronize databases' section with buttons for 'Remove unrelated events' and 'Remove unrelated event series'. Below this, there are tabs for 'Collection <-> TaxonNames', 'Family and order', 'Collection <-> Exsiccatae', and 'Collection <-> Gazetteer'. The 'Gazetteer' tab is active, displaying a table with columns 'Country in DiversityCollection' and 'Anzahl'.

Annotations on the left side of the screenshot:

- 'Optional Project' points to the 'Project:' dropdown menu.
- 'Optional inclusion of the accession number to check single datasets' points to the 'Include accession numbers' checkbox.
- 'The new entry for the country' points to the 'Change the selected country to:' dropdown menu.
- 'Optional Note about the original content' points to the 'Add original to notes:' checkbox and the 'Ori. Country: Argentina' text field.

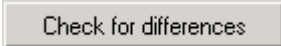
Annotations at the bottom of the screenshot:

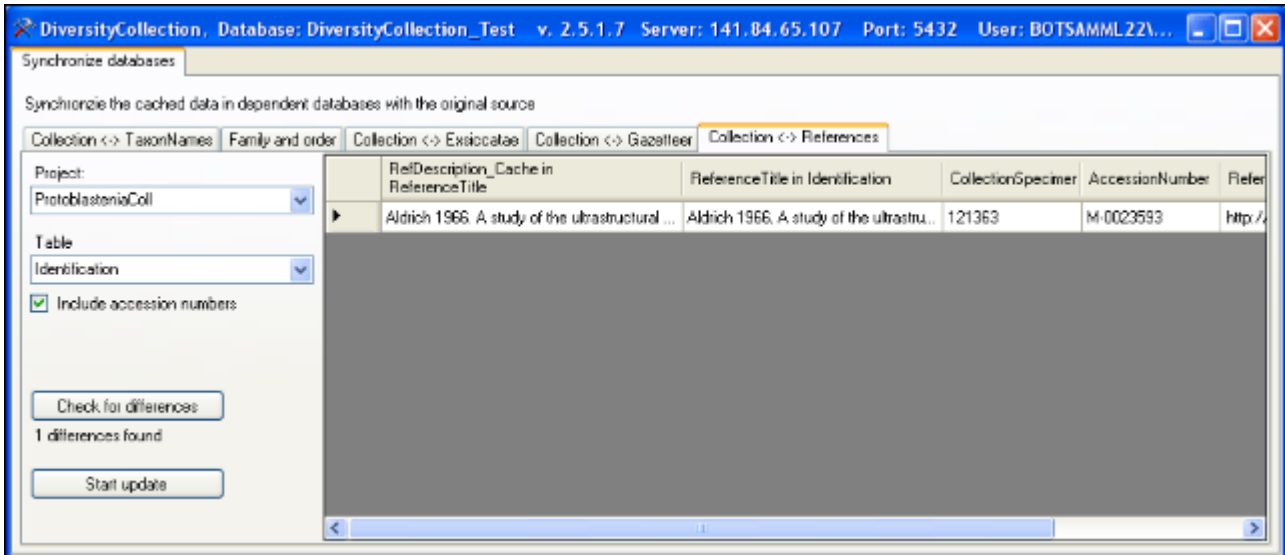
- An arrow points from the text 'Original content that does not match any entry in the country list of DiversityGazetteer' to the 'Ori. Country: Argentina' field.
- An arrow points from the text 'The number of the occurrences of an entry' to the 'Anzahl' column of the table.

Country in DiversityCollection	Anzahl
(The World)	103
Antarctica	1
Argentina	20
Bosnia-Herzegovina	2
Guayana	1
honolulu	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

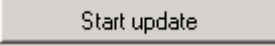
The image above summarizes the options for an update of the country. You can restrict your query to one of the projects you have access to. If you want to check single datasets, check the **include accession numbers** option before you start the query. To keep the old entry in the Notes field check the **Add original to notes** option.

Maintenance - References

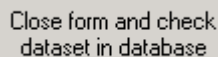
To synchronize the titles of the references that are linked to the module DiversityReferences choose **Administration -> Maintenance** from the menu. A form as shown below will open. On the tab page **Collection <-> References** select the project for which the reference titles should be synchronized. There are 3 tables which may contain links to DiversityReferences: [CollectionEvent](#), [CollectionSpecimen](#) and [Identification](#). Choose one of these tables for the synchronization. Then start the query with a click on the  button.

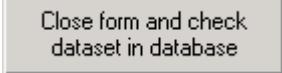


The form will list all differences found. To update the database click on the

 button.

If you want to have a more detailed look on one of the datasets in the list data you have to check the "Include accession number" checkbox before starting




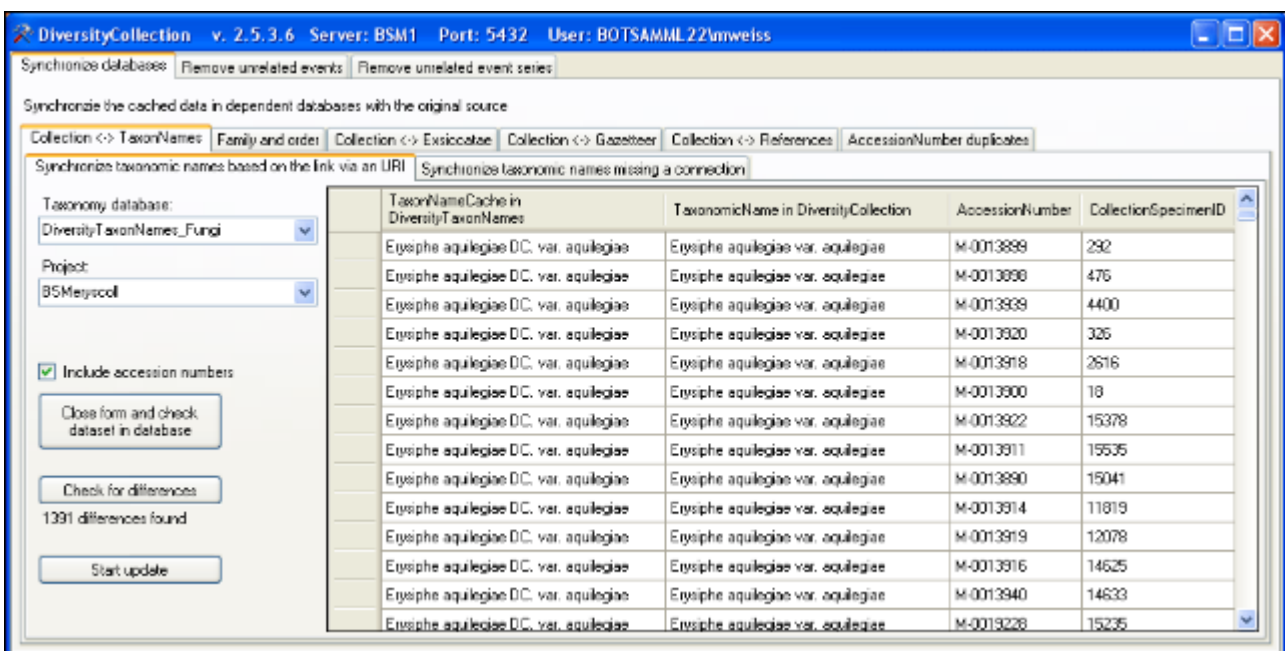
the Query. A button  will appear that will take you back to a single dataset in the database.

Maintenance - Taxonomic names

To synchronize the entries for the taxonomic names derived from the module DiversityTaxonNames choose **Administration -> Maintenance** from the menu. A form as shown below will open. 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 can 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 can **Synchronize taxonomic names missing a connection**, where no link is established and you can query for identical names in one of the databases.

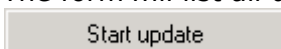
Synchronize taxonomic names based on the link via an URI

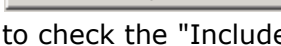
The taxonomic names are stored in the field TaxonomicName in the table Identification. Select a taxonomic database and a project that should be synchronized. Then start the query with a click on the  button.

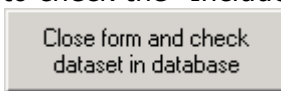



TaxonomicNameCache in DiversityTaxonNames	TaxonomicName in DiversityCollection	AccessionNumber	CollectionSpecimenID
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013889	292
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013990	476
Erysiphe aquilegiae DC. var. aquilegiae	Erysiphe aquilegiae var. aquilegiae	M-0013909	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

The form will list all differences found. To update the database click on the



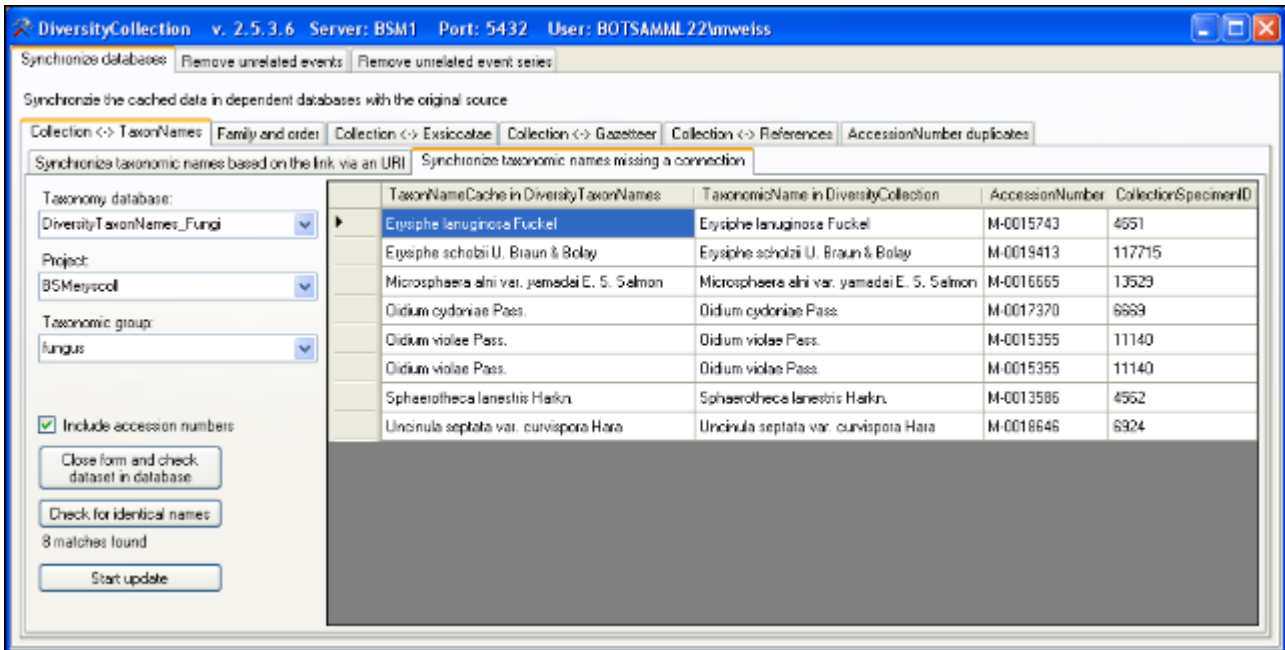
 button. If you want to have a more detailed look on your data you have to check the "Include accession number" checkbox before starting the Query. A button



 will appear that will take you back to a single dataset in the database.

Synchronize taxonomic names missing a connection

Select a taxonomic database, a project and a taxonomic group to search for identical names. Then start the query with a click on the **Check for identical names** button.



The form will list all matches found. To insert the links to the database click on the

Start update

button. If you want to have a more detailed look on your data you have to check the "Include accession number" checkbox before starting the Query. A button

Close form and check dataset in database

will appear that will take you back to a single dataset in the database.

Maintenance - Unrelated data

Collection events

Provided you have the proper rights, you can remove unlinked datasets in the tables CollectionEvent and CollectionEventSeries. To delete events that are not linked to any data in the database, use the tab page **[Remove unrelated events]**. These unrelated dataset may e.g. stem from specimen that were transferred to another collection event. Click on the **[List unrelated events]** button to list all events that are not related to a specimen. The found collection events will be listed in the upper part of the form. The lower parts show the localisations and the event properties related to these collection events. These must be deleted to delete the related events. Otherwise only the events with no relations to localisations or properties will be deleted.

The screenshot shows the DiversityCollection v. 2.5.2.3 interface. The 'Remove unrelated events' tab is active. It contains three data tables:

CollectionEventID	Version	SeriesID	CollectorsEventNum	CollectionDate	CollectionDay	CollectionMonth	CollectionYear	Color
45360	1							
45910	1							
46388	1							
48453	1							
48813	1							
48905	1							

CollectionEventID	LocalisationSystem	Location1	Location2	LocationAccuracy	LocationNotes	DeterminationDate	DistanceToLocatio	Dirac
45360	7	Hildesheim, Kreis ...	http://id.smb.inf...			17.11.2003 07:51		
46388	7	Hildesheim, Kreis ...	http://id.smb.inf...			17.11.2003 07:51		
48813	7	Hildesheim, Kreis ...	http://id.smb.inf...			17.11.2003 07:51		

CollectionEventID	PropertyID	DisplayText	PropertyURI	PropertyHierarchyC	PropertyValue	ResponsibleName	ResponsibleAgentL	Notes

Collection event series

To delete collection event series with no relation to collection events or other event series, choose the tab page **[Remove unrelated event series]**. Click the **[List unrelated event series]** to list these series and the **[Delete unrelated event series]** button to delete them. .

The screenshot shows the DiversityCollection v. 2.5.2.3 interface. The 'Remove unrelated event series' tab is active. It displays a table of event series:

SeriesID	SeriesParentID	Description	SeriesCode	Notes	DateCache	LogCreatedWhen	LogCreatedBy	LogUp
-1536		New EventSeries				04.01.2008 13:36	BSM1Vbeck	04.01.2
-1531		Germany, Bayern...		Germany, Bayern...	09.08.1946	03.01.2008 13:47	dbo	03.01.2
-1525		Germany, Bayern...		Germany, Bayern...	17.11.1941	03.01.2008 13:47	dbo	03.01.2
-1524		Germany, Bayern...		Germany, Bayern...	10.04.1920	03.01.2008 13:47	dbo	03.01.2
-1520		Germany, Bayern...		Germany, Bayern...	23.09.1919	03.01.2008 13:47	dbo	03.01.2
-1519		Germany, Bayern...		Germany, Bayern...	04.08.1946	03.01.2008 13:47	dbo	03.01.2
-1513		New EventSeries				21.11.2007 17:29	BSM1Vriebe1	21.11.2
-1511		New EventSeries				21.11.2007 11:00	BSM1Vriebe1	21.11.2
-1510		New EventSeries				09.11.2007 14:11	BSM1Vriebe1	09.11.2

Import and export

For the import and export you have several options:

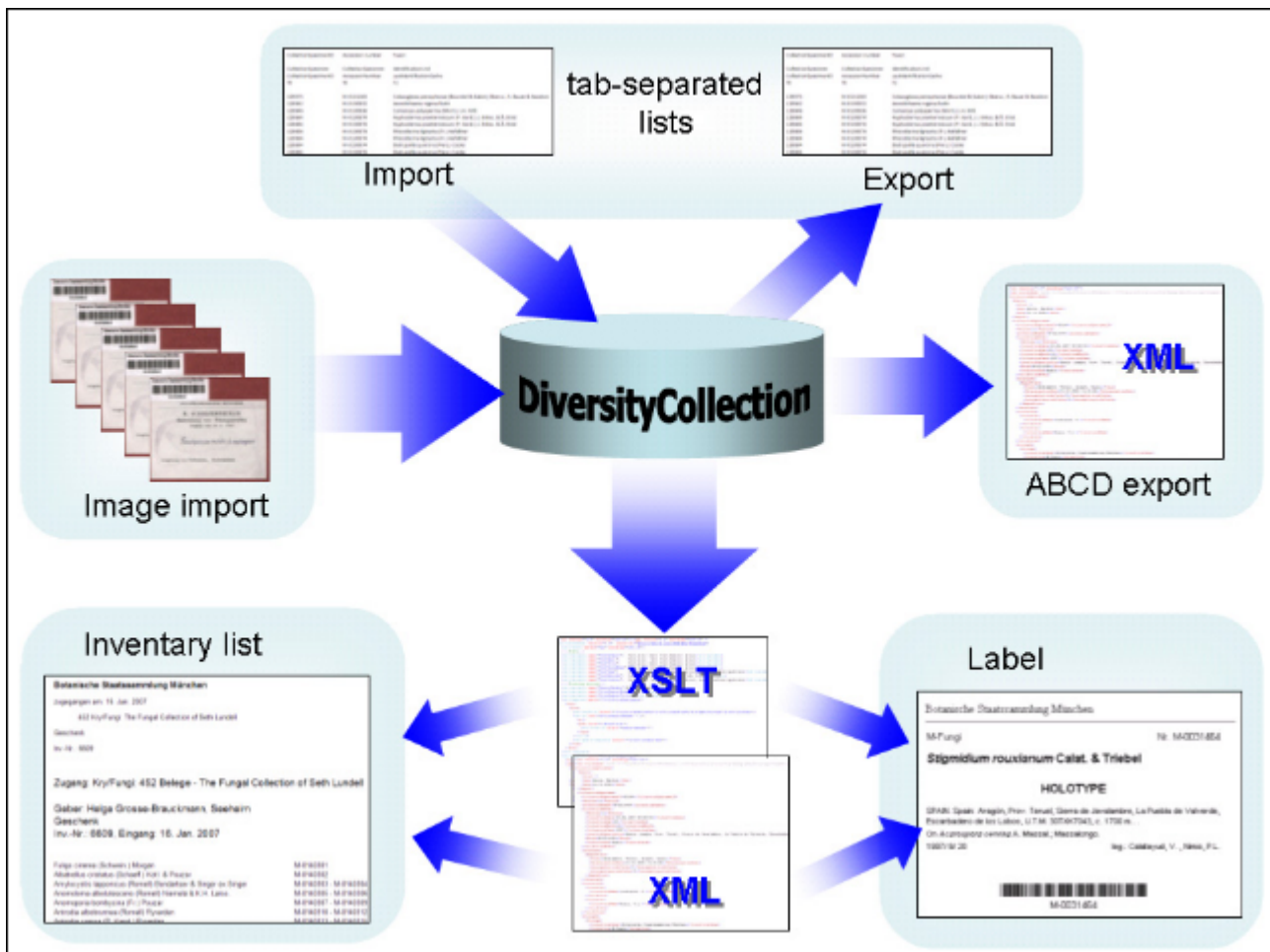
[Import of images](#): Images that are named according to the accession number can be imported together with default informations to the whole batch.

Import and export of tab-separated list: To import data from foreign sources and to export data e.g. for reimport after external editing.





Export of XML data according to ABCD.

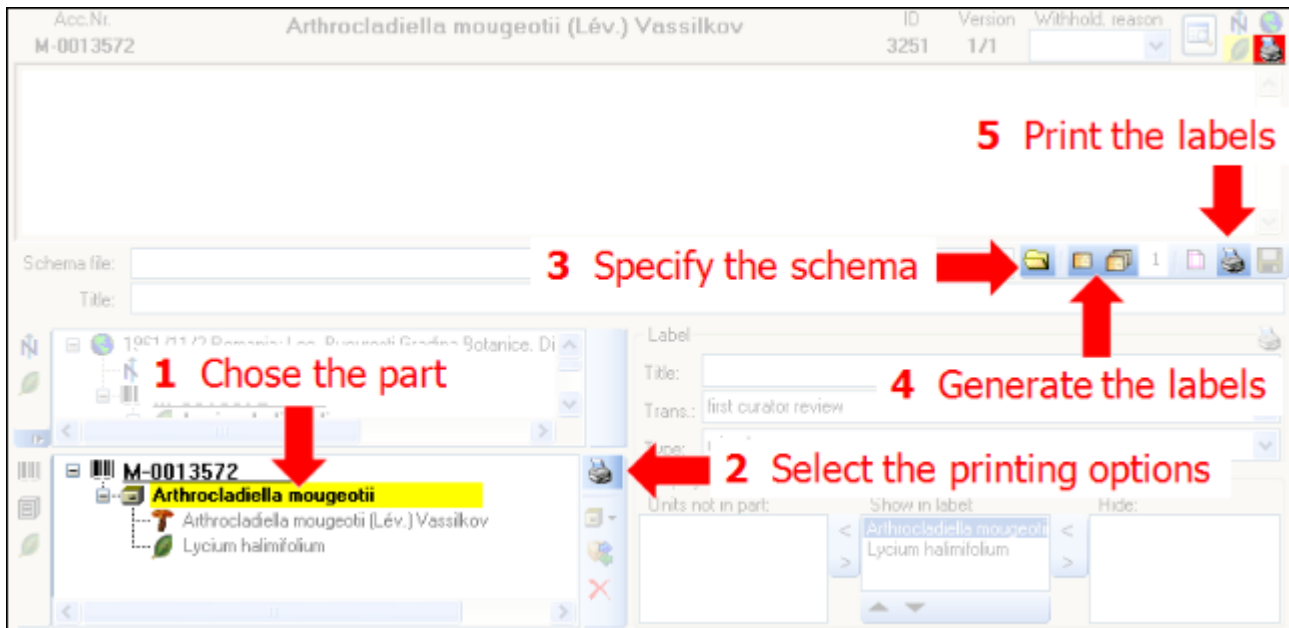
Generation of [labels](#).

Generation of [inventory list](#).

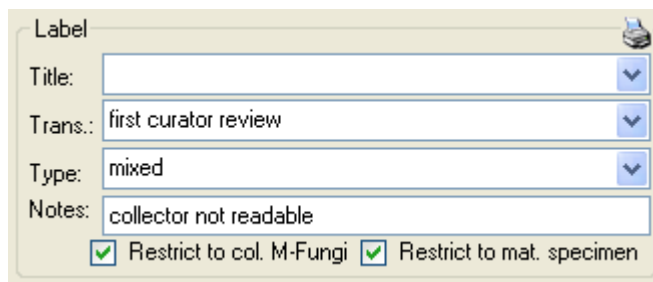


Label

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.



If you want to print label for all the specimens in the specimen list you can restrict these to the collection and the material category of the current specimen part. These options are active by default as shown in the image below.







Information about an existing label is entered in this label section. The data are stored in the table [CollectionSpecimen](#).


label types:
 handwriting = all data in handwriting
 mixed = data typed with handwriting comments
 typed = all data typed


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 resp. change to your own needs or create new ones. 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 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 to the desired value. You can print 1 - 99 duplicates of a label. If there are more than 20 specimens in the list, you get a warning if you really want to create all these labels, as this could be somewhat time consuming. The labels are generated as XML files with XSLT-Schema files and depicted in a browser. To print the label click on the  button. If you use a different browser than that included in DiversityCollection make sure, that the browser can interpret XSLT/XML (e.g. MS-Internet Explorer).



If you want to save the generated files for later printing click on the  button to do this. Note that the program will by default create a file Label.xml in the LabelPrinting directory that will be overwritten everytime you generate a new label. So you have to save the file under a different name or in a different directory to prevent the program to erase these data.

If you use Code 39 for your labels and want to print the barecodes on the labels you need the font  code39.ttf , which is included in the DiversityCollection packet. 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 omit to give a Schema file, you will see the generated XML-file as shown in the image below. The XML file is the base for all label types you want to generate. To create your own labels just design your own XSLT-schema file. See e.g. <http://www.w3.org/TR/xslt> for further informations about schema files.


```
<CollectionDay>20</CollectionDay>
<CollectionMonth>10</CollectionMonth>
<CollectionYear>1841</CollectionYear>
<CollectionDateCategory>collection
  date</CollectionDateCategory>
<LocalityDescription>Africa, Ethiopia, In
  montibus
  Djeladjeranne</LocalityDescription>
<Notes>M-0011595</Notes>
</CollectionEvent>
```

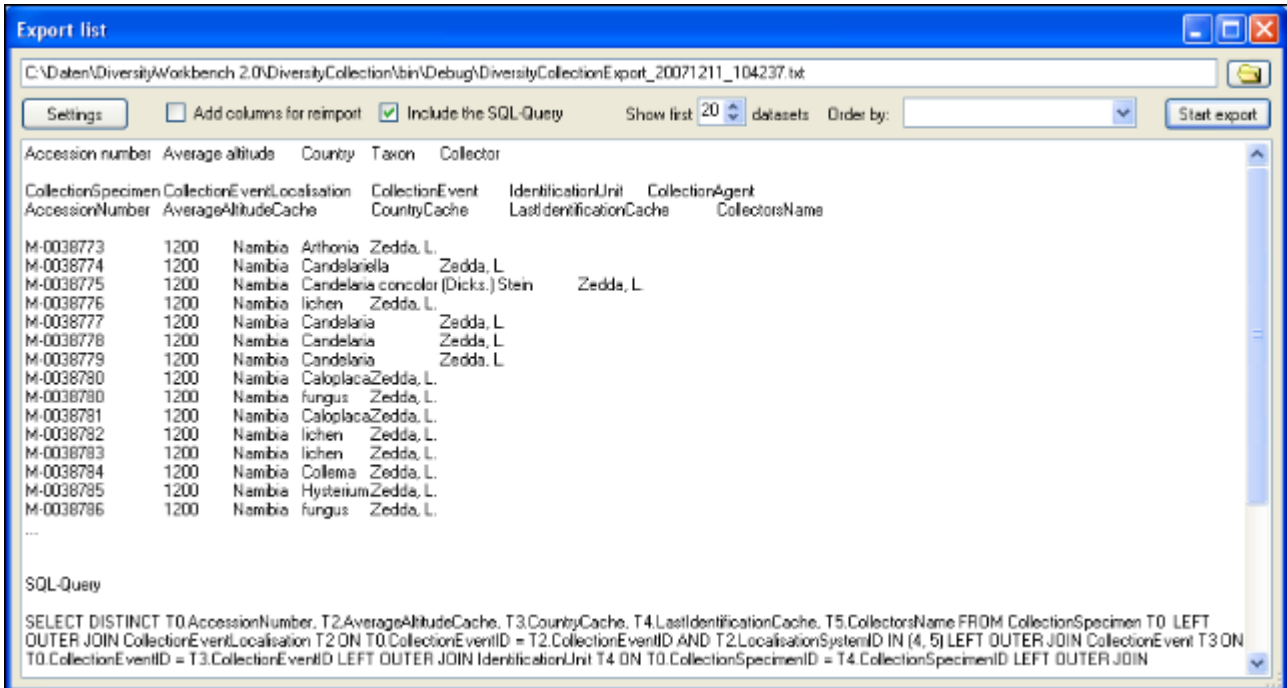
Schema file:

Title:


Coll. / Mat.: M-VascularPlants / herbarium sheets

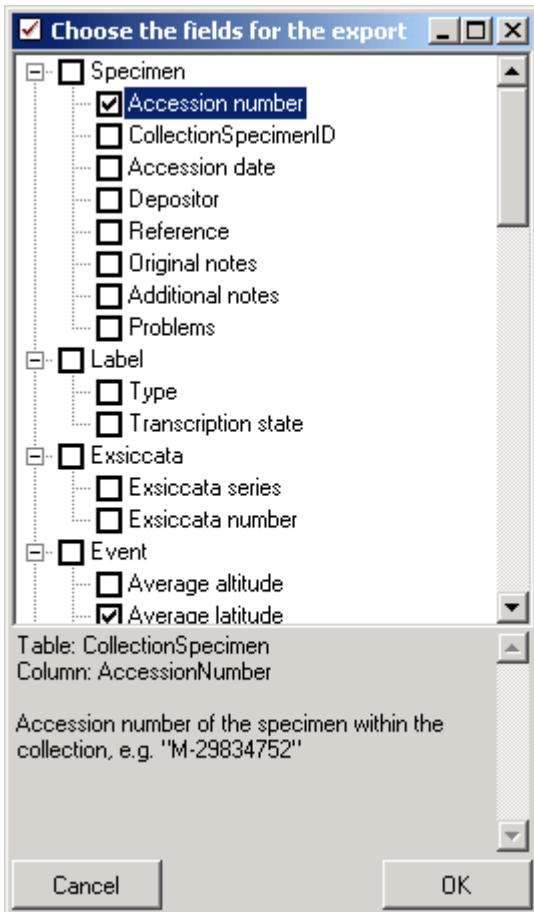
Export

For an analysis of the data within the database, you can export the contents of the datasets listed in the specimen list into a tab-separated list. Choose **Data - Export - Export list...** from the menu. A form as shown below will open. To change the preset path of the export file use the  button.



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 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 ordering the results **[Order by:]** will be filled. So if you need your results ordered 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  button. A form will open as shown below, where you can choose the fields you want to export.



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.

Accession number
CollectionSpecimen
AccessionNumber

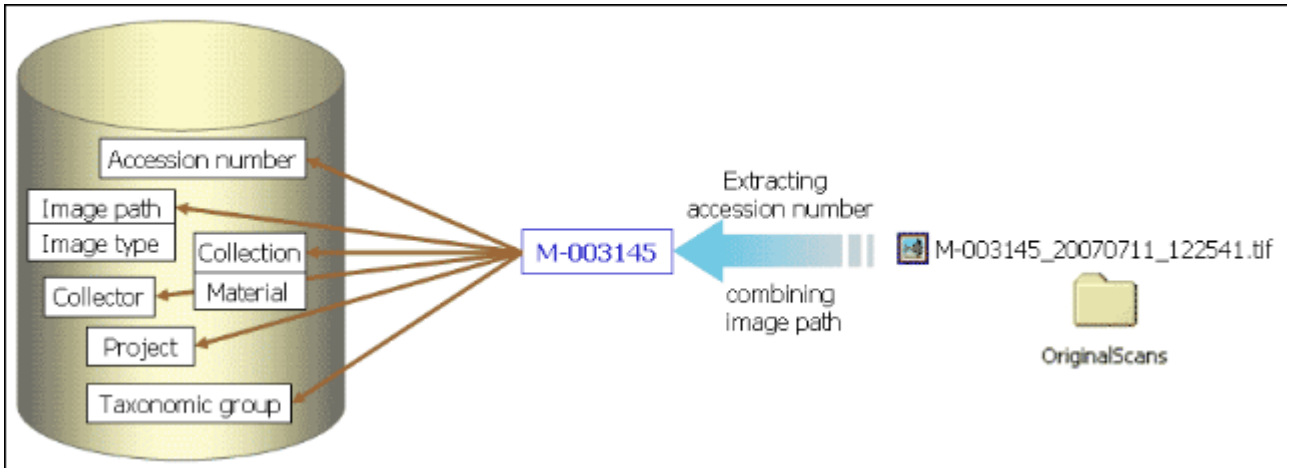
M-0013579
M-0013579
M-0013579
M-0013579
M-0013579
M-0013579

Taxon
IdentificationUnit
LastIdentificationCache

Arthrocladiella mougeotii (Lev.) Vassilkov
Arthrocladiella mougeotii (Lev.) Vassilkov
Blumeria graminis (DC.) Speer
Blumeria graminis (DC.) Speer
Lycium barbarum
Lycium barbarum

Import specimen scans

With this import routine, you can import new datasets along with new images into the database. To achieve this the image files should be named corresponding to the accession numbers of the datasets that should be imported and an optional trailing identifier. The image below shows an overview of the whole import process.



To import images like scanned label from specimen choose **Data - Import - Specimen scans...** from the menu. A form for the import of images will open.

Import scans of specimen

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**


DK	Acc. Nr.	Source file	Path in database	Error	App
<input checked="" type="checkbox"/>	M-0039137	M-0039137_20070730_170350.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039137_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0017745	M-0017745_20070604_130620.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0017745_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039119	M-0039119_20070604_130314.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039119_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039120	M-0039120_20070604_125832.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039120_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039121	M-0039121_20070604_131042.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039121_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039122	M-0039122_20070604_131400.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039122_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039123	M-0039123_20070604_125306.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039123_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039124	M-0039124_20070730_172436.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039124_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039125	M-0039125_20070730_172632.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039125_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039126	M-0039126_20070730_172014.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039126_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039127	M-0039127_20070730_172158.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039127_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039128	M-0039128_20070730_171704.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039128_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039129	M-0039129_20070730_171048.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039129_20...		<input type="checkbox"/>
<input checked="" type="checkbox"/>	M-0039130	M-0039130_20070730_171420.jpg	http://pictures.snsb.info/BSMSchieferdecker/M-0039130_20...		<input type="checkbox"/>

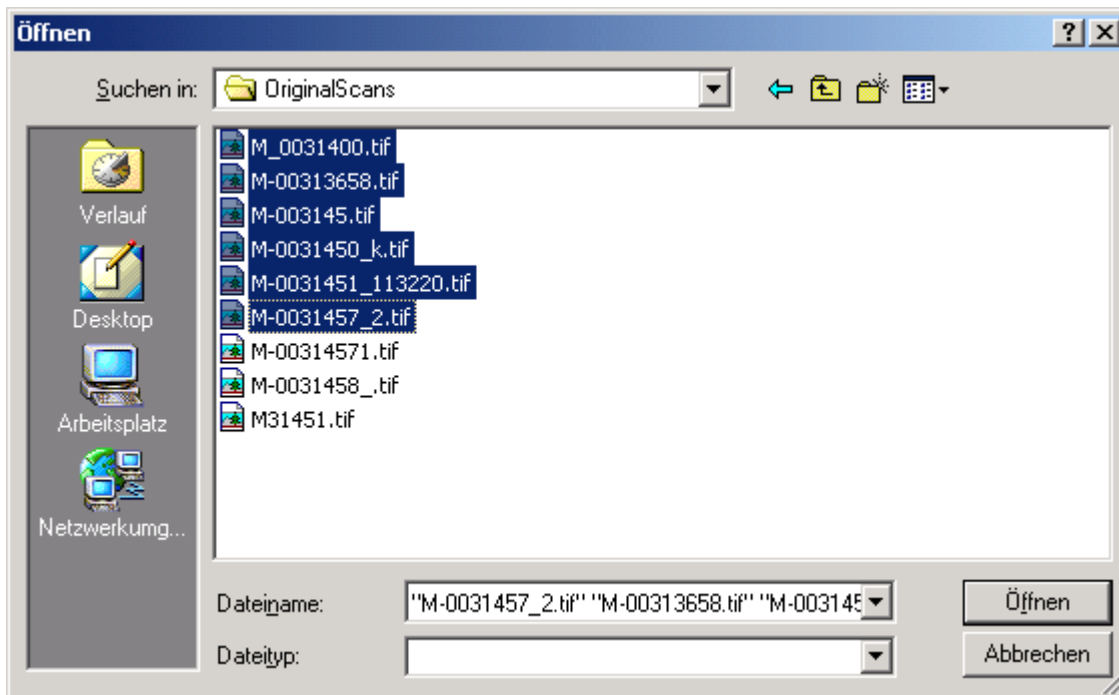
Database
 Parameters for the import in the database
 Locality or place: Collector: Collection date: -- Suppl.:
 Collector: **M-Fungi** Material: **specimen** Project: **BSMSchieferdecker** Image type: **label**
 Identifier: Ident. by: Taxon group: **Fungus**
 Exsiccate: Label type: **handwriting**
 Import the image not with the original path as specified above but as URL BaseURL: **http://pictures.snsb.info/BSMSchieferdecker/web/**

Create log file Logfile for report: C:\Daten\diversity\work\bench 2.0\diversity\collection\Nbn\Ndebug\Log\import_mweiss_20070914_130546.log

The fields marked with **red** are obligate.

Image source

To select the images you want to import in the database click on the  button. A dialog will open, where you can select the images that you want to import into your Database.



This will enter the selection of the images in the list in the form.

Import options and security checks

If you want to replace datasets for images already in the database, check the **Overwrite existing images** checkbox. If the images are located in a subfolder, that is named according to the first characters of the AccessionNumber, check the **Place images in subfolder of length** checkbox and specify the length of the name of the folder. If you want to check the URI's of the images check the corresponding checkbox. The datasets will then only be imported when the images are available on the web. If the filename next to the accession number contains a trailing identifier, this must be separated by a unique character. Check the corresponding box and enter the separating character. If you want to check if 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 images selected for the import. If the file name passed the specified checks, the OK field for the image will be checked. Otherwise an explanation for not passing the checks will be shown in the **Error** section. The list shows the accession number extracted from the file name, the file name of the original image file and if selected the file names for the web and preview images. If a dataset for an image already exists in the database, the checkbox **Append** at the right end of the table will be checked.

Database


You can set several obligate and optional values that will be written in the database for all imported data. The fields marked with **red** are obligate. These are the collection in which the specimen are located, the material of the specimen, the project, the image type of the scans and the taxonomic group of the main organism in the specimen. If you want to refer to a web source for the label instead of a local file you must give the base URL as well. Optional fields are a place according to the DiversityGazetteer and the date of the collection, 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](#) .

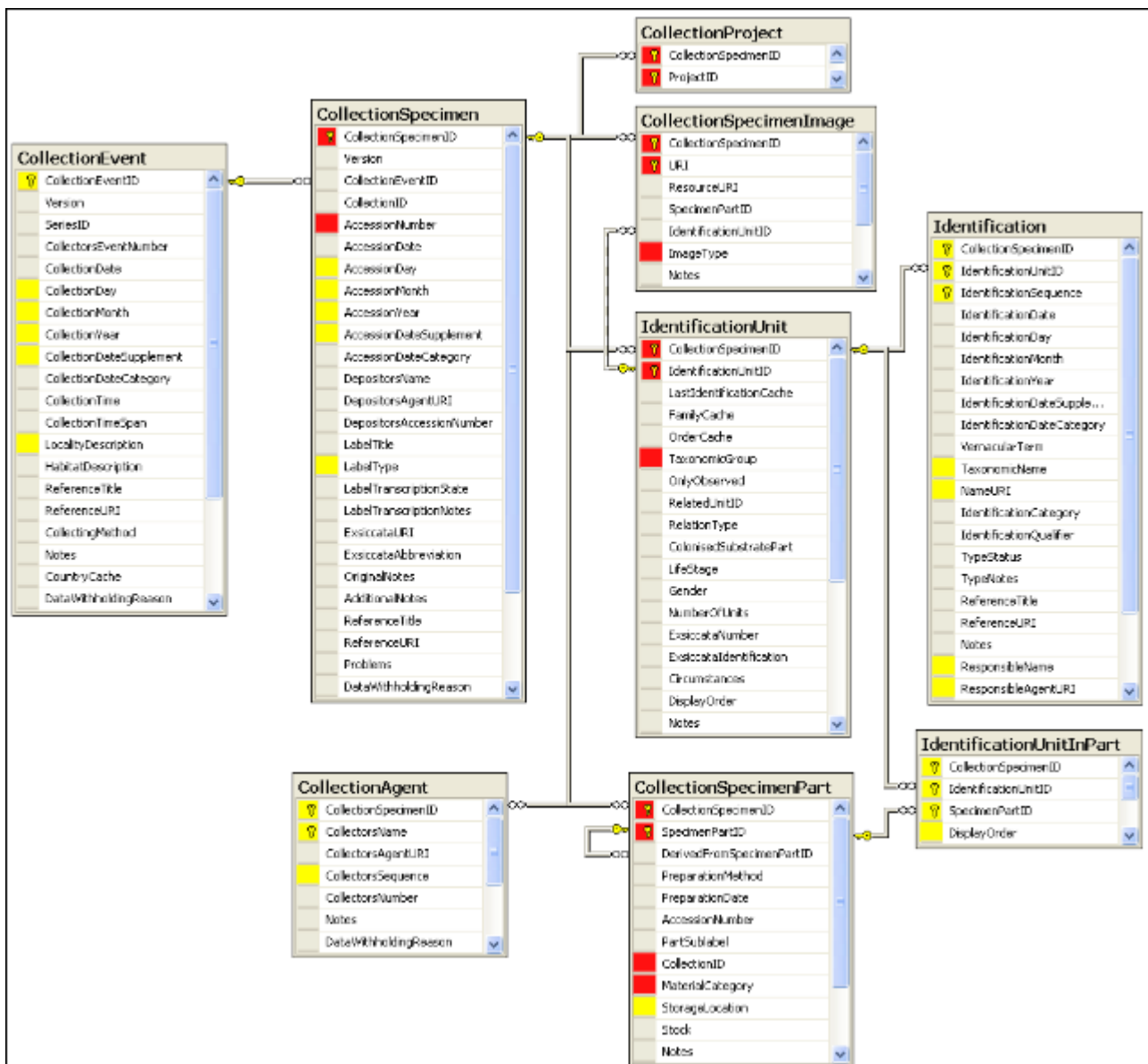
To test the import and if the images are present in the database click on the  button.

If everything is fine click on the  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 and the date and time of the import in the directory where the image files are archived.



The program will check, if an accession number is already present in the database. It will then only import data, when the option Append images if accession number is present is checked. Otherwise these data will not be imported.


If the images will be provided by a webservice, check the appropriate checkbox and specify the folder or click on the  button of search for the website.

In the overview below the obligate fields are marked with red, the optional fields with yellow.




Import tab-separated lists

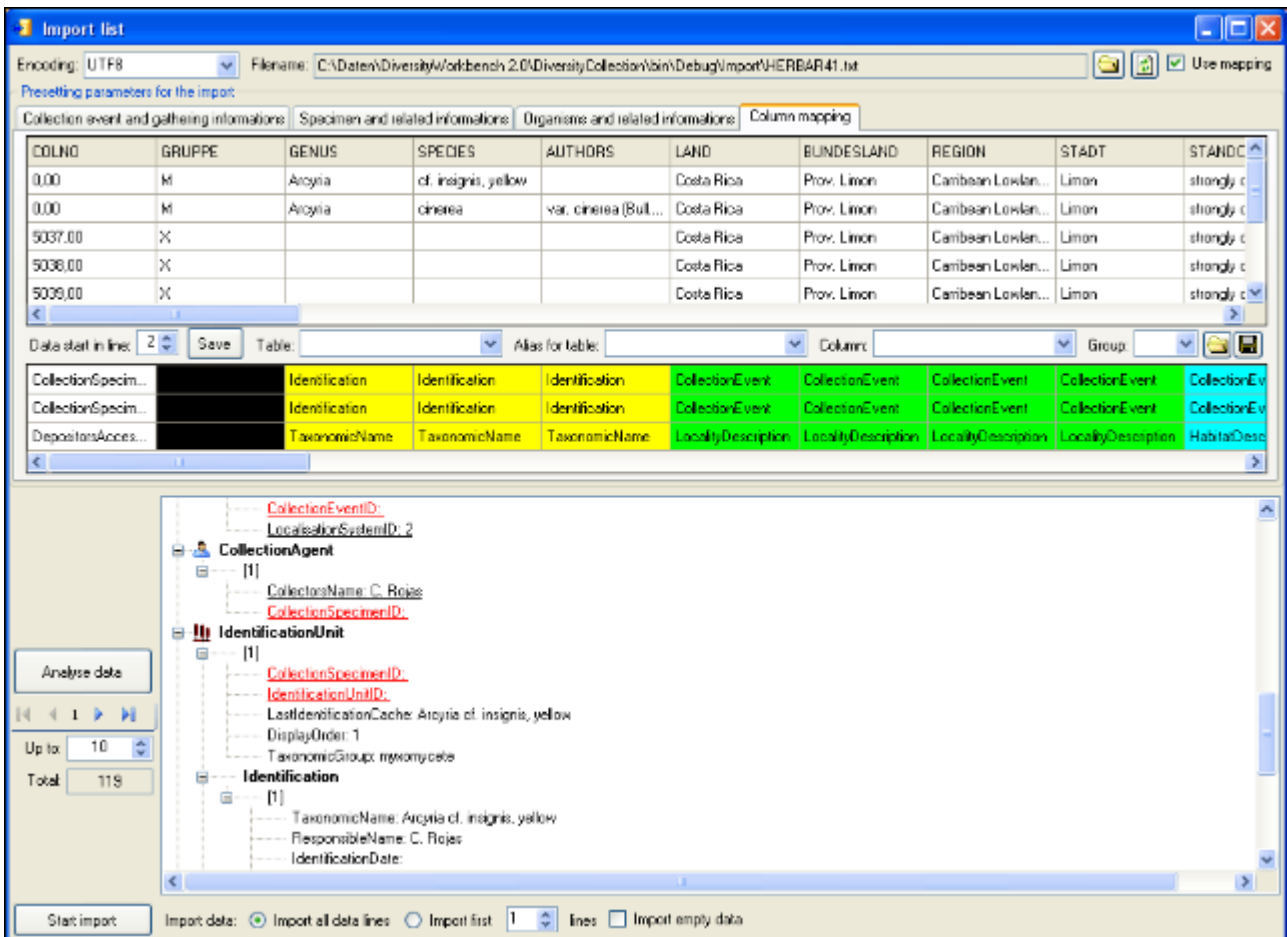
With this import routine, you can import data in tab-separated lists into the database. Choose **Data -> Import -> Import list...** from the menu to open the form for the import. In the form click on the  button to select the file with the data you want to import. Use the proper **[encoding]** to ensure 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 the **[Data start in line]** to set the area for the import. Preceding 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

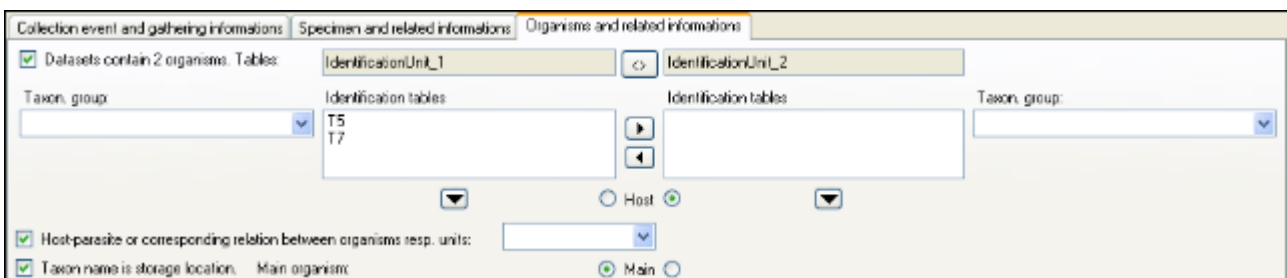
For a column that should not be imported, choose the **black** color from the Group as shown for the second column in the image below. These columns will be ignored for the analysis and the import. For all other columns choose the **[Table]** and the **[Column]** your data correspond to. If you want to import two different datasets in the same table, you have to change the **[Alias for table]** to a unique value for this dataset.

If some columns should be transferred into one field, you have to choose a group for these column as shown below for columns 3 to 5, 6 to 9, To do this, just choose a color from the Group combobox other than white or black. To save the current mapping, click on the  button.



To analyse the data in the file click on the **[Analyse]** button. During the analysis you may be asked to give additional information, like the taxonomic groups of the imported organisms. In the upper part of the form you can preset diverse informations that should 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 in your data if there is e.g. a parasite and a host. The data tables that 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.




By default for every dataset one collection event will be created.




If the events should be taken together on the bases of the entries in the file, you can choose the second option as shown below. The import will create a new event if there is a change in any of the data related to the collection event, like the description of the locality, the altitude, the coordinates etc.




If all the dataset belong to one event series, e.g. an expedition, you can choose the option as shown below and enter the code and description of the event series in the corresponding fields.

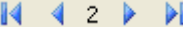
All collection events belong to an event series, e.g. an expedition 

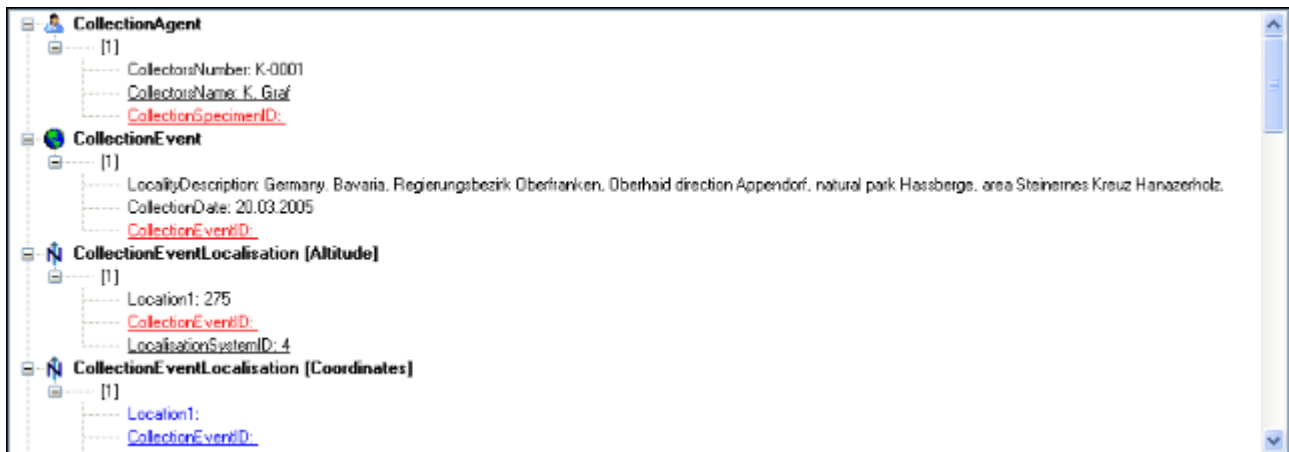
Code	Description	Notes
Elbe06	Elbsandsteingebirge, 25.9. - 4.10.2006	

If you want to use an existing event series, 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 a successful analysis, the form 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 dataset will be shown in the form. If you want to check more datasets, set the number of the last position you want to check and click on the **[Analyse]** button. The data are presented according to the tables in the database where they will be inserted. Underlined columns 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 dataset contains no values and will therefore not be imported into the database, the columns will be shown in **blue**. To import these entries in any case, choose the **[import empty values]** option. To browse through the datasets in the preview use the  buttons.

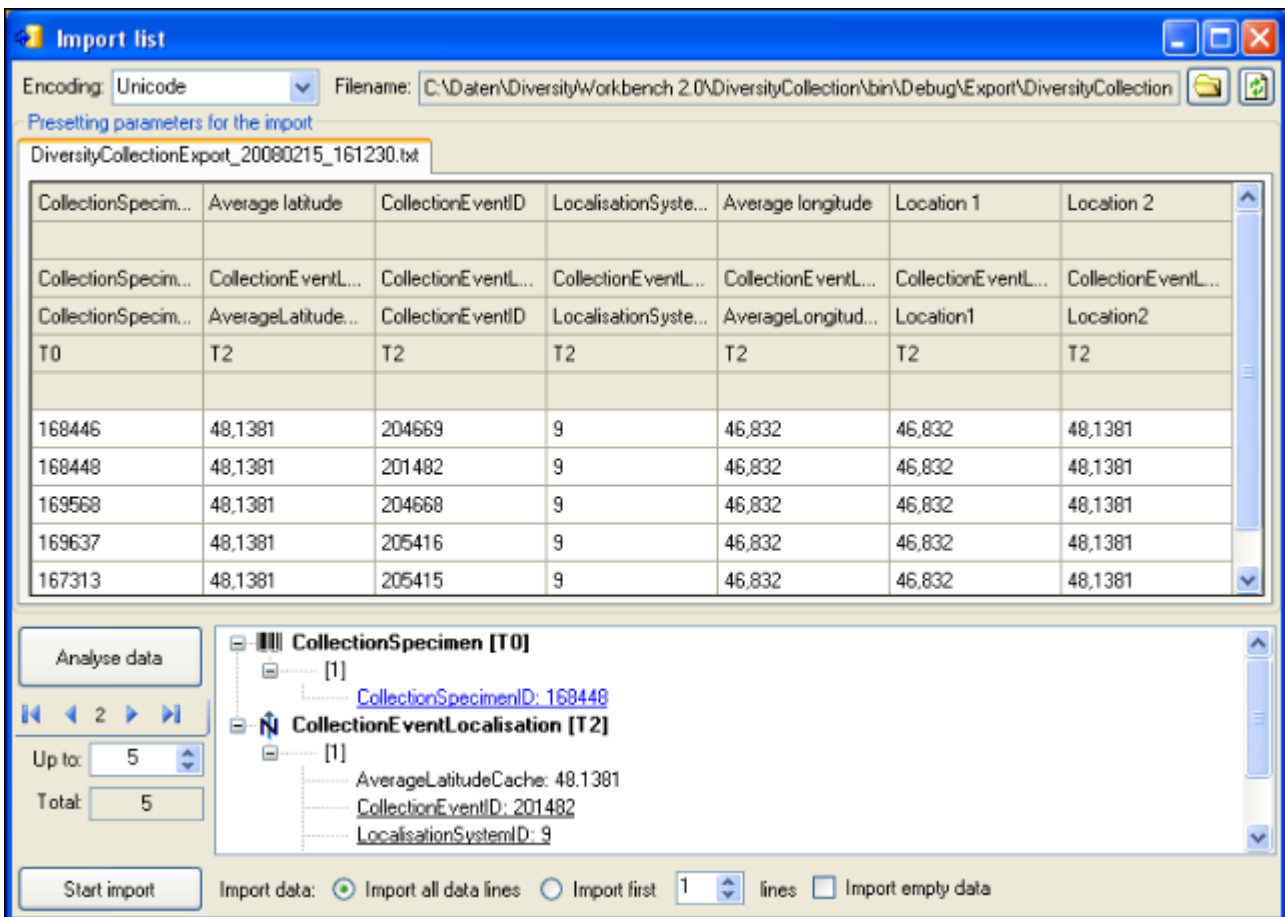



To import your data, click on the **[Start import]** button. If you want to import just a part of the data, e.g. for a test, choose the **[Import first ... lines]** option.

Reimport tab-separated lists

With this import routine, you can reimport data in tab-separated lists that had been exported from the database into the database. Choose **Data -> Import -> Reimport list...** from the menu to open the form for the reimport. To reimport data, these must have been exported using the option **[add columns for reimport]** to ensure correct header lines in your file. As there is no possibility to change data on the bases of lists, you may export the respective data to a tab-separated list, change your values and than reimport it.

In the form click on the  button to select the file with the data you want 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.






To analyse the data in the file click on the **[Analyse]** button. After a successful analysis, the form will show you the result as shown in the image below. The first dataset will be shown in the form. If you want to check more datasets, set the number of the last position you want to check and click on the **[Analyse]** button. The data are 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 dataset contains no values and will therefore not be imported into the database respectively updated, the columns will be shown in **blue**. To import these entries in any case, choose the **[import empty values]** option. To browse through the datasets in the preview use the  buttons.

To import your data, click on the **[Start import]** button. If you want to import just a part of the data, e.g. for a test, choose the **[Import first ... lines]** option.

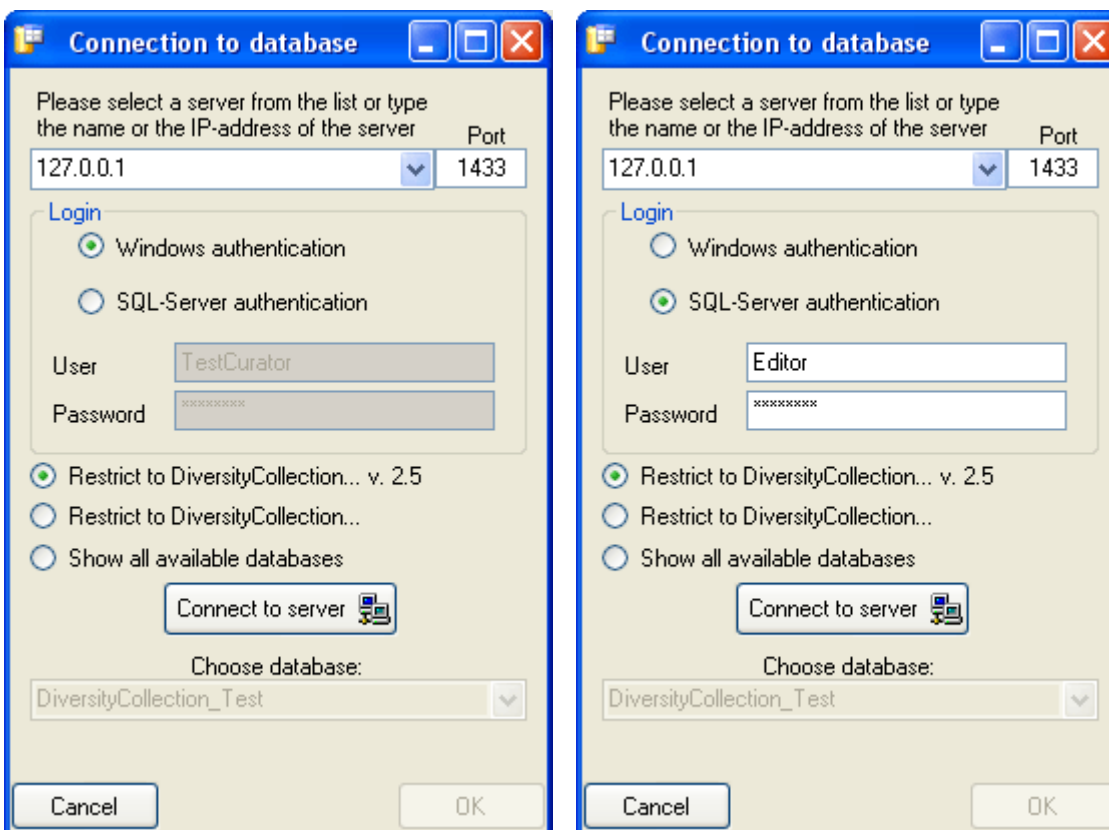
Database - access

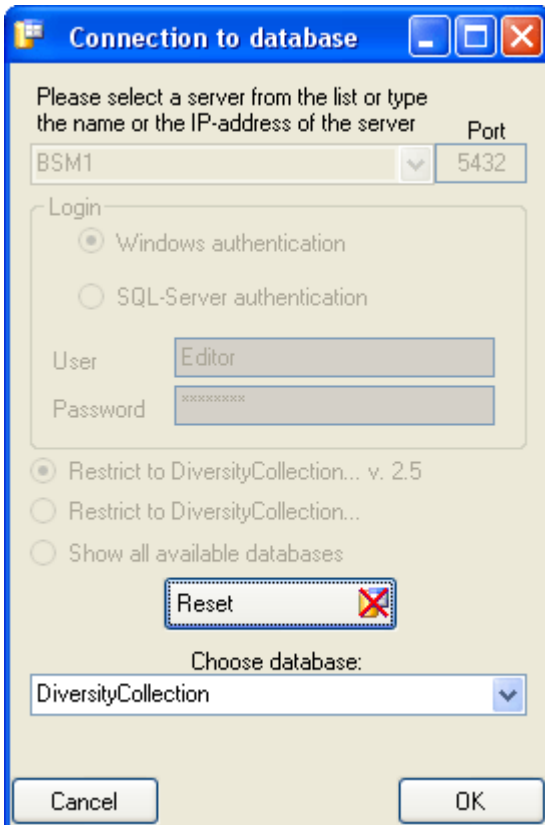
The database engine for DiversityCollection is Microsoft SQL-Server 2005.

If you are connected to a database this is indicated by the icon of the connection button  in left upper corner. If you are not connected this will be indicated by the icon . To access any database, you must specify the server where the database is located. For the configuration of this connection choose **Connection, Database...** from the menu or click on the  button.

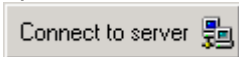
Database name, IP-address and Port

A dialog will open, to specify the name or IP-address and port number of the server and to select the authentication mode. You can either choose Windows authentication (see left image below) or SQL-Server authentication (see below - central middle image).





The standard port number for SQL-Server is 1433 and will be set as a default. If the database server is configured using a port different from that port, you must give the port number in

the field Port. Click on the  button to connect to the server. If the connection informations are valid, you can choose a database from the server from the combobox at the base of the form (see right image above). To restart the connecting process

click on the  button.

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Table Analysis

Analysis types used within the database

Column	Data type	Description
<u>AnalysisID</u>	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
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table AnalysisTaxonomicGroup

The types of analysis that are available for a taxonomic group

Column	Data type	Description
<u>AnalysisID</u>	int	Analysis ID, foreign key of table Analysis.
<u>TaxonomicGroup</u>	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 <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

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 (255)	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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionAgent

The collector(s) of collection specimens

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to ID of CollectionEvent (= Foreign key and part of primary key)
<u>CollectorsName</u>	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 <i>Default value: getdate()</i>
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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionCurator

Curators within DiversityCollection, responsible of specimen transactions

Column	Data type	Description
<u>LoginName</u>	nvarchar (50)	A login name which the user uses for access the DivesityWorkbench, Microsoft domains, etc..
<u>AdministratingCollectionID</u>	int	ID for the collection for which the curator has the right to administrate the transaction. Corresponds to AdministratingCollectionID in table Transaction.

Table CollectionEvent

The collection event where the specimen was collected

Column	Data type	Description
<u>CollectionEventID</u>	int	Unique ID for the collection event (= Primary key)
Version	int	The version of the dataset. Automatically set by the system. <i>Default value: (1)</i>
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 calculated 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 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
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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>

LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>
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Table CollectionEventImage

The images showing the site of the collection event

Column	Data type	Description
<u>CollectionEventID</u>	int	Unique ID for the collection event (= Primary key)
<u>URI</u>	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
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionEventLocalisation

The geographic localisation of a collection event

Column	Data type	Description
<u>CollectionEventID</u>	int	Refers to the ID of CollectionEvent (= Foreign key and part of primary key)
<u>LocalisationSystemID</u>	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. <i>Default value: [dbo].[CurrentUserName]()</i>
ResponsibleAgentURI	varchar (255)	URI of the person or organisation responsible for the data (see e.g. module DiversityAgents)
AverageAltitudeCache	real	Calculated altitude as parsed from the location fields
AverageLatitudeCache	real	Calculated latitude as parsed from the location fields
AverageLongitudeCache	real	Calculated longitude as parsed from the location fields
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionEventProperty

A property of a collection site, e.g. exposition, slope, vegetation. May refer to Diversity Workbench module DiversityScientificTerms

Column	Data type	Description
<u>CollectionEventID</u>	int	Refers to the ID of

		CollectionEvent (= Foreign key and part of primary key)
<u>PropertyID</u>	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. <i>Default value: [dbo].[CurrentUserName]()</i>
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 collection site.
AverageValueCache	float	For numeric values - a cached average value according to the
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionEventSeries

The series within which collection events take place

Column	Data type	Description
<u>SeriesID</u>	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
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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionEventSeriesImage

The images showing the sites of a collection event series, e.g. an expedition or sampling plot

Column	Data type	Description
<u>SeriesID</u>	int	Unique ID for the collection event series (= Foreign key and part of primary key)
<u>URI</u>	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
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this

		dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionProject

The projects within which the collection specimen were placed

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of 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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionSpecimen

The data directly attributed to the collection specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Unique reference ID for the collection specimen record (primary key)
Version	int	The version of the dataset <i>Default value: (1)</i>
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
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
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionSpecimenImage

The images of a collection specimen or of an identification unit within this specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)

<u>URI</u>	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. label
Notes	nvarchar (MAX)	Notes about the specimen image
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table **CollectionSpecimenPart**

Parts of a collection specimen. Includes a possible hierarchy of the parts

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>SpecimenPartID</u>	int	ID for a part of a specimen (part of primary key) <i>Default value: (1)</i>
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 prepared 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 duplicates 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) <i>Default value: N'specimen'</i>
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	tinyint	Number of stock units if the specimen is stored in separated units e.g. several boxes or vessels
Notes	nvarchar (MAX)	Notes concerning the storage of the sample
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionSpecimenProcessing

The processing that was applied to a collection specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>ProcessingDate</u>	datetime	Date and time of the start of the processing <i>Default value: getdate()</i>
ProcessingID	int	ID of the processing. Refers to ProcessingID in table Processing (foreign key) <i>Default value: (1)</i>
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 in seconds
ResponsibleName	nvarchar (255)	Name of the person or institution responsible for the determination <i>Default value: [dbo].[CurrentUserName]()</i>
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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table **CollectionSpecimenRelation**

The relations of a collection specimen to other collection specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Unique reference ID for the collection specimen record (primary key)
<u>RelatedSpecimenURI</u>	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 <i>Default value: (1)</i>
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table CollectionSpecimenTransaction

The transactions in which a specimen was involved

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>TransactionID</u>	int	Unique ID for the transaction (= Foreign key and part of primary key)
<u>SpecimenPartID</u>	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. <i>Default value: user_name()</i>
LogInsertedWhen	smalldatetime	Date and time when the data

		were first entered (typed or imported) into this database. <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Name of user who last updated the data. <i>Default value: user_name()</i>
LogUpdatedWhen	smalldatetime	Date and time when the data were last updated. <i>Default value: getdate()</i>

Table Identification

The identifications of the organisms within a specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>IdentificationUnitID</u>	int	Refers to the ID of IdentificationUnit (= foreign key and part of primary key)
<u>IdentificationSequence</u>	smallint	The sequence of the identifications. The last identification (having the highest sequence) is regarded as valid <i>Default value: (1)</i>
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
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 <i>Default value:</i> <i>[dbo].[CurrentUserName]()</i>
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 <i>Default value:</i> <i>getdate()</i>
LogCreatedBy	nvarchar (50)	Login of the user who created the dataset <i>Default value:</i> <i>user_name()</i>
LogUpdatedWhen	datetime	Date and time when the dataset was changed

		<i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Login of the user who changed the dataset <i>Default value: user_name()</i>

Table IdentificationUnit

Organism that is present in or on a collection specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>IdentificationUnitID</u>	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,
<u>LastIdentificationCache</u>	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. <i>Default value: (0)</i>
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 exsiccate.
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 occurrence 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. <i>Default value: (1)</i>
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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>

LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table IdentificationUnitAnalysis

The analysis values taken from an identification unit

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>IdentificationUnitID</u>	int	Refers to the ID of IdentificationUnit (= foreign key and part of primary key)
<u>AnalysisID</u>	int	Analysis ID, foreign key of table Analysis.
<u>AnalysisNumber</u>	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 <i>Default value: [dbo].[CurrentUserName]()</i>
ResponsibleAgentURI	varchar (255)	URI of the person or institution responsible for the determination (= foreign key) as stored in the module DiversityAgents.
AnalysisDate	datetime	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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset

		<i>Default value: user_name()</i>
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Table IdentificationUnitInPart

The list of the organisms that are found in a part of the specimen

Column	Data type	Description
<u>CollectionSpecimenID</u>	int	Refers to the ID of CollectionSpecimen (= Foreign key and part of primary key)
<u>IdentificationUnitID</u>	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,
<u>SpecimenPartID</u>	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. <i>Default value: (1)</i>
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. <i>Default value: user_name()</i>
LogInsertedWhen	smalldatetime	Date and time when the data were first entered (typed or imported) into this database. <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Name of user who last updated the data. <i>Default value: user_name()</i>
LogUpdatedWhen	smalldatetime	Date and time when the data were last updated. <i>Default value: getdate()</i>

Table LocalisationSystem

The geographic localisation systems, e.g. coordinates

Column	Data type	Description
<u>LocalisationSystemID</u>	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, geographic 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
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Table Processing

The processings of the specimen

Column	Data type	Description
<u>ProcessingID</u>	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
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table ProcessingMaterialCategory

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) <i>Default value: (1)</i>
<u>MaterialCategory</u>	nvarchar (50)	Material category of specimen. Examples: 'herbarium sheets', 'drawings', 'microscopic slides' etc. <i>Default value: N'specimen'</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated

		<i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table Property

The list of the properties that can be specified for the collection site

Column	Data type	Description
<u>PropertyID</u>	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)	-
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

Table Transaction

Transactions like loan, borrow, gift, exchange etc. of specimen if they are e.g. permanently or temporary transferred from one collection to another

Column	Data type	Description
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<u>TransactionID</u>	int	Unique ID for the transaction (= Primary key)
ParentTransactionID	int	The ID of a preceding 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 <i>Default value: N'exchange'</i>
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) <i>Default value: ''</i>
MaterialCategory	nvarchar (50)	Material category of specimen. Examples: 'herbarium sheets', 'drawings', 'microscopic slides' etc. <i>Default value: N'specimen'</i>
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
FromTransactionPartnerAgent URI	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 transferred, 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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

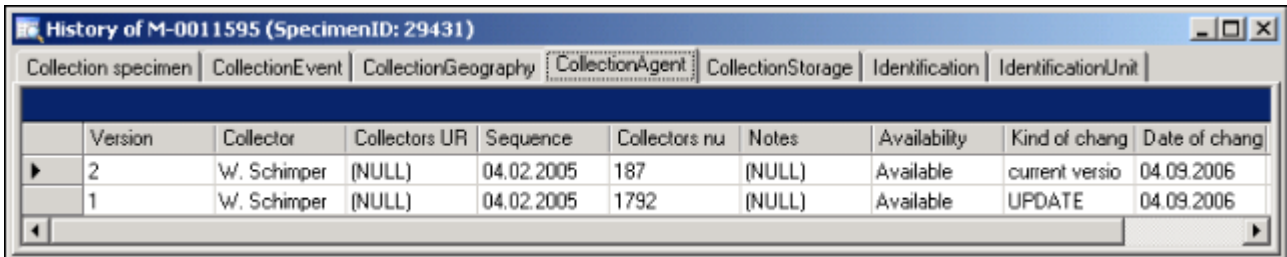
Table TransactionDocument

The history of transactions resp. the documents connected to the transactions

Column	Data type	Description
<u>TransactionID</u>	int	Unique ID for the Transaction, refers to table Transaction (= Part of primary key and foreign key)
<u>Date</u>	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 <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

History

To inspect the history of a dataset click on the  button. A form will open, showing all former states of the data in the tables with the current dataset at the top. The database DiversityCollection handles 2 different histories - one for the collection specimen and one for the collection event. The version shown in the header of the main form 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 collection event, e.g. 2 / 1 means version 2 of the specimen and version 1 of the collection event.



Version	Collector	Collectors UR	Sequence	Collectors nu	Notes	Availability	Kind of chang	Date of chang
2	W. Schimper	(NULL)	04.02.2005	187	(NULL)	Available	current versio	04.09.2006
1	W. Schimper	(NULL)	04.02.2005	1792	(NULL)	Available	UPDATE	04.09.2006

The version will be set automatically. If a dataset 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](#)).

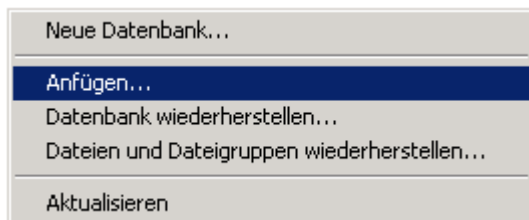
Backup

If you need to backup your database, you have to use the functionality provided by SQL-Server. To do this, you need administration rights in the database you want to create a backup. Open the 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 store a copy of the ..._Data.MDF File to keep it as a backup.

After storing the backup you have to attach the database.



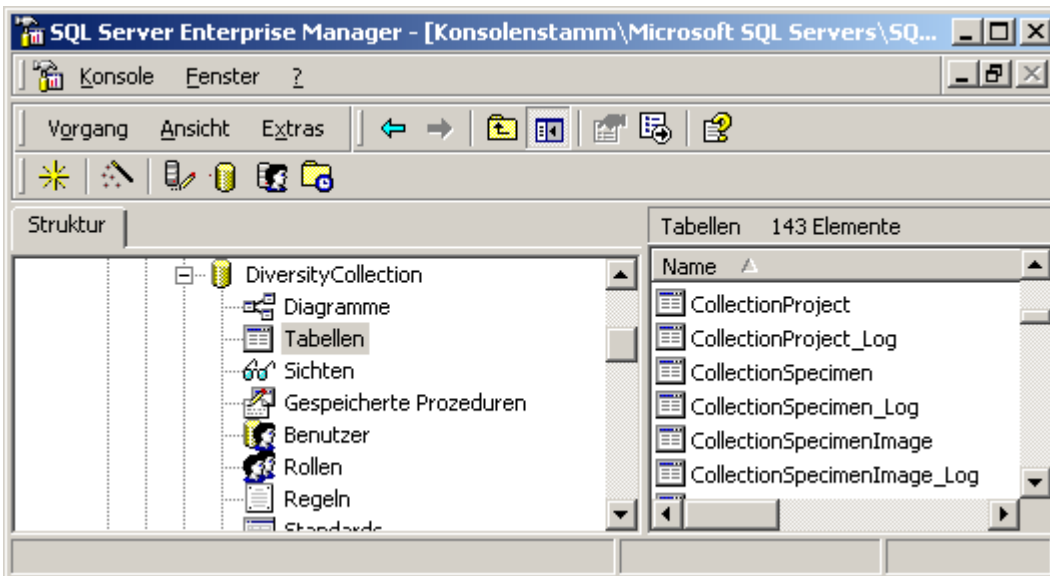
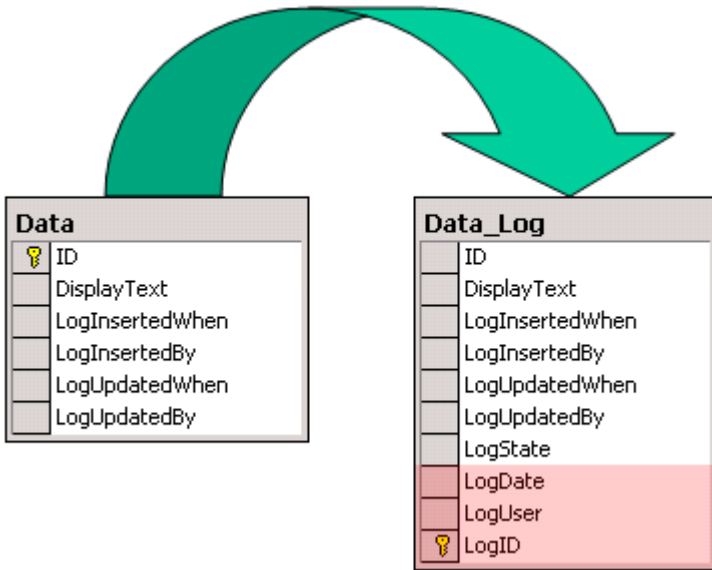
A dialog will appear where you have to select the original database file in your directory.

Logging

Changes within the database will be documented for each dataset together with the time and the responsible user in the columns shown in the image below.




Spaltenname	Datentyp/Form	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	smal datetime	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	smal datetime	Date and time when record was last updated.

All main tables have a corresponding logging table. If you change or delete a dataset the original dataset will be stored in this logging table together with informations about who has done the changes and when it happend.



Version of datasets

The **Version** of a dataset consists of two parts, e.g. 3 / 1 as shown in the header of the [specimen](#) in the main form. The first part of the number refers to the version of the dataset as stored in table CollectionSpecimen. The second part refers to the version as stored in the table CollectionEvent. Both versions will be set to a higher number if the data in the tables themselves or in dependent tables are changed, e.g. the insertion of a new identification in the table Identification will increase the specimen part of the version from 3 to 4 resulting in a version 4 / 1 for the whole dataset. 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 dataset within 24 hours and the version will only be increased by 1.

Acc.No.	Erysiphe aquilegiae var. ranunculi (Grev.) U. Braun	ID (Specimen / Event)	Version	Withhold. reason			
M-0040397		135548 / 211558	3 / 1	<input type="text"/>			

The data are stored in the tables [CollectionSpecimen](#) and [CollectionEvent](#).

Database - Application tables

Informations concerning the application are stored in the application tables. The table ApplicationSearchSelectionStrings hold the SQL-strings of the predefined queries for the users. The table ApplicationEntityDescription holds the description of the database entities, if these are different from the description in the database, especially if other languages then English are to be supported.

Index

- [ApplicationEntityDescription](#)
- [ApplicationSearchSelectionStrings](#)
- [ProjectProxy](#)
- [ProjectUser](#)
- [UserProxy](#)

Table ApplicationEntityDescription

The description of the columns in different languages

Column	Data type	Description
TableName	varchar (50)	The name of the table within the database
ColumnName	varchar (50)	The name of the column of the table within the database
DisplayText	nvarchar (50)	The text for the column as shown e.g. in a user interface
Description	nvarchar (MAX)	The description of the content of the column
LanguageCode	nvarchar (50)	ISO 639: 2-letter codes for the language of DisplayText and Description
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table ApplicationSearchSelectionStrings

Selection strings for customized queries for users

Column	Data type	Description
UserName	varchar (50)	The name of the user who created this SQL string <i>Default value: user_name()</i>
SQLStringIdentifier	varchar (50)	The identifier for the selection string as shown in user interface

ItemTable	varchar (50)	The main table from which the datasets should be selected <i>Default value: 'TaxonName'</i>
SQLString	varchar (MAX)	SQL string for selecting datasets from the database
Description	nvarchar (MAX)	Description of the resultset and the purpose of the query
LogCreatedWhen	datetime	The time when this dataset was created <i>Default value: getdate()</i>
LogCreatedBy	nvarchar (50)	Who created this dataset <i>Default value: user_name()</i>
LogUpdatedWhen	datetime	The last time when this dataset was updated <i>Default value: getdate()</i>
LogUpdatedBy	nvarchar (50)	Who was the last to update this dataset <i>Default value: user_name()</i>

Table ProjectProxy

The projects as stored in the module DiversityProjects

Column	Data type	Description
<u>ProjectID</u>	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)
Project	nvarchar (50)	The name or title of the project as shown in a user interface (Projects are defined in DiversityProjects)

Table ProjectUser

The projects that a user can access

Column	Data type	Description
<u>LoginName</u>	nvarchar (50)	A login name which the user uses for access the DivesityWorkbench, Microsoft domains, etc..
<u>ProjectID</u>	int	ID of the project to which the specimen belongs (Projects are defined in DiversityProjects)

Table UserProxy

The user as stored in the module DiversityUsers

Column	Data type	Description
<u>LoginName</u>	nvarchar (50)	A login name which the user uses for access the DivesityWorkbench, Microsoft domains, etc..
CombinedNameCache	nvarchar (255)	The short name of the user, e.g. P. Smith <i>Default value: NULL</i>
UserURI	varchar (255)	URI of a user in a remote module, e.g. referring to UserInfo.UserID in database DiversityUsers

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 DiversityProjects, DiversityResources, DiversityExsiccatae, DiversityGazetteer, DiversityScientificTerms, DiversityTaxonNames, DiversityAgents, DiversityUsers and DiversityReferences as illustrated in the image below.



The [modules](#) communicate with each other to provide their services for the other modules.

Modules

The [Diversity Workbench](#) is a set of components for building and managing biodiversity information, each of which focuses on a particular domain.

Dive

rsity Administration of the agents, i.e. people and institutions which should be documented with e.g. their addresses
Age
nts

Dive

rsity
Coll Administration of the scientific collections and specimens within these collections
ecti
on

Dive

rsity
Des Administration of descriptive data
cript
ions

Dive

rsity
Exsi Administration of [exsiccatal series](#)
ccat
ae

Dive

rsity A data collection to enable the linking of [geographical records](#) with the Getty Thesaurus of Geographical Names (TGN), the German Gaze geographical names.

tteer

Dive

rsity
Scie Data collections of [scientific terms](#) from foreign sources like vegetation, stratigraphy, soil science etc.
ntifi
cTer
ms

Dive

rsity Administration of [projects](#) within the Diversity Workbench
Proj
ects

Dive

rsity
Refe Administration of [references](#)
renc
es

Dive

rsity
Res Administration of [resources](#) like images, etc.
ourc
es

Dive

rsity
Tax Administration of [taxonomic names](#), their synonyms and hierarchical position
onN
ame
s

Dive

rsity Administration of the [users](#) and their permissions within the Diversity Workbench
User
s



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

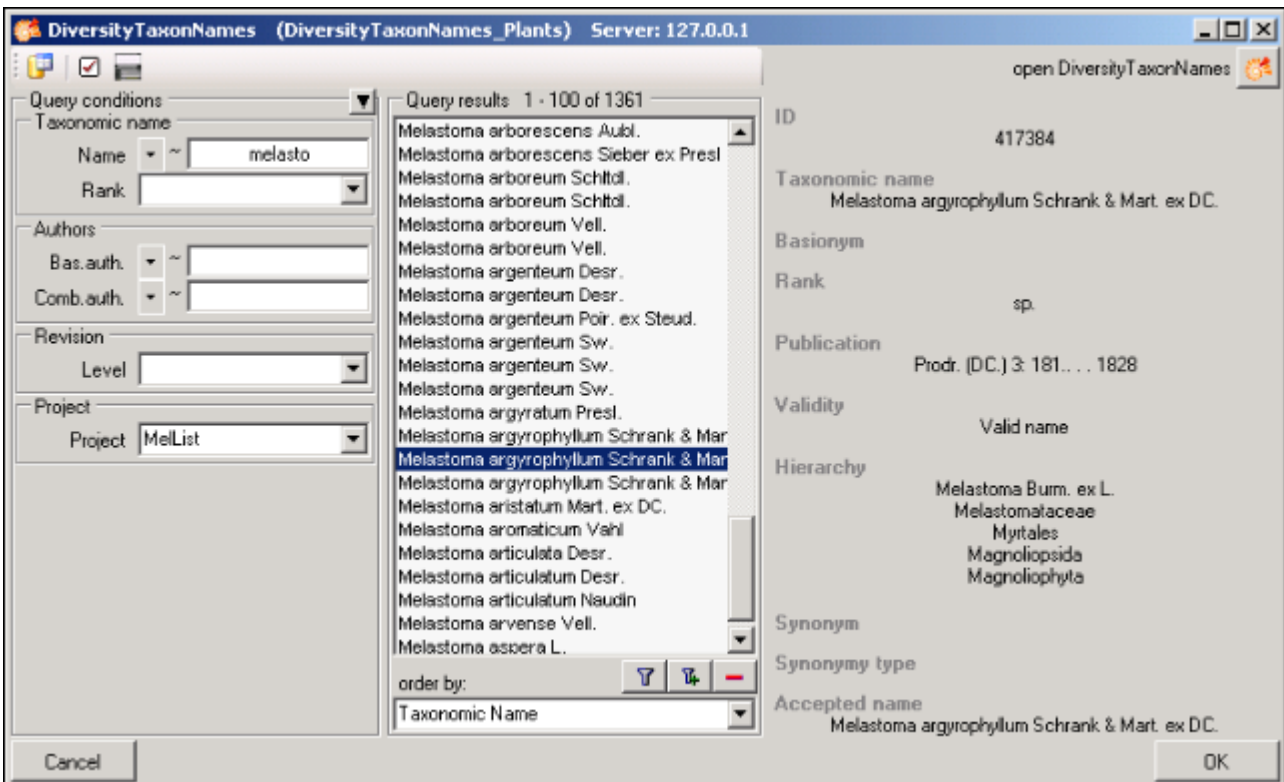
Module related entry

The Diversity Workbench is a set of components for building and managing biodiversity information, each of which focuses on a particular domain. Each module provides services for the other [modules](#). To use the service of a module, you need access to the database of the module and optionally the module application placed in your application directory. Entries related to an external module have a standard interface in the main form. There are 2 states of this interface:

1 - the value is only set in the local database with no connection to the remote module

Tax.name: 



In this state, you can either type the value or select it from the values that are already available in the database. To get a list of the available values type the beginning of the value (you may use wildcards) and click on the  button. If you want to set a relation to the remote module, click on the  button. A form will open where you may select an entry from the foreign database.





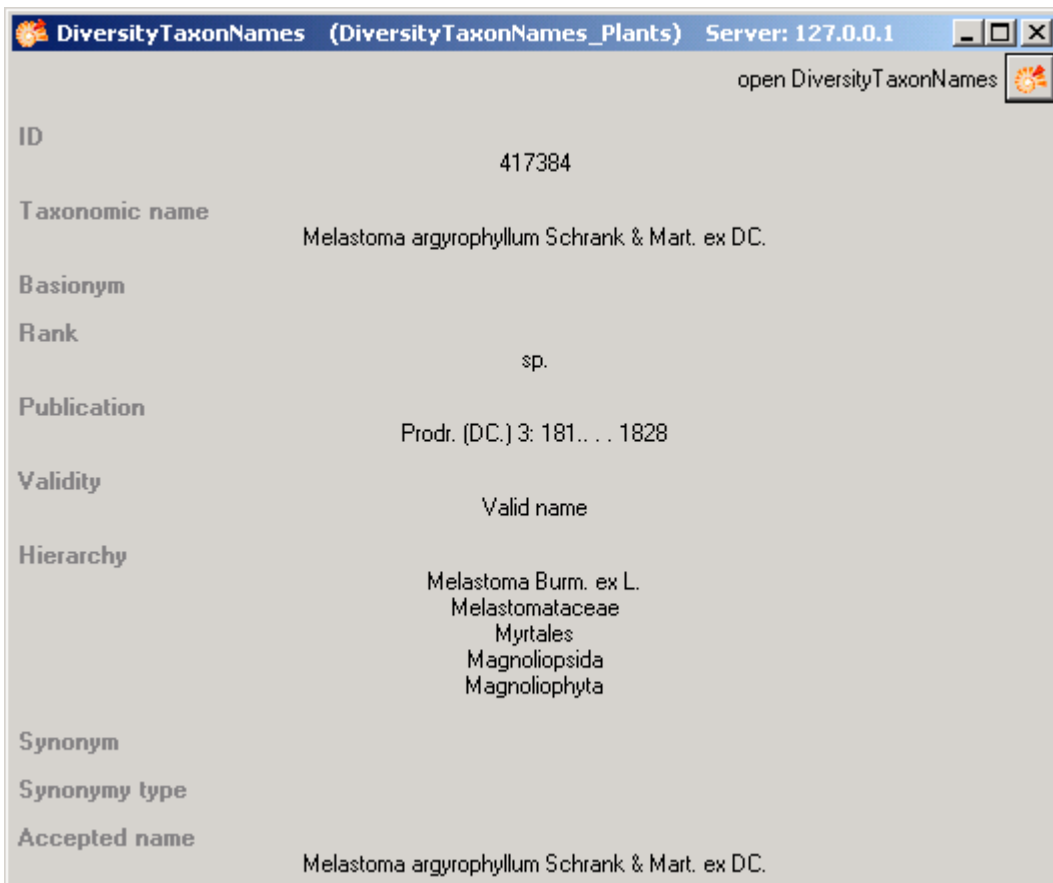
The screenshot shows the 'DiversityTaxonNames' application window. The title bar indicates 'Server: 127.0.0.1'. The main interface is divided into several sections:


- Query conditions:** Includes fields for 'Taxonomic name' (Name: ~ melasto, Rank: dropdown), 'Authors' (Bas. auth., Comb. auth.), 'Revision' (Level: dropdown), and 'Project' (Project: MeList).
- Query results:** A list of 1361 results, with 'Melastoma argyrophyllum Schrank & Mart. ex DC.' highlighted. Below the list are 'order by:' options (Taxonomic Name) and sorting icons.
- Details panel:** Shows information for the selected entry, including ID (417384), Taxonomic name, Basionym, Rank (sp.), Publication (Prodr. (DC.) 3: 181... 1828), Validity (Valid name), Hierarchy (Melastoma Bum. ex L., Melastomataceae, Myrtales, Magnoliopsida, Magnoliophyta), Synonym, Synonymy type, and Accepted name (Melastoma argyrophyllum Schrank & Mart. ex DC.).

2 - the value is related to the remote module

Tax.name:  


If the value has a relation to the remote module, the interface will appear as shown above. To release the connection to the remote module click on the  button. If you need further information about the value, click on the  button. This will open a form, showing an overview of the related value.



If the client application of the module is available you can inspect the details of the entry. To start the client application of the remote module, just 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.

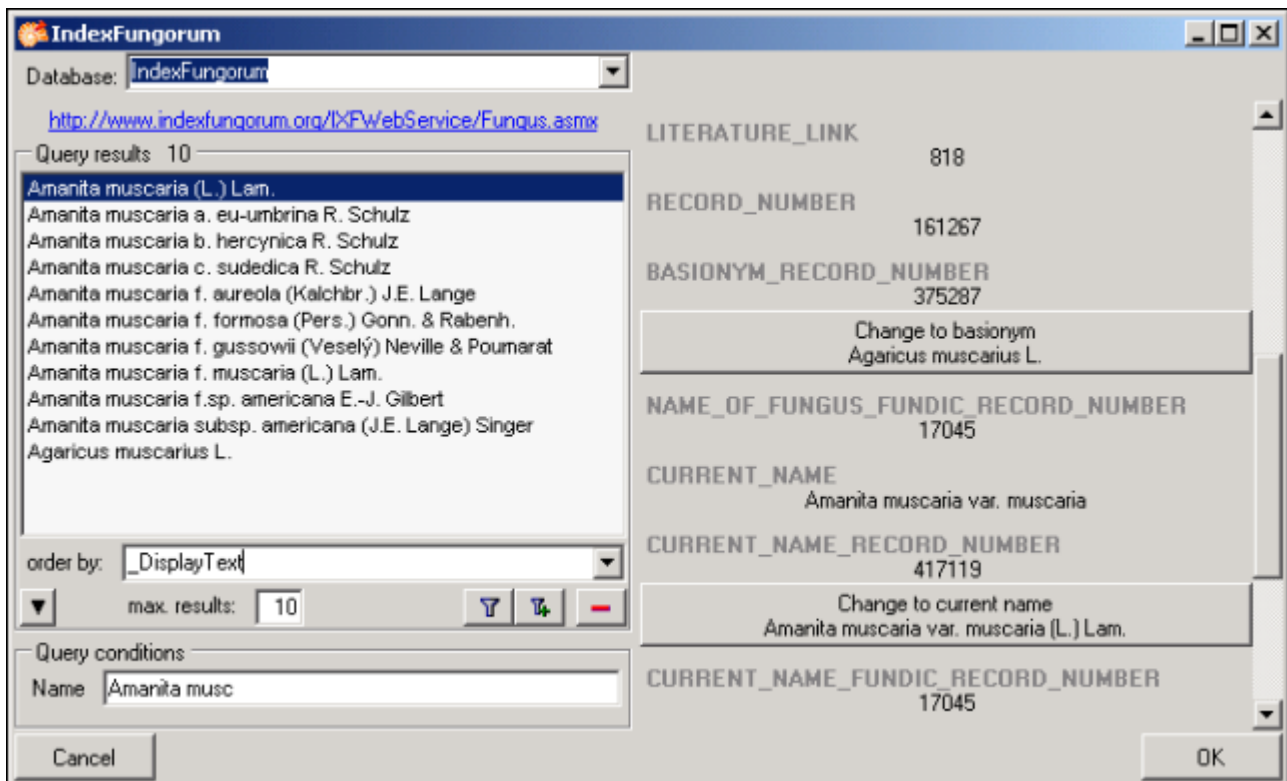
To establish a connection to an external webservice, click on the  button. As with the link to modules within the Diversity Workbench a form will open where you can choose from either Diversity Workbench modules or external Webservices. See [Webservice](#) for further details

4 - relation to a local service

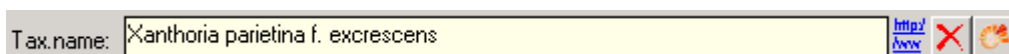
Some modules provide the possibility to link your data to a local installed service. For example DiversityTaxonNames gives you access to the taxonomic names of the Catalogue of life. See [Catalogue of Life](#) for further details


Webservice - foreign sources

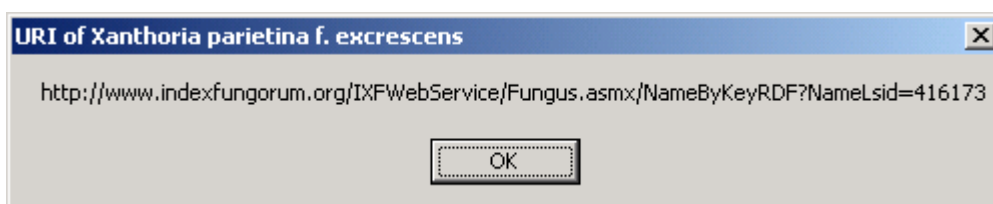
Some modules within the Diversity Workbench provide the possibility to link your data to an external webservice. For example DiversityTaxonNames gives you access to the taxonomic names of IndexFungorum. To establish a connection to an external webservice, click on the  button. A form will open where you can choose from either Diversity Workbench modules or external Webservices.




If you choose a webservice the form will change as shown in the above image. Enter the query condition for your search and the maximal number of records you want to get in the max. results field (choose a low number if you have a slow connection to the internet). Then click on the search button to start the query. In the right part of the form additional information is shown as provided by the webservice. For certain entries buttons will appear, as e.g. shown above for the basionym and the current name of a scientific name. Click on these buttons if you want to change to one of these related datasets from the webservice. To take the link from the webservice into your database choose one of the entries and click OK. The entry will change as shown below.

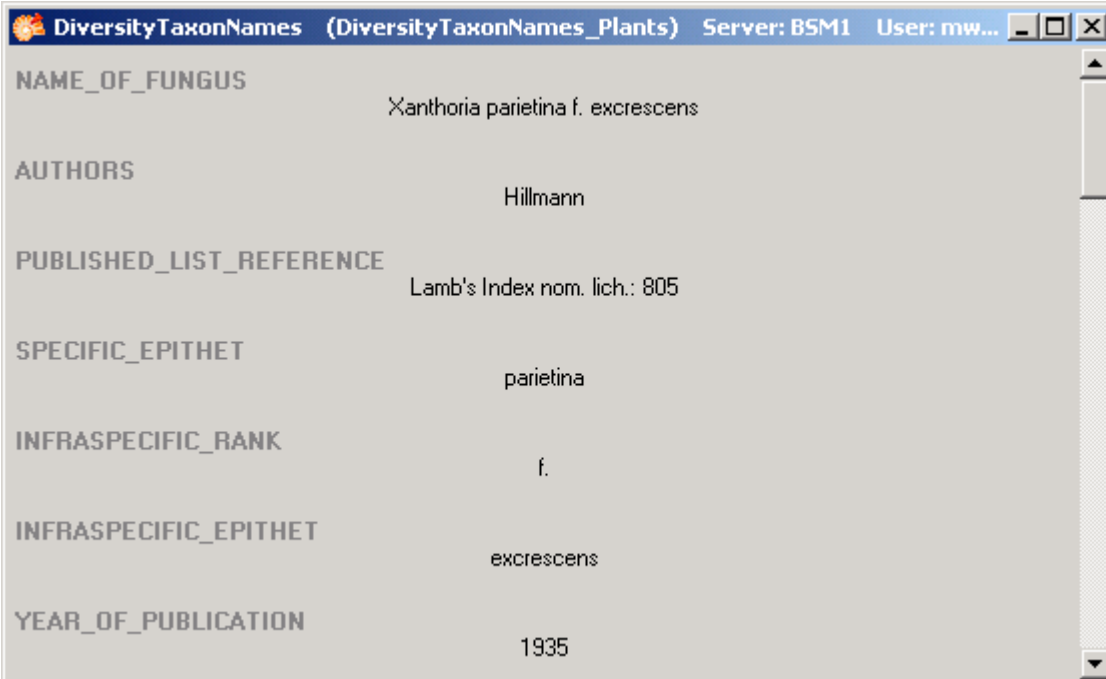


If you double-click on the link area  a window will open, providing you with the retrieval information of the webservice.




To get the whole information related to this entry as provided by the webservice, click on the


 button. A window will open as shown below where the informations of the webservice are listed.




Field Name	Value
NAME_OF_FUNGUS	Xanthoria parietina f. excrescens
AUTHORS	Hillmann
PUBLISHED_LIST_REFERENCE	Lamb's Index nom. lich.: 805
SPECIFIC_EPITHET	parietina
INFRASPECIFIC_RANK	f.
INFRASPECIFIC_EPITHET	excrescens
YEAR_OF_PUBLICATION	1935

If you want to remove the link to the webservice, click on the  button. This will only remove the relation to the webservice, not the cached name.

Catalogue of life

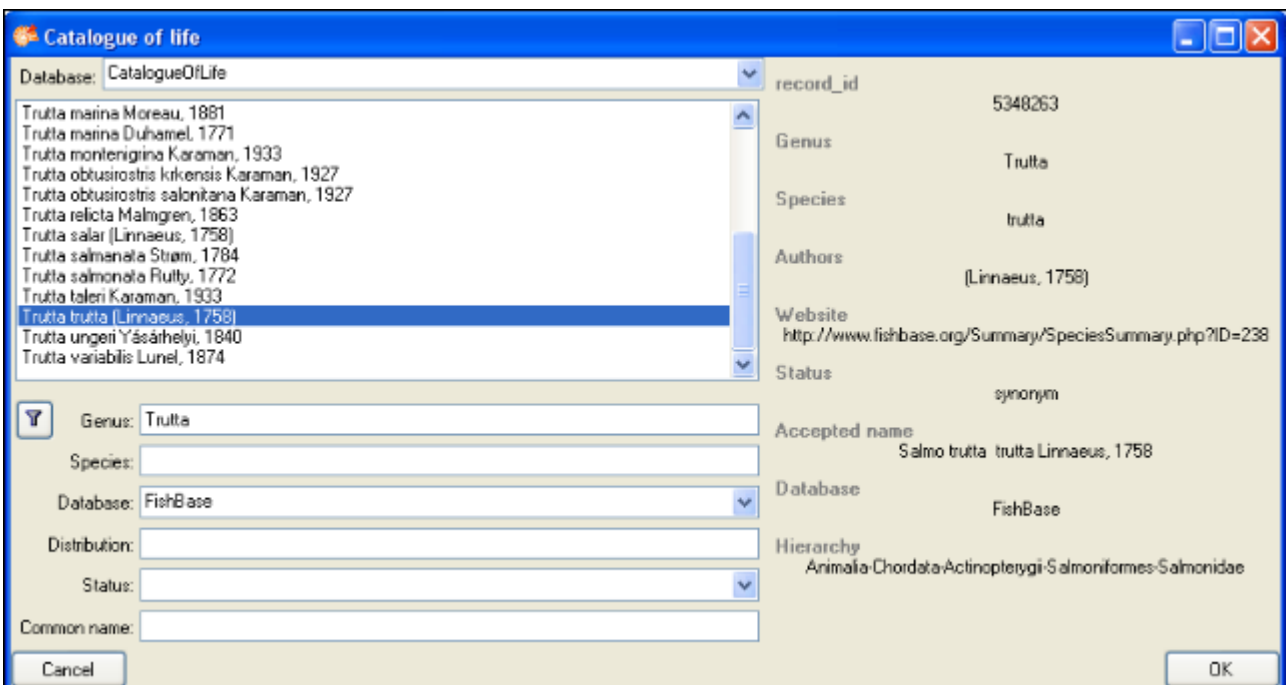
Some modules within the Diversity Workbench provide the possibility to link your data to a foreign source. For example DiversityTaxonNames gives you access to the taxonomic names of the Catalogue of life. To establish a connection to this source, click on the  button. As with the link to modules within the Diversity Workbench a form will open where you can choose from either Diversity Workbench modules, external Webservices or foreign sources. If you need the service of the catalogue of life, you have to install this according to the installation instructions provided at http://www.catalogueoflife.org/annual-checklist/2008/info_about_col.php. If you have the catalogue of life installed on your local machine, you have access to this service provided the service is started. Start the service e.g. by choosing **Programs -> Catalogue of Life -> 2008 Annual Checklist** from your Windows Start menu (the exact path depends on your local installation).






An icon  will appear in your Windows Task panel, showing that the MicroWeb server is running. Then choose the Catalogue of life from the list as shown below. If you forget to start this service, the program will try to start it. To stop this service, right-click on this symbol and choose Exit.



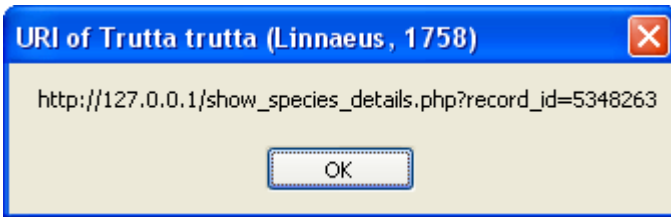
If the service is started you can search the names provided by the Catalogue of life as shown below.




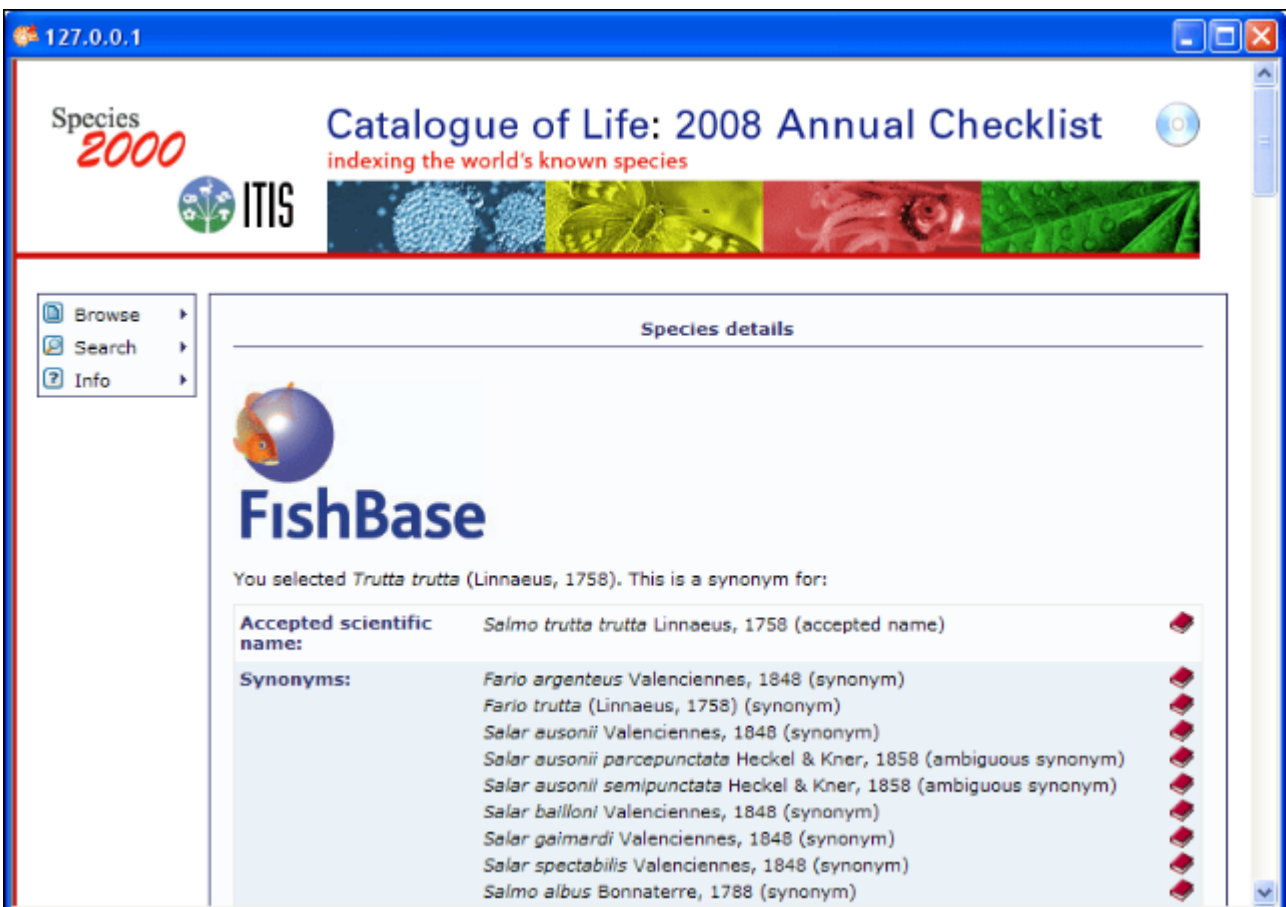
You can choose one of the databases provided by the Catalogue of Life and enter the query conditions for your search. Then click on the search button  to start the query. In the right part of the form additional information is shown as provided by the service. To take the link from the service into your database choose one of the entries and click OK. The entry will change as shown below.


Tax.name: [http://127.0.0.1](#)  

If you double-click on the link area [http://](#) a window will open, providing you with the retrieval information of the service.




To get the whole information related to this entry as provided by the service, click on the  button. A window will open as shown below where the informations of the service are listed.



If you want to remove the link to the service, click on the  button. This will only remove the relation to the service, not the cached name.

Resources

Images for specimen and the collection event can either be stored in DiversityCollection with their file path or in more detail in the module DiversityResources. For directly changing to DiversityResources click on the  button.

For direct access to the resources in this module, you need the application **DiversityResources.exe** in your application directory, the database DiversityResources and a valid account in the database DiversityUsers.

Reference

Details about References are stored in the module DiversityReferences. You can 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 need the application **DiversityReferences.exe** in your application directory. To use the application DiversityReferences.exe you need access to the database DiversityReferences.