



# GOTIT 1.1 HELP LIBRARY

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## **1. WHAT IS GOTIT???**

GOTIT (Gene, Occurrence and Taxa in Integrative Taxonomy<sup>1</sup>) is a Web user interface for managing and mapping data and metadata on species occurrence. It differs from conventional species occurrence web interfaces in that it incorporates species taxa delimited on different criteria, especially morphological and molecular criteria. GOTIT includes species taxa with binomial names (which were historically most often delimited based on morphology) and species taxa delimited based on molecular criteria. The latter are referred to as molecular operational taxonomic units (MOTU). These different species taxa are linked into a coherent framework.

Also, in accordance to the scientific rigor of taxonomy, GOTIT provides full traceability of methods and biological material related to species occurrence data. It allows tracking information about the sampling site and method, the biological material collected at a site (i.e. specimen lot and individual specimen used for morphological and molecular analysis), the molecular method (DNA extraction, PCR) and metadata (chromatogram, DNA sequence) used to delimit MOTUs, the storage of biological material (specimen lot, individual specimen, specimen slide and specimen DNA) and literature references.

GOTIT has been conceived as an “an everyday working laboratory resource” that can be used to manage data and metadata produced on a-day-by-day basis by a biodiversity laboratory involved in the delimitation and distribution of species taxa. In addition, it incorporates species occurrence data and molecular metadata (i.e. DNA sequence) from external sources (e.g. literature). GOTIT is a Web user interface that stores and retrieves information from a relational database, the structure of which is briefly described in the following section.

<sup>1</sup> “Integrative taxonomy’ is defined as the science that aims to delimit the units of life’s diversity from multiple and complementary perspectives.” (Dayrat B. 2005. Towards integrative taxonomy. Biological Journal of the Linnean Society, 85(3): 407–417).

## **2. THE DATA BASE BEHIND GOTIT**

Figure 1 provides the simplified structure of the relational data base in which GOTIT stores and retrieves information (see document ” GOTIT\_help\_database.pdf” for a detailed description of the data base).

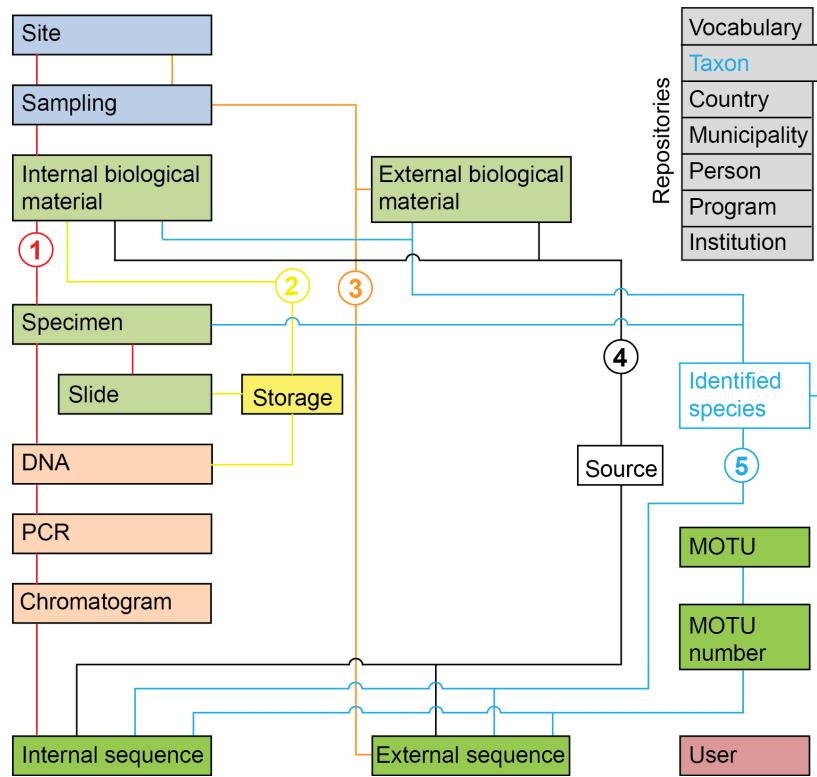


Figure 1: Simplified structure of the relational data base connected to GOTIT.

The database structure follows a classical data-production procedure along which a site is visited (table: site) and sampled (table: sampling). Sampling provides specimen lots (table: internal biological material) among which some specimens are isolated (table: specimens) and used for dissecting and mounting (table: slides) and/or producing DNA sequences (tables: DNA, PCR, chromatogram, internal sequence). This procedure generates biological material that is physically stored at identified locations (table: storage for specimen lots, specimen slides and DNA solution). The data base also incorporates data from the literature, either species occurrence data (table: external biological material) or DNA sequence data (table: external sequence), to which we refer as to external data. Biological materials and sequences (either internal or external) are linked to literature references (table: source). Taxa names are attributed to biological material, specimens and sequences and the attribution process specifies which delimitation criterion is used (tables: species taxa). At last, MOTUs (tables: MOTU and MOTU numbers) are attributed to DNA sequences, specifying well-defined delimitation methods and data sets. Overall, the data table structure provides the necessary traceability for recovering the set of methods and biological material linked to any species delimitation and occurrence.

### 3. DASHBOARD

The dashboard provides summary of data stored in the relational data base as well as the last updates made in GOTIT. It also provides direct links to a number of data uploading tools (Tools). The help button (?) on the upper right corner provides short information on how to use each form as well as links to sections of GOTIT HELP document for further details. The menu on the upper right corner allows the user to change his account (option “profile” available for administrator and project member only), to switch to the English/French version of GOTIT and to log out.

#### 4. GOTIT menu

The GOTIT menu contains 9 headings each containing a number of sub-headings. The lists of headings and sub-headings are provided in table 1, together with their corresponding tables in the relational data base. The content and use of headings and sub-headings are detailed in the ensuing document.

Table 1: Headings of GOTIT menu and their corresponding items in the simplified structure of the relational data base (cf. Fig. 1). Colors as in Figure 1.

GOTIT headings	GOTIT sub-headings	Table in the simplified database structure (Fig. 1)
Field data	Site	Site
	Sampling	Sampling
Morphological analysis	Biological material (internal)	Bio. Mat. (internal)
	Specimen	Specimen
	Specimen slide	Slides
	External biological material	Bio. Mat. (external)
Molecular analysis	DNA	DNA
	PCR	PCR
	Chromatogram	Chromatogram
DNA sequence	Internal sequence	Sequence (internal)
	External sequence	Sequence (external)
	MOTU	MOTU & MOTU number
Storage	Biological material	Storage
	Specimen slide	Storage
	DNA	Storage

Sources		Sources
Repositories	Vocabulary	Repository tables
	Taxon	Taxon
	Person	Repository tables
	Program	Repository tables
	Institution	Repository tables
	Country	Repository tables
	Municipality	Repository tables
User		User
Species search	COI data set	
	MOTU	
	Species hypotheses	
	Distribution data	
	Species hypotheses	

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Each sub-heading gives access to a content web page showing the content of selected fields for records of the targeted table (Figure 2). The content page features buttons to delete records, upload many records at a time and to access individual record forms for creating, reading and updating records. Other buttons direct the user to the next step of the data production process, such as for example, the DNA extracts and microscope slides generated from the specimens. Record forms provide the fields to be completed for each record: data entry is made as often as possible by means of menus scrolling down the items entered in the repository tables (Figure 2). A number of specialized tools are included into the report forms. A tool example is the self-generation of informative identifier codes from data entries made in the report form (e.g. the two specimen codes in Figure 2, see also section 15. of GOTIT HELP). Another useful tool is the cartographic visualization in the site creation form of already existing sites in the vicinity of a candidate site. This prevents users to create several names for the same site.

**a**

Headings

**b**

Sub-headings

**c**

Specimen content page

**d**

Specimen update form

Figure 2: Overview of GOTIT web interface showing extracts of the dashboard headings (a), its sub-headings (b), a content page (c) and a record form (d). The “User profile” and “Switch button” button at the top right of the interface screen (a) is for modifying login details (accessible to project members only) and changing the language of the interface, respectively. The “?” button in (a) provides the main purposes of the active screen and guides the user towards the corresponding section of GOTIT help document. Color patterns in (b) are the same as in Figure 1 to show the links between sub-headings of the interface and tables of the relational database. The list of fields shown in (c) can be modified by the user.

## **5. FIELD DATA**

### 5.1. SITE

#### 5.1.1. Site list

Use this page to browse, create, import, show, edit and delete sampling sites. Deleting a site may not be possible until all data related to a site have been deleted. Additional fields can be listed using the top right button. To access to sampling carried out at a site, click the "col" button. The search button applies to the field "site code".

#### 5.1.2. Create new site

Use this form to fill in data of a new site. See appendix 5.1.2 in GOTIT HELP for content of fields. Use the button "See nearby sites" to obtain a distribution of sites nearby the new site, once latitude and longitude of this new site have been filled in.

#### 5.1.3. Import new set of sites and related data

Use this form to upload data from multiple sites and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: country, municipality, vocabulary);
- use and upload the template file "site" to follow appropriate data format.

Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 5.1.4. Show site

Use this form to consult data of a site. See appendix 5.1.2 in GOTIT HELP for content of fields.

#### 5.1.5. Edit site

Use this form to edit data of a site. See appendix 5.1.2 in GOTIT HELP for content of fields.

#### 5.1.6. Delete site

Use this button to delete a site. Deletion may not be possible until all data related to a site have been deleted.

### 5.1.7. Linked data

The button "col" provides access to the list of sampling carried out at a site.

## 5.2. SAMPLING

### 5.2.1. Sampling list

Use this page to browse, create, import, show, edit and delete sampling surveys. Deleting a sampling may not be possible until all data related to a sampling have been deleted. Additional fields can be listed using the top right button. To access to internal biological materials, external biological materials and external sequences linked to sampling, respectively click the "Lot", "LotExt" and "SqcExt" buttons (option: ). Also, use these same buttons (option +) to create internal biological materials, external biological materials and external sequences for a sampling. The search button applies to the field "Sample code".

### 5.2.2. Create new sampling

Use this form to fill in data of a new sampling. See appendix 5.2.2 in GOTIT HELP for content of fields.

### 5.2.3. Import new set of sampling and related data

Use this form to upload data from multiple samplings and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: program, person, taxon, vocabulary);
  - use and upload the template file "sampling" to follow appropriate data format.
- Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

### 5.2.4. Show sampling

Use this form to consult data of a sampling. See appendix 5.2.2 in GOTIT HELP for content of fields.

### 5.2.5. Edit sampling

Use this form to edit data of a sampling. See appendix 5.2.2 in GOTIT HELP for content of fields.

### 5.2.6. Delete sampling

Use this button to delete a sampling. Deletion may not be possible until all data related to a sampling have been deleted.

### 5.2.7. Linked data

The button "Lot", "LotExt" and "SqExt" (option:  ) provide access to the list of internal biological materials, external biological materials and external sequences linked to a sampling, respectively. The button "Lot", "LotExt" and "SqExt" (option: +) allow to create internal biological materials, external biological materials and external sequences for a sampling, respectively.

## 6. MORPHOLOGICAL ANALYSIS

### 6.1. BIOLOGICAL MATERIAL

#### 6.1.1. Biological material list

Use this page to browse, create, import, show, edit and delete internal biological materials (i.e. specimen lots). Deleting a biological material may not be possible until all data related to a biological material have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Biological material code". To access to specimens extracted from a specimen lot and to the list of specimens for a site, respectively click the "Ind(s)" and "Ind/St" buttons (option:  ). Also, use the "Ind(s)" button (option +) to create specimens for a biological material.

#### 6.1.2. Create new biological material

Use this form to fill in data of a new internal biological material. See appendix 6.1.2 in GOTIT HELP for content of fields.

#### 6.1.3. Import new set of biological material and related data

Use this form to upload data from multiple biological materials and related data sets.

Proceed by step:

- (if necessary) upload the referential files (templates: box, taxon, vocabulary, person, source);
- use and upload the template file "internal\_biological\_material" to follow appropriate data format.

Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 6.1.4. Show biological material

Use this form to consult data of an internal biological material. See appendix 6.1.2 in GOTIT HELP for content of fields.

#### 6.1.5. Edit biological material

Use this form to edit data of an internal biological material. See appendix 6.1.2 in GOTIT HELP for content of fields.

#### 6.1.6. Delete biological material

Use this button to delete a biological material. Deletion may not be possible until all data related to a biological material have been deleted.

#### 6.1.7. Linked data

The buttons "Ind(s)" and "Ind/St" (option: ) provide access to the list of specimens extracted from a biological material and to the list of specimens for a site, respectively. The button "Ind(s)" (option +) allows to create specimens for a biological material.

### 6.2. SPECIMEN

#### 6.2.1. Specimen list

Use this page to browse, create, import, show, edit and delete specimens. Deleting a specimen may not be possible until all data related to a specimen have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Specimen morphological code". To access to DNA extract and microscope slide of a specimen, respectively click the "DNA" and "Slide" buttons (option: ) . Also, use the "DNA" and "Slide" buttons (option +) to create DNA extract and microscope slide for a specimen.

#### 6.2.2. Create new specimen

Use this form to fill in data of a new specimen. See appendix 6.2.2 in GOTIT HELP for content of fields.

#### 6.2.3. Import new set of specimens and related data

Use this form to upload data from multiple specimens and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: taxon, vocabulary, person);

- use and upload the template file "specimen" to follow appropriate data format.

Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 6.2.4. Show specimen

Use this form to consult data of a specimen. See appendix 6.2.2 in GOTIT HELP for content of fields.

#### 6.2.5. Edit specimen

Use this form to edit data of a specimen. See appendix 6.2.2 in GOTIT HELP for content of fields.

#### 6.2.6. Delete specimen

Use this button to delete a specimen. Deletion may not be possible until all data related to a specimen have been deleted.

#### 6.2.7. Linked data

The buttons "DNA" and "Slide" (option:  ) provide access to the list of DNA extracts and microscope slides of a specimen, respectively. The buttons "DNA" and "Slide" (option +) allow to create DNA extract and microscope slide for a specimen.

### 6.3. SPECIMEN SLIDE

#### 6.3.1. Specimen slide list

Use this page to browse, create, import, show, edit and delete specimen slides. Deleting a specimen slide may not be possible until all data related to a specimen slide have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Specimen morphological code".

#### 6.3.2. Create new slide

Use this form to fill in data of a new specimen slide. See appendix 6.3.2 in GOTIT HELP for content of fields.

### 6.3.3. Import new set of slides and related data

Use this form to upload data from multiple specimen slides and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: box, vocabulary, person);
  - use and upload the template file "specimen\_slide" to follow appropriate data format.
- Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

### 6.3.4. Show slide

Use this form to consult data of a specimen slide. See appendix 6.3.2 in GOTIT HELP for content of fields.

### 6.3.5. Edit slide

Use this form to edit data of a specimen slide. See appendix 6.3.2 in GOTIT HELP for content of fields.

### 6.3.6. Delete slide

Use this button to delete a specimen slide. Deletion may not be possible until all data related to a specimen slide have been deleted.

## 6.4. EXTERNAL BIOLOGICAL MATERIAL

### 6.4.1. External biological material list

Use this page to browse, create, import, show, edit and delete external biological materials (i.e. specimen lots from the literature). Deleting an external biological material may not be possible until all data related to an external biological material have been deleted.

Additional fields can be listed using the top right button. The search button applies to the field "External biological material code".

### 6.4.2. Create new external biological material

Use this form to fill in data of a new external biological material. See appendix 6.4.2 in GOTIT HELP for content of fields.

### 6.4.3. Import new set of external biological material and related data

Use this form to upload data from multiple external biological materials and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: taxon, vocabulary, person, source);
- use and upload the template file “external\_biological\_material” to follow appropriate data format.

Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 6.4.4. Show external biological material

Use this form to consult data of an external biological material. See appendix 6.4.2 in GOTIT HELP for content of fields.

#### 6.4.5. Edit external biological material

Use this form to edit data of an external biological material. See appendix 6.4.2 in GOTIT HELP for content of fields.

#### 6.4.6. Delete external biological material

Use this button to delete an external biological material. Deletion may not be possible until all data related to an external biological material have been deleted.

### 7. MOLECULAR ANALYSIS

#### 7.1. DNA

##### 7.1.1. DNA list

Use this page to browse, create, import, show, edit and delete DNA extracts. Deleting a DNA extract may not be possible until all data related to a DNA extract have been deleted. Additional fields can be listed using the top right button. To access to PCRs made from a DNA extract, click the "PCR" button (option: ). Also, use the same button (option +) to create PCR from a DNA extract. The search button applies to the field "DNA code".

##### 7.1.2. Create new DNA

Use this form to fill in data of a new DNA extract. See appendix 7.1.2 in GOTIT HELP for content of fields.

### 7.1.3. Import new set of DNA and related data

Use this form to upload data from multiple DNA extracts and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: box, vocabulary, person);

- use and upload the template file "DNA" to follow appropriate data format.

Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

### 7.1.4. Show DNA

Use this form to consult data of a DNA extract. See appendix 7.1.2 in GOTIT HELP for content of fields.

### 7.1.5. Edit DNA

Use this form to edit data of a DNA extract. See appendix 7.1.2 in GOTIT HELP for content of fields.

### 7.1.6. Delete DNA

Use this button to delete a DNA extract. Deletion may not be possible until all data related to a DNA extract have been deleted.

### 7.1.7. Linked data

The button "PCR" (option:  ) provides access to the list of PCRs made from a DNA extract. The same button (option +) allows to create PCRs for a DNA extract.

## 7.2. PCR

### 7.2.1. PCR list

Use this page to browse, create, import, show, edit and delete PCRs. Deleting a PCR may not be possible until all data related to a PCR have been deleted. Additional fields can be listed using the top right button. To access to chromatograms obtained from a PCR click the "Chr(s)" button (option :  ). The same button (option +) allows to create "Chr(s)" for a PCR. The search button applies to the field "Specimen molecular code".

### 7.2.2. Create new PCR

Use this form to fill in data of a new PCR. See appendix 7.2.2 in GOTIT HELP for content of fields.

#### 7.2.3. Import new set of PCR and related data

Use this form to upload data from multiple PCRs and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: vocabulary, person);
- use and upload the template file "PCR" to follow appropriate data format.

Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 7.2.4. Show PCR

Use this form to consult data of a PCR. See appendix 7.2.2 in GOTIT HELP for content of fields.

#### 7.2.5. Edit PCR

Use this form to edit data of a PCR. See appendix 7.2.2 in GOTIT HELP for content of fields.

#### 7.2.6. Delete PCR

Use this button to delete a PCR. Deletion may not be possible until all data related to a PCR have been deleted.

#### 7.2.7. Linked data

The button "Chr(s)" (option : ) provides access to the list of chromatograms obtained from a PCR. The same button (option +) allows to create "Chr(s)" for a PCR.

### 7.3. CHROMATOGRAM

#### 7.3.1. Chromatogram list

Use this page to browse, create, import, show, edit and delete chromatograms. Deleting a chromatogram may not be possible until all data related to a chromatogram have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Chromatogram code".

#### 7.3.2. Create new chromatogram

Use this form to fill in data of a new chromatogram. See appendix 7.3.2 in GOTIT HELP for content of fields.

#### 7.3.3. Import new set of chromatograms and related data

Use this form to upload data from multiple chromatograms and related data sets. Proceed by step:

- (if necessary) upload the referential files (templates: institution, vocabulary);
  - use and upload the template file "chromatogram" to follow appropriate data format.
- Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 7.3.4. Show chromatogram

Use this form to consult data of a chromatogram. See appendix 7.3.2 in GOTIT HELP for content of fields.

#### 7.3.5. Edit chromatogram

Use this form to edit data of a chromatogram. See appendix 7.3.2 in GOTIT HELP for content of fields.

#### 7.3.6. Delete chromatogram

Use this button to delete a chromatogram. Deletion may not be possible until all data related to a chromatogram have been deleted.

### 8. DNA SEQUENCE

#### 8.1. Internal sequence

##### 8.1.1. Internal sequence list

Use this page to browse, create, import, show, edit and delete internal sequences. Additional fields can be listed using the top right button. Deleting an internal sequence may not be possible until all data related to an internal sequence have been deleted. The search button applies to the field "Sequence code".

##### 8.1.2. Create new sequence

Use this form to fill in data of a new internal sequence. See appendix 8.1.2 in GOTIT HELP for content of fields.

#### 8.1.3. Import new set of sequences and related data

Use this form to upload data from multiple internal sequences and related data sets.

Proceed by step:

- (if necessary) upload the referential files (templates: source, vocabulary, person, taxon);
- Use and upload the template “internal\_sequence” to follow appropriate data format.

Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 8.1.4. Show sequence

Use this form to consult data of an internal sequence. See appendix 8.1.2 in GOTIT HELP for content of fields.

#### 8.1.5. Edit sequence

Use this form to edit data of an internal sequence. See appendix 8.1.2 in GOTIT HELP for content of fields.

#### 8.1.6. Delete sequence

Use this button to delete an internal sequence. Deletion may not be possible until all data related to an internal sequence have been deleted.

### 8.2. External sequence

#### 8.2.1. External sequence list

Use this page to browse, create, import, show, edit and delete external sequences. Deleting an external sequence may not be possible until all data related to an external sequence have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "External sequence code".

#### 8.2.2. Create new external sequence

Use this form to fill in data of a new external sequence. See appendix 8.2.2 in GOTIT HELP for content of fields.

### 8.2.3. Import new set of external sequences and related data

Use this form to upload data from multiple external sequences and related data sets.

Proceed by step:

- (if necessary) upload the referential files (templates: source, vocabulary, person, taxon);
  - Use and upload the template file “external\_sequence” to follow appropriate data format.
- Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

### 8.2.4. Show external sequence

Use this form to consult data of an external sequence. See appendix 8.2.2 in GOTIT HELP for content of fields.

### 8.2.5. Edit external sequence

Use this form to edit data of an external sequence. See appendix 8.2.2 in GOTIT HELP for content of fields.

### 8.2.6. Delete external sequence

Use this button to delete an external sequence. Deletion may not be possible until all data related to an external sequence have been deleted.

## 8.3. MOTU

### 8.3.1. MOTU list

Use this page to browse, create, import, show, edit and delete data and metadata related to molecular operational units (MOTU). WARNING: confirming deletion would not only delete metadata but also all the MOTU data imported under a particular data set.

Additional fields can be listed using the top right button. The search button applies to the field "MOTU title".

### 8.3.2. Create new MOTU

Use this form to fill in metadata for a new set of MOTUs to be imported. See appendix 8.3.2 in GOTIT HELP for content of fields.

### 8.3.3. Import new set of MOTU and related data

Use this form to upload a new set of MOTUs and related data sets. Use and upload the template file "MOTU" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 8.3.4. Show MOTU

Use this form to consult metadata for a set of MOTUs. See appendix 8.3.2 in GOTIT HELP for content of fields.

#### 8.3.5. Edit MOTU

Use this form to edit metadata for a set of MOTUs. See appendix 8.3.2 in GOTIT HELP for content of fields.

#### 8.3.6. Delete MOTU

Use this button to delete data and metadata for a set of MOTUs. WARNING: confirming deletion would not only delete metadata but also all the MOTU data imported under a particular data set.

### 9. STORAGE

#### 9.1. Box biological material

##### 9.1.1. Box biological material list

Use this page to browse, create, show, edit and delete storing boxes for biological material. Deleting of a box may not be possible until all biological materials stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.1.3 and 9.1.4 in GOTIT HELP to this end). Also use this page to store sets of biological materials in boxes and move sets of biological materials from one box to another. Additional fields can be listed using the top right button. The search button applies to the field "Box code".

##### 9.1.2. Create new box biological material

Use this form to fill in characteristics of a new storing box for biological material. See appendix 9.1.2 in GOTIT HELP for content of fields.

##### 9.1.3. Store biological material as file

Use this form to store sets of biological materials that have not yet been allocated to boxes. Use and upload the template file “biological\_material\_store” to follow appropriate data format. Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 9.1.4. Move or delete biological material as file

Use this form to move or remove sets of biological materials that are already stored in boxes. Use and upload the template file “biological\_material\_move” to follow appropriate data format. Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 9.1.5. Show box biological material

Use this form to consult characteristics and content of a storing box for biological material. See appendix 9.1.2 in GOTIT HELP for content of fields.

#### 9.1.6. Edit box biological material

Use this form to edit characteristics of a storing box for biological material. See appendix 9.1.2 in GOTIT HELP for content of fields.

#### 9.1.7. Delete box biological material

Use this button to delete a box for biological material. Deletion of a box may not be possible until all biological materials stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.1.3 and 9.1.4 in GOTIT HELP to this end).

### 9.2. Box specimen slide

#### 9.2.1. Box specimen slide list

Use this page to browse, create, show, edit and delete storing boxes for specimen slides. Deleting of a box may not be possible until all specimen slides stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.2.3 and 9.2.4 in GOTIT HELP to this end). Also, use this page to store sets of specimen slides in boxes and move sets of specimen slides from one box to another. Additional fields can be listed using the top right button. The search button applies to the field "Box code".

#### 9.2.2. Create new box specimen slide

Use this form to fill in characteristics of a new storing box for specimen slides. See appendix 9.2.2 in GOTIT HELP for content of fields.

#### 9.2.3. Store slides as file

Use this form to store sets of specimen slides that have not yet been allocated to boxes. Use and upload the template file “slide\_store” to follow appropriate data format. Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 9.2.4. Move or delete slides as file

Use this form to move or remove sets of specimen slides that are already stored in boxes. Use and upload the template file “slide\_move” to follow appropriate data format. Also, refer to the section “uploading tools” in GOTIT HELP for further details on the uploading procedure.

#### 9.2.5. Show box specimen slide

Use this form to consult characteristics and content of a storing box for specimen slides. See appendix 9.2.2 in GOTIT HELP for content of fields.

#### 9.2.6. Edit box specimen slide

Use this form to edit characteristics of a storing box for specimen slides. See appendix 9.2.2 in GOTIT HELP for content of fields.

#### 9.2.7. Delete box specimen slide

Use this button to delete a box of specimen slides. Deletion of a box may not be possible until all specimen slides stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.2.3 and 9.2.4 in GOTIT HELP to this end).

### 9.3. Box DNA

#### 9.3.1. Box DNA list

Use this page to browse, create, show, edit and delete storing boxes for DNA extracts. Deleting of a box may not be possible until all DNA extracts stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.3.3 and 9.3.4 in GOTIT HELP to this end). Also, use this page to store sets of DNA extracts in boxes and move

sets of DNA extracts from one box to another. Additional fields can be listed using the top right button. The search button applies to the field "Box code".

#### 9.3.2. Create new box DNA

Use this form to fill in characteristics of a new storing box for DNA extracts. See appendix 9.3.2 in GOTIT HELP for content of fields.

#### 9.3.3. Store DNA boxes as file

Use this form to store sets of DNA extracts that have not yet been allocated to boxes. Use and upload the template file "DNA\_store" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 9.3.4. Move or delete DNA boxes as file

Use this form to move or remove sets of DNA extracts that are already stored in boxes. Use and upload the template file "DNA\_move" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 9.3.5. Show box DNA

Use this form to consult characteristics and content of a storing box for DNA extracts. See appendix 9.3.2 in GOTIT HELP for content of fields.

#### 9.3.6. Edit box DNA

Use this form to edit characteristics of a storing box for DNA extracts. See appendix 9.3.2 in GOTIT HELP for content of fields.

#### 9.3.7. Delete box DNA

Use this button to delete a box of DNA extracts. Deletion of a box may not be possible until all DNA extracts stored in that box have been removed and/or moved to another box (use the appropriate tools in 9.3.3 and 9.3.4 in GOTIT HELP to this end).

### 10. SOURCE

#### 10.1. Source list

Use this page to browse, create, import, show, edit and delete reference sources.   
WARNING: confirming deletion would not only delete the reference source but also all the attributions of that source to biological materials, external biological materials, internal sequences and external sequences. Also, use this page to attribute reference sources to biological materials and internal sequences that are not linked to a reference source. Additional fields can be listed using the top right button. The search button applies to the field "Source code".

#### 10.2. Create new source

Use this form to fill in characteristics of a new reference source. See appendix 10.2 in GOTIT HELP for content of fields.

#### 10.3. Import new set of sources

Use this form to upload data for multiple reference sources and related data sets. Proceed by step:

- (if necessary) upload the referential files (template: person);
- use and upload the template file "source" to follow appropriate data format.

Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 10.4. Source to biological material as file

Use this form to attribute reference sources to biological materials that are not linked to reference sources. Use and upload the template file "source\_attribute\_to\_lot" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 10.5. Source to sequence as file

Use this form to attribute reference sources and accession numbers or reference sources alone to internal sequences that are not linked to reference sources and do not have an accession number. Use and upload the template file "source\_attribute\_to\_sequence" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 10.6. Show source

Use this form to consult data of a reference source. See appendix 10.2 in GOTIT HELP for content of fields.

## 10.7. Edit source

Use this form to edit data of a reference source. See appendix 10.2 in GOTIT HELP for content of fields.

## 10.8. Delete source

Use this button to delete a reference source. **WARNING:** confirming deletion would not only delete the reference source but also all the attributions of that source to biological materials, external biological materials, internal sequences and external sequences.

# 11. REPOSITORIES

## 11.1. Vocabulary

### 11.1.1. Vocabulary list

Use this page to browse, create, import, show, edit and delete vocabulary. Deletion may not be possible until all data links pointed to a vocabulary have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Title". In case a bilingual version of GOTIT is installed, the list of vocabularies is provided into the two languages selected during installation.

### 11.1.2. Create new vocabulary

Use this form to fill in characteristics of a new vocabulary. See appendix 11.1.2 in GOTIT HELP for content of fields.

### 11.1.3. Import new vocabulary

Use this form to upload multiple vocabulary repository data. Use and upload the template file "vocabulary" to follow appropriate data format. Also, refer to the section 13.26 "uploading tools: Upload vocabulary" in GOTIT HELP for further details on the uploading procedure and the defined list of names for the "parent" field.

Note: The 'vocabulary' template used for uploading vocabularies should not contain parent codes that are not defined in GOTIT. Doing so will create a new parent code that is however not accessible in the scrolling list of parents. This issue will be fixed in the next release of GOTIT.

### 11.1.4. Show vocabulary

Use this form to consult characteristics of a vocabulary. See appendix 11.1.2 in GOTIT HELP for content of fields.

#### 11.1.5. Edit vocabulary

Use this form to edit characteristics of a vocabulary. See appendix 11.1.2 in GOTIT HELP for content of fields.

#### 11.1.6. Delete vocabulary

Use this button to delete a vocabulary. Deletion may not be possible until all data links pointed to a vocabulary have been deleted.

### 11.2. Taxon

#### 11.2.1. Taxon list

Use this page to browse, create, import, show, edit and delete species taxa. Deletion may not be possible until all data links pointed to a species taxon have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Taxon name".

#### 11.2.2. Add taxon name

Use this form to fill in characteristics of a species taxon added to the list. See appendix 11.2.2 in GOTIT HELP for content of fields.

#### 11.2.3. Import new set of taxa

Use this form to upload multiple taxon metadata. Use and upload the template file "taxon" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 11.2.4. Show taxon name

Use this form to consult characteristics of a species taxon. See appendix 11.2.2 in GOTIT HELP for content of fields.

#### 11.2.5. Edit taxon name

Use this form to edit characteristics of a species taxon. See appendix 11.2.2 in GOTIT HELP for content of fields.

#### [11.2.6. Delete taxon name](#)

Use this button to delete a species taxon. Deletion may not be possible until all data links pointed to a species taxon have been deleted.

### [11.3. Person](#)

#### [11.3.1. Person list](#)

Use this page to browse, create, import, show, edit and delete person characteristics. Deletion may not be possible until all data links pointed to a person have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Person list".

#### [11.3.2. Create new person](#)

Use this form to fill in characteristics of a new person. See appendix 11.3.2 in GOTIT HELP for content of fields.

#### [11.3.3. Import new set of persons](#)

Use this form to upload multiple person metadata. Use and upload the template file "person" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### [11.3.4. Show person](#)

Use this form to consult characteristics of a person. See appendix 11.3.2 in GOTIT HELP for content of fields.

#### [11.3.5. Edit person](#)

Use this form to edit characteristics of a person. See appendix 11.3.2 in GOTIT HELP for content of fields.

#### [11.3.6. Delete person](#)

Use this button to delete a person. Deletion may not be possible until all data links pointed to a person have been deleted.

## 11.4. Program

### 11.4.1. Program list

Use this page to browse, create, import, show, edit and delete characteristics of a funding program. Deletion may not be possible until all data links pointed to a funding program have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Program code".

### 11.4.2. Create new program

Use this form to fill in characteristics of a new funding program. See appendix 11.4.2 in GOTIT HELP for content of fields.

### 11.4.3. Import new set of programs

Use this form to upload multiple program metadata. Use and upload the template file "program" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

### 11.4.4. Show program

Use this form to consult characteristics of a funding program. See appendix 11.4.2 in GOTIT HELP for content of fields.

### 11.4.5. Edit program

Use this form to edit characteristics of a funding program. See appendix 11.4.2 in GOTIT HELP for content of fields.

### 11.4.6. Delete program

Use this button to delete a funding program. Deletion may not be possible until all data links pointed to a funding program have been deleted.

## 11.5. Institution

### 11.5.1. Institution list

Use this page to browse, create, import, show, edit and delete characteristics of an institution. Deletion may not be possible until all data links pointed to an institution have

been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Institution name".

#### 11.5.2. Create new institution

Use this form to fill in characteristics of a new institution. See appendix 11.5.2 in GOTIT HELP for content of fields.

#### 11.5.3. Import new set of institutions

Use this form to upload multiple institution metadata. Use and upload the template file "institution" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 11.5.4. Show institution

Use this form to consult characteristics of an institution. See appendix 11.5.2 in GOTIT HELP for content of fields.

#### 11.5.5. Edit institution

Use this form to edit characteristics of an institution. See appendix 11.5.2 in GOTIT HELP for content of fields.

#### 11.5.6. Delete institution

Use this button to delete an institution. Deletion may not be possible until all data links pointed to an institution have been deleted.

### 11.6. Country

#### 11.6.1. Country list

Use this page to browse, create, import, show, edit and delete a country. Deletion may not be possible until all data links pointed to a country have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Country code".

#### 11.6.2. Create new country

Use this form to fill in characteristics of a new country. See appendix 11.6.2 in GOTIT HELP for content of fields.

### [11.6.3. Import new set of countries](#)

Use this form to upload multiple country metadata. Use and upload the template file "country" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

### [11.6.4. Show country](#)

Use this form to consult characteristics of a country. See appendix 11.6.2 in GOTIT HELP for content of fields.

### [11.6.5. Edit country](#)

Use this form to edit characteristics of a country. See appendix 11.6.2 in GOTIT HELP for content of fields.

### [11.6.6. Delete country](#)

Use this button to delete a country. Deletion may not be possible until all data links pointed to a country have been deleted.

## [11.7. Municipality](#)

### [11.7.1. Municipality list](#)

Use this page to browse, create, import, show, edit and delete characteristics of a municipality. Deletion may not be possible until all data links pointed to a municipality have been deleted. Additional fields can be listed using the top right button. The search button applies to the field "Municipality name".

### [11.7.2. Create new municipality](#)

Use this form to fill in characteristics of a new municipality. See appendix 11.7.2 in GOTIT HELP for content of fields.

### [11.7.3. Import new set of municipalities](#)

Use this form to upload multiple municipality metadata. Use and upload the template file "municipality" to follow appropriate data format. Also, refer to the section "uploading tools" in GOTIT HELP for further details on the uploading procedure.

#### 11.7.4. Show municipality

Use this form to consult characteristics of a municipality. See appendix 11.7.2 in GOTIT HELP for content of fields.

#### 11.7.5. Edit municipality

Use this form to edit characteristics of a municipality. See appendix 11.7.2 in GOTIT HELP for content of fields.

#### 11.7.6. Delete municipality

Use this button to delete a municipality. Deletion may not be possible until all data links pointed to a municipality have been deleted.

### 12. SPECIES SEARCH

#### 12.1. COI data set

Use this request to explore the availability and distribution of COI sequences for a species taxon as well as the distribution of that species taxon. See section 12.1 in GOTIT HELP for more details about the functionalities of this request.

Select a species taxon using the scroll bars and press the “search” button. The “Results” table provides for the selected species taxon:

- Field “Taxon”: The name of the selected species taxon. Clicking on the species taxon name opens the taxon referential show form containing the characteristics of that species taxon.
- Heading “Specimen samples”; Field “Sites”: the number of sampling sites in the data base
- Heading “Specimen samples”; Field “LMP (Deg)": the latitudinal midpoint of the species range in decimal degrees.
- Heading “Specimen samples”; Field “MLE (km)": the maximum linear extent of the species range in km, defined as the straight-line distance between the two most distant known localities.
- Heading “COI samples”; the same three fields as above but for those sites at which a COI sequence is available for the selected species taxon.
- Field “Loc”: clicking the “Loc” button provides the geographic distribution of sites, including those of internal and external biological materials and those with COI sequences. You can zoom in and out the map and download the maps as .png file.

Activate labels to show site characteristics (i.e. button “Toggle show closest data on hover”).

Notes:

- By clicking on the “on” green button to its “off” position, results are provided for the entire set of species taxa in the data base.
- The results table can be copied to the clipboard or be exported either as a .csv file or .xlsx file.

## 12.2. MOTU

Use this request to explore the number of molecular operational taxonomic units (MOTU) within a species taxon as well as the list of COI sequences attributed to MOTUs for that species taxon. See section 12.2 in GOTIT HELP for more details about the functionalities of this request.

Under the heading “Search by species”

- Select a species taxon using the scroll bars.

Under the heading “Molecular method”

- Select a data set using the scroll bar (See sub-section “MOTU” in section “DNA Sequence” of GOTIT web user interface for more details about the selected data set).
- Check boxes to select molecular methods used to delimit MOTUs (See sub-section “MOTU” in section “DNA Sequence” of GOTIT web user interface for more details about the molecular delimitation methods).

Under the heading “Species identification”

- Select the table in which the species taxon name is attributed. For example, by selecting the table “DNA sequence”, only those COI sequences which were attributed to the requested species taxon name will be considered. By selecting the table "Specimen", only those COI sequences belonging to specimens which were attributed to the requested species taxon name will be considered. By selecting the table "Biological material", only those COI sequences belonging to biological materials (i.e. internal and external biological materials) which were attributed to the requested species taxon name will be considered.
- Check boxes to select the identification criteria. For example, by selecting the table “DNA sequence” and the criterion “Morphology”, only those COI sequences which were attributed to the requested species with the identification criterion “Morphology” will be considered. By selecting the table “Specimen” and the criterion “Morphology”, only those COI sequences belonging to specimens which were attributed to the requested species with the identification criterion “Morphology” will be considered.

Press the “search” button. The “Results” table provides for the selected species taxon:

- Field “Taxon”: The name of the selected species taxon. Clicking on the species taxon name opens the taxon referential show form containing the characteristics of that species taxon.

- Field “Molecular method”: The abbreviation of the molecular methods used to delimit MOTUs.
- Field “Data set”: The code of the data set used to delimit MOTUs.
- Field “Sequences”: The number of COI sequences for the selected species taxon and for the molecular methods and data set selected.
- Field “MOTUS”: The number of MOTUs for the selected species taxon and for the molecular method and data set selected.
- Field “Details”: clicking the “Details” button opens a second results table which provides the list of COI sequences for the different MOTUs delimited for the selected species taxon and for the molecular method and data set selected. This second table contains the following fields:
  - Field “Seq. code”: The code of the COI sequence. Clicking on the sequence code opens the internal sequence show form containing information on that sequence.
  - Field “Accession”: The accession number of the COI sequence. Clicking on the accession number opens the nucleotide GenBank form (NCBI) for that sequence.
  - Field “Gene”: The gene
  - Field “Type”: The type of sequence, either internal (laboratory data) or external (literature data).
  - Field “MOTU”: the MOTU number to which a COI sequence belongs to.
  - Field “Criterion”: The identification criterion which was used while allocating a species taxon name to the sequence, specimen, or biological material (depending on the table selection specified during the search process).

Notes:

- By clicking on the “on” green button to its “off” position, results are provided for the entire set of species taxa in the data base.
- The two results tables can be copied to the clipboard or be exported either as .csv files or .xlsx files.

### 12.3. Species hypotheses

Use this request to find out the nature of molecular operational taxonomic units (MOTU), in particular, whether a MOTU is a match, a split, a lump, or a reshuffling of species taxa delimited using morphological criteria. See section 12.3 in GOTIT HELP for more details about the functionalities of this request.

The “Species hypotheses” request is based upon the principle that several sets of species taxa delimited from the same set of individuals but using different delimitation criteria can be compared by means of only four terms: match, lump, split and reshuffling. Species taxa are species hypotheses (SHs) that are delimited based on specific criteria. The use of different criteria and/or delimitation methods provide different sets of SHs which differ in the number of species taxa. Still, it is possible to document the change in taxonomic pattern when shifting from one criterion to another. In the request results, we use four terms to

document the changes when shifting from one set of SHs ( $S_a, b, c, d, e, f$ ) delimited using a criterion to another set of SHs delimited using another criterion ( $S_\alpha, \beta, \gamma, \delta, \varepsilon, \zeta$ ) (Fig. 1).

- 1) Match: the individuals in  $S_\alpha$  are from a single SH (e.g.  $S_a$ ) and include all the individuals of that SH.
- 2) Lump: the individuals in  $S_\beta$  are from more than one SH (e.g.  $S_b$  and  $S_c$ ) and include all the individuals of those SHs.
- 3) Split: the individuals in  $S_\gamma$  are from a single SH (e.g.  $S_d$ ) but do not include all the individuals of that SH.
- 4) Reshuffling: the individuals in  $S_\varepsilon$  are from more than one SH (e.g.  $S_e$  and  $S_f$ ) and do not include all the individuals of those SHs.

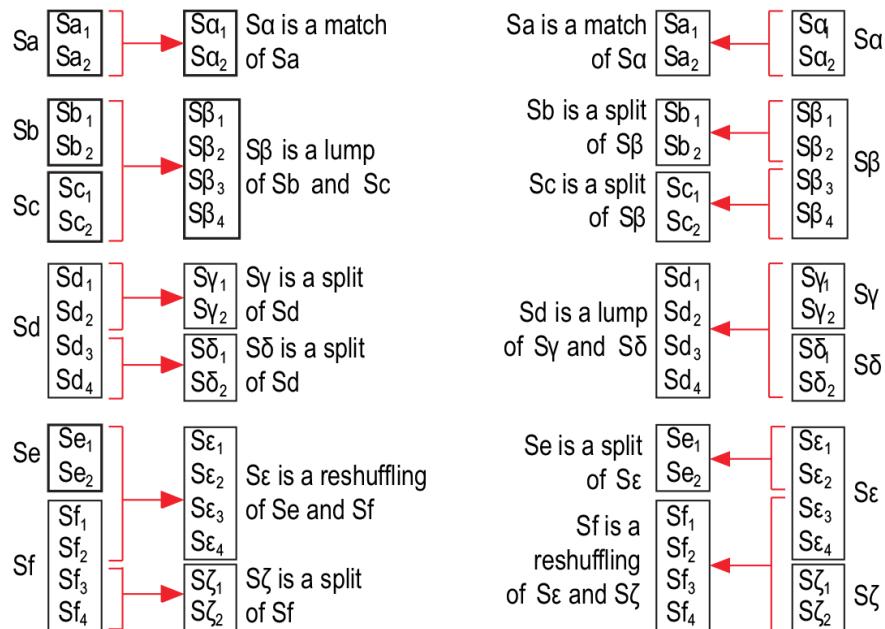


Figure 3. Schematic illustration of the four possible types of changes – match, lump, split and reshuffling – when shifting from one set of species hypotheses to another (in Eme D., Zagmajster M., Delić T., Fišer C., Flot J.-F., Konecny-Dupré L., Pálsson S., Stoch F., Zakšek V., Douady C. J. & Malard F. 2017. Do cryptic species matter in macroecology? Sequencing European groundwater crustaceans yields smaller ranges but does not challenge biodiversity determinants. *Ecography*, 41(2): 424-436).

Under the heading “Reference method”, select either “Morphology”, “Taxon”, or “Molecular method”.

- Morphology: The species taxa that were attributed a species name (delimitation most often based on morphology) will be compared with MOTUs delimited using the different molecular methods specified in the target data set below (see heading “Target dataset”).
- Taxon: The same comparison as above but for a single selected species taxon.

- Molecular method: By selecting one data set and one molecular method, the MOTUs delimited using that molecular method will be compared with the MOTUs obtained with the other molecular methods within that data set.

Under the heading “Target dataset”, select the target data set that has to be used when the option “Morphology” has been selected in the heading ““Reference method”.

Results are simultaneously provided using bar plots and a table. Click the two labels “Reference method ---> Target dataset” and “Target dataset ---> Reference method” at the top of the figure to change the direction of the comparison between the sets of species taxa (the table will change accordingly). Color interactive labels on the figure provide the number of matches, splits, lumps, and reshuffling as expressed by the bars. The result table provides for the different molecular methods:

- Data set: the code of the data set used for comparison
- Match, Split, Lump, and Reshuffling: the number of species hypotheses (i.e. species taxa) belonging to these 4 different cases out of the total number of species hypotheses included in the selected data set.
- Seq. count: the number of COI sequences in the selected data set
- Sites count: the number of sampling sites in the selected data set.

Notes:

- The result table can be copied to the clipboard or be exported either as .csv files or .xlsx files.

#### 12.4. Distribution data

Use this request to explore the spatial distribution of molecular operational taxonomic units (MOTU) within a species taxon. See section 12.4 in GOTIT HELP for more details about the functionalities of this request.

Under the heading “Search by species”, select a species taxon using the scroll bars.  
Under the heading “Select molecular delimitation method”, select the data set and molecular delimitation method.  
Press the “search” button.

The “Results” table provides for the selected species taxon:

- Field “Taxon”: The name of the selected species taxon. Clicking on the species taxon name opens the taxon referential show form containing the characteristics of that species taxon.
- Field “Seq. code”: The code of the COI sequence. Clicking on the sequence code opens the internal sequence show form containing information on that sequence.

- Field “Type”: The type of sequence, either internal (laboratory data) or external (literature data).
- Field “Accession”: The accession number of the COI sequence. Clicking on the accession number opens the nucleotide GenBank form (NCBI) for that sequence.
- Field “MOTU”: the MOTU number to which a COI sequence belongs to.
- Field “Lat.”: The latitude (in decimal degree) of the site at which the sequence-bearing specimen was collected.
- Field “Long.”: The longitude (in decimal degree) of the site at which the sequence-bearing specimen was collected.
- Field “Site”: The code of the site at which the sequence-bearing specimen was collected.
- Field “Municipality”: The name of the municipality at which the sequence-bearing specimen was collected.
- Field “Country”: The name of the country at which the sequence-bearing specimen was collected.

Clicking the “MOTU map” button provides the geographic distribution of MOTUs for the selected species taxon. You can zoom in and out the map and download the maps as .png file. Activate labels to show site characteristics (i.e. button “Toggle show closest data on hover”). Mapping of individual MOTUs can be activated / deactivated by clicking on the items of the legend.

#### Notes:

- The result table can be copied to the clipboard or be exported either as .csv files or .xlsx files.

### 12.5. Species names

Use this request to select among different correspondence cases among species names attributed to biological materials, specimens, and DNA sequences. See section 12.5 in GOTIT HELP for more details about the functionalities of this request.

In the data base, species names are attributed together with a species criterion to three different items, namely, internal biological material, specimens and internal sequences (i.e. here, the request does not consider external biological materials and external DNA sequences). Although a DNA sequence is issued from a specimen which is itself issued from a biological material (i.e. a specimen lot), different species names can be attributed to these three items. For example, the species name “*Proasellus cavaticus*” with the criterion “Morphology” can be attributed to a biological material because at least one mature specimen has been morphologically identified as such. Yet, another specimen from the same biological material can be attributed to “*Proasellus sp.*” simply because that specimen is a juvenile (species identification to species level is not possible for juveniles). Then, upon obtaining a DNA sequence, the user may indeed realize based on molecular similarities with other sequences that the sequence belongs to *Proasellus cavaticus*. The user may thus

attribute the species name “*Proasellus cavaticus*” with the accompanying species criterion “temporary molecular assignment” to the DNA sequence.

From times to times, the user may need to check the correspondence between species names attributed to biological materials, specimens and DNA sequences. The request addresses this need by enabling the user to select among multiple cases of correspondence and list the items falling under these different cases.

Successively, select one item under the heading “Biological material”, “Specimen”, and “DNA sequence”. For example, successively selecting A, B, and C consists in requesting cases when the three species names attributed to biological material, specimen and DNA sequence, are different. Select the item “Any” in the heading “Biological material” and “Specimen” when you want all three possible items among A, B and C. Select the item “Any” in the heading “DNA sequence” when you want all four possible items among A, B, C and undefined. The item “undefined” in the heading “DNA sequence” is for cases when they are no DNA sequences available.

Press the search button. The “Results” table provides for each line:

#### Heading “Biological material”

Bio. mat. code: The code of the biological material. Clicking opens the biological material show form.

Taxon: The taxon name attributed to the biological material. Clicking opens the taxon show form.

Criterion: The criterion used to attribute the taxon name.

#### Heading “Specimen”

Specimen mol. code: The molecular code of the specimen. Clicking opens the specimen show form.

Specimen morph. code: The morphological code of the specimen. Clicking opens the specimen show form.

Taxon: The taxon name attributed to the specimen. Clicking opens the taxon show form.

Criterion: The criterion used to attribute the taxon name.

#### Heading “DNA sequence”

Seq. code: The sequence code. Clicking opens the internal sequence show form.

Taxon: The taxon name attributed to the DNA sequence. Clicking opens the taxon show form.

Criterion: The criterion used to attribute the taxon name.

#### Notes:

- The result table can be copied to the clipboard or be exported either as .csv files or .xlsx files.

## 13. UPLOADING TOOLS

All data uploading tools work with ready-to-use files that have to be recorded with the options:

- character encoding in UTF-8;
- the "semicolon" as record delimiter;
- quotation marks ("") as text field delimiter.

it is highly recommended to use LibreOffice Calc to handle spreadsheets: this facilitates the management of CSV formats and UTF-8 character encoding (free download to <https://www.libreoffice.org/download/download/> )

## Import Files CSV

(1) Select the file to be imported using the scroll bar

(2) Upload the csv file to be imported

The csv file has to be saved with the options:  
- character encoding in UTF-8  
- the semicolon as record delimiter  
- quotation mark as text field delimiter

Internal\_biological\_material

Internal\_biological\_material

Box

Source

Taxon

Vocabulary

Person

---

Figure 4: The uploading window in GOTIT

There are two types of files:

- template files which contain information to be stored in core tables of the data base (e.g. file "Internal\_biological\_material" in Figure 4).
- referential files which contain reference information to be stored in referential tables of the data base (e.g. box, source, taxon, vocabulary, and person in Figure 4).

Whenever the template files to be uploaded contain reference information that are not yet included in referential tables, referential files have to be uploaded first.

Also, template files have to be uploaded in sequential order because data tables are linked via foreign keys in the data base. For example, uploading a "sampling" template file containing samplings that have no corresponding sites (foreign key) in the "site" data table will necessarily result in a message error that will halt the uploading process.

Upon successful uploading of either a template or referential file, the following message will show up:

Import : file name.csv (Template name.csv)  
Data import is successful. Number of records Imported = X  
Date of data set import : YYYY-MM-DD HH:MM:SS

During uploading, horizontal and vertical tabulation marks, line breaks and carriage returns left in the .csv file are automatically deleted. When other errors are detected during uploading, uploading is prevented and the full list of encountered errors are listed. Then, errors must be corrected in the uploading csv file, until uploading is successful.

The most common errors are due to:

- Occurrence in the template file of reference terms that do not have corresponding reference terms in referential tables of the data base. Reference terms may be incorrectly spelled in the template file or, if new, they should be uploaded into the database using one of the referential files.
- Occurrence in the template file of foreign keys with no correspondence in the data base (i.e. sampling at a site that has not been included into the table "site" of the data base). Foreign keys may be incorrectly spelled in the template file or, if new, another template file with the corresponding foreign key should be uploaded first.
- Occurrence in the template file of code terms (most often foreign keys) which already exist in the data base and must be unique. For example, uploading a site while that site is already present in the data base will halt the uploading process.
- Incorrect data format for the filed content.

All templates files are stored in ~/install/1.1/template directory. Copy these files onto your computer before filling them. Be careful! Do not to change the column headers and do not delete any column, otherwise the uploading process won't work.

To assist users in solving uploading errors, we provide below for each template file (c.f. sections 13.1 to 13.21) :

- The field titles
- The field contents (c.f. also appendixes 5.1.2 to 10.2)
- The fields that are linked to referential tables
- The fields that are used as foreign keys

### 13.1. Upload Site

Template file: site

Referential files: country, municipality, vocabulary

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
station.code_station	Y	Site code	VARCHAR(255)			Foreign key (link to sampling).	Capitals	BERKELSP
station.nom_station	Y	Site name	VARCHAR(1024)				Capitals	BERKELEY SPRINGS
station.pays_fk(pays.nom_pays)	Y	Country name	VARCHAR(1024)		country		Capitals	UNITED STATES
station.commune_fk(commune.code_com mune)	Y	Municipality code	VARCHAR(255)		municipality		Enter code as follows: Municipality name Region name Country name. All space must be replaced with " ". (1)	BERKELEY_SPRINGS WEST_VIRGINIA UNITED_STATES
station.habitat_type_voc_fk(voc.code)	Y	Habitat type (code)	VARCHAR(255)	Multiple habitat codes separated by " \$"	vocabulary		See habitat type codes in the vocabulary table.	ODOUSOU
station.point_acces_voc_fk(voc.code)	Y	Access type (code)	VARCHAR(255)	Multiple access codes separated by " \$"	vocabulary		See access codes in the vocabulary table.	SOU
station.lat_deg_dec	Y	Latitude Dec Deg	FLOAT					39.62 or 39,62
station.long_deg_dec	Y	Longitude Dec Deg	FLOAT					-78.23 or -78,23
station.altitude_m	N	Elevation m asl	INTEGER					192

station.precision_lat_long_voc_fk(voc.code)	Y	Coordinate precision (code)	VARCHAR(255)		vocabulary		See precision codes in the vocabulary table.	INF100M
station.info_description	N	Site description	TEXT					Morgan county
station.commentaire_station	N	Site comments	TEXT					Thermal spring site

- (1) When uploading the .csv file, if the community code is new to the data base, the script inserts a new record into the Municipality table. The new record contains the Municipality code and the Municipality name and the Region name are extracted from the Municipality code. The “\_” signs replacing spaces in the Municipality code are not reported in the Municipality name and Region name. If the community code already exists in the data base, the uploaded site record is linked to that community code in the data base.

## 13.2. Upload sampling

Template file: sampling

Referential files: program, person, taxon, vocabulary

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
collecte.station_fk(station.code_station)	Y	Site code	VARCHAR(255)			Foreign key (link to site).	Capitals	BERKELSP
collecte.code_collecte	Y	Sampling code	VARCHAR(255)			Foreign key (link to internal biological material, external biological material, external sequence).	Expressed as "site code_sampling year sampling month" see 15.2.	BERKELSP_201704 BERKELSP_201700 if sampling month not known; BERKELSP_00000 if sampling month and year not known.
collecte.date_collecte	N	Sampling date	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	29/04/2017
collecte.date_precision_voc_fk(voc.code)	Y	Date precision (code)	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J
collecte.duree_echantillonage_mn	N	Sampling duration	INTEGER				Expressed in minutes.	60
collecte.conductivite_micro_sie_cm	N	Specific conductance (microsiemens per cm)	FLOAT				Expressed in microsiemens per cm.	125.5 or 125,5

collecte.temperature_c	N	Temperatur e (Celcius)	FLOAT				Expressed in degree Celcius.	12.5 or 12,5
collecte.leg_voc_fk(voc.code)	Y	Donation (code)	VARCHAR (255)		vocabulary		See Donation codes in the vocabulary table : "NON" if the sample is collected by your own's laboratory staff, "OUI" in the contrary case, and "NA" if the sample is not stored in your own laboratory (i.e. sampling of an external biological material).	OUI
collecte.a_faire	Y	Status (code)	VARCHAR (255)				See Status codes in the vocabulary table : "OUI" when the sample has been sorted and "NON" in the contrary case.	NON
collecte.commentaire_collecte	N	Sampling comments	TEXT					Rainy day
a_pour_fixateur.fixateur_voc_fk(voc.code)	Y	Fixative(s) (code)	TEXT	Multiple codes separated by "\$"	vocabulary		See codes in the vocabulary table	ALC \$ CRYO
a_pour_sampling_method.sampling_method_voc_fk(voc.code)	Y	Sampling method(s) (code)	TEXT	Multiple codes separated by "\$"	vocabulary		See codes in the vocabulary table.	INC \$ SUR
a_cibler.referentiel_taxon_fk(referentiel_taxon.taxname)	Y	Targeted taxa	VARCHAR(255)	Multiple targeted taxa separated by "\$"	taxon		See taxon names in the taxon table.	ASELLIDAE \$ AMPHIODA
est_finance_par.programme_fk(programme.code_programme)	Y	Funding program(s) (code)	TEXT	Multiple funding programs	program		See program code in the program table.	N_AM_ASEL \$ SMITH

				codes separated by "\$ "				
est_effectue_par.per sonne_fk(personne.n om_personne)	Y	Name(s) of person who samples	TEXT	Multiple persons separated by "\$ "	person		See person names in the person table.	LEWIS J \$ SMART F

### 13.3. Upload biological material (internal)

Template file: internal\_biological\_material

Referential files: box, taxon, vocabulary, person, source

Field title	Compu Isory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
lot_materiel.collecte_fk(collecte.code_collecte)	Y	Sampling code	VARCHAR(255)			Foreign key (link to sampling, external biological material, external sequence).	Expressed as "site code_sampling year sampling month" see 15.2.	BERKELSP_201704 BERKELSP_201700 if sampling month not known; BERKELSP_00000 if sampling month and year not known.
lot_materiel.code_lot_materiel	Y	Biological material code	VARCHAR(255)			Foreign key (link to specimen).	Expressed as "Name of species taxon sampling code" see 15.3.	LIRCEUS_BRACHYURUS BERKELSP_201704
composition_lot_mat eriel.commentaire_compo_lot_materiel	N	Comments on composition of biological material	TEXT					A1=1 male mounted on slide
composition_lot_mat eriel.nb_individus+ty pe_individu_voc_fk(v oc.code)	Y	Composition of biological material: number and types of specimens (code)	TEXT	Multiple "numbers of individuals followed by specimen type codes" separated by " \$" (see example)	vocabulary		Expressed as numbers of specimens of a type separated by " \$" (see vocabulary for specimen type codes)	7A \$ 2B \$ 1BOV \$ P (A stands for males, B female, etc...)

lot_materiel.date_lot_materiel	Y	Biological material date (processing date)	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	22/02/2018
lot_materiel.date_precision_voc_fk(voc.code)	Y	Date precision (code)	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J
lot_materiel.yeux_vo_c_fk(voc.code)	Y	Vision (code)	VARCHAR(255)		vocabulary		See codes in the vocabulary table	O (for oculated)
lot_materiel.pigmentation_voc_fk(voc.cod e)	Y	Pigmentation (code)	VARCHAR(255)		vocabulary		See codes in the vocabulary table	P (for pigmented)
lot_materiel.a_faire	Y	Status of biological material (code)	VARCHAR (255)				"1" when specimens have to be analyzed and "0" in the contrary case.	0
lot_materiel.comme ntaire_conseil_sqc	N	Sequencing advice	TEXT					Please sequence A1=47
lot_materiel.comme ntaire_lot_materiel	N	Biological material comments	TEXT					Vial 21: 10 individuals
lot_materiel.boite_fk (boite.code_boite)	N	Storing box (code)	VARCHAR(255)		box		See box codes in the box table	LOT_aAsel4
lot_materiel_est_real ise_par.personne_fk(personne.nom_perso nne)	Y	Name of person who processed the biological material.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	MALARD F
espece_identifiee.ref erentiel_taxon_fk(ref erentiel_taxon.taxna me)	Y	Name of species taxon attributed to	VARCHAR(255)		taxon		See name of species taxa in the taxa table	LIRCEUS_BRACHYUR US

		biological material.						
espece_identifiee.dat e_identification	Y	Species taxon identification date.	DATE (DD /MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	22/02/2018
espece_identifiee.dat e_precision_voc_fk(v oc.code)	Y	Date precision for species taxon identification (code).	VARCHAR = { J,M,A} with J for day, M for month and A for year }		vocabulary		J for day, M for month and A for year.	J
espece_identifiee.crit ere_identification_vo c_fk(voc.code)	Y	Species taxon identification criterion (code).	VARCHAR(255)		vocabulary		See codes in the vocabulary table	M
espece_identifiee.co mmentaire_esp_id	N	Species taxon identification comments.	TEXT					No need to check.
est_identifie_par.per sonne_fk(personne.n om_personne)	Y	Name(s) of person(s) who identified the species taxon.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	LEWIS J \$ MALARD F

lot_est_publie_dans. source_fk(source.cod e_source)	N	Source (i.e. literature reference) in which the biological material is published (code).	VARCHAR(255)	Multiple source codes separated by " \$"	source		See sources codes in the source table	Sidorov_Holsinger_2 007_Crustaceana_80 _4_417_430
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### 13.4. Upload specimen

Template file: specimen

Referential files: taxon, vocabulary, person

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
individu.lot_materiel_fk(lot_materiel.code_lot_materiel)	Y	Biological material code	VARCHAR(255)			Foreign key (link to biological material).	Expressed as "Name of species taxon sampling code" see 15.3.	LIRCEUS_BRACHYURUS BERKELSP_201704
individu.code_ind_biomol	N	Specimen molecular code	VARCHAR(255)				Expressed as "Code for name of species taxon_sampling code_specimen molecular number" See example. See table "taxon" for codes of species taxa names. Unique code. See 15.6.	LIRbrachyurus_BERKE LSP_201704_1ID
individu.code_ind_tri_morpho	Y	Specimen morphologic al code	VARCHAR(255)				Expressed as "Name of species taxon sampling code[specimen code tube]" See example. Unique code. See 15.5.	LIRCEUS_BRACHYURUS BERKELSP_201704[A1]
individu.type_individual_voc_fk(voc.code)	Y	specimen type (code)	VARCHAR(255)		vocabulary		See vocabulary for specimen type codes.	A (for male)
individu.code_tube	Y	Code of the tube containing the specimen	VARCHAR(255)				No space in the code	A1

individu.num_ind_biomol	N	Molecular number of the specimen.	VARCHAR(255)				No space in the code	1ID
individu.commentaire_ind	N	Comments about the specimen	TEXT					MALE MOUNTED ON SLIDE
espece_identifiee.reference_taxon_fk(reference_taxon.taxoname)	Y	Name of species taxon attributed to specimen.	VARCHAR(255)		taxon		See name of species taxa in the taxa table	LIRCEUS_BRACHYURUS
espece_identifiee.date_identification	Y	Species taxon identification date.	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	22/02/2018
espece_identifiee.date_precision_voc_fk(voc.code)	Y	Date precision for species taxon identification (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J
espece_identifiee.criterie_identification_voc_fk(voc.code)	Y	Species taxon identification criterion (code).	VARCHAR(255)		vocabulary		See codes in the vocabulary table	M
espece_identifiee.commentaire_esp_id	N	Species taxon identification comments.	TEXT					Little doubt
est_identifie_par.personne_fk(personne.nom_personne)	Y	Name(s) of person(s) who identified	VARCHAR(255)	Multiple persons separated by "\$"	person		See person names in the person table	LEWIS J \$ MALARD F

		the species taxon.						
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### 13.5. Upload specimen slide

Template file: specimen\_slide

Referential files: box, vocabulary, person

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
individu_lame.individu_fk(individu.code_in_d_tri_morpho)	Y	Specimen morphologic al code	VARCHAR(255)			Foreign key (link to specimen).	Expressed as "Name of species taxon sampling code[specimen code tube]" See example. See 15.5.	LIRCEUS_BRACHYUR US BERKELSP_201704[A1]
individu_lame.code_lame_coll	Y	code of the specimen microscope slide	VARCHAR(255)				Unique code.	23_23
individu_lame.date_lame	Y	Specimen slide processing date.	DATE (DD /MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	22/02/2018
individu_lame.date_precision_voc_fk(voc. code)	Y	Date precision for specimen slide processing date (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J
individu_lame.libelle_lame	Y	Title of the specimen microscope slide	VARCHAR(1024)					A1 Lirceus brachyurus BERKELSP_201704, Berkeley Springs.
individu_lame.nom_dossier_photos	N	Name of the folder in which photos of	VARCHAR(1024)					Lirceus_brachyrus_B ERKELSP_2017

		the slide are stored						
individu_lame.comm entaire_lame	N	Comments about the specimen slide	TEXT					Nice slide
individu_lame.boite_fk(boxe.code_boxe)	N	Code of the box in which the slide is stored (code)	VARCHAR(255)		box		See box codes in the slide box table	LAM_23
individu_lame_est_re alise_par.personne_fk(personne.nom_per sonne)	Y	Name(s) of person(s) who processed the slide.	VARCHAR(255)	Multiple persons separated by " \$ "	person		See person names in the person table	MALARD F

### 13.6. Upload external biological material

Template file: external\_biological\_material

Referential files: taxon, vocabulary, person, source

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
lot_materiel_ext.collecte_fk(collecte.code_collecte)	Y	Sampling code	VARCHAR(255)			Foreign key (link to sampling).	Expressed as "site code_sampling year sampling month". See 15.2.	FTBOUIL_197000
lot_materiel_ext.code_lot_materiel_ext	Y	External biological material code	VARCHAR(255)				Expressed as "Name of species taxon sampling code". See 15.4.	PROASELLUS_MERIDIANUS FTBOUIL_197000
lot_materiel_ext.pigmentation_voc_fk(voc.code)	Y	Pigmentation (code)	VARCHAR(255)		vocabulary		See codes in the vocabulary table	DP (for depigmented partially)
lot_materiel_ext.yeu_x_voc_fk(voc.code)	Y	Vision (code)	VARCHAR(255)		vocabulary		See codes in the vocabulary table	O (for oculated)
lot_materiel_ext.commentaire_lot_materiel_ext	N	Comments about the external biological material	TEXT					No comments.
lot_materiel_ext.nb_individuals_voc_fk(voc.code)	Y	An indication of the number of specimens in the external biological material (code).	VARCHAR(255)		vocabulary		See codes in the vocabulary table	PLUDIZ (for several dozens of individuals)

lot_materiel_ext.com mentaire_nb_individuals	N	Comments about the number of specimens in the external biological material.	TEXT					82 individuals
lot_materiel_ext.date_creation_lot_materiel_ext	Y	External biological material date (creation date)	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	01/01/1970
lot_materiel_ext.date_precision_voc_fk(voc.code)	Y	Date precision (code)	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	A (for year)
lot_materiel_ext.est_realise_par.personne_fk(personne.nom_personne)	Y	Name(s) of person(s) who processes the external biological material	VARCHAR(255)	Multiple persons separated by " \$ "	person			BERTRAND J Y
espece_identifiee.reference_taxon_fk(reference_taxon.taxname)	Y	Name of species taxon attributed to external biological material.	VARCHAR(255)		taxon		See name of species taxa in the taxa table	PROASELLUS_MERIDIANUS
espece_identifiee.criterie_identification_voc_fk(voc.code)	Y	Species taxon identification criterion (code).	VARCHAR(255)		vocabulary		See codes in the vocabulary table	M (for morphology)
espece_identifiee.date_identification	Y	Species taxon identification date.	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	01/01/1970

espece_identifiee.dat e_precision_voc_fk(v oc.code)	Y	Date precision for species taxon identification (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table (J for day, M for month and A for year)	M (for month)
espece_identifiee.co mmentaire_esp_id		Species taxon identification comments.	TEXT					No comments.
est_identifie_par.per sonne_fk(personne.n om_personne)	N	Name(s) of person(s) who identified the species taxon.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	BERTRAND J Y
lot_materiel_ext_est _reference_dans.sou rce_fk(source.code_s ource)	Y	Source (i.e. literature reference) in which the external biological material is published (code).	VARCHAR(255)	Multiple source codes separated by " \$"	source		See sources codes in the source table	Bertrand_1971_Bull_ Assoc_nat_orléan_Lo ire_moy_53

### 13.7. Upload DNA

Template file: DNA

Referential files: box, vocabulary, person

Field title	Compulsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
adn.individu_fk(individu.code_ind_biomol)	Y	Specimen molecular code	VARCHAR(255)			Link to specimen table.	Expressed as "Code for name of species taxon_sampling code_specimen molecular number" See example. See table "taxon" for codes of species taxa names. Unique code. See 15.6.	LIRbrachyurus_BERKE LSP_201704_1ID
adn.code_adn	Y	Code of the DNA extract	VARCHAR(255)			Foreign key (link to PCR).	No space in the code	LiBrB1
adn.date_adn	N	DNA extraction date	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	07/03/2018
adn.date_precision_voc_fk(voc.code)	Y	Precision of DNA extraction date	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J (for day)
adn.methode_extraction_adn_voc_fk(voc.code)	Y	DNA extraction method	VARCHAR(255)		vocabulary		See codes for DNA extraction methods in the vocabulary table.	C (for Chelex)
adn.concentration_ng_microlitre	N	DNA concentration	Double precision				12.5 or 12,5	

adn.commentaire_adn	N	Comments about the DNA extract	TEXT					Chelex_47
adn.est_realise_par.personne_fk(personne.nom_personne)	Y	Name(s) of person(s) who extracted DNA.	VARCHAR(255)	Multiple persons separated by " \$ "	person		See person names in the person table	KONECNY L
adn.boite_fk(boxe.code_boxe)	N	Code of the box in which the DNA extract is stored.	VARCHAR(255)		box		See DNA box codes in the box table	ADN_CA6
adn.qualite_adn_voc_fk(voc.code)	Y	Quality of the DNA extract	VARCHAR(255)		vocabulary		See DNA quality codes in the vocabulary table	OK

### 13.8. Upload PCR

Template file: PCR

Referential files: vocabulary, person

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
pcr.adn_fk(adn.code _adn)	Y	Code of the DNA extract	VARCHAR(255)			Foreign key (link to DNA).	No space in the code.	LiBrB1
pcr.est_realise_par.p ersonne_fk(personne .nom_personne)	Y	Person(s) who performs the PCR	VARCHAR(255)	Multiple persons separated by " \$ "	person		See person names in the person table	KONECNY L
pcr.gene_voc_fk(voc. code)	Y	Targeted gene (code)	VARCHAR(255)		vocabulary		See table vocabulary for codes of genes	COI
pcr.code_pcr	Y	PCR code	VARCHAR(255)			Foreign key (link to chromatogram).	Expressed as "DNA code_PCRnumber_PCR forward primer_PCR reverse primer" See 15.7.	LiBrB1_COI952_COIL CO1490_COILKR3
pcr.num_pcr	Y	PCR number	VARCHAR(255)				No space	COI952
pcr.date_pcr	N	Date of the PCR	DATE (DD /MM/YYYY)				DD=01 if sampling is not known, MM=01 if month is not known, left field blank if date is not known.	20/03/2018
pcr.date_precision_v oc_fk(voc.code)	Y	PCR date precision	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J (for day)

pcr.primer_pcr_start_voc_fk(voc.code)	Y	PCR forward primer (code)	VARCHAR(255)		vocabulary		See vocabulary table for PCR forward primer codes	COILCO1490
pcr.primer_pcr_end_voc_fk(voc.code)	Y	PCR reverse primer (code)	VARCHAR(255)		vocabulary		See vocabulary table for PCR reverse primer codes	COILKR3
pcr.qualite_pcr_voc_fk(voc.code)	Y	PCR quality (code)	VARCHAR(255)		vocabulary		See vocabulary table for PCR quality codes	TB (for very good)
pcr.specificite_voc_fk(voc.code)	Y	PCR specificity (code)	VARCHAR(255)		vocabulary		See vocabulary table for PCR specificity codes	N (for nested PCR)
pcr.detail_pcr	N	PCR details	TEXT					semi nested
pcr.remarque_pcr	N	PCR comments	TEXT					PCR blank contaminated

### 13.9. Upload chromatogram

Template file: chromatogram

Referential files: institution, vocabulary

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
chromatogramme.pc r_fk(pcr.code_pcr)	Y	PCR code	VARCHAR(255)			Foreign key (link to PCR).	Expressed as "DNA code_PCRnumber_PCR forward primer_PCR reverse primer". See 15.7.	LiBrB1_COI952_COIL CO1490_COILKR3
chromatogramme.co de_chromato	Y	Chromatogram code	VARCHAR(255)			Foreign key (link to internal DNA sequence).	Expressed as "YAS number chromatogram primer" See 15.8.	YAI170 COILKR3
chromatogramme.nu m_yas	Y	YAS number (i.e. chromatogram number).	VARCHAR(255)				No space	YAI170
chromatogramme.pri mer_chromato_voc_fk(voc.code)	Y	chromatogram primer (code)	VARCHAR(255)		vocabulary		See chromatogram primer codes in the vocabulary table	COILKR3
chromatogramme.qu alite_chromato_voc_fk(voc.code)	Y	Chromatogram quality (code)	VARCHAR(255)		vocabulary		See chromatogram quality codes in the vocabulary table	OK
chromatogramme.co mmentaire_chromat o	N	Comments about the chromatogram	TEXT					tb
chromatogramme.et ablissement_fk(etablis sement.nom_etablis sement)	Y	Institution which performs sequencing	VARCHAR(255)		institution		See institution names in the table "institution"	BIOFIDAL

### 13.10. Upload internal sequence

Template file: internal\_sequence

Referential files: source, vocabulary, person, taxon

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
sequence_assemblee .code_sqc_ass	Y	Sequence code	VARCHAR(1024)		Foreign key (link MOTU).		Expressed as: "Sequence status_molecular specimen code_concatenation of chromatogram codes PCR specificity code" Use"- " for concatenation. Do not include sequence status if VALIDATED. See 15.9.	LIRbrachyurus_BERKE LSP_201704_1ID_YAI 170 COILKR3 C- YAI179_COILCO1490  C
sequence_assemblee .code_sqc_alignmen t	Y	Sequence alignment code	VARCHAR(1024)				Expressed as: "Sequence status_species taxon code attributed to DNA sequence_sampling code_specimen molecular number_concatenation of chromatogram codes PCR specificity code" Use"- " for concatenation. Do not include sequence status if VALIDATED. See 15.10.	LIRbrachyurus_BERKE LSP_201704_1ID_YAI 170 COILKR3 C- YAI179_COILCO1490  C
sequence_assemblee .accession_number	N	Sequence accession number	VARCHAR(255)					FJ791877997
sequence_assemblee .statut_sqc_ass_voc_fk(voc.code)	Y	Sequence status	VARCHAR(255)		vocabulary		See codes for sequence status in the vocabulary table	VALIDATED

sequence_assemblee.date_creation_sqc_ass	N	Date of sequence creation	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	18/09/2018
sequence_assemblee.date_precision_voc_fk(voc.code)	Y	Date precision for sequence creation (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J (for day)
sequence_assemblee.commentaire_sqc_ass	N	Comments about the sequence	TEXT					No comments.
sequence_assemblee.est_realise_par.personne_fk(personne.nom_personne)	Y	Name of person who assembled the sequence.	VARCHAR(255)	Multiple persons separated by " \$ "	person		See person names in the person table	KONECNY L
espece_identifiee.reference_taxon_fk(reference_taxon.taxoname)	Y	Name of species taxon attributed to the sequence.	VARCHAR(255)		taxon		See name of species taxa in the taxa table	LIRCEUS_BRACHYURUS
espece_identifiee.criterie_identification_voc_fk(voc.code)	Y	Species taxon identification criterion (code).	VARCHAR(255)		vocabulary		See codes for identification criteria in the vocabulary table	AMP (for Provisional molecular assignment)
espece_identifiee.date_identification	N	Species taxon identification date.	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if sampling is not known, left field blank if date is not known.	18/09/2018
espece_identifiee.date_precision_voc_fk(voc.code)	Y	Date precision for species taxon identification (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table ( J for day, M for month and A for year)	J (for day)
espece_identifiee.commentaire_esp_id	N	Species taxon identification comments.	TEXT					Species name temporarily attributed based on 16S gene similarity

est_identifie_par.personne_fk(personne.nom_personne)	Y	Name(s) of person(s) who identified the species taxon.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	MALARD F
est_aligne_et_traite.chromatogramme_fk(chromatogramme.code_chromato)	Y	Chromatogram code	VARCHAR(255)	Multiple chromatogram codes separated by " \$"		Foreign key (link chromatogram).	Chromatogram code expressed as "YAS number chromatogram primer". See 15.8.	YAI170 COILKR3 \$ YAI179 COILCO1490
sqc_est_publie_dans.source_fk(source.code_source)	N	Source (i.e. literature reference) in which the sequence is published (code).	VARCHAR(255)	Multiple source codes separated by " \$"	source		See source codes in the source table	Sidorov_Holsinger_2007_Crustaceana_80_4_417_430

### 13.11. Upload external sequence

Template file: external\_sequence

Referential files: source, vocabulary, person, taxon

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
sequence_assemblee_ext.code_sqc_ass_ext	Y	External sequence code	VARCHAR(1024)		Foreign key (link to MOTU table)		Expressed as "Sequence status_species taxon code attributed to DNA sequence at creation_sampling code_sequence specimen number_accession number sequence origin. Do not include sequence status if VALIDATED. See 15.11.	LIRCEObisetus_GOR MAN_000000_GM1_AY566531 NCBI
sequence_assemblee_ext.code_sqc_ass_ext_alignement	Y	External sequence alignment code	VARCHAR(1024)				Expressed as "Sequence status_last species taxon code attributed to DNA sequence_sampling code_sequence specimen number_accession number sequence origin. Do not include sequence status if VALIDATED. See 15.12.	LIRCEObisetus_GOR MAN_000000_GM1_AY566531 NCBI
sequence_assemblee_ext.accession_number_sqc_ass_ext	Y	External sequence accession number	VARCHAR(255)					AY566531

sequence_assemblee_ext.num_individu_sqc_ass_ext	Y	External sequence specimen number	VARCHAR(255)				No space	GM1
sequence_assemblee_ext.taxon_origine_sqc_ass_ext	N	External sequence primary taxon	VARCHAR(255)				The taxon name originally associated to the external sequence in the literature	Lirceolus bisetus
sequence_assemblee_ext.origine_sqc_ass_ext_voc_fk(voc.code)	Y	External sequence origin	VARCHAR(255)		vocabulary		See table vocabulary for codes of sequence origin	NCBI
sequence_assemblee_ext.gene_voc_fk(voc.code)	Y	Targeted gene (code)	VARCHAR(255)		vocabulary		See table vocabulary for codes of genes	COI
sequence_assemblee_ext.statut_sqc_ass_voc_fk(voc.code)	Y	Sequence status	VARCHAR(255)		vocabulary		See codes for sequence status in the vocabulary table	VALIDATED
sequence_assemblee_ext.date_creation_sqc_ass_ext	N	Date of sequence creation	DATE (DD/MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	15/09/2017
sequence_assemblee_ext.date_precision_voc_fk(voc.code)	Y	Date precision for sequence creation (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table (J for day, M for month and A for year)	J (for day)
sequence_assemblee_ext.collecte_fk(collecte.code_collecte)	Y	Sampling code	VARCHAR(255)			Foreign key (link to sampling)	Expressed as "site code_sampling year sampling month" See 15.2.	GORMAN_000000
sequence_assemblee_ext.commentaire_sqc_ass_ext	N	Comments on external sequence	TEXT					No comments
sqc_ext_est_realise_par.personne_fk(personne.nom_personne)	Y	Name of person who enters the sequence.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	MALARD F

espece_identifiee.ref erentiel_taxon_fk(ref erentiel_taxon.taxna me)	Y	Name of species taxon attributed to the sequence.	VARCHAR(255)		taxon		See name of species taxa in the taxa table	LIRCEOLUS_BISETUS
espece_identifiee.crit ere_identification_vo c_fk(voc.code)	Y	Species taxon identification criterion (code).	VARCHAR(255)		vocabulary		See codes for identification criteria in the vocabulary table	INC (for not known)
espece_identifiee.dat e_identification	N	Species taxon identification date.	DATE (DD /MM/YYYY)				DD=01 if day is not known, MM=01 if month is not known, left field blank if date is not known.	15/09/2017
espece_identifiee.dat e_precision_voc_fk(v oc.code)	Y	Date precision for species taxon identification (code).	VARCHAR (255)		vocabulary		See Date precision codes in the vocabulary table (J for day, M for month and A for year)	J (for day)
espece_identifiee.co mmentaire_esp_id	N	Species taxon identification comments.	TEXT					No indication for the identification criterion in NCBI
est_identifie_par.per sonne_fk(personne.n om_personne)	Y	Name(s) of person(s) who identified the species taxon.	VARCHAR(255)	Multiple persons separated by " \$"	person		See person names in the person table	MALARD F
sqc_ext_est_referenc e_dans.source_fk(so urce.code_source)	Y	Source (i.e. literature reference) in which the sequence is published (code).	VARCHAR(255)	Multiple source codes separated by " \$"	source		See source codes in the source table	Krejca_2005_PhD_Th esis_Austin_Texas_U SA

### 13.12. Upload MOTU

Template file: MOTU

To upload MOTUs use the following procedure.

- 1) Provide the metadata for the new set of MOTUs to be imported.

Click the button “Create new set of MOTU” in subsection “DNA sequence / MOTU” of the web user interface (see section 8.3.2. Create new MOTU and appendix 8.3.2 in GOTIT HELP for more details) and fill in the fields below. We provide a fictitious example along which a new delimitation method entitled “TNNEW” is used to generate MOTUs (see column “example”). Five delimitation methods are already incorporated into the vocabulary table: HAPLO, TH, PTP, BPTP, and GMYC.

Section / Field label	Content type	Description	Rules	Note	Compu lsory	Example
csv file name	VARCHAR(255)	Provide name of the MOTU csv file containing the MOTU data set to be imported.			Y	HAPLO_TH_PTP_ <b>THNEW</b> _COI_2018
MOTU title	VARCHAR(255)	Provide title for the MOTU data set.			Y	Malard_et_al._2018
MOTU date	DATE	Provide date when the MOTU numbers are generated, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	12/12/2018
MOTU comments	TEXT	Provide comments if necessary.			N	MOTUs generated using the COI gene with methods HAPLO, TH, PTP and <b>THNEW</b> (see source Malard_et_al_2018_Internal_Report)
is generated by	LIST OF SELECTION	Provide name of person who generated the MOTU data set using the scroll bar.			Y	MALARD F

2) If necessary, provide the necessary “vocabulary”.

In this factious example, the MOTU file to be uploaded (i.e. HAPLO\_TH\_PTP\_THNEW\_COI\_2018) contains four methods, HAPLO, TH, PTP and THNEW. Three of these methods, HAPLO, TH and PTP are listed in the vocabulary table, one, THNEW, is not. Incorporate the new method into the vocabulary table by clicking the button “Create new vocabulary” of the subsection Repositories/Vocabulary in the web user interface (see section 11.1.2. Create new vocabulary and appendix 11.1.2 in GOTIT HELP for more details).

3) Upload the template file “MOTU” with the following fields:

Field title	Co mp ulso ry	Field content	Content type	Single - multiple items	Link to referenti al table	Link to tables	Rules (internal)	Example
code_seq_ass	Y	Sequence code	VARCHAR(1024)			Foreign key (link to internal sequence and external sequence).	<u>Internal sequence</u> : Expressed as: "Sequence status_molecular specimen code_concatenation of chromatogram codes PCR specificity code". Use "-" for concatenation. Do not include sequence status if VALIDATED. See 15.9.  <u>External sequence</u> : Expressed as "Sequence status_species taxon code attributed to DNA sequence at creation_sampling code_sequence specimen number_accession number sequence origin. Do not include sequence status if VALIDATED. See 15.11.	<u>Internal sequence</u> : LIRbrachyurus_BERKELSP_201704_1D_YAI170 COILKR3 CYAI179_COILCO1490 C <u>External sequence</u> : LIRCEObisetus_GORMAN_000000_GM1_AY566531 NCBI
num_motu	Y	MOTU number	INTEGER				Use integers	183

code_methode_motu	Y	The method used to delimit MOTUs.	VARCHAR(255)		vocabulary		See codes of methods used to delimit MOTUs in the vocabulary table.	HAPLO
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### 13.13. Store biological material as file

Template file: biological\_material\_store

Notes:

- 1) Use this procedure to store sets of biological materials that have not yet been allocated to boxes.
- 2) All codes for storing boxes of biological materials should already be in the box table.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_lot_materiel	Y	Biological material code	VARCHAR(255)			Foreign key (link to biological material).	Expressed as "Name of species taxon sampling code". See 15.3.	LIRCEUS_BRACHYURUS BERKELSP_201704
code_boite	Y	Storing box (code)	VARCHAR(255)		box		See box codes in the box table	LOT_aAsel4

### 13.14. Move or delete biological material as file

Template file: biological\_material\_move

Notes:

- 1) Use this form to move or remove sets of biological materials that are already stored in boxes.
- 2) For removing a biological material from its box, leave box field blank.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_lot_materiel	Y	Biological material code	VARCHAR(255)			Foreign key (link to biological material).	Expressed as "Name of species taxon sampling code" See 15.3.	LIRCEUS_BRACHYURUS BERKELSP_201704
code_boite	Y	Storing box (code)	VARCHAR(255)		box		See box codes in the box table. Left field blank to remove a biological material from storage.	LOT_aAsel4

### 13.15. Store slides as file

Template file: slide\_store

Notes:

- 1) Use this form to store sets of specimen slides that have not yet been allocated to boxes.
- 2) All codes for storing boxes of specimen slides should already be in the box table.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_lame_coll	Y	code of the specimen microscope slide	VARCHAR(255)			Link to specimen slide table		23_23
code_boite	y	Code of the box in which the slide is stored (code)	VARCHAR(255)		box		See box codes in the slide box table	LAM_23

### 13.16. Move or delete slides as file

Template file: slide\_move

Notes:

- 1) Use this form to move or remove sets of specimen slides that are already stored in boxes.
- 2) For removing a specimen slide from its box, leave box field blank.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_lame_coll	Y	code of the specimen microscope slide	VARCHAR(255)			Link to specimen slide table		23_23
code_boite	y	Code of the box in which the slide is stored (code)	VARCHAR(255)		box		See box codes in the slide box table. Left field blank to remove a slide from storage.	LAM_23

### 13.17. Store DNA boxes as file

Template file: DNA\_store

Notes:

- 1) Use this form to store sets of DNA extracts that have not yet been allocated to boxes.
- 2) All codes for storing boxes of DNA extracts should already be in the box table.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_adn	Y	Code of the DNA extract	VARCHAR(255)			Foreign key (link to DNA).	No space	LiBrB1
code_boite	Y	Code of the box in which the DNA extract is stored.	VARCHAR(255)		box		See DNA box codes in the box table	ADN_CA6

### 13.18. Move or delete DNA boxes as file

Template file: DNA\_move

Notes:

- 1) Use this form to move or remove sets of DNA extracts that are already stored in boxes.
- 2) For removing a DNA extract from its box, leave box field blank.

Field title	Compulsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
code_adn	Y	Code of the DNA extract	VARCHAR(255)			Foreign key (link to DNA).	No space	LiBrB1
code_boite	Y	Code of the box in which the DNA extract is stored.	VARCHAR(255)		box		See DNA box codes in the box table. Left field blank to remove a DNA extract from storage.	ADN_CA6

### 13.19. Upload set of sources

Template file: source

Referential file: person

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
source.code_source	y	Reference source code	VARCHAR(255)				Expressed as "Author_year_journal_abbreviation_volume number_issue number_pages (see example)."	Brunke_Gonser_1999_J_North_Am_Benthol_Soc_18_3_344_362
source.annee_source	N	Publication date of the source	INTEGER				Expressed publication as "YYYY"	1999
source.libelle_source	Y	Full title of the source	VARCHAR(2048)				See example for source format.	Brunke M., Gonser T. 1999. Hyporheic invertebrates - the clinal nature of interstitial communities structured by hydrological exchange and environmental gradients. Journal of the North American Benthological Society, 18(3), 344-362.
source.commentaire_source	N	Comments about the source.	TEXT					No comments.
source_a_ete_integre_par.personne_fk(personne.nom_personne)	Y	Name(s) of person(s) who inputs the slide.	VARCHAR(255)	Multiple persons separated by " \$ "	person		See person names in the person table	MALARD F

### 13.20. Source to biological material as file

Template file: source\_attribute\_to\_lot

Referential files: person, source

Notes:

- 1) Use this procedure to attribute reference sources to biological materials that are not linked to reference sources.
- 2) All codes of reference sources should already be in the source table.

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
source.code_source	y	Reference source code	VARCHAR(255)			Foreign key (link to source).	Expressed as "Author_year_journal abbreviation_volume number_Issue number_pages (see example).	Brunke_Gonser_1999 _J_North_Am_Benth ol_Soc_18_3_344_36 2
code_lot_materiel	Y	Biological material code	VARCHAR(255)			Foreign key (link to biological material).	Expressed as "Name of species taxon sampling code" See 15.3.	LIRCEUS_BRACHYUR US BERKELSP_20170 4

### 13.21. Source to sequence as file

Template file: source\_attribute\_to\_sequence

Referential files: person, source

Notes:

- 1) Use this form to attribute reference sources and accession numbers or reference sources alone to internal sequences that are not linked to reference sources and do not have an accession number.
- 2) All codes of reference sources should already be in the source table.
- 3) To attribute reference sources alone keep the field "accession number empty"

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
source.code_source	y	Reference source code	VARCHAR(255)			Foreign key (link to source).	Expressed as "Author_year_journal abbreviation_volume number_Issue number_pages (see example)."	Brunke_Gonser_1999_J_North_Am_Benthol_Soc_18_3_344_362
code_sqc_ass	Y	Sequence code	VARCHAR(1024)			Foreign key (link to internal sequence).	Expressed as: "Sequence status_molecular specimen code_concatenation of chromatogram codes PCR specificity code" Use "-" for concatenation. Do not include sequence status if VALIDATED. See 15.9.	LIRbrachyurus_BERK_ELSP_201704_1ID_YAI170 COILKR3 C-YAI179_COILCO1490 C
accession_number	N	Sequence accession number	VARCHAR(255)					FJ791877997

## 13.22. Upload person names

Template file: person

Referential file: institution

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
personne.nom_perso nne	Y	Person name	VARCHAR(255)				Capitals. Write CLINTON B	KONECNY L
personne.nom_complet	N	Person full name	VARCHAR(1024)				Capitals. Write CLINTON BILL	KONECNY LARA
personne.nom_perso nne_ref	N	Second name of person (if any).	VARCHAR(255)				See example.	KONECNY DUPRE LARA
personne.etablissement_fk(etablissement .nom_etablissement)	N	Name of institution to which the person belongs.	VARCHAR(1024)		Link to institution table		See institution names in the institution table	UNIVERSITY LYON 1
personne.commentai re_personne	N	Comments	TEXT					No comments.

### 13.23. Upload institutions

Template file: institution

Referential file: person

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
établissement.nom_établissement	Y	Name of the institution	VARCHAR(1024)		Link to person table		Capitals	DTAMB
établissement.commentaire_établissement	N	Comments about the institution	TEXT					Développement de Techniques et Analyse Moléculaire de la Biodiversité. Villeurbanne. France.

### 13.24. Upload program

Template file: program

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
programme.code_programme	Y	Code of funding program	VARCHAR(255)				Capitals. No space.	N_AM_ASEL
programme.nom_programme	Y	Name of funding program	VARCHAR(1024)					Distribution and diversity of north American asellids
programme.noms_responsables	Y	Name(s) of coordinator(s) of funding program.	TEXT				Capitals. No space. Write as follows: CLINTON B or CLINTON B \$ OBAMA B H when more than one coordinator	LEWIS JJ
programme.type_financeur	N	Name or code of funding agency for the funding program	VARCHAR(1024)				Capitals	SMITHSONIAN INSTITUTE
programme.annee_debut	N	Starting year of funding program	INTEGER					2016
programme.annee_fin	N	Ending year of funding program	INTEGER					2019

### 13.25. Upload taxon

Template file: taxon

Field title	Compulsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
referentiel_taxon.taxname	Y	Name of species taxa	VARCHAR(255)				Capitals, no space (see example). Must be unique.	ASELLUS_AQUATICUS_CARSICUS
referentiel_taxon.rank	Y	Taxonomic rank	VARCHAR(255)				Capitals. See list. NA stands for not applicable	SUBSPECIES
referentiel_taxon.subclass	N	Subclass	VARCHAR(255)				Capitals	EUMALACOSTRACA
referentiel_taxon.ordre	N	Order	VARCHAR(255)				Capitals	ISOPODA
referentiel_taxon.family	N	Family	VARCHAR(255)				Capitals	ASELLIDAE
referentiel_taxon.genus	N	Genus	VARCHAR(255)				Capitals	ASELLUS
referentiel_taxon.species	N	Species	VARCHAR(255)				Capitals	AQUATICUS
referentiel_taxon.subspecies	N	Subspecies	VARCHAR(255)				Capitals	CARSICUS
referentiel_taxon.commentaire_ref	N	Comments about the species taxon	TEXT					No comments.
referentiel_taxon.validity	Y	Whether species taxon name is valid	SMALL INTEGER				YES or NO	YES

		(yes) or not valid (no)						
referentiel_taxon.code_taxon	Y	Abbreviated taxon code	VARCHAR(255)				No space. Code must be unique.	Aaquaticuscarsicus
referentiel_taxon.clade	N	Clade to which the species taxa belongs	VARCHAR(255)				No space. Capitals.	
referentiel_taxon.taxname_ref	N	Provide species taxa synonym, if any	VARCHAR(255)					

### 13.26. Upload vocabulary

Template file: vocabulary

Field title	Compu lsory	Field content	Content type	Single - multipl e items	Link to referential table	Link to tables	Rules (internal)	Example
voc.code	Y	Code for the vocabulary	VARCHAR(255)				No space	18S
voc.libelle	Y	Title for the vocabulary	VARCHAR(255)					18S gene
voc.parent	Y	Parent to which the vocabulary belongs to.	VARCHAR(255)				Use French codes of parents listed in the table foonote.	gene
voc.commentaire	N	Comments about the vocabulary	TEXT					No comments.

Code list of parents (English translation in brackets): codeCollection (Code collection); criterelidentification (Identification criteria); datePrecision (Date Precision); fixateur (Fixative); gene (Gene); habitatType (Habitat Type); leg (Donation); methodeExtractionAdn (DNA extraction method); methodeMotu (method Motu); nbIndividus (Number of specimen); origineSqAssExt (External sequence origin); pigmentation (Pigmentation); pointAcces (Access type); precisionLatLong (Coordinate precision); primerChromato (Primer Chromato); primerPcrEnd (Primer PCR End); primerPcrStart (Primer PCR Start); qualiteAdn (DNA quality); qualiteChromato (Chromatogram quality); qualitePcr (PCR quality); samplingMethod (sampling method); specificite (PCR specificity); statutSqAss (Sequence status); typeBoite (Box type); typeCollection (Collection type); typeIndividu (Specimen type); yeux (Vision).

### 13.27. Upload box

Template file: box

Referential file: vocabulary

Field title	Compulsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
boite.code_boite	Y	Box code	VARCHAR(255)				No space	ADN_CNC1
boite.type_boite_voc_fk(voc.code)	Y	Type of box	VARCHAR(255)		Link to vocabulary		For codes of box types see vocabulary table (i.e. LOT for biological material, LAME for specimen slide and ADN for DNA extract).	ADN
boite.libelle_boite	Y	Box title	VARCHAR(1024)					ADN_chelex NewCaledonia1
boite.code_collection_voc_fk(voc.code)	Y	Collection code	VARCHAR(255)		Link to vocabulary		For codes of collections see vocabulary table	ADN_NC
boite.type_collection_voc_fk(voc.code)	Y	Collection type	VARCHAR(255)		Link to vocabulary		For codes of collection types see vocabulary table (i.e. LOT for biological material, LAME for specimen slide and ADN for DNA extract).	ADN
boite.commentaire_boite	N	Comments about the box	TEXT					No comments.

### 13.28. Upload municipalities

Template file: municipality

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
commune.code_commune	Y	Code of municipality	VARCHAR(255)				Concatenate name of municipality, name of region and code of country as in example. Spaces must be replaced by “_”	LOW_MUNICIPALITY  HIGH_REGION  BOSNIA_AND_HERZE GOVINA
commune.nom_commune	Y	Name of municipality	VARCHAR(1024)				Capitals	LOW MUNICIPALITY
commune.nom_region	Y	Name of region	VARCHAR(1024)				Capitals	HIGH REGION
commune.pays_fk(pays.co de_pays)	Y	Code of country	VARCHAR(1024)		Link to country		Capitals, space replaced by –	BOSNIA_AND_HERZE GOVINA

Note. The municipality data table contains four fields: municipality code, municipality name, region name, and country name (see appendix 11.7.2 in GOTIT HELP). These four fields can also be filled in by the user when uploading the template file “site” (see section 13.1 Upload site in GOTIT HELP).

### 13.29. Upload country

Template file: country

Field title	Compu lsory	Field content	Content type	Single - multiple items	Link to referential table	Link to tables	Rules (internal)	Example
pays.code_pays	Y	County code	VARCHAR(255)				Capitals, no space.	BOSNIA_AND_HERZE GOVINA
pays.nom_pays	Y	Country name	VARCHAR(1024)		Link to municipality		Capitals	BOSNIA AND HERZEGOVINA

## **14. LOGIN AND USER**

### 14.1. Login

Use this page to login and access to GOTIT web user interface. Enter your user name and password. See section 14.2. below for usage restrictions associated with different user types.

### 14.2. User type

The section “User” is for administrator only. Administrator can set up four different types of user account.

- Administrator

An administrator has full access to all functionalities and data in GOTIT.

- Project member

A project member has access to almost all functionalities and data in GOTIT but the following restrictions apply (see Appendix 14.2.1. for a full description of functionalities offered to project members).

- Partial access to repositories, including no access to referential files “vocabulary”, “taxon”, “country” and “municipality”.
- No access to uploading tools “Move or delete biological material, slide and DNA boxes as file” in section “storage”.
- Read access only to the MOTU section with no possibility to upload MOTUs.
- No access to a number of fields (most often, foreign keys) in the editing mode

- Collaborator

A collaborator has restricted access to data and functionalities of GOTIT (see Appendix 14.2.2. for a full description of functionalities offered to a collaborator). He can create and read data but he can only edit data that he created. The following restrictions apply to collaborator:

- No access to repositories, except the referential file “person”
- No access to uploading tools in the following sections: site, sampling, internal and external biological materials, specimen, specimen slide, sources, and storage (i.e. no access to uploading tools “Move or delete biological material, slide and DNA boxes as file”).
- Read access only to the MOTU section with no possibility to upload MOTUs
- No access to a number of fields (most often, foreign keys) in the editing mode

- Invited member:

Invited members only have a read access to the data with no possibility to export data when using the “Species search” tools.

### 14.3. User form

#### 14.3.1. User list

Use this page to browse, create, show, edit and delete user accounts. WARNING: Deleting a user account would erase contents of technical fields (e.g. user creation). Rather, lock a user account using the option “LOCKED” in the edit session (see appendix 14.3.1 in GOTIT HELP for further details). Additional fields can be listed using the top right button. The search button applies to the field "Username".

#### 14.3.2. Create new user

Use this form to fill in data of a new user. See appendix 14.3.1 in GOTIT HELP for content of fields.

#### 14.3.3. Show user

Use this form to consult data of a user. See appendix 14.3.1 in GOTIT HELP for content of fields.

#### 14.3.4. Edit user

Use this form to edit data of a user. See appendix 14.3.1 in GOTIT HELP for content of fields.

#### 14.3.5. Delete user

Use this button to delete a user account. WARNING: Deleting a user account would erase contents of technical fields (e.g. user creation). Rather, lock a user account using the option “LOCKED” in the edit session (see appendix 14.3.1 in GOTIT HELP for further details).

## **15. SELF-GENERATION OF INFORMATIVE IDENTIFIER CODES**

### 15.1. Principle

Many informative identifier codes (e.g. see list below) are generated automatically upon creation of a new record. An informative identifier code is both unique and informative in that sense that its reading makes sense to a user (i.e. it is not only an identifier number as stored in the database). Informative identifier codes are needed at different steps of the laboratory workflow, for example for labelling tubes and biological vouchers. Self-generation of codes is from concatenation of data entered in different fields of a single data table, or more rarely from concatenation of data contained in different tables. In most cases, self-generation is active only in the creation mode. Then, informative identifier codes and the content of fields used to build them can be updated by administrators only, thereby ensuring the stability of codes (see privileges according to different user roles in section 14.). We describe below the assembly rules of informative identifier codes that are automatically generated in GOTIT.

**Important:** The assembly rules should also be followed when filling the template files used to upload many data at a time

### 15.2. Sampling code

The sampling code in the sampling creation form (cf. section 5.2.2.) is assembled as follows:

Site code\_YYYYMM

Where: Site code is the code of the sampling site (capitals) and “YYYY” and “MM” are the sampling year and month, respectively. If the sampling month is not known (sampling date precision=YEAR), then “MM”=”00”. If the sampling date is not known (sampling date precision=NOT KNWOW), then “YYYY”=”0000” and “MM”=”00”.

Examples: SITECODE\_201901; SITECODE\_201900; SITECODE\_000000

### 15.3. Biological material code

The biological material code in the biological material creation form (cf. section 6.1.2.) is assembled as follows:

Taxon name|sampling code

Where: Sampling code is the code of sampling as described in section 15.2. and taxon name is the name of the taxon as declared in the field “taxa” of the section “identified species”.

Example: ASELLUS\_AQUATICUS|SITECODE\_201901

### 15.4. External biological material code

The external biological material code in the external biological material creation form (cf. section 6.4.2.) is assembled in exactly the same way as for the biological material code (i.e. Taxon name | sampling code, see section 15.3.).

### 15.5. Specimen morphological code

The specimen morphological code in the specimen creation form (cf. section 6.2.2.) is assembled as follows:

Taxon name | sampling code[tube code]

Where: sampling code is the code of sampling as described in section 15.2., taxon name is the name of the taxon as declared in the field “taxa” of the section “identified species”, and tube code is the code of the tube in which the specimen is stored.

Example: ASELLUS\_AQUATICUS|SITECODE\_201901[A1]

### 15.6. Specimen molecular code

The specimen molecular code in the specimen edit form (cf. section 6.2.5.) is assembled as follows:

Taxon code\_sampling code\_specimen molecular number

Where: sampling code is the code of sampling as described in section 15.2., taxon code is the code of the taxon as declared in the repository table “taxon”, and the specimen molecular number is the molecular number assigned to the specimen by the user in the specimen creation form (see section 62.2.),

Example: Aaquaticus\_SITECODE\_201901\_01

Where “Aaquaticus” is the taxon code attributed to ASELLUS\_AQUATICUS in the repository table “taxon” and “01” is the specimen molecular number assigned to that specimen by the user.

Note 1: For the selection of specimen molecular numbers, it is strongly recommended to increment numbers for all specimens collected at a site and this independently of the taxon to which these specimens belong. This avoids creating duplicates of specimen molecular codes, especially when the taxon code is made to be changed. To this end, GOTIT provides in the biological material menu a button entitled "Ind / St" which allows to list all specimens collected at a site.

Note 2: the specimen molecular code is automatically generated in the edit mode, instead of the creation mode, because the laboratory workflow implies that a morphological specimen is selected and coded before it can be used and coded for molecular analysis. Note also that a morphological specimen can be isolated for morphological analysis (e.g. the specimen can be mounted on slide for microscopic analysis) without necessarily being used for molecular analysis.

#### 15.7. PCR code

The PCR code in the PCR creation form (cf. section 7.2.2.) is assembled as follows:

DNA code\_PCR number\_forward primer code\_reverse primer code

Where: DNA code is the code attributed to the DNA extract by the user (see section 7.1.2.), PCR number is the number assigned to the PCR by the user, and the forward primer and reverse primer codes are the codes set in the vocabulary tables for the two primers used to perform the PCR.

Example: ADNcode1\_01\_16SarDr\_16Sbr

#### 15.8. Chromatogram code

The chromatogram code in the chromatogram creation form (cf. section 7.3.2.) is assembled as follows:

YAS number|chromatogram primer code

Where: YAS number if the number attributed to the chromatogram by the user and chromatogram primer code is the code of the chromatogram primer as set in the vocabulary table.

Example: YAD125|16SPcavR1

#### 15.9. Sequence code

The sequence code in the internal sequence creation form (cf. section 8.1.2.) is assembled as follows:

Sequence status\_Specimen molecular code\_chromatogram code1|PCR specificity-chromatogram code2|PCR specificity-....

Example 1: Aaquaticus\_AINCROTE\_201410\_01\_YASNUMBER3|16Sbr|C

Example 2: NUMT\_Aquaticus\_AINCROTE\_201410\_01\_YASNUMBER3|16Sbr|C-YASNUMBER|16SPcavR1|C

Where: Sequence status indicates the status of the sequence as selected from the different status cases incorporated in the vocabulary repository table, specimen molecular code is the molecular code of the specimen as described in section 15.6., and “chromatogram code|PCR specificity” is the code of chromatogram as described in section 15.8., together with the specificity of the PCR as provided in the PCR creation form (cf. section 7.2.2.). The symbol “|” is added between the chromatogram code and PCR specificity and all “chromatogram code|PCR specificity” are separated by the symbol “-”, when several chromatograms are used to assemble a sequence (see example 2).

Note 1: When the sequence status is "VALID", that status is not indicated in the sequence code (see example 1)

#### 15.10. Sequence alignment code

The sequence alignment code in the internal sequence creation form (cf. section 8.1.2.) is assembled as follows:

Sequence status\_Taxon code\_sampling code\_specimen molecular number  
\_chromatogram code1|PCR specificity- chromatogram code2|PCR specificity-....

Example 1: Aaquaticuscarsicus\_AINCROTE\_201410\_01\_YASNUMBER3|16Sbr|C

Example 2: NUMT\_Aquaticuscarsicus\_AINCROTE\_201410\_01\_YASNUMBER3|16Sbr|C-YASNUMBER|16SPcavR1|C

Where: Sequence status indicates the status of the sequence as selected from the different status cases incorporated in the vocabulary repository table, taxon code is the code of the taxon assigned to the sequence in the field “taxa” of the section “identified species”, sampling code is the code of sampling as defined in section 15.2., specimen molecular number is the molecular number assigned to the specimen by the user in the specimen edit form (see section 6.2.5.), and “chromatogram code|PCR specificity” is the code of chromatogram as described in section 15.8., together with the specificity of the PCR as provided in the PCR creation form (cf. section 7.2.2.). The symbol “|” is added between the chromatogram code and PCR specificity and all “chromatogram code|PCR specificity” are separated by the symbol “-”, when several chromatograms are used to assemble a sequence (see example 2).

Note 1: In the above examples, the taxon assigned to the sequence of specimen formerly named ASELLUS\_AQUATICUS (see examples 1 and 2 in section 15.9.) is ASELLUS\_AQUATICUS\_CARSICUS (i.e. taxon code Aaquaticuscarsicus).

Note 2: When the sequence status is "VALID", that status is not indicated in the sequence code (see example 1)

Note 3: It is a good practice to keep the sequence code unmodified while the sequence alignment code can be modified when the taxon name attributed to the sequence is changed. The sequence alignment code provide a link between a fixed sequence code as stored in the database and a potentially variable sequence alignment code which is used in various sequence alignments by the user.

#### 15.11. External sequence code

The external sequence code in the external sequence creation form (cf. section 8.2.2.) is assembled as follows:

Sequence status\_taxon code\_sampling code\_external sequence specimen number\_external sequence accession number|external sequence origin

Example 1: Aaquadicuscarsicus\_2BUSTA\_201110\_01\_SL150150|NCBI

Example 2: NUMT\_Aaquadicuscarsicus\_2BUSTA\_201110\_01\_SL150150|NCBI

Where: Sequence status indicates the status of the sequence as selected from the different status cases incorporated in the vocabulary repository table, taxon code is the code of the taxon assigned to the sequence in the field "taxa" of the section "identified species", sampling code is the code of sampling as defined in section 15.2., external sequence specimen number is the molecular number assigned to the specimen by the user, external sequence accession number is the accession number of the sequence (if none, indicate "0"), and external sequence origin provides the source of the external sequence (e.g. NCBI).

Note 1: When the sequence status is "VALID", that status is not indicated in the sequence code (see example 1)

#### 15.12. External sequence alignment code

Same assembly rules as for the external sequence code (section 15.11).

#### 15.13. Municipality code

The municipality code in the municipality creation form (cf. section 11.7.2.) is assembled as follows:

Municipality name|Region name|Country name

Where: Municipality name is the name of the municipality in capital letters, region name is the name of the region in capital letters, and country name is the name of the country in capital letters. Upon creation of the municipality code, all spaces between words are replaced by “\_”.

Example: MUNICIPALITY\_NAME1|REGION\_NAME2|CAYMAN\_ISLANDS

#### 15.14. Country code

The country code is generated from the country name by replacing all spaces, if any, by the symbol “\_”.

## **APPENDICES**

### **Note to all appendices**

Four technical fields are automatically generated while creating / editing a form in GOTIT.

- Creation date: the datetime when a form is created.
- Updating date: the datetime when a form is updated.
- User create: the id of the user\_db table of the user who created the form.
- User update: the id of the user\_db table of the user who updated the form.

The field “Restriction” indicates when access to the field is blocked to project member (PM) and/or collaborator (CM) in the editing mode. This indication is provided only when the form is accessible to PM and/or CM (see section 14 “LOGIN AND USER” and Appendices 14.2.1 and 14.2.2 in GOTIT HELP for further details).

## Appendix 5.1.2 SITE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Site code	LIST OF SELECTION	Provide site code	Capitals		Y	PM, CM
Site name	VARCHAR(1024)	Provide site name	Capitals		Y	
Site description	TEXT	Provide short description of site	Avoid special characters		N	
Country table	LIST OF SELECTION	Provide country using the scroll bar			Y	
Municipality table	LIST OF SELECTION	Provide municipality using the scroll bar		Only those municipalities belonging to the country selected in field "Country table" appear.	Y	
Municipality table	BUTTON : "Add new Municipality"	Use this button to add a new Municipality for a selected country. Open a modal [Municipality]				
Municipality table / [Municipality] Municipality code	VARCHAR(255)	Municipality code generated automatically from municipality name, region name and country table	Self-generated code. See 15.13.			
Municipality table / [Municipality] Municipality name	VARCHAR(1024)	Provide name of municipality	Capitals		Y	
Municipality table / [Municipality] Region name	VARCHAR(1024)	Provide name of region	Capitals		Y	
Municipality table / [Municipality] Country table	LIST OF SELECTION	As in field Country table				
Habitat type	LIST OF SELECTION	Provide type of habitat using the scroll bar			Y	

Access type	LIST OF SELECTION	Provide type of access to the habitat using the scrollbar			Y	
Latitude Dec Deg	FLOAT	Provide latitude in decimal degrees			Y	
Longitude Dec Deg	FLOAT	Provide longitude in decimal degrees			Y	
		Look at distribution of nearby sites, once latitude and longitude of the new site have been filled in. Use buttons + and - to zoom in and out and button "camera" to download map as .png file.				
Coordinate precision	LIST OF SELECTION	Provide precision of latitude and longitude using the scrollbar			Y	
Coordinate precision	BUTTON : "See nearby sites"	Use this button to see the distribution of nearby sites, once latitude and longitude of the new site have been filled in. Use buttons + and - to zoom in and out and button "camera" to download map as .png file.				
Elevation m asl	INTEGER	Provide elevation of site as meters above sea level			N	
Site comments	TEXT	Provide comments if necessary			N	

## Appendix 5.2.2 SAMPLING: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Site table	LIST OF SELECTION	Select site code using the scroll bar.	Capitals		Y	PM, CM
Sampling code	VARCHAR(255)	Sampling code generated automatically from site code and sampling date. See 15.2.	Capitals. Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
Sampling date	DATE	Provide sampling date day as DD , MM, YYYY	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	PM, CM
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Sampling method	BUTTON : "Add sampling method"	Use this BUTTON to select more than one sampling method.			Y	
Sampling method	LIST OF SELECTION	Provide sampling method using the scroll bar.			Y	
Fixative	LIST OF SELECTION	Provide sample fixative using the scroll bar.			Y	
Fixative	BUTTON : "Add fixative"	Use this BUTTON to select more than one sample fixative.				

Funding program	LIST OF SELECTION	Provide funding program using the scroll bar. Select "INC" when funding program is not known.			Y	
Funding program	BUTTON : "Add program"	Use this BUTTON to select more than one funding program.				
Funding program	BUTTON : "Add new program"	Use this BUTTON to create a new funding program (not yet in the list of programs). Open a modal [Program]				
Funding program / [Program] Program code	VARCHAR(255)	Provide code of funding program.	Capitals		Y	
Funding Program / [Program] Program name	VARCHAR(1024)	Provide name of funding program.			Y	
Funding program / [Program] Program coordinator	TEXT	Provide the name(s) of coordinator(s) of funding program.		Write as follows: CLINTON B or CLINTON B \$ OBAMA B H when more than one coordinator	Y	
Funding program / [Program] Funding agency	VARCHAR(1024)	Provide name or code of funding agency for the funding program.	Capitals		N	
Funding program / [Program] Starting year	INTEGER	Provide starting year of funding program.	YYYY		N	
Funding program / [Program] Ending year	INTEGER	Provide ending year of funding program.	YYYY		N	
Funding program / [Program] Program comments	TEXT	Provide comments about the program if necessary.			N	
is done by	LIST OF SELECTION	Provide name of person who sampled using the scroll bar.			Y	
is done by	BUTTON "Add person"	Use this BUTTON to select more than one person.				

is done by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
is done by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is done by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is done by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is done by / [Person] Institution table	LIST OF SELECTION	Select name of institution to which the person belongs using the scroll bar.			N	
is done by / [Person] Person comments	TEXT	Provide comments if necessary.			N	
Targeted taxa	LIST OF SELECTION	Provide taxon targeted during sampling using the scroll bar.			Y	
Targeted taxa	BUTTON "Add targeted taxa"	Use this BUTTON to select more than one targeted taxon.				
Sampling duration	INTEGER	Provide duration of sampling in minutes.	Minutes		N	
Temperature (Celcius)	FLOAT	Provide temperature during sampling in degree Celcius.	Degree Celcius		N	
Specific conductance (micro_sie_cm)	FLOAT	Provide specific conductance of water during sampling in micro-siemens per centimeter.	Micro-siemens per centimeter		N	
Status	CHECK BOX	Indicate whether the sample has been sorted.	Select "YES" when the sample has been sorted and "NO" in the contrary case.		Y	
Sampling comments	TEXT	If necessary, provide comments about sampling.			N	

Donation	CHECK BOX	Indicate whether the sample is a donation.	Select "YES" when the sample has been collected by your own's laboratory staff, "NO" in the contrary case, and "NOT APPLICABLE" when the sample is not stored in your own laboratory (i.e. sampling connected to external biological material).		Y	
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## Appendix 6.1.2 BIOLOGICAL MATERIAL: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Sampling table	LIST OF SELECTION	Select sampling code using the scroll bar.			Y	PM, CM
Biological material code	VARCHAR(255)	Biological material code generated automatically from sampling code and identified species taxa (field: taxa table). See 15.3.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
Biological material date	DATE	Provide sampling date day as DD , MM, YYYY	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
is done by	LIST OF SELECTION	Provide name of person who processed the biological material using the scroll bar.			Y	
is done by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is done by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
is done by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	

is done by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is done by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is done by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
is done by / [Person] Person comments	TEXT	Provide comments if necessary.			N	
Identified species	BUTTON "Add species taxa"	Use this button to add more than one species taxa.				
Identified species / Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	
Identified species / Identification criterion	CHECK BOX	Select the identification criterion			Y	
Identified species / Identification date	DATE	Provide date when the species taxa is identified, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Identified species / Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Identified species / Identified species comments	TEXT	Provide comments if necessary.			N	
Identified species / is identified by	LIST OF SELECTION	Provide name of the person who attributes the species name using the scroll bar.			Y	
Identified species / is identified by	BUTTON "Add person"	Use this button to select more than one person.				

Vision	LIST OF SELECTION	Select eye characteristics using the scroll bar.			Y	
Pigmentation	LIST OF SELECTION	Select pigmentation using the scroll bar.			Y	
Status	CHECK BOX	Indicate whether specimens of the biological material have to be analyzed.	Select "YES" when specimens have to be analyzed and "NO" in the contrary case.		Y	
Sequencing advice	TEXT	If necessary provide guidance for sequencing individual specimens.			N	
Biological material comments	TEXT	If necessary provide comments about the biological material.			N	
Box table	LIST OF SELECTION	Select storing box using the scroll bar.			N	
Composition of biological material	BUTTON "Add composition of biological material"	Use this button to select more than one composition (i.e. specimen type) for the biological material				
Composition of biological material / Number of specimens	INTEGER	Provide number of specimens for a specimen type (see next field)			N	
Composition of biological material / Specimen type	LIST OF SELECTION	Select specimen type using the scroll bar.			Y	
Composition of biological material / Biological material composition comments	TEXT	If necessary provide comments about the composition of the biological material.			N	
is published in	BUTTON "Add source"	Use this button to select one or more than one source (i.e. literature reference) for the biological material				

is published in / Source table		Select source (i.e. literature reference) using the scroll bar			N	
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## Appendix 6.2.2 SPECIMEN: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Biological material table	LIST OF SELECTION	Select biological material code using the scroll bar.			Y	PM, CM
Tube code	VARCHAR(255)	Provide name of the tube containing the specimen.			Y	PM, CM
Specimen morphological code	VARCHAR(255)	Specimen morphological code generated automatically from species taxa (field: taxa table), sampling code and tube code. See 15.5.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
Specimen type	LIST OF SELECTION	Select specimen type using the scroll bar.			Y	
Specimen molecular number	VARCHAR(255)	Provide molecular number of the specimen.			Y	PM, CM. Edit mode but only once the field has been filled in.
Specimen molecular code	VARCHAR(255)	Specimen molecular code generated automatically from species taxa code (field: taxa table), sampling code and specimen molecular number. See 15.6.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM. Edit mode but only once the field has been filled in.
Specimen comments	TEXT	If necessary, provide comments about the specimen.			N	
Identified species	BUTTON "Add species taxa"	Use this button to add more than one species taxa.				
Identified species / Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	

Identified species / Identification criterion	C	Select the identification criterion			Y	
Identified species / Identification date	DATE	Provide date when the species taxa is identified, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Identified species / Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Identified species / Identified species comments	TEXT	Provide comments if necessary.			N	
Identified species / is identified by	LIST OF SELECTION	Provide name of the person who attributes the species name using the scroll bar.			Y	
Identified species / is identified by	BUTTON "Add person"	Use this button to select more than one person.				

### Appendix 6.3.2 SPECIMEN SLIDE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Specimen table	LIST OF SELECTION	Select specimen morphological code using the scroll bar			Y	PM, CM
Collection slide code	VARCHAR(255)	Provide the code for the microscope slide			Y	PM, CM
Slide title	VARCHAR(1024)	Provide title of the microscope slide (text written on the slide)			Y	
Slide date	DATE	Provide date when the slide is mounted as DD MM YYYY.		Error messages if wrong date format	y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Photo folder name	VARCHAR(1024)	Provide name of the folder in which photos of the slide are stored			N	
Slide comments	TEXT	Provide comments about the slide, if necessary.			N	
Box table	LIST OF SELECTION	Select the code of the box in which the slide is stored, using the scroll bar			N	
is mounted by	LIST OF SELECTION	Select the name of the person who mounted the slide.			Y	
is mounted by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is mounted by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				

is mounted by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is mounted by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is mounted by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is mounted by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar.			N	
is mounted by / [Person] Person comments	TEXT	Provide comments if necessary.			N	

## Appendix 6.4.2 EXTERNAL BIOLOGICAL MATERIAL: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Sampling table	LIST OF SELECTION	Select sampling code using the scroll bar.			Y	PM, CM
External biological material code	VARCHAR(255)	External biological material code generated automatically from sampling code and identified species taxa (field: taxa table). See 15.4.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
Pigmentation	LIST OF SELECTION	Select pigmentation using the scroll bar.			Y	
Vision	LIST OF SELECTION	Select eye characteristics using the scroll bar.			Y	
External biological material comments	TEXT	If necessary provide comments about the external biological material.			N	
Number of specimens	LIST OF SELECTION	Select an indication of the number of specimens in the external biological material using the scroll bar.			Y	
Number of specimens comments	TEXT	If necessary provide comments about the number of specimens in the external biological material.			N	
External biological material creation date	DATE	Provide date when the external biological material is processed, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	

is done by	LIST OF SELECTION	Provide name of person who processes the external biological material using the scroll bar.			Y	
is done by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is done by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
is done by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is done by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is done by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is done by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
is done by / [Person] Person comments	TEXT	Provide comments if necessary.			N	
Identified species	BUTTON "Add species taxa"	Use this button to add more than one species taxa.				
Identified species / Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	
Identified species / Identification criterion	CHECK BOX	Select the identification criterion			Y	
Identified species / Identification date	DATE	Provide date when the species taxa is identified, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Identified species / Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	

Identified species / Identified species comments	TEXT	Provide comments if necessary.			N	
Identified species / is identified by	LIST OF SELECTION	Provide name of the person who attributes the species name using the scroll bar.			Y	
Identified species / is identified by	BUTTON "Add person"	Use this button to select more than one person.				
is published in	BUTTON "Add source"	Use this button to select one or more than one source (i.e. literature reference) for the biological material				
is published in / Source table	LIST OF SELECTION	Select source (i.e. literature reference) using the scroll bar			N	

## Appendix 7.1.2 DNA: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Specimen table	LIST OF SELECTION	Select specimen molecular code using the scroll bar.			Y	PM, CM
DNA code	VARCHAR(255)	Provide DNA code			Y	PM, CM
DNA date	DATE	Provide date when DNA is extracted, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	Y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
DNA extraction method	LIST OF SELECTION	Select DNA extraction method using the scroll bar.			Y	
Concentration ng per micro litre	FLOAT	Provide DNA concentration	Expressed in ng per micro litre		N	
DNA comments	TEXT	If necessary, provide comments about the DNA extract			N	
DNA quality	LIST OF SELECTION	Select DNA quality using the scroll bar.			N	
Box table	LIST OF SELECTION	Select DNA storing box using the scroll bar.			N	
is extracted by	LIST OF SELECTION	Provide name of person who extracted DNA using the scroll bar.			Y	
is extracted by	BUTTON "Add person"	Use this BUTTON to select more than one person.				

is extracted by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
is extracted by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is extracted by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is extracted by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is extracted by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar.			N	
is extracted by / [Person] Person comments	TEXT	Provide comments if necessary.			N	

## Appendix 7.2.2 PCR: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
DNA table	LIST OF SELECTION	Select DNA code using the scroll bar.			Y	PM, CM
PCR code	VARCHAR(255)	PCR code generated automatically from DNA code, PCR number, forward primer and reverse primer. See 15.7.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
PCR number	VARCHAR(255)	Provide PCR number.			Y	PM, CM
Gene	LIST OF SELECTION	Select gene using the scroll bar.			Y	
PCR forward primer	LIST OF SELECTION	Select forward primer using the scroll bar.			Y	PM, CM
PCR reverse primer	LIST OF SELECTION	Select reverse primer using the scroll bar.			Y	PM, CM
PCR date	DATE	Provide date when PCR is performed as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	Y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
PCR quality	LIST OF SELECTION	Select PCR quality using the scroll bar.			Y	
PCR specificity	LIST OF SELECTION	Select PCR specificity using the scroll bar.			Y	
PCR details	TEXT	Provide PCR details, if any.			N	
PCR comments	TEXT	Provide comments about the PCR, if necessary.			N	
PCR is done by	LIST OF SELECTION	Provide name of person who performed the PCR, using the scroll bar.			Y	
PCR is done by	BUTTON "Add person"	Use this BUTTON to select more than one person.				

PCR is done by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
PCR is done by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
PCR is done by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
PCR is done by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
PCR is done by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
PCR is done by / [Person] Person comments	TEXT	Provide comments if necessary.			N	

### Appendix 7.3.2 CHROMATOGRAM: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
PCR table	LIST OF SELECTION	Select PCR code using the scroll bar.			Y	PM, CM
Chromatogram code	VARCHAR(255)	Chromatogram code generated automatically from YAS number (i.e. chromatogram number) and chromatogram primer. See 15.8.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
YAS number	VARCHAR(255)	Provide YAS number (i.e. chromatogram number).			Y	PM, CM
Chromatogram primer	LIST OF SELECTION	Select chromatogram primer using the scroll bar.			Y	PM, CM
Chromatogram quality	LIST OF SELECTION	Select chromatogram quality using the scroll bar.			Y	
Institution table	LIST OF SELECTION	Select institution which performs sequencing using the scroll bar			Y	
Chromatogram comments	TEXT	Provide comments about the chromatogram, if necessary.			N	

## Appendix 8.1.2 INTERNAL SEQUENCE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Gene	LIST OF SELECTION	Select gene using the scroll bar.			Y	PM, CM
Specimen table	LIST OF SELECTION	Select specimen molecular code using the scroll bar.			Y	PM, CM
Sequence code	VARCHAR(1024)	Sequence code generated automatically from sequence status, specimen molecular code (i.e. field: specimen table), and chromatogram code   Specificity. See 15.9.	Code automatically generated only once at creation (not in editing mode).		Y	CM
Sequence accession number	VARCHAR(255)	Provide accession number for the internal sequence, if any.			N	
Sequence alignment code	VARCHAR(1024)	Sequence alignment code generated automatically from sequence status, species taxa code (i.e. field: taxa table), sampling code (i.e. field: sampling table in appendix 6.1.2), specimen molecular number (in appendix 6.2.2), and chromatogram code   Specificity. See 15.10.	Code automatically generated only once at creation (not in editing mode).		Y	
Sequence comments	TEXT	Provide comments about the internal sequence, if necessary.			N	
Sequence creation date	DATE	Provide date when internal sequence is generated, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not	Error messages if precision does not correspond to sampling date.	Y	

			known: all date fields left blank.			
Sequence status	LIST OF SELECTION	Provide sequence status using the scroll bar.			Y	CM
is assembled	BUTTON "Add chromatogram"	Use this button to select more than one Chromatogram code   Specificity.				
is assembled / Chromatogram code   Specificity	LIST OF SELECTION	Provide Chromatogram code   Specificity using the scroll bar.			Y	CM
is generated by	LIST OF SELECTION	Provide name of person who performed the PCR, using the scroll bar.			Y	
is generated by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is generated by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person]				
is generated by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is generated by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is generated by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is generated by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
PCR is done by / [Person] Person comments	TEXT	Provide comments if necessary.			N	

Identified species	BUTTON "Add species taxa"	Use this button to add more than one species taxa.				
Identified species / Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	
Identified species / Identification criterion	CHECK BOX	Select the identification criterion			Y	
Identified species / Identification date	DATE	Provide date when the species taxa is identified, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	Y	
Identified species / Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Identified species / Identified species comments	TEXT	Provide comments if necessary.			N	
Identified species / is identified by	LIST OF SELECTION	Provide name of the person who attributes the species name using the scroll bar.			Y	
Identified species / is identified by	BUTTON "Add person"	Use this button to select more than one person.				
is published in	BUTTON "Add source"	Use this button to select one or more than one source (i.e. literature reference) for the biological material				
is published in / Source table		Select source (i.e. literature reference) using the scroll bar			N	

## Appendix 8.2.2 EXTERNAL SEQUENCE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Sampling table	LIST OF SELECTION	Select sampling code using the scroll bar.			Y	PM, CM
External sequence code	VARCHAR(1024)	External sequence code generated automatically from sequence status, species taxa code (i.e. field: taxa table), sampling code (i.e. field: sampling table), external sequence specimen number, external sequence accession number and external sequence origin. See 15.11.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
External sequence alignment code	VARCHAR(1024)	External sequence alignment code generated automatically from sequence status, species taxa code (i.e. field: taxa table), sampling code (i.e. field: sampling table), external sequence specimen number, external sequence accession number and external sequence origin. See 15.12.	Code automatically generated only once at creation (not in editing mode).		Y	PM, CM
External sequence accession number	VARCHAR(255)	Provide accession number for the internal sequence, if any.			N	PM, CM
External sequence specimen number	VARCHAR(255)	Provide specimen number for the external sequence.	Write "0" if not known		Y	PM, CM
External sequence primary taxon	VARCHAR(255)	Provide original species taxa name attributed to the sequence in the literature.			N	
External sequence origin	LIST OF SELECTION	Select origin of the sequence using the scroll bar.			Y	PM, CM
Gene	LIST OF SELECTION	Select gene using the scroll bar.			Y	
Sequence status	LIST OF SELECTION	Select sequence status using the scroll bar.			Y	PM, CM
External sequence creation date	DATE	Provide date when internal sequence is generated, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	

Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
External sequence comments	TEXT	Provide comments about the external sequence, if necessary.			N	
is integrated by	LIST OF SELECTION	Provide name of person who entered the data using the scroll bar.			Y	
is integrated by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is integrated by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal [Person].				
is integrated by / [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is integrated by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is integrated by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is integrated by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
is integrated by / [Person] Person comments	TEXT	Provide comments if necessary.			N	
Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	
Identification criterion	CHECK BOX	Select the identification criterion.			Y	
Identification date	DATE	Provide date when internal sequence is generated, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	

Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Identified species	BUTTON "Add species taxa"	Use this button to add more than one species taxa.				
Identified species / Taxa table	LIST OF SELECTION	Select species taxa using the scroll bar.			Y	
Identified species / Identification criterion	CHECK BOX	Select the identification criterion			Y	
Identified species / Identification date	DATE	Provide date when the species taxa is identified, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
Identified species / Date precision	CHECK BOX	Provide date precision by selecting either day, month, year or not known.	day: DD/MM/YYYY; month: 01/MM/YYYY. year: 01/01/YYYY; not known: all date fields left blank.	Error messages if precision does not correspond to sampling date.	Y	
Identified species / Identified species comments	TEXT	Provide comments if necessary.			N	
Identified species / is identified by	LIST OF SELECTION	Provide name of the person who attributes the species name using the scroll bar.			Y	
Identified species / is identified by	BUTTON "Add person"	Use this button to select more than one person.				
is published in/ Source table	LIST OF SELECTION	Select source (i.e. literature reference) using the scroll bar.			N	

### Appendix 8.3.2 MOTU: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
csv file name	VARCHAR(255)	Provide name of the MOTU csv file containing the MOTU data set to be imported.			Y	The whole form is not accessible to PM and CM
MOTU title	VARCHAR(255)	Provide title for the MOTU data set.			Y	
MOTU date	DATE	Provide date when the MOTU data are generated, as DD MM YYYY.	DD = [ 1 to 31] MM = [1 to 12] YYYY = [1000 to 2999]	Error messages if wrong date format	y	
MOTU comments	TEXT	Provide comments if necessary.			N	
is generated by	LIST OF SELECTION	Provide name of person who generated the MOTU data set using the scroll bar.			Y	
is generated by	BUTTON “Add person”	Use this BUTTON to select more than one person.				
is generated by	BUTTON “Add new person”	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal “Person”.				
Provide name and initials of the person.	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
is generated by / [Person] Person name	VARCHAR(1024)	Provide full name of the person	Capitals	Write CLINTON BILL	N	
is generated by / [Person] Person name	VARCHAR(255)	Provide second name of person (in any)	Capitals		N	
is generated by / [Person] Person name	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar	Capitals		N	



## Appendix 9.1.2 BOX BIOLOGICAL MATERIAL: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Box code	VARCHAR(255)	Provide code for the box.	Begin with "LOT_", do not include space (e.g. LOT_Pcav1). Code must be unique.		Y	PM, CM
Box title	VARCHAR(255)	Provide name for the box.	Title must be unique.		Y	
Box comments	TEXT	Provide comments about the box, if necessary.			N	
Collection type	LIST OF SELECTION	Select collection type (i.e. LOT) using the scroll bar.			Y	
Collection code	LIST OF SELECTION	Select collection code using the scroll bar.			Y	
Box type	LIST OF SELECTION	Selection list is fixed (see note).		Selection list is fixed to LOT for biological material, LAME for specimen slide and ADN for DNA extract.	Y	
Biological material	FIELD NOT MODIFIABLE	Show biological material codes of biological materials stored in a box.		Mode show and edit only.		

## Appendix 9.2.2 BOX SPECIMEN SLIDE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Box code	VARCHAR(255)	Provide code for the box.	Begin with "LAM_", do not include space (e.g. LAM_14). Code must be unique.		Y	PM, CM
Box title	VARCHAR(255)	Provide name for the box.	Title must be unique.		Y	
Box comments	TEXT	Provide comments about the box, if necessary.			N	
Collection type	LIST OF SELECTION	Select collection type (i.e. SLIDE) using the scroll bar.			Y	
Collection code	LIST OF SELECTION	Select collection code using the scroll bar.			Y	
Box type	LIST OF SELECTION	Selection list is fixed (see note).		Selection list is fixed to LOT for biological material, LAME for specimen slide and ADN for DNA extract.	Y	
Specimen slide	FIELD NOT MODIFIABLE	Show collection slide code of a specimen slide stored in a box.		Mode show and edit only.		

### Appendix 9.3.2 BOX DNA: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Box code	VARCHAR(255)	Provide code for the box.	Begin with "ADN_", do not include space (e.g. ADN_CA1). Code must be unique.		Y	PM, CM
Box title	VARCHAR(255)	Provide name for the box.	Title must be unique.		Y	
Box comments	TEXT	Provide comments about the box, if necessary.			N	
Collection type	LIST OF SELECTION	Select collection type (i.e. DNA) using the scroll bar.			Y	
Collection code	LIST OF SELECTION	Select collection code using the scroll bar.			Y	
Box type	LIST OF SELECTION	Selection list is fixed (see note).		Selection list is fixed to LOT for biological material, LAME for specimen slide and ADN for DNA extract.	Y	
DNA	FIELD NOT MODIFIABLE	Show DNA code of DNA extracts stored in a box.		Mode show and edit only.		

## Appendix 10.2 SOURCE: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Source code	VARCHAR(255)	Provide reference source code.	Write as follows (with no space): Dole_Olivier_et_al_2009 _Freshwat_Biol_54_4_7 97_813.		Y	PM, CM
Source year	INTEGER	Provide publication year for the reference source.			N	
Source title	VARCHAR(255)	Provide full description of the reference source.	Write as follows: Dole Olivier M.J., Malard F., Martin D., Lefebure T., Gibert J. 2009. Relationships between environmental variables and groundwater biodiversity at the regional scale. Freshwater Biology, 54(4), 797-813.		Y	
Source comments	TEXT(2048)	Provide comments about the reference source if necessary.			N	
is integrated by	LIST OF SELECTION	Provide name of person who entered the reference source using the scroll bar.			Y	
is integrated by	BUTTON "Add person"	Use this BUTTON to select more than one person.				
is integrated by	BUTTON "Add new person"	Use this BUTTON to create a new person (not yet in the list of persons). Open a modal "Person".				
is integrated by [Person] Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	

is integrated by / [Person] Person full name	VARCHAR(1024)	Provide full name of the person.	Capitals	Write CLINTON BILL	N	
is integrated by / [Person] Person name bis	VARCHAR(255)	Provide second name of person (in any).	Capitals		N	
is integrated by / [Person] Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar			N	
is integrated by / [Person] Person comments	TEXT	Provide comments if necessary.			N	

## Appendix 11.1.2 VOCABULARY: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Code	VARCHAR(255)	Provide code for the vocabulary.			Y	
Title	VARCHAR(2014)	Provide title for the vocabulary.			Y	
Parent	LIST OF SELECTION	Provide the parent to which the vocabulary belongs to.		Titles of parents are defined in dictionaries (see files messages.fr.yml [French] and messages.en.yml [English])	Y	
Comments	TEXT	Provide comments if necessary.			N	

## Appendix 11.2.2 TAXON: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Taxon name	VARCHAR(255)	Provide name of species taxa	Capitals, no space (e.g. ASELLUS_AQUATICUS_C AVERNICOLUS). Must be unique.		Y	
Taxon rank	VARCHAR(255)	Provide taxonomic rank	Capitals. See list. NA stands for not applicable		Y	
Subclass	VARCHAR(255)	Provide Subclass	Capitals.		N	
Order	VARCHAR(255)	Provide Order	Capitals.		N	
Family	VARCHAR(255)	Provide Family	Capitals.		N	
Genus	VARCHAR(255)	Provide Genus	Capitals.		N	
Species	VARCHAR(255)	Provide Species	Capitals.		N	
Subspecies	VARCHAR(255)	Provide Subspecies	Capitals.		N	
Taxon code	VARCHAR(255)	Provide abbreviated taxon code	No space. Must be unique.		Y	
Clade	VARCHAR(255)	Provide clade to which the species taxa belongs			N	
Taxon name synonym	VARCHAR(255)	Provide species taxa synonym, if any			N	
Taxon validity	CHECK BOX	Indicate whether species name is valid (yes) or not valid (no)			Y	
Taxon comments	TEXT	Provide comments if necessary.			N	

### **Appendix 11.3.2 PERSON: Create, show, edit**

<b>Section / Field label</b>	<b>Content type</b>	<b>Description</b>	<b>Rules</b>	<b>Note</b>	<b>Compulsory</b>	<b>Restriction</b>
Person name	VARCHAR(255)	Provide name and initials of the person.	Capitals	Write CLINTON B	Y	
Person full name	VARCHAR(1024)	Provide full name of the person.	Capitals	Write CLINTON BILL	N	
Person name bis	VARCHAR(255)	Provide second name of person (in any).	Capitals		N	
Institution table	LIST OF SELECTION	Provide name of institution to which the person belongs using the scroll bar.			N	
Person comments	TEXT	Provide comments if necessary.			N	

#### Appendix 11.4.2 PROGRAM: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Program code	VARCHAR(255)	Provide code of funding program.	Capitals		Y	
Program name	VARCHAR(1024)	Provide name of funding program.			Y	
Program coordinator	TEXT	Provide the name(s) of coordinator(s) of funding program.	Capitals	Write as follows: CLINTON B or CLINTON B \$ OBAMA B H when more than one coordinator	Y	
Funding agency	VARCHAR(1024)	Provide name or code of funding agency for the funding program.	Capitals		N	
Starting year	INTEGER	Provide starting year of funding program.	YYYY		N	
Ending year	INTEGER	Provide ending year of funding program.	YYYY		N	
Program comments	TEXT	Provide comments about the program if necessary.			N	

## **Appendix 11.5.2 INSTITUTION: Create, show, edit**

<b>Section / Field label</b>	<b>Content type</b>	<b>Description</b>	<b>Rules</b>	<b>Note</b>	<b>Compulsory</b>	<b>Restriction</b>
Institution name	VARCHAR(1024)	Provide institution name.	Capitals		Y	
Institution comments	TEXT	Provide comments (e.g. Institution address), if necessary			N	

## Appendix 11.6.2 COUNTRY: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Country code	VARCHAR(255)	Country code automatically generated. See 15.14.		Code automatically generated. Same as Country name but spaces are replaced by _ (e.g. ANTIGUA_AND_BARBUDA).	Y	
Country name	VARCHAR(1024)	Provide country name.	Capitals		Y	

## Appendix 11.7.2 MUNICIPALITY: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Municipality code	VARCHAR(255)	Municipality code generated automatically from municipality name, region name and country table. See 15.13.			Y	
Municipality name	VARCHAR(1024)	Provide name of municipality	Capitals		Y	
Region name	VARCHAR(1024)	Provide name of region	Capitals.		Y	
Country table	LIST OF SELECTION	Select country using the scroll bar.				

## Appendix 14.2.1 PROJECT MEMBER: rights

\* CRUD: A user can “create, read, update, delete” data

\*\* crud: A user can “create, read, update, delete” data but only those data that he created.

Section	Sub-section	Level 1	Level 2	Rights	Field restriction (edit mode)
Field data	Site	Form	General	CRUD	Site code
Field data	Site	Import new set of sites	General	YES	
Field data	Site	Import new set of sites	Site	YES	
Field data	Site	Import new set of sites	Country	NO	
Field data	Site	Import new set of sites	Vocabulary	NO	
Field data	Sampling	Form	General	CRUD	Site code, Sampling code, Sampling date
Field data	Sampling	Import new set of sampling	General	YES	
Field data	Sampling	Import new set of sampling	Sampling	YES	
Field data	Sampling	Import new set of sampling	Program	YES	
Field data	Sampling	Import new set of sampling	Person	YES	
Field data	Sampling	Import new set of sampling	Taxon	NO	
Field data	Sampling	Import new set of sampling	Vocabulary	NO	
Morphol. analysis	Biological material	Form	General	CRUD	Sampling, Biological material code
Morphol. analysis	Biological material	Import new set of biological material	General	YES	
Morphol. analysis	Biological material	Import new set of biological material	Internal_biological_material	YES	
Morphol. analysis	Biological material	Import new set of biological material	Box	YES	
Morphol. analysis	Biological material	Import new set of biological material	Taxon	NO	
Morphol. analysis	Biological material	Import new set of biological material	Vocabulary	NO	
Morphol. analysis	Biological material	Import new set of biological material	Person	YES	
Morphol. analysis	Biological material	Import new set of biological material	Source	YES	

Morphol. analysis	Specimen	Form	General	CRUD	Internal Biological material, Specimen morphological code, Tube code, Specimen molecular code*, Specimen molecular number* (* only once the field has been filled in).
Morphol. analysis	Specimen	Import new set of specimens	General	YES	
Morphol. analysis	Specimen	Import new set of specimens	Specimen	YES	
Morphol. analysis	Specimen	Import new set of specimens	Taxon	NO	
Morphol. analysis	Specimen	Import new set of specimens	Vocabulary	NO	
Morphol. analysis	Specimen	Import new set of specimens	Person	YES	
Morphol. analysis	Specimen slide	Form	General	YES	Specimen, Slide title
Morphol. analysis	Specimen slide	Import new set of slides	General	YES	
Morphol. analysis	Specimen slide	Import new set of slides	Specimen_slide	YES	
Morphol. analysis	Specimen slide	Import new set of slides	Box	YES	
Morphol. analysis	Specimen slide	Import new set of slides	Vocabulary	NO	
Morphol. analysis	Specimen slide	Import new set of slides	Person	YES	
Morphol. analysis	Ext biological material	Form	General	CRUD	Sampling, External biological material code
Morphol. analysis	Ext biological material	Import new set of ext biological material	General	YES	
Morphol. analysis	Ext biological material	Import new set of ext biological material	external_biological_material	YES	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Source	YES	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Taxon	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Vocabulary	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Person	YES	
Molecular analysis	DNA	Form	General	CRUD	Specimen, DNA code
Molecular analysis	DNA	Import new set of DNA	General	YES	
Molecular analysis	DNA	Import new set of DNA	DNA	YES	
Molecular analysis	DNA	Import new set of DNA	Box	YES	

Molecular analysis	DNA	Import new set of DNA	Vocabulary	NO	
Molecular analysis	DNA	Import new set of DNA	Person	YES	
Molecular analysis	PCR	Form	General	CRUD	DNA, PCR code, PCR number, PCR forward primer, PCR reverse primer
Molecular analysis	PCR	Import new set of PCR	General	YES	
Molecular analysis	PCR	Import new set of PCR	PCR	YES	
Molecular analysis	PCR	Import new set of PCR	Vocabulary	NO	
Molecular analysis	PCR	Import new set of PCR	Person	YES	
Molecular analysis	Chromatogram	Form	General	CRUD	PCR, Chromatogram code, YAS number, Chromatogram primer
Molecular analysis	Chromatogram	Import new set of chromatograms	General	YES	
Molecular analysis	Chromatogram	Import new set of chromatograms	chromatogram	YES	
Molecular analysis	Chromatogram	Import new set of chromatograms	Institution	YES	
Molecular analysis	Chromatogram	Import new set of chromatograms	Vocabulary	NO	
Molecular analysis	Chromatogram	Import new set of chromatograms	Person	YES	
DNA Sequence	Internal sequence	Form	General	CRUD	Gene, Specimen
DNA Sequence	Internal sequence	Import new set of sequences	General	YES	
DNA Sequence	Internal sequence	Import new set of sequences	internal_sequence	YES	
DNA Sequence	Internal sequence	Import new set of sequences	Source	YES	
DNA Sequence	Internal sequence	Import new set of sequences	Vocabulary	NO	
DNA Sequence	Internal sequence	Import new set of sequences	Person	YES	
DNA Sequence	Internal sequence	Import new set of sequences	Taxon	NO	

DNA Sequence	External sequence	Form	General	CRUD	Sampling, External sequence code, External sequence alignment code, External sequence accession number, External sequence specimen number, External sequence origin, Sequence status
DNA Sequence	External sequence	Import new set of external sequences	General	YES	
DNA Sequence	External sequence	Import new set of external sequences	external_sequence	YES	
DNA Sequence	External sequence	Import new set of external sequences	Source	YES	
DNA Sequence	External sequence	Import new set of external sequences	Vocabulary	NO	
DNA Sequence	External sequence	Import new set of external sequences	Person	YES	
DNA Sequence	External sequence	Import new set of external sequences	Taxon	NO	
DNA Sequence	MOTU	Form	General	Read only	
DNA Sequence	MOTU	Import new set of MOTU	General	Read only	
Storage	Biological material	Form	General	CRUD	Box code
Storage	Biological material	Store biological material as file	biological_material_store	YES	
Storage	Biological material	Move or delete biological material as file	biological_material_move	NO	
Storage	Specimen slide	Form	General	CRUD	Box code
Storage	Specimen slide	Store slides as file	slide_store	YES	
Storage	Specimen slide	Move or delete slides as file	slide_move	NO	
Storage	DNA	Form	General	CRUD	Box code
Storage	DNA	Store DNA boxes as file	DNA_store	YES	
Storage	DNA	Move or delete DNA boxes as file	DNA_move	NO	
Source	Source	Form	General	CRUD	Source code
Source	Source	Import new set of sources	Source	YES	
Source	Source	Import new set of sources	Person	YES	

Source	Source	Source to biological material as file	source_attribute_to_lot	YES	
Source	Source	Source to biological material as file	Person	YES	
Source	Source	Source to biological material as file	Source	YES	
Source	Source	Source to sequence as file	source_attribute_to_sequence	YES	
Source	Source	Source to sequence as file	Person	YES	
Source	Source	Source to sequence as file	Source	YES	
Repositories	Repositories	Vocabulary	General	NO	
Repositories	Repositories	Taxon	General	NO	
Repositories	Repositories	Person	General	YES	
Repositories	Repositories	Program	General	YES	
Repositories	Repositories	Institution	General	YES	
Repositories	Repositories	Country	General	NO	
Repositories	Repositories	Municipality	General	NO	
Species search	COI data set	COI data set	General	YES	
Species search	MOTU	MOTU	General	YES	
Species search	Species hypotheses	Species hypotheses	General	YES	
Species search	Distribution data	Distribution data	General	YES	
Species search	Species names	Species names	General	YES	

## Appendix 14.2.2 COLLABORATOR: rights

\* CRUD: A user can “create, read, update, delete” data

\*\* crud: A user can “create, read, update, delete” data but only those data that he created.

Section	Sub-section	Level 1	Level 2	Rights	Field restriction (edit mode)
Field data	Site	Form	General	crud	Site code
Field data	Site	Import new set of sites	General	NO	
Field data	Site	Import new set of sites	Site	NO	
Field data	Site	Import new set of sites	Country	NO	
Field data	Site	Import new set of sites	Vocabulary	NO	
Field data	Sampling	Form	General	crud	Site code, Sampling code, Sampling date
Field data	Sampling	Import new set of sampling	General	NO	
Field data	Sampling	Import new set of sampling	Sampling	NO	
Field data	Sampling	Import new set of sampling	Program	NO	
Field data	Sampling	Import new set of sampling	Person	NO	
Field data	Sampling	Import new set of sampling	Taxon	NO	
Field data	Sampling	Import new set of sampling	Vocabulary	NO	
Morphol. analysis	Biological material	Form	General	crud	Sampling, Biological material code
Morphol. analysis	Biological material	Import new set of biological material	General	NO	
Morphol. analysis	Biological material	Import new set of biological material	Internal_biological_material	NO	
Morphol. analysis	Biological material	Import new set of biological material	Box	NO	
Morphol. analysis	Biological material	Import new set of biological material	Taxon	NO	
Morphol. analysis	Biological material	Import new set of biological material	Vocabulary	NO	
Morphol. analysis	Biological material	Import new set of biological material	Person	NO	
Morphol. analysis	Biological material	Import new set of biological material	Source	NO	

Morphol. analysis	Specimen	Form	General	crud	Internal Biological material, Specimen morphological code, Tube code, Specimen molecular code*, Specimen molecular number* (* only once the field has been filled in).
Morphol. analysis	Specimen	Import new set of specimens	General	NO	
Morphol. analysis	Specimen	Import new set of specimens	Specimen	NO	
Morphol. analysis	Specimen	Import new set of specimens	Taxon	NO	
Morphol. analysis	Specimen	Import new set of specimens	Vocabulary	NO	
Morphol. analysis	Specimen	Import new set of specimens	Person	NO	
Morphol. analysis	Specimen slide	Form	General	crud	Specimen, Slide title
Morphol. analysis	Specimen slide	Import new set of slides	General	NO	
Morphol. analysis	Specimen slide	Import new set of slides	Specimen_slide	NO	
Morphol. analysis	Specimen slide	Import new set of slides	Box	NO	
Morphol. analysis	Specimen slide	Import new set of slides	Vocabulary	NO	
Morphol. analysis	Specimen slide	Import new set of slides	Person	NO	
Morphol. analysis	Ext biological material	Form	General	crud	Sampling, External biological material code
Morphol. analysis	Ext biological material	Import new set of ext biological material	General	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	external_biological_material	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Source	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Taxon	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Vocabulary	NO	
Morphol. analysis	Ext biological material	Import new set of ext biological material	Person	NO	
Molecular analysis	DNA	Form	General	crud	Specimen, DNA code
Molecular analysis	DNA	Import new set of DNA	General	YES	
Molecular analysis	DNA	Import new set of DNA	DNA	YES	
Molecular analysis	DNA	Import new set of DNA	Box	NO	

Molecular analysis	DNA	Import new set of DNA	Vocabulary	NO	
Molecular analysis	DNA	Import new set of DNA	Person	YES	
Molecular analysis	PCR	Form	General	crud	DNA, PCR code, PCR number, PCR forward primer, PCR reverse primer
Molecular analysis	PCR	Import new set of PCR	General	YES	
Molecular analysis	PCR	Import new set of PCR	PCR	YES	
Molecular analysis	PCR	Import new set of PCR	Vocabulary	NO	
Molecular analysis	PCR	Import new set of PCR	Person	YES	
Molecular analysis	Chromatogram	Form	General	crud	PCR, Chromatogram code, YAS number, Chromatogram primer
Molecular analysis	Chromatogram	Import new set of chromatograms	General	YES	
Molecular analysis	Chromatogram	Import new set of chromatograms	chromatogram	YES	
Molecular analysis	Chromatogram	Import new set of chromatograms	Institution	NO	
Molecular analysis	Chromatogram	Import new set of chromatograms	Vocabulary	NO	
Molecular analysis	Chromatogram	Import new set of chromatograms	Person	YES	
DNA Sequence	Internal sequence	Form	General	crud	Gene, Specimen, Sequence code, Sequence alignment code, Sequence status, Chromatogram code   Specificity
DNA Sequence	Internal sequence	Import new set of sequences	General	YES	
DNA Sequence	Internal sequence	Import new set of sequences	internal_sequence	YES	
DNA Sequence	Internal sequence	Import new set of sequences	Source	NO	
DNA Sequence	Internal sequence	Import new set of sequences	Vocabulary	NO	
DNA Sequence	Internal sequence	Import new set of sequences	Person	YES	
DNA Sequence	Internal sequence	Import new set of sequences	Taxon	NO	

DNA Sequence	External sequence	Form	General	crud	Sampling, External sequence code, External sequence alignment code, External sequence accession number, External sequence specimen number, External sequence origin, Sequence status
DNA Sequence	External sequence	Import new set of external sequences	General	YES	
DNA Sequence	External sequence	Import new set of external sequences	external_sequence	YES	
DNA Sequence	External sequence	Import new set of external sequences	Source	NO	
DNA Sequence	External sequence	Import new set of external sequences	Vocabulary	NO	
DNA Sequence	External sequence	Import new set of external sequences	Person	YES	
DNA Sequence	External sequence	Import new set of external sequences	Taxon	NO	
DNA Sequence	MOTU	Form	General	Read only	
DNA Sequence	MOTU	Import new set of MOTU	General	Read only	
Storage	Biological material	Form	General	crud	Box code
Storage	Biological material	Store biological material as file	biological_material_store	YES	
Storage	Biological material	Move or delete biological material as file	biological_material_move	NO	
Storage	Specimen slide	Form	General	crud	Box code
Storage	Specimen slide	Store slides as file	slide_store	YES	
Storage	Specimen slide	Move or delete slides as file	slide_move	NO	
Storage	DNA	Form	General	crud	Box code
Storage	DNA	Store DNA boxes as file	DNA_store	YES	
Storage	DNA	Move or delete DNA boxes as file	DNA_move	NO	
Source	Source	Form	General	crud	Source code
Source	Source	Import new set of sources	Source	NO	
Source	Source	Import new set of sources	Person	YES	
Source	Source	Source to biological material as file	source_attribute_to_lot	YES	
Source	Source	Source to biological material as file	Person	YES	

Source	Source	Source to biological material as file	Source	NO	
Source	Source	Source to sequence as file	source_attribute_to_sequence	YES	
Source	Source	Source to sequence as file	Person	YES	
Source	Source	Source to sequence as file	Source	NO	
Repositories	Repositories	Vocabulary	General	NO	
Repositories	Repositories	Taxon	General	NO	
Repositories	Repositories	Person	General	YES	
Repositories	Repositories	Program	General	NO	
Repositories	Repositories	Institution	General	NO	
Repositories	Repositories	Country	General	NO	
Repositories	Repositories	Municipality	General	NO	
Species search	COI data set	COI data set	General	YES	
Species search	MOTU	MOTU	General	YES	
Species search	Species hypotheses	Species hypotheses	General	YES	
Species search	Distribution data	Distribution data	General	YES	
Species search	Species names	Species names	General	YES	

### Appendix 14.3.1 USER ACCOUNT: Create, show, edit

Section / Field label	Content type	Description	Rules	Note	Compulsory	Restriction
Username	VARCHAR(255)	Provide user name			Y	
Password (8 char min)	VARCHAR(255)	Provide password	Minimum 8 characters, maximum 50 characters		Y	
Repeat Password	VARCHAR(255)	Confirm password	Minimum 8 characters, maximum 50 characters		Y	
Email address	VARCHAR(255)	Provide e-mail address			N	
User full name	VARCHAR(255)	Provide user full name			Y	
Institution	VARCHAR(1024)	Provide institution name for the user			N	
Role	CHECK BOX	Select the type of account to be opened for a user: ADMIN, PROJECT, COLLABORATION, INVITED, LOCKED.	See section 14.2. in GOTIT HELP for details of functionalities offered to different user types.		Y	
Version	CHECK BOX	Default version (i.e. French or English) for the interface			Y	
User comment	TEXT	If necessary, provide further details about the user.			N	