Hdb2Win 2.6.0
Application *Oliva*
Service Release 5 (March 2025)

Content

1 Introduction

Oliva is the newest application of the database system, currently consisting of 43 tables that are interconnected with each other. *Oliva* was primarily designed to record data of extant molluscs. The main focus is the registration of collection material (and observations) of marine extant organisms. The structure has a clear research focus and supports the recording and analysing of morphometric data of the organisms, their geographical distribution and distribution among different sediment types. While it is designed for molluscs, *Oliva* may also serve for other extant marine organisms. For the labels of data fields in the *Oliva* data acquisition forms the languages English, German and Spanish are supported. The programmes, output, and others are only in the languages of English or German.

Be aware that this document only describes the application and does not describe not the powerful database system. There is a general introduction to the database system (Hd26Eng.pdf, Hdb26Ger.pdf), and an older PDF document for version 2.1. Information on later versions, as well as a description of the interpreter and allied programmes (PaleoTax/Map, PaleoTax/Graph, PaleoTax/ Measure) are available from the Internet page of the programme.

There are two versions of the present document: oliva-5.pdf is the version without modifications marked in a different colour (compared to oliva-4.pdf), whereas in oliva-5m.pdf all modifications compared to oliva-4.pdf are marked in a different colour. In the case of a new chapter, only the title of the chapter is marked in this colour.

Oliva was created from the experiences with the preceding Hdb2Win applications such as *PaleoTax* and *PalCol*. *PaleoTax* is clearly taxon-based and *PalCol* is specimen-based, but both applications are dedicated to fossil material and have, therefore, a special focus on time and rocks. *Oliva* is specimen-based and dedicated to extant material. Hence, there are no stratigraphy or lithology data, but there are data on marine areas, water depth, and the sediment type. *Oliva* is clearly specimen-based, and to date the taxonomic background is basic. The structure was developed in a stepwise manner from November 2017 in order to carry out a small-scale research project in the Gulf of California. Its first version (Service Release 1) was published in May 2020, followed by the second to fifth version (Service Release) in 2021- 2025.

Be aware that *Oliva* is still an ongoing project and future versions may bring changes, probably not so much with the data structure, but in forms and programmes. You may also note that some programme functions of the application are still disabled because they are not yet designed, or they need adaptation to the present data structure. It is possible that *Oliva* will meet your needs in some aspects, but not in others. Therefore, please do not hesitate to present a proposal on ways in which the design could be improved. Such suggestions on possible improvements might easily be included in a future *Service Release*, which can also be applied to existing structures.

When you are new to the database system you should first read the introduction to the database system (hdb26eng.pdf). Chapter 2 of this manual introduces to the structure of data and you need to check it because you have to know whether it meets your requirements. Note that Oliva is specimen based, not taxon based. In the centre stands the collection material. The taxonomy part only encompasses tables necessary for name the material. There are no tables for quotations in the literature (but for synonymy), no types or type species tables.

Please read this manual carefully. That is, without understanding the concept behind a structure, method or concept, one will not gain success. Therefore, read this manual completely before starting to record data. It will assist in making any principal decisions that need to be taken at the beginning. If you have already data in a different format be aware that the importation of data is not a difficult procedure. With Service Release 2, programmes for data importation are provided.

1.1 Compared to Service Release 1

Changes compared to Service Release 1 are here briefly listed.

1. Various data acquisition forms were modified. There is a new type of data fields in the orange colour. These fields are disabled when adding or editing records but can be searched for. So it is now possible to search in the principal table of the SPECIMENS for the family and genus of the species, or the country, region and marine body of the locality.
2. The main menu is modified and has two more boxes: SPECIMENS TO PICTURES and REFERENCES.
3. The table SPECIMEN has a new output format Table.
4. The table SPECIES has a new output format Data sheet.
5. The table LOCALITIES has a new output format Species list.
6. The table PICTURES TO SPECIMENS has been modified. You are able to search for images of a family, genus, species, or specimen. The image is shown in the data acquisition form.
7. The table FACIES was renamed into SEDIMENT TYPE. This is a much clearer denomination.
8. It is possible to import data from a text file into a new or already existing database.
9. There are more programmes available for data analysis.
10. The RTF output of labels was improved.
11. In the tables of GENERA and SPECIES are now buttons to add literature.
12. The fields to tag and untag the marker fields in the tables of SPECIMENS and SPECIES can be set from the search form.
13. In order to display graphs created with *Oliva* it is not necessary to start the programme Paleo-Tax/Graph since the functions of this programme are now included into the database system.

To be able to use Service Release 2 you need to install Hdb2Win (at least version 2.5) in a first step. In a second step you need to apply Service Release 2 to your existing database (see below under Structural modifications).

1.2 Compared to Service Release 2

1. The selection of species in the programme 'Create a species list (V.2)' is improved.
2. There are several new programmes for data analysis.
3. Right click in the main menu at the table families shows a short-list of families (only families that are marked with 'Include in selection list') and allows single or multiple selection. Records will be edited.
4. Some tables are expanded by new data fields and various data acquisition forms were modified.

Please install first the new database version (2.5.1) and afterwards bring your database to Service Release 3. There is a document (https://www.paleotax.de/sr.pdf) that explains this step by step.

1.3 Compared to Service Release 3

Changes compared to Service Release 3 are here briefly listed and also marked in the text with a different colour. There is also a version of this document without marked modification, principally for persons who start with Service Release 4.

1. Numerous programmes were improved and there are also some new programmes.
2. New data fields were added to some tables.
3. Some forms were modified (principally enlarged).
4. PaleoTax/Graph – now version 2.5 – was improved and programmes make use of new functions.

Please install first the new database version (2.5.2) and afterwards bring your database to Service Release 4. There is a document (https://www.paleotax.de/sr.pdf) that explains this step by step. You cannot install only SR4 and not the new programme version 2.5.2. There are modifications in the interpreter and the updated programmes make use of these changes. Of course you can work with Hdb2Win 2.5.2 and Oliva SR3, but this is not recommended since SR4 also removes some programme errors.

1.4 Compared to Service Release 4

Changes compared to Service Release 4 are here briefly listed and also marked in the text with a different colour. There is also a version of this document without marked modification, principally for persons who start with Service Release 5.

1. Various programmes were improved and there are also some new programmes. Not all is explained in this manual.
2. New data fields were added to some tables. Not all is shown in this version of the manual.
3. All data acquisition forms were modified and adapted to the new concept introduced with Hdb2Win 2.6.
4. An image cache was added for the albums (species, genera, families).

Please install first the new database version (2.6.0) and afterwards bring your database to Service Release 5. There is a document (https://www.paleotax.de/sr.pdf) that explains this step by step. You cannot install only SR5 and not the new programme version 2.6. There are modifications in the data acquisition forms that are unknown to former versions. Of course you can work with Hdb2Win 2.5.2 and Oliva SR4, but why? You cannot work with Hdb2Win 2.5.2 and Oliva SR5. You cannot work with Hdb2Win 2.6 and Oliva SR4.

Please be aware that the general fucntion of the database system is not included in the present document anymore. Please compare to the manual file hdb26eng.pdf.

2 Data structure

2.1 Introduction

A database is a complex compound structure of tables (such as a spreadsheet) that are interconnected with each other. The structure of the database (which tables are used, how they are interconnected) depends on the rules of the relational data model, on the one hand, and on the focus of the database, on the other hand. The database is scalable, which means that you may modify the structure, e.g. enlarge it. **It is not recommendable to remove data fields, to rename them, or to change their attributes**; this will cause errors. The start screen (Figure 2.1) shows the principal tables, which are those tables that are usually searched.
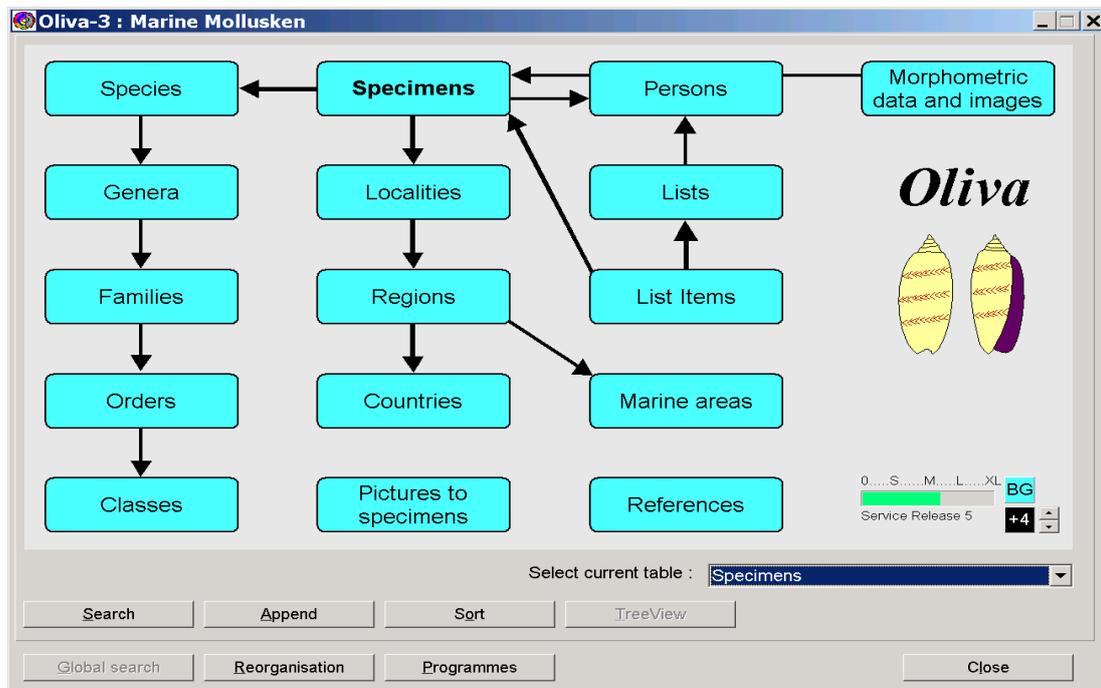
Figure 2.1. Start screen of the *Oliva* database application. The size of the form can be modified.

Each table has data fields that may represent characters, numbers, dates, a logical status, or interconnections with other tables. Since the tables are interconnected with each other, records can be edited or appended with respect to tables that are interconnected with the current table.

Below we describe the tables step-by-step. The order is not alphabetical, but according to the subjects and how they are related to the main table of SPECIMENS. Each table has a data acquisition form. This form always has the same structure.

In the following description of the tables, the fields (or group of fields) are marked with a number.

① A number with a green background indicates fields that should be recorded.

② Yellow circles indicate fields that should be recorded if data are available.

③ Fields marked with numbers with a white background should be recorded when you considers this to be necessary.

④ Blue circles mark fields that are set automatically by programmes.

⑤ Fields with numbers on a red background should not be touched.

2.2 Specimen data

2.2.1 Specimens

Figure 2.2. Data acquisition form of the table SPECIMENS, page 1.

The table SPECIMENS is the central table of the structure. All other data can be controlled from here, and adding new data will mainly be realised through this table. The form has two pages, the main page with information about a specimen, or numerous specimens, and a second page to handle the sub-numbers.

Page 1 (Specimen)

1   Number of a single specimen or numerous specimens. Observations normally have no number. If you want to record observations as sub-numbers (mainly images of living organisms that are not re-moved from their habitat) you would be better off assigning a number in the table SPECIMENS. That makes the automatic import of images easier. If you want to record only the size of a specimen that remains in the field, it is not necessary to enter an observation number.

2   Quantity of specimens. Zero for observations. The small buttons increase and decrease the amount of specimens.

3   Old or alternative number.

4a   Family and genus names are both set automatically. These fields cannot be modified, but it can be searched for.

4b   Species name that refers to the table SPECIES. Select according to the name of the species, not the genus.

5   Field for nomenclature information such as confer (cf.), affinis (aff.), ex grupo (ex gr.), etc.

6   If no species name is available, a family or group name can be recorded here.

7a   The country, region, and the marine area are set automatically and cannot be edited, but searched.

7b   Locality that refers to the table LOCALITIES. Select according to the name of the country, region, and site.

8   Sampling describes a visit of a locality by a certain person, on a certain day. During one act of sampling, various specimens can be collected, as well as many specimens can derive from different visits (samplings) at the same locality. Since the conditions at a specified site may change according to the season, this information can be of interest. Click on the button Sampling to select a visit, or append a new visit. Be aware that a locality must be recorded beforehand. The button below just assigns another specimen (or many specimens) to the same sampling. If you attempt to assign a sampling of a different locality to the current record, you get a warning message and you may then select a correct sampling. **Think** well whether you need these data.

9   Tick this box if the locality is an assumption or according to the distribution of the species.

10   The location (shelf, drawer, box) of the material.

11   Person who has donated the material, and the date. It refers to the table DEDITUR. Select according to the name of the person and date.

12   Person who has assigned the scientific name to the material of the current record. There exists the option to define a default person that is always set (in the case the database is maintained by only one person). See below under 'Options of the database'.

13   The modification date is updated automatically when the record is modified.

14   Select here an item from the table PUBLICATIONS. Another place to assign a literary reference to a species is in the table SPECIES.

15   Measurements can be recorded here or – with much greater detail and more options for further data processing – in the table MORPHOMETRIC DATA AND IMAGES. See also the second page of this form.

16   Three fields are free for the user. Two of these fields are interconnected with other tables, one field is not interconnected with other tables. You are free to record additional data. To modify the labels, open the file RCSpecms.frm (with Notepad.exe or with the editor of the interpreter of Hdb2Win), go to the very end of the file and follow the instructions that are there.

17   User specified. Mark records for output or any further action. This field can also be set automatically (Search > Process > Action).

18   Add one or more specimens of the current record to a trade list. The quantity (see number 2) will be automatically reduced by this amount. It is therefore not possible that the number of specimens for the trade is higher than the current number of specimens in this lot.

19   Feel free to record a comment or note.

20   Images of the specimens can be recorded here or in the table MORPHOMETRIC DATA AND IMAGES. It is recommended to add images to the latter table. Also see the second page of this form.

21   Place for an image of the record. This can be the first image or a specified image if more than one image is available. After appending new images – either in this table or the table of MORPHOMETRIC DATA AND IMAGES – the image will not immediately shown. The reason is that some programmes that organise the images need update rounds that are only started once a day.

Figure 2.3. Data acquisition form of the table SPECIMENS, page 2.

Page 2 (Sub-numbers)

A sub-number is one specimen out of many specimens. A single specimen can be selected to record morphometric data or to take an image. The table lists all sub-numbers with their number and principal measurement. Here, you may add new sub-numbers, edit an existing sub-number or delete one sub-numbers. The sub-numbers are managed in the table MORPHOMETRIC DATA AND IMAGES, and when marking one item and clicking an 'Edit' the corresponding record of this table is opened. Please refer to this table for details.

2.2.2 Morphometric data and images

Figure 2.4. Data acquisition form of the table MORPHOMETRIC DATA AND IMAGES.

The table separates single specimens from many specimens that are recorded in the table SPECIMENS. This separation can have two purposes, taking morphometric data (measurements, counts, weight) or taking images. If you want to record field observations (as described above under SPECIMENS) you should assign an observation number (table SPECIMENS) when images should be added to the sub-number. There exists a programme that shows a graph of morphometric data. See below in the chapter 'Search and output' for details.

1a   Genus and species names are both set automatically. These fields cannot be modified, but it can be searched for.

1b   The specimen lot to which the selected specimen belongs. If this record is managed from the table SPECIMENS, this value is set by default. If no specimen number is available, in this field appears NN. It is only possible to search for specimens or lots that have a number.

2   The consecutive sub-number of the specimen. Note that if you want to take an image of the whole lot you can create a sub-number zero and attach the image to this number. The field ID Number below can be used for any additional number. Key F7 replaces the field with the next free sub-number.

3   The morphological characteristics are defined with the genus and the characteristics within this table are set automatically. You may or may not record these data. But at least one value should be recorded in the case where the image has no scale. This can be measurements, counts or the weight. The names of the characteristics are sourced from the table CHARACTERISTICS.

4   Any pertinent comment on the specimen. The space for this field was enlarged compared to SR3.

5   Quality of the specimen according to the internationally applied scale from COM to GEM, price, and currency.

6   Add images here (or – much easier – use the import function described below). Note, that in the SPECIES table, for the moment, only those images are shown that are attached to the table MORPHOMETRIC DATA AND IMAGES. You may also see the images here one by one.

7   The first image of the specimen is shown.

2.2.3 Characteristics

Figure 2.5. Data acquisition form of the table CHARACTERISTICS.

1   Short name for the characteristic. This abbreviation is shown in interconnected tables. **Keep the name short**.

2   The unit can be millimetre, gram, or remain empty (e.g. when something is counted, or it deals with an index without unit).

3   The explanation leaves more space. Use the first field for your own language. When different from English, use the second field for the explication in English (this can be useful for the HTML export or the species data sheet).

2.3 Taxonomy

2.3.1 Species

Figure 2.6. Data acquisition form of the table SPECIES, page 1.

This table is probably the most important following the SPECIMENS. It offers much information on a species, and it allows to visualise occurrence data (a map, the distribution among different sediment types), size distribution, and shows the images of one species. If other data are important to be shown, as for instance depth distribution or seasonal aspects of occurrences, please do not hesitate to contact the support.

Figure 2.7. Showing the images of one species. Click on the image to enlarge it. Click on the image again or press ESC to return to the general view. One image can be selected by clicking on 'Select', and after selection the corresponding record of the IMAGE table is opened. For the moment, only images attached to the table MORPHOMETRIC DATA and images are displayed.

1a　　Taxonomic data. Family and subfamily names are both set automatically. These fields cannot be modified, but it can be searched for.

1b　　The genus and subgenus refer to an entry in the table GENERA.

2　　Data about author and year refer to a corresponding table. Remember to mark the box if the original genus differs from the current genus, and the author has to be in parentheses.

3　　Various data about the species, that are all calculated on the basis of provided data or they are all set automatically. It gives information on the number of localities for the species, the number of specimens, the frequency (for the calculation of the frequency please refer to the chapter 'Programmes' below), the percentage of localities of this species compared to all localities within the same marine area, the average number of specimens per locality, an endemic area, the average sediment type, the modification date, and the HTML version.

4　　Internet resources can be managed here.

5　　'Mark' can be used to mark a species, 'Trade' marks the species to be made available for trade and 'Output HTML' to mark species that are included in the HTML output. 'Output Text' to mark species that are included in a not further specified text output. With 'Exclude' species can be marked that will not be included in the observation lists (see 6.2 List of species...).

6　　Feel free to record a comment or note.

7　　The species can be connected to a literary reference. A click on the button will permit you to select a reference and/or edit the information, for instance, to add a page or a different name that is used in this publication. If you do not want that a specific reference is not shown in an output (e.g. the data sheet) mark the box 'No output'.

8　　All three buttons visualise data. 'Images' collects all images and shows them in a type of album. For options and limitations see below in the separate chapter Album. 'Size' shows in a graph the different measurements of specimens of this species, and 'Sedim.' shows the distribution of the species among the sediment types.

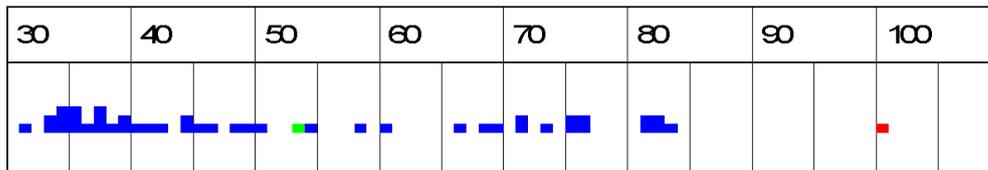| 30	40	50	60	70	80	90	100

Figure 2.8. Size distribution of one species. The red dot marks the maximum size (as recorded in the species table), the green dot marks the average of the recorded specimens. Note that it is from SR3 on possible to include only measurements of material collected by a specific person. See under 6.6 Options of the database. The person is defined through the options but to get this option working, the reorganisation must be started regularly.

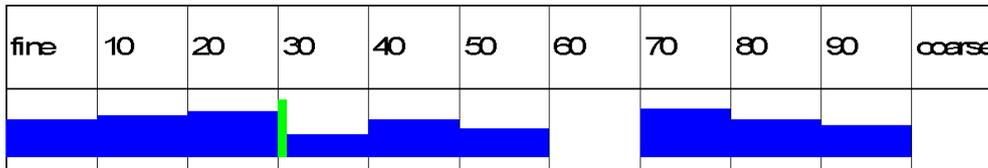| fine	10	20	30	40	50	60	70	80	90	coarse

Figure 2.9. The distribution of one species among the sediment type. The scale is from left with fine sediment to the right with coarse grained sediment. The green bar marks the average. It has to be noted that – as in the shown example – the average does not necessarily marks the average of the distribution shown in the graph, but of the distribution based on sites that were admitted to deliver sediment data.

9　　Maximum size according to the literature and/or Internet resources. This value is shown in the size graph as a red dot.

10　A list of localities with the specimen number and the amount of samples is automatically compiled for each species.

11　If exact positions are recorded with the localities, distribution maps can be created and are shown here. To know how to create the maps, please refer to the section 'Programmes' below. Maps must be stored in a path PLOTS within the data directory. Click on the map to increase its size.

Figure 2.10. Data acquisition form of the table Species, page 2.

Specified data can be recorded on the second page. The idea of this function is to create user-defined own fields (data classes) without touching the database structure. Here, recorded data can be output, for instance, in the HTML application.

1　　The left table contains the data classes that are created by the user. As you can see, data classes on the frequency and the size of a species were created, as well as a field for remarks. It is not only possible to record texts, but also to record numerical values, file names, and references to records of other tables. The data classes can be created, edited or deleted. See below (chapter 'Text comments') for further explanation.

2　　The right table encompasses the recorded data. 'New' creates a new item of a data class marked in the left table, 'Edit' allows to edit an item, and 'Remove' marks it as deleted.

2.3.2 Genera

Figure 2.11. Data acquisition form of the table GENERA, page 1.

1   Taxonomic data. The family and subfamily refer to entries in the tables of FAMILIES and SUB-FAMILIES. Authorship of the genus is optional.

2   The number of currently assigned species (counted are only species with species name and author) is calculated automatically by a programme (see below under 'Programmes').

3   Feel free to record a comment or note.

3a   It is possible to attach a reference to the genus.

3b   Images of species that belong to the genus. Only those images are shown that are marked as Principal image in the table IMAGES OF SPECIMENS. For options and limitations see below in a separate chapter Album.

4   A list of species, together with their localities is compiled automatically.

5   When you consider recording morphometric data in the table MORPHOMETRIC DATA AND IMAGES, it is highly recommended to fill in those fields which are connected to the table CHARACTERISTICS. The main characteristic is that used in the album, the size distribution graph and in the HTML output. Hence, you should at least fill in the main characteristic and the first characteristic.

An image can be recorded on the second page This can be a table of how to distinguish the species within one genus, or a compound image of common species.

2.3.3 Families

Figure 2.12. Data acquisition form of the table FAMILIES, page 1.

1   Taxonomic data. The superfamily and order refer to entries in the tables of SUPERFAMILIES and ORDERS. No authorship here.

1a   Mark here those families that are shown when doing a right click in the main menu on the family box.

2   Feel free to record a comment or note.

2a   It is possible to attach a reference to the family.

2b   Images of species that belong to the family. Only those images are shown that are marked as Principal image in the table IMAGES OF SPECIMENS. For options and limitations see below in a separate chapter Album.

3   A list of genera and species is compiled automatically. If the species is within the database endemic to a marine area, this area is shown in brackets.

An image can be recorded on the second page. This can be a table of how to distinguish the genera within the family, or a compound image of common genera.

2.3.4 Superfamilies

This table has on the first page the name of the subfamily and a list of families and genera, on a second page place for an image, and on the third page place for comments as in other tables such as SPECIES or GENERA.

2.3.5 Subfamilies

This table has on the first page the name of the subfamily and a list of species, on a second page place for an image, and on the third page place for comments as in other tables such as SPECIES or GENERA.

2.3.6 Orders

This table has the name of the order, the class to which it is assigned, and a list of all families.

2.3.7 Classes

This table has the name of the class, and the phylum to which it is assigned.

2.3.8 Phyla

This table has only the name of the phylum.

2.3.9 Author of Taxa

Figure 2.13. Data acquisition form of the table AUTHOR OF TAXA.

This table records the author(s) of taxa (species, genera).

1   First, second, and third author, and author within a larger work.

2   Year of the publication.

3   Feel free to record here the publication if needed.

4   List of species of this author and year.

2.3.10 Authors

This table records the first name and family name of an author.

2.4 Geography

2.4.1 Localities

The table LOCALITIES is important.

1a   Country and marine area are both set automatically. These fields cannot be modified, but it can be searched for.

1b   Select the region from the table REGIONS according to country and region name.

2   Name of the sample site.

3   An optional sample point or station number.

4   Two fields to be used for any purpose that are of interest to you.

5   Environmental data. If you wish to analyse the sediment distribution of a species, this field should be used. It is possible to exclude selected localities from the sediment analysis. The water depth can be added here.

6   The geographic position. This can be a transect or a point with a certain radius.

7   The radius of the circle around the given position in km.

8   The code that will be displayed on the map when output to PaleoTax/Map.

9   The number of species, the number of specimens and the number of species that occurs only at the locality is calculated by a database programme.

10   Feel free to record a comment or note.

11   You may add images of the locality. The first is shown on the right side of the form.

12   A document can be attached to the record (e.g. a PDF file).

The second page provides three lists: the list of species found a this locality, the list of species restricted to this locality, and the list of visits at this locality. The list of species that only occur at a specific locality may show more entries than such species are indicated for the locality. This happens if the frequency analysis is restricted to one specific collector.

Figure 2.14. Data acquisition form of the table LOCALITIES.

2.4.2 Regions

Figure 2.15. Data acquisition form of the table REGIONS.

1   Select the country from the table COUNTRIES and enter the region name.

2   The marine area or province should be recorded if distribution data are interesting for your project. A marine area can be defined as a marine water body that has clear (or not so clear) boundaries with other marine water bodies. There exist established biogeographical provinces that could be too large or too small for your needs. On the next page you can see one design (out of many), published by Hanske & Löser (2006).

3   Feel free to record a comment or note.
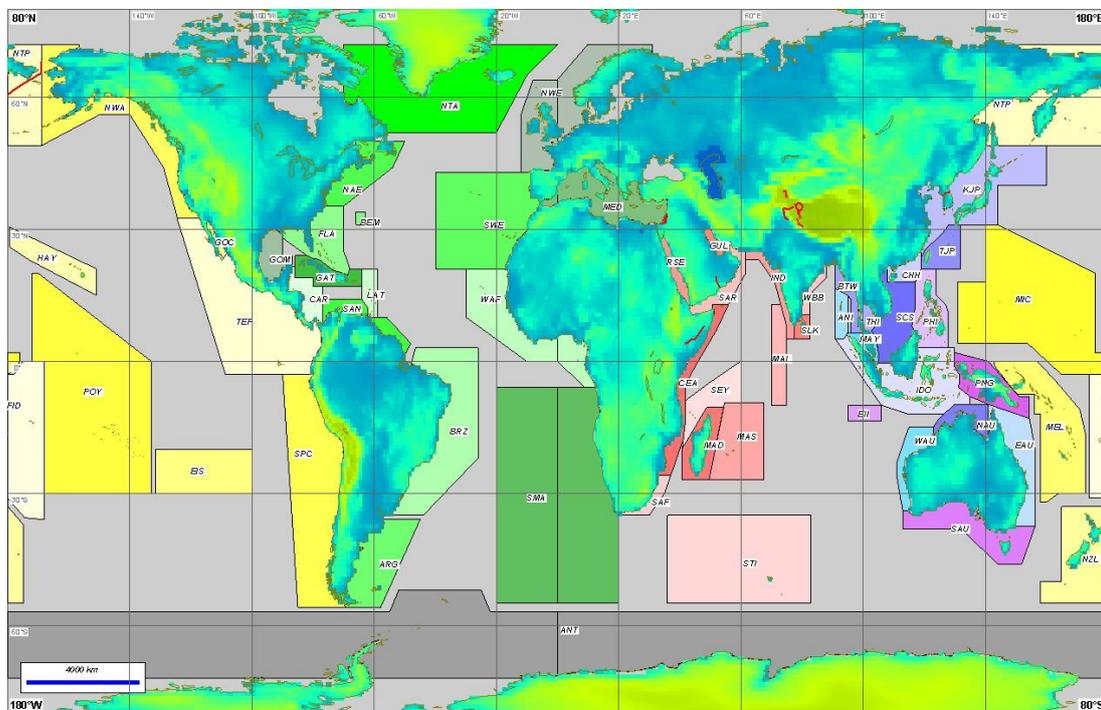
4   List of localities of this region.

Figure 2.16. A possible classification of marine areas following Hanske & Löser (2006).

2.4.3 Countries

This table has the name of the country and its abbreviation.

2.4.4 Marine areas

A marine area is a large body of marine water. As explained above, there exist various standards.

1   The name of the marine area.
2   The number and list of the localities are calculated automatically.
3   The number and list of the species are calculated automatically.

Figure 2.17. Data acquisition form of the table MARINE AREAS.

2.4.5 Sediment type

Figure 2.18. Data acquisition form of the table SEDIMENT TYPE.

The tables contains the different sediment types.

1   The name of the sediment type.
2   An index between one (very fine silty sediment) to 100 (pure rocks) allows to analyse which type of sediment is preferred by a species.
3   A colour can be assigned to the sediment type. This can be interesting in the correlation of localities.
4   A list of localities is shown.

The distribution can be analysed only if the correct index values are recorded,. The following table should give you some ideas about the sediment grain size.

Index	Example
5	Large sandy beach, partly muddy or silty
	Estuary, sandy-silty
	Tidal flats
10	Large sandy beach
15	Medium large bay with sandy beach, that has rocky margins
20	Sandy beach with little gravel
30	Sandy beach with some gravel
40	Rocky ground with sandy-silty sediment
45	Medium large sandy bay with rocky margins
50	Mixed environment with near-shore living corals
55	Rock mixed with sand
	Gravel (20-50mm)
60	Poorly consolidated rocks
70	Small sandy bay with rocky margins
	Rocky beach with small beaches
	Small bay with rocky margins, beach with gravel
80	Large bay with beach, but ground is rocky
	Rocky promontory with lateral sandy areas
90	Rocky beach with large loose boulders
100	Only solid rocks, no loose rocks

For the definition of the sediment distribution of a species, only clean assignments (very low and very high sediment indices, above in green) should be used. It is, therefore, possible to exclude localities with a mixed sediment type from the analysis.
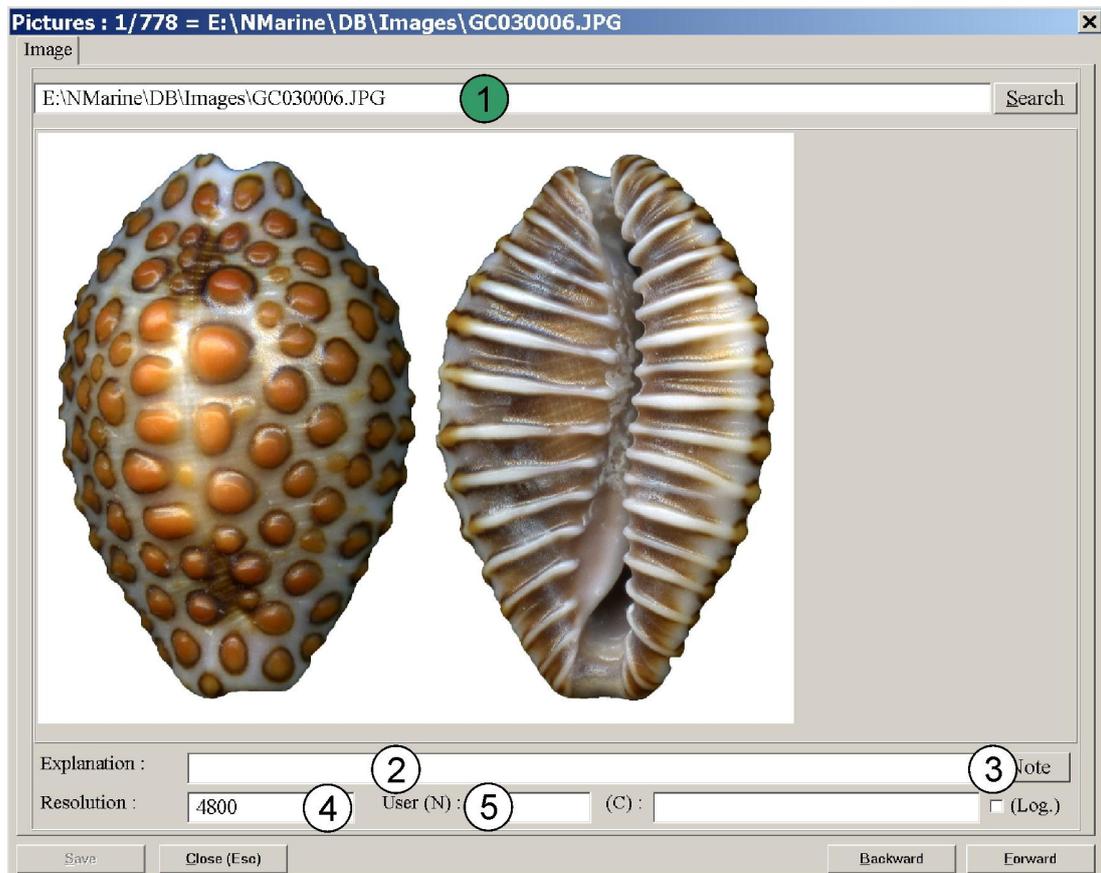
2.5 Images

2.5.1 Images

Figure 2.19. Data acquisition form of the table IMAGES.

The table contains all images of the database. Please remember that it is possible to import images automatically into this table. See below (Programmes > Import of images) for details.

1   The file name of the image. Images are not part of the database. In the database, only the links are recorded. Files of the types JPG, BMP, GIF, and WMF are displayed.

2   Place for an optional explication (on the image, not on the specimen).

3   Feel free to record a comment or note on the image.

4   If the resolution (dpi) of the image is known, it can be recorded here.

5   There are three fields that you may use for your data. The first is an integer number, the second is a string, and the third a logical value.

2.5.2 Images of specimens

The table interconnects the table IMAGES with that of SPECIMENS or MORPHOMETRIC DATA AND IMAGES. It is better to not directly append new items to this table, but rather to use the import function or the buttons in both tables mentioned above.

1   If it is envisaged to use this image in the HTML output, you may put a number here. The image with the first number will be shown first.

2   If it is envisaged to use this image in the Text output, you may put a number here. The image with the first number will be shown first.

3   Define this picture as the principal picture of a of many specimens of one record of the table SPECIMENS. This specimen will be shown. If no image is marked, the first found is shown.

4   Family, genus, and species names as well as the specimen number are set automatically. These fields cannot be modified, but it can be searched for.

5   Information about the owner of this image. Do not modify this field.

6   The link to the table IMAGES. Do not modify.

Figure 2.20. Data acquisition form of the table IMAGES OF SPECIMENS.

2.5.3 Images of localities

The table connects the table IMAGES with the table LOCALITIES and it is better to not touch this table, but rather to use the button in the table LOCALITIES. Its structure is similar to that of IMAGES OF SPECIMENS.

2.6 Sampling data

2.6.1 Sampling

The table contains the samplings of material. If control on sampling is not important to you, just use one record and also modify the field Date. If a strict control on sampling is important for your work, create a new record for each visit at a collection site. If you add single specimens to an existing lot of specimens, also add the sampling.

1   The field is interconnected with the locality.

2   The field is interconnected to the person who did the sampling.

3   The sampling date can be a date or time period. Press F7 to replace the current field with today's date.

4   Feel free to record a comment or note on the sampling.

5   The list of species found during this sampling. It is not a complete list of species of this locality because there may exist various samplings.

Figure 2.21. Data acquisition form of the table SAMPLING.

2.6.2 Sampling of specimens

This table connects the table SPECIMENS with the table SAMPLING. It is recommended that you do not touch this table, but rather use only the function of the table SPECIMENS.

2.6.3 Persons

This table encompasses only the names of persons that collected or donated (sold) material to you.

2.6.4 Donated

The table has the name of the person you received (bought) the material from, a date and a field for an additional note.

2.7 Literature

2.7.1 References

Figure 2.22. Data acquisition form of the table REFERENCES.

1   Five fields of authors refer to the table AUTHORS.

2   The year of publication. In parenthesis, the publication date as given in the book/article (only when different from the real publication date).

3   A reference letter serves to distinguish publications by the same author or team of authors that appeared in the same year.

4   The title of the book or article.

5   If the article is published in a book, the book can be selected here from the table BOOKS.

6   If the reference is a book itself or is published in a journal, this data can be selected from the interconnected table of JOURNALS.

7   Place for the volume, the issue, pages, and plates.

8   Two fields that are interconnected with other tables. The use of these fields is up to the user.

9   Mark or unmark references.

10   Feel free to record a comment or note on the reference.

11   A document can be attached to the record (e.g. a PDF file). Clicking on the '+' button allows to select a document.

The second page shows the citations of the reference. These citations are recorded in the table of SPECIES.

2.7.1.1 Authors

The table of AUTHORS has solely the family and given name as fields.

2.7.2 Books

Figure 2.23. Data acquisition form of the table BOOKS.

1   Up to three editors refer to the table AUTHORS.
2   Title of the book.
3   The publishing house refers to the table PUBLISHING HOUSES.
4   Field for the number of pages and plates.

2.7.3 Journals

Figure 2.24. Data acquisition form of the table JOURNALS.

1   The name of the journal.
2   The publishing house refers to a separate table.
3   The place of publication is interconnected with the table TOWNS.
4   The field serves to record the Internet URL address of the journal.
5   Feel free to record a comment or note on the journal.

2.7.4 Publishing houses

The table has only the name of the publishing house.

2.7.5 Towns

The table has the name of the town and is interconnected with the table COUNTRIES.

2.7.6 References of tables

Figure 2.25. Data acquisition forms of the table REFERENCES OF TABLES (below) with the corresponding record of the table SPECIES (above).

This table interconnects various tables, mostly that of the taxonomy, with a reference. It also holds information about a differing taxonomic opinion. The references with their citations attached to the species table are also shown as a list in the table of REFERENCES.

1   Information about the owner of this reference. Do not modify these fields.

2   Link to an item of the table REFERENCES.

3   The name of the species in the reference. In the above example, Keen cites the species as *Hipponix pilosus*, but the current name is *Pilosabio trigona*. This field should only be used when the species name differs. It is normal, that the generic assignment of a species may vary through time.

4   Place for the page and/or figure of the species within the given reference.

5   Currently unused field. In the future, it will be possible to suppress the output of this item e.g. in the HTML output.

2.7.7 Internet

Figure 2.26. Data acquisition form of the table INTERNET.

This table interconnects the tables of the species with the Internet URL addresses. It is more easy to manage from the table SPECIES.

1   Information about the owner of this reference. Do not modify this field.

2   Internet URL address.

3   A field to mark deleted records. A deleted record is not shown in the list in the table SPECIES.

2.8 Documents

2.8.1 Documents

Figure 2.27. Data acquisition form of the table DOCUMENTS.

A document can be a file on your computer or an Internet URL address.

1   Name of the document.

2   Comment or note on the document.

3   The button lets you select a file.

4   The button opens the file, either with the standard application defined by the operating system or as defined in Hdb2Win > Application library > Options > Tools > List of programmes.

2.8.2 Documents of tables

The table interconnects the documents with the tables and should be only managed by the tables.

2.9 Trade

2.9.1 Lists

Figure 2.28. Data acquisition form of the table LISTS.

A list is a compilation of various specimens (parts of many). The trade is more easy realised from the main table of SPECIMENS.

1   Name of the list.

2   The person who received the material from the list.

3   Comment or note on the list.

4   Items contained in this list.

2.9.2 List items

Figure 2.29. Data acquisition form of the table LIST ITEMS.

A list item is the assignation of a specimens to a list. Here, it is also possible to print labels of selected items.

1   The list as a reference to a record in the table LISTS.

2   The item refers to a record in the table SPECIMENS.

3   The number of specimens.

2.10 Text comments

The tables for text comments can be interconnected with any table. For the moment it is interconnected with the tables SPECIES, GENERA, and FAMILIES. The user may define own data classes and add notes, texts, files, etc. This is easier than modifying the data structure when a new piece of information should be added. The disadvantage is that a search for items is not possible. The principal function of this table is to add specific text-related information to species or genera. This can be a description, discussion, or any specific comment.

2.10.1 Data types

This table is predefined and should not be altered. It contains the data types that may select for the table DATA CLASSES (that can be defined by the user).

2.10.2 Data Classes

Figure 2.30. Data acquisition form of the table DATA CLASSES.

The data classes can be created by the user, but it is recommendable to use the function of the comment sheets (here, in this version, only in the table SPECIES). Only the fields marked with a white background may be modified later.

1   Name of the data class in your language.

2   Name of the data class in English.

3   The data type.

4   If this data type is only valid for one table, this table is given here.

5   Internal.

6   An optional sorting code can be recorded here.

7   Mark the box if this data type should be included in the HTML output.

8   Mark the box if this data type should be included in the future text output.

2.10.3 Comments

Figure 2.31. Data acquisition form of the table COMMENTS.

This is the principal table of the group and contains the text comments themselves. As above, it is recommendable to use the function of the comment sheets (here, in this version, only in the SPECIES table).

1   Table within which the comment belongs.

2   The data class of the comment.

3   The content (that can be text, numerical data, or a reference to a record of another table).

4   The record to which the comment belongs.

5   A longer text (as an alternative data type).

6   A field that marks deleted records.

3 Data recording

Data recording begins with the download and installation of the programme. You need to install the application of *Oliva*. You do not need the other applications (PaleoTax, PalCol). You need to install Paleo-Tax/Map when you want to plot your material on a map. PaleoTax/Graph is included in the database but is also available as stand-alone version. To create a new database follow the steps described in the manual Hdb26Eng.pdf. Usually, you will start recording data with the table SPECIMENS. From this table you may also record species and localities. It is not necessary to change from one table to another to append records.

Before starting, it is useful to think about the following topics:

- Do you want to record single specimens, many specimens, or both? All can be recorded in the table SPECIMEN, but if you want to image specimens or take measurements, it should be decided where to store the image(s) – with the specimen or with the sub-numbers (MORPHOMETRIC DATA AND IMAGES).

- Think about a system of numbering for your material. A self-explanatory number – consisting of a locality code and a current number – can be easier to manage than a current number. It generally causes problems when the number contains spaces, points, or slashes. A short number only consisting of characters and digits is recommended. This makes later the automatically import of images easier.

- If you want to take morphometric data, please fill in the fields of the morphometric characteristics for each genus (in the table GENERA; Figure 2.12), always when recording a new genus.

It is easy to import pre-existing data into the database. The import of genera, countries, or marine areas, e.g. tables that are not interconnected with many other tables, can be realised without any programming. For importing more complex data (species, localities, specimens) a programme is available from SR2 on. See below in the chapter 'Data import from text files'.

4 Search and output

For the function of search and output data please compare to the general introduction on the database. Here we talk only about specific output modes in *Oliva*.

4.1 Various tables : specimen and species labels

Probably, the most common output of the RTF format will be the specimen label. Four tables offer this option. Whereas in the tables of LOCALITIES and SPECIES the design of the label is fixed, the design of labels in the tables of SPECIMENS and LIST ITEMS can be defined by the user. When selecting one of the latter tables, you have to decide which data the label should have.
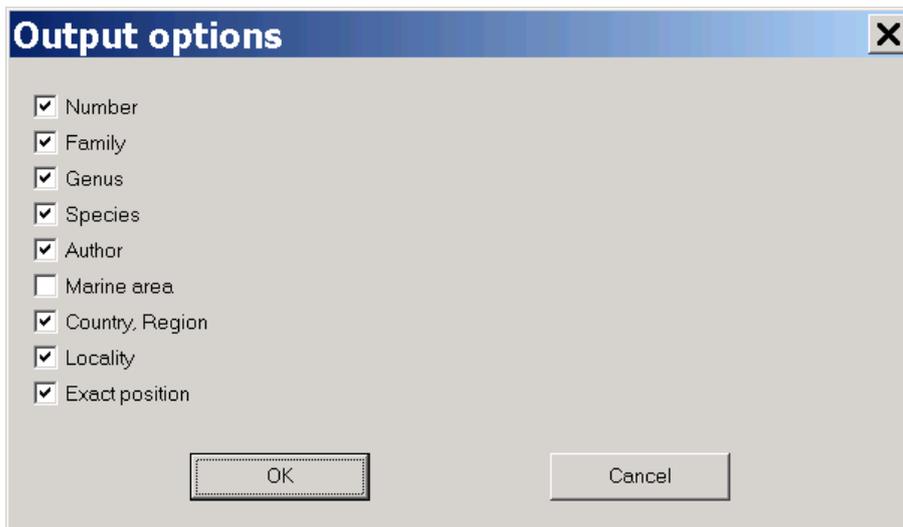

Figure 4.1. Options for the label.

The RTF output creates a file where characters are formatted and each label is marked with a frame.
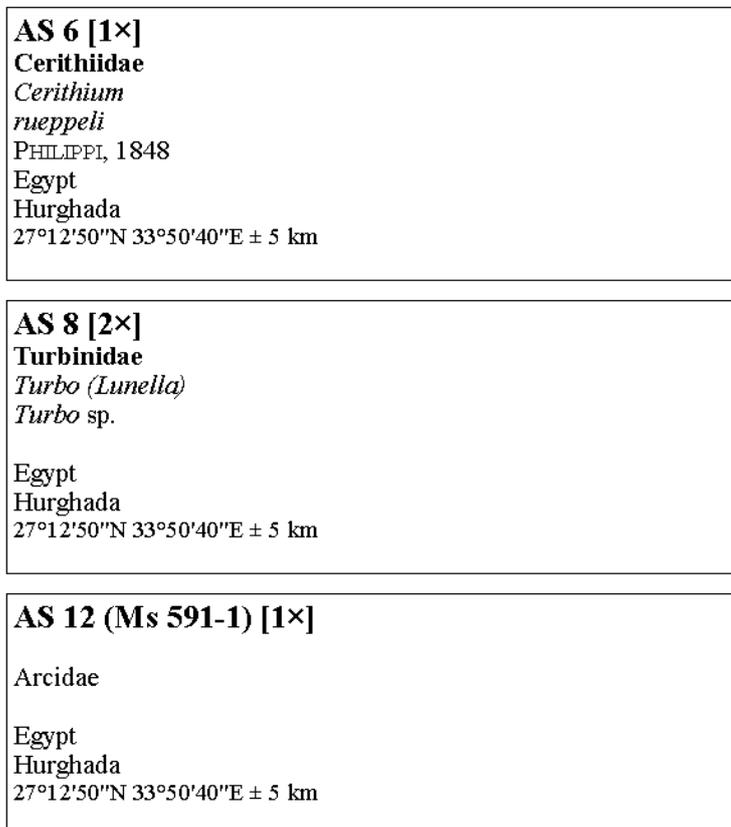

Figure 4.2. Label output.

In order to obtain more narrow labels, you should increase the number of columns. The exact values for the width of the columns and their distance depends on the used paper format. If you want to modify the box around the text (line thickness, line style, line colour, distance to the text) you should only modify these characteristics in the paragraph style "Standardtext".

Figure 4.3. Label with formatted columns and boxes.

4.2 Specimens : table

The output produces a text file in the PaleoTax/Graph (PGR) format that is converted into a table. The table may extend over several pages. The total number of lines is 10240, what corresponds to approximately 170 pages of 60 lines each. You will be able to select specific records from the table of SPECIMENS, or output all. Let's assume a search for all species from the marine area Red Sea. Select then Table (PGR) and the output format is automatically set to PGR.

After clicking on 'Output', a list of the possible data are shown. It does not make much sense to select all levels, just because of the limited space in the table. In the next step you need to define the number of lines per page (a value between 10 and 200 is expected). A message at the end informs about the page number.

Figure 4.4. Selection of data.

If in the above list the species was selected, you are asked in a second question whether you want to output the author of the species and its frequency. The frequency is taken from the SPECIES table. If no frequency is available the abbreviation 'n/a' is shown.
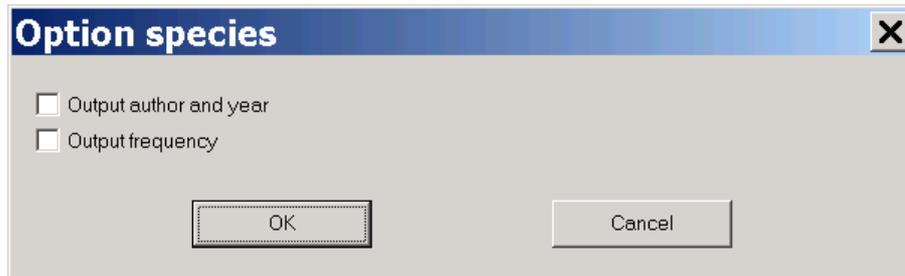
Figure 4.5. Options for the species.

Now PaleoTax/Graph is started and the resulting table is shown. You may change the paper format, margins, the width of each column, the thickness of lines, the height of lines, the text format and size, etc. (all this is explained in the documentation file on PaleoTax/Graph). The table is written in the WMF format and can easily imported by many programmes.

Order	Family	Genus	Species
Arcida	Arcidae	Barbatia	sp.
Cardiida	Tellinidae	Quidnipagus	palatam
		Tellina	sp.
Cycloneritida	Neritidae	Nerita (Theliostyla)	sanguinolenta
Littorinimorpha	Cymatiidae	Cymatium	aquatile
	Naticidae	Natica	gualtieriana
	Strombidae	Strombus (Canarium)	mutabilis
		Strombus (Gibberulus)	gibberulus albus
		Strombus (Laevistrombus)	fasciatus
		Strombus	ochroglottis
	Tonnidae	Tonna	canaliculata
	Velutinidae	Lamellaria	sp.
Lucinida	Lucinidae	Codakia	
Neogastropoda	Conidae	Conus (Hermes)	nussatella
		Conus (Pionoconus)	achatinus
	Costellariidae	Vexillum	sp.
	Muricidae	Murex (Murex)	aduncospinosus
	Pisaniidae	Engina	mendicaria
		Pisania	ignea
			sp.
Patellogastropoda	Patellidae	Patella (Patella)	
Sorbeconcha	Cerithiidae	Cerithium	rueppeli
Venerida	Mactridae	Mactra (Mactra)	sp.
Vetigastropoda	Trochidae	Clanculus (Clanculus)	pharaonius
	Turbinidae	Turbo (Lunella)	sp.

Figure 4.6. Resulting table.

4.3 *Specimens : rarefaction*

Rarefaction helps to analyse how complete is a collection within a defined area. Rarefaction sets the number of specimens and the number of species into relation and shows a curve. A global analysis does not make sense, it is better to limit the analysis to a specific region or marine area.

4.4 *Species : data sheet*

The data sheet function is offered by the table of SPECIES. It collects information about a species that is presented in a text file of the RTF format. The programme is complex and offers a wide range of options. You may select one or multiple species. All selected species are written into one file, but each species starts on a new page. You may sort the table before using this function.
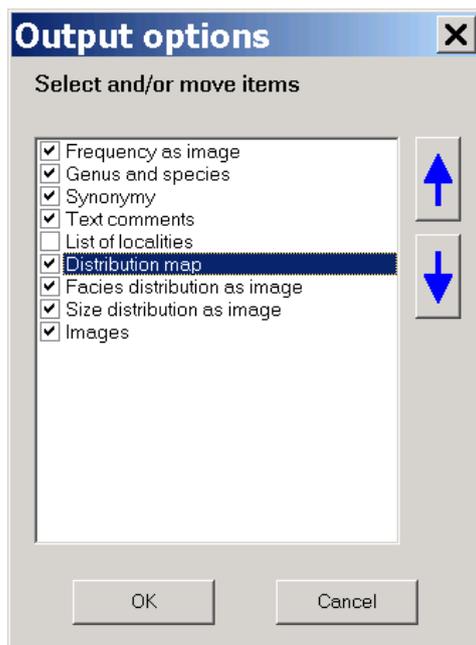
Figure 4.7. Data for the data sheet.

The first step is the selection which data will appear in the data sheet (Figure 4.9). The following items are available:

- Frequency as image – The frequency of a species is coded in a small image.
- Genus and species – Name of the species with author and year.
- Synonymy – List of citations of the species.
- Text comments – Text comments from the second page in the data acquisition form of the table SPECIES.
- List of localities – List of localities where the species was found.
- Sediment distribution as image – A small table showing the distribution of the species among sediments of different grain size.
- Size distribution as image – A small table of the distribution of measured specimens.
- Distribution map – A map where the occurrence of the species is plotted
- Images – Images of the species. The images are not included in the RTF file, only links to them.

It is not only possible to select or deselect items, it is also possible to modify their order. Only the genus and species name cannot be removed, and this item and the frequency cannot be moved to another place. For some topics, there are options. As in most other programmes, once selected options are stored in the Hdb2Win Registry and proposed in another execution of the programme. Following the various items and possible options are explained.

4.4.1 Frequency as image

A full circle indicates a very common species, a circle with three quarters filled a common species, etc. up to an empty circle for very rare species. A cross in a circle indicates the absence of frequency data. The images of the PCX type are found in the data folder. You may modify them but you should take care not to modify their size of 239x239 pixel and the resolution of 600dpi. It is not possible to modify the position of this topic within the data sheet.

4.4.2 Genus and species

Shown is the genus, subgenus, species, subspecies, variety, form, and author. This topic is fixed. It cannot be removed and its position cannot be modified.

4.4.3 Synonymy list

The synonymy list is compiled from the data recorded in the SPECIES table under the button 'Literature'.

4.4.4 Text comments

Text comments are only shown when either attached to the table of SPECIES or no to any table at all, and if the field Output (Text) in the table COMMENTS : DATA CLASSES is set. Moreover, the field Sorting in the same table must be set. If the sorting value is missed in one data class, the programme asks to complete the data.
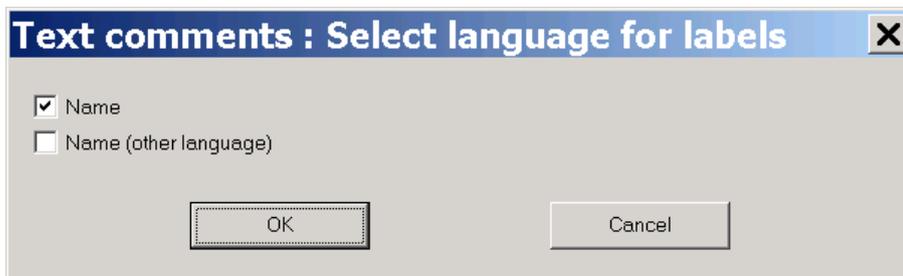
Figure 4.8. Language for the text comments.

You are also asked which language should be used for the labels of the comments. These names are defined in the table COMMENTS : DATA CLASSES.

4.4.5 List of localities

The list of localities is compiled from data of the SPECIMEN table.

4.4.6 Sediment distribution as image

The sediment distribution image is the same that can be compiled in the SPECIES acquisition form. If the WMF file is not available, the programme will ask whether the file should be created.
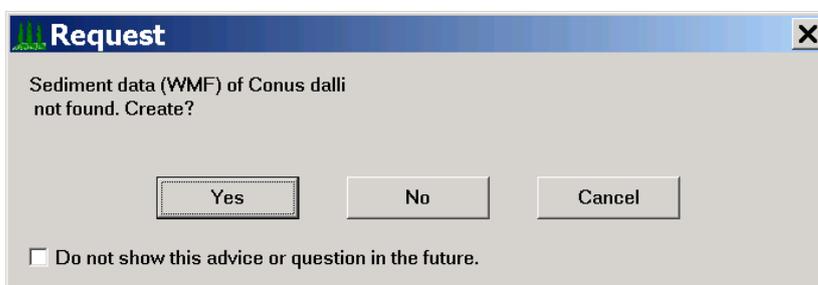
Figure 4.9. Absence of the sediment distribution image.

If you decide the create the file, you need to answer the questions as described above (description of the SPECIES data acquisition form). The PaleoTax/Graph plug-in is called and shows the file. You do not need to do anything; the plug-in writes the WMF file and closes automatically.

When selecting the option 'Do not show this advice ...' the programme will in future automatically create the file, without asking, applying the options set the last time. This auto-mode can be switched off the in the *Oliva* options.

4.4.7 Size distribution as image

The size distribution image is the same that can be compiled in the SPECIES acquisition form. For the image caption there are options for the name of measurement type. You need to decide which data from the table MORPHOLOGICAL CHARACTERISTICS is used to describe the size.
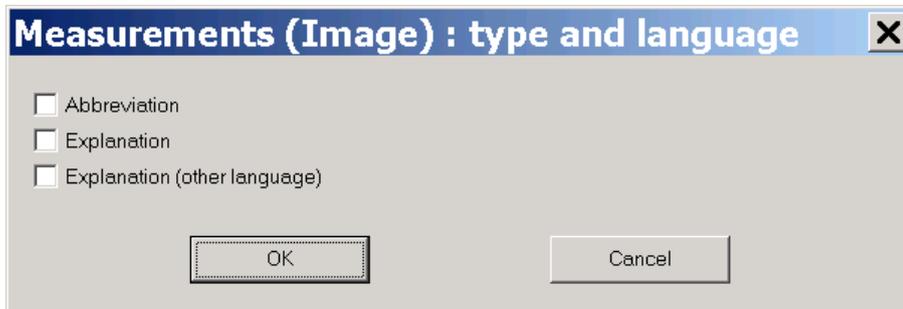
Figure 4.10. Selection of the caption for the image.

If the WMF file is not available, the programme creates the file automatically. The PaleoTax/Graph plug-in is called and shows the file. You do not need to do anything; the plug-in writes the WMF file and closes automatically.

4.4.8 Distribution map

The distribution map is the same that is shown in the Species acquisition form. If the file is not available, it is not created because this programme is too complex to be called as a sub-routine.

4.4.9 Images

The images are taken from the table MORPHOMETRIC DATA AND IMAGES. First you need to select the images to be shown.
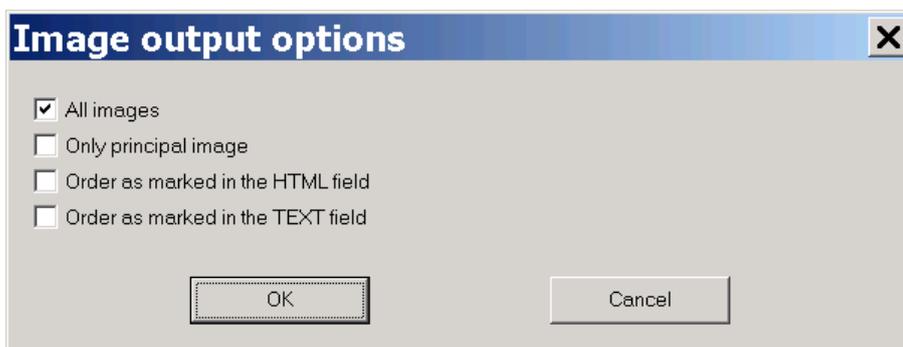
Figure 4.11. Selection of images.

For the image captions exist various options.
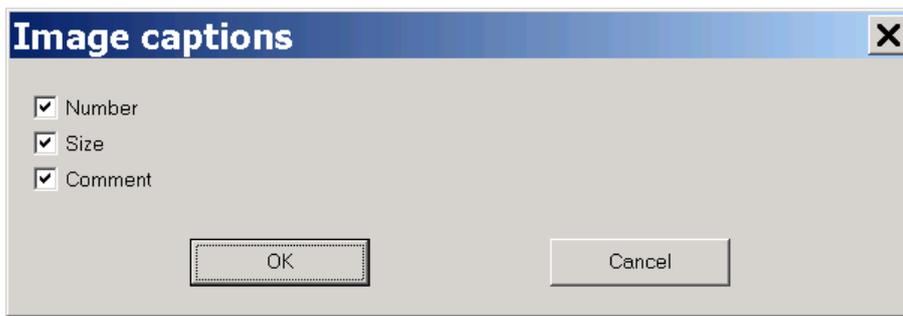
Figure 4.12. Selection of image caption.

The comment is taken from the table MORPHOMETRIC DATA AND IMAGES. If you have decided the size to be included, you also need to decide which data from the table MORPHOLOGICAL CHARACTERISTICS is used to describe the size.
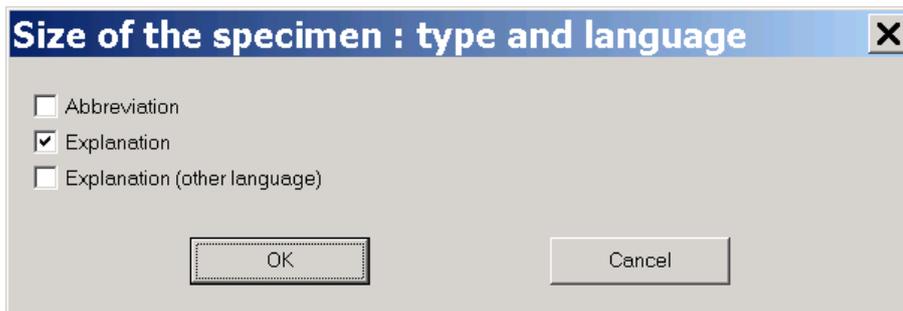
Figure 4.13. Selection of the caption for the size of the specimen.

In RTF files it is not possible to define the size of bitmap images. Conventional text processors do not read the resolution of the image, they assume a value of 120dpi or 180dpi. In some programmes, when the image is wider than 16cm, it will be reduced to this size. In some text processors, the wide of the image is adapted to the wide of the page or columns, in others not. The problem is generally known. A recommendation is, to limit the size of the image with a one-cell-table, but this does not change the size of the image, it only crops it. So do not wonder when your images appear much to large.

4.4.10 Paper format

There are presently two options for the paper format. The correct selection guarantees that the size of the columns fits to the selected paper.
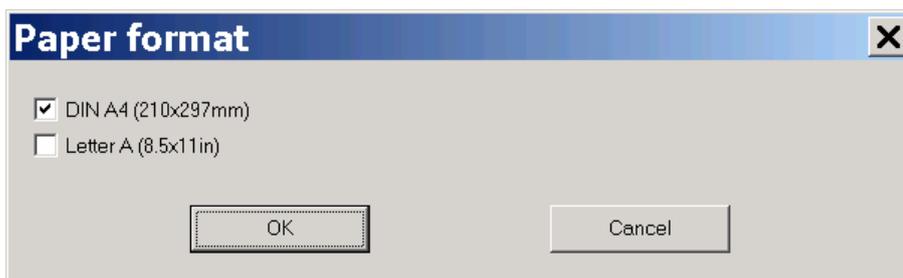
Figure 4.14. Selection of the paper format.

Figure 4.15 shows the result for one species. Note that the RTF was not modified.

Pseudozonaria annettae (DALL, 1909)

KEEN (1971) Sea shells of tropical West America. Marine Mollusks from Baja California to Peru. – p. 495

BRUSCA (1980) Common intertidal marine invertebrates of the Gulf of California. 2nd edition. – p. 170

BURGESS (1985) Cowries of the world. – p. 102

BERTSCH & AGUILAR ROSAS (2016) Invertebrados Marinos del Noroeste de México. Marine Invertebrates of Northwest Mexico. – p. 199 – (as *Zonaria annettae*)

Size and remarks. Internet resources report a maximum length of 55mm. Specimens nearly up to this size can be found, but most are between 30 and 50mm.

GC063009/0.

GC034009/3. Length 37.8mm.

Geographic distribution.

Distribution according to the facies.

Distribution of the length.

Figure 4.15. Example of the result.

4.5 Species : distribution of species among the sediment type

The function shows the average sediment type of the selected species (as for instance, one genus or one family) in a graph. The species are sorted according to the genus and the sediment type (not according to the species name).

4.6 Morphometric data : graphs of morphometric data

The table offers with SR2 the export of morphometric data into a graph. Several conditions must be fulfilled. Characteristics need to be recorded with the genus of interest, and at least two values must be recorded for each specimen.

After making your selection of records (that can be a genus, species, or a specified lot in the table of the SPECIMENS) the programme checks whether all selected specimens belong to same genus. If not, the message '(E1) all specimens must belong to the same genus.' is displayed. If for the genus an insufficient number of characteristics is recorded (less than two), the message '(E2) insufficient number of characteristics.' is displayed. If no error occurred, the programme starts with several questions.

Select language for labels ✕ ☑ Explanation (your language) ☐ Explanation (other language) OK Cancel	The first step is the selection of the language. Remember that there are two fields in the table CHARACTERISTICS, one for your own language and another for another language (as for instance English).
Select two characteristics ✕ ☐ Small diameter (mm) ☐ Larger diameter (mm) ☐ Length (mm) ☐ Length last worl (mm) ☐ Weight (g) ☐ Sediment type OK Cancel	In the second step you have to select at least two characteristics. If you select more than two characteristics, only the first two are evaluated. If you select only one, a error message is displayed. From SR3 on, the sediment index can be used as one characteristic. This may serve to see whether the size of the organism depends on the grain size.
Label for Oliva incrassata ✕ ☐ Specimen number ☐ Sub number ☐ ID Number OK Cancel	In the third step you may decide how the data points are labelled.
The data are written into a PaleoTax/Graph file. If no data are found, an error message is shown. Otherwise the plug-in of this programme is started and the graph is displayed. Please be aware that PaleoTax/Graph offers multiple options and you should consult the manual.	
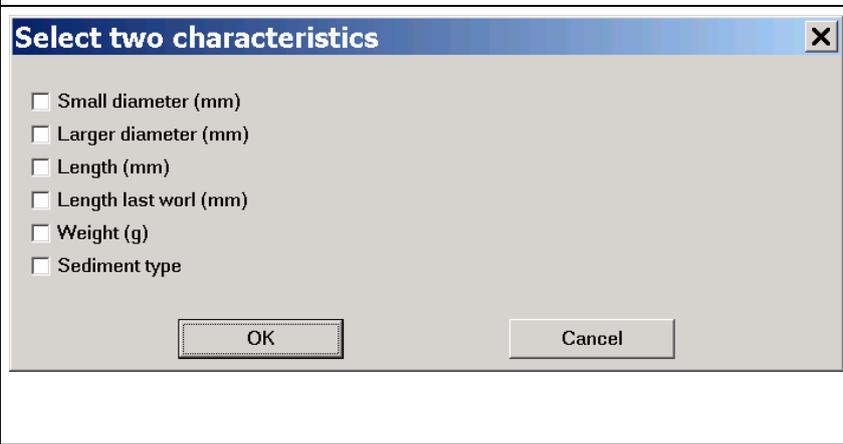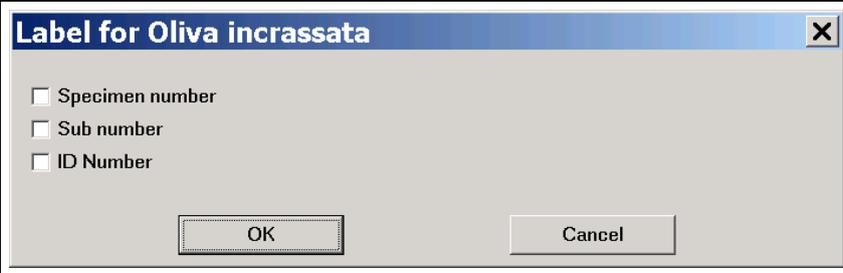
4.7 Localities : species list

This output produces a text file in the Rich Text Format (RTF). You will be able to select specific records from the table of LOCALITIES, or output all.

4.8 Localities : species per family

This output produces a graph file in the PaleoTax/Graph format (PRG). This graph shows in the form of a percentage bar how the species of one or multiples localities are distributed among families. If no data are found, no graph is shown. Otherwise the plug-in of this programme is started and the graph is displayed. Please be aware that PaleoTax/Graph offers multiple options and you should consult the manual. It does not make much sense to include too many localities. A maximum of 128 families is shown.

4.9 Localities : records per visit

This output produces a graph file in the PaleoTax/Graph format (PRG). This graph shows in the form of horizontal bars the numbers of records per visit for the selected localities. If no data are found, no graph is shown. Otherwise the plug-in of this programme is started and the graph is displayed. Please be aware that PaleoTax/Graph offers multiple options and you should consult the manual. It does not make much sense to include too many localities.

4.10 Localities : frequency of species

This output produces a graph file in the PaleoTax/Graph format (PRG). This graph shows in the form of a bar chart the number of very rare, rare, occasional, common and very common species. Per default, very rare species are shown first (left). This can be changed in the options. There is a limit of 32 localities.

4.11 Localities : distribution of species/order

This output produces a graph file in the PaleoTax/Graph format (PRG). This graph shows in the form of a bar chart the distribution of the species among the orders. There is a limit of 16 localities and 256 orders. Works better for less than 20 orders.

4.12 Localities : export position into geocaching (LOC)

Note that the name of the locality (or the short name) must not contain any special character, only letters and numbers.

4.13 Localities: R- and V-index

Both indices can only be calculated when frequency data for the species are available. The first one, the 'index of rarity' (r-index), varies between zero and hundred and it is based on percentage values of very rare to very common species at this locality. So the percentage value for very common species is multiplied with one, the value for common species with two, and so on. The resulting values are summarised, reduced by 100, and then divided by four. The lowest value is zero for a locality where all species are very common and the highest value is 100 for a locality where all species are very rare. Of course, such extreme values are never reached in collections that encompasses at least 30 species. See the equation below.

$$index = \frac{\left(\sum_{i=1}^{5} p_i \cdot i\right) - 100}{4}$$

Equation for calculating the rarity index for a specific locality: **p** vector with the percentage values starting with very common species.

The second index can be called an index of interest (i-index). It combines the total number of species and the index of rarity.

$$index = \frac{\left(\dfrac{ns \cdot 100}{sx}\right) + ri}{2}$$

Equation for calculating the overall index of interest for a specific locality: **ns** number of species of the specific locality; **mx** highest number of species for all sites within the examined area; **ri** rarity index from above.

5 Programmes

Complex data analysis and output (as RTF text files or WMF graphs) is either attached to the tables from where data are obtained (see above under chapter 'Search and output') or – when independent from any table – behind the button 'Programmes' in the main menu of the database. Most of these programmes have numerous options. The individual settings are saved by the system, hence when starting a programme again, the former selected options will be set by default. Of course, you will be asked whether you agree with the settings or not and you may modify the settings.
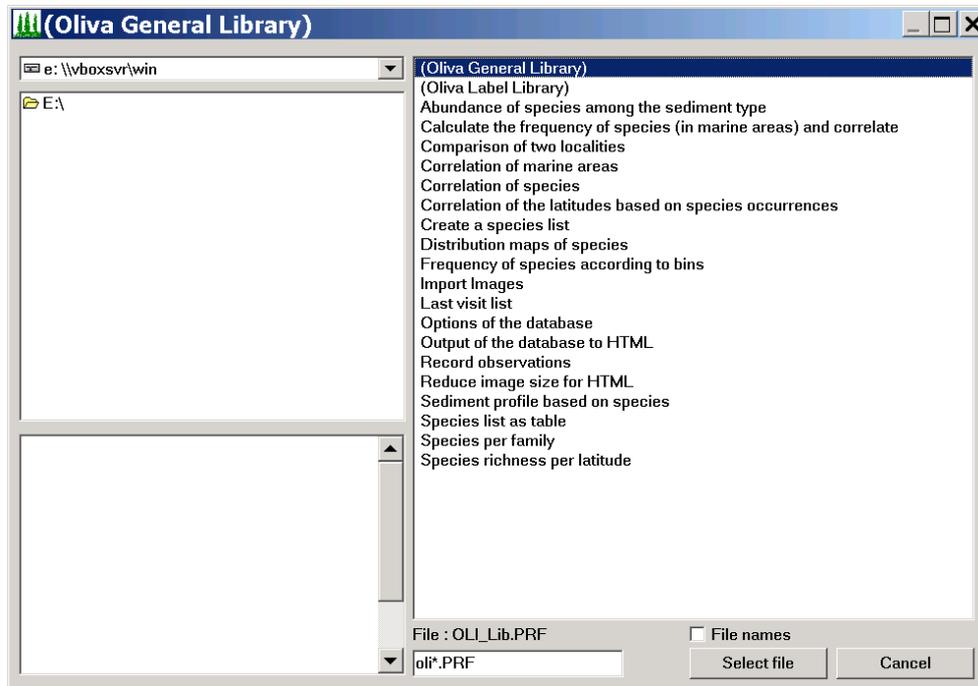

Figure 5.1. Programmes available in Service Release 5.

All programmes are written with the database interpreter (the same as what you see in the main menu when starting the programme). For the very complex interpreter, there exists an extensive manual that is regularly updated and which can be found on the manual page of the database system. Be very careful when applying changes and work only with copies. If you want to modify a programme that is part of the *Oliva* package, make a local copy under a different name. If you want to modify OLI4_AB.PRF, make a copy and call it OLI4_ABmod.PRF. Keep the first three letters so you do not need to search when clicking on the button 'Programmes'. Modify the description in the heading of the programme.

Please note that most programmes are expecting a certain amount of records in some tables (principally SPECIMENS, SPECIES, LOCALITIES). So before starting the programmes you have to record some data. It can be that the programme simple will not start when the number of records is too low.

In the following sections all programmes are described. Following a dot (•) the place and/or name of the programme is given, the programme name in parentheses.

5.1 *Data estimation, statistics, and consistency*

5.1.1 Analysis, statistics, and reorganisation

- Application library > Reorganisation > Reorganisation and various index files

The programme updates fields in red with the current data (tables GENERA, LOCALITIES, MARINE AREAS, SPECIES, SPECIMENS). It also gives a short report about how many genera, species and specimens are recorded in the database. The programme also resets the assignation of images of sub-numbers to specimens.

5.1.2 Check database

- Application library > Reorganisation > Consistency check.

The programme checks the database for double records (same species and same locality), records with a number but without specimens, and records with specimens but without number. At the end of the routine, a brief report list shown.

5.1.3 Frequency of species and correlation

- Programmes > Calculate frequency of species (in marine areas) and correlate (OLI4_AB.PRF)

This programme is complex and it will only work properly if the regions of the localities have a marine area. The programme is only interesting for collectors who work within a small area. Since it estimates only one marine area, the sediment distribution and the frequency of the species are only valid within the selected area.
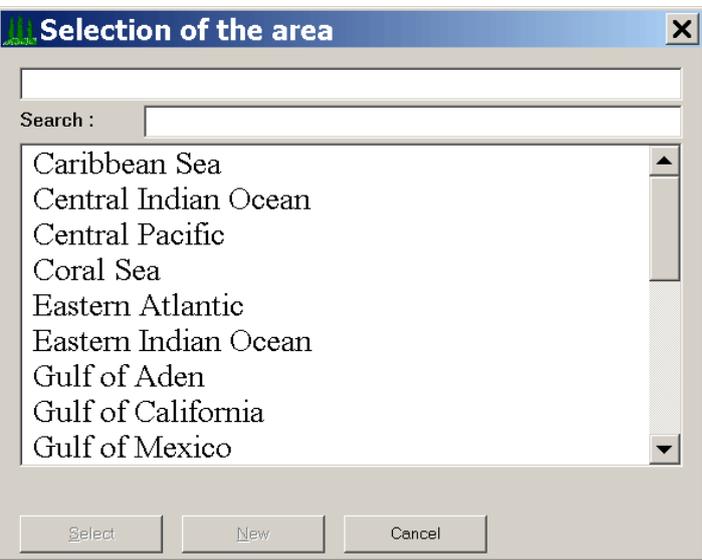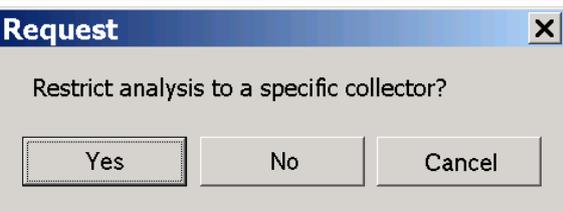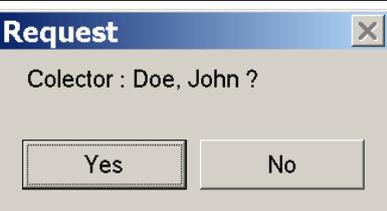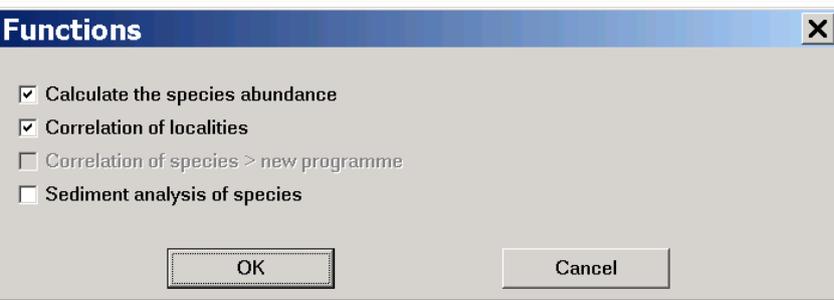
The frequency (as shown in the data acquisition form of the table SPECIES) is based on the number of localities where a species was found, in relation to all localities. The localities can be limited. It makes no sense to include localities that have only a few species because obviously they were not thoroughly sampled and only common species are recorded.

The frequency of species is anyhow tricky. Generally, if collecting material you will find out quickly which species are common and which not. There are species that seem to occur everywhere, whereas other species seem to be extremely rare. It is a normal experience that there exist few really abundant species and many rare species.
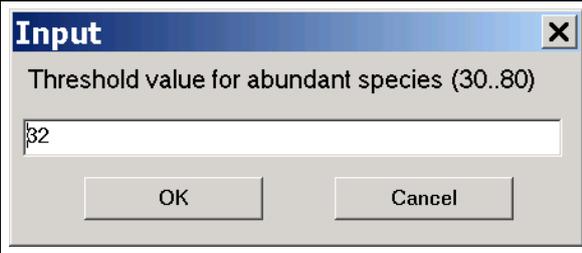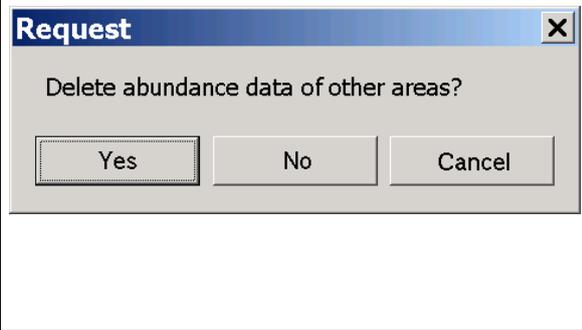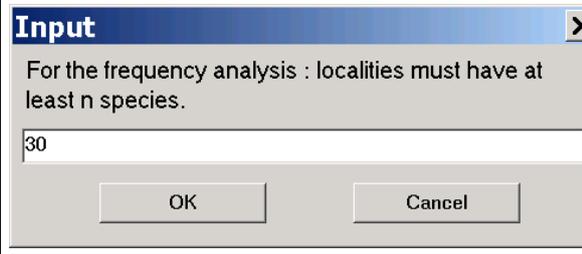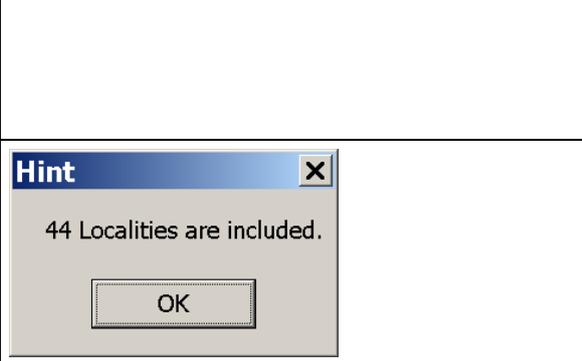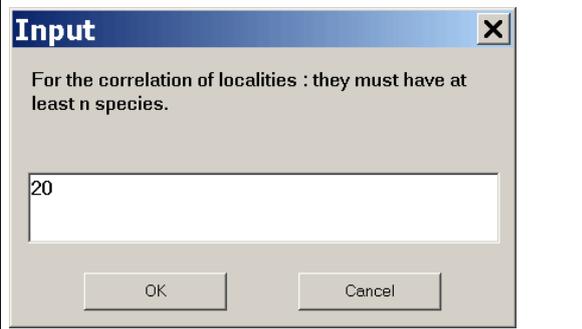
The frequency is calculated with a logarithmic approach. First an initial threshold value is defined, let's assume 60. This means that all species that occur at more than 60% of all included localities are very common. The initial value is divided by two: species occurring at 31 to 60% of the localities are considered common. Species occurring at 16 to 30% of the localities are considered occasional. For rare species, a value from 8% to 15% is assumed. The remaining species occurring at less than 8% of the included localities are considered very rare. A high initial values reduces the number of very common species and increases the values for rare and very rare species. A low initial value has a contrary effect. The analysis of the frequency does not work well with a low amount of species per marine area. If a marine area has about 100 species, the initial threshold should be a high value, such as 60 or 80. If the sediment type has a strong influence on your organism group, you better start with a lower value.

The analysis can be restricted to a specific collector in order to exclude material that was purchased or exchanged, where the a correct place of collection is unknown. This restrictions does only works well when the specimens have got all sampling data, e.g. a person and a date when the specific specimen was collected or observed.

When correlating and using afterwards a MDS analysis, please note that the name of the locality should be short (the correlation offers various options for labeling) and must not contain any spaces. When applying MDS, apply 'User similarity'.

Request ☒ Area "Gulf of California"? [Yes] [No]	The first step is the selection of the marine area. If the programme was already executed once, the formerly selected area is proposed.
Selection of the area ☒ [ ] Search : [ ] Caribbean Sea Central Indian Ocean Central Pacific Coral Sea Eastern Atlantic Eastern Indian Ocean Gulf of Aden Gulf of California Gulf of Mexico [Select] [New] [Cancel]	If no area was formerly selected or the area should be modified, it will be selected from a list.
Request ☒ Restrict analysis to a specific collector? [Yes] [No] [Cancel]	In a second question is asked if the analysis is restricted to a certain collector (material taken by other persons will be not included).
Request ☒ Colector : Doe, John ? [Yes] [No]	If confirmed, the collector from former programme executions is proposed.
Selection of the collector ☒ [ ] Search : [ ] (unknown, local dealer) ▲	If it is not convenient or no collector was selected before, the collector is selected from a list.
Functions ☒ ☑ Calculate the species abundance ☑ Correlation of localities ☐ Correlation of species > new programme ☐ Sediment analysis of species [OK] [Cancel]	Now the programme offers various execution options. 1, calculation of the species frequency, 2, output of a correlation of the localities based on the species occurrence, 3, the correlation of the species is now in another programme (see below), 4, sediment analysis of the species.

(1) Species frequency

Input ✕ Threshold value for abundant species (30..80) `32` [OK] [Cancel]		The first step is the selection of the initial threshold. It should be a value between 30 and 80. If the programme was already executed once, the formerly selected value is proposed.
Request ✕ Delete abundance data of other areas? [Yes] [No] [Cancel]		You may keep the frequency data calculated for other marine areas (No) or discard these data (Yes). Note that the frequency is based on the total number of species per area, so in one area a species may be common when indicated at 10 localities, in another area at 25 localities.
Input ✕ For the frequency analysis : localities must have at least n species. `30` [OK] [Cancel]		An analysis of the frequency only makes sense when the data are representative. If, on average, at one locality 50 species are observed, a locality with only five species should not be included because it is very likely that this locality was not thoroughly sampled. Therefore, here a minimum number of species can be defined.
Hint ✕ 44 Localities are included. [OK]		The number of included localities is reported.
Input ✕ For the correlation of localities : they must have at least n species. `20` [OK] [Cancel]		

The resulting graph below shows the number of species for each bin.

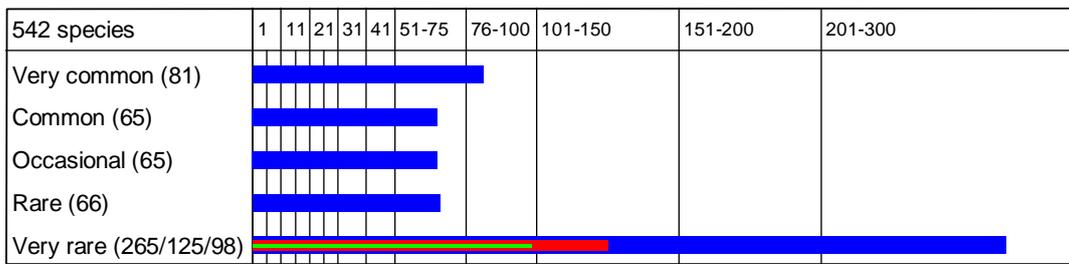| 542 species	1	11	21	31	41	51-75	76-100	101-150	151-200	201-300
Very common (81)										
Common (65)										
Occasional (65)										
Rare (66)										
Very rare (265/125/98)										

Figure 5.2. Results of species frequency. The last line shows three values. The thickest (blue) line correspond to all species, the red line shows the species with only one locality, and the green line shows the species with only one specimen (singleton) available.

(2) Correlation of localities

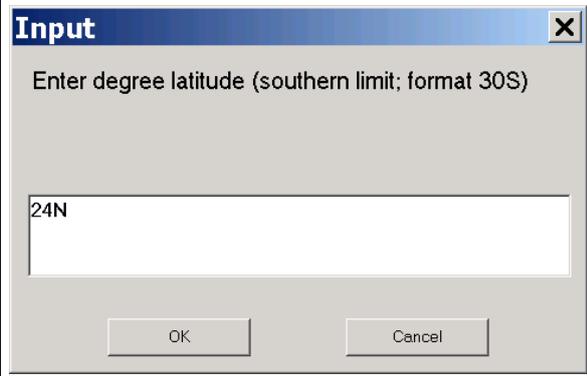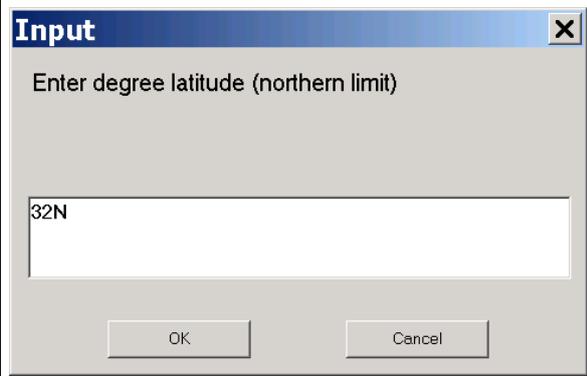|	
Input × Correlation of localities : they must have at least n species. 50 [OK] [Cancel]	A minimum number of species per locality can be defined. It does not make sense to compare localities with 100 species to a locality with 10 species.
Options output × ☐ Country ☐ Region ☑ Site ☐ Sample point ☑ Number of species ☑ Sediment data ☑ Sediment data with colour [OK] [Cancel]	The correlation data are written into a PaleoTax/Graph file. You may select which locality data are shown in the graph. The plug-in of this programme is started and the graph is displayed. Please be aware that this programme offers multiple options and you should consult the manual.

(4) Sediment analysis

Request × Sites marked in the field <No analysis> exclude from sediment analysis [Yes] [No] [Cancel]	You may decide whether marked localities are not used for the sediment analysis. This can be the case if the locality is very large or correct facies data are unknown, or the locality represents mixed sediment types.

5.1.4 Correlation of the latitudes

- Programmes > Correlation of the latitudes based on species occurrences (OLI2_CRLA.PRF)
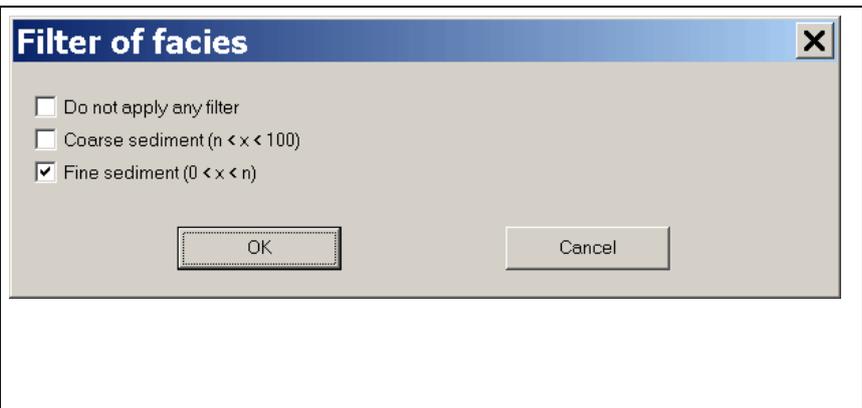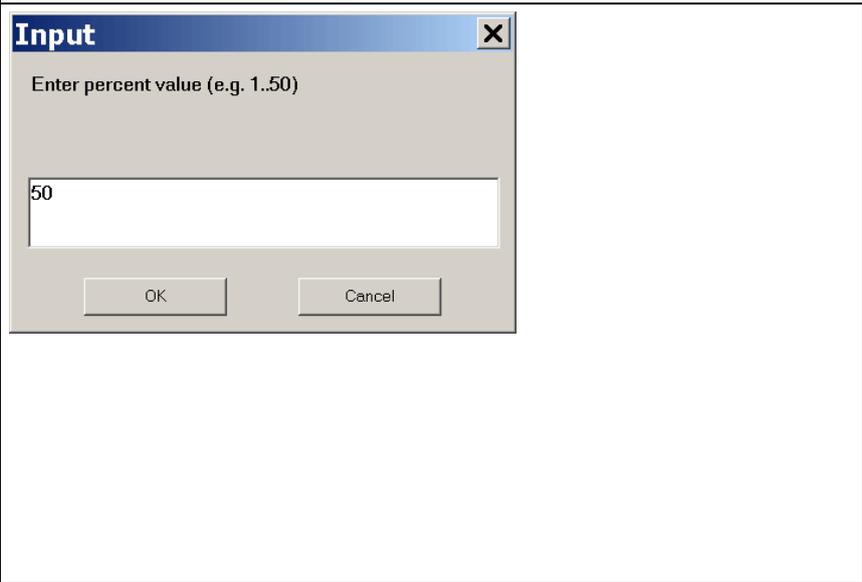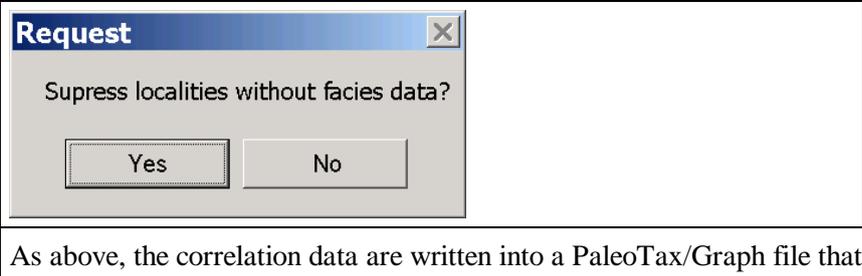
The distribution pattern of marine organisms depends much on the geographic latitude. This programme correlates the latitude based on the occurrence of species.

Input ✕ Enter degree latitude (southern limit; format 30S) `24N` OK Cancel		The first step is the selection of the southern limit in full degree (no decimals are allowed here). The hemisphere (N or S) must be indicated.
Input ✕ Enter degree latitude (northern limit) `32N` OK Cancel		The second step is the selection of the northern limit. As above, no decimals are allowed and a hemisphere (N or S) must be indicated.
Input ✕ The selected area covers 8 degrees. Enter the raster in minutes. `20` OK Cancel		The third step is the definition of the raster in minutes. If the value is too high, the results may be to imprecise, is the value too small, more data is needed for correlation. No decimals are allowed.
Selection of the area ✕ Search : Caribbean Sea Central Indian Ocean Central Pacific Coral Sea Eastern Atlantic Eastern Indian Ocean Gulf of Aden Gulf of California Gulf of Mexico Select New Cancel		The next step is the selection of the marine area. If the programme was already executed once, the formerly selected area is proposed. If no area was formerly selected or the area should be modified, it will be selected from a list.
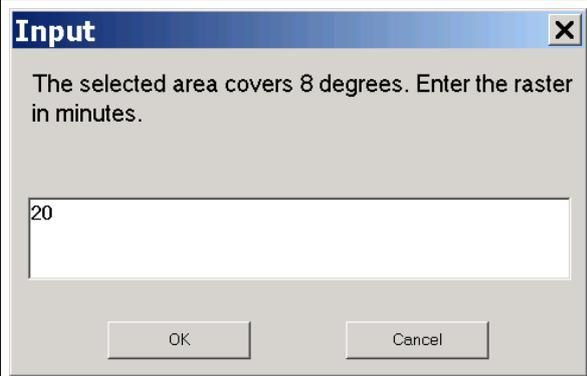
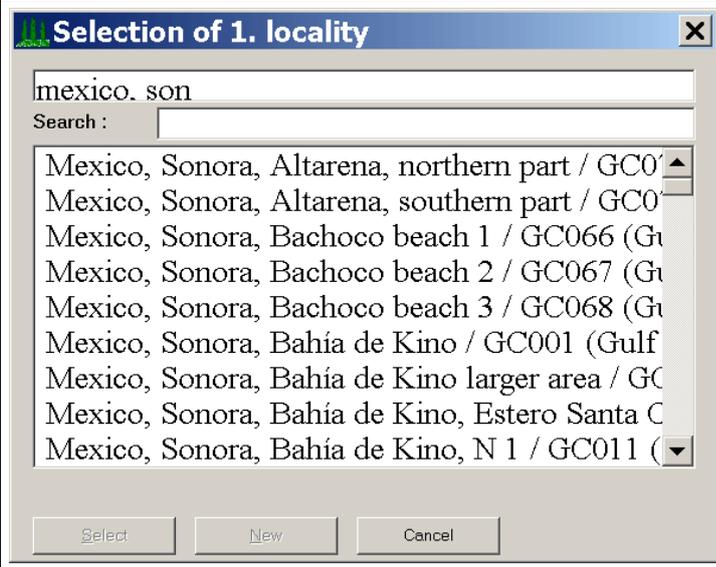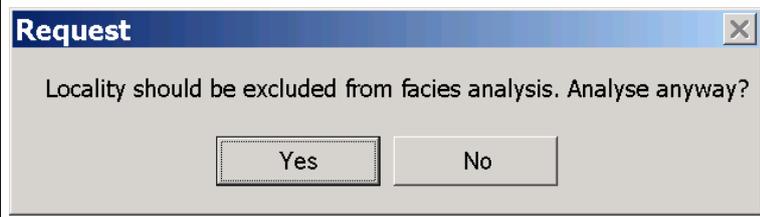|	
Filter of facies ☒ ☐ Do not apply any filter ☐ Coarse sediment (n < x < 100) ☑ Fine sediment (0 < x < n) [OK] [Cancel]	Sediment type limitation is a very helpful filter. If the examined organisms vary much depending on the sediment type, it is better to restrict the correlation analysis to a certain sediment type. The first option does not apply any filter, the second option applies to rocky shores, and the third option to sandy-silty areas.
Input ☒ Enter percent value (e.g. 1..50) 50 [OK] [Cancel]	If you have chosen the second or third option, you need to define the limit. Generally, a value between 40 and 60 is reasonable. If here you set a value of 50, then for the second option all species within a sediment preference between 50 and 100 will be listed, otherwise, for the third option, all species above zero and below 51 will be included. Setting a low value for a fine-grained sediment (e.g. 30) or a high value for coarse sediment (e.g. 70) will reduce the amount of data.
Request ☒ Supress localities without facies data? [Yes] [No]	Localities without sediment data can be suppressed.
As above, the correlation data are written into a PaleoTax/Graph file that is shown immediately.	

5.1.5 Sediment profile

• Programmes > Sediment profile based on species (OLI2_FP.PRF)

This programme gives for one locality the distribution of the sediment type value assigned to the species occurring at this locality. Preferably, in the locality that should be analysed, the field 'Do not include in sediment type analyses' should be marked. The programme gives only results when – on the one hand – at least some localities have sediment data, and – on the other hand – the analysis 'Calculate frequency of species (in marine areas) and correlate' is carried out. If the species have no sediment type values, the programme cannot give results.

Selection of 1. locality ✕ mexico, son Search : [ ] Mexico, Sonora, Altarena, northern part / GC0 Mexico, Sonora, Altarena, southern part / GC0 Mexico, Sonora, Bachoco beach 1 / GC066 (G Mexico, Sonora, Bachoco beach 2 / GC067 (G Mexico, Sonora, Bachoco beach 3 / GC068 (G Mexico, Sonora, Bahía de Kino / GC001 (Gulf Mexico, Sonora, Bahía de Kino larger area / GC Mexico, Sonora, Bahía de Kino, Estero Santa C Mexico, Sonora, Bahía de Kino, N 1 / GC011 ([Select] [New] [Cancel]	The first step is the selection of the locality.
Request ✕ Locality should be excluded from facies analysis. Analyse anyway? [Yes] [No]	If the locality is not suppressed for the sediment type analysis, a warning message is shown.

The data are written into a PaleoTax/Graph file. The plug-in of this programme is started and the graph is displayed. Please be aware that PaleoTax/Graph offers multiple options and you should consult the manual.

5.1.6 Frequency of species

• Programmes > Frequency of species according to bins (OLI2_FREQU.PRF)
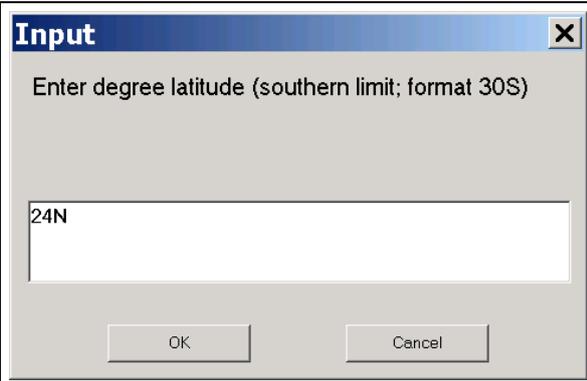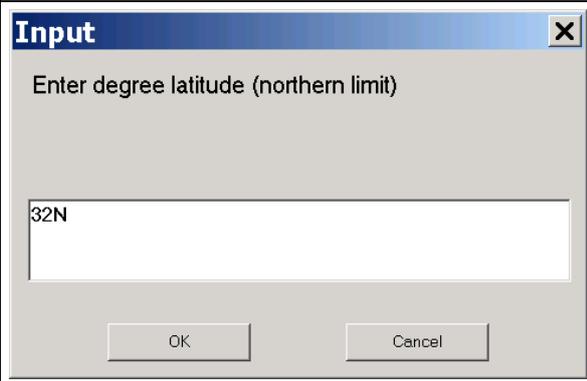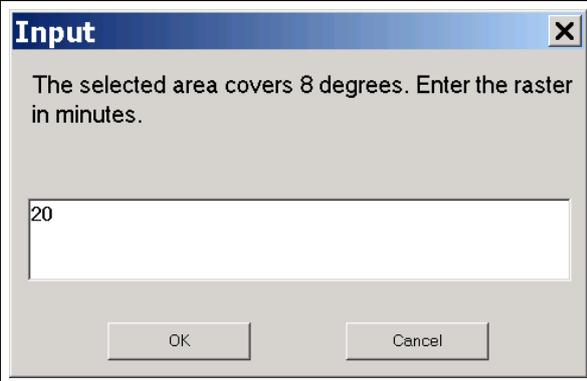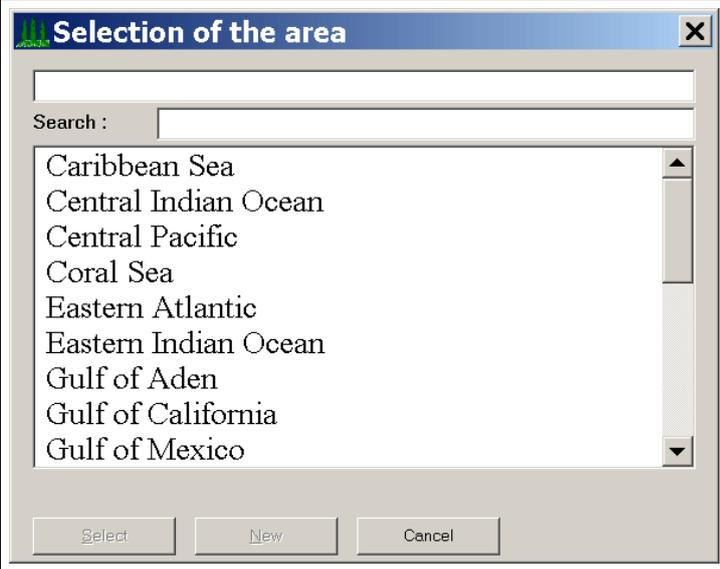
The frequency of species as shown in the SPECIES table is calculated on the basis of the number of localities where a species occurred (see 7.1.3). But there is another method to calculate the frequency. The total number of occurrences (localities per species) is divided by five to obtain the class or bin size. The species are sorted descending according to the number of their localities. Then, the number of occurrences is summarised. When the bin size is reached, a bin is closed and the number of occurrences is summarised again. In this way, five frequency bins are obtained, from very abundant to very rare.

The frequency is only calculated for species with frequency data obtained through the above mentioned programme (Calculate frequency of species (in marine areas) and correlate), and it makes only sense when it is calculated for one marine area. In the mentioned analysis it is therefore important to delete the frequency data of other areas. The number of specimens is not taken into account. The results are shown as text file.

5.1.7 Species richness per latitude

- Programmes > Species richness per latitude (OLI2_SUMLA.PRF)

The programme summarises the amount of species according to the latitude.

Input [×] Enter degree latitude (southern limit; format 30S) 24N [OK] [Cancel]	The first step is the selection of the southern limit. No decimals are allowed here, and a hemisphere (N or S) must be indicated.
Input [×] Enter degree latitude (northern limit) 32N [OK] [Cancel]	The second step is the selection of the northern limit. As above, no decimals are allowed and the hemisphere (N or S) must be indicated.
Input [×] The selected area covers 8 degrees. Enter the raster in minutes. 20 [OK] [Cancel]	The third step is the definition of the raster in minutes. If the value is too high, the results may be imprecise, is the value too small, an overflow error is indicated (increase the amount!). No decimals are allowed.
Selection of the area [×] Search : Caribbean Sea Central Indian Ocean Central Pacific Coral Sea Eastern Atlantic Eastern Indian Ocean Gulf of Aden Gulf of California Gulf of Mexico [Select] [New] [Cancel]	The next step is the selection of the marine area. If the programme was already executed once, the formerly selected area is proposed. If no area was formerly selected or the area should be modified, it will be selected from a list.
As above, the graph written into a PaleoTax/Graph file that is shown immediately.	

5.1.8 Last visit list

- Programmes > Last visit list (OLI2_VL.PRF)

The programme compiles a list of localities and adds the date of the last visit. The data are taken from the table SAMPLING. It is possible to restrict the selection of localities to a specific country (region, marine area), to a specific collector, and a start date. The resulting list might be helpful when several sample points in a limited area are regularly visited. The items on the top of the list are those that have not been visited for long and the localities at the bottom of list are those visited just recently.

5.1.9 Correlation of marine areas

- Programmes > Correlation of marine areas (OLI2_CORRMA.PRF)

The programme correlates all marine areas based on the species. There are two possible settings. First, species without author (e.g. in open nomenclature) can be suppressed. This makes sense because a positive correlation between all specimens assigned to Patella sp. is not a real correlation because very probably these specimens represent different species. Second, species restricted to one marine area (or only known from one locality) can be suppressed. A species that occurs only in one marine area would not correlate with any other species, as well as species that occurs at only one locality. The are limitations. Not more than 10,000 marine areas, and not more 10,000 species can be correlated, and the maximal number of pairs is 50,000. This programme is only useful if you work – as for instance – with one taxonomic group, but on a global scale. The programme will not deliver good results if you are working regionally and most of your specimens come from one marine area, and only few from other areas.

The data are written into a PaleoTax/Graph file. The plug-in of this programme is started and the graph is displayed. Please be aware that PaleoTax/Graph offers multiple options and you should consult the manual.

5.1.10 Abundance of species among the sediment type

- Programmes > Abundance of species among the sediment type (OLI3_FA.PRF)

The programme plots all species in the database according to their average sediment type. The resulting polygon shows the number of species per sediment type (on average). The table of SPECIES must have at least ten records and the species must have sediment type values.

5.1.11 Comparison of two localities

- Programmes > Comparison of two localities (OLI3_COMS.PRF)

The programme compares two localities and creates three lists of species:

1) Species that co-occur at both localities.

2) Species that occur at the first locality but not at the second.

3) Species that occur at the second locality but not at the first.

The table of SPECIMENS must have at least 50 records and the table of LOCALITIES at least two. The result is a RTF file.
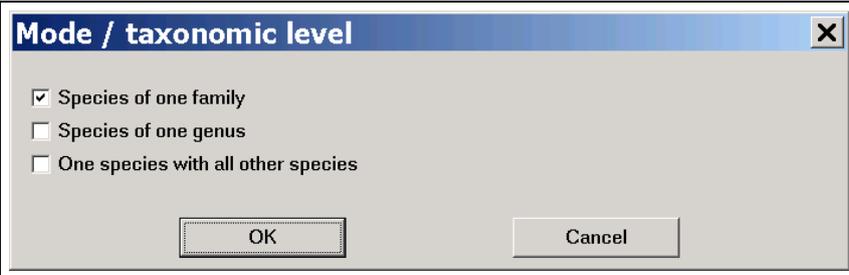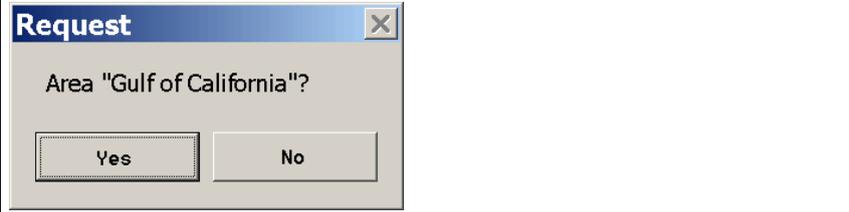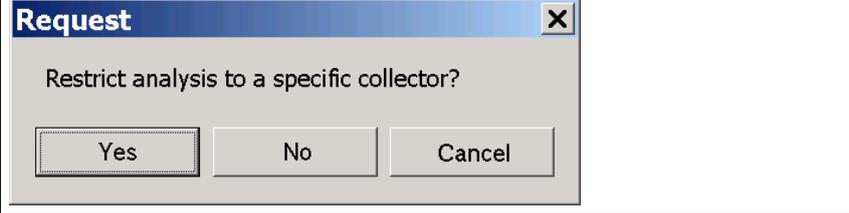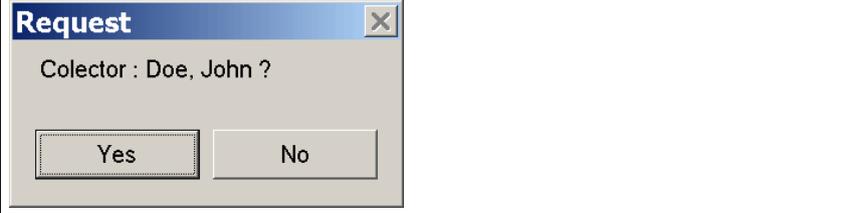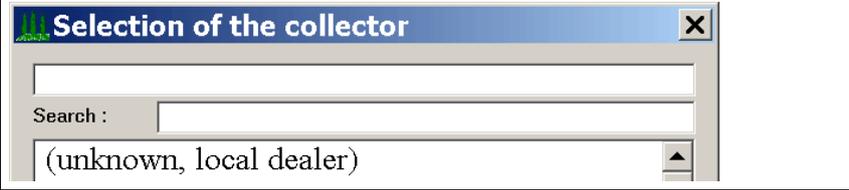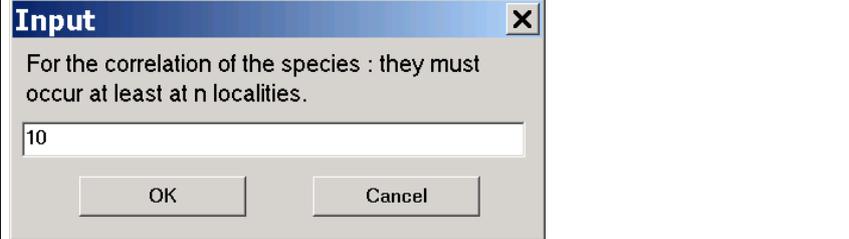
5.1.12 Species per family

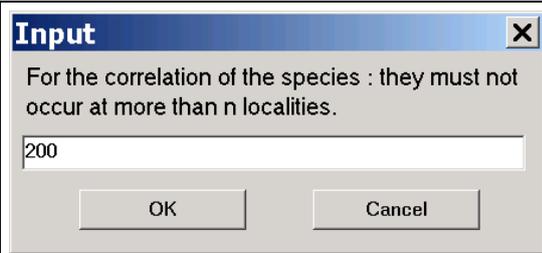- Programmes > Species per family (Chart) (OLI4_SPF.PRF)

The programme gives a chart on the number of species per family. It is possible to restrict the output to one locality or one marine area. The output is a chart.

5.1.13 Correlation of species

- Programmes > Correlation of species (OLI4_CRS.PRF)

The programme has been removed from the programme 'Frequency of species' and is extended.

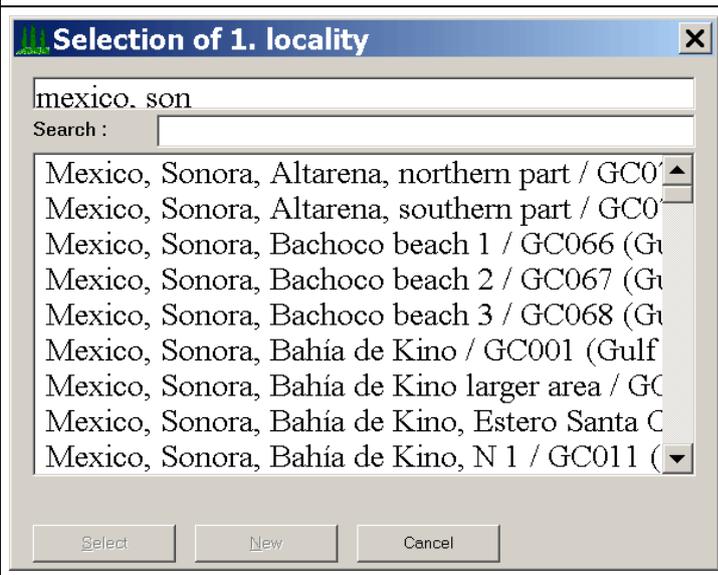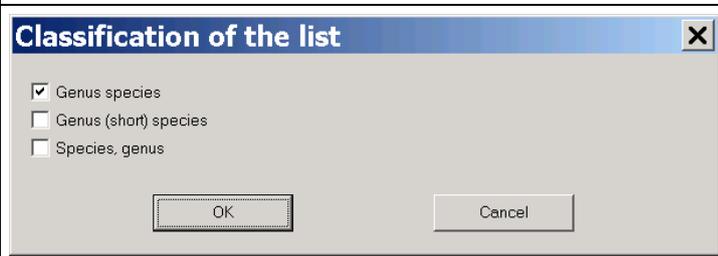|	
Mode / taxonomic level ☒ ☑ Species of one family ☐ Species of one genus ☐ One species with all other species [OK] [Cancel]	In a first step you have to decide the mode. When selecting the first option, a family must be selected, a genus for the second, or a species for the third option.
Request ☒ Area "Gulf of California"? [Yes] [No]	The first step is the selection of the marine area. If the pro-gramme was already executed once, the formerly selected area is proposed.
Selection of the area ☒ Search : Caribbean Sea Central Indian Ocean Central Pacific Coral Sea Eastern Atlantic Eastern Indian Ocean Gulf of Aden Gulf of California Gulf of Mexico	If no area was formerly selected or the area should be modified, it will be selected from a list.
Request ☒ Restrict analysis to a specific collector? [Yes] [No] [Cancel]	In a second question is asked if the analysis is restricted to a certain collector (material taken by other persons will be not in-cluded).
Request ☒ Colector : Doe, John ? [Yes] [No]	If confirmed, the collector from former programme executions is proposed.
Selection of the collector ☒ Search : (unknown, local dealer)	If it is not convenient or no col-lector was selected before, the collector is selected from a list.
Input ☒ For the correlation of the species : they must occur at least at n localities. 10 [OK] [Cancel]	As above: it does not make sense to compare very rare to very common species and it is there-fore recommendable to exclude very rare species.

| | | It is also possible to exclude very common species. As above, the correlation data are written into a PaleoTax/Graph file, the plug-in of this programme is started and the graph is displayed. |

5.2 List of species and record of observations

- Programmes > Create a species list (OLI4_SL.PRF)
- Programmes > Species list as table (OLI4_SLV.PRF)
- Programmes > Record observations (OLI5_RECOB.PRF)

If you are not solely interested in recording material, but you are also in observations in the field, the application supports you with three programmes. The first programme – Create a species list – creates a list of species of selected localities and marks already observed or already collected material.
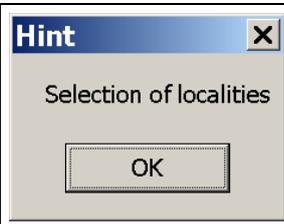
| | | The first step is the selection of the localities. |

| | | Select up to ten localities. Press ESC to finish the selection. If you wish to visit localities that are new to you, you may also skip the selection of localities and create only a species list. |

| | | Decide how the items should be sorted in the list, according to the genus or the species name, and if the genus name should be abbreviated (three letters). |

Filter acording to abundance ✕ ☑ All species (no filter) ☐ All species with abundance data ☐ Rare to very abundant species ☐ Occasional to very abundant species ☐ Abundant and very abundant species ☐ Only very abundant species ☐ Enter percent value [OK] [Cancel]	Decide which species should be shown in the list.
Input ✕ Species must occur at n % of the localities 10 [OK] [Cancel]	If you have selected 'Enter percent value', decide regarding at how many localities the species must occur. It is not wise to add very rare species to the list because this makes the list very long and difficult to handle. In the case of rare species, you may note these on a separate list or take them home to confirm identity.
Filter of facies ✕ ☐ Do not apply any filter ☐ Coarse sediment (n < x < 100) ☑ Fine sediment (0 < x < n) [OK] [Cancel]	Sediment type limitation is a very helpful filter. If you plan to visit only beaches with fine-grained sediment it does not make much sense to also include species that are restricted to rocky shores. The first option does not apply any filter, the second option applies to rocky shores, and the third option to sandy-silty areas.
Input ✕ Enter percent value (e.g. 1..50) 50 [OK] [Cancel]	If you have chosen the second or third option, you need to define the limit. Generally, a value between 40 and 60 is reasonable. If here you set a value of 50, then for the second option all species within a sediment preference between 50 and 100 will be listed, otherwise, for the third option, all species above zero and below 51 will be listed. Setting a low value for a fine-grained sediment will reduce the number of species.
Request ✕ Take field <Exlude> in the species tabel into account? [Yes] [No] [Cancel]	You can exclude those species that are marked as 'Exclude' in the SPECIES table.

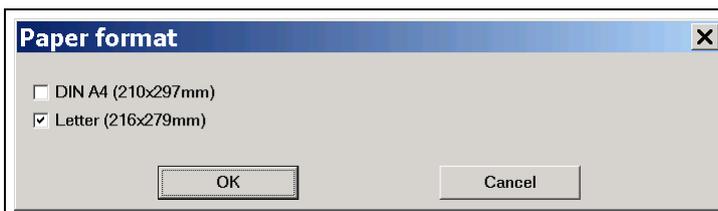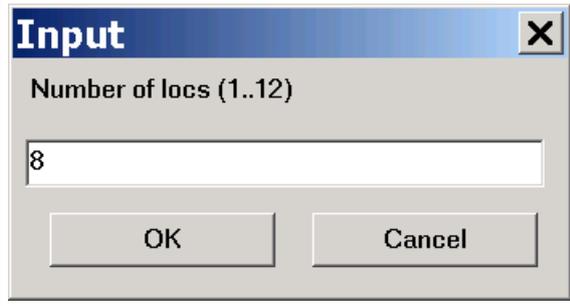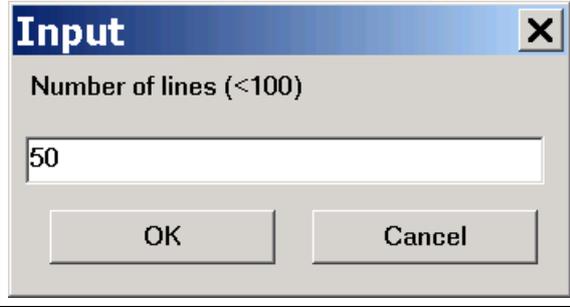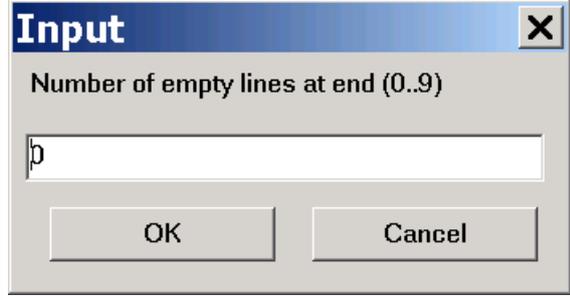|	
Request ✕ 76 species found. Modify search options? [Yes] [No] [Cancel]	The programme now counts the species that fall into the limits. If the number is too high or too low, you may modify the options until the number of species is convenient. A number between 70 and 90 species is easy to handle.
Result is in OLI_SL.TXT: ✕ ☐ Show resulting file ☑ Create table [OK] [Cancel]	The resulting list is stored in an ANSI text file. You may see this file in the notepad.exe (and copy it to another application) or you may proceed and create – based on this text file – a table. For a more detailed description see below.
OLI_SL.TXT - Editor _ ☐ ✕ Datei Bearbeiten Format Ansicht ? 1 = Altarena, northern part 2 = Altarena, southern part Species 1 2 Fusinus ambustus Tivela byronensis × × Tagelus californianus × × Cerithideopsis californica Donax californicus Chione californiensis Cancellaria cassidiformis Semicassis centiquadrata Pholas chiloensis × × Strigilla chroma Petricola cognata × Lamelliconcha concinna × × Sinum debile	If you have selected the first option, the result will be shown in a text file.

1 = Altarena, northern part
2 = Altarena, southern part

Species	1	2				
Fusinus ambustus		
Tivela byronensis	×	×
Tagelus californianus	×	×
Cerithideopsis californica		
Donax californicus		
Chione californiensis		
Cancellaria cassidiformis		
Semicassis centiquadrata		
Pholas chiloensis	×	×

Species	1	2
Eupleura muriciformis		
Cerithium muscarum		
Hexaplex nigritus	×	×
Architectonica nobilis		
Tellina ochracea	×	
Serpulorbis oryzata		
Arca pacifica		
Saccostrea palmula		
Melongena patula		
Anadara perlabiata		

You may copy this file into a text processor and convert it into a table.

The second programme – Species list as table – helps to convert the species list obtained in the first step into a table. This programme can be started from the first programme, but also works as a stand-alone-version.

Paper format ✕ ☐ DIN A4 (210x297mm) ☑ Letter (216x279mm) [OK] [Cancel]	In a first step you are asked for the used paper format.

		The second step is to define the number of localities. The shown number is the number of selected localities. You may increase this values and leaving some localities empty. The maximum value is 12.
		The third question concerns the number of lines (including one head line).
		The fourth question concerns the number of empty lines at the bottom of the list. This value is per default zero, but you may increase it up to 9.

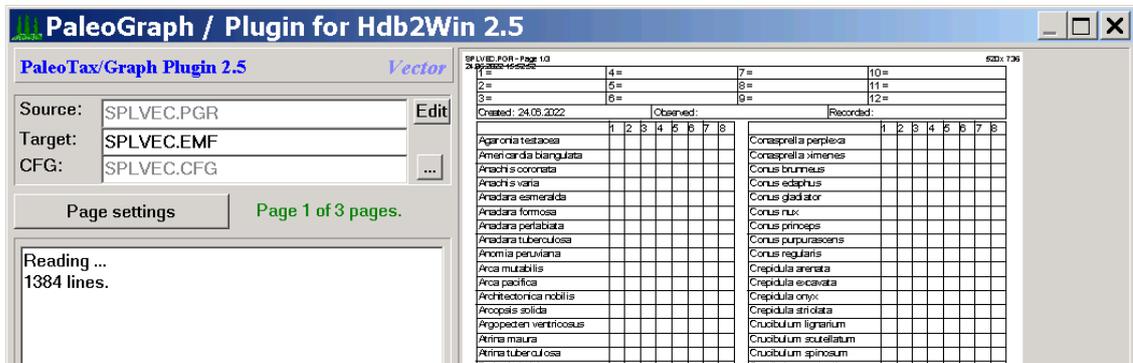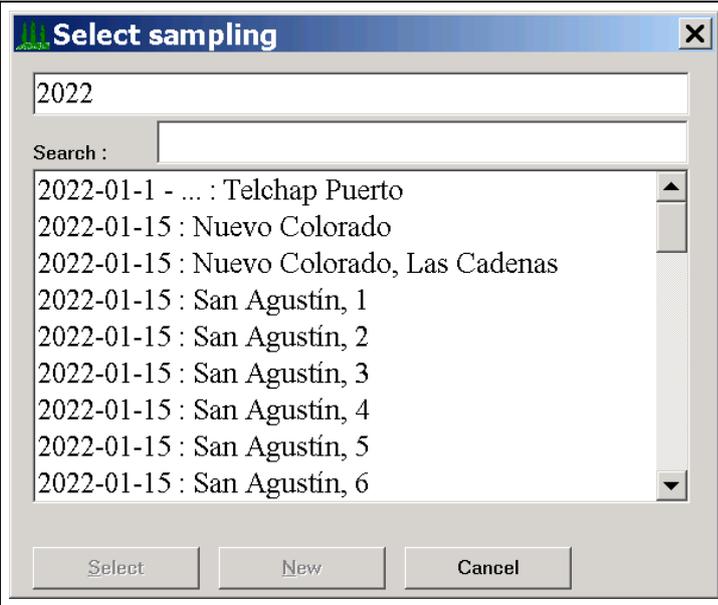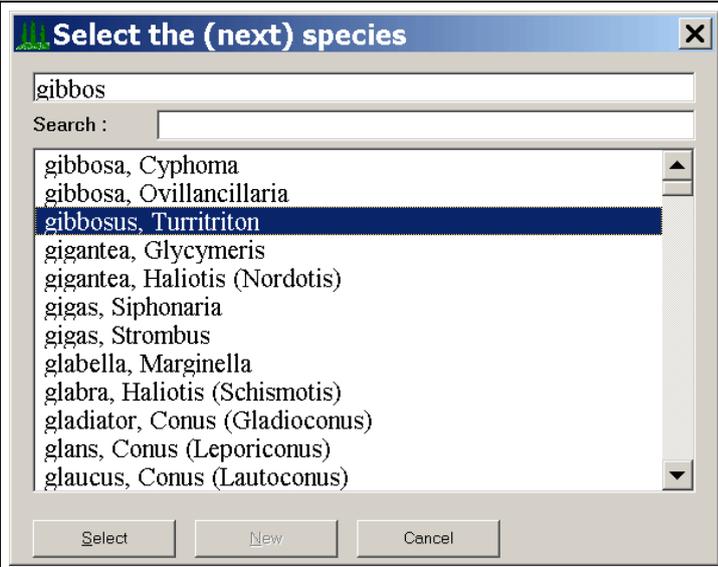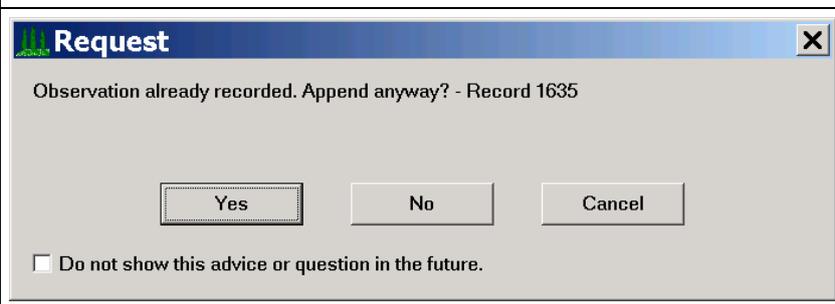Now the programme creates the tables in the form of a vector graphic.

Figure 5.3. List of species as vector graphic.

The margins are kept narrow. The table may extend over various pages. For details compare to the manual of PaleoTax/Graph.

The third programme – Record observations – helps to incorporate observations from the list into the database.

Select sampling ☒ 2022 Search : 2022-01-1 - ... : Telchap Puerto 2022-01-15 : Nuevo Colorado 2022-01-15 : Nuevo Colorado, Las Cadenas 2022-01-15 : San Agustín, 1 2022-01-15 : San Agustín, 2 2022-01-15 : San Agustín, 3 2022-01-15 : San Agustín, 4 2022-01-15 : San Agustín, 5 2022-01-15 : San Agustín, 6 Select New Cancel	The first step is the selection of the sampling. Sampling is sorted according to the date, beginning with the year, followed by month and day. No collector is indicated anymore. If no sampling is selected, a locality needs to be selected.
Request ☒ Person who determined the species : John Doe Yes No Cancel	In the second step, the person who determined the sample is confirmed or selected.
Select person who determined the species ☒ Search : (unknown, local dealer)	Selection of the person who determined the specimens.
Input ☒ Modification date of the records 15.10.2019 OK Cancel	The modification date of the record needs to be confirmed.

Select the (next) species gibbos Search : gibbosa, Cyphoma gibbosa, Ovillancillaria **gibbosus, Turritriton** gigantea, Glycymeris gigantea, Haliotis (Nordotis) gigas, Siphonaria gigas, Strombus glabella, Marginella glabra, Haliotis (Schismotis) gladiator, Conus (Gladioconus) glans, Conus (Leporiconus) glaucus, Conus (Lautoconus) Select New Cancel	The process of recording your observations now starts. The list will appear again until you click on 'Cancel'.
Request Observation already recorded. Append anyway? - Record 1635 Yes No Cancel ☐ Do not show this advice or question in the future.	If the species is already recorded from the locality (not taking into account the sampling), you will receive a warning message.

5.3 Import of images

- Programmes > Import Images (OLI_IMPC.PRF)

The programme allows import automatically images into the database. This is helpful if you are taking many images of your material. The image files will be attached to the table MORPHOMETRIC DATA AND IMAGES, not to the table SPECIMENS. The file names must adhere to the following pattern:

<specimen number>_<sub-number>[-<image number>].<extension>

for instance

RC0451_12-1.JPG

The underscore (_) separates by default the specimen number and the sub-number. If this character is otherwise used in your numbering system, replace this symbol by another symbol (that separates specimen number and the sub-number in your case) in the file OLI_IMPC.PRF, line 20

```
define     subnumsep,c,default,0,'_'
```

If the character that you have selected to separate specimen number and sub-number is for instance the $ symbol, the line should be modified as follows:

```
define     subnumsep,c,default,0,'$'
```

The sub-number corresponds to the field Sub-No in the table MORPHOMETRIC DATA AND IMAGES. If you want to import an image of the whole lot, you should create a sub-number zero.

The image number is optional. It only makes sense if you have taken multiple images of one specimen.

During the importation process, you will be asked where the images are stored (source directory) and where they will be copied to (the target directory). Both folders must not be identical. The target directory can be a sub-directory in your *Oliva* data folder. Moreover, you are asked for the file extension. Please be aware that the programme may import any file, but only images of the BMP, GIF, JPG, and WMF format are displayed. The programme **does not copy the files** from the source to the target directory. **You must do this manually**.

During the importation of images, the program writes an importation log file (oli_impc.txt). If any error, occurs then the programme stops.
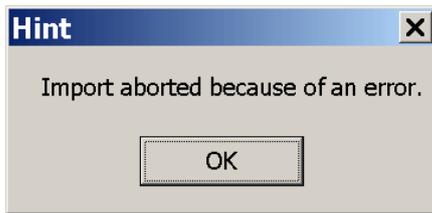

Figure 5.4. The import of images was not successful.

The programme shows a log file within which it is indicated which files could be imported and which could not be imported (and which files created an error message).
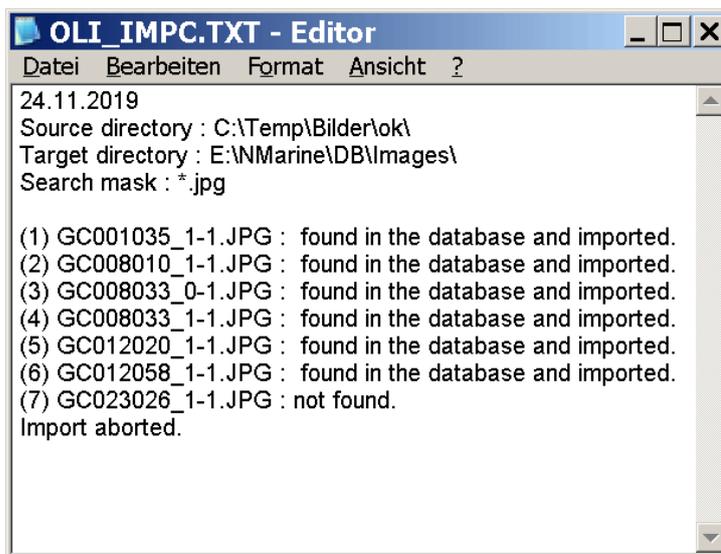

Figure 5.5. Log file.

Therefore, copy the files which have been successfully imported into the target directory, handle the error, and start the programme again. Otherwise, you will get a message that the import was successful.

Figure 5.6. The import of images was successful.

If you try to import an image which name already exists in the database you get a warning error.

In the case where you follow this system to use the specimen numbers to name the image file, one problem may occur. Imagine you have taken an image from specimen T0241_1. This is the first sub-number of the lot T0241. Later, you find out that this specimen does not belong to this species and it would need to be transferred to another species, let us assume to T0340. What you have to do would be the following steps,

1. Go to lot T0340 and check whether there already does exist a sub-number _1. If not, no problem, if yes, you note the first free sub-number.

2. Go to sub-number T0241_1 and change the lot number from T0241 to T0340 (select the new lot). Change the sub-number – if necessary – from _1 to the next free number of T0340.

3. Select 'Reorganisation' from the main menu within the application and activate 'Reorganisation and various index files'.

You will see that the image is with the correct lot T0340. You do not need to modify the name of the image file but it is recommendable. In this case, you shall also need to modify the name of the image in the database. To do so – to take the above example – go to the sub-number of lot T0340, click on Illustrations, select the image, click on Edit, go the field Image file, double click, change the name, and save the record.

5.4 HTML output

5.4.1 Reduction of the image size

- Programmes > Reduce image size for HTML (OLI_ABB.PRF)

The HTML output consists of two programmes. The first programme – Reduce image size for HTML – helps to reduce the size of the images. Normally, the images are too large to show them on the Internet. In its place, to reduce the size of them manually, this short programme helps to make the process automatic.
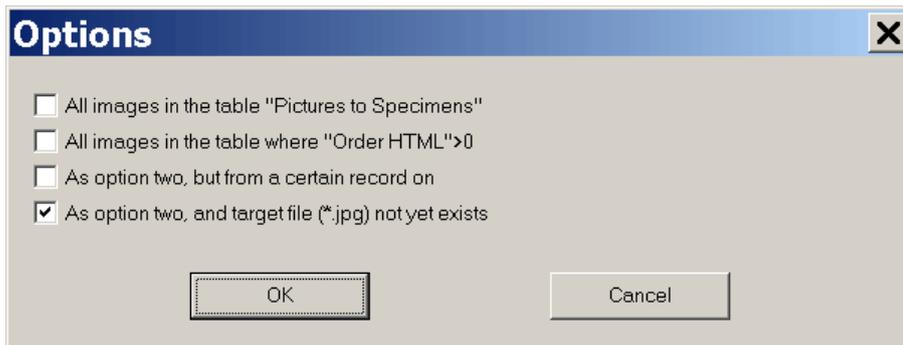
Figure 5.7. (1) First, you need to decide which images should be exported.
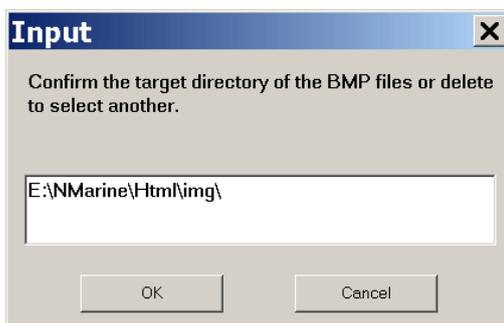
Figure 5.8. (2) Confirm the target path or empty the field to select another.
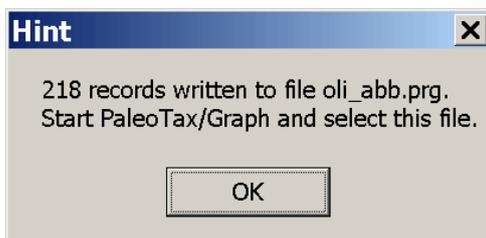

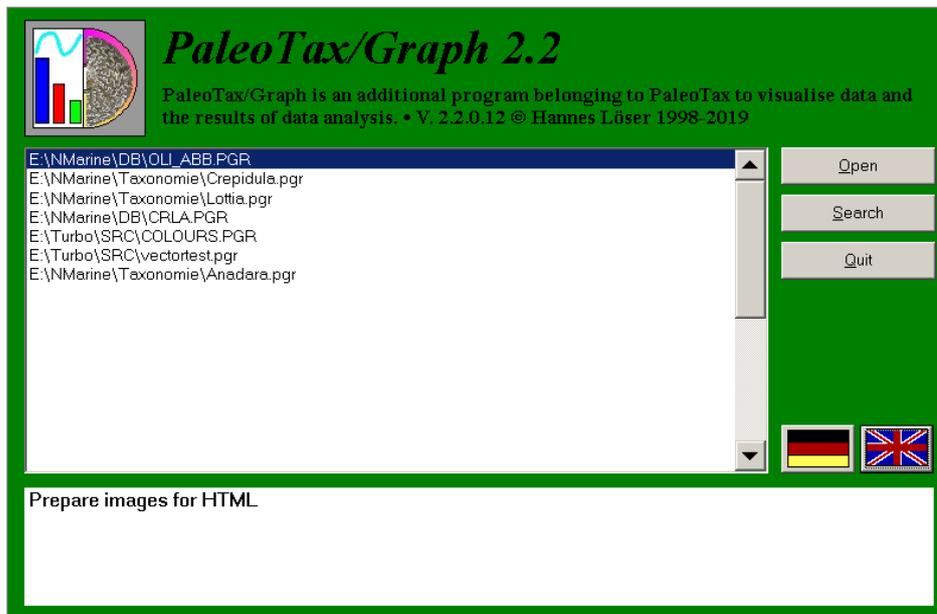Figure 5.9. (3) The programme writes a small parameter file.

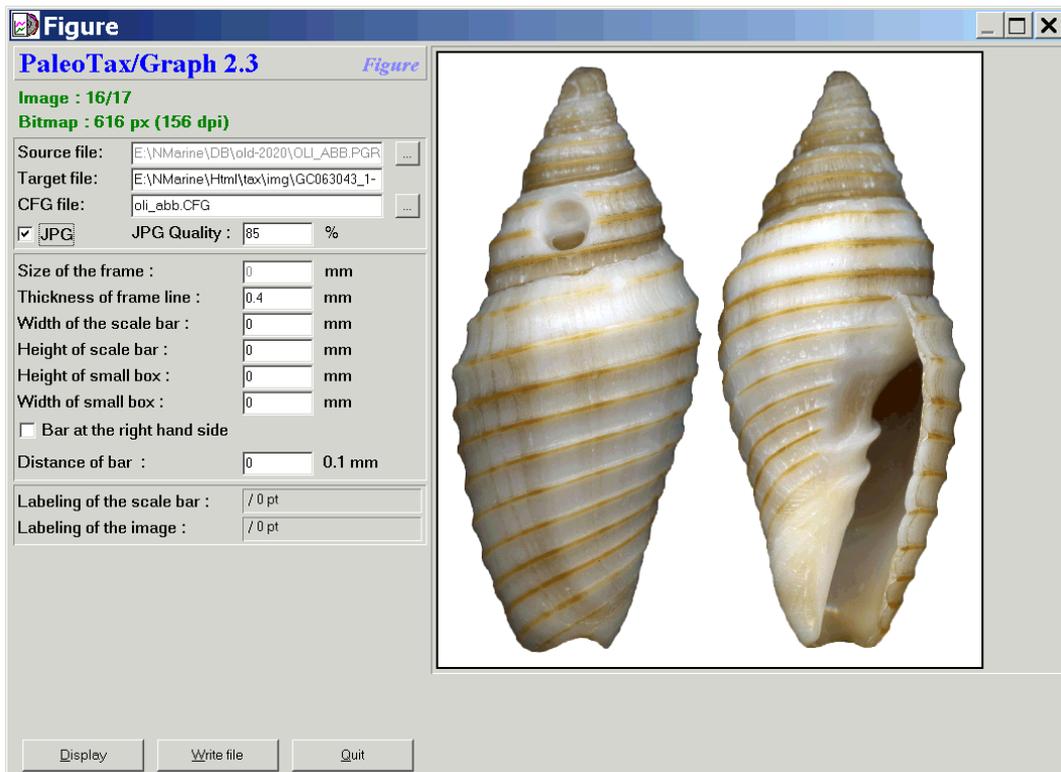Figure 5.10. (4) Open PaleoTax/Graph and open this file.

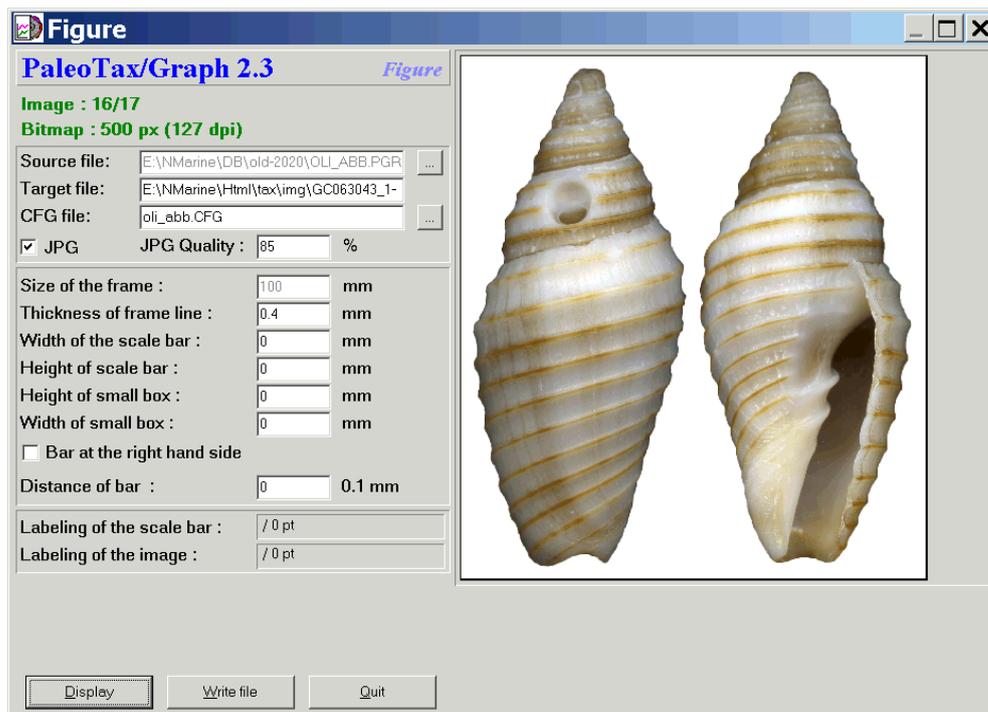Figure 5.11. (5) The target size of the image is given in the upper left.

Figure 5.12. (6) The size of the windows has been modified to reach the desired size. Then, click on 'write file' until you reach the end of the list. The use of the programme only makes sense if the height and width of your images are more or less equal. The files can be created as JPG or BMP. When JPG is selected, the JPG quality can be set. This is a percent value, where 100 corresponds to the lowest compression rate, best quality, and largest file size. If you choose the target format BMP, then you probably need another programme to convert the files automatically into JPG or GIF.

5.4.2 Output to HTML

• Programmes > Output of the database to HTML (OLI_HTML.PRF)

The second one is a complex programme with about 1000 lines and it is still under construction. The programme will not be explained in greater detail here, because there are currently too many changes entailed. For successful use of the programme, some preparation is necessary.

Header and Footer – Each HTM file has at least a header that comes before the data. Although the programme works without it, it is better to create a header file. Its name must be header.htm and it must be located in the data path. You do not need to create a footer file, but you can modify the footer in the file oli_html.prf (at the very end).

Version – The count of versions helps to mark those species that are new compared to an older version. The version is shown in the SPECIES data acquisition form. When a new output version is created, the programme replaces the field *htmlv* in the table SPECIES with this value and – when this option is selected – these species that are new to the output are marked with an asterisk on the family and genera pages.

Images – Images can be attached to the table SPECIMENS and to the table MORPHOMETRIC DATA AND IMAGES. It is a good idea to use the field *Order HTML* in the table IMAGES OF SPECIMENS. This can be done in the table SPECIES: click on Images and mark the image (you can only select one image at a time) with which status you want to change.

Maps – The programme allows you to include the maps created by the programme described below, but you should probably create these files in the JPG format. The programme file oli_plot.prf in this case would need modification (around line 40, variable file_extension must be changed to JPG). When creating the maps, you should note, that the extension of the JPG depends on the size of the window. Smallest size is (PaleoTax/Map 2.2) 425x425 pixels. The file extension must be also modified in the file oli_html.prf (around line 60, variable file_extension) into .JPG. Do not forget the point before the extension.
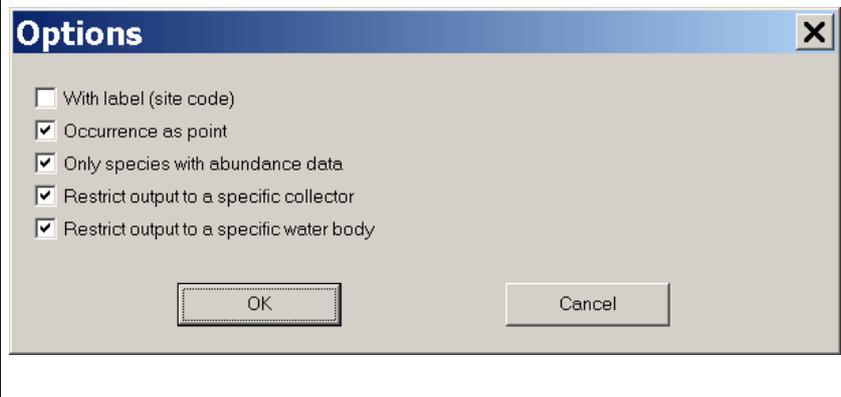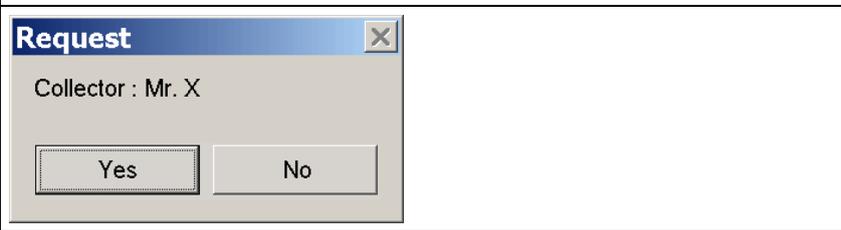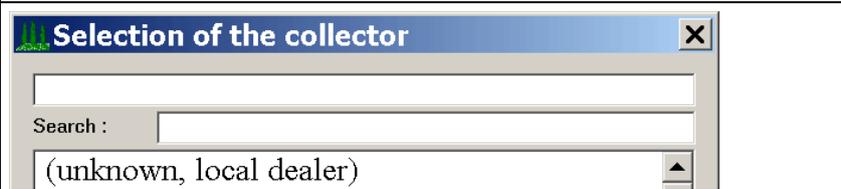
Source and target path – You need to select a target path for the HTML files that must exist. You need to select relative path names for the maps and the images.
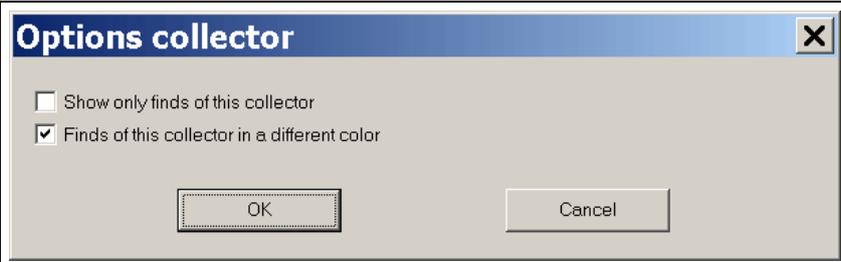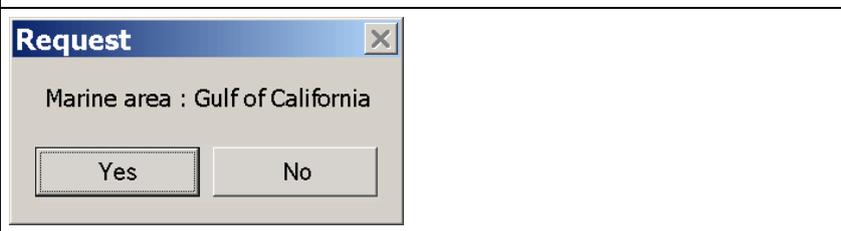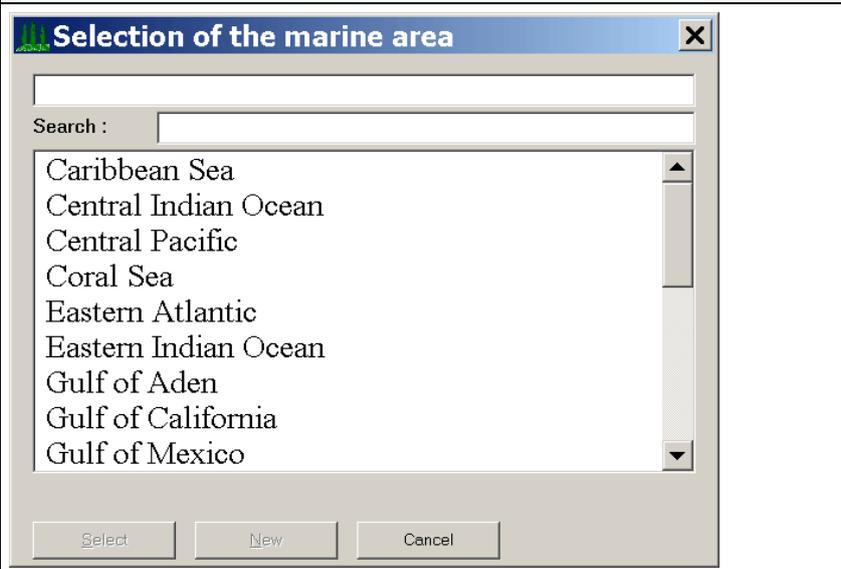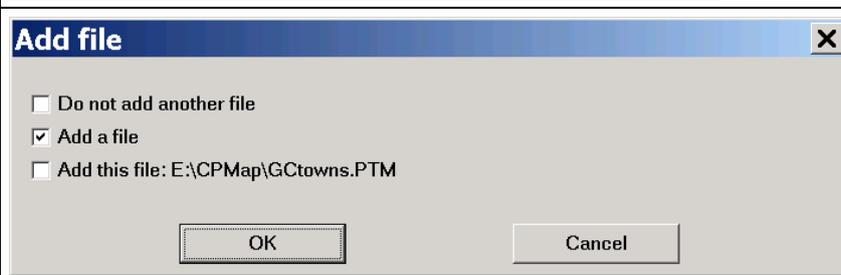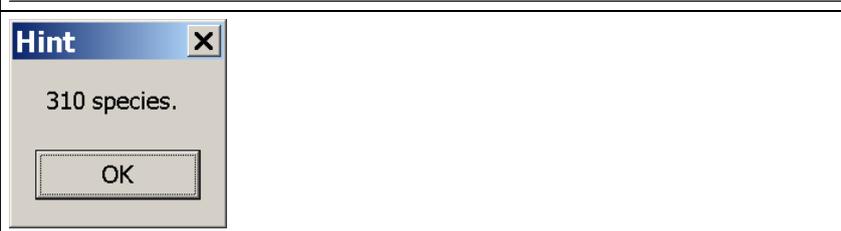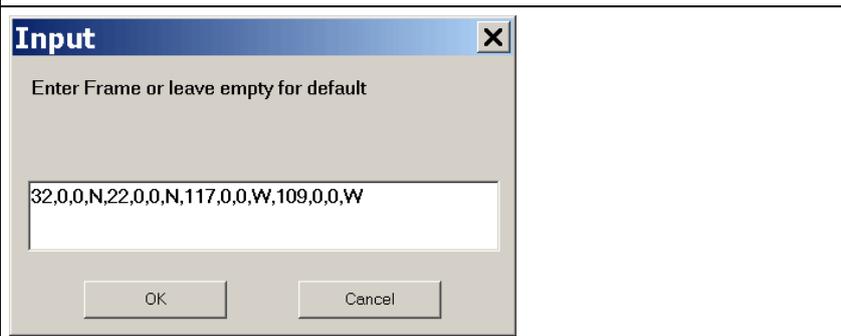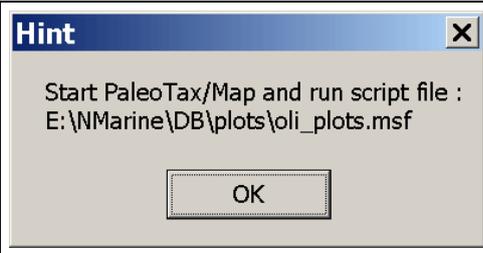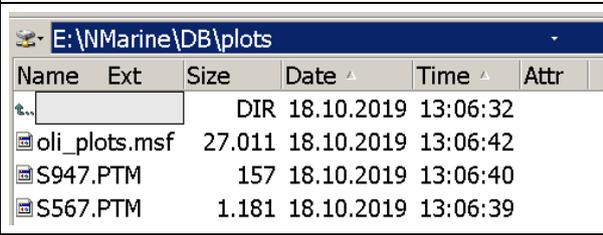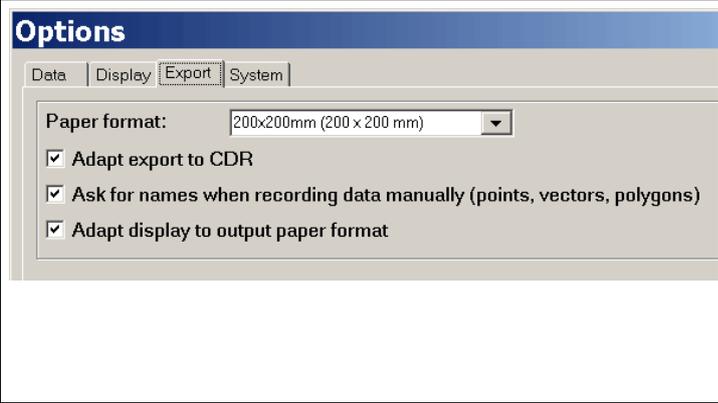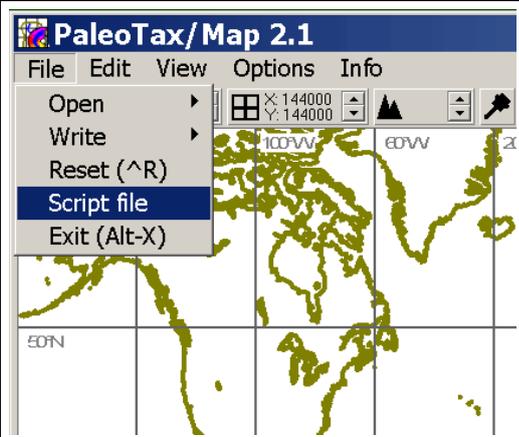
5.5 *Distribution maps of species*

In order to produce distribution maps of your finds, you need to (1) record the exact geographic position of your localities and (2) have installed PaleoTax/Map (at least version 2.2.1). The registration of the exact position of the localities is easy, either by a GPS device or an application such as Google Earth®. The programme PaleoTax/Map can be installed together with the database programme. Before starting the programme that creates the map files, some points should be considered.

1. The database application has a strong focus on biogeography. If you collect at the world-wide scale, you will probably not restrict the map to a certain area. If, in contrast, your activities are restricted to a specified area, you probably only wish that area to be shown. Hence, no disrespect intended, please try to understand the concept of marine areas in advance.

2. It makes a difference if you are not collecting yourself, but rather buying or exchanging material, or mostly collecting and observing species yourself.

3. It is possible that you collect in various marine areas, for instance, in the Gulf of Mexico, the Eastern Pacific, and also in Hawaii. All of these are different marine areas that probably should be shown on different maps. Please note that any geographic (political) region (that borders a marine body) can be assigned to a marine area. Moreover, there are regions that may have borders with two areas (as, for instance, the Mexican state of Baja California that has borders with the Gulf of California and the Eastern Pacific). Please compare to the descriptions of the table REGIONS and the table MARINE AREAS.

4. If you choose to work with marine areas, note that for one species only one map of one marine area is shown. Depending on the size of the area, a species may occur in various areas. For the moment, it is possible to select one or two marine areas at the same time. If there is a desire to include more areas, it is surely no problem to adapt the programme. Just make a request.

5. Before creating the maps you should adapt the line thickness, colours and font size in PaleoTax/Map to your needs. Please note that the standard installation does not encompass the full data set.

If you are finished with these considerations, then start the programme 'Create distribution maps of species' (oli_plot.prf).

	There are various options. 1, the locality code is shown or not. 2, the occurrences are shown as point, or as line transect 3, all species or only species with frequency data are shown 4, only material collected by a specific collector is shown 5, restrict the output to a specific marine area
	If option 4 is set and in another execution of the programme a collector was selected, this collector is offered here.
	If no collector was selected beforehand or if you wish to change the collector, you may select he/she here.

Options collector [×] ☐ Show only finds of this collector ☑ Finds of this collector in a different color 〔OK〕 〔Cancel〕	If option 4 is set, collections/ observations not realised by the selected person can be marked in a different colour.
Request [×] Marine area : Gulf of California 〔Yes〕 〔No〕	If option 5 is set on, a formerly selected marine area is offered.
Selection of the marine area [×] [ ] Search : [ ] Caribbean Sea Central Indian Ocean Central Pacific Coral Sea Eastern Atlantic Eastern Indian Ocean Gulf of Aden Gulf of California Gulf of Mexico 〔Select〕 〔New〕 〔Cancel〕	If no area was formerly selected or if you wish to change the area, it can be selected here. Afterwards, a second area can be selected (when cancelled with ESC, only one area is shown).
Add file [×] ☐ Do not add another file ☑ Add a file ☐ Add this file: E:\CPMap\GCtowns.PTM 〔OK〕 〔Cancel〕	From SR3 on exists the opportunity to include an additional file with PaleoTax/Map data. This file must be a file in the PTM format. Please consult the PaleoTax/Map manual. This file is loaded first.
Hint [×] 310 species. 〔OK〕	Now the data files are created.
Input [×] Enter Frame or leave empty for default [32,0,0,N,22,0,0,N,117,0,0,W,109,0,0,W] 〔OK〕 〔Cancel〕	You may select a certain map frame to be shown. This frame should cover the selected marine area. If you work with several marine areas, the programme remembers the frame for each of them.

Hint ✕ Start PaleoTax/Map and run script file : E:\NMarine\DB\plots\oli_plots.msf OK	The programme writes a script file that will produce the maps.
E:\NMarine\DB\plots ▾ Name Ext Size Date Time Attr ↰.. DIR 18.10.2019 13:06:32 oli_plots.msf 27.011 18.10.2019 13:06:42 S947.PTM 157 18.10.2019 13:06:40 S567.PTM 1.181 18.10.2019 13:06:39	In the selected folder you will see the script file and the data files, one for each species.
Options Data Display Export System Paper format: 200x200mm (200 x 200 mm) ▾ ☑ Adapt export to CDR ☑ Ask for names when recording data manually (points, vectors, polygons) ☑ Adapt display to output paper format	Start PaleoTax/Map now, then go to options, and select as paper format 200x200mm. You should probably also modify the font size and the line thickness for the frame and grid lines. Switch off the topographic data setting. Otherwise, huge WMF files are created (not a problem when working with BMP or JPG formats).
PaleoTax/Map 2.1 File Edit View Options Info Open ▸ X: 144000 Write ▸ Y: 144000 Reset (^R) Script file Exit (Alt-X)	Select 'File/Script file' and select the above indicated file. The maps are created. Each map is a small file in the WMF format. This file will be shown in the species record. If you want to create files in the BMP format, you need to adapt the file extension in OLI_Plot.prf (line 40) and species.ent (lines 112 and 115).

In the case where you are not satisfied with the selected map frame, you may just modify the frame in the script file (oli_plots.msf). The first line gives the map frame. There are two options: change the first line or delete it and set the frame manually before starting the script.

If you wish to have a date stamp of the map, you need to include this command in the source file since you have to define the position in the map (this is a geographic position). Please compare to the file OLI_Plot, from line 250 on. The line number is shown on the bottom line in the Interpreter.

If you wish to adapt manually the raster width (distance between grid lines) you may change that from programme line 285 on. The raster width is in seconds, so choose a value that corresponds to the size of your areas. Try to choose a value that is easy to be labelled by the programme (such as 5, 10, 15, 20, 30, 60, 120, 300, 600, 1200, 1800, 3600, 7200, 14400 etc.). Per default, this option is switched off.

From Service Release 2 on, the files are per default written into the folder PLOTS in your data directory. If the folder does not exist, it will be created. When the files are stored in another folder, they cannot be shown in the SPECIES table or you have to modify the RCSPECS.ENT programme (variable mappath in the top section):

```
MOV        mappath,'PLOTS\'      ; change to your map path here
```

If you wish to create the maps in a different format than WMF, you have to modify the programme file OLI_Plot. First the file extension must be changed from WMF to the desired format (BMP or JPG). This happens in about line 40:

```
define    file_extension,c,default,0,'WMF'
```

Second, you need to modify the RCSPECS.ENT programme (variable rcspec_format in the top section):

```
DEFINE     rcspec_format,c,default,0,'WMF' ; modify here the format
```

to the applied format (BMP or JPG).

5.6 Options of the database (SR5)

This programme allows to make some settings of the application.

1. Form Species - PGR Files : Delete PGR files (sizes, sediment distribution) after showing – Defines whether these temporary files are deleted after the images were shown.
2. Form Specimens - Detitur : Define a person that is set into the field Detitur (taxonomic assignation by...) by default. This makes sense if only one person maintains the database and does all the taxonomy.
3. Form Specimens - Display images : It is possible to suppress that images are shown. If they are very large, is takes more time to go through the table via Edit.
4. Form Species - Width of the Album : select a value between 40 and 100% of the screen width.
5. Form Species - Chart of Measurements : the chart can be restricted to a specific collector. This can be the case when only collected but not purchased material should be included. This function works only properly when the reorganisation is started regularly, and it affects only new records.
   If you wish to the change the collector, you need to modify the REORG.PRF programme. Open the file with the Interpreter and search the title line
   ```
   ; - MM Collector
   ```
   About ten lines below you will find these two lines
   ```
   cmp  sbcoll,0 ; only new items
   jne  MMCollNF ; only new items
   ```
   and set before these two lines a semicolon:
   ```
   ;cmp sbcoll,0 ; only new items
   ;jne MMCollNF ; only new items
   ```
   In a second question you are asked whether data without exact position should be suppressed.
6. Option for the sediment type in the data sheet : the auto-mode can be switched on or off here.
7. Folder names for images can be checked. This may have sense when absolute and relative pathes are mixed.
8. A right click on the family box offers various options that can be predefined here.

6 Data import from text files

6.1 General remarks

Data import from a text file is not a difficult task when following the instructions. Before importing data you need to have created an *Oliva* database. The database can be new (completely empty) or can have data, this does not make any difference. But the work with a completely empty database is easier because it can be discarded as a whole when the import was not successful with the first attempt.

6.2 Import file format

The file to be imported can be a text file (such as Word®) or a spread sheet (such as Excel®). The data should be in the form of a table as shown below (Figure 8.1). Fields may remain empty; you are not obliged to have all data.

Subclass	Order	Super family	Family	Subfamily	Genus	Species	Autor	Orig. name	Latitud	Longitud	Sitio	Entidad	Region
Caenogastropoda	Littorinimorpha	Littorinoidea	Littorinidae	Littorininae	Echinolittorina	*Echinolittorina modesta*	Philippi, 1846	Littorina modesta Philippi, 1846	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Caenogastropoda	Littorinimorpha	Littorinoidea	Littorinidae	Littorininae	Echinolittorina	*Echinolittorina modesta*	Philippi, 1846	Littorina modesta Philippi, 1846	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Caenogastropoda	Littorinimorpha	Littorinoidea	Littorinidae	Littorininae	Echinolittorina	*Echinolittorina modesta*	Philippi, 1846	Littorina modesta Philippi, 1846	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Caenogastropoda	Neogastropoda	Muricoidea	Muricidae	Muricinae	Hexaplex	*Hexaplex nigritus*	Philippi, 1845	Murex nigritus Philippi, 1845	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Caenogastropoda	Neogastropoda	Muricoidea	Muricidae	Muricinae	Hexaplex	*Hexaplex nigritus*	Philippi, 1845	Murex nigritus Philippi, 1845	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Caenogastropoda	Neogastropoda	Muricoidea	Muricidae	Muricinae	Hexaplex	*Hexaplex nigritus*	Philippi, 1845	Murex nigritus Philippi, 1845	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Neritimorpha	Cycloneritida	Neritoidea	Neritidae	Neritinae	Nerita	*Nerita scabricosta*	Lamarck, 1822	Nerita scabricosta Lamarck, 1822	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Neritimorpha	Cycloneritida	Neritoidea	Neritidae	Neritinae	Nerita	*Nerita scabricosta*	Lamarck, 1822	Nerita scabricosta Lamarck, 1822	28.892053	-112.050835	San Fernando	Sonora, México	Golfo de California
Neritimorpha	Cycloneritida	Neritoidea	Neritidae	Neritinae	Nerita	*Nerita scabricosta*	Lamarck, 1822	Nerita scabricosta		-112.050835	San Fernand	México	Golfo de California

Figure 6.1. Data format for importing data into *Oliva*.

The columns must be in the order as shown below. Not all columns must be present because you will be able to select data (columns) of your file during the importation process. But you cannot change the order of columns.

Number	A specimen or current number.
Phylum	Name of the phylum.
Class	Name of the class.
Subclass	The subclass will be not imported, unless there is a data field subclass in the table of Orders and a table Subclass (file name RCSCLASS) with the data field sclname (c, 80). Per default such a table SUBCLASS and a field subclass does not exists in the table Orders and you have to create the table (Application library > Options > Tools > Create new table) and modify the table of the Orders (Application library > Options > Tools > Modify structure) on your own.
Order	Name of the order with or without author. The author is stored in the field of the name of the order.
Superfamily	Name of the superfamily with or without author. The author is stored in the field of the name of the superfamily.
Family	Name of the family with or without author. The author is stored in the field of the name of the family.
Subfamily	Name of the subfamily with or without author. The author is stored in the field of the name of the subfamily.
Genus	Name of the genus with or without author. The author is stored in the field of the name of the genus.
Species	Name of the species with or without genus, but without author. If the genus name is repeated in the field of the species, it is suppressed in this field during importation. A sub species name is possible. See valid examples for the same species: Cypraecassis testiculus senegalica testiculus senegalica Cypraecassis testiculus testiculus

Author	The author group can have the following format: Author, year Author, year-year Author & author, year Author, author & author, year Author in author, year Author in author & author, year but not Author year or Author & author & author, year Names of authors and the year must be always separated by a comma. The author group can be in parenthesis.
Original name	The original name is only imported if such a field exists in your table of SPECIES (oriname, c, 80). Per default such a field does not exists in this table and you have to create it on your own (Application library > Options > Tools > Modify structure).
Latitude, Longitude	The geographic position must have the decimal format (as for instance shown by Google Maps®). Latitude south and longitude west are negative values. If your position data are in a different format, contact the author and send some examples.
Site	Name of the outcrop or station.
Region	Can be a country name, or the country followed by a comma and the region name. No comma indicates a country. A comma indicates the format country, region: Mexico Mexico, Sonora but not Sonora or Sonora, Mexico.
Area	The area is the marine area or water body.
User data	Two fields are designated for your own data. For the first a table will be created. This field is therefore for data that are frequently repeating in the whole table. The second will be included in the main table as it is, without creating a table.

The conversion itself consists of three steps, carried out by three programmes. After each step you have the opportunity to revise whether the conversion was so far successful.

6.3 Conversion Pass 1

In order to prepare your data remove a possible title row in the table. Convert then the table into a text and separate the fields by tabulators.

Figure 6.2. Text file with tabulators separating fields.

Follow these steps:

1. Save the file as simple text file in the DOS format ('MS-DOS Text (*.txt)').

2. Copy the resulting file into your data directory.

3. Start Hdb2Win and select Interpreter. Do not start the programme from the running *Oliva* application.

4. Search in your data directory via 'Load' for the file IMPORT1.PRF ('Text Import Oliva (Pass 1)').

5.   Start the programme ('Run').

6.   Select the above created text file.

Now you are asked in two steps which fields are present in the table. The fields must be exactly in the same order in your text file. Not to mark a field means that this field is not present in the table; it does not mean, it is present in the table, but you do not want to import it. The choice which fields you want to import and which not must be taken when preparing the text file.
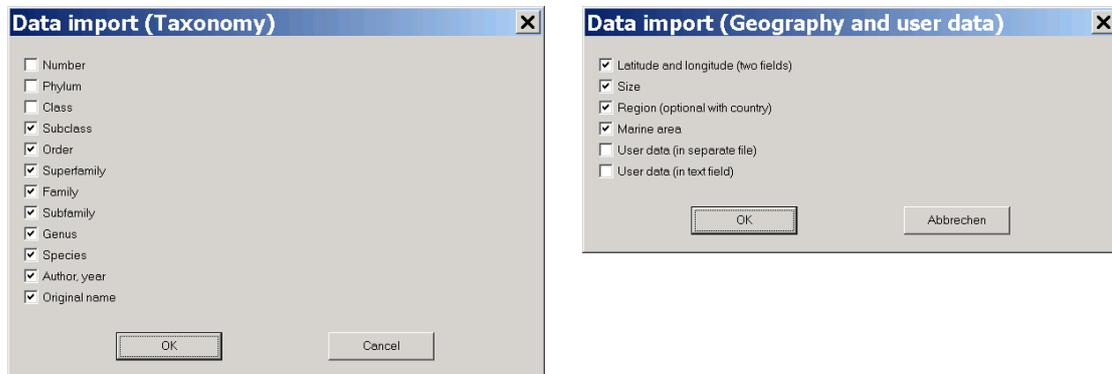

Figure 6.3. Import options.

When the programme was successfully executed, you will see a message telling you how many lines were imported and how many errors occurred. If there occurred at least one error, a log files is opened with the editor. There are two possible errors. Either there are too many characters for a certain data field, or one of the geographic positions is an invalid number. Please revise your source text file and try again.

To see the imported data, leave the Interpreter with 'Quit' and start the CommandLine.

1.   Change the directory to your data directory via
      CD ?

2.   Type
      USE imp1p

3.   You can now via EDIT or BROW see your imported text file.

Figure 6.4. See your data with EDIT or BROW.

4.   Leave the command line with QUIT.

When you find errors you want to correct, you can do it in this table. But you may also make the modifications in the text file and repeat the first pass of the import.

6.4 Conversion Pass 2

Pass 2 should only be executed when you are satisfied with the data in the table IMP1P.

1.   Start Hdb2Win and select Interpreter.

2.   Search via 'Load' the programme IMPORT2.PRF ('Text Import Oliva (Pass 2)'). Do not start the programme from the running *Oliva* application.

3.   Click on Run. Note errors. A message is shown when the conversion was successful. Two errors may be generated. The first ('(1) File imp1p.dbf not found.') when the first conversion pass was not executed. The second ('(2) Nothing to import!') when the file imp1p.dbf is present but empty, this means, it has no records.

You may now see the result.

1.   Leave the Interpreter and select CommandLine.

2.   Change the directory to your data directory via
         CD ?

3.   Type the following command
        USE imp2p

4.   You can now via EDIT or BROW see your modified data file. Finish the command line with QUIT.

Figure 6.5. See your data with EDIT or BROW.

As you can see, there are more fields and those fields that had complex data (species, author, region) are now separated into single fields. Also the geographic position was adapted to the format used by the *Oliva* application.

6.5 Conversion Pass 3

The third pass imports the data in an existing *Oliva* database. It is not matter, whether the database contains data or not. If your database already contains data, it is highly recommended to create backup copies before importing data. As explained above, an empty database is easier to handle in the case of importation errors because it can be deleted as a whole and created again.

1.   Start Hdb2Win and select Interpreter.

2.   Search via Load for the programme IMPORT3.PRF ('Text Import Oliva (Pass 3)'). Do not start the programme from the running *Oliva* application.

3.   Click on Run.

4.   Three errors may be generated. The first ('(1) File rcspecms.dbf not found.') when the programme is not stored in the data directory and does not have access to the tables of your *Oliva* data. The second ('(2) File imp2p.dbf not found.') when the second pass was not executed. The third ('(3) Nothing to import!') when the file imp2p.dbf is present but is without records.

If you are unhappy with the result of the import you may restore backup copy (in case your database had already data) or delete the complete database and create a new one (if the database was virgin and had no data before importation).

6.6 Open database and reorganisation

After the third conversion pass was executed successfully, open the database, select 'Reorganisation' and set the options as shown below.
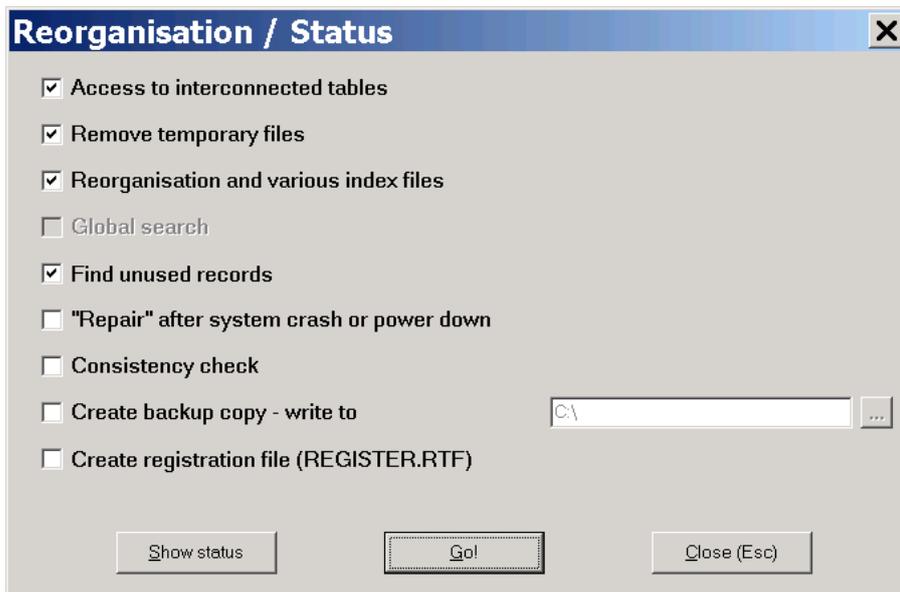
Figure 6.6. Reorganisation.

7 Album

The Album function (tables SPECIES, GENERA, FAMILIES) can show presently up to 60 images at the same time (this is defined within the database kernel). In the table of SPECIES, all images assigned to the current species are shown, in the other tables only items that are marked as 'Principal image' in the table PICTURES TO SPECIMENS. In the album you may click on the image to see it in full screen size (when more than two images are shown). In the table of species you may click on 'Select' to go to the corresponding record in the table of PICTURES TO SPECIMENS.

Please take into account that the time to read an image from your hard disk and the required memory depends on the size of the image. A colour image that measures 6000x4000 pixels may occupy 4 MB on your hard disk. In the memory it occupies (6000x4000*3) 70 MB. If you want to show 24 of them, you must have 1.7 GB of free memory.

Hdb2Win limits the memory used for the album to 512MB. If this limit is reached, further images are not shown. If this memory exceeds the available main memory of your computer a handle error is reported:
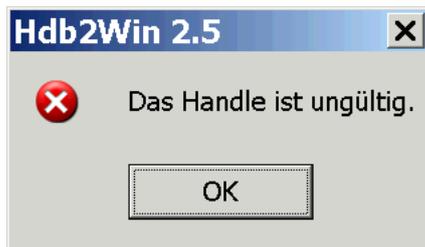

Figure 7.1. Album handle error.

There are several options to avoid these problems.

Increase the memory available for the album. To do so, got to Hdb2Win > Application library > Options > Tools > Extended Options > Application library > '[139] Available memory ... '. Modify this value (a maximum value is 3072 MB).

If you have already set the maximum value but still missing images, there is another option. You can activate the internal image cache. To do so, go to Hdb2Win > Application library > (open database) > Programmes > Set image caching. Answer the questions and ready. Image caching means, that within your image folder a folder imgcache is created. When an image is added is added to an album, the programme looks whether a smaller version exists in this folder. If not, the smaller image will be created and stored in this folder. The former version of small and medium sized versions was discarded. If you have created such files, just create the folder imgcache in your image folder and move this file into this folder.

8 Literature

Hanske, H. & Löser, H. 2006. Annotated Bibliography on Extant Corals (1758-2002). – Coral Research Bulletin, 8: 1-35, CD-ROM; Dresden (CPress Verlag).

9 Imprint

Hdb2Win / PaleoTax © H. Löser 1993-2025

Application Library Oliva

Published	March 2025
Version	SR5
History	May 2020 • Version 1
	May 2021 • Version 2
	May 2022 • Version 3
	May 2023 • Version 4
	March 2025 • Version 5
E-Mail	info@paleotax.de
Internet	https://www.paleotax.de
Document	E:\T\DOK\OLIVA\OLIVA-5.DOC