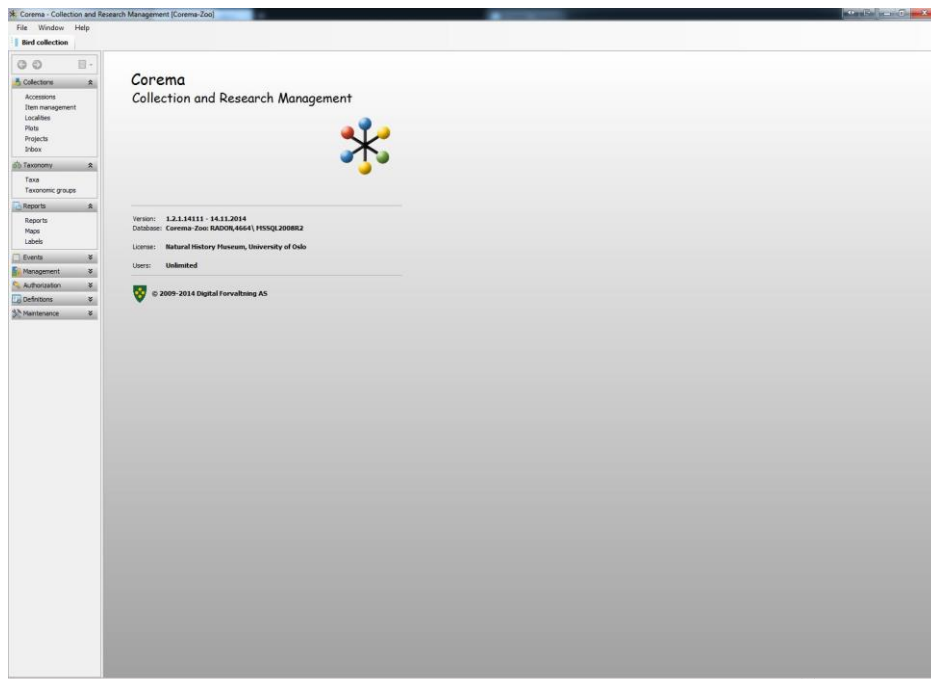


COREMA

Collection and Research Management

A BRIEF INTRODUCTION



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Special fonts used in the document:

- Button** On-screen buttons
- Field** Field names (as they appear on-screen)
- Form** Forms (Modules)
- Help Menu selections

INTRODUCTION

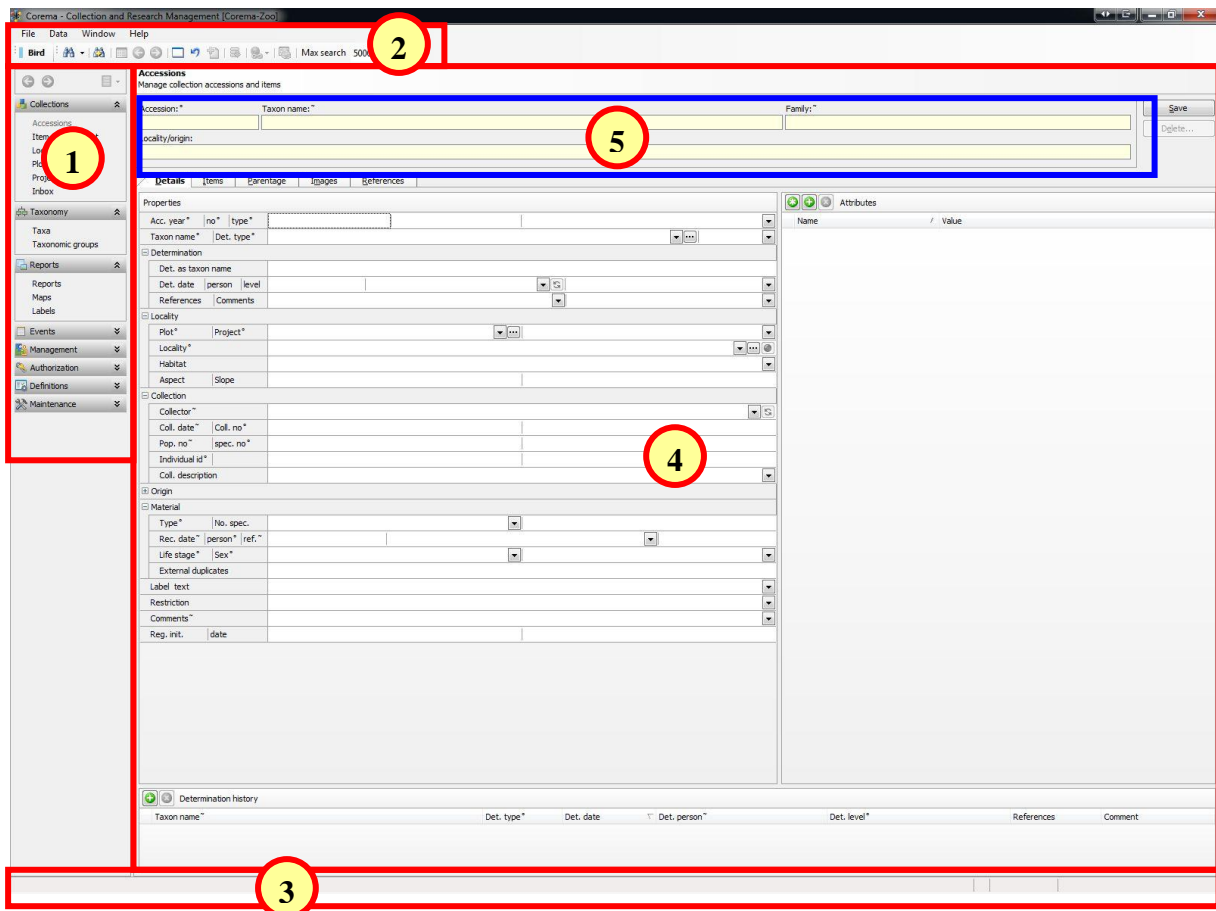
This is a brief introduction to the most central parts of Corema. Because several parts of Corema are not mentioned at all, or only briefly, anyone intending to use the program should also have a look at the Corema *Help* section (menu `Help>Contents . . .`). In fact, that should be done even if you just intend to use the parts treated in this introduction.

NB! For additions and changes made in versions after the one this manual refers to (see front page), please refer to the Corema *Version history* for an overview of these.

Some Corema basics

- The basic unit in Corema is the individual specimen, which is registered as an *accession*. Several samples from the same individual and sampling event should be registered as *items* belonging to the same *accession* (see below for more details about different types of item)
- Thus, several samples taken from e.g. a bird during one sampling event should be registered as different items under one accession
- If, on the other hand, the bird is recaptured later the same day/season/etc., samples taken during this sampling event should be registered as items under a new accession. **Individual id**, or some other individual specific ID field, should in such cases be identical so that all accessions of an individual can be identified
- In botany, “population samples” of e.g. 10 individuals of the supposedly same taxon from a restricted, small area would typically be registered as 10 accessions, each with one e.g. tissue item, sharing the same **Pop. no** but with different **Pop. spec. no**
- Further, when e.g. DNA is extracted from a tissue or blood sample, this should be registered as a new *DNA extract* item under the same accession as where the tissue/blood sample is registered. The relationship to a specific item may also be recorded in the **Item ref.** field (may be useful if e.g. several tissue and/or blood items exist)
- There is no limit to the number of items that can be registered on an accession, and it is also possible to register several items of the same type on one accession
- In `File>Options` some global settings for the program interface can be set;
 - *Confirm unsaved*: Choose *True* to get a warning if you try to leave a form with unsaved data in it (recommended)
 - *Language*: Choose interface language (so far only English [en] is available)
 - *Large toolbar*: Choose *True* to increase the size of the toolbar buttons
 - *Image max resolution*: Images can either be saved in original size (*Original*; not recommended due to storage space requirements), or reduced to a smaller or larger extent upon saving in Corema (*MegaPix_1-MegaPix_5*)
 - *Long location code*: Choose *False* to avoid unnecessarily long location codes (the full code will still be visible in drop-down lists)
- On-screen field names: All field names appear to the left of the actual fields, in the same order as the fields themselves. Field names starting with lowercase letters should be read as having the first word in common with the first field on the same line (e.g. the field names **Det. date**, **person** and **level** should be understood as fields **Det. date**, **Det. person** and **Det. level**).
- Numbers in curly brackets (e.g. {1}) in the text refer to numbers on figures within the same sections of the text.

PROGRAM INTERFACE



1 Navigation bar

Provides access to all the different forms (modules), such as **Accessions**, **Taxa**, etc.

2 Menus & tool bar

Commands related to the current form. Also shows the current collection to the far left

3 Status bar

Messages and other information

4 Main area

Viewing and entering of data

5 Express search fields

Quick searching for accession numbers, barcodes containing either accession numbers or UUIDs, taxon or family names and locality information

COLLECTIONS

Corema exists in to “versions” at NHM; *Corema-Bot* and *Corema-Zoo*, for the botanical and zoological DNA bank collections, respectively. Further, each of these contain several *collections*, corresponding roughly to major taxonomic groups within their fields. These are:

Version	Collection	Collection acronym
Botany	DNA Plant Collection	O-DP
	DNA Moss Collection	O-DM
	DNA Fungi & Lichens Collection	O-DFL
Zoology	Bird Collection (also “non-DNA” collections; sperm, eggs, skins etc.)	NHMO-BI
	DNA Fish & Herptile Collection	NHMO-DFH
	DNA Mammal Collection	NHMO-DMA
	DNA Arthropod Collection	NHMO-DAR
	DNA Other groups Collection	NHMO-DOT

Accession is given to each of these collections individually, meaning that any user may have access to one or more collection(s). Further, there are several levels of access; most users will start with *Reader* access, to allow them getting used to the program and “play around” without having to worry about deleting data or otherwise “messing anything up”.

With *Reader* access you can read all available data, but editing is possible only in the **Tasks** form, including creating new tasks. This has been made so because tasks are such a useful way to work with data in Corema, and may be most useful even to users without any further editing access. Have a look in the *Tasks* section below and try it out!

Whenever you feel comfortable with the software and have a need for a higher access level, typically allowing entering new and changing existing data, just contact the [Corema administrator](#) to have your authorization upgraded.

ITEM TYPES

A number of different item types are available in Corema, some of which are derived from other item types. Which item types are available differs among the collections. Below is a brief description of these, including whether they are derived and which collections they are available in.

Item type	Description	NHMO					O		
		BI	DFH	DMA	DAR	DOT	DP	DM	DFL
Tissue	Tissue sample stored for genetic analyses	X	X	X	X	X	X	X	X
DNA extract	Extracted DNA [derived]	X	X	X	X	X	X	X	X
Preserved specimen	Preserved study specimen, e.g. study skin, mounted specimen, herbarium sheet etc.	X	X	X	X	X	X	X	X
Blood	Blood sample stored for genetic analyses	X							
Feather	Preserved feather	X							
Sperm	Sperm sample stored for morphological analyses	X							
Sperm slide	Microscope slide prepared for sperm morphological analyses [derived]	X							
Sperm recording	Footage of live sperm swimming behaviour	X							
Testes	Testes stored for further analyses	X							
Seminal glomera	Seminal glomera stored for further analyses	X							
Egg	Complete clutches or single emptied eggshells	X							
Living	Living specimens, typically kept in the phytotron						X	X	X
Seeds	Seed samples stored for further propagation or analyses						X		

SEARCH

There are three ways to search for data in Corema;

- Enter search criteria in the yellow *Express search fields* at the top of the form
- Enter search criteria directly in the relevant fields of any given form (*Regular search*), or
- Use the *Advanced search criteria*

If a search returns more than one match, the result will be presented in a search result list. To select an item in the list, double click or highlight the item and press the space bar. If only one match is found, the item will be presented directly in the relevant form.

In forms where the search may return a large result set, a **Max search** value for limiting the number of returned results is shown in the tool bar. The default value for this is 5000. If your search returns more than 5000 accessions, only the first 5000 will be shown and the background colour of **Max search** will change to yellow to inform you that not all matches are shown. In this case, preferably constrain your search by adding more/stricter search criteria, or alternatively choose a higher value for **Max search**. The unlimited option (∞) should be used with care, as this may result in slow searches.

Express search

The *Express search fields* are the yellow fields at the top of the **Accessions** and **Taxa** forms that has a circle (°) or a tilde (~) at the end of the field name, viz. **Accession number**, **Taxon name** and **Family**. These can be used to perform quick searches for these data types.




The **Taxon** field has the special function that if you write the first letter(s) of the genus and species names, separated by a space, you will get all accessions or taxa with **Genus** and **Species** beginning with the given letters.

Regular search


You may search for accessions by entering search criteria in one or more of the searchable fields of any form. Searchable fields are indicated by either a small circle (°) or a tilde (~) following the field name. For fields marked with a circle (°) *exact* matches are used, while fields with a tilde (~) uses *like* matches. In fields with a tilde (~) it is, however, also possible to use *exact* match, by ending the selection criterion with “|” (two “pipes”; |).

Wildcard searches are also supported; the wildcard character is “%”.

To perform a search:




1. Navigate to the relevant form, click  (**Clear/New**; Ctrl+E) and fill in your search criteria in one or more fields
2. Execute the search;
 - Click  (**Search**; Ctrl+F) to show a list of *accessions* matching the search criteria
 - Click on the arrow at the right of the same button () and choose *Search Items* (Ctrl+I) to show a list of *items* matching the search criteria

Advanced search

A more advanced search is also available; click  (**Adv. search**; Ctrl+S) to access this. This is advanced in several respects;

- There are more search fields available
- Several types of searches can be selected for most fields
- Search criteria will remain in the search fields and searches may thus easily be refined

To use the *Advanced search*:

1. Navigate to the relevant form, click (**Clear/New**; Ctrl+E) and then click  (**Adv. search**; Ctrl+S)
2. Tick off the search field(s) you want to use
3. Select type of search from the first drop-down menu
4. Enter your search criteria, or choose these from the drop-down menu if available
5. Repeat this for all fields you want to include in the search (all ticked-off criteria will be combined in the search)
6. Execute the search;
 - Click  (**Search**; Ctrl+F) to show a list of *accessions* matching the search criteria
 - Click on the arrow at the right of the same button () and choose *Search Items* (Ctrl+I) to show a list of *items* matching the search criteria

TASKS

Tasks is a very powerful and useful function in Corema, and is used to create “bundles” of e.g. accessions, items or taxa in the collection. Tasks can then be used as a simple search criterion in the **Accessions**, **Taxa** and **Item management** forms, and as a selection criterion for **Reports** and **Maps**. As mentioned above, tasks can be created and edited also by users with only *Reader* access.

A task can consist of accessions, items or taxa (and actually more; see *Corema Help* for more info), but any one task can only contain entries of one type.

Whenever you will be working with the same selection of e.g. accessions or items more than once, it will probably save you time to store these in a task. You would then have to do the job of searching out all relevant accessions or items during the making of the task, but whenever you need to retrieve the same accessions or items later on, you just have to enter one search criteria, viz. the task number. And accessions, items or taxa can also be added or removed from a task at a later stage.


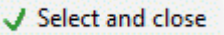

You may also add comments to each entry of a task, as well as label them as *Open*, *Completed* or *Excluded*. Both comments and labels will only be stored within the task, and will thus not influence the “original” accessions.

All tasks will by default be assigned to the user currently logged in, but this may be changed as desired. All Corema users can, however, access all tasks, irrespective of who created or owns them. Feel free to use other’s tasks, if useful, but please do not change them without consulting the owner!


To show all existing tasks, go to the **Tasks** form, click (**Clear/New**; Ctrl+E) to clear the form if necessary, and then hit Ctrl+F.

To register a task:

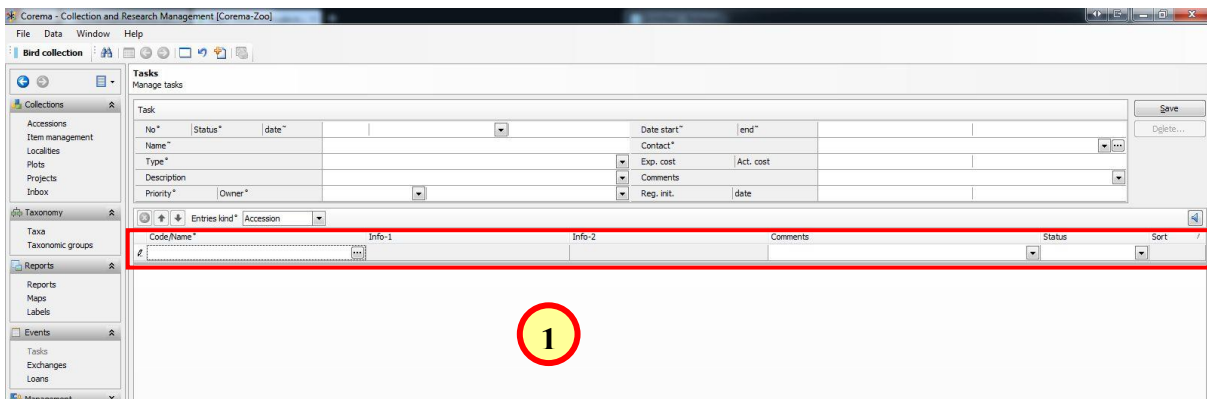
1. Go to the **Tasks** form, under the *Events* heading in the Navigation pane
2. If necessary, click (**Clear/New**; Ctrl+E) to clear the form
3. Fill in a meaningful and descriptive name for the task in **Name** – this should be meaningful also to other users!
4. Choose a **Type** for the task, depending on whether it is intended just for temporary use (*Temporary*) or to be permanent (*Permanent*)
 - *Permanent tasks* will never be deleted, e.g. masters project or samples used in a scientific paper
 - *Temporary tasks* can be deleted by the administrator after 6 months, or when they are marked with Status = *Closed*
5. You may also add more info about the task, especially if it is a permanent one, in **Description** and/or **Comments**
6. The following fields will be filled in automatically upon save;
 - **No** (next vacant number) – this is the number you should use to search for a task
 - **Status** (*Open*)
 - **Date** (current date)
 - **Priority** (*0: none*; may be changed as desirable)
 - **Owner** (currently logged in user name)
 - **Reg. init.** (currently logged in user initials [user name])
 - **Reg. date** (current date)

7. Choose what kind of objects are to be stored in the task from the drop-down menu in **Entries kind**
8. Finally, add the actual objects in the area indicated on the figure below, by either of these methods;
 - Type the accession number in **Code/Name** and press the *Enter* key to validate it; if it is valid the accession will be added to the task
 - Click  in **Code/Name** to open the **Accessions** form, from which you can search for records as described in the *Search* section above. When you have selected one or more records to be included in the task, press  to copy the records back to the **Event** form
 - Paste one or multiple newline-delimited values (e.g. from an Excel spreadsheet) into **Code/Name**. The entered accession numbers will then be validated and any invalid numbers indicated by empty lines and a red/white X symbol . Any invalid lines will have to be deleted before the task can be saved
9. When all objects have been added to the task, the task has to be saved by clicking the **Save** button in upper right corner

All objects associated with a task will be listed in the lower part of the **Tasks** form { 1 }, with accession number (and species and location, depending on type of objects) and any comments and status entered. To get more details for the objects, there are two options:

- Select one object (line) and click  to go to the relevant form for that entry
- Create a report (e.g. *Items - Most often used data*) for all objects in the task by entering the task number in the **Event name** selection criteria field

Similarly, the task number can be used as search/selection criterion to search for accessions, create maps etc.



REPORTS

To get data out from Corema, use any of the pre-defined reports found in the **Reports** form.

The reports are arranged in sections according to their main focus; generally, they are listed so that the first ones in any one section are the more relevant to most users. When a report is selected, some more details about what it will contain is presented in the upper right panel (above the search fields). Here is a brief explanation of the various groups of reports:

Report section	Report contents
Accession objects	<i>Accession level data</i> : taxonomy, locality, collection event, images, restrictions, ...
Accession items	<i>Item level data</i> : same as previous plus item level data such as item types, item details (e.g. extraction data), storage location etc.
Taxa	Taxon-specific data, and counts per taxa, including images for taxa
Events	Data for tasks, including data for the elements stored in the task (accessions, items etc.)
Management	Data for contacts, labels with contact data, library items and storage locations
Statistics	Various statistical reports; counts of collections, accessions, items etc. Mostly relevant only for collection administrators
Miscellaneous	DarwinCore exports, code list contents and locality data

To create a report:

1. Select a report in the list
2. Fill in the desired selection criteria. Only criteria selected by ticking off the checkbox next to it will be used. Empty criteria (even if selected) will be ignored.
3. Indicate sorting order (ascending/descending) and sequence by choosing 1 for the first sorting variable, 2 for the next and so on. If left unchanged (i.e. = 0) the data will not be sorted by that variable.
4. Depending on report type, one or more of the buttons **View**, **Print** and **Export** will be available in the upper right corner; use either of these to produce the report;
 - **View**: Open the report for viewing (most reports will produce an *MS Excel* file and thus be opened in this program). If a large number of accessions are included in the report, the viewing of the report might fail. In that case, using the **Export** button to create a text file (*.txt) which may be opened from within *MS Excel* may help
 - **Print**: Print a hard copy of the report. Specify printer in the appearing dialog box
 - **Export**: Save the report to a file;
 - In the appearing dialog box the location as well as the format of the file may be specified; available file formats will vary depending on report type
 - If you choose to save to an already existing file, a dialog box gives you the choice of *appending* the current data set to the file (default) or to *overwrite* the file (i.e. replace all data in the file with the current data set)

MAPS

Maps can be plotted for accessions and localities, provided that these have valid coordinates registered;

- *Accessions map* will produce a map with separate points for each accession, with certain accession details available as labels for the map points, and more details available by clicking on the labels and in a file which may be saved together with the map image (see below)
- *Localities map* will produce a map with separate points for each locality, with certain locality details available as labels for the map points, and more details available by clicking on the labels and in a file which may be saved together with the map image

A number of base maps are available, including e.g. various Google, Bing and Yahoo maps as well as “Norgeskart” from the Norwegian Mapping Authority. These can be selected after the map has been plotted. Further, the appearance of the map points can be altered by the user (however, only for all plots in a map simultaneously).

How much info to display in the point labels, and whether they should be permanent or just show up when hovering over the point, can also be selected by the user.

Clicking on a map point in an *Accessions map* brings up either the **Accessions** form (if only one) or a result list (if several) for all accessions associated with that map point. If more than one accession is associated with a map point, this will be indicated by e.g. “+ 14 additional” in the label. Similarly, for a *Localities map*, the **Localities** form is brought up.

The maps can be printed or saved to files (image file and Excel file with accompanying data), and finally your favourite selection of map type, markers etc. can be stored as defaults for new maps.

Explanations of the controls available in the map window are provided in the figure on next page. For further details about maps, see the *Maps* section in the *Corema Help*.

NB1! Remember that only accessions/localities with valid coordinates will be shown in a map, meaning that Corema has been able to convert the originally entered coordinates to latitude and longitude (see [below](#) for more on this). There may be more accessions/localities matching the selection criteria but lacking valid coordinates, and the map may therefore not provide a good impression of the true distribution of the accessions/localities intended to be plotted!

NB2! To show maps an internet connection is required.

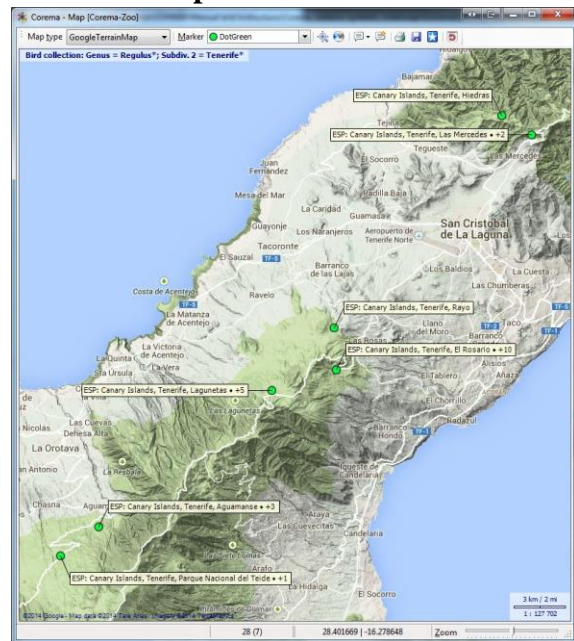
Map examples

Below is an example of the same accessions plotted with the two different map types.

Accessions map



Localities map



Map controls & customizing



1. Background map type
2. Marker shape & colour
3. Zoom to include all markers in the map at maximum zoom
4. Swap between colour and grayscale map
5. Add labels to markers
 - Permanent or dynamic (i.e., showing only when pointing to a marker)
 - Various levels of details
6. Reposition labels
 - If there are many markers and labels on the map, some will often be hidden behind others; use this button to try various repositions of the labels
7. Print map
8. Export map
9. Set map defaults
10. Clear map cache

WHERE TO FIND THE DATA YOU'RE LOOKING FOR

Although most Corema data fields hopefully are informatively named, it may still sometimes be hard to guess in which field the data you are looking for is stored.

Below is a brief guide to where the most common data are located, along with hints about some of the perhaps less logical field names (**in this font**).

Accessions – Details

1. Taxonomy

2. Locality

3. Collection data

- Collector, collection date, field/sample ID (**Coll. no**), Pop. no, ring number (**Individual id**)

4. Samples originating from other collections (NHM or other museums)

- Voucher collection, voucher ID (**Origin ref.**)

5. Various sample info

- Age (**Life stage**), sex, restrictions (on whole accession)

6. Various “custom attributes”

- Biometry, additional IDs (Ind. no., Nest no., ...), BOLD/GenBank info, culture, host, ...

7. Determination history

8. Express search fields

Accessions – Items

The screenshot shows the COREMA software interface. The main window displays a list of items with columns for Item no., Type, Location, Loc. ref., Status, and Date. Five red circles are placed over the first five rows of data, labeled 1 through 5. To the right, the 'Item properties' panel is visible, showing detailed information for the selected item, including references, location, status, condition, date, label, and material. A text box with arrows points to the 'Cons. no.' and 'Restriction' fields in the material section, explaining their content.

Item no.	Type	Location	Loc. ref.	Status	Date
1	Bird	B04-R05		Unknown	21.02.2014
2	Bird	S08-R007		Unknown	21.02.2014
3	Sperm	S01-R003		OK	21.02.2014
4	Sperm	S03-R002		OK	21.02.2014
5	Sperm				

Item properties for Item no. NHFO-BI-18202/1-B:

- Current:
- Type: Blood
- References: Cons. no. 26438, External ref.
- Location: Location code B04-R05, Location name Rack in freezer Bank04, Location ext. subref. SSS
- Status: Unknown
- Condition: No. specimens
- Date: 21.02.2014, Person Johannesssen, Lars Erik
- Label: no. ok
- Material: Content, Prep. Ethanol, Storage medium, Creation person
- Restriction: Sperm
- Comments: larsejo
- Reg. inst. 11.04.2014

Old database/journal number (Cons. no.)

Restrictions (only single item)

1. Registered items
2. Item type
3. Storage location for items
4. Item status
5. Item details
 - Sample type, storage container, storage medium, extraction method, ...

Accessions – Images

The screenshot shows the 'Accessions' window in the COREMA software. The window title is 'Corema - Collection and Research Management [Corema-Zoo]'. The main area displays taxonomic information for an accession: 'Accessions: *', 'Taxon name: *', 'Family: *', 'Rank: 1', 'Item: 1', 'Date: 23.03.2009', 'Origin: *', 'Provider: *', 'File name: C:\...', 'Properties: Image: *', 'Comments: *', 'Reg. init. date: larsejo', 'date: 02.03.2014'. The 'Images' tab is active, showing a list of three images with their ranks. A large preview of a selected image is shown on the right, with a toolbar above it containing buttons for 'Copy', 'Save', and other actions. Red circles with numbers 1, 2, 3, and 4 highlight specific features: 1. A list of three images with their ranks. 2. A table showing image details like rank, date, item, origin, provider, file name, properties, and comments. 3. A large preview of a blue and white bird perched on a hand. 4. A toolbar above the preview with buttons for Copy, Save, and other actions.

1. Available images linked to accession
2. Image details
3. Preview of selected image
4. Buttons for *Copy*, *Save* etc.

Accessions – References

The screenshot shows the 'Accessions' management interface. The main area displays details for an accession (NHMO-BI-18202) and a table of references. Two red circles with numbers 1 and 2 highlight specific buttons in the 'References' table. Circle 1 points to a button in the 'Item' column, and circle 2 points to a button in the 'Text' column. Two text boxes with arrows provide instructions: 'Buttons to access more details in the Library and Events forms, respectively' and 'Button to open linked documents (e.g. PDFs, Excel files etc.) directly'.

Author(s)	Year	Title	Pages	Comments	Item	Type
Lars Erik Johannessen	2014	Cyanistes 2011.			NHMO-BI-18202/4-55	Sperm morphology image ...

Event kind	Text	Item	Status	Status date	Priority	Start date	End date
Exchange	Exchange 33: 44 - Pele-Synek	NHMO-DSE-18202/2-D	Completed	07.03.2014	0: None		
Task	Task 24: PhD project - Jostein Gohli		Completed	21.03.2014	0: None		

1. References, permits, data sets etc. linked to the accession (or single item; if so this is indicated in the *Item* column)
2. Tasks, loans or exchanges in which the accession is involved

ENTERING NEW ACCESSIONS

New accessions can of course be entered directly in Corema, although for larger data sets it will probably be more efficient to import the data via Excel template files. Below both alternatives are described, focusing on the most common and important fields for the former.

Entering data in Corema

To start entering data for a new accession, go to the **Accessions** form and, if necessary, click (**Clear/New**; Ctrl+E) to clear the form. Then fill in as much information as you can for the accession and associated items; main pieces of info are mentioned below, with those most important and/or most often used in **bold** face:

1. **Determination (taxon)**
2. **Locality**
3. **Collection data**
4. Origin; for samples obtained from other collections (also within NHMO), museums or similar
5. **Sex & age**
6. Restrictions
7. Biometry etc.
8. Permits etc.
9. Images
10. Parentage
11. **Items**

The screenshot shows the 'Accessions' form in the Corema web application. The form is divided into several sections, with red circles highlighting specific fields corresponding to the list above. A red box at the top highlights the 'Details', 'Items (4)', 'Parentage', 'Images (3)', and 'References (3)' tabs.

1. Determination (taxon): Taxon name* (Cyanistes teneriffae), Det. type* (Cyanistes teneriffae), Det. as taxon name (Cyanistes teneriffae), Det. date (2014), Det. person (Jan Terje Lifjeld), Det. level (Species), Original det. (Cyanistes teneriffae)

2. Locality: Locality* (ESP: Canary Islands, Aguanarse, 28 21 25 N | 16 30 9 W), Plot* (Macaronesia)

3. Collection data: Collector* (Jan Terje Lifjeld), Coll. date* (23.03.2009), Coll. no* (C011), Pop. no* (L1933), spec. no* (L1933), Coll. description (Sperm)

4. Origin: Contact* (type*), Origin* (ref.), Provenance* (Prop. hist.)*

5. Sex & age: Type* (No. spec. Blood), Rec. date* (person* ref.), Life stage* (2K+), Sex* (Male)

6. Restrictions: Label text, Restriction, Comments* (Sperm), Reg. init. date (larsjojo) (21.02.2014)

7. Biometry etc.: Attributes table showing Name, Value, and Value

Name	Value
BOLDProcessID	BONM4022-10
LUIDAcc	http://purl.org/nhmuis/ld/1c1e809f-6395c7c3767c
WingLength	65,00

8. Permits etc.: Permits*

9. Images: Images (3)

10. Parentage: Parentage

11. Items: Items (4)

Determination history

Taxon name*	Det. type*	Det. date	Det. person*	Det. level*	References	Comment
Cyanistes teneriffae		23.03.2009	Jan Terje Lifjeld			Original det.: Cyanistes...


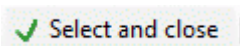

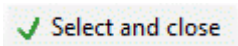
Properties											
Acc. year°	no°	type°	2014		18202					▼	
Taxon name°	Det. type°	Cyanistes teneriffae								▼ ... ▼	
Determination											
Det. as taxon name		Cyanistes teneriffae									
Det. date	person	level	23.03.2009		Jan Terje Lifjeld		▼	🔄		▼	
References	Comments								▼	Original det.: Cyanistes teneriffae	▼
Locality											

Determination (taxon identity)

- Start typing the taxon name in **Taxon name** {1}; if the taxon is already registered in Corema, it will show up in the list and you can select it **2**
- If the taxon cannot be found in the list **1** will have to be added to the taxon registry. Feel free to contact the [Corema administrator](#) to get help with this, or continue **3** add it yourself as follows:
 - Click on in **Taxon name** to go to the **Taxa** form
 - First search for all registered species in the relevant genus by entering the genus name in **Genus** and search (Ctrl+F)
 - Check to see if the desired taxon indeed is on the resulting list – perhaps only a typo or slightly different way of spelling prevented it from popping up in the taxon list?
 - If you do find the correct taxon, select it and click to copy the taxon back to the **Accessions** form
 - If not, continue below
 - Clear the **Taxa** form by clicking (**Clear/New**; Ctrl+E)
 - Choose genus from the **Genus** field
 - If you cannot find the genus in the **Genus** list, contact the [Corema administrator](#) to have it registered
 - Enter the new species name in **Species** and species author in **Species Author** (and similar for subspecies in **Infra name** and **Infra Author**, if relevant)
 - Select a source for the new taxon (preferably one of those available in the drop-down menu). Any new species added should be based on some authoritative source, like the IOC Bird list for birds, Fauna Europaea for most of the arthropods, Mammal Species of the World for mammals etc.
 - Click **Save** and then to copy the taxon back to the **Accessions** form
- Other relevant fields in the *Determination* and *Properties* panels:
 - Uncertain species identity may be indicated in **Det. type** {2} at the lower right of the *Properties* panel
 - If the species identity has been confirmed by genetic analyses, by a specialist or similar, this can be indicated in **Det. level** {3}
 - Det. date** and **Det. person** will default to the same as **Coll. date** and **Collector**, respectively (see below)

Locality

Locality		Macaronesia		3
Plot*	Project*			
Locality*		ESP: Canary Islands, Tenerife, Aguananse, 28 21 25 N 16 30 9 W		1
Habitat				2
Aspect	Slope			

- Click  in **Locality** {1} to go to the **Localities** form
- First check to see if the locality is already registered, by filling in **Country** etc. and performing a search (Ctrl+F)
 - If you find the locality, select it and click  to copy the locality back to the **Accessions** form
 - If not, continue below
- Fill in as many as possible of the fields **Country**, **Ocean**, **Subdiv. 1** (i.e., county), **Subdiv. 2** (i.e., municipality), **Locality**, **Alt. from** (altitude, or lower bound of altitude range), **Alt. to** (only to be used for upper bound of altitude range), **Alt. unit** (defaults to meters), **Org. coord** (coordinates) and **Datum**.
- If the coordinates given do not refer to an exact locality, but e.g. a larger sampling area, an island or similar, indicate the radius of a circle in which the true sampling localities are located in **Trueness. Precision** is to be used for coordinate uncertainty, e.g. as indicated on a GPS device (e.g. +/- 5 m).
- Some comments on coordinates:
 - There are two **Org. coord.** fields; latitudes should be entered in the first and longitude in the second of these. Remember to include *N* or *S* and *E* or *W*, respectively, at the end
 - UTM coordinates* should be entered in the first of the two **Org. coord.** fields only, and *has to be* on the format *ZoneNumberZoneLetter Easting Northing*, i.e. the parts *have to be* separated by a space and this is thus the only valid format:
 - 32V 598995 6643642
 - MGRS coordinates* should also be entered in the first of the two **Org. coord.** fields only, and on the format *ZoneNumber ZoneLetter Square Easting Northing*. Spaces may or may not be included. Easting and northing can be indicated with 1-5 digits each (but they have to have the same number of digits), reflecting the precision of the coordinates; 1 digit = 10.000 m, 5 digits = 1 m precision. All of these (and more) are therefore valid:
 - 32VNM9899543642
 - 32 V NM 98995 43642
 - 32 V NM 98995 43642
 - 32V NM 990 436
 - Provided that the original coordinates are entered according to the specifications, they will be converted to decimal degrees in the **Dec. deg. lat.** and **Dec. deg. long.** fields when the locality is saved. After this, click  to verify that the locality is indeed plotted where you expected it to be. If not, please correct the errors before proceeding.
- When all data have been filled in, click **Save** and then  to copy the locality back to the **Accessions** form
- Other relevant fields in the *Location* panel:
 - {2} **Habitat** (ecology etc.), **Aspect** (direction [N, S, etc.] in which the locality faces) and **Slope** (terrain steepness)

- **Project** {3}; if the accession is part of a larger project, the project can be registered in the **Projects** form and then selected in this field

Collection data

Collection	
Collector™	Jan Terje Lifjeld 1
Coll. date™	Coll. no.™ 23.03.2009 4
Pop. no.™	spec. no.™ 2
Individual id.°	L1933 3
Coll. description	


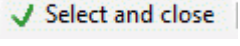

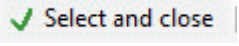
Enter any relevant collection information in the corresponding fields in the *Collection* section.

- {1} **Collector** and **Coll. date** should always be filled in
- {2} **Pop. no.** and **spec. no** should be filled in for botanical population samples. **Pop. no. has to be unique, i.e. not used in Corema before!**
- **Individual id** {3} should be filled in if the sample is from a uniquely marked individual (e.g. banded birds or tagged fish). **Any number or code entered in this field should be unique within the current Corema collection!**
- **Coll. no** {4} can be used e.g. for field sample numbers or other “semi unique” identifiers

Origin

Origin	
Contact°	type° 1
Origin™	ref. 2
Provenance°	Prop. hist.°

For samples originating from other NHMO collections, other museums, collections etc., register the institution, person etc. of origin as well as any reference or ID number for the specimen in that collection:

1. Click  in **Contact** {1} to go to the **Contacts** form
2. First check to see if the contact is already registered by showing all contacts (Ctrl+F)
 - If you find the contact, select it and click  to copy the contact back to the **Accessions** form (all registered NHMO collections start with “NHMO...”)
 - If not, continue below
3. Fill in as much info as possible about the contact, including at least the following: **Name**, **Country** and preferably some contact info (**Phone**, **E-mail**, **Web site**). **Code**, **Id** and **Status** will be filled in automatically.
4. Do also add a **Role** by clicking  in the **Roles** panel and selecting one of the available roles
5. When all data have been filled in, click **Save** and then  to copy the contact back to the **Accessions** form
6. Finally, in **Origin ref.** {2}, register any accession, registration or other ID number associated with the sample(s) in the collection of origin

Sex & age

Material		
Type°	No. spec.	Blood 3
Rec. date~	person°	ref.~
Life stage°	Sex°	2K+ 2 Male 1
External duplicates		

Information on sex and age should be entered in the *Material* section, in **Sex** {1} and **Life stage** {2}, respectively. **Material Type** {3} in this section should only be used if e.g. a DNA extract or some other derived item type is received and the source from which this is derived therefore cannot be registered as a separate item. In this case, choose source type from the **Material** drop-down menu. However, as far as possible, both the source and derived objects should be registered as separate items of the relevant type, and the derived item should be linked to the source item by use of the **Item ref.** field for items (see [below](#)).

Label text	
Restriction	
Comments~	Sperm
Reg. init.	date
	larsejo
	21.02.2014

Restrictions

The default assumption for all material entering the NHMO DNA bank is that there are no restrictions on the publication or use of the samples, as long as this is in accordance with the DNA bank grant policy and MTA (see [DNA bank website](#) for more details). It is, however, possible to place restrictions of various kinds on accessions, items and taxa, but this will then have to be cleared with the DNA bank before doing so.

An overview of the various restriction types can be found in the **Restriction types** form under the *Definitions* heading in the Navigation pane. There are three levels of restrictions (*None*, *Limited* and *Prohibited*), and these can be set independently for publication and usage of the accessions, items or taxa to which the restriction type is applied. Further, restrictions are hierarchical so that taxon restrictions override accession restrictions, and accession restrictions override item restrictions.

For changes in taxon restrictions contact the [Corema administrator](#). Restrictions on samples should normally be registered on the accession level, i.e. in **Restrictions** {1} at the bottom of the *Details* tab. This is because any restrictions usually will apply to all items of an accession. For restrictions applying only to some but not all items of an accession, see [below](#).

Biometry etc.


Attributes	
Name	Value
1	2
BOLDProcessID	BONMA022-10
UIJIDAcc	http://purl.org/nhmuio/id/1c3bb492-8175-4229-a0...
WingLength (mm)	65,00

A range of additional fields are available for various other pieces of information not included among the main fields in Corema; these appear in the *Attributes* panel at the right side of the **Accessions** form. To see the full list of available attributes (different for zoology and botany) and what type of data they accept (unit, if applicable, is included as part of the attribute

name), go to **Custom attributes** in the *Definitions* part of the Navigation bar. Below some of the custom attributes are mentioned:

- **Zoology:** Several biometric measurements; Colour codes or other additional individual identifiers; Nest ID, BOLD info; GenBank accession number, Host info; Hatching info (species and stadium hatched from); Culture info for cultured individuals.
- **Botany:** Ploidy level; Host species; BOLD info, GenBank accession number

To add data in a custom attribute field:




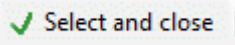
1. Click  in the *Attributes* panel and select which attributes to add data for in the drop-down menu of the blank field becoming available {1}
2. Fill in the relevant value or information in the *Value* field {2} for that attribute

Permits etc.



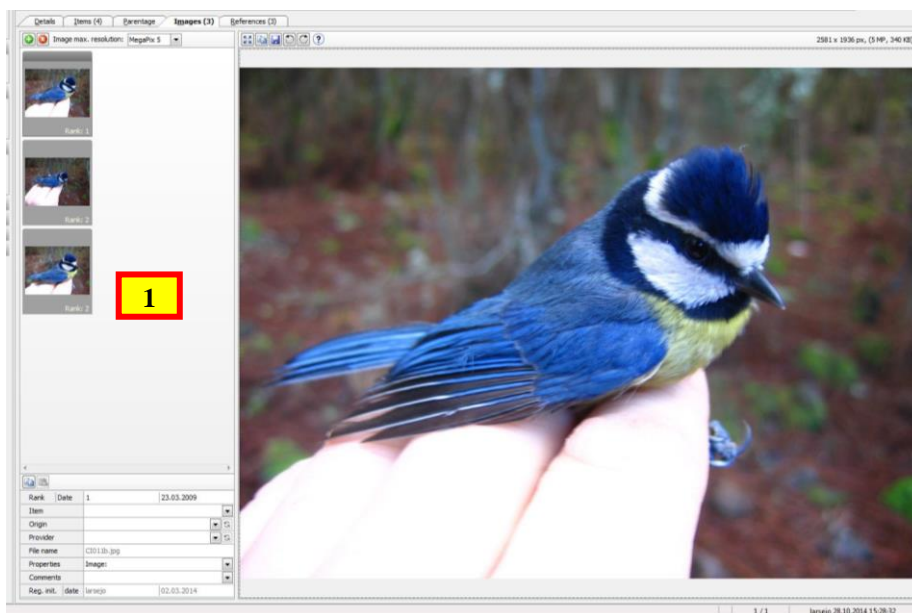
Any permits or other documentation relating to the sample should be properly registered before the sample itself is entered into any collection. It is also highly desirable to have all relevant documentation registered in Corema, to facilitate subsequent use of the samples. It is advisable to register PDFs of all collection, export, import, CITES etc. permits, as well as any other relevant documents (PIC, MAT, MTA) in the **Library** form in Corema, and then link these to all related accessions.


To add documentation:

1. Go to the *References* tab and click  in the *Library items* panel
2. If the documentation is already registered, this can be selected from the drop-down menu in **Author(s)**
3. If not, click  in **Author(s)** to go to the **Library** form
4. Fill in enough relevant info to enable yourself and others to recognize the document on a later occasion. For permits etc. this should at least include the fields **Author** (e.g. issuing agency), **Year**, **Title** and **Type**.
5. Add the PDF by clicking  in **E-Document**, selecting the PDF file and clicking **Open**
6. Click **Save** and then  to copy the documentation back to the **Accessions** form

You can add as many documents as you like for each accession.

Images


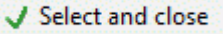


Images can be added in the *Images* tab. Just drag and drop image files from Windows Explorer into the large open field at the left side of the form { 1 }, or add them by clicking  at the top left of the form and navigate to the file(s). If available, some info for the image info fields at the lower left will be taken from EXIF info in the image files during import, but you may also add or change this info yourself after having imported the images.

Parentage

4

Parent-offspring relations among accessions (e.g. tissue samples from parents and offspring) can also be recorded, in the *Parentage* tab:

1. Register the parent accession(s) as normally
2. Register the offspring accession
3. In the *Parentage* tab, use the  button in **Parent-1** (mother) and **Parent-2** (father) { 1 } to search for and add the parent accessions. Remember to click the  after having found the right accessions to copy them back to the **Accessions** form.
4. **Sex** ({ 2 }); conventionally Parent-1 should be the mother) and whether the parentage is considered certain (**certain** { 3 }) can then be filled in

In the parent individual accessions all registered offspring will then be listed in the *Progeny* panel in the *Parentage* tab {4}.

Items

Item no.*	Type*	Location*	Loc. ref.**	Status*	Date**
1	Blood	B04-R05	555	Unknown	21.02.2014
2	C	B08-RP0	07SE	Un	25.09.2014
3	S	S01-R00	27	OK	26.02.2014
4	Sperm slide	S03-R00.2	98	OK	26.02.2014

Item properties

Item no. Current **NHMO-BI-18202/1-B**

Type* Blood

References

Cons. no.* External ref.* 26438

Storage no.* Item ref.*

Location

Location code* B04-R05

Location name* Rack in freezer Bank04

Location ref.* subref. 555

Status

Status* Unknown

Condition* No. specimens

Date* Person* 21.02.2014 Johannessen, Lars Erik

Label* no. ok*

Material

Content

Prep. type* quality

Storage container* medium* Ethanol

Created date* person*

Restriction*

Comments* Sperm

Reg. int. date larsetjo 11.04.2014

Finally, *do not forget to register the actual items!* This is done in the *Items* tab, starting in the *Items* panel on the left side of the form {1}:

1. Select item type in **Type** {2}
2. Specify a storage location for the item in **Location** {3}. This has to be chosen from the list of available locations, which typically refers to racks in specific freezers, shelves in cabinets etc. By sorting on the *Code long* column the available locations will be sorted by room number, freezer/cabinet and rack/shelf. If you do not know the location at the time of registration, or you will hand the items over to the DNA bank curator for further storage, choose *Code short* = “?” in this field, as it cannot be left empty.
3. Further sublocations can be entered in **Location. ref.** {4} or **Location subref.** {5}. These can be e.g. box number within a rack or shelf (**Loc. ref.**), recording number within a video (**Loc. ref.**), well number within a plate or tube number within a box (**Loc. subref.**), or start and stop times within a video recording (**Loc. subref.**).
4. Specify a status for the item in **Status** {6}. Hopefully this will be “OK” as long as the item is not already used up, damaged or similar
5. Depending on type of item, several other fields, especially in the *Material* section of the right panel {7}, should also be filled in, including **Prep. type** (item subtype, or extraction protocol for DNA extracts), **Storage container**, **Storage medium**, **Created date** and **Created person**.
6. Restrictions should in most cases be registered for the accession in general (i.e. in the **Restrictions** field in the *Details* tab; see [above](#)), as they normally will apply to all items of an accession. However, any restrictions applying only to specific items should be registered in **Restrictions** {8} in the *Items* tab.

Import of data

To register larger chunks of samples it will probably be most efficient to use the *MS Excel* template sheets available for several of the collections. In these data can easily be copied from existing field note or other files, and registration of collection dates or other repetitive data can be done very quick and efficiently. After having filled in the import file, send it to the [Corema administrator](#) to have it validated and imported into Corema.

Before you start to fill in your data, be sure to download the latest version of the import template file from the [DNA Bank section](#) of the NHM best Practice Wiki. These files are constantly changed, and using the old version you have stored on your local hard drive – even if it's just a few days old! – can cause a lot of extra work during import!

Do also take the time to read the information in the *Info* tab of the file – it will probably both save you time when filling in the file, and increase the chances that the file can be easily imported to Corema ☺.