# Import DaRWIN

1 HOW IT WORKS

The principle is to convert data into a pre-established structured data format, allowing mapping between the original data and DaRWIN fields.

The import is done in three parts:

- Import of taxonomy : import missing taxons in DaRWIN (optional - maybe created during import, but if many taxons are missing, can be time consuming)

- Import of localities : import missing sampling localities in DaRWIN, using an unique code

- Import of specimens

DaRWIN import tool reads "tab-delimited" files, that can be created from Excel/Calc.

To allow the link between the 3 templates, the system uses the scientific name (taxon) of the specimen and the code of the station. When a specimen is imported, it will be subsequently linked to its taxon and sampling locality pre-existing or previously imported.
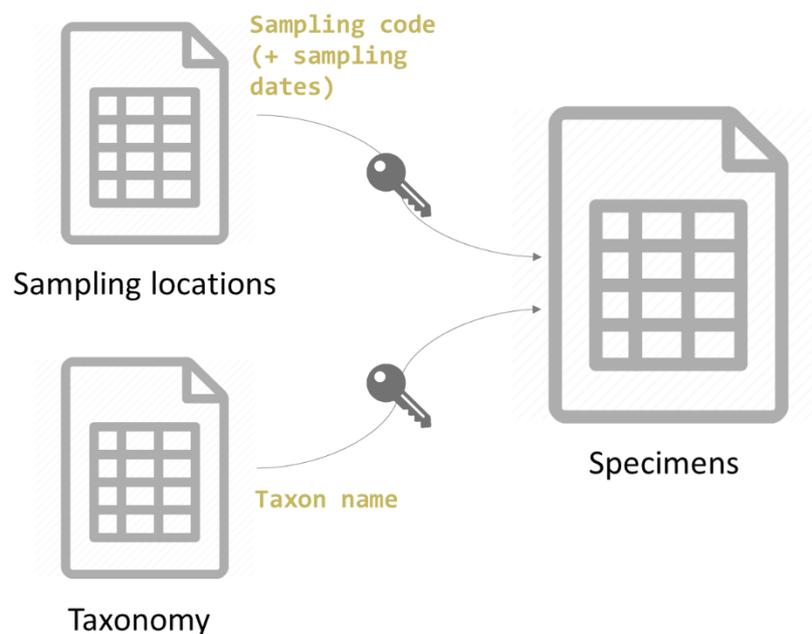
2 TAXONOMY IMPORT

2.1 PRELIMINARY INFORMATION

WARNING ! Intra-data problems: half of corrections after import originates from **errors in original file**. Import has to be prepared with care. Errors in the file will be imported…

→ Examples and consequences:

- Different hierarchy within a file => *duplicated taxon with different hierarchy* (can have sense if really different, but not if only some levels are missing like sub and supra levels)

- Misspelling => *duplicated taxon*

- Taxon in the wrong level (wrong column) => *bad hierarchy*

- Vernacular names used in higher levels taxonomy => *bad taxon and bad hierarchy*

This kind of errors has consequences for import: if taxon is not unique, it will not be automatically recognized. During an import, when a specimen is linked to a taxon for which duplicates exist in Darwin, taxonomy cannot be automatically attributed. Human action is therefore needed to select which taxon is correct.

What if duplicates can have a scientific basis?

They need to be considered in the database.

Solution: parallel taxonomies

Two types:

- **Reference taxonomy: one taxon is only present once**

  = combination name + author + level is unique in all reference taxonomic levels

- **Non-reference:** if you need a parallel taxonomical hierarchy (historical data to store with historical taxon name, temporary taxonomy, user-based taxonomy, etc); can store duplicates

=> Possibility to group taxa in a specific named hierarchy

New specimens imported by Excel (CSV/TXT) can be compared with all, one or several taxonomies.

2.2 STEP 1: PREPARE YOUR FILE

You should prepare a file with the list of taxa that are missing in DaRWIN and should be imported. To do so, you first need to know what already exist in DaRWIN and then, what is missing and need to be imported. The missing taxa should be stored in a tab-delimited file, for import.

2.2.1 Check taxonomy

A tool for checking taxonomy is available here:
http://nautilus.rbins.be/natural_heritage_webservice/taxonomy/

Technical information on how to format file are available here:

Mail field to allow mail alert is not yet available.

You can upload a tab-delimited file with taxon names from the file you wish to import, following the structure below:

scientificName	kingdom	phylum	order	family
Mandatory	Optional	Optional	Optional	Optional
Name you wish to check	Used to focus on a group of taxon (allows to avoid homonyms in groups that don't interest you			

You can check on what catalogue you wish to validate your taxonomy.

This tool will help you to know what is in DaRWIN and with which taxonomical hierarchy, and to complete missing taxonomical trees with the system of your choice (GBIF, IUCN, WoRMS).

It is also possible to use the tool available on GBIF website (https://www.gbif.org/tools/species-lookup) or on WoRMS website (http://www.marinespecies.org/aphia.php?p=match).

2.2.2 Import missing taxonomy

The file has to be saved in tab-delimited format (*.txt).

The list of fields for taxonomy import file is available in Annex 1.

Please, use the exact same spelling.

The final file for import should contain all missing taxa that you wish to load in DaRWIN. Each line therefore contains all missing levels and the lower known parent in DaRWIN. Example: you wish to import a new species name. If the genus already exists in DaRWIN, you only need to mention this genus in your file. If you want, you can add all higher levels, but it is not necessary.

A name that is already present in DaRWIN, and also present in import file with the exact same form will be recognized by the system during import and will not be imported. On the contrary, a new name will be imported if a parent if in the file. If you aim to match an existing taxonomical tree in DaRWIN, to connect a new sub-tree by import, you have to refer to the exact same names to ensure the matching between DaRWIN and import.

Example 1 : "Alligatoridae Cuvier" exists in DaRWIN – reference Taxonomy. If you use "Alligatoridae" in your file, it will not be recognized, and nothing will be imported.

Example 2 : if you use "Alligatoridae Cuvier" as family and "Melanosuchus" as genus in your file for import in reference taxonomy, "Melanosuchus" will be created and it ends in appearance of a duplicate taxon, i.e. "Melanosuchus" and "Melanosuchus Gray, 1862".

If you need parallel taxonomies, you must prepare one file by taxonomy (example: one for Reference taxonomy, and a second for a temporary taxonomy).

2.3   STEP 2: IMPORT IN DaRWIN

Import itself is a quiet rapid process. Enter the import tool, through menu ADMINISTRATION > IMPORTS > TAXONOMY
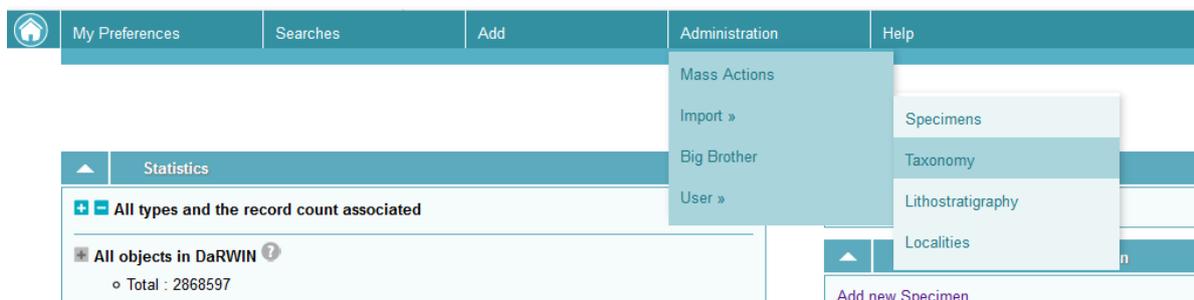
A summary table with all previous imports appears. From this page, you can :

1) filter taxonomy imports by filename, state of import or show only finished files
2) sort results by id and date
3) ask to import a new file

At the bottom of this table, click on "Import taxons". You will be redirected to the import file form.

In this form, you mention:

- the source database, as a reminder. Ex: "Collection Congo 1956"
- click on the "File" field, a file explorer opens, and you can select the *.txt file containing the taxonomy you wish to import
- select in which taxonomy you wish to import, mainly "RBINS Reference (is reference)"
- precise kingdom, basically "Animalia (RBINS Reference)"

Then, you click on submit.

The system has now your file in memory and waits for you to ask him to load the data in its intermediate table, called "staging", that is where all checks will be implemented.

Click on "Load in staging" at the end of the line that concerns your current import.

When file is loaded in staging, system waits for you to ask him to check information and import what it can import. You could need to refresh the page to see this new state appear.

At the end of the check process, import is finished. And you can see the result by clicking on icon at the end of the line.

Here are the errors that can appear:

imported_taxon	The taxon has been imported
taxonomic_hierarchy_already_exists	The taxon already exists with the same hierarchy
taxonomic_conflict	The taxon already exists in the taxonomy, with another hierarchy
taxon_to_be_created_without_suitable_parent	The taxon is new, but is dependant of a parent that already exists in the same taxonomy with another hierarchy

taxon_to_be_created	The taxon exists on same taxonomy with different author.
	It is also an error that can appear for other technical reasons. If you are not sure, you can contact administrator.
	You can try to import your specimens anyway.

Keep in mind that existing hierarchies' warnings are normal for parent taxa that you use to connect your new taxonomical tree.

3 SPECIMENS IMPORT

3.1 STEP 1: PREPARE YOUR FILE

Your data have to be stored in a spreadsheet (Excel/LibreOffice) and then be converted into a tab-delimited file (*.txt).
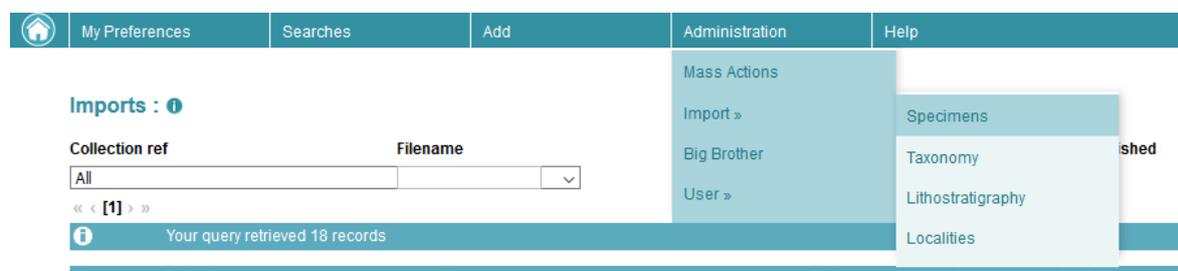
The fields available in the template is listed in Annex 2.

Unrecognized columns will be imported as a property. You can therefore use any other column name to create a property.

Please, use the exact same spelling.

3.2 STEP 2: LOAD YOUR FILE

Import itself is a rapid process. Enter the import tool, through menu ADMINISTRATION > IMPORTS > SPECIMENS

A summary table with all previous imports appears. From this page, you can:

1) filter specimens imports by filename, state or collection or show only finished files
2) sort results by id, date
3) ask to import a new file
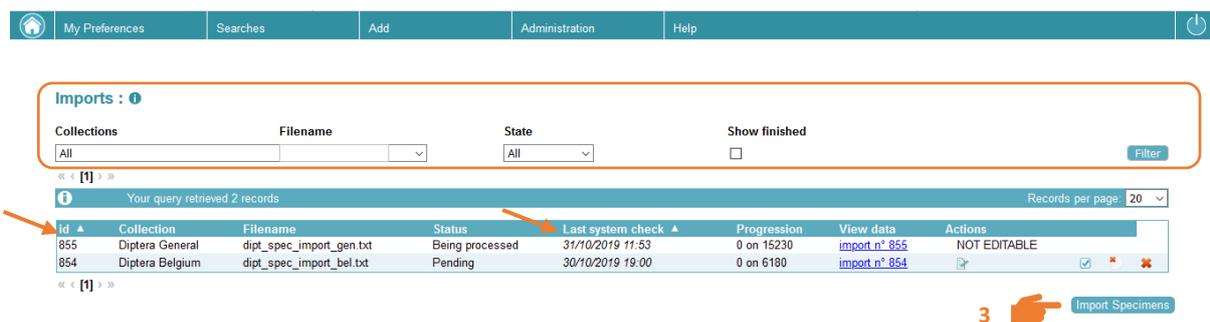
At the bottom of this table, click on "Import specimens". You will be redirected to the import file form.

Import Specimens

Source database :	
File :	
Format :	ABCD ⌄
Collection :	Choose !
Specimen taxonomy ref :	All ⌄
Enforce code unicity :	☑

Submit

In this form, you mention:

- the source database, as a reminder. Ex: "Collection Congo 1956"
- click on the "File" field, a file explorer opens, and you can select the *.txt file containing the specimens you wish to import
- select the collection in which specimens will be imported
- select which taxonomy you wish to use for your file (see below for more info)
- select/unselect checkbox "Enforce code unicity" if you wish the system to control if you use unique unit ID in your file and collection. For data without unique ID, the checkbox should be unselected, otherwise import will be stopped.

Then, you click on submit.

Your import appears in the table, and you have to click on "Load import".

After a few minutes, data are loaded, and system has to check them. If you refresh the page, you will see "Check import" at the end of the line. You can click. The system proceeds to a check on your data.

When state is "Being processed", the system is working, and no action are allowed.

Actions available are:

☑	Import ok lines :	you can import all lines for which system did not detect any problem, lines with errors will remain
📝	Edit import :	to access to the validation/correction interface, allowing you to correct data not validated by the system and being then able to import them
✖	Abort import :	cancel process
✖	Delete import :	delete import

Which taxonomy?

New specimens imported can be compared with all, one or several taxonomies. You can work iteratively, starting with one taxonomy, then import specimens matching this taxonomy. Then, choose another taxonomy, check the data, import specimens matching this second taxonomy, etc. For example, if you have taxa from RBINS Reference taxonomy and from Open Nomenclature, you can start by select "RBINS Reference". And after a first check, you can recheck with "Open Nomenclature". If you use "All", the matching will be done on all existing taxonomies. If you choose a precise taxonomy, for example a temporary taxonomy that you have created, the matching will be done only in entries of this taxonomy.

Practical info on how to proceed are detailed below, in *3.3. STEP 3 : CORRECT ERRORS IF EXISTING*.

3.3 STEP 3: CORRECT ERRORS IF EXISTING

Once your file has been checked, some lines could need validation.

You can see lines necessitating action when you click on edit icon at the end of the summary imports table.

You are redirected to a validation screen, listing all lines in error.

What does it mean?

Some information stored in your file are linked to table in DaRWIN. It means that the system has to compare your value and see if it can be matched with an existing value in DaRWIN.

Your value can match several entries, like a person name. Take Wilson as an example. Several occurrences appear for this name. But the system cannot presume which is the one your target. Wilson M.? Wilson Brad? You have to precise.

Your value could also not be recognized. This is a common situation in taxonomy. You have to give precision.

What can be done?

In both case, you have to click on edit icon at the beginning of each line. You are then redirected to a form, that allows you, for each value in error, to search for the value in DaRWIN through the magnifier icon next to the field.
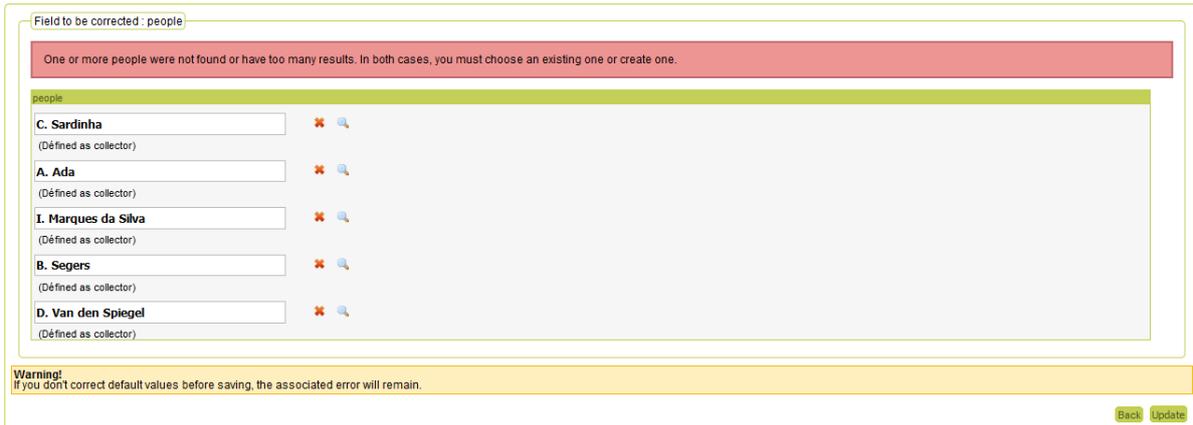
It will then open a pop-up window, that is the same as what you are used to in DaRWIN (creation of records, selecting linked info like taxon when adding a new specimen, etc.). You search for your value, and click on "Choose", or you can create it, and then choose it.
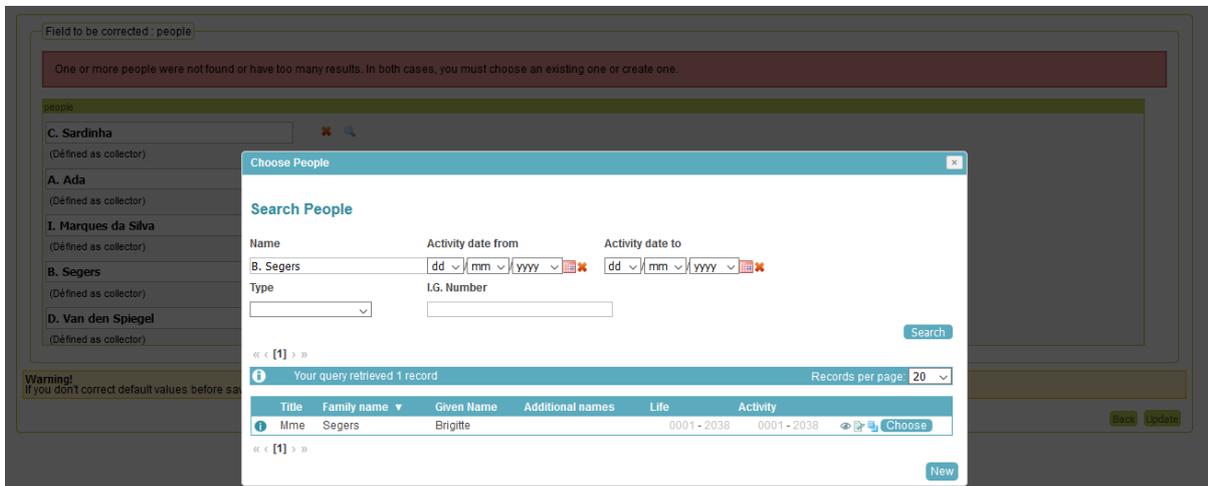
When you are done with corrections, you can click on "Update". You can also leave the correction for later and click on "Back" that send you back to the list of errors.

When you click on "Update", the system will update info from data you have imported in temporary file, to make them match existing data in DaRWIN. If an error is present more than one time, one correction is enough. The system will update all lines for the concerned value.

And what about taxonomy?

As previously mentioned, it is possible to use several taxonomies during one import.

At the beginning of the import process, when you load the file, you choose one taxonomy.

Through the correction interface, for taxa not recognized after the first check, you can choose another taxonomy, and click on check for the system to be able to compare and see if unrecognized taxa can be linked to this other taxonomy. By doing so, you will be redirected to the summary table page, letting the system work on the recheck. When it is done, icons for edition, import, abort import or delete import will be available again.

And so on, for each taxonomy you wish to use, iteratively.

Show only row with errors ☑
◉ Zoology
◯ Geology

Search
« ‹ [1] › »

	Your query retrieved 11 records												Records per page: 50 ▾

Actions	Error(s) found	Status	Linked Info	Codes	Category	Expedition	Sampling Location	Taxon.	I.G.	Acquisition	Part	Status	Institution	Number
✎ ✖	1	Error	9	M.T.38360				Cichlidogyrus sclerosus, Cichlidogyrus thurstonae, Scutogyrus longicornis (3x)						5
✎ ✖	1	Error	9	M.T. 38363				Cichlidogyrus thurstonae (2x), Scutogyrus longicornis						3
✎ ✖	1	Error	10	M.T.38377				Cichlidogyrus Cichlidogyrus sclerosus, Cichlidogyrus halli						2
✎ ✖	1	Error	10	M.T.50				Cichlidogyrus halli (3x), tilapiae ?						4
✎ ✖	1	Error	10	M.T.51				Cichlidogyrus halli (3x) (Price & Kirk, 1967)						3
✎ ✖	1	Error	10	M.T.52				Cichlidogyrus halli (4x) (Price & Kirk, 1967)						4
✎ ✖	1	Error	10	M.T.55				Cichlidogyrus thurstonae (1x), tilapiae (3x)						4
✎ ✖	1	Error	10	M.T.57				Cichlidogyrus tilapiae (3x) Paperna, 1960						3
✎ ✖	1	Error	10	M.T.58				Cichlidogyrus thurstonae (1x), halli (1x), tilapiae (1x)						3
✎ ✖	2	Error	11	M.T.69				Paperna, 1960 tilapiae						
✎ ✖	1	Error	10	M.T.96				Cichlidogyrus C. halli, C. tilapiae						2

Taxonomic reference : All ▾
Back to Import   Try to create missing peoples   Recheck   Import "OK" lines

There can also appear errors if you use the wrong format, for example for numeric fields like totalNumber. Import file *.txt must be corrected and reimported in that case.

3.4   STEP 4: IMPORT OK LINES

You can import "OK" lines when you are done with corrections. It is also possible to import all ok lines, when some lines are still to be corrected.

It could happen if you have corrected a part of lines, and wish to already send them in DaRWIN, leaving remaining corrections for later.

Or it can also be necessary if you wish to check data on 2 different taxonomies. You will then correct all lines that concern taxonomy you selected in the beginning of the import process. Then import them. And after, re-check data against another taxonomy.

<div style="border:1px solid red; color:red;">

!!! WARNING: Don't "import ok lines" for more than one file at the same time. Once you click on "import ok lines" for an import, you have to wait for this file to be proceeded and imported before importing other lines.

</div>

4 LOCALITIES IMPORT

4.1 STEP 1: PREPARE YOUR FILE

Your data have to be stored in a spreadsheet (Excel/LibreOffice) and then be converted into a tab-delimited file (*.txt).

The fields available in the template are listed in Annex 3.

Please, use the exact same spelling.

4.2 STEP 2: LOAD YOUR FILE

Import itself is a rapid process. Enter the import tool, through menu ADMINISTRATION > IMPORTS > LOCALITIES

A summary table with all previous imports appears. From this page, you can:

1) filter localities imports by filename, state or collection or show only finished files
2) sort results by id, date
3) ask to import a new file

At the bottom of this table, click on "Import Localities". You will be redirected to the import file form.

Import Locality

Source database :	
File :	
Format :	Locality
Collection :	Choose !
	Submit

In this form, you mention:

- the source database, as a reminder. Ex: "Collection Congo 1956"
- click on the "File" field, a file explorer opens, and you can select the *.txt file containing the specimens you wish to import
- (optional) select the collection in which specimens will be imported; in this case, you can only access it through this collection. Not advised for a classical use of import tool.

Then, you click on submit.

Your import appears in the table, and you have to click on "Load import".

After a few minutes, data are loaded, and system has to check them. If you refresh the page, you will see "Load GTU in DB" at the end of the line. You can click. The system imports all data without error.

After import, you can access a summary of import by clicking on edit icon . Lines in green were imported. Lines in orange are in error.

List of errors for code:

- Duplicate code inside file: line is equivalent to another line in the file.
- Code already in DaRWIN: a sampling location with the same code already exists in database. It is the possible to correct your code or to force import.

sampling_code
33768/Witches Hat change code and import Force import with current code
33768/Intertidal change code and import Force import with current code

WARNING !! If you change a sampling code because it already exists in database, don't forget to update your specimens, in order to link the correct locality…

There can also appear errors if you use the wrong format, for example for coordinates. You will then see 'wrong_dms_coordinate_format'. Import file *.txt must be corrected and reimported in that case.

5 ANNEXES

5.1 ANNEX 1 – TEMPLATE FIELDS TAXONOMY

domain
kingdom
super_phylum
phylum
sub_phylum
super_class
class
sub_class
infra_class
super_order
order
sub_order
infra_order
section
sub_section
super_family
family
sub_family
super_family
family
sub_family
super_tribe
tribe
infra_tribe
genus
sub_genus
species
sub_species
variety
sub_variety
form
sub_form
abberans
author_team_and_year

5.2 ANNEX 2 – TEMPLATE FIELDS SPECIMENS

Field	Widget	Widget field	Short description
Sample identification			
unitID	Codes	Code (with category "Main" by default)	MANDATORY - Unique alphanumeric identifier of specimen
additionalID	Codes	Code (with category "Additional" by default)	Additional alphanumeric identifier
accessionNumber	I.G. number	-	I.G. number
acquiredFrom	Donators or sellers	-	How gived or sold the specimen (if more than one person, separate each name with ";")
acquisitionType	Acquisition	Acquisition category	Donation, purchase, mission?
acquisitionYear	Acquisition	Acquisition date	Date of acquisition
acquisitionMonth	Acquisition	Acquisition date	Date of acquisition
acquisitionDay	Acquisition	Acquisition date	Date of acquisition
Sampling location: who, where and when collected?			
samplingCode	Sampling location	Sampling location code; link to Sampling location catalogue, should the exact same code as in DaRWIN	Code in Sampling locations catalogue, that identifies collecting or observation station
collectionStartDay	Sampling location	Gtu from date	Collecting date
collectionStartMonth	Sampling location	Gtu from date	Collecting date
collectionStartYear	Sampling location	Gtu from date	Collecting date
collectionStartTimeH	Sampling location	Gtu from date	Collecting date
collectionStartTimeM	Sampling location	Gtu from date	Collecting date
collectionEndDay	Sampling location	Gtu to date	Collecting date (end if needed)
collectionEndMonth	Sampling location	Gtu to date	Collecting date (end if needed)
collectionEndYear	Sampling location	Gtu to date	Collecting date (end if needed)
collectionEndTimeH	Sampling location	Gtu to date	Collecting date (end if needed)

collectionEndTimeM	Sampling location	Gtu to date	Collecting date (end if needed)
collectedBy	Collectors	-	How collected specimens (if more than one person, separe each name with ";")
expedition_project	Expedition	-	Expedition
localityText	Comments	Notion "Sampling locations"	Comment on locality, for this particular specimen
Specimen description			
kindOfUnit	Part	Specimen part	Part(s) of organism or class of materials represented (animal, mounted specimen, microscopic preparation, part of organism, fossil, etc.)
typeStatus	Type	-	Type (paratype, holotype, etc.)
lifeStage	Stage	-	Phase or life stage (juvenile, larva, caterpillar)
socialStatus	Social status	-	Social status (worker, etc.)
sex	Sex	-	M or male = Male, F or female = Female, U or unknown = Unknown, N = Not applicable (for a fungus in a herbarium), X = Mixed (mixed specimens, males and females).
totalNumber	Count	Specimen count	Total number
maleCount	Properties	Value (Property type: "N males")	Number of males
femaleCount	Properties	Value (Property type: "N females")	Number of females
sexUnknownCount	Properties	Value (Property type: "N sex unknown")	Number of unknown gender
fixation	Properties	Value (Property type: "fixation")	Fixative or anesthetics used prior to tissue preservation
samplingMethod	Collecting method		Material and/or method used to collect the specimen

Identification information			
fullScientificName	Taxonomy	link to Taxonomy Catalogue, should be the exact same name as in DaRWIN	Taxon in Taxonomy catalogue, that identifies specimen taxon
identifiedBy	Identifications	Identifier	Identifier name (of more than one person, separate each name with ";")
identificationYear	Identifications	Date	Date of identification
identificationMonth	Identifications	Date	Date of identification
identificationDay	Identifications	Date	Date of identification
identificationNotes	Comments	Value (Notion: "Identifications")	Additional information/remark about identification of specimen
referenceString	External Links OR Comment	If link, goes to External Links; if character string, goes to comments with notion "Identifications"	References that were used by the identifier to provide the identification
Mineralogical identification information for unique name as identification			
mineralogicalIdentification	Identifications	Mineralogical identification without classification hierarchy stored in "Subject" field (category "Mineralogy")	Taxon in Taxonomy catalogue, that identifies specimen taxon
mineralogicalIdentifier	Identifications	Identifier	Identifier name (of more than one persone, separate each name with ";")
mineralogicalIdentificationYear	Identifications	Date	Date of identification
mineralogicalIdentificationMonth	Identifications	Date	Date of identification
mineralogicalIdentificationDay	Identifications	Date	Date of identification
Chronostratigraphy/Paleontological specimen			
geologicalEpoch	Chronostratigraphy		
age	Properties	Value (Property type: "age")	
age_bis	Properties	Value (Property type: "age_bis")	

Storage information: how and where?			
Institution	Localisation	Institution	Institution (RBINS)
Building	Localisation	Building	Building (De Vestel)
Floor	Localisation	Floor	Floor (Conservatory)
Room	Localisation	Room	Room
Row	Localisation	Row	Row
Column	Localisation	Column	Column
Shelf	Localisation	Shelf	Shelf
ContainerType	Container	Container type	Container type (jar, minigrip, etc.)
ContainerStorage	Container	Container storage	Conservation middle (dry, alcohol)
ContainerName	Container	Container	Name or number of container
SubcontainerType	Container	Subcontainer type	Subcontainer type, if existing
SubcontainerStorage	Container	Subcontainer storage	Conservation middle (dry, alcohol)
SubcontainerName	Container	Subcontainer	Name or number of subcontainer
Specimen properties			
Property1 to 30	Properties	Property type	Type of property (length, weight, etc.)
PropertyValue1 to 30	Properties	Value	Value
Multimedia			
externalLink	External Links	Url	External link (to a global repository for files or to additional info relevant for specimen)
Specimen comments			
notes	Comments	Value (Notion "General")	General comment about specimen
Relationships between taxas			
HostClass	Properties	Value (Property type: "Host - class")	Host information
HostOrder	Properties	Value (Property type: "Host - order")	
HostFamily	Properties	Value (Property type: "Host - family")	

HostGenus	Properties	Value (Property type: "Host - Genus")	
HostFullScientificName	Properties	Value (Property type: "Host - Taxon name")	
HostAuthority	Properties	Value (Property type: "Host - Authority")	
HostCollector	Properties	Value (Property type: "Host - collector")	
HostIdentifier	Properties	Value (Property type: "Host - Identifier")	
HostRemarks	Properties	Value (Property type: "Host - Remark")	
ParasiteClass	Properties	Value (Property type: "Parasite - class")	Parasite information
ParasiteOrder	Properties	Value (Property type: "Parasite - order")	
ParasiteFamily	Properties	Value (Property type: "Parasite - family")	
ParasiteGenus	Properties	Value (Property type: "Parasite - Genus")	
ParasiteFullScientificName	Properties	Value (Property type: "Parasite - Taxon name")	
ParasiteAuthority	Properties	Value (Property type: "Parasite - Authority")	
ParasiteCollector	Properties	Value (Property type: "Parasite - collector")	
ParasiteIdentifier	Properties	Value (Property type: "Parasite - Identifier")	
ParasiteRemarks	Properties	Value (Property type: "Parasite - Remark")	
Specimen association with another specimen			
associatedUnitInstitution	Relationships	Owner institution	
associatedUnitCollection	Relationships	Collection in owner institution	
associatedUnitID	Relationships	Unit ID	If in DaRWIN, link is established
associationType	Relationships	Unit type	Specimen in Darwin, external, taxon or mineral

Identification revision (1 to 50)			
IdentificationHistory1DateYear	Identifications	Date	Date of identification
IdentificationHistory1DateMonth	Identifications	Date	Date of identification
IdentificationHistory1DateDay	Identifications	Date	Date of identification
IdentificationHistory1Notion	Identifications	Category	**Mandatory** to create an identification, use "taxonomy" for taxon
IdentificationHistory1Value	Identifications	Subject	Taxon name
IdentificationHistory1Status	Identifications	Det. St.	Level of identification (% certitude)
IdentificationHistory1Identifier	Identifications	Identifier	Identifier name (of more than one persone, separate each name with ";")

5.3 ANNEX 3 – TEMPLATE FIELDS LOCALITIES

Name of field	Content	Comment
station_type	Station and expedition info	"station" or "event" (if part of an expedition)
sampling_code	Station and expedition info	**Mandatory**
sampling_field_number	Station and expedition info	
event_cluster_code	Station and expedition info	
event_order	Station and expedition info	
ig_num	Station and expedition info	
collectors	Station and expedition info	list separated by ;
collector	Station and expedition info	
expeditions	Station and expedition info	list separated by ;
expedition	Station and expedition info	
countries	General	list separated by ;
country	General	
ocean	General	
continent	General	
sea	General	
natural_site	General	
archipelago	General	
island	General	
state_territory	General	
province	General	
region	General	
district	General	
county	General	
department	General	
city	General	
municipality	General	
populated_place	General	
original_administrative_data	General	
exact_site	General	
collecting_day_start	Temporal information	For expedition only
collecting_month_start	Temporal information	For expedition only
collecting_year_start	Temporal information	For expedition only
collecting_day_end	Temporal information	For expedition only
collecting_month_end	Temporal information	For expedition only
collecting_year_end	Temporal information	For expedition only
collecting_time_start	Temporal information	For expedition only
collecting_time_end	Temporal information	For expedition only
ecology	Ecology and habitat	
habitat	Ecology and habitat	
collections	Link to specimens in collection	list separated by ; (integer id of Darwin collection)

collection	Link to specimens in collection	integer id of Darwin collection
sampling_method	Link to specimens in collection	
sampling_fixation	Link to specimens in collection	
iso3166	Link with thesaurii and maps	ISO 3166-1 (2 letters)
iso3166_subdivision	Link with thesaurii and maps	ISO 3166-2 values
coordinates_format	Georeferencing	DMS/DD/UTM
latitude_1	Georeferencing	Lat of point 1
longitude_1	Georeferencing	Lat of point 1
latitude_2	Georeferencing	Lat of point 2 (if bounding box)
longitude_2	Georeferencing	Lat of point 2
gis_type	Georeferencing	POINT/LINE/POLYGON
coordinates_datum	Georeferencing	EPSG code
coordinates_original	Georeferencing	
coordinates_accuracy	Georeferencing	
coordinates_accuracy_text	Georeferencing	
station_baseline_elevation	Elevation and depth	
station_baseline_accuracy	Elevation and depth	
sampling_elevation_start	Elevation and depth	
sampling_elevation_end	Elevation and depth	
sampling_elevation_accuracy	Elevation and depth	
original_elevation_data	Elevation and depth	
sampling_depth_start	Elevation and depth	
sampling_depth_end	Elevation and depth	
sampling_depth_accuracy	Elevation and depth	
original_depth_data	Elevation and depth	
locality_text	Freehand description	
ecology_text	Freehand description	
habitat_text	Freehand description	
station_notes	Freehand description	
sampling_notes	Freehand description	
sampling_property_type_[1…N]	Properties	Mandatory for the property
sampling_property_lower_value_[1…N]	Properties	Mandatory for the property (if no upper value this is the only value field)
sampling_property_upper_value_[1…N]	Properties	
sampling_property_is_quantiative_[1…N]	Properties	yes/no
sampling_property_unit_[1…N]	Properties	