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Organiser

Organiser will help you manage your datafiles and database quickly, consistently and efficiently. You can import a variety of different file types containing occurrence and IGD data and import them to your database or save them in a different file format. Conflicts are highlighed and you are able to edit details of individual data items or entire datasets. In addition, you can make use of functionality previously accessible through separate StrataBugs applications.

> ***Note: Organiser*** *has been designed to replace Index and the Import/Export applications previously found in Tools. Early releases of v1.8 will not have all of the functionality in place but we recommend its use for import of DEX files and management of data therein. There are also a large number of built in functions that are not fully documented but for which you will receive specific instructions from* ***StrataData*** *if you need to use them.*

How to...

This section provides information on how to use the HELP and how to carry out basic tasks in the Organiser application.

How to use HELP

This HELP is designed to explain how Organiser works and to help you carry out specific tasks. It also provides a detailed description of the function of all the dialogs in the application. It can be accessed from any of the HELP buttons or HELP menu items in the Organiser application or by pressing the F1 key on your keyboard.

The main HELP dialog comprises a main text display pane with a navigation pane on the lefthand side.

Text coloured red refers to dialog titles. These appear in the Title strip of each dialog. Bold black text relates to important menu items and dialog buttons.

Click on blue text to get more help; underlined text provides internal links which guide you from one part of the HELP to another. Blue text which is not underlined will generate pop-ups containing an example of a specific dialog. To dismiss pop-ups click anywhere within in the HELP dialog.

You can search the HELP in four ways using the tabs in the navigation pane:

- The **Table of Contents** is organised like the sections in a book with related items grouped together hierachically. Select one to see a description in the main display pane.
- The **Index** provides a list of topics organised in alphabetical order. Select one to see a description in the main display pane.
- The **Glossary** explains technical terms. These are grouped together logically and arranged in alphabetic groups. Select a term from the list in the navigation bar and the explanation appears in a pane beneath. Alternatively, you can search the entire glossary by typing a text string in the Find text box.
- If you cannot find what you are looking for using the "Table of Contents" or the "Index" then try using full-text "**Search**" facility. Select the Search tab (magnifying glass) and type a word or phrase in the Find text box. HELP will search for text matching your request and display the number of matching items in the Navigation bar. The circle in the first column indicates the ranking of the matches for that topic.The more filled-in the circle is, the higher the ranking. The number in the second column indicates the number of times the query was matched and the text indicates the name of the section in which the matches occur. Select the section most appropriate to your request and scroll through the text to see the matching text which is highlighed in blue.
- There is also a **Favorites** feature which enables you to save particular pages of the Help for future reference. Select the Add to Favorites Button (filled right arrow) while a page is displayed and it is automatically added to your list of Favorites. To view the list select the Favorites icon. To display a Favorite select one on the list.

To close/open the navigation pane use the two small arrows on the frame between the navigation pane and the main HELP display pane. You can also resize the panes by dragging the frame borders.

How to use Organiser buttons

The buttons on the tool bar of the main window are shortcuts for routine tasks.

The buttons currently available are Import, Export and Select Well, View database and Help.

Import and **Export** buttons guide you through the essential steps for importing some of the most common types of data. You can exit this procedure at any time by pressing Cancel.

Select Well enables you to select a well or wells from the database.

View database enables you to select the data types you want to display for each dataset.

Help activates the Organiser Help

How to use Organiser menus

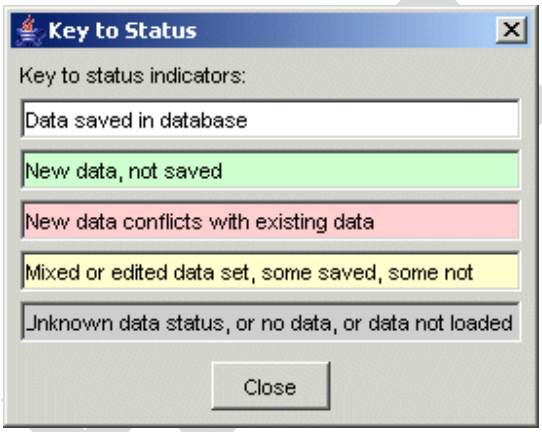
You will probably use Organiser most frequently to import and export data from your database. If you are not familiar with the way Organiser works the quickest way of achieving results is to use the **Organiser buttons** to guide you through the import or export procedure. When you are familiar with Organiser you can work with your data using the menus following these steps.

Step 1 - Open a file - Open a variety of file types or a dataset from your database in your workspace. You will need to do this as a prelude to the following steps.

To do this: Select **File | Open...**

Select a file from the directory list or navigate to a folder containing the correct file. The file can contain information about a single well of a number of wells. There are separate menu options for different source file formats (XML, StrataBugs, CSV, etc.). Alternatively, you can open a dataset in your database.

The Well name(s) and data will be displayed in the Data view pane. The **Key to status dialog** will also appear.



This provides a key to the colours of the data type displayed in the Data view pane. Typically data will be displayed in Green as they has not yet been compared to the database and therefore considered as new data.

Step 2 - View data - Drill down into the datasets in your workspace, view your data and make editorial changes if required. You may wish to do this before proceeding to step 3 or 4.

To do this: **View | Selected data...**

Before you make your selection first highlight the appropriate cell on the main window data table. A dialog displaying the data of the selected type for the selected well will appear. Press the **Close** button to dismiss the dialog. You can carry out the following optional steps if you wish or proceed directly to the next stage (**Step 3 - Match data**)

2.1 - Select displayed data types (optional)

To do this: Select **View | Data types...**

By default the main window will display all the data types which are contained in the file. If you want to remove some data columns from the display select off the checkboxes for the data types you don't want in your workspace.

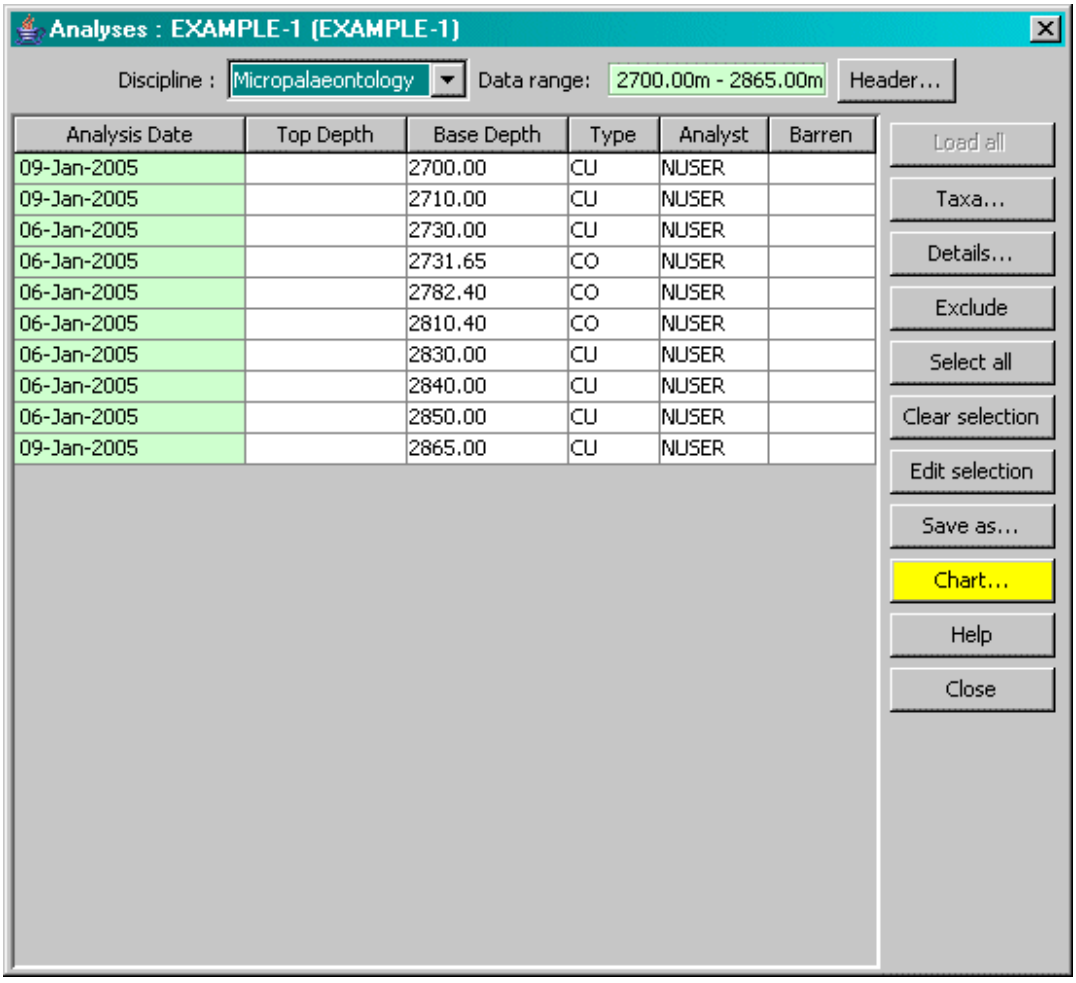
> ***Note:*** *although they disappear from view these data still remain part of your workspace data. It is important to remember this when you save data to your database.*

2.2 - Edit the data (optional)

You can edit the source data in your workspace before it is entered to the database.

To do this for Taxom occurrences (Micro-, Nanno-, Macropalaeontology and Palynology):

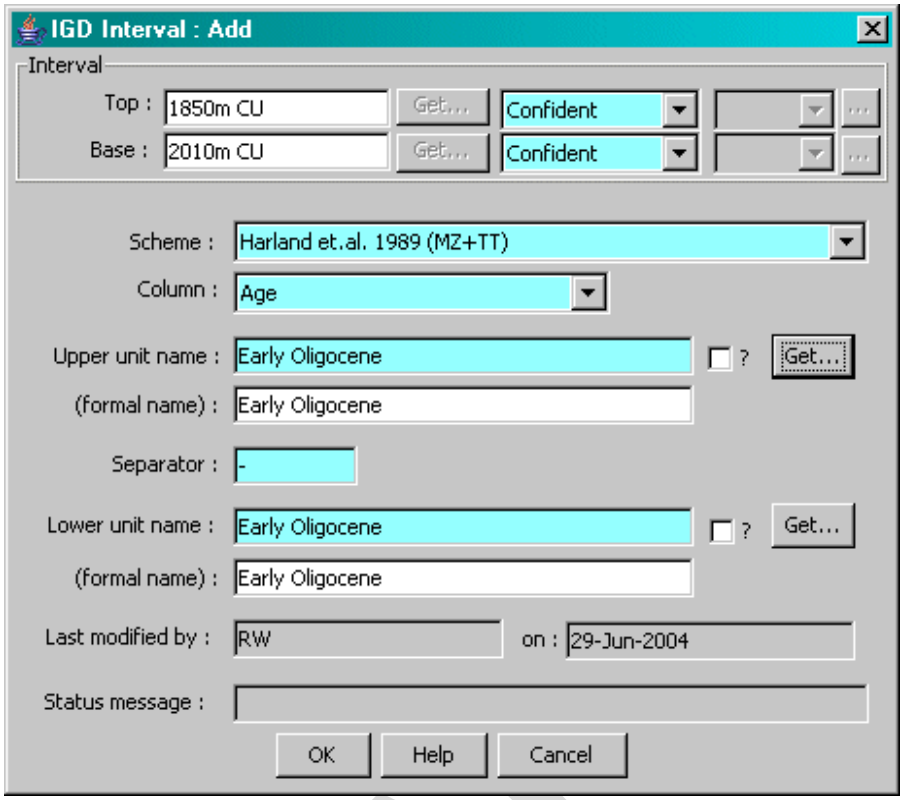
Ensure that the correct discipline is displayed in the list box at the top of the **Analyses dialog**.



Highlight a sample and press the **Taxa...** button. A dialog displaying taxon occurrences for the selected discipline and sample are displayed. To delete taxa from the list, first highlight the one(s) you want to remove and press the **Remove Selection** button. To scroll through the samples use the **Previous** and **Next** buttons. Press the **Close** button to finish.

To do this for IGD (Lithostratigraphy, Chronostratigraphy, Sequences, Biozones - not Lithology or Comments):

Highlight the data item in the **IGD data dialog** and press the **Edit...** button. The **IGD interval dialog** will appear.

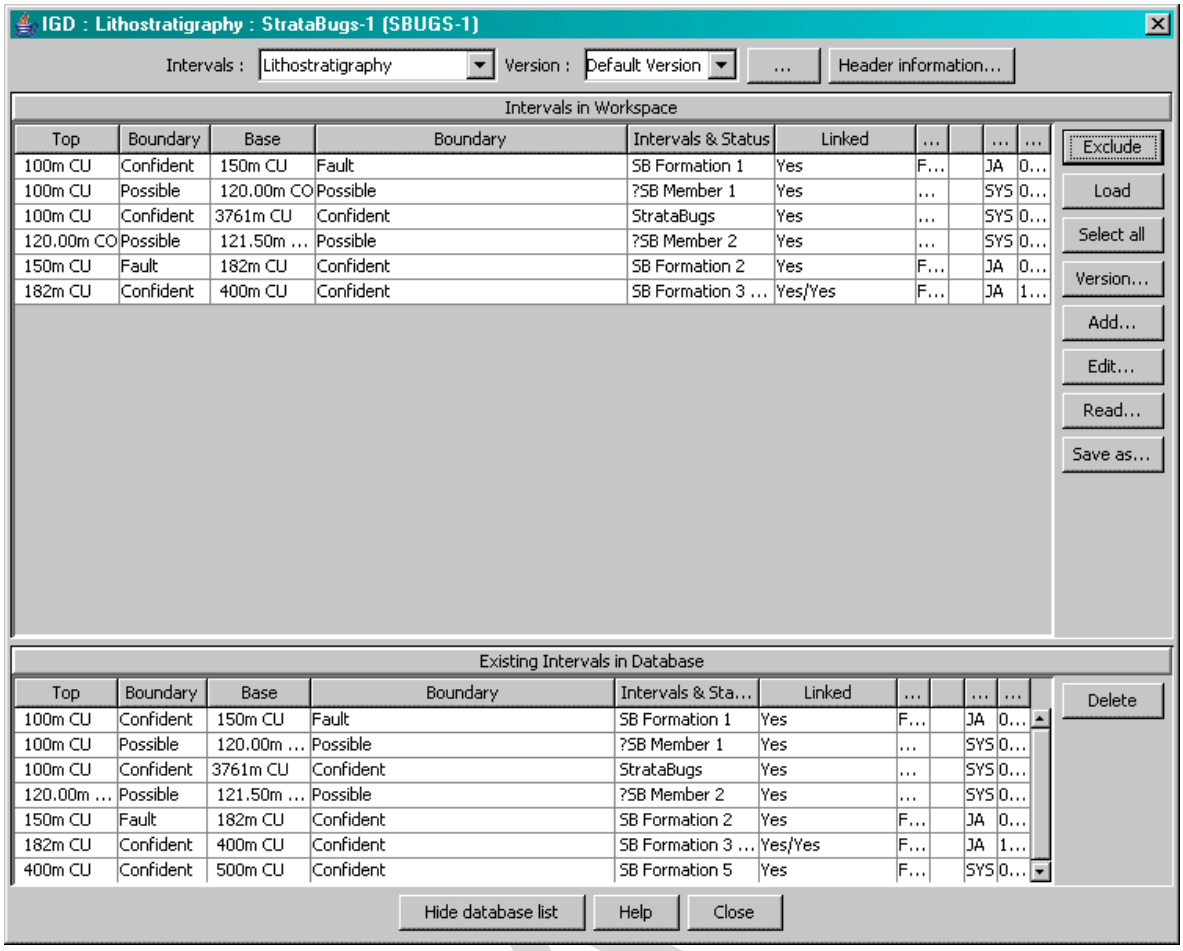


Edit the contents of the dialog as you wish and press the **OK** or **Cancel** button.

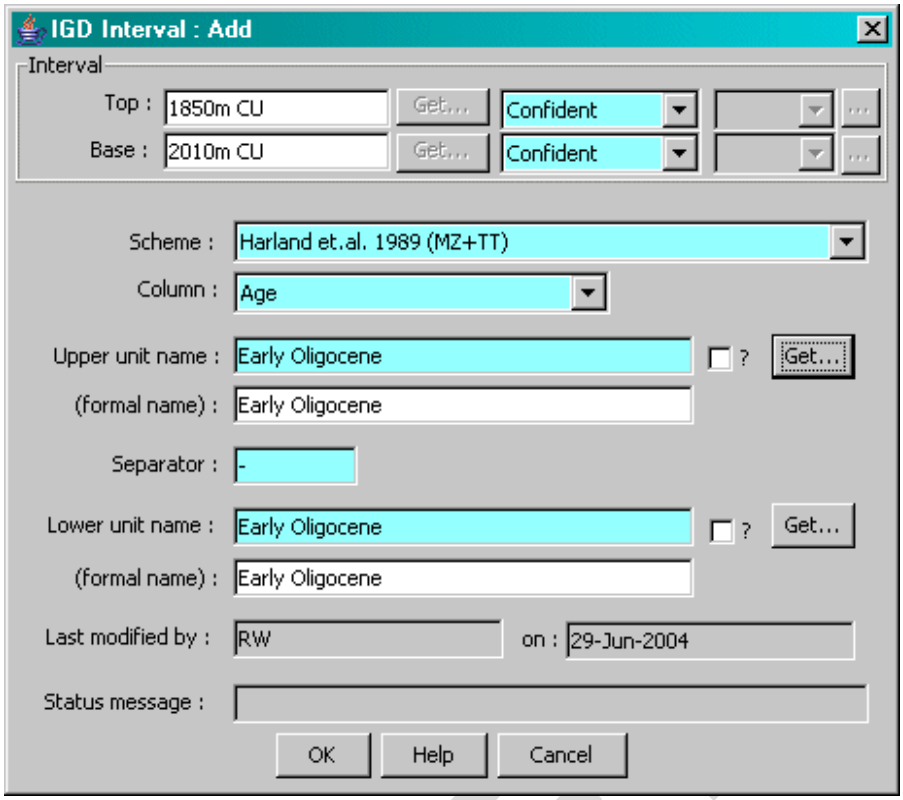
2.3 - Add to the data (IGD only - optional)

To do this:

In the **IGD data dialog** press the **Add...** button.



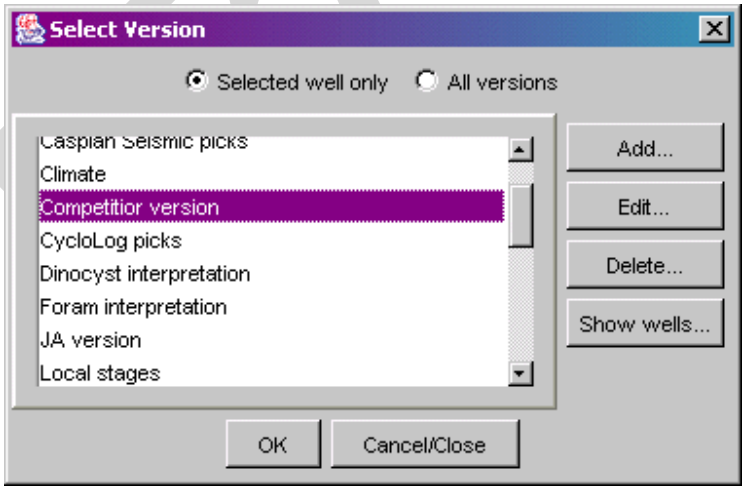
The **IGD interval dialog** will appear. Add an interval as you wish and press the **OK** or **Cancel** button.



2.4 - Select version (IGD only - optional) You can have more than one version of IGD data for a specific well in StrataBugs. If you want to import data to a version other than the default version select another version to which to import the data.

To do this:

In the **IGD data dialog** press the **Version...** button. The **Select version dialog** will appear.



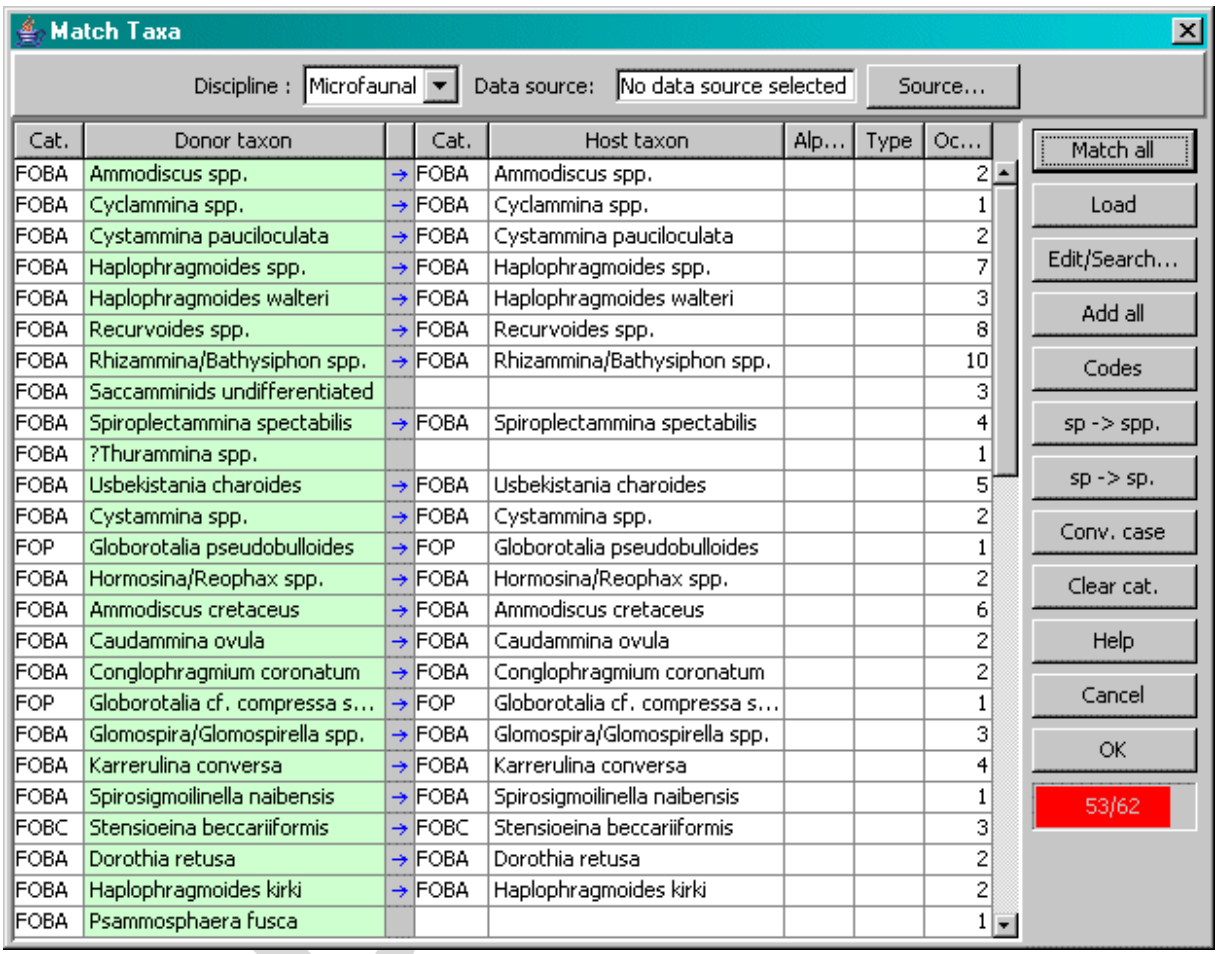
This displays a list of version names (you can choose either version names which have prevously been used for the **Selected well** only or **All versions**).If the name is not on the list you can add it using the **Add...** button. To see in which wells existing version names have been used previously push the **Show wells...** button. Press the **OK** or **Cancel** button.

Step 3 - Match the data - Match Taxa, IGD and Well name independently against your database and add data items and resolve conflicts if required. You will need to do this if your are going to import data to your database.

3.1 First, match taxa (only necessary if taxa in the dataset)

To do this: Select **Match | Taxa...**

The **Match Taxa dialog** will appear.



Cat.	Donor taxon		Cat.	Host taxon	Alp...	Type	Oc...
FOBA	Ammodiscus spp.	→	FOBA	Ammodiscus spp.			2
FOBA	Cyclammina spp.	→	FOBA	Cyclammina spp.			1
FOBA	Cystammina pauciloculata	→	FOBA	Cystammina pauciloculata			2
FOBA	Haplophragmoides spp.	→	FOBA	Haplophragmoides spp.			7
FOBA	Haplophragmoides walteri	→	FOBA	Haplophragmoides walteri			3
FOBA	Recurvoides spp.	→	FOBA	Recurvoides spp.			8
FOBA	Rhizammina/Bathysiphon spp.	→	FOBA	Rhizammina/Bathysiphon spp.			10
FOBA	Saccamminids undifferentiated						3
FOBA	Spiroplectammina spectabilis	→	FOBA	Spiroplectammina spectabilis			4
FOBA	?Thurammina spp.						1
FOBA	Usbekistania charoides	→	FOBA	Usbekistania charoides			5
FOBA	Cystammina spp.	→	FOBA	Cystammina spp.			2
FOP	Globorotalia pseudobulloides	→	FOP	Globorotalia pseudobulloides			1
FOBA	Hormosina/Reophax spp.	→	FOBA	Hormosina/Reophax spp.			2
FOBA	Ammodiscus cretaceus	→	FOBA	Ammodiscus cretaceus			6
FOBA	Caudammina ovula	→	FOBA	Caudammina ovula			2
FOBA	Conglophragmium coronatum	→	FOBA	Conglophragmium coronatum			2
FOP	Globorotalia cf. compressa s...	→	FOP	Globorotalia cf. compressa s...			1
FOBA	Glomospira/Glomospirella spp.	→	FOBA	Glomospira/Glomospirella spp.			3
FOBA	Karrerulina conversa	→	FOBA	Karrerulina conversa			4
FOBA	Spirosigmoilinella naibensis	→	FOBA	Spirosigmoilinella naibensis			1
FOBC	Stensioeina beccariiformis	→	FOBC	Stensioeina beccariiformis			3
FOBA	Dorothia retusa	→	FOBA	Dorothia retusa			2
FOBA	Haplophragmoides kirki	→	FOBA	Haplophragmoides kirki			2
FOBA	Psammosphaera fusca						1

Select the appropriate discipline from the list box at the top of the dialog to display all the taxa for that discipline in the dataset in the Data view pane of the main window. Use the **Global**, **Load** and **Edit/Search** buttons to match the taxon names to the database or to add new ones.

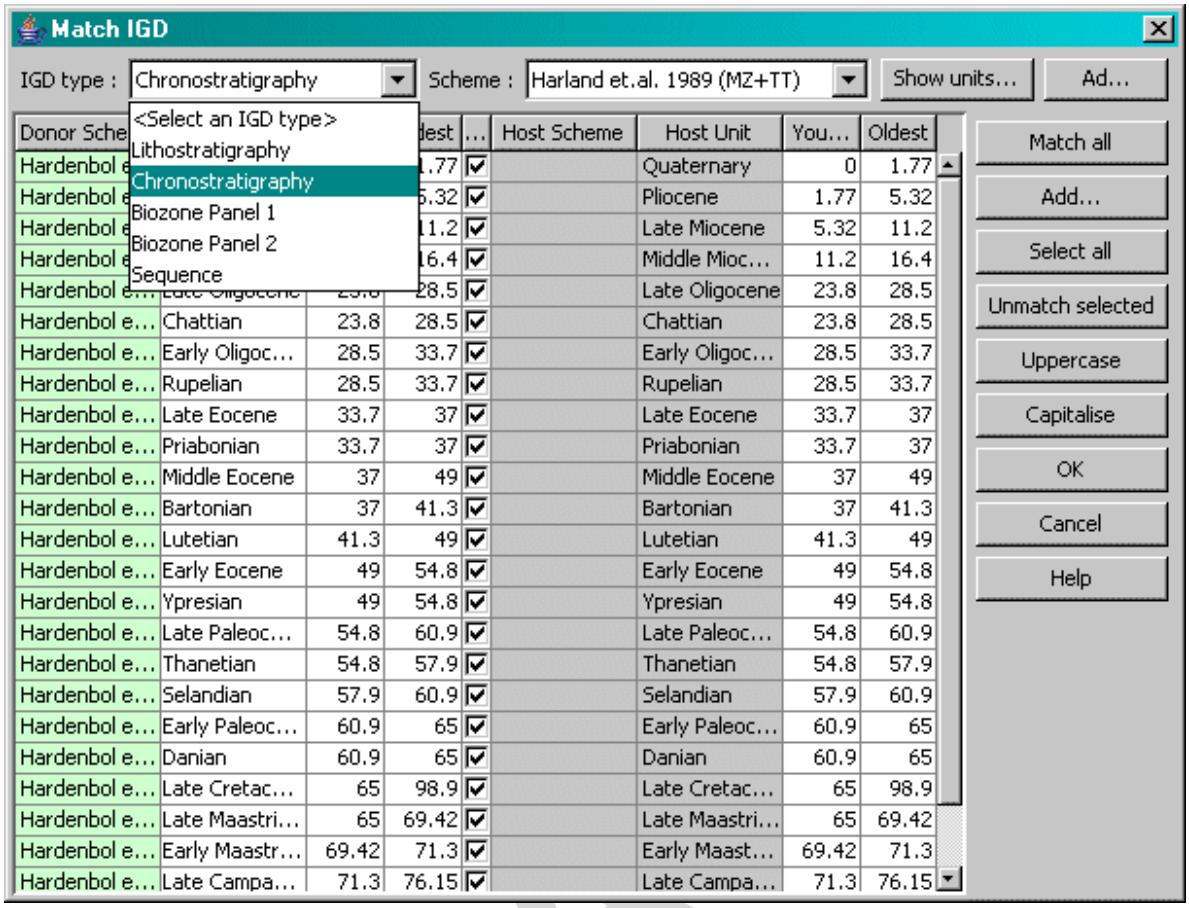
Press the **Source** button and select a source or add one if the one you want is not on the list.

Press the **Codes** button to match taxa on the basis of company codes instead of names. Press **Cancel** or **OK** when finished.

3.2 Next, match taxa (optional if no taxa in dataset)

To do this: Select **Match | IGD...**

The **Match IGD dialog** will appear.



Donor Sche					Host Scheme	Host Unit	You...	Oldest
Hardenbol e...			1.77	☑		Quaternary	0	1.77
Hardenbol e...			5.32	☑		Pliocene	1.77	5.32
Hardenbol e...			11.2	☑		Late Miocene	5.32	11.2
Hardenbol e...			16.4	☑		Middle Mioc...	11.2	16.4
Hardenbol e...			28.5	☑		Late Oligocene	23.8	28.5
Hardenbol e...	Chattian	23.8	28.5	☑		Chattian	23.8	28.5
Hardenbol e...	Early Oligoc...	28.5	33.7	☑		Early Oligoc...	28.5	33.7
Hardenbol e...	Rupelian	28.5	33.7	☑		Rupelian	28.5	33.7
Hardenbol e...	Late Eocene	33.7	37	☑		Late Eocene	33.7	37
Hardenbol e...	Priabonian	33.7	37	☑		Priabonian	33.7	37
Hardenbol e...	Middle Eocene	37	49	☑		Middle Eocene	37	49
Hardenbol e...	Bartonian	37	41.3	☑		Bartonian	37	41.3
Hardenbol e...	Lutetian	41.3	49	☑		Lutetian	41.3	49
Hardenbol e...	Early Eocene	49	54.8	☑		Early Eocene	49	54.8
Hardenbol e...	Ypresian	49	54.8	☑		Ypresian	49	54.8
Hardenbol e...	Late Paleoc...	54.8	60.9	☑		Late Paleoc...	54.8	60.9
Hardenbol e...	Thanetian	54.8	57.9	☑		Thanetian	54.8	57.9
Hardenbol e...	Selandian	57.9	60.9	☑		Selandian	57.9	60.9
Hardenbol e...	Early Paleoc...	60.9	65	☑		Early Paleoc...	60.9	65
Hardenbol e...	Danian	60.9	65	☑		Danian	60.9	65
Hardenbol e...	Late Cretac...	65	98.9	☑		Late Cretac...	65	98.9
Hardenbol e...	Late Maastri...	65	69.42	☑		Late Maastri...	65	69.42
Hardenbol e...	Early Maastr...	69.42	71.3	☑		Early Maast...	69.42	71.3
Hardenbol e...	Late Campa...	71.3	76.15	☑		Late Campa...	71.3	76.15

Select the appropriate IGD type from the list box at the top of the dialog to display all the Schemes and Units for that datatype in the dataset displayed in the main window table.

You must select a Scheme. Press the **Scheme** button and select a Scheme from the list box. If you want to see the component units for a selected Scheme push the **Scheme...** button.

Use **Capitalise/Uppercase** buttons to modify the case of the text as required.

Press the **Cancel** or **OK** button when finished.

Step 4 - Save the data- Decide whether to save the data in your workspace to a file or to your database or to quit.

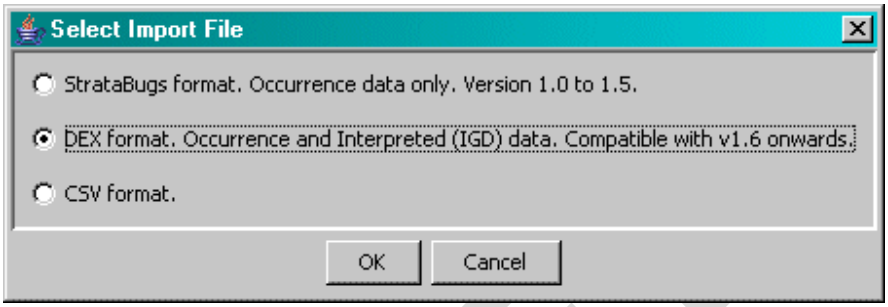
To do this: Select **File | Save**

To save the data to your database select **in Database**. Alternatively, to save your data to an XML file select **XML**.

How to import DEX, CSV and StrataBugs data (guided)

If you are importing one of the most common types of data file (StrataBugs, DEX and CSV formats) Organiser can guide you through the import process. To do this select the **Import data** icon from the tool bar at the top of the Main window. You can go through the same procedure without being guided by opening the file from the **File** menu and selecting each of the items on the **Match** menu in turn.

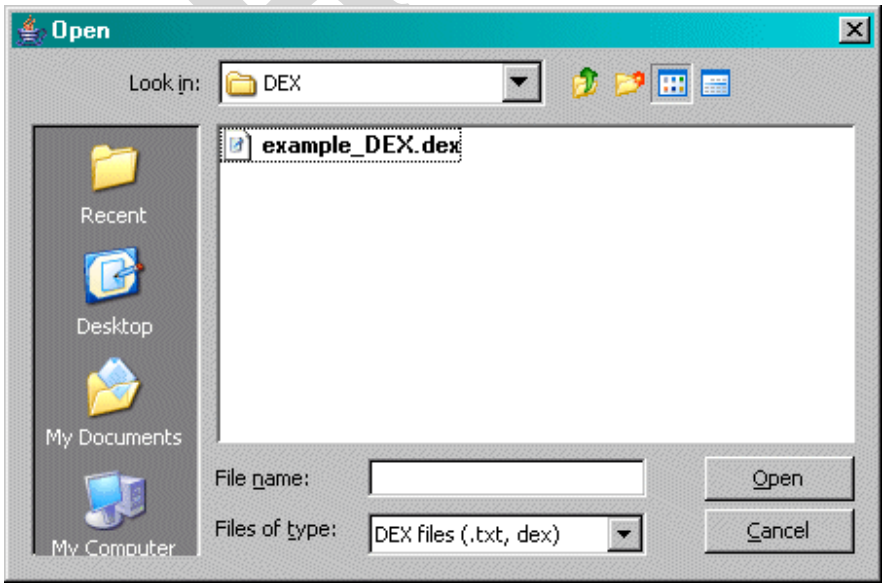
Select from one of the following import file types .



StrataBugs format (*.txt) is a data exchange format used in versions 1.0-1.5 for fossil occurrence data only.
DEX format (*.dex) is the current data exchange format for StrataBugs users compatible with v1.6 onwards.
CSV format (*.csv) is used to import occurence data from spreadsheets.

There are some procedural differences for importing each file type.

To import any of these file types navigate to the folder containing the file you wish to import and press **OK**.

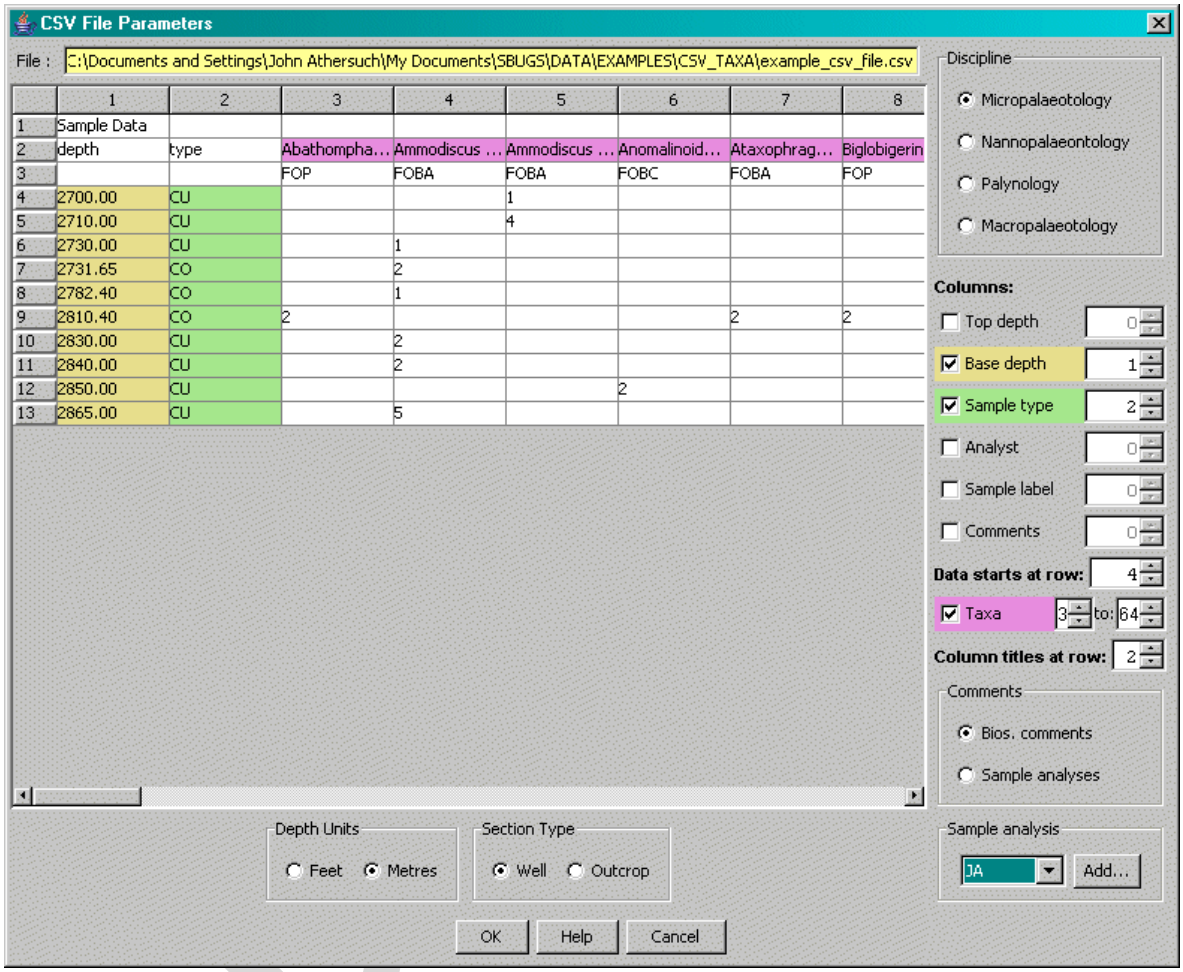


> ***Note:*** *Subsequently, you will be automatically navigated to the location of the files of the selected type.*

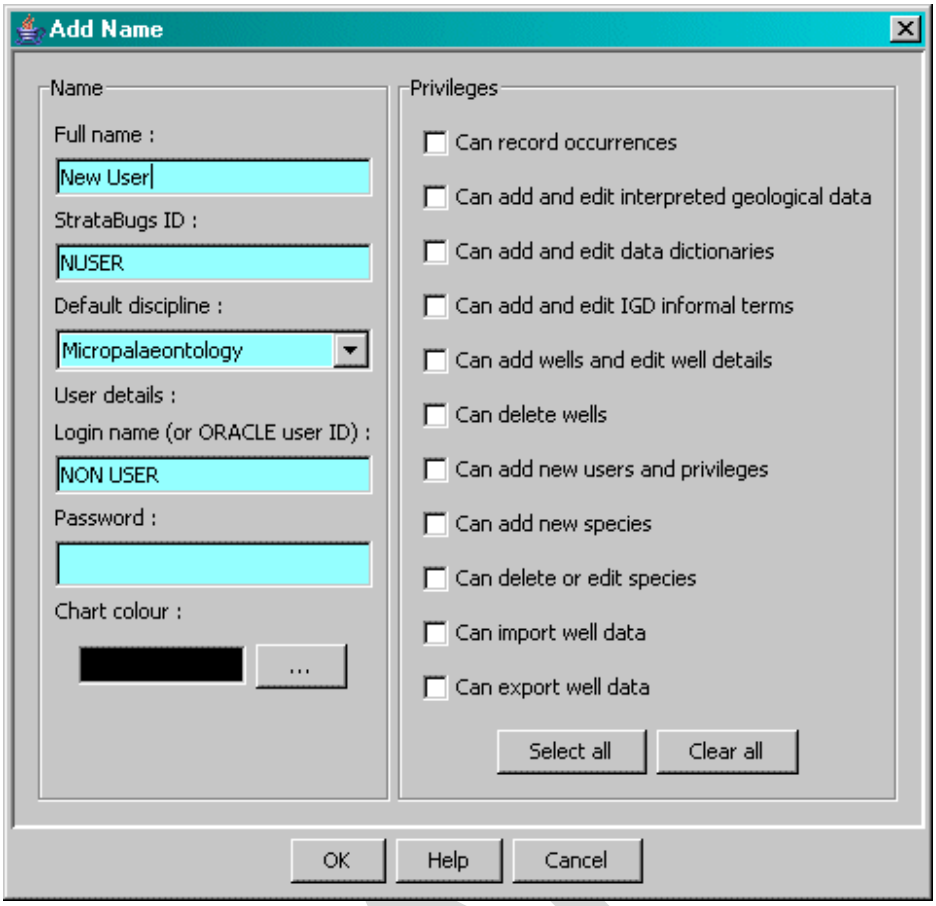
Select a file from the list and press **Open**.

For CSV files only you must take the next step.

The contents of the file will be displayed in the **CSV File Parameters dialog**.

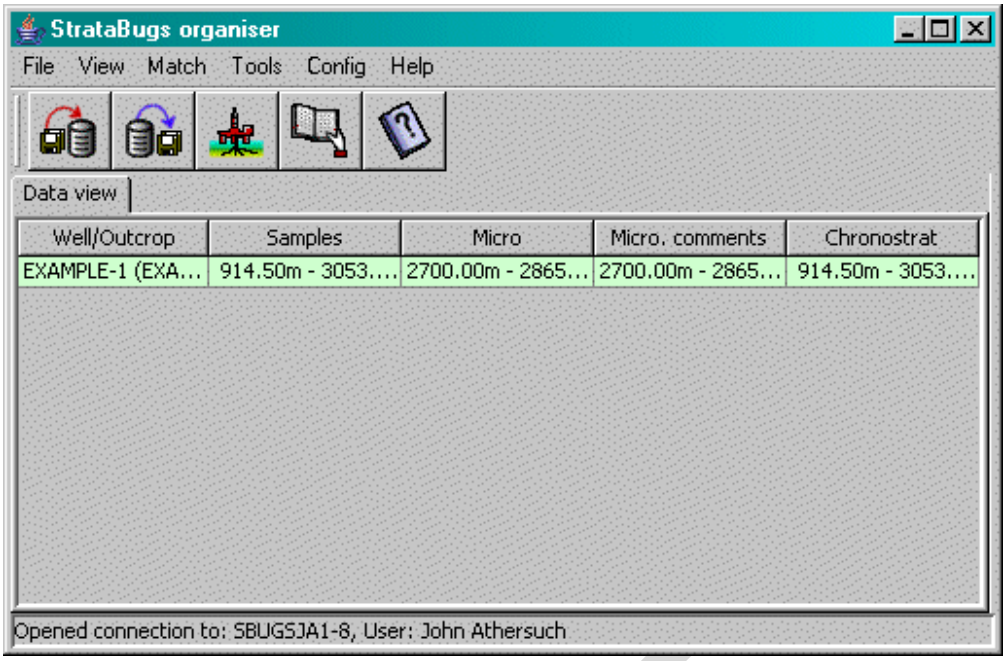


The data are displayed as a spreadsheet. Colours help identify sample (top and base) depth, sample type, analyst, sample label, comments and taxon names. StrataBugs uses a number of rules in an attempt to identify the data items correctly. If it fails then you can intervene using the check boxes and scroll arrows to reposition the clours and thus identify the data types. You must also use the appropriate radio buttons to select the correct depth units, section type (well or outcrop) and discipline. You can select to import any comments as Biostratigraphic Comments or as Sample Analysis comments. Finally you must select an analyst from the drop down list. If the one you want is not there you can add one to the database by pressing the **Add...** button to add a new analyst ID in the **Add Name dialog**.



Fill in the Full name of the new analyst. Because the analyst is not a user of your StrataBugs system there is no need to add a Password or provide any privileges. Press OK.

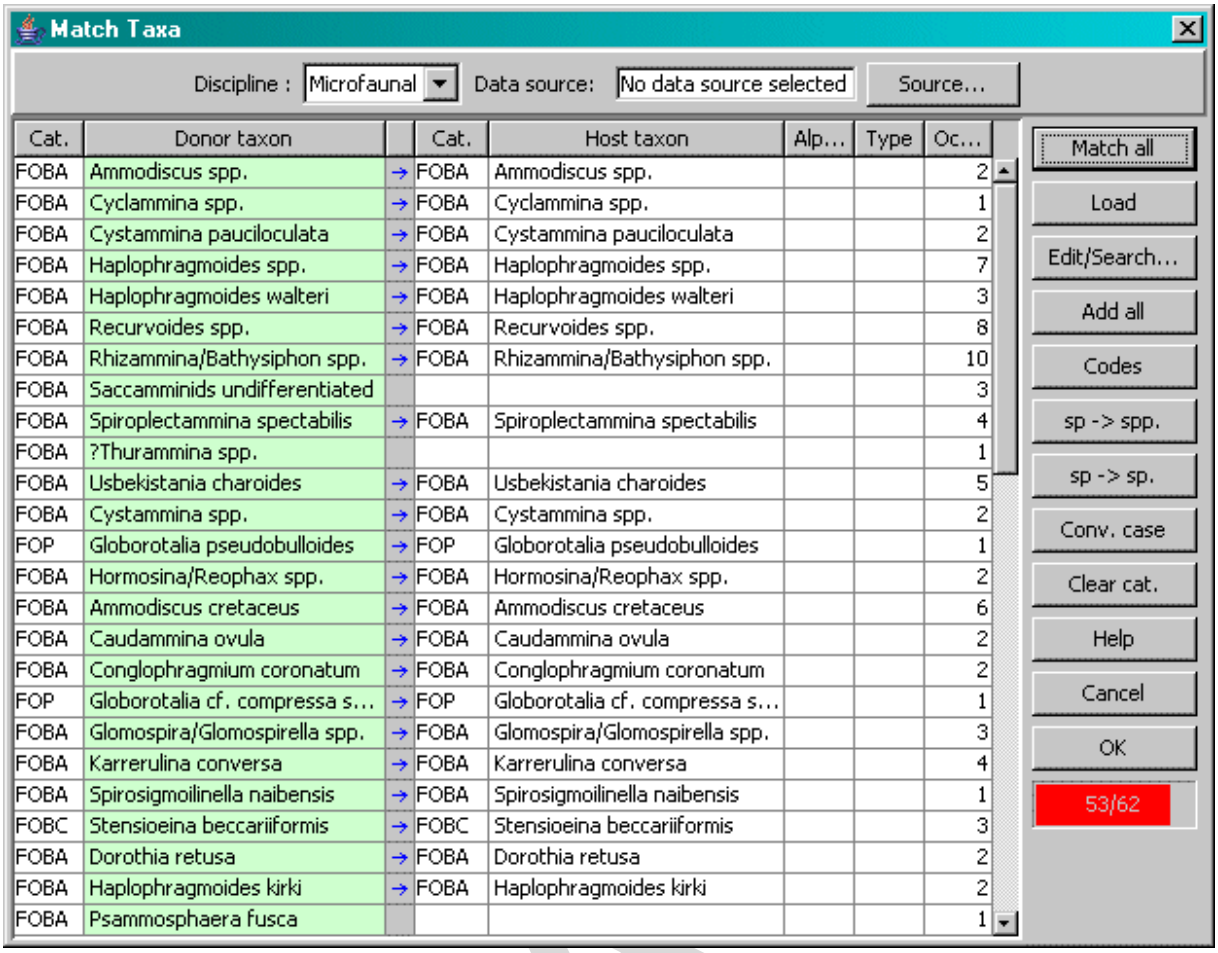
For StrataBugs, DEX and CSV files the contents of the file will immediately be displayed in the Data view tab workspace of the Organiser. Data for each well in the dataset are displayed in separate rows with depth ranges of different data types displayed in columns.



Simultaneously the first of a succession of dialogs appears, each reflecting a data type in the import file. You will next be required to **Match data** in the import file against the database. For instructions on each dialog press the **Help** button.

> ***Note:*** *If you cancel during the import process the data in the workspace will be left in the same state as the last dialog visited, rather than at the start. This may result in a partially unmatched dataset. Any data can be Excluded before the process is restarted.*

If there are taxon occurrences in the file the first dialog to appear will be the **Match Taxa dialog**.



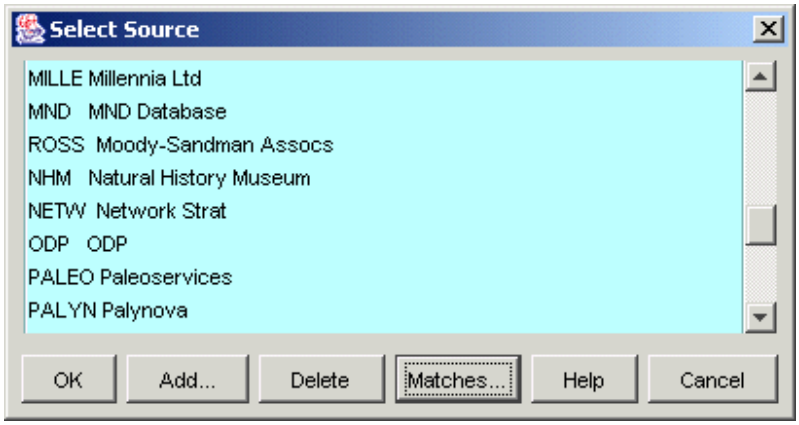
The donor taxa (i.e. those listed in the import file) are listed on the lefthand side of the dialog highlighted in green with their category listed to the left. The number of occurrences of each taxon in the file is recorded on the righthand side. The purpose of this matching process is to find matching names in the database for each of the taxa on the list.

The Discipline to which the displayed taxa belong is shown at the top of the dialog. If there is more than one discipline represented in the data you can select another dicipline from the drop down list. You should repeat the following matching procedure for each discipline you want to import.

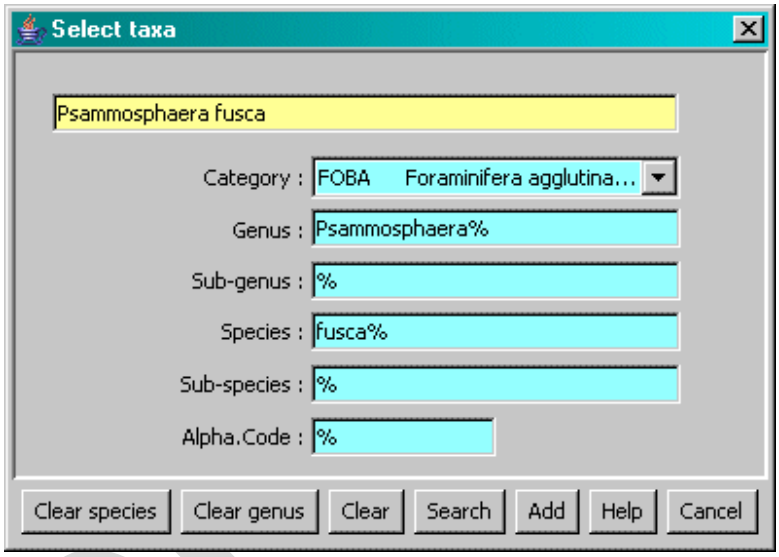
You may wish to press the relevant button on the right hand side to remove common inconstencies from the dataset by converting entries "sp" to "spp." or "sp" to "sp." according to your preference. If the taxon names are in upper case the "Conv.case" button will correctly capitalise each donor name.

Press the "Match all" button and any matching host taxon names (i.e. those already in the database) will appear to the right of the donor taxa.

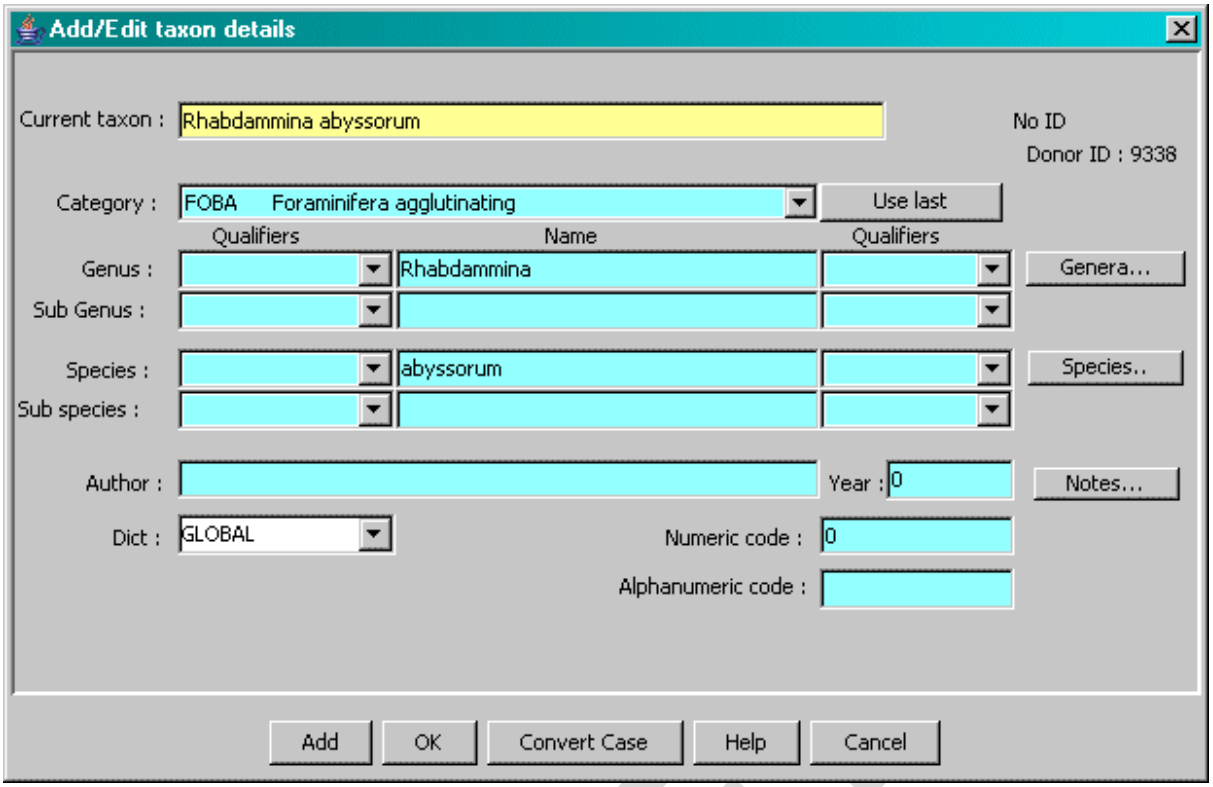
If you have imported data from the same data provider (source) previously you can chose to use any matches specific to that data source by pressing the **Source...** button at the top right hand corner and selecting the Source from the **Select Source dialog**.



It is unusal to match all the taxa in this way so any remaining unmatched taxa must be added to the database one by one until all the taxa are matched. Any taxa remaining unmatched at the the end of this process will not be imported. To add an unmatched taxon, double click on the row to open the **Select taxa dialog**.



This dialog will display the unmatched taxon name in full at the top of the dialog followed by separate fields for Category, Genus, Sub-genus, Species, Sub-species and Alpha code containing various parts of the name. If all you want to do is add the name without modification press the **Add** button. However, be sure to check the name and the way in which it is formatted before you do this and edit any of the fields so that the name is correct. Use the Clear species, Clear genus and Clear buttons to help edit the name. If the Category is incorrect select the right one from the drop down menu. If you are not sure how to spell or format a name use the wildcards (%) and press Search to look for a matching name in the database. When you are sure you have the correct name press the Add button to open the **Add/Edit taxon details dialog**.



Most likely you will just need to check once more that the name is correct and then press **Add**.

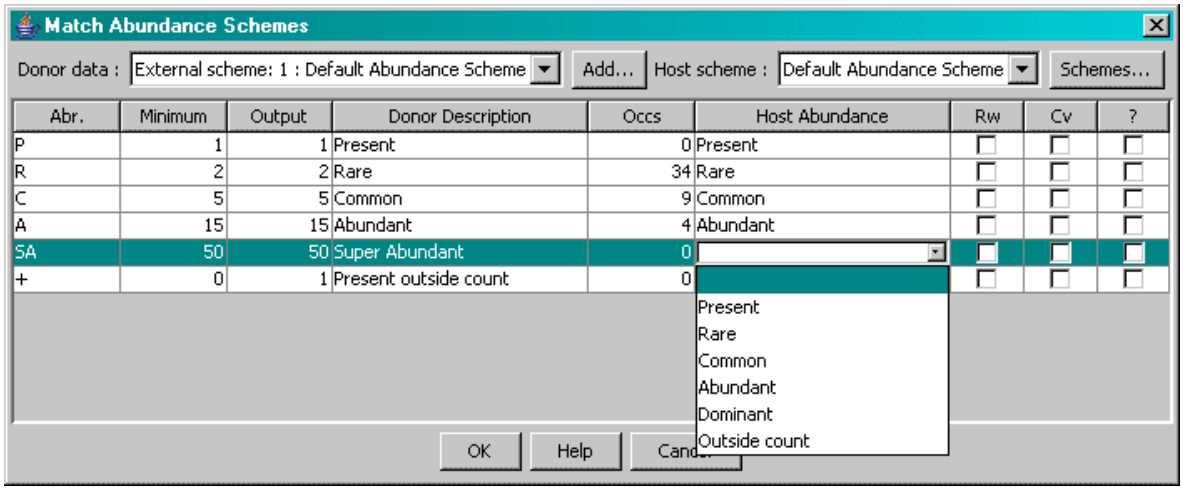
You will either receive a message informing you that the taxon is about to be added to the database or **?????????????????? what.**

Confirm this message to continue.

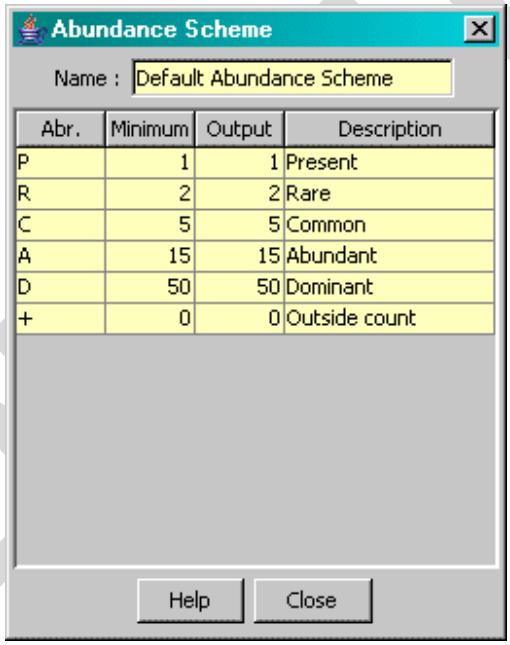
You can use the **Add all** button to add all unmatched taxa to the database. Use this only if you are absolutely certain that all the remaining unmatched names on the list are correct. An example of when this may be adviseable is if you are transferring data which you have recorded on one PC to another. Never trust other user's spelling!

When you have finished matching taxa on the list, either select another discipline form the drop down list or press OK to continue to the next dialog. If you leave any taxa unmatched or skip a discipline you will receive warning messages.

If there are fossil occurrence records in the file there will also be abundance schemes which must be matched in the **Match Abundance Schemes dialog**.

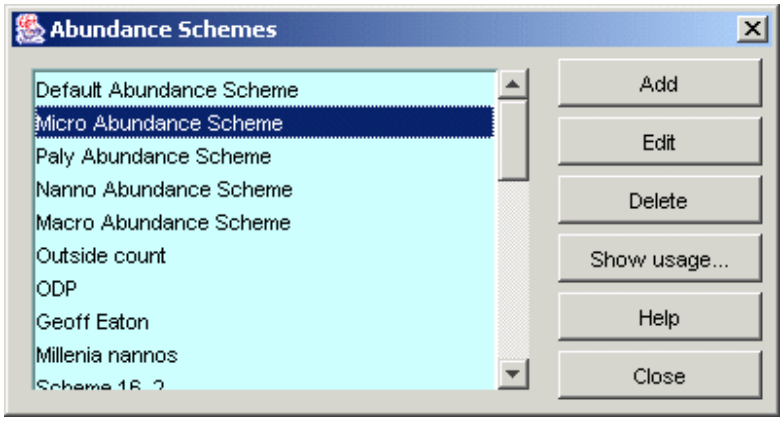


The donor abundance scheme is displayed on the lefthand side of the dialog. For each item in the scheme there is an abbreviation, minimum value, output value and description. The number of occurrences in the dataset is also recorded. If there is a match or partial match in the database it will be displayed on the righthand side. If the displayed match is not correct select another from the the drop down list to see other schemes which match. Each time you select a scheme the **Abundance Scheme dialog** will appear displaying all the values for the selected scheme.



You will often find that the donor and host schemes do not quite match (as in the example above). To match an individual item in the host abundance scheme click on it and select a term from the drop down list.

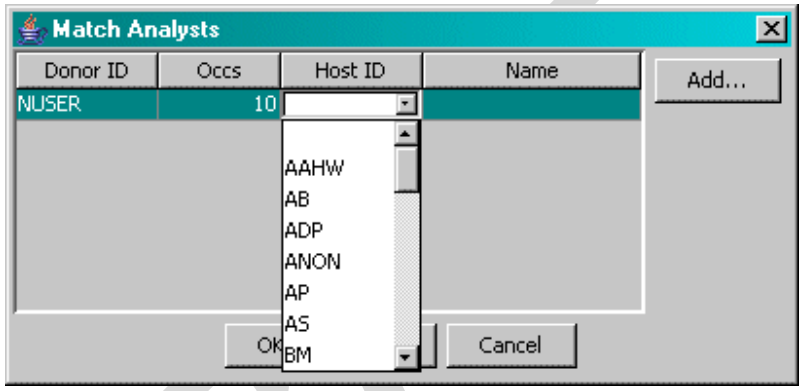
For a full list of schemes press the **Schemes...** button to open the **Abundance Schemes dialog**.



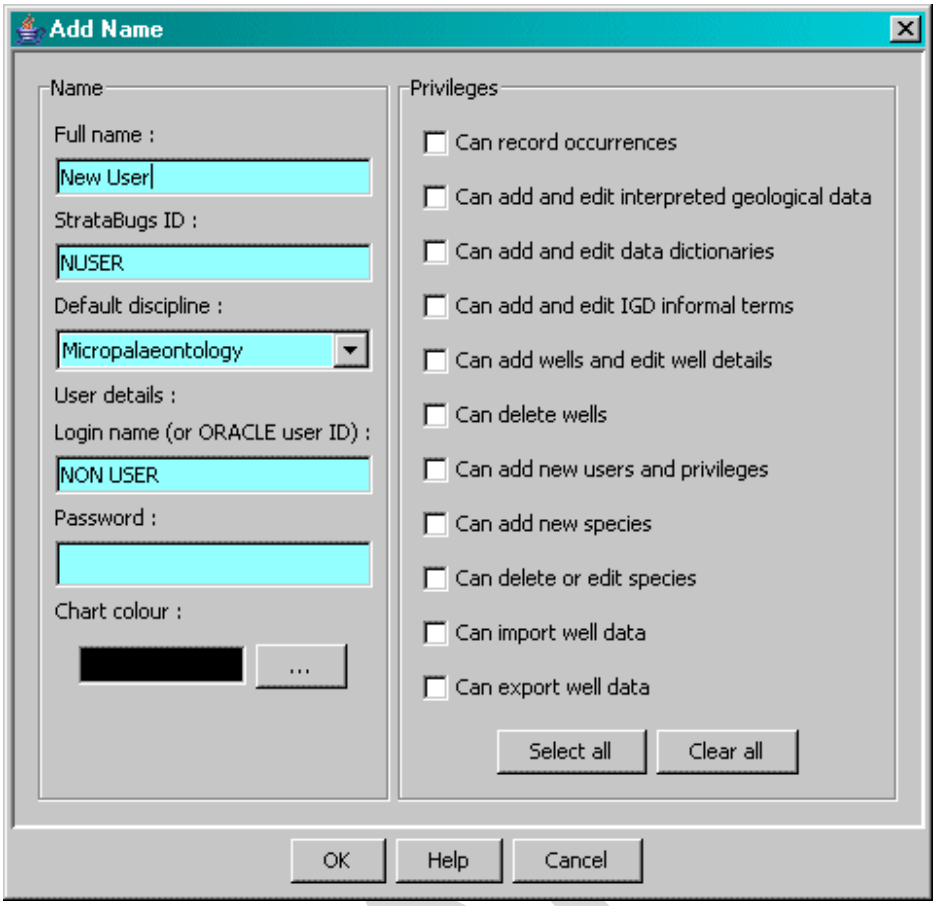
From this dialog you can Add, Edit, Delete or Show Usage of a particular scheme.

When you have matched the abundance scheme(s) for the dataset press OK.

For StrataBugs and DEX files the next dialog to appear will be the **Match Analysts dialog**.



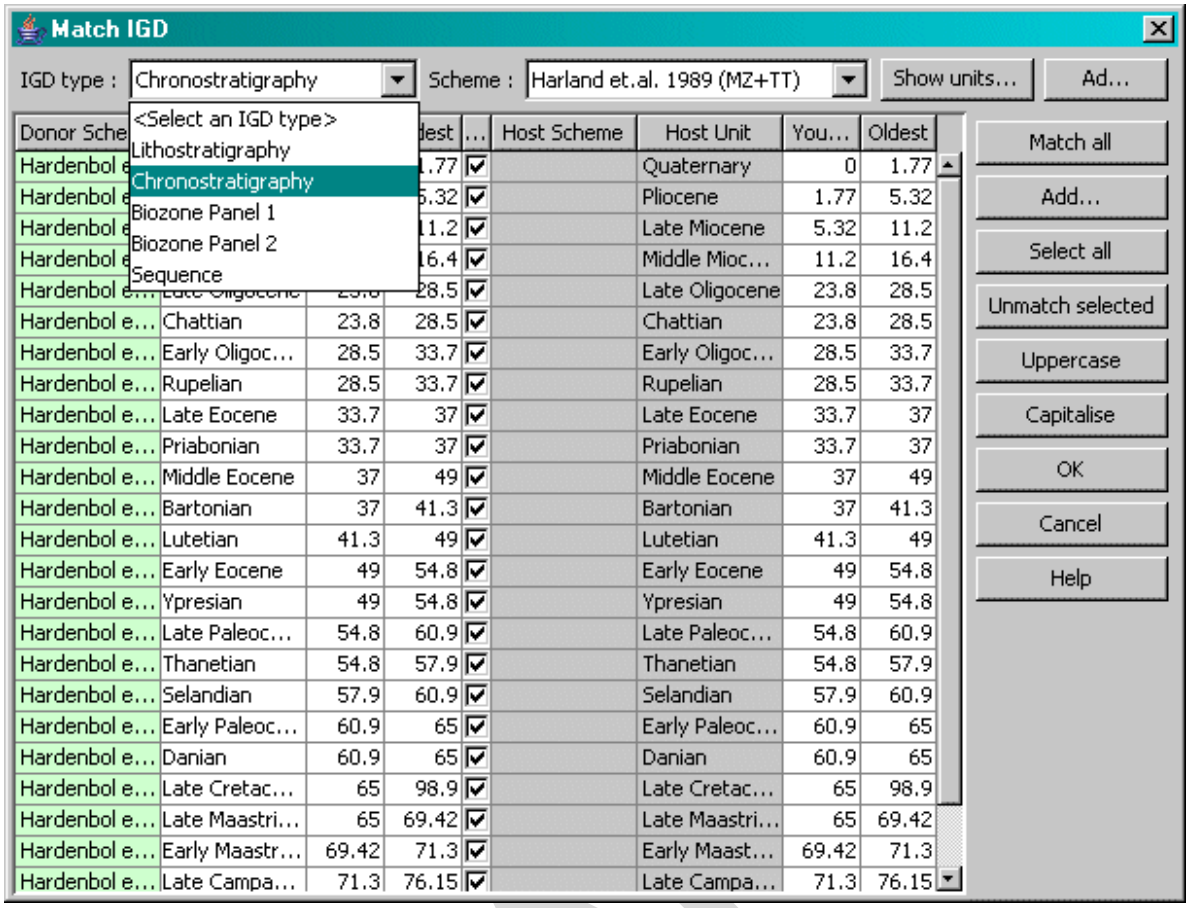
The donor analyst ID is displayed on the lefthand side of the dialog. If there is a matching analyst name in the database this will be displayed on the righthand side. To select a match for the analysts ID selct one form the drop downlist or press the **Add...** button to add a new add a new analysts ID in the **Add Name dialog**.



Fill in the Full name of the new analyst. Because the analyst is not a user of your StrataBugs system there is no need to add a Password or provide any privileges. Press OK.

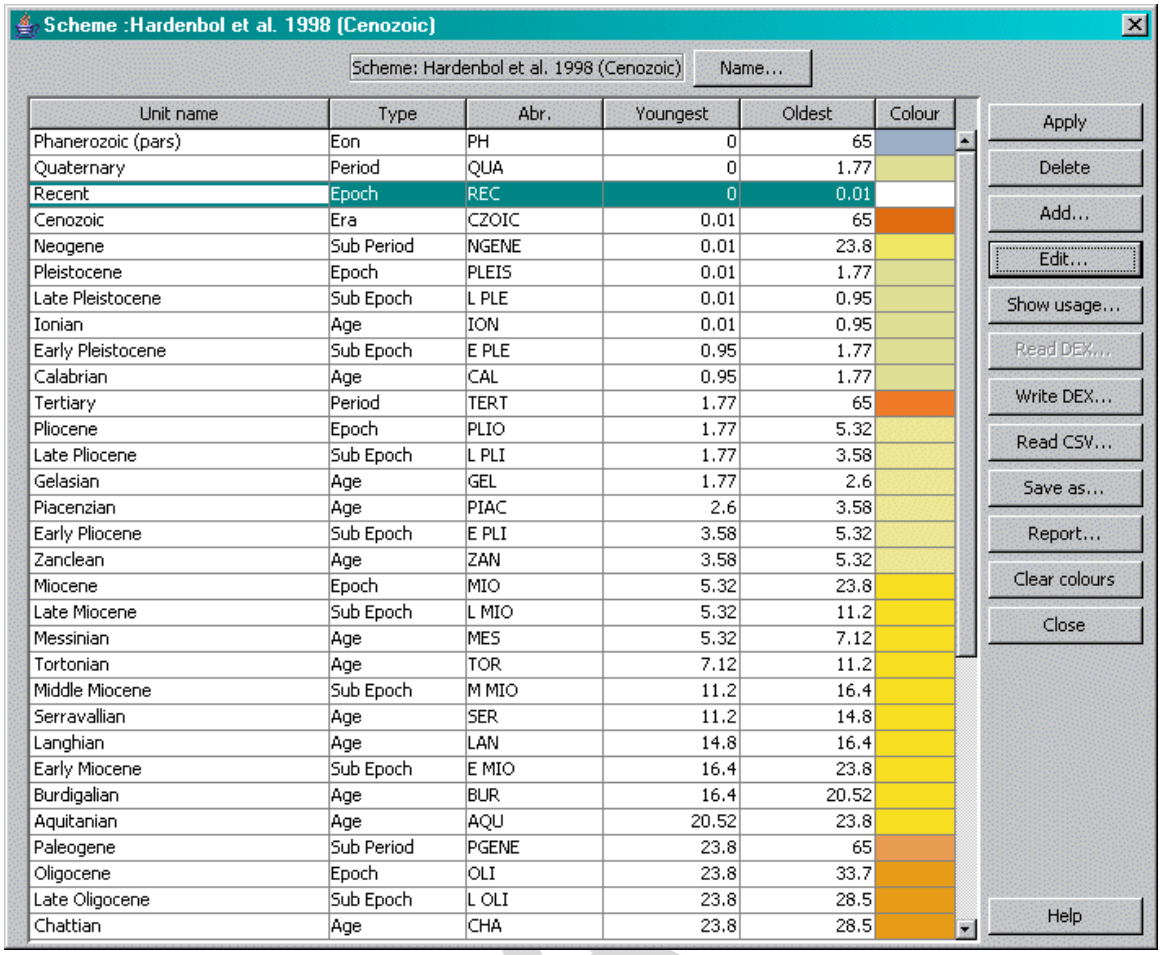
For StrataBugs and CSV files skip to the Match wells section below

For DEX files containing IGD (Interpreted Geological Data) in the dataset the **Match IGD dialog** will appear next.



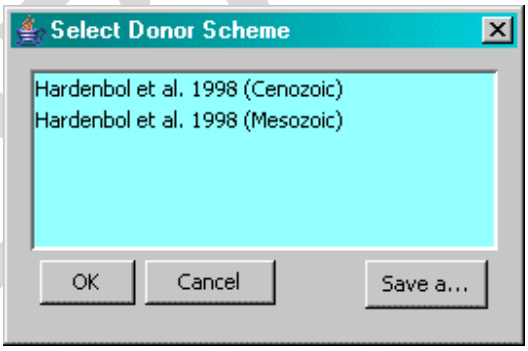
Donor Sche					Host Scheme	Host Unit	You...	Oldest
Hardenbol e...			1.77	☑		Quaternary	0	1.77
Hardenbol e...			5.32	☑		Pliocene	1.77	5.32
Hardenbol e...			11.2	☑		Late Miocene	5.32	11.2
Hardenbol e...			16.4	☑		Middle Mioc...	11.2	16.4
Hardenbol e...			28.5	☑		Late Oligocene	23.8	28.5
Hardenbol e...	Chattian	23.8	28.5	☑		Chattian	23.8	28.5
Hardenbol e...	Early Oligoc...	28.5	33.7	☑		Early Oligoc...	28.5	33.7
Hardenbol e...	Rupelian	28.5	33.7	☑		Rupelian	28.5	33.7
Hardenbol e...	Late Eocene	33.7	37	☑		Late Eocene	33.7	37
Hardenbol e...	Priabonian	33.7	37	☑		Priabonian	33.7	37
Hardenbol e...	Middle Eocene	37	49	☑		Middle Eocene	37	49
Hardenbol e...	Bartonian	37	41.3	☑		Bartonian	37	41.3
Hardenbol e...	Lutetian	41.3	49	☑		Lutetian	41.3	49
Hardenbol e...	Early Eocene	49	54.8	☑		Early Eocene	49	54.8
Hardenbol e...	Ypresian	49	54.8	☑		Ypresian	49	54.8
Hardenbol e...	Late Paleoc...	54.8	60.9	☑		Late Paleoc...	54.8	60.9
Hardenbol e...	Thanetian	54.8	57.9	☑		Thanetian	54.8	57.9
Hardenbol e...	Selandian	57.9	60.9	☑		Selandian	57.9	60.9
Hardenbol e...	Early Paleoc...	60.9	65	☑		Early Paleoc...	60.9	65
Hardenbol e...	Danian	60.9	65	☑		Danian	60.9	65
Hardenbol e...	Late Cretac...	65	98.9	☑		Late Cretac...	65	98.9
Hardenbol e...	Late Maastri...	65	69.42	☑		Late Maastri...	65	69.42
Hardenbol e...	Early Maastr...	69.42	71.3	☑		Early Maast...	69.42	71.3
Hardenbol e...	Late Campa...	71.3	76.15	☑		Late Campa...	71.3	76.15

At the top lefthand corner of the dialog there is a drop down list of IGD data types in the dataset. By default the first IGD type on the list is displayed. You should match each IGD data type in turn using the following procedure. The donor IGD scheme will be displayed on the lefthand side. Each unit in the scheme will be displayed together with their youngest and oldest ages (if available) and a check box indicating that the units are "linked" in a scheme. The host unit names and ages are displayed on the righthand side but you must select a matching scheme from the drop down list. If you are unsure what units are contained within a scheme, select the scheme on the list and then press the **Show units...** button. The details of the selected IGD scheme will be displayed in the **IGD Scheme dialog**.

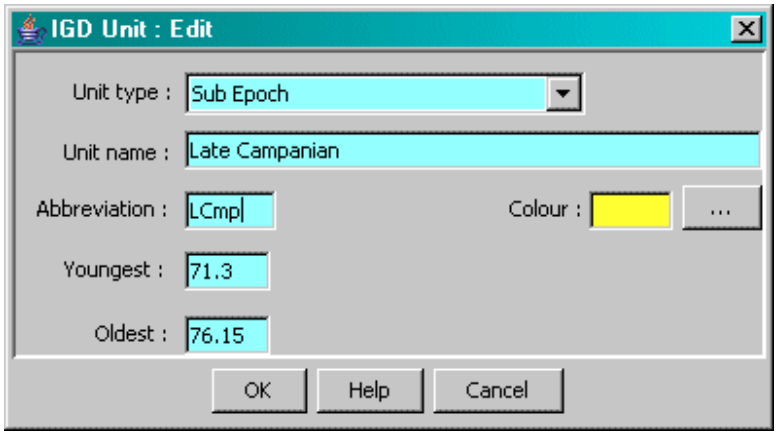


Unit name	Type	Abr.	Youngest	Oldest	Colour
Phanerozoic (pars)	Eon	PH	0	65	
Quaternary	Period	QUA	0	1.77	
Recent	Epoch	REC	0	0.01	
Cenozoic	Era	CZOIC	0.01	65	
Neogene	Sub Period	NGENE	0.01	23.8	
Pleistocene	Epoch	PLEIS	0.01	1.77	
Late Pleistocene	Sub Epoch	L PLE	0.01	0.95	
Ionian	Age	ION	0.01	0.95	
Early Pleistocene	Sub Epoch	E PLE	0.95	1.77	
Calabrian	Age	CAL	0.95	1.77	
Tertiary	Period	TERT	1.77	65	
Pliocene	Epoch	PLIO	1.77	5.32	
Late Pliocene	Sub Epoch	L PLI	1.77	3.58	
Gelasian	Age	GEL	1.77	2.6	
Piacenzian	Age	PIAC	2.6	3.58	
Early Pliocene	Sub Epoch	E PLI	3.58	5.32	
Zanclean	Age	ZAN	3.58	5.32	
Miocene	Epoch	MIO	5.32	23.8	
Late Miocene	Sub Epoch	L MIO	5.32	11.2	
Messinian	Age	MES	5.32	7.12	
Tortonian	Age	TOR	7.12	11.2	
Middle Miocene	Sub Epoch	M MIO	11.2	16.4	
Serravallian	Age	SER	11.2	14.8	
Langhian	Age	LAN	14.8	16.4	
Early Miocene	Sub Epoch	E MIO	16.4	23.8	
Burdigalian	Age	BUR	16.4	20.52	
Aquitanian	Age	AQU	20.52	23.8	
Paleogene	Sub Period	PGENE	23.8	65	
Oligocene	Epoch	OLI	23.8	33.7	
Late Oligocene	Sub Epoch	L OLI	23.8	28.5	
Chattian	Age	CHA	23.8	28.5	

To add a donor scheme as a new scheme to your database press the **Add...** button, select the scheme and press OK.



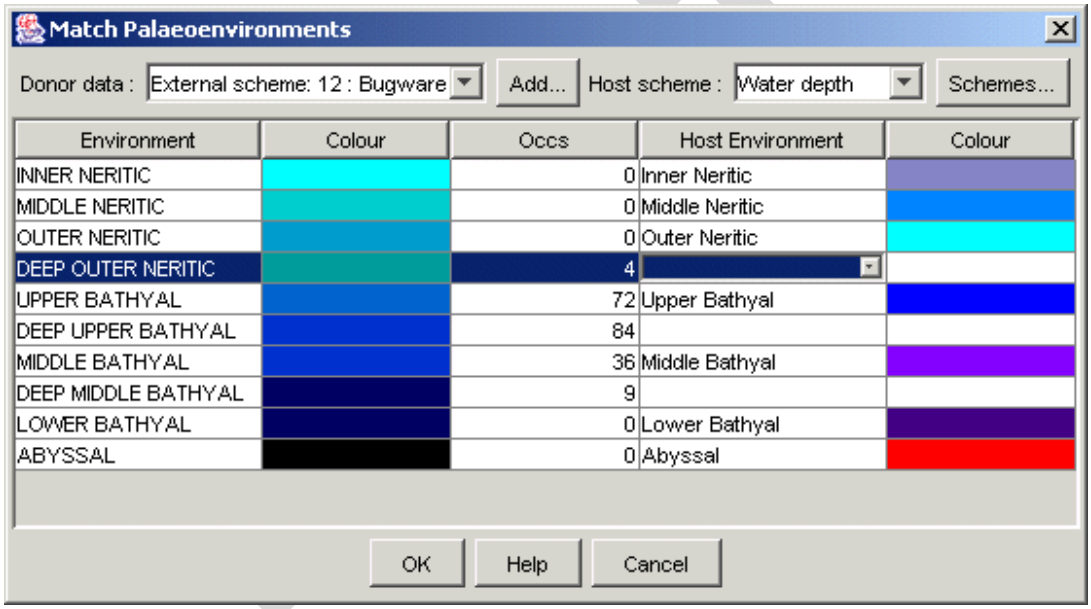
When you have finally selected the appropriate Scheme press the **Match all** button. If any of the units are not matched you can match them to another scheme by selecting one from the drop down list or add them to the selected scheme by double clicking to open the **Scheme dialog** and the **IGD Unit dialog**.



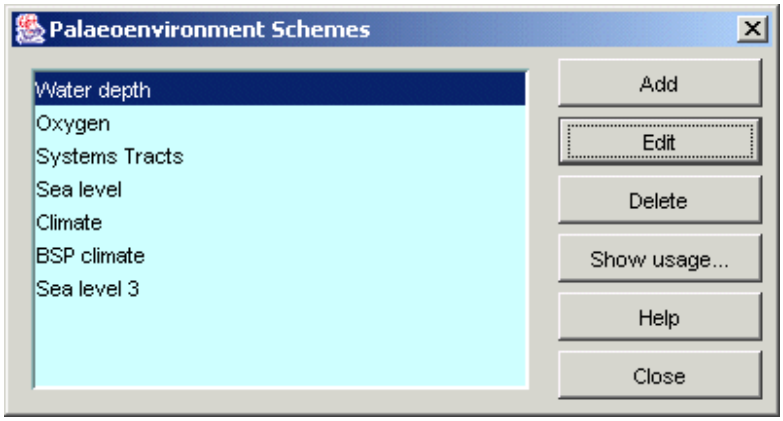
Select the unit type from the drop down list and a suitable abbreviation, edit any of the other fields and select a colour for the unit as appropriate. Press OK and the new unit willappear on the list of units in the Scheme dialog.

When you have finished one IGD type select another from the drop down list or press OK to continue.

If there are any palaeoenvironmental data the next dialog to open will be the **Match Palaeoenvironments dialog**.

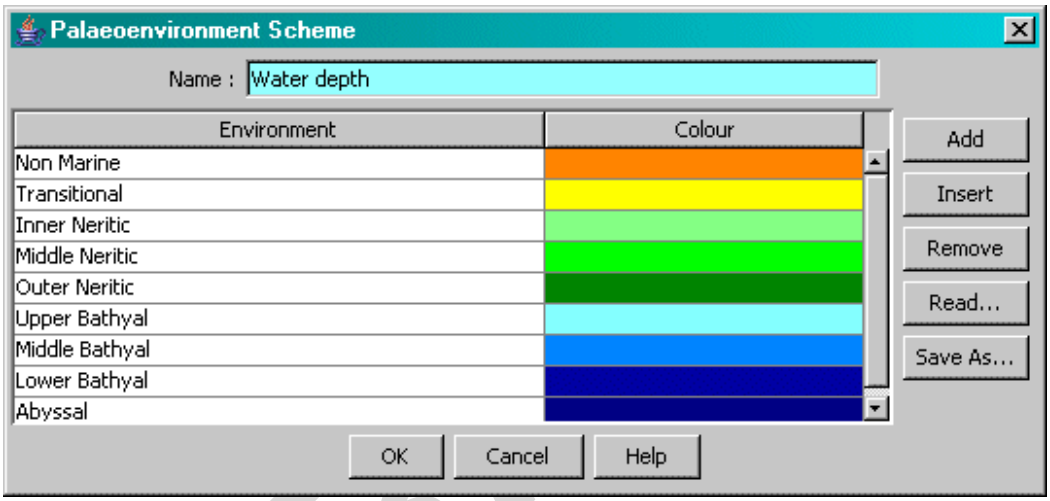


The donor Palaeoenvironemt scheme will be displayed on the lefthand side. Each unit in the scheme will be displayed together with their display colours and the number of occurrences in the donor dataset. The host unit names and display colours are displayed on the righthand side. You can select an alternative scheme from the drop down list. A list of schemes appears in the **Palaeoenvironmental schemes dialog**.



From here you can add, edit, delete or show the usage of the schemes.

If you want to add the Donor scheme to your database press the **Add...** button next to the Donor data field and the **Palaeoenvironment Scheme dialog** will appear.

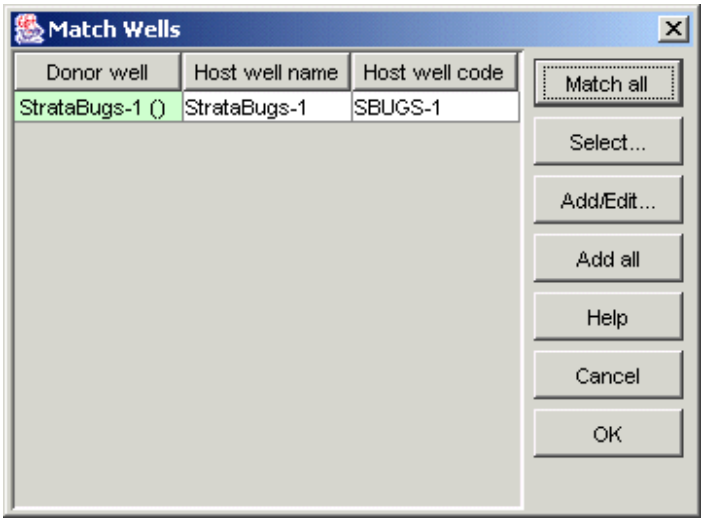


From here you can add insert or Remove units from a scheme.

> ***Note:*** *do not insert units within a scheme for which there are data as this will modify existing interpretations.*

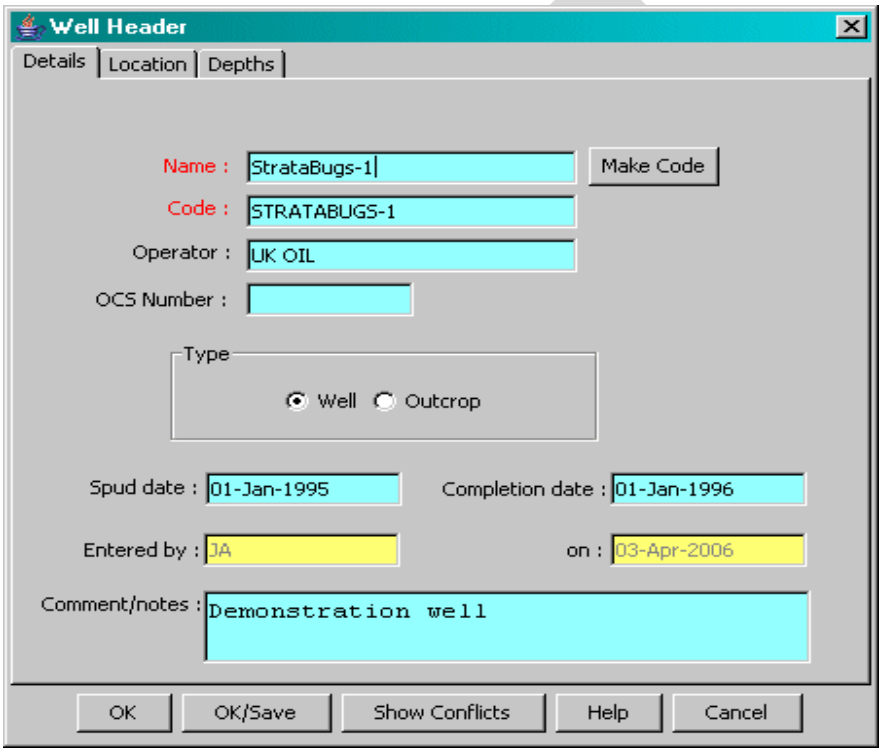
Press OK to add the new scheme to your database.

For StrataBugs, DEX and CSV files the next dialog in the matching process to appear irrespective of what data you are importing is the **Match Wells dialog**.



If the Donor well(s) is/are already in your database then you can press the **Match all** button to select the Host well names. You can also add new wells and add wells under different names. To add one or more new wells you can use the **Add all** button.

To add a new well press the **Add/Edit** button. The **Well header dialog** will appear.



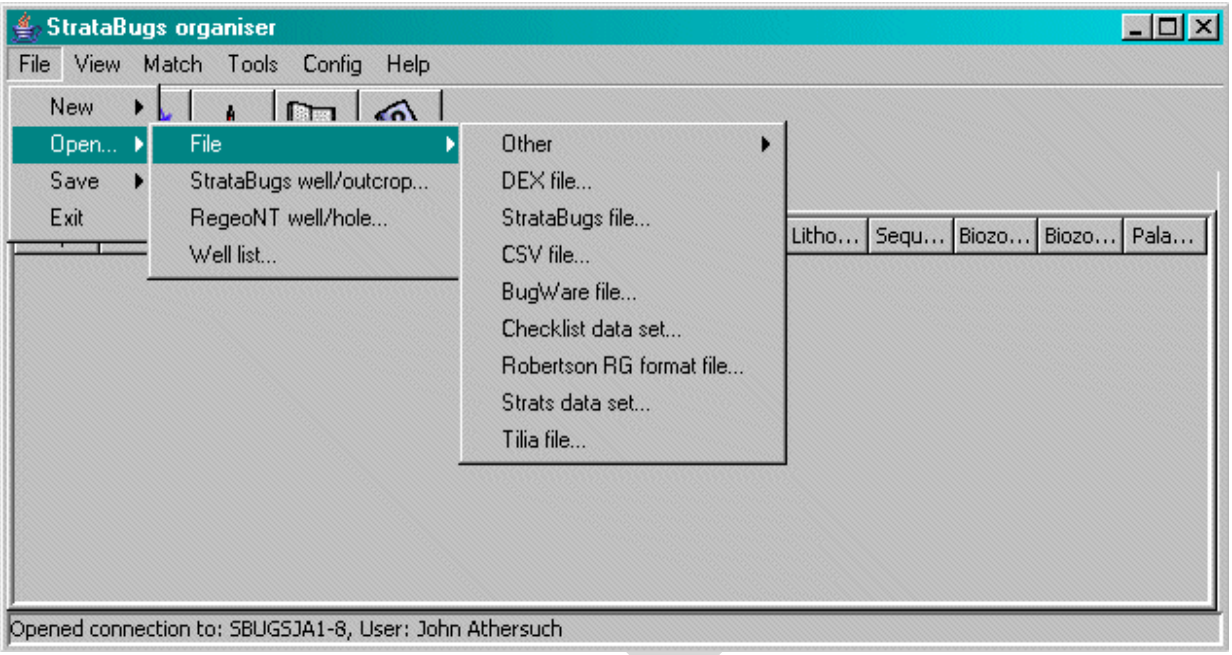
By default all the mandatory fields will be filled and you can just press OK. If you want to make any additions or modifications for the well header information you may do so at this stage.

Press OK and all the data are imported. The entries in the workspace that were green should now be white. If any of them are red please press the **Show Conflicts** button and resolve the conflicts by editing either the donor or host well header data.

If you want to quit at any time press **Cancel**. When you have completed the matching process **Organiser** will automatically **Save data** to the database.

How to import biostratigraphic data

You can import a number of data types by selecting the menu options yourself. You can import DEX, CSV and StrataBugs files using the assistance of the Import button (see above).



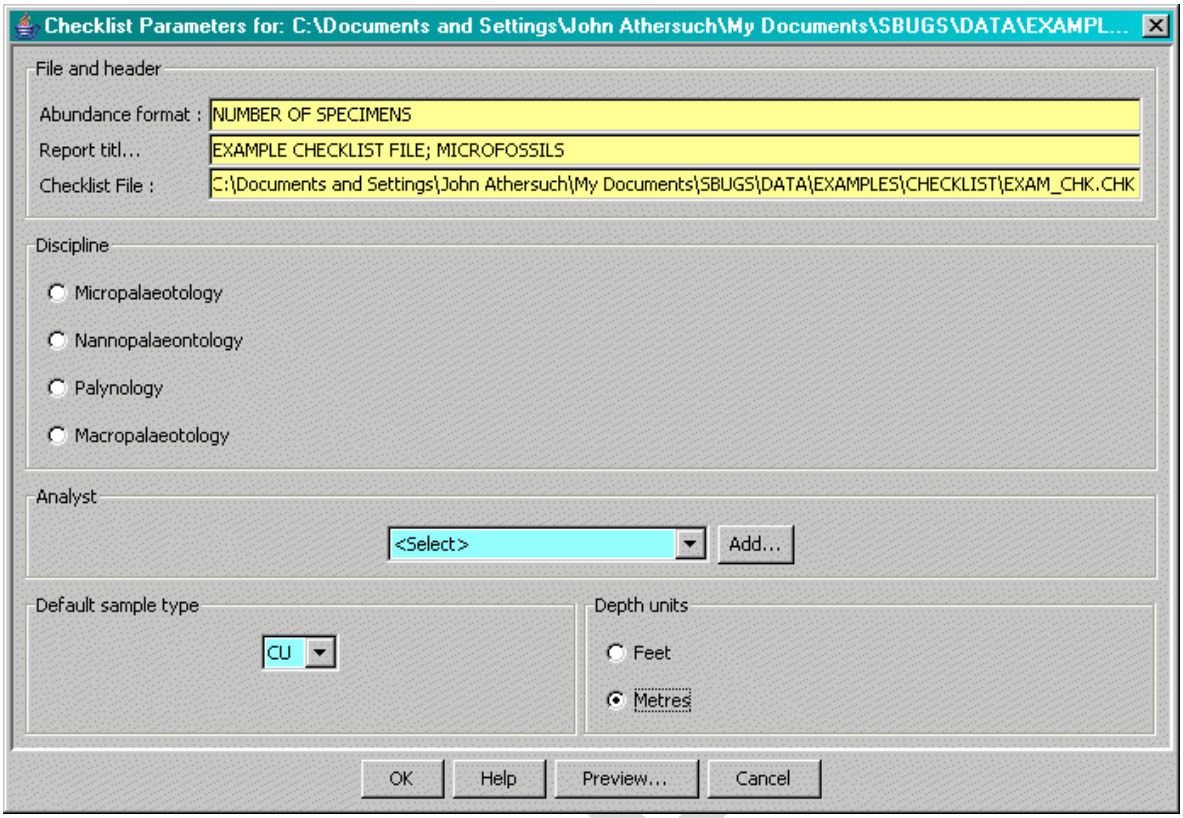
First select the files type you want to import (**File | Open | File | *filename***).

For StrataBugs, DEX and Strats files the contents of the file will immediately be displayed in the Data view tab workspace of the Organiser. Data for each well in the dataset are displayed in separate rows with depth ranges of different data types displayed in columns.

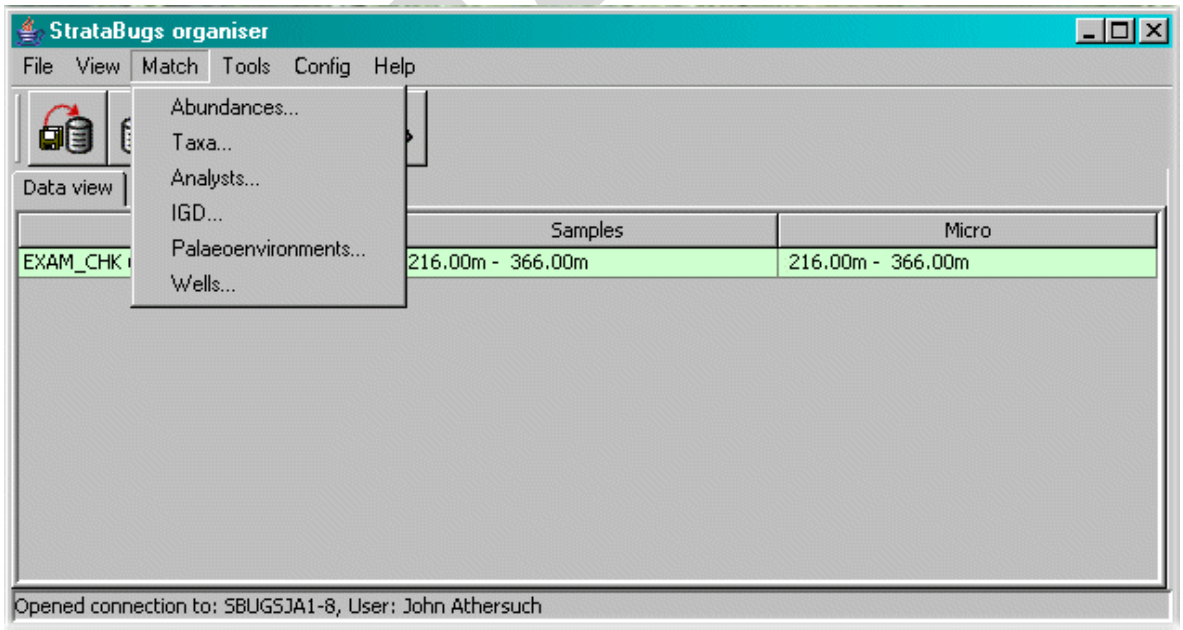
For CSV, Bugware, Checklist, Robertson's RG and Tilia files it is necessary to do some preparation of the dataset before it can go through the import process. This is because these file types do not contain sufficient parameters to allow them to be imported correctly. In each case complete the required information that will enable Organiser to process the data correctly.

The **CSV File Parameters dialog** is described above in "How to import DEX, CSV or StrataBugs data from a file into the database".

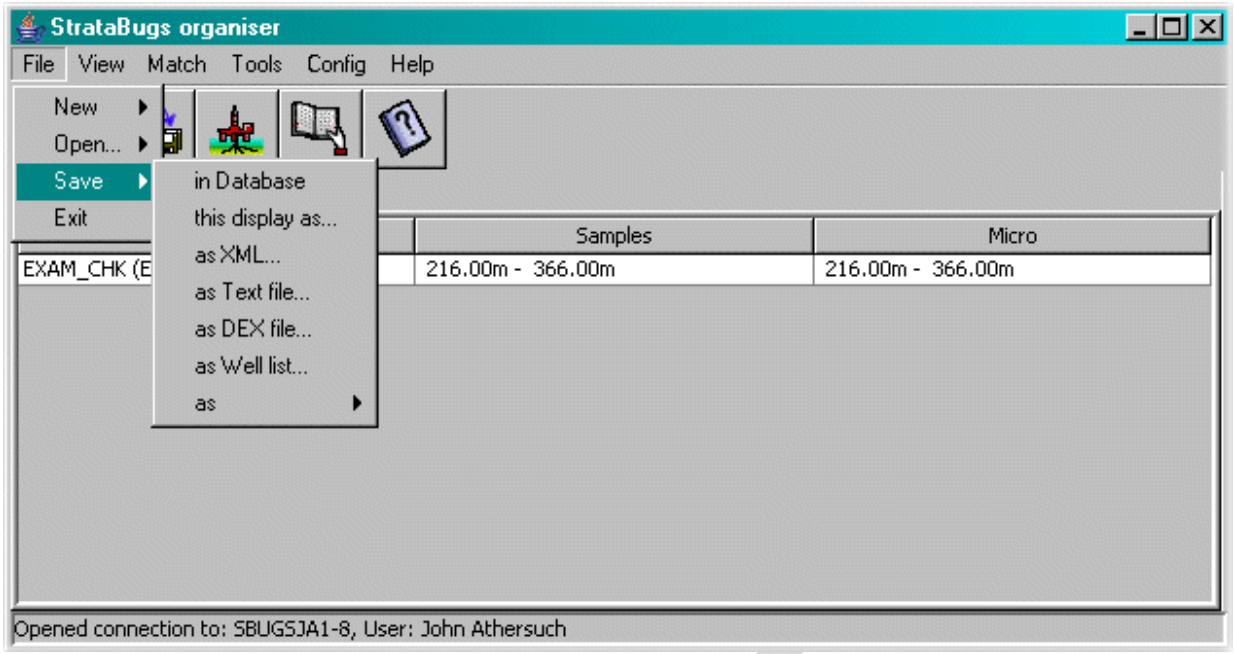
Another example is the **Checklist Parameters dialog**.



When the data are displayed in the workspace you must match each data type in turn by selecting each of the items on the **Match** menu in turn. Not all files will contain all data types and you will be warned if you try to match a data type for which there are no data. You will also be warned if you skip a data type without matching it. In these cases you can proceed if you wish but the unmatched data will not be imported.



When all the data are matched select File | Save | in database.



The data will be saved in the database and the imported datatypes displayed in the workspace should turn white.

How to import lithology data

The StrataBugs DEX export/import process has been designed so that lithology data remains consistent between users. You may wish to use lithology data from sources other than other StrataBugs users. To maintain this consistency lithotypes and graphics are not user definable. Each lithotype has a unique StrataBugs code and associated graphic. If you can't find a suitable match for a term contact StrataData who may create a bespoke lithology for you. This will be added to the lithologies available from the StrataData website and can be downloaded and integrated into your existing lithology scheme.

Installing new lithology patterns

From time to time new lithology patterns become available for use with StrataBugs. These are downloadable from the StrataData website. Copy them to a temporary folder on your hard drive. Then from the StrataBugs control panel select Accessories | Config | Database and then scroll down the list of Actions until you get to "Import lithology pattern from file" and press Run.

If you want to rearrange the order of the patterns on your lithology pallette you can edit a file called lithsort.csv (also downloadable from the StrataData website) Then from the StrataBugs control panel select Accessories | Config | Database and then scroll down the list of Actions until you get to" Import lithology sort order and descriptions from file" and press Run.

There are two styles of lithology display in StrataBugs.

Sample lithology. Recorded on a sample by sample basis. Sample lithotypes are displayed in the Sample lithology panel as horizontal bars subdivided according to the % of each lithotype recorded. There is only one type of data file for the sample lithologies at present. To import Sample Lithology refer to the description of the **Sample Lithology import**.

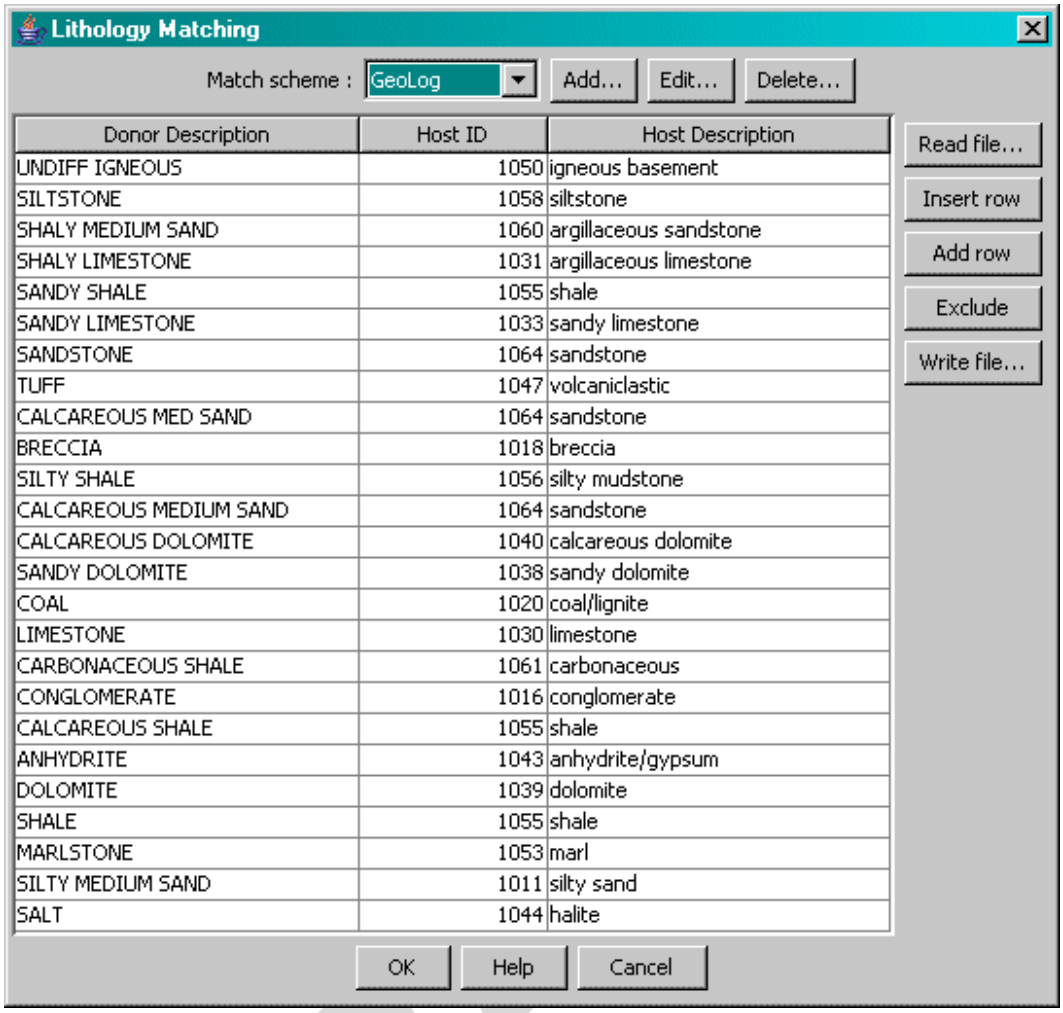
Interpreted Lithology. Based on an interpretation of the sample lithology and logs. Interpreted Lithologies are displayed in the Lithology panel and are recorded as intervals. There are numerous file formats for interpreted lithology. StrataBugs is set up to recognise the formats which we have encountered.

For both lithology styles if you want to display lithology data from a datafile in your workspace so that your can later save it to your database or to a datafile, you must first create a match between the "Donor" lithotype dictionary and the "Host" StrataBugs lithologies. This is called a **Lithology match scheme** and you can create one by reading an existing dictionary from a datafile or from scratch. In either case the Lithology match scheme provides a "translation" of the terms in a Lithology datafile to terms recognised by your database.

Procedure for importing Interpreted Lithology

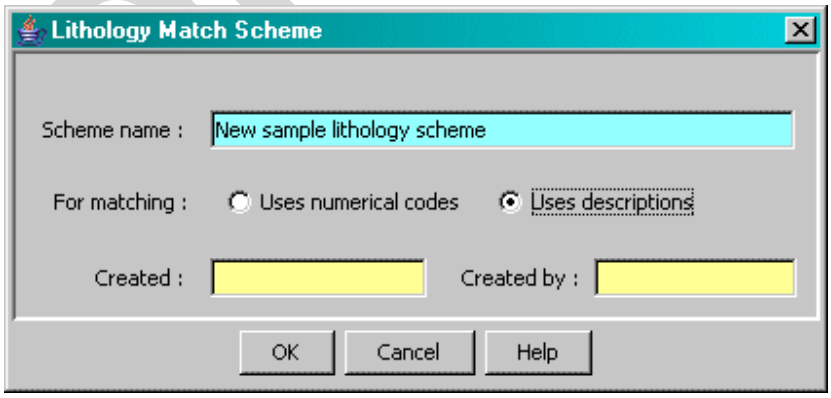
Step 1 - Create Lithology Match Scheme. If this is the first occassion on which you have imported data in a particular format or from a particular source you may first need to import a Lithology Match Scheme for the data. To do this, go to Tools | Lithology Matching. If you do not need to create a Lithology Match Scheme go straight to Step 2 (below).

Answer yes if Organiser needs to create some tables. When the **Lithology Matching dialog** opens the last used scheme will be displayed.



Donor Description	Host ID	Host Description
UNDIFF IGNEOUS	1050	igneous basement
SILTSTONE	1058	siltstone
SHALY MEDIUM SAND	1060	argillaceous sandstone
SHALY LIMESTONE	1031	argillaceous limestone
SANDY SHALE	1055	shale
SANDY LIMESTONE	1033	sandy limestone
SANDSTONE	1064	sandstone
TUFF	1047	volcaniclastic
CALCAREOUS MED SAND	1064	sandstone
BRECCIA	1018	breccia
SILTY SHALE	1056	silty mudstone
CALCAREOUS MEDIUM SAND	1064	sandstone
CALCAREOUS DOLOMITE	1040	calcareous dolomite
SANDY DOLOMITE	1038	sandy dolomite
COAL	1020	coal/lignite
LIMESTONE	1030	limestone
CARBONACEOUS SHALE	1061	carbonaceous
CONGLOMERATE	1016	conglomerate
CALCAREOUS SHALE	1055	shale
ANHYDRITE	1043	anhydrite/gypsum
DOLOMITE	1039	dolomite
SHALE	1055	shale
MARLSTONE	1053	marl
SILTY MEDIUM SAND	1011	silty sand
SALT	1044	halite

Create a new scheme by pressing **Add...**, and make sure that you select the correct option from **Numerical codes** or **Descriptions** is selected in the **Lithology Match Scheme dialog**. If you are importing AppleCore data make sure you have selected the **Numerical** option.

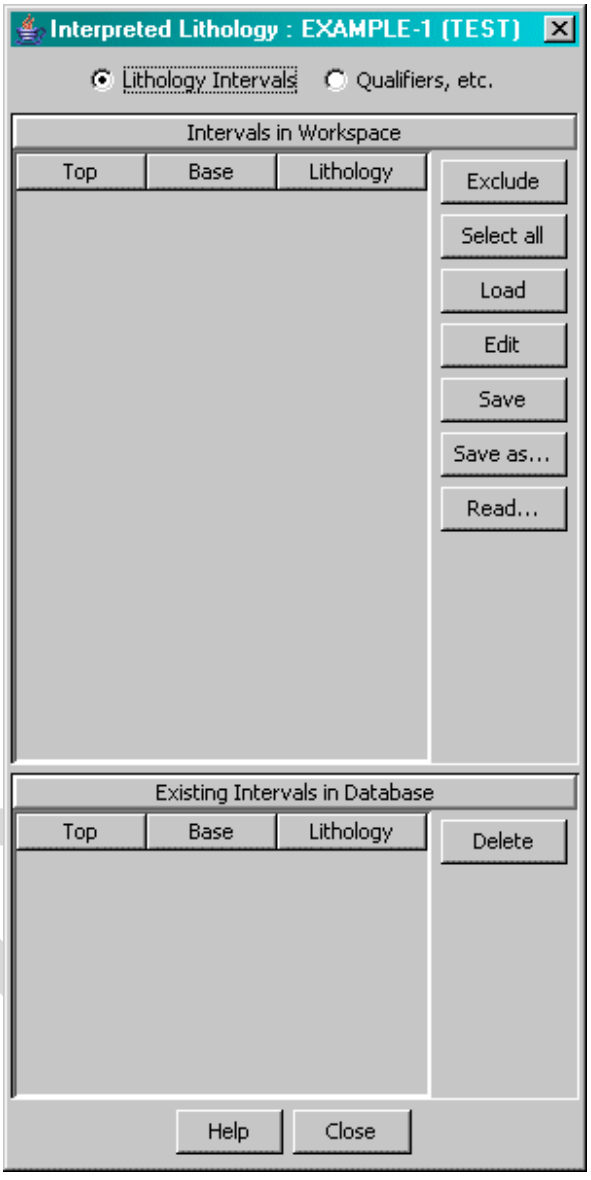


Press **OK** and you will return to the blank **Lithology Matching dialog**.

Import the scheme file by pressing **Read file** button. Check the descriptions in the file translate correctly. Change or add any new matches according to your needs. Many schemes

are not rigid over the assignment of codes, some of them are user defined so will vary between users. To do this click on the blank Host descriptions one at a time and select a description from the drop down list. If you're unsure about lithology codes and translations consult StrataData. Press **OK** to save the scheme.

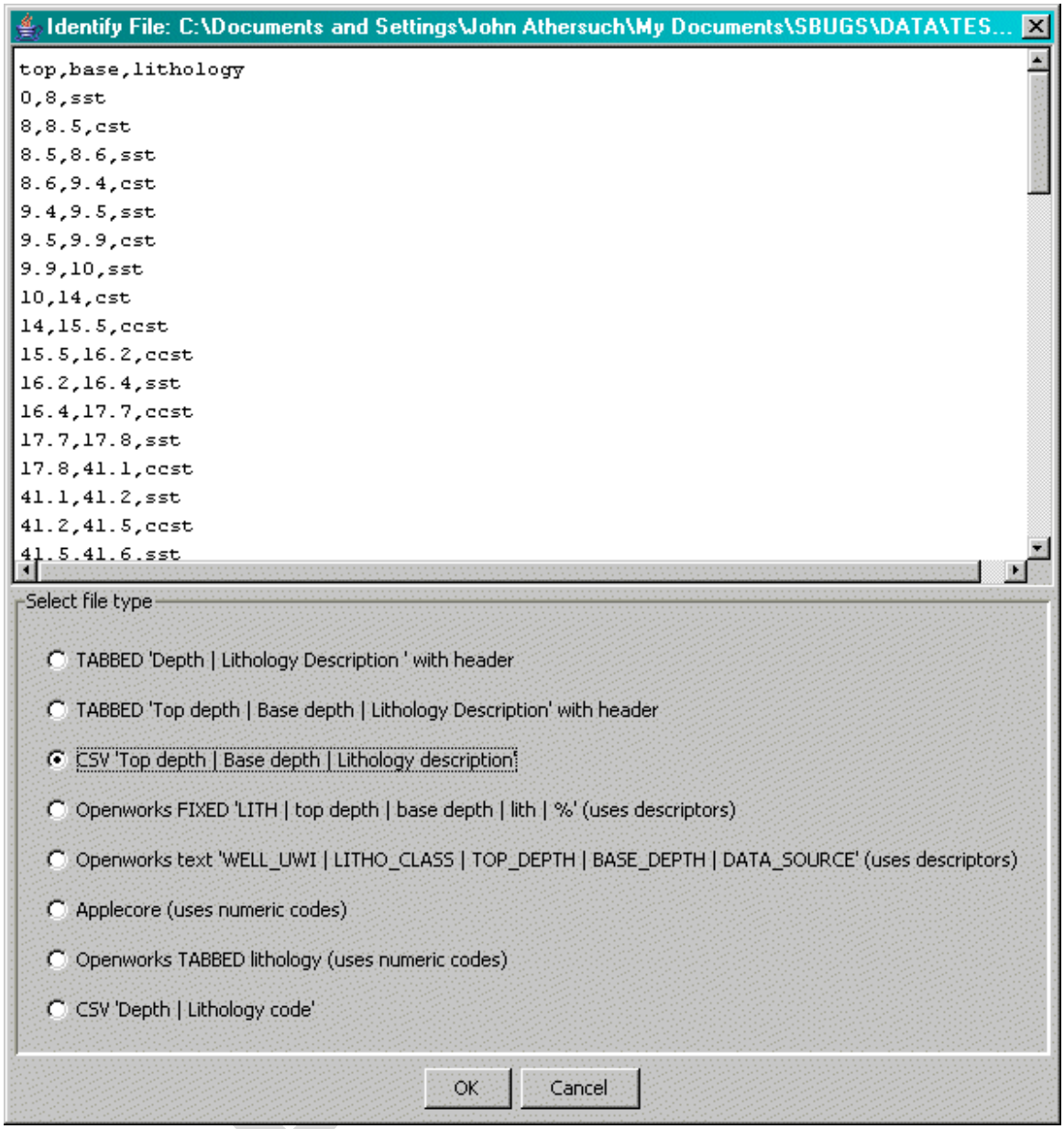
Step 2 - import the lithology data. Once you have imported a suitable scheme you can match data from any number of wells against it. To do this press the **Select well** button on the toolbar to select a target well. Then select the Data type button on the toolbar and select Interpreted Lithology. Double-click the Interpreted Lithology cell for a well to open a blank **Interpreted Lithology dialog**.



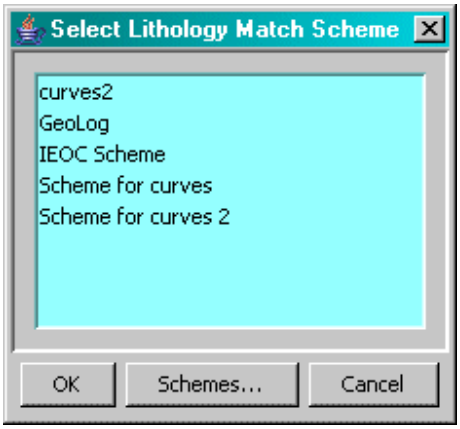
Press the **Read** button. Select the data file. Press OK to read the contents of a lithology datafile.

In the next dialog part of the file contents will be displayed to enable you to dentify the import file type. A brief description of each file type we have encountered is given to help you identify the correct option.

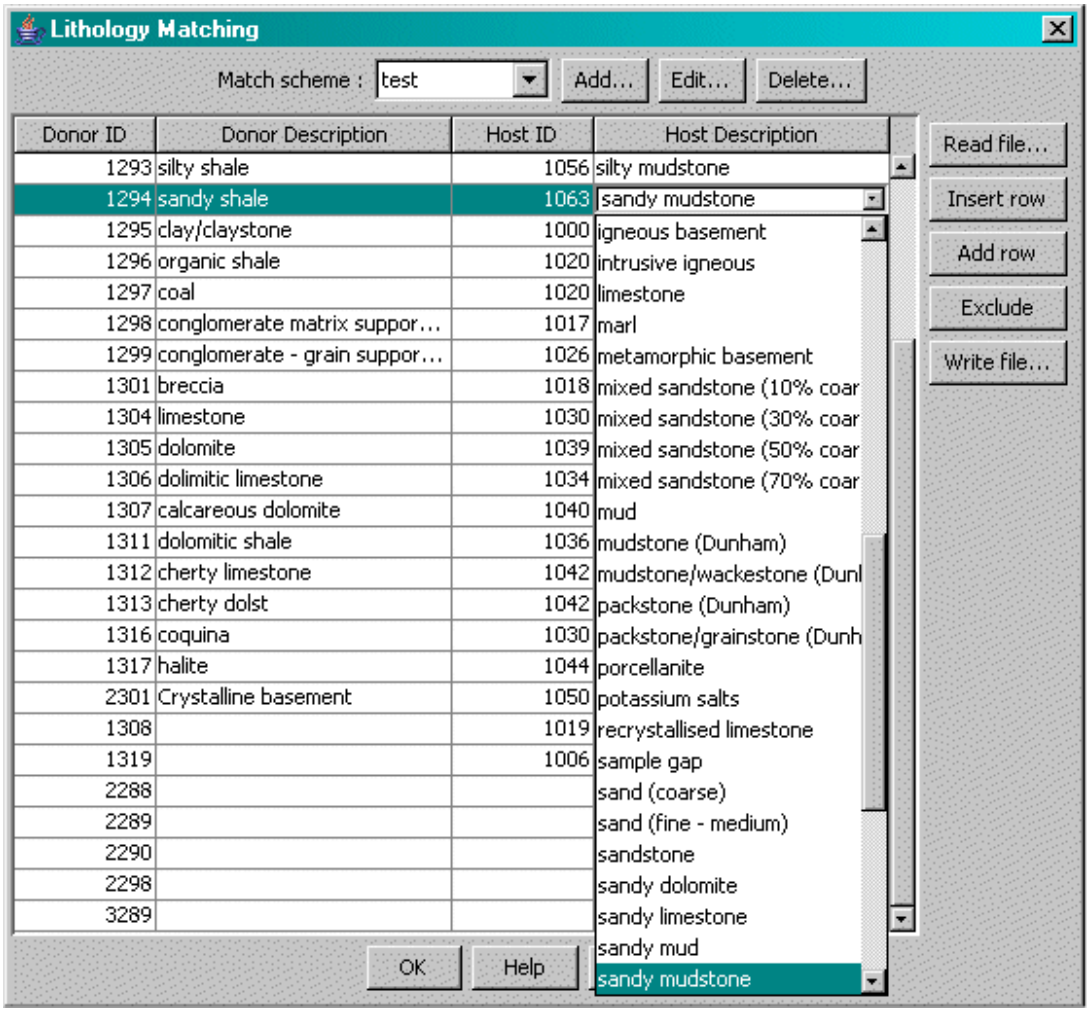
Press **OK**.



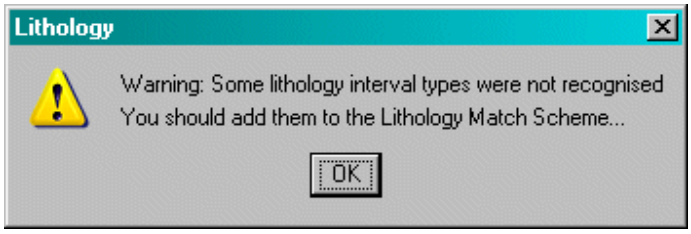
You will then be asked to select the name of a scheme in the **Select Lithology Match Scheme dialog**.



Select an appropriate one from the list and press **OK**. If you don't know which scheme to select you can press the Schemes button instead. You can then select any match scheme from the drop down list and display all the lithology matches.



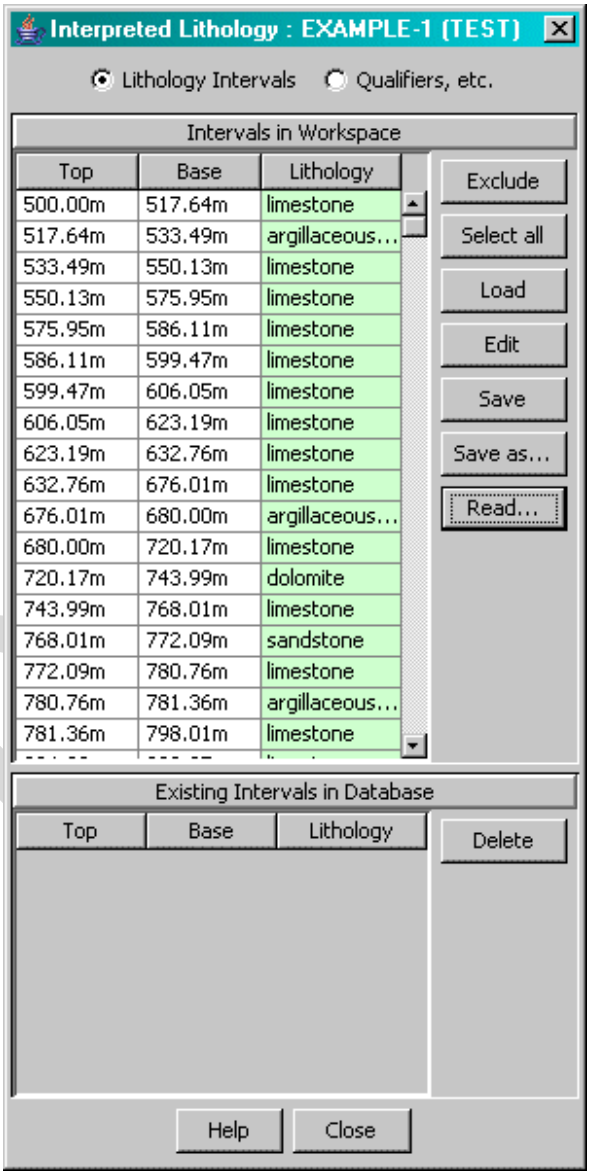
You may get messages about missing translations which you can then add to the scheme.



To do this click on the blank Host descriptions one at a time and select a description from the drop down list. If you're unsure about lithology codes and translations consult StrataData.

Press **OK**. You will be asked to confirm that the want to commit the data to the database. Press **Yes**.

You should end up with a list of lithology intervals displayed in green in the **Interpreted Lithology dialog**.



Press **Save** on that dialog to save the data in the database.

Press close and the Interpreted Lithology cell in the workspace will display the data range in white showing thatthe data are saved inthe database.

How to import other data

If you need to import a specific data type you can do so while you have the appropriate dialog open

Open a well in your database and select a data type. If there is a **Read** button on the dialog press it. This will enable you to navigate to the import file and select it. Datatypes that can currently be imported in this way are listed below. Specific instructions are provided in the HELP for each dialog.

Cores

Interpreted Lithology

Sample Lithologies

Comments

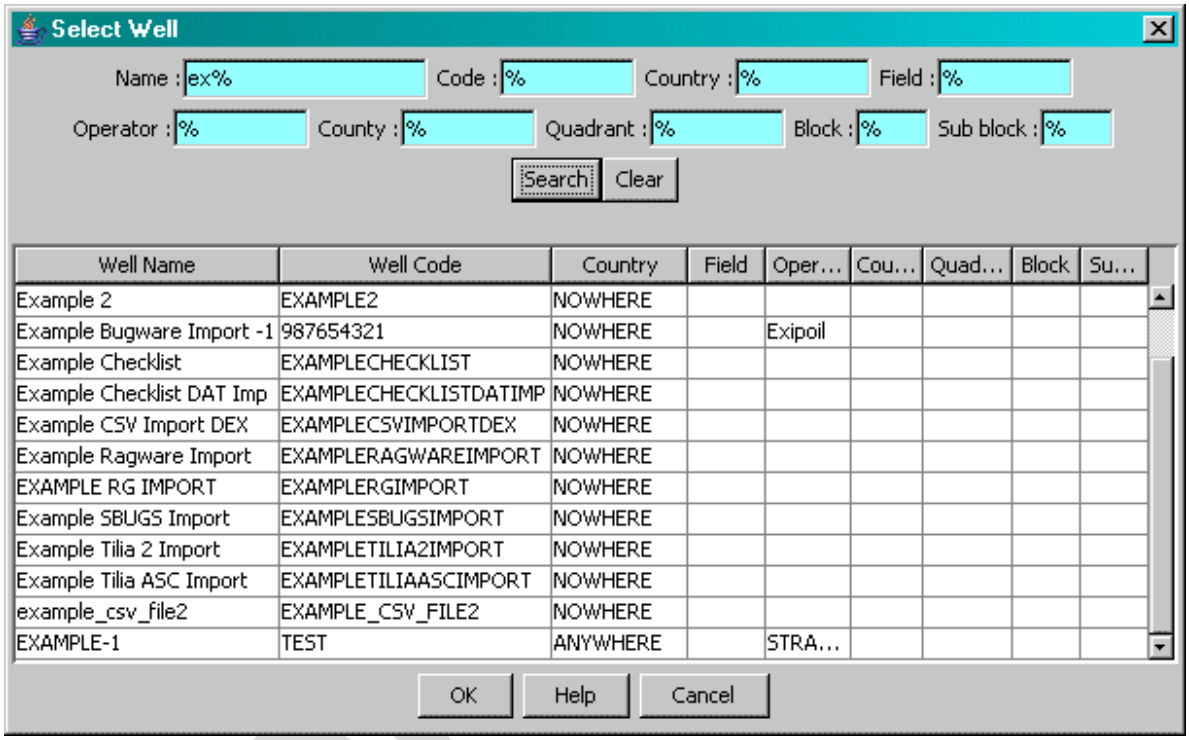
IGD (Lithostratigraphy, Chronostratigraphy, Sequences, Biozones)

Composite standards

How to export data to a DEX file (guided)

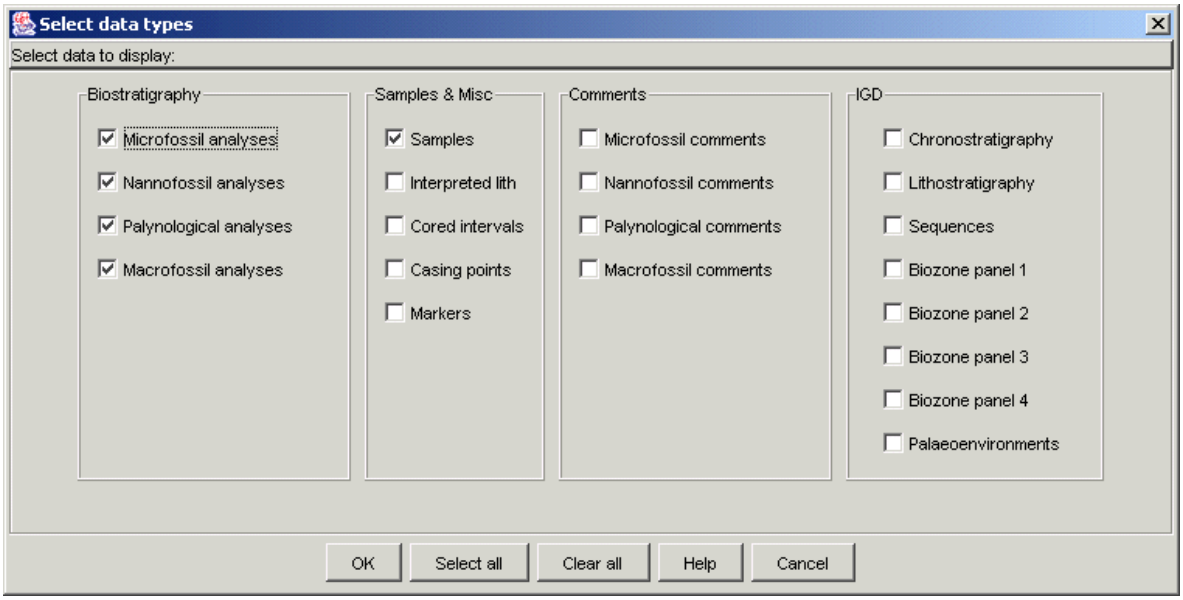
If you are exporting data in DEX format Organiser can guide you through the process. To do this select the **Export data** icon from the tool bar at the top of the Main window. (You can of course export data in DEX format without being guided by first opening the dataset from the **File** menu then loading the data to the workspace from the **View** menu and finally saving the file as a DEX file from the **File** menu.)

Select the **Export button** from the tool bar at the top of the Main window. The **Select Well dialog** will appear.

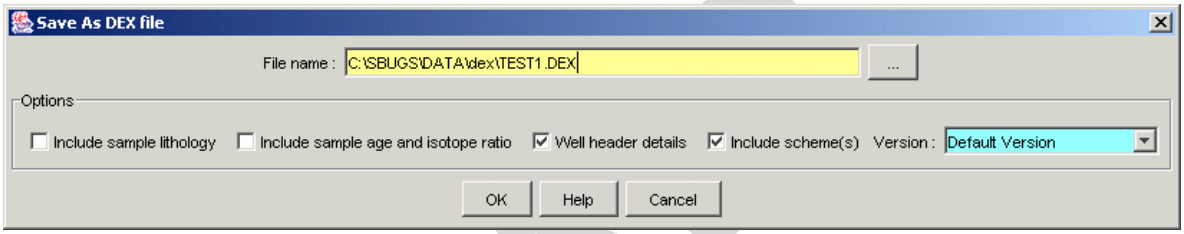


Select the well or wells from the database and press **OK**.

Then select the datatypes you want to export from the **Select data types dialog**.



The depth ranges of the selected data types will be displayed in the workspace and simultaneously a **Save as DEX file dialog** appears.



Provide a suitable file name and press **OK**.

Export data (other formats)

If you need to export a specific data type you can do so while you have the appropriate dialog open.

Open a dataset in a file or in your database and select a particular data type. If there is a **Read** button on the dialog press it. This will enable you to navigate to the import file and select it. Datatypes that can currently be imported in this way are listed below. Specific instructions are provided in the HELP for each dialog.

Analyses - Press **Save as** and select or add a filename to save analyses as a **CSV file**.

Interpreted Lithology - Press **Save as** and select or add a filename to save the lithology intervals as a **Landmark .TXT file**.

Comments - Press **Save as** and select or add a filename to save comments as a **CSV file**.

IGD (Lithostratigraphy, Chronostratigraphy, Sequences and Biozones) **-** Press **Save as** and select or add a filename to save Lithostratigraphic intervals as a **CSV file** (all columns), **OpenWorks style CSV file** or **Tab delimited TXT file.**

Palaeoenvironments - Press **Save as** and select or add a filename to save palaeoenvironmental intervals as a **CSV file (all columns)** or **Tab delimited TXT file** (all columns)**.**

Events - Press **Save as** and select or add a filename to save events as a **CSV file**.

Event dictionary - Press **Save as** and select or add a filename to save an event dictionary as a **DEX file**.

LOC's - Press **Save as** and select or add a filename to save LOC's as a **DEX file**.

Lithology index file - Press **Write file** and select or add a filename to save a lithology index as a **CSV file**.

Composite Standard - Press **Save as** and select or add a filename to save a composite standard as a **DEX file**.

How to view data in the database

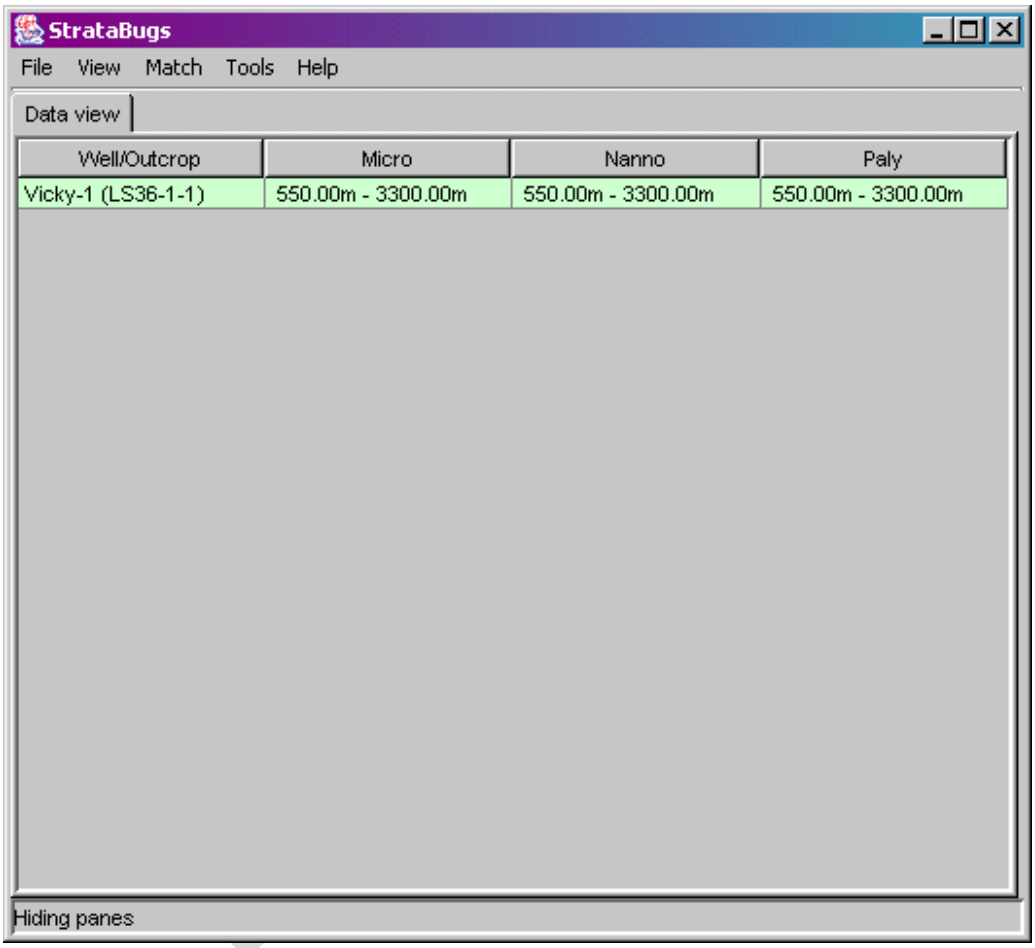
First select a well (or wells) using the **Well button** (well icon) in the tool bar at the top of the Main Window. Then select the data type(s) you want to view using the **View data button** (open book icon). The depth range of all available data will be shown for each well in the Main Window. Double click on each data range to see details of data in your database.

Dialogs

This section of the help provides a functional description of each of the dialogs used in the **Organiser application**. To find out how to use Organiser to accomplish a specific task refer to the **How to...** section.

Main Organiser window

The main Organiser application window is a tabbed **Dataview pane** from which all functions of the application are accessible. By default, when the application is first started the **Dataview pane** will be blank.



You must populate the workspace with data from data files or your database or both. To do this select **File**, then **View** and finally **Match**. These terms are explained below. The status of individual data items displayed in the **Data view pane** is displayed according to a simple colour scheme. This shows data in your data base (white), data which are new and not in saved your database (green), data which conflict in some way with data already in your database or is internally inconsistent (red), data with mixed status some of which need saving to your database (yellow) and data for which the status is for some reason unknown (grey) or which is not loaded into the workspace. Using this system it is easy to spot new information, omissions and conflicts when dealing with large datasets.

There are five drop-down menus on the menu bar which enable you to select, display and organise your data:

File enables you to open data files, view and modify them in your workspace and save data to your database or to XML data files. You can also view and edit your database and perform other tasks like adding new wells.

View enables you to display different types of data on screen and to organise the way they are displayed.

Match enables you to match the data in a data file with data in your database and if necessary to translate individual data items.

Tools enables you to access a number of useful applications for managing your data.

Config enables you to set up StrataBugs Names for users and analysts and user permissions.

Help enables access to on-screen help and to select the **Status colours dialog** . Help buttons on individual dialogs will also provide contextual help.

File enables you to select data from data files or your database, to save data to your database or to a file, and to create new wells in your StrataBugs database.

There are four options:

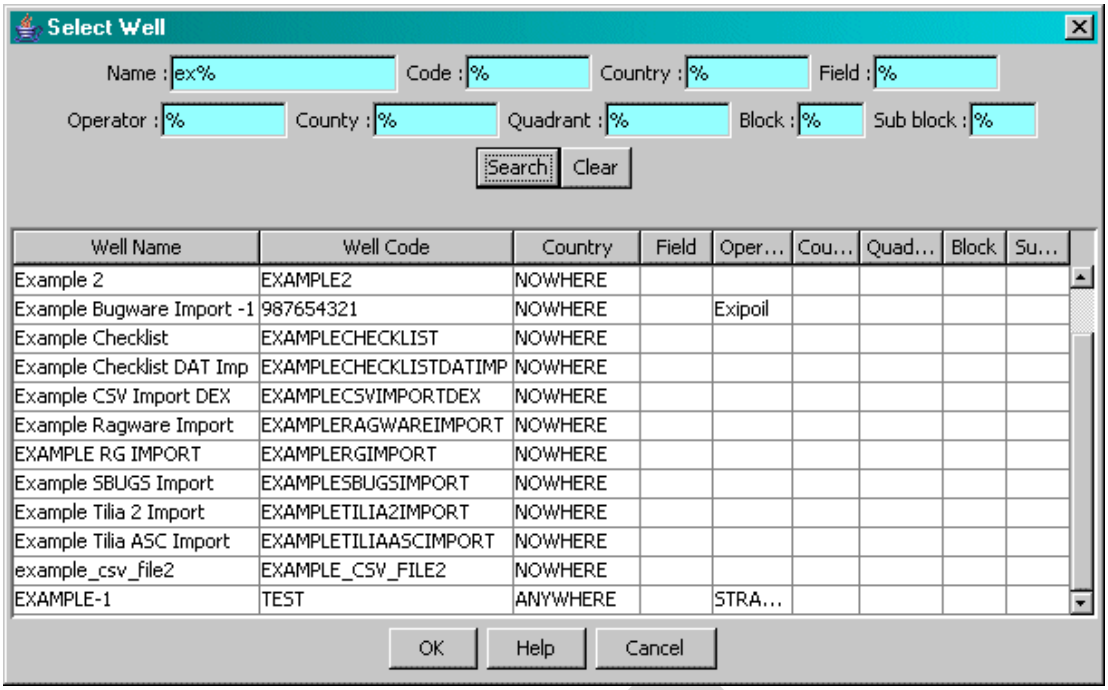
New There is currently only one sub-menu item:

Select **Well** to add a new well to StrataBugs. The **Well header dialog** appears.

Open enables you to open a variety of different formats of data file or to select data for one or more wells in your database.

To view the contents of a data file, select the file type from the **Open...** submenu and navigate to the folder containing your data file. Highlight the filename and press **Open**. If the file contains well/outcrop data will be displayed in the Organiser workspace and the depth range of each data type in each well will be displayed in rows and columns in the **Data view pane**. If the file contains dictionary data the data will be displayed in a separate dialog. Detailed procedures for importing the main dsata types are give in the **Composites Standards dialog** displays a list of the existing composite sections in your database. **Composites Standards dialog** displays a list of the existing composite sections in your database. How to... section of Organiser Help.

To view the data for wells in your database select **StrataBugs well/outcrop** from the **Open...** submenu. The **Select well dialog** appears.



Enter a text string in one or more of the search fields or leave them blank. Press the **Search** button to search for matching wells. Highlight one or more well names on the list and press **OK**. Data for the selected wells will be displayed in the Organiser workspace and the depth range of each data type in each well will be displayed in rows and columns in the **Data view pane**.

To view a data file select the **Open... | File** submenu. Then select the correct file type for the dataset. There are a large number of different file types supported.

> ***Note:*** *this area of Organiser is under development and additional items are continually being added. Most of these items will have been developed to deal with specific data management queries from clients and will be of limited use. Consequently, only those items of wider interest are described in full here. For further information please contact* **StrataData***.*

When you have selected the file type, a standard file selection box will open. Navigate to the file you want to open, select it and press **Open**.

> ***Note:*** *the first time you do this you will have to navigate to the correct folder where the file resides; thereafter the same folder will open automatically.*

Data from the selected file will be displayed either in the Organiser workspace, in which case the depth range of each data type in each well will be displayed in rows and columns in the **Data view pane,** or in a special data dialog.

> ***Note:*** *The status of individual data items is displayed according to a simple colour scheme. To access a key to this colour scheme press* ***Help | Status colours...*** *at any time.*

Note: *To see the details of each data type for each well, double click to select the appropriate data item. A dialog displaying the data will appear.*

Note: *By default, when you open a datafile only the columns for which there are data available in the selected dataset will be displayed. When you select wells from the database the default will be the last selected.*

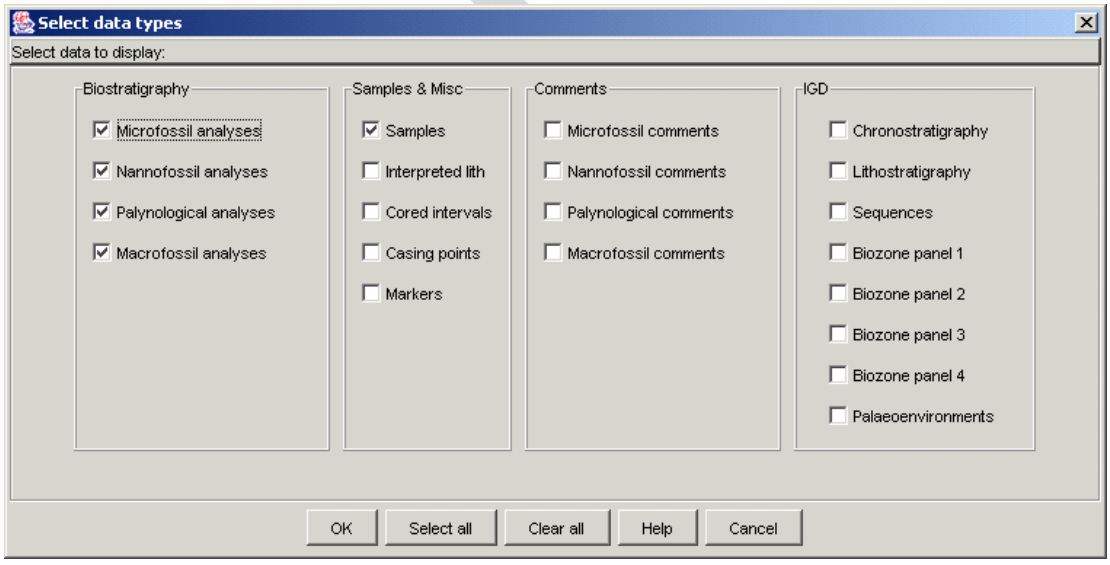
Save enables you to save data to the database or in a number of different file formats as follows:

in Database. Select this option to save the data in your workspace to your database. You will warned if there are conflicting data which need to be corrected before you can save the dataset.

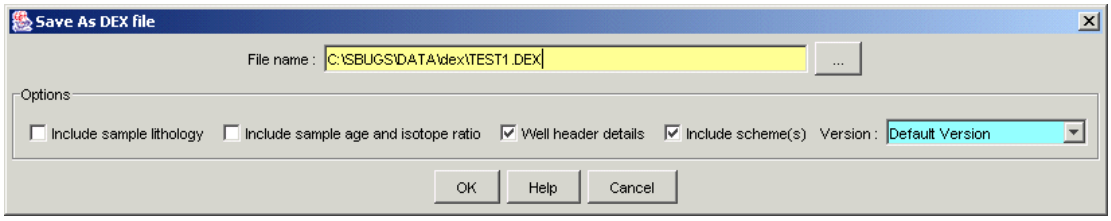
as XML...(all data types). Select this option to save the data in your workspace as an XML file.

as Text file... (Chronostratigraphy, Biozones and Comments only). Select this option to save the data in your workspace as a Text file.

as DEX file...(all data types). Select this option to save the data in your workspace as a DEX file. You will have the opportunity to de-select data items which you do not wish to export using the **Select data types dialog**.



Press **OK** and the **Save as DEX file dialog** appears.



This enables you to include or exclude sample lithology, sample ages and isotope ratios, well header details and IGD schemes. You can also select the IGD Version to save (if there is more than one) from the drop down list in the Version field.

Exit closes the Organiser application.

View enables you to display different types of data in your workspace and to organise the way they are arranged.

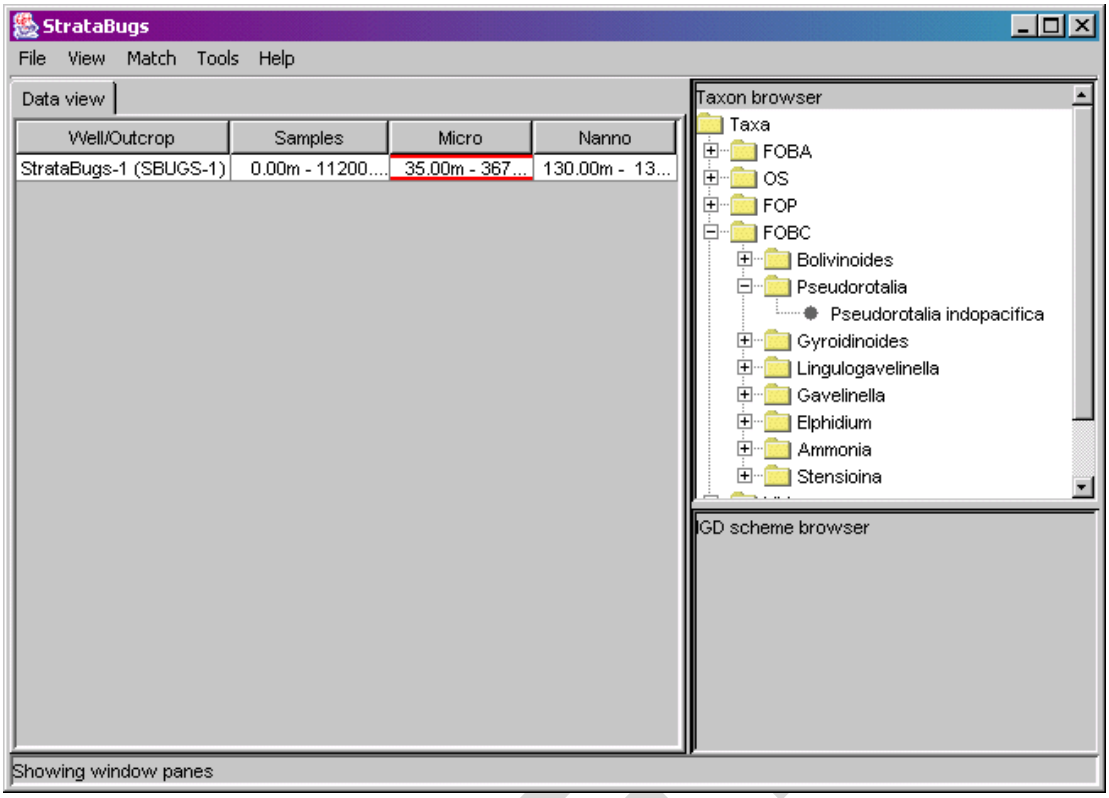
There are six items on the menu:

Selected data... enables you to view the details of any particular data type for a well. You must first highlight the appropriate cell in the table of the **Data view pane**. Alternatively, double-click the cell to make a data dialog appear. This dialog will have a different layout for each main data type:

Wells | Samples | IGD | Lithology | Comments

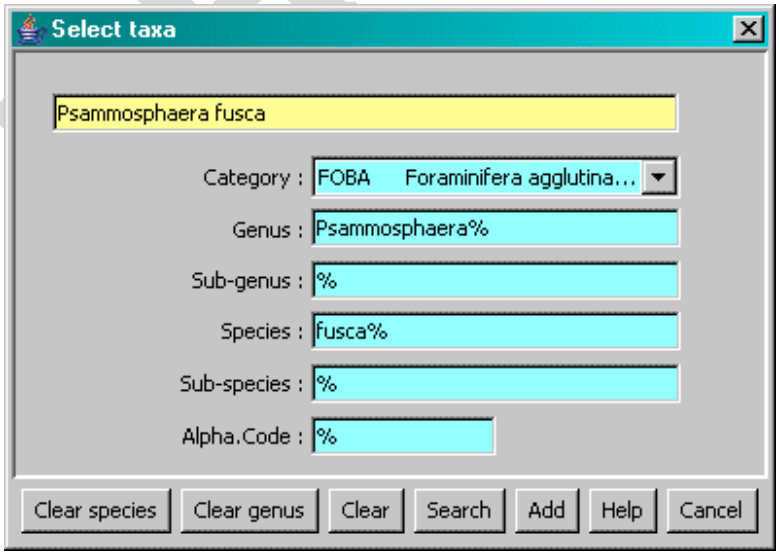
Data types... opens the **Select data types dialog** which enables you to choose which data types from your selected dataset are displayed in the table of the main application window. Once displayed the order of the default ordering of the data types can be changed by grabbing the appropriate table column header and sliding it into the preferred position.

Browser panes opens/closes other display panes within the main Organiser window. (Currently only the Taxon browser is enabled). Browser panes enable you to view data in other ways.

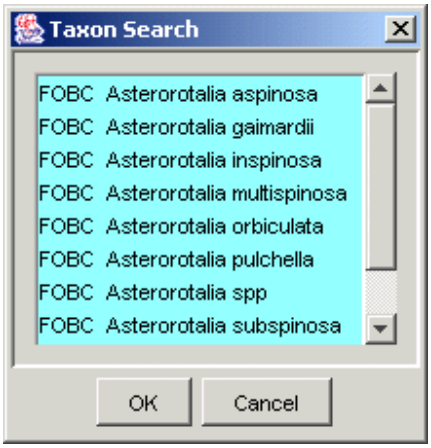


Select **View | Browser panes** and the **Taxon browser** will appear. This enables you to view all the taxa from the selected dataset arranged hierachically.

There are several ways of populating the Taxon browser pane. If you open a data file containing taxon names these will be automatically posted in the browser. To select individual taxa you should choose **Tools | Taxon dictionary | Select taxon...** and then search for the taxon using the **Select taxa dialog**.



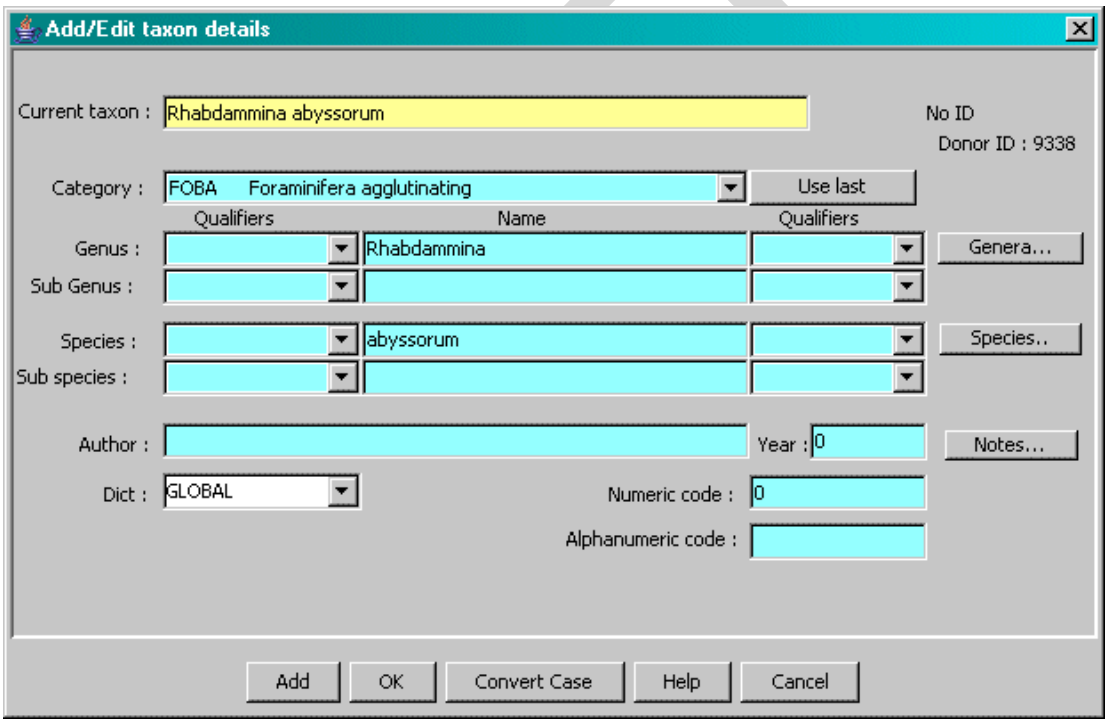
Select a name from the list in the **Taxon search dialog** and press **OK**.



To display all of the taxa in your database select **Tools | Taxon dictionary | Load all taxa**.

> ***Note:*** *This may take several minutes if you have a lot of taxa in your database).*

You can drill down to individual species names and view or edit them in the **Add/Edit Taxon details dialog**.



Units enables you to display all the data in metres or feet, or in the drilled units for each well.

Exclude selected wells enables you to exclude from your workspace individual highlighted wells in multiwell datasets.

Load all data for selected wells will load all the data for selected wells to your workspace so that it immediately available for viewing. Alternatively, each data display dialog will have the option to load data for an individual well.

Move default to version enables you to import data displayed in the workspace directly to a version other than the default version of the host well. When you select this **Move default to version** option the **Select version dialog** will appear.

Match enables you to match the data in a file with data in your database and if necessary to translate individual data items.

You can match **Taxa**, **IGD, Wells, Abundances** and **Palaeoenvironments** separately. Before you can match a well you must first match any taxa or IGD.

Taxa. Select the **Taxa...** item on the **Match** menu in order to match taxa in a file with those already in your database, to check for spelling or formating errors and make decisions about if and how you want to import the taxonomic names. The **Match taxa dialog** appears.

IGD. Select the **IGD...** item on the **Match** menu to match IGD units and schemes in a file with those already in the database. The **Match IGD dialog** appears.

Wells. Select the **Wells...** item on the **Match** menu to match wells in a file with those already in the database. The **Match Wells** dialog appears.

Abundances. Select the **Abundances...** item on the **Match** menu to manage abundance class assignments. The **Match Abundance Schemes** dialog appears. From here you can add the scheme associated with data in the data file, select a matching scheme from the database, and qualify those occurrences which should be Reworked, Caved or Questionable.

Palaeoenvironments. Select the **Palaeoenvironments...** item on the **Match** menu to match palaeoenvironmental schemes in a file with those already in the database. The **Match Palaeoenvironments** dialog appears.

Analysts. Select the **Analysts...** item on the **Match** menu to match the analysts in a file with those already in the database. The **Match analysts** dialog appears.

Tools are small utilities that implement a limited set of functions and help you perform specific data management tasks. The principal items on the Tools menu are described below but new items will be added as required:

Lithology matching enables you to match the a lithology scheme in a data file to the one in your database. You must do this before you can import lithology data for a well. You can also create new schemes from scratch and save them as data files. Select **Lithology matching...** from the **Tools** menu and the **Lithology matching dialog** appears.

Composite Standards... enables you to manage Composite standards. You can add new ones, edit exiting ones or import composites from DEX files.

Select **Composite standards...** from the **Tools** menu and the **Composite Standards dialog** appears.

Event Dictionary... enables you to manage Event dictionary. Select the **Event dictionary...** item from the **Tools** menu and the **Event Dictionary dialog** appears.

IGD Schemes enables you to add, edit, delete and view the usage of your IGD Schemes. Select **Chronostratigraphy, Lithostratigraphy, Biozones** or **Sequence** from a sub-menu. (For Biozones there is a further selection of Microfossil, Nannofossil, Palynomorph or Macrofossil schemes). The appropriate **IGD Schemes dialog** will appear.

Chart Tools. There are currently two tools available for managing Charts:

> **Chart Manager...** enables you to view charts and their constituent panels and to delete them if you wish. You may wish to do this if you are removing a large number of panels from an existing chart or if for some reason a particular panel corrupts your chart. You can check which panels may be causing problems from the information dialog which displays the panel reference when the chart is loading. Select the **Chart Manager...** item from the **Tools** menu and the **Chart Manager dialog** appears.
>
> **Edit Log Path References** enables you to reassign the path for log file references used in Charts.

Abundance Schemes... enables you to add an abundance scheme, or to edit or delete an existing scheme. Select the **Abundance schemes...** item from the **Tools** menu and the **Abundance Schemes dialog** appears.

Palaeoenvironment Schemes... enables you to add a palaeoenvironment scheme or to edit or delete an existing scheme. Select the **Palaeoenvironment Schemes** item from the **Tools** menu and the **Palaeoenvironment Schemes dialog** appears.

Taxon dictionary enables you to add and edit taxon names in your workspace. First select **Browser panes** item from the **View** menu and then select the **Taxon Dictionary** item from the **Tools** menu. This will provide a submenu from which you can choose to load all the taxa in the database or a selection of taxa only. The selected taxa will appear in the **Taxon Browser pane**.

Note: loading all the taxa may take several minutes!

Analyses enables you to manage analyst assignments.

Fix Data [under construction]

Create Database objects [under construction]

Config currently has only one option:

> **Names...** enables you to manage the user names, passwords, privileges and permissions of users (if you have the privilege to do so). Select the **Names...** item from the **Config** menu. A list of existing StrataBugs Names will appear.

Help provides three options:

This window provides a link to the on screen help contents. In addition, other help buttons on individual dialogs will give context sensitive help.

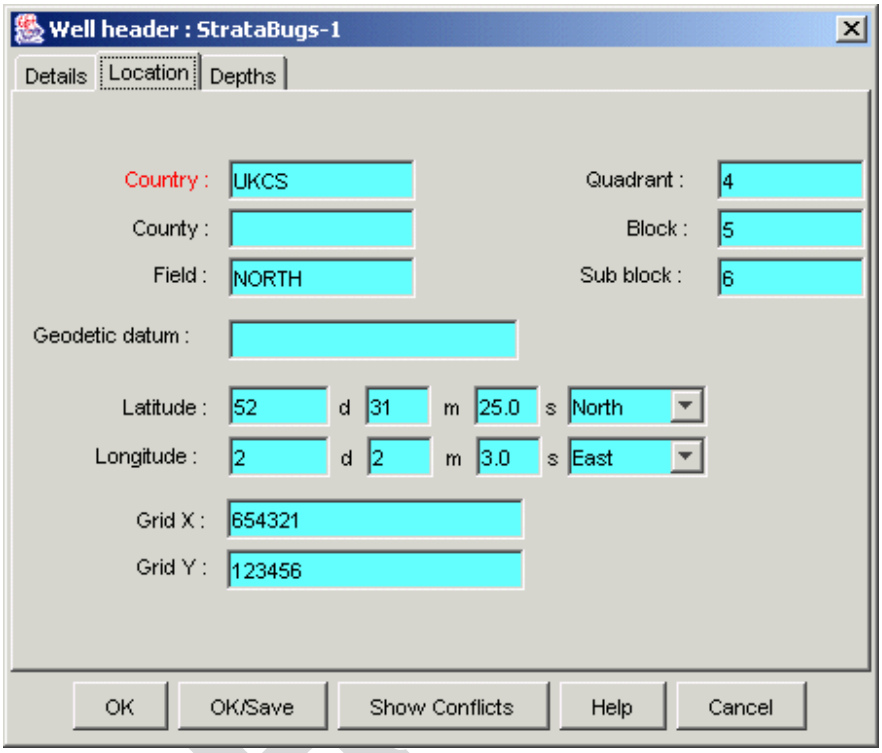
About provides information about the release date of the current version of the StrataBugs Java application.

Status colours... provides a floating key of the data status colours.

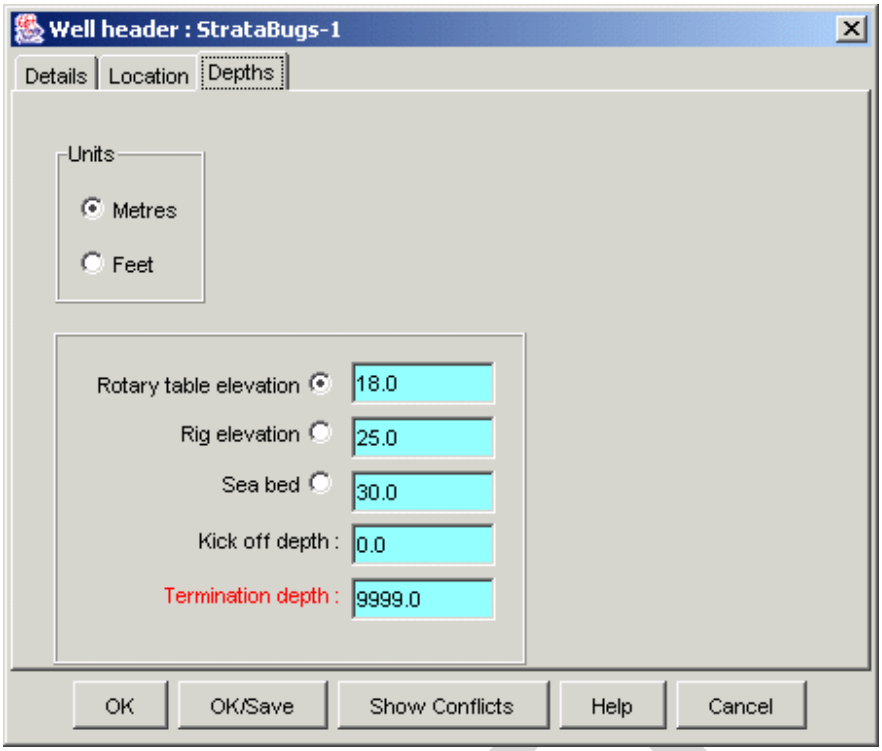
Well header dialog

There are three tabs on the **Well header dialog**. Select them one at a time and complete the necessary fields.

On the **Details tab** fill in the Name and Code fields with the Well name and code (mandatory). You may also complete the other editable fields with Operator name, OCS Number, Spud date and Completion date. Select either Well or Outcrop as the Type of section you are entering. You can also add Comments or notes about the well.

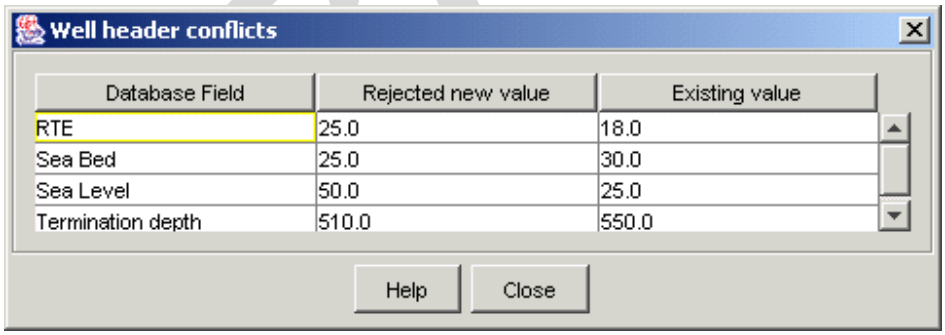


On the **Location tab** enter the Country (mandatory), and County, Field, Quadrant, Block and Sub-block if required. You may also enter Geodetic datum and coordinates as Lat/Long and/or as Grid X/Y values. These data will be used in future versions of StrataBugs when linked to a mapping application.



On the **Depths tab** select the appropriate depth Units option (meters or feet). You may also enter the Rotary table elevation, Rig elevation and Sea bed and (for side track wells) the Kick off depth. These data are not currently used. It is mandatory to enter a Termination depth. If you don't know this value enter a large number which is likely to exceed the deepest sample (eg 9999.0m).

Conflicts between data in a datafile and the database will cause the well name in the Data view pane to be highlighted in red. To resolve these conflicts press the **Show conflicts** button to display the **Well header conflicts dialog**.



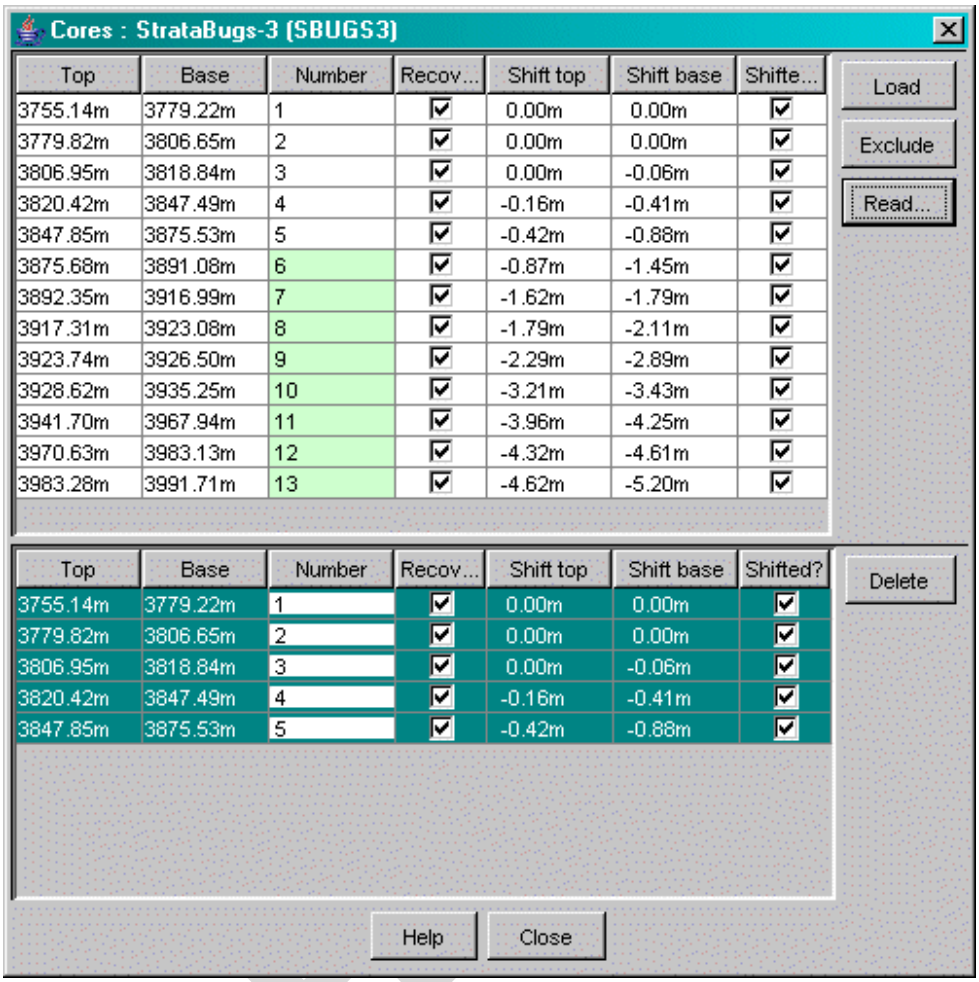
The fields where there are conflicts between new and existing values will be displayed. Press the **Close** button to return to the appropriate Tab on the Well header dialog and make the necessary changes to the appropriate fields.

Press the **OK** button to save the matching well name but not add it to the database yet. You may wish to do this if you are re-exporting the data without loading it to your database.

Press the **OK/Save** button to save the matching well name to the database.

Press the **Cancel** button to exit the dialog without saving the matching well name.

Cores dialog



To access the **Cores dialog** highlight the dataset for a well in the **Data view panel** and select **View | Selected data...** Alternatively, you can double click on the dataset to select it.

For each well the Cores dialog displays the top and base depth of each core, its number, and recovery status. If a core shift has been calculated this can be displayed and whether or not the core shift is applied. Data from files will be displayed in the upper pane. If there are data in the database for the same well this will be displayed in a lower pane, otherwise the pane will not appear.

> ***Note:*** You must **Match Wells** first for the database data to appear.

To core data for the selected well to the workspace from your database press the **Load** button.

To exclude an item from the list highlight it on the list and press the **Exclude** button.

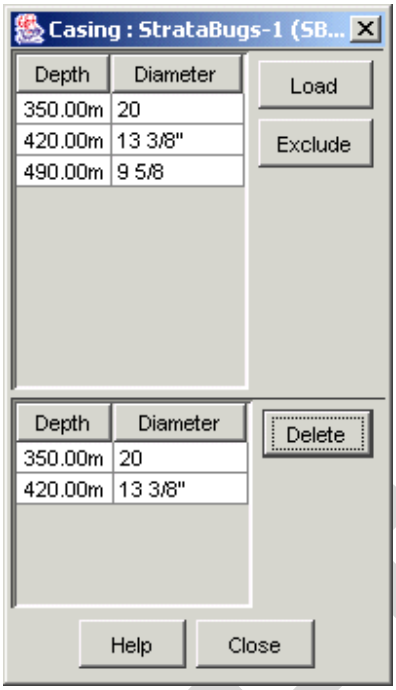
To delete core data from the database, highlight an item in the lower (database) pane and press the **Delete** button. You will be asked to confirm that you want to delete it.

The **Read** button enables you to view the contents of an Excel spreadsheet file (.XLS) containing cored interval and core shift data. The format must be in the same format as this:

CORE #	CDEPTH	CDEPTH_1	LDEPTH	CDEN_1	CKHL_1	CKHLOB_1	CKVL_1	CPOR_1	CPOROB_1	CSOR_1	CSW_1	CPFS_1	shift
	feet	METRES	METRES	G/C3	MD	MD	MD	V/V	V/V	V/V	V/V	V/V	M
4	12589.8469	3837.43	3837.12		0.15	0.032555	-	0.083	0.077329	0.044	0.746	0.063	-0.31
4	12590.8475	3837.74	3837.43		0.23	0.057279	0.20	0.106	0.100308	0.174	0.445	0.128	-0.31
4	12592.0188	3838.09	3837.79		0.22	0.054029	-	0.091	0.085713	0.125	0.664	0.075	-0.31
4	12592.8456	3838.35	3838.04		0.27	0.070671	0.19	0.109	0.103227	0.145	0.608	0.105	-0.31
4	12600.8474	3840.79	3840.50		0.35	0.093082	0.23	0.115	0.109065	0.092	0.484	0.129	-0.29
4	12601.8481	3841.09	3840.81		0.27	0.070671	-	0.103	0.097389	0.092	0.613	0.098	-0.29
4	12602.8487	3841.40	3841.11		0.37	0.106481	0.35	0.123	0.116849	0.168	0.450	0.158	-0.28
4	12603.8461	3841.70	3841.42		0.57	0.185651	-	0.143	0.136309	0.207	0.556	0.108	-0.28
4	12604.8467	3842.00	3841.73		0.06	0.003466	0.04	0.033	0.029279	0.000	0.830	0.020	-0.28
4	12605.8474	3842.31	3842.03		0.04	0.005423	-	0.027	0.023441	0.000	0.758	0.052	-0.28
4	12606.848	3842.61	3842.34		0.04	0.005423	0.04	0.032	0.028306	0.000	0.728	0.033	-0.27
4	12607.8454	3842.92	3842.64		0.12	0.024171	-	0.085	0.079875	0.088	0.706	0.071	-0.28
4	12608.846	3843.22	3842.93		0.16	0.035471	0.13	0.105	0.099335	0.015	0.769	0.099	-0.29
4	12609.8467	3843.53	3843.23		0.18	0.041463	-	0.088	0.082794	0.000	0.746	0.063	-0.30
4	12610.8473	3843.83	3843.53		0.20	0.047655	0.23	0.110	0.104200	0.125	0.663	0.106	-0.31
4	12611.848	3844.14	3843.82		0.28	0.074110	-	0.121	0.114903	0.097	0.487	0.120	-0.32
4	12612.8453	3844.44	3844.12		0.19	0.044535	0.19	0.120	0.113930	0.134	0.596	0.129	-0.32

Press the **Close** button when you have finished.

Casing dialog



To access the **Casing dialog** highlight the dataset for a well in the **Data view panel** and select **View | Selected data...**. Alternatively, you can double click on the dataset to select it.

The Casing dialog displays all the casing diametres and casing shoe depths for the selected well. Data from files will be displayed in the upper pane. If there are data in the database for the same well this will be displayed in a lower pane, otherwise the pane will not appear.

> ***Note:*** You must **Match Wells** first for the database data to appear.

To casing data for the selected well to the workspace from your database press the **Load** button.

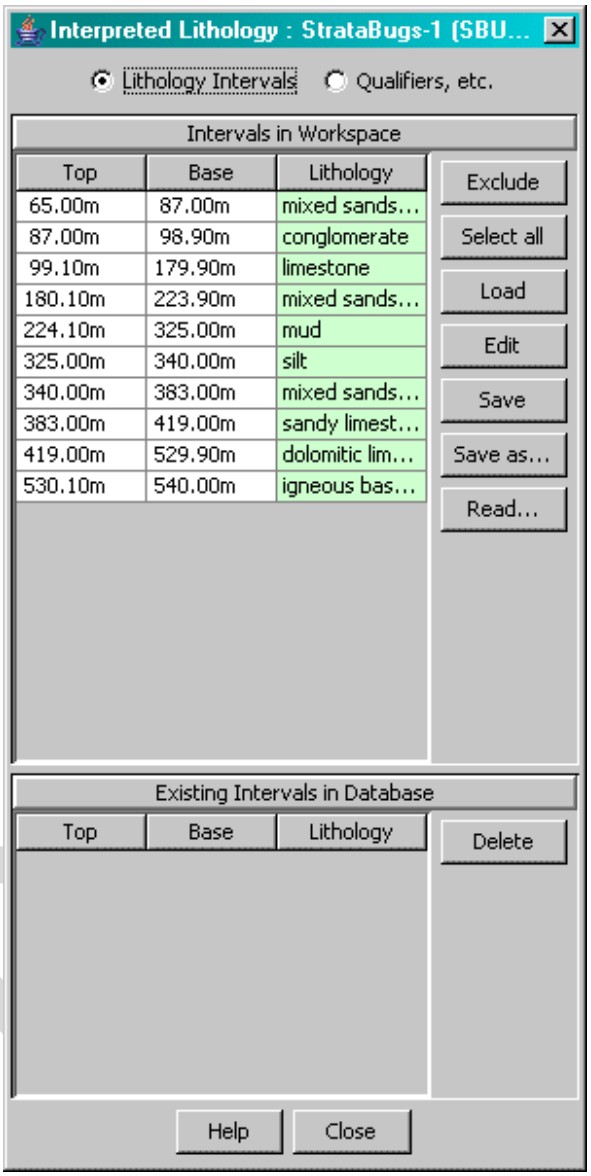
To exclude an item from the list highlight it on the list and press the **Exclude** button.

To delete casing data from the database, highlight an item in the lower (database) pane and press the **Delete** button. You will be asked to confirm that you want to delete it.

Press the **Close** button when you have finished.

Lithology dialog

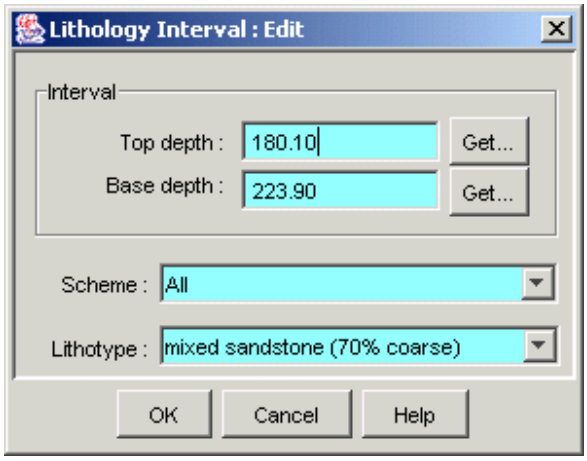
To access the **Lithology dialog** highlight the dataset for a well in the Data view panel and select **View | Selected data**. Alternatively, you can double click on the dataset to select it. By default all samples in the selected well will be displayed. Sample data from a data file are shown in the upper workspace pane. If there are data in the database for the same sample/discipline this will be displayed in a lower database pane, otherwise the pane will not appear.



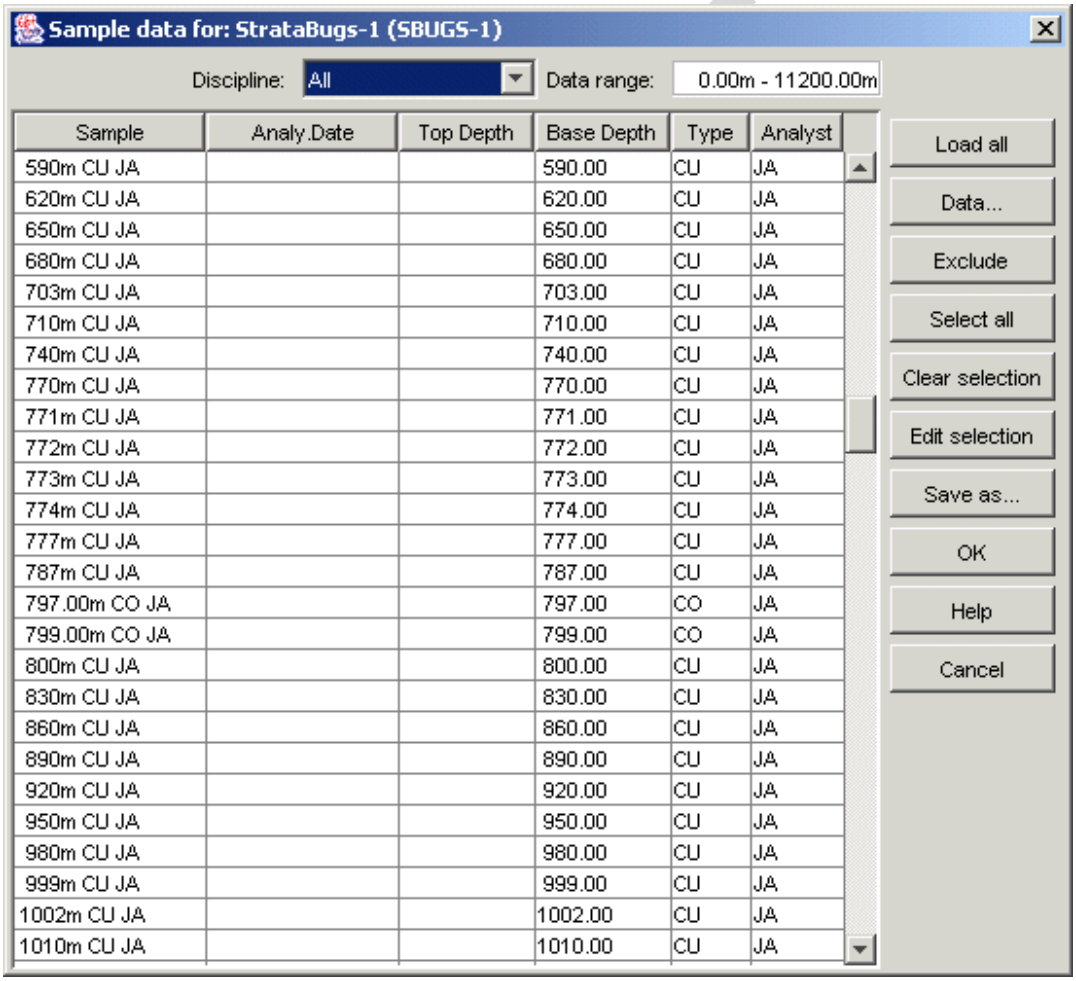
Select one of the option buttons for viewing **Lithology intervals** or **Qualifiers, etc.**

If you select the **Lithology intervals** option the data are arranged in columns displaying Top depth, Base depth and Lithology of the selected sample. By default the lithological intervals will be sorted in depth order. To sort them based on other columns in the table, select the appropriate table column header(Shift + select to reverse order).

Press **Edit** if you want to edit the details of individual data items. The **Lithology Interval dialog** will appear.



To edit the Top depth and Base depth of the interval press the appropriate **Get...** button and select a sample depth from the **Sample data dialog** which appears.



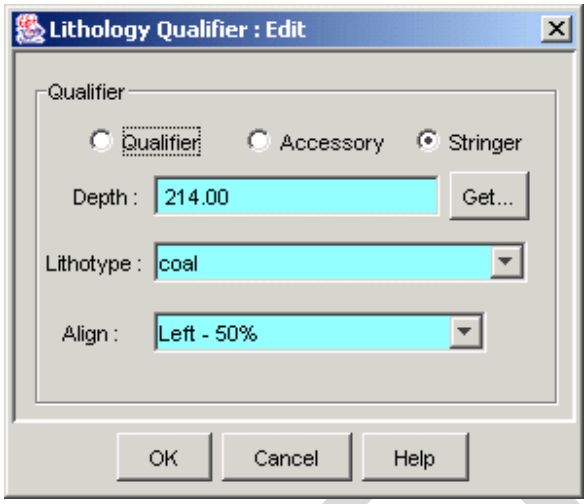
Sample	Analy.Date	Top Depth	Base Depth	Type	Analyst
590m CU JA			590.00	CU	JA
620m CU JA			620.00	CU	JA
650m CU JA			650.00	CU	JA
680m CU JA			680.00	CU	JA
703m CU JA			703.00	CU	JA
710m CU JA			710.00	CU	JA
740m CU JA			740.00	CU	JA
770m CU JA			770.00	CU	JA
771m CU JA			771.00	CU	JA
772m CU JA			772.00	CU	JA
773m CU JA			773.00	CU	JA
774m CU JA			774.00	CU	JA
777m CU JA			777.00	CU	JA
787m CU JA			787.00	CU	JA
797.00m CO JA			797.00	CO	JA
799.00m CO JA			799.00	CO	JA
800m CU JA			800.00	CU	JA
830m CU JA			830.00	CU	JA
860m CU JA			860.00	CU	JA
890m CU JA			890.00	CU	JA
920m CU JA			920.00	CU	JA
950m CU JA			950.00	CU	JA
980m CU JA			980.00	CU	JA
999m CU JA			999.00	CU	JA
1002m CU JA			1002.00	CU	JA
1010m CU JA			1010.00	CU	JA

To change the name of the Lithology scheme select one from the drop down menu attached to the **Scheme** field. To change the lithology type from the selected scheme select one from

the drop down menu attached to the **Lithotype** field. When you have finished press **OK** or **Cancel** to return to the Lithology dialog.

If you select the **Qualifiers,etc.** option the data are arranged in columns displaying Depth, Type (Qualifier, Accessory or Stringer) and its Label. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order).

Press **Edit** if you want to edit the details of individual data items. The **Lithology Qualifier dialog** will appear.



Select one of the three option buttons for **Qualifier, Accessory** or **Stringer**. To edit the depth of the qualifier press the **Get...** button and select a sample depth from the **Sample data dialog** which appears. To change the Lithotype select one from the drop down menu attached to the **Lithotype** field. To change the position of a qualifier or accessory edit the value in the **Position** field (this is % from the left hand margin of the display panel), or the alignment of a stringer from the drop down list attached to the **Align** field. When you have finished press **OK** or **Cancel** to return to the Lithology dialog.

To remove a Lithology unit or Qualifier from the workspace pane first highlight it and then press the **Exclude** button.

Press the **Select all** button to select all the items on the list.

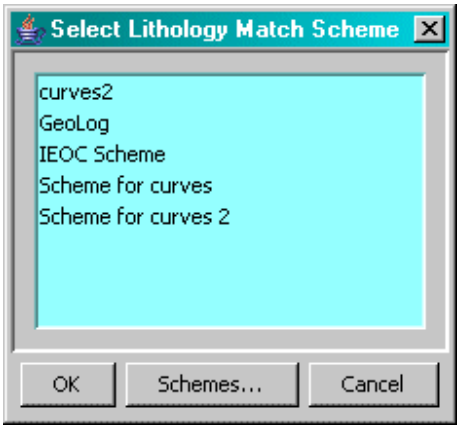
Press the **Load** button to display data from your database in your workspace.

Press **Save** to commit the data in your workspace to the database.

Press **Save as...** to save the data to a datafile (currently only Landmark format text file).

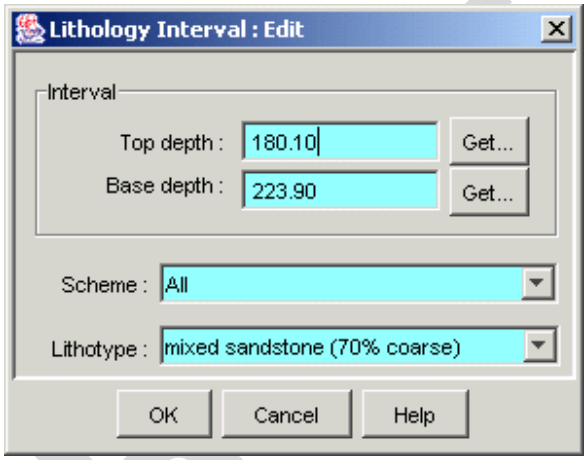
To import lithology data from a CSV file you must have opened the host well and selected the Lithology data type in the **Data view** pane. You must also have an appropriate **Lithology match scheme** available. Press the **Read...** button and a file selector dialog appears. Select the correct datafile, press **Open** and the data will be loaded into your workspace using the selected lithology match scheme to translate the lithotype terms.

If there is more than one available lithology match scheme the **Select lithology match scheme dialog** will appear.



Select the appropriate scheme and press **OK**.

If lithologies types cannot be imported because you have not provided a translation in the selected lithology match scheme you will be shown a list of intervals in the **Lithology types not imported dialog**. To edit any of the intervals press the **Edit** button (or double click on the interval on the list). The **Lithology interval dialog** appears.

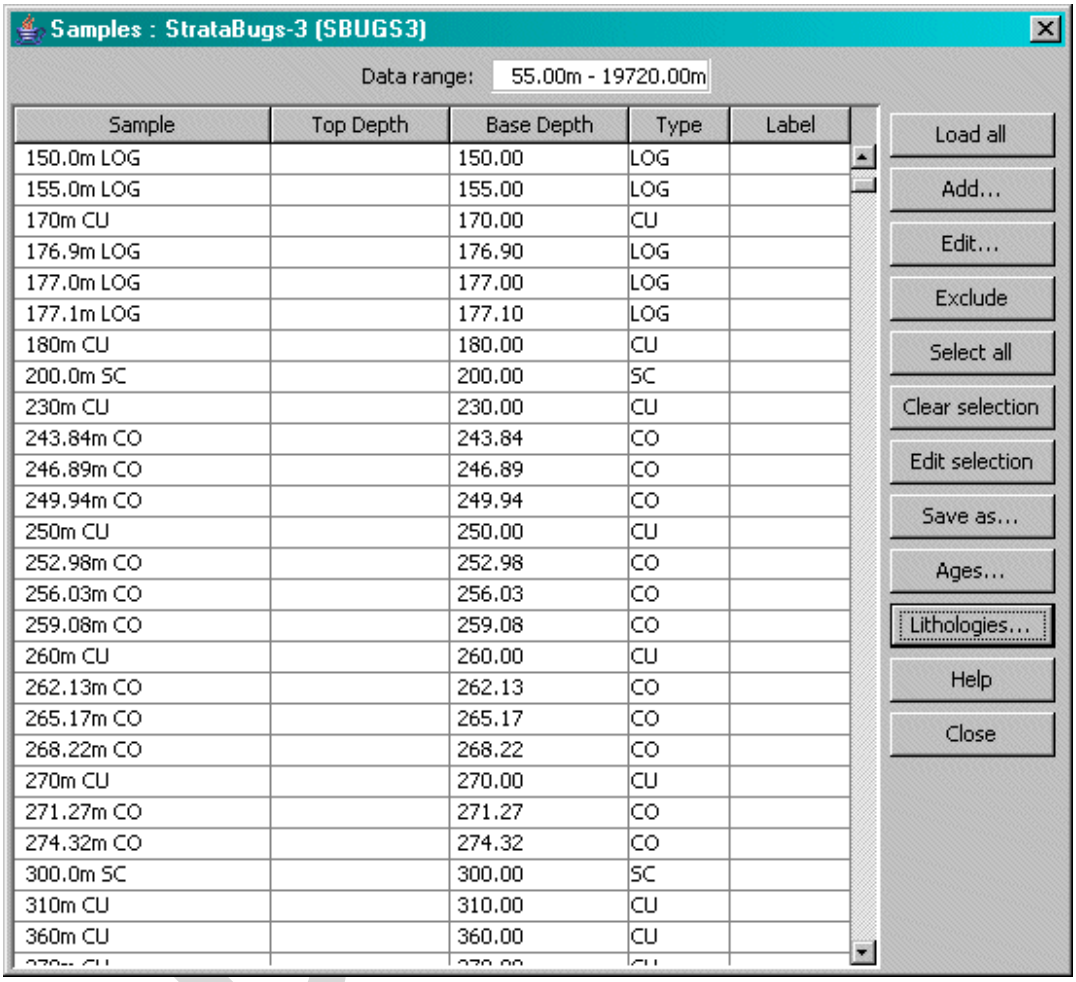


If you want to delete items from the database first highlight them in the database pane and then press the **Delete** button.

Press the **Close** button when you have finished.

Samples dialog

To access this dialog, highlight the dataset for a well in the Data view panel and select **View | Selected data**. Alternatively, you can double click on the dataset in the Samples column to open it. If you select a dataset from your database the table the samples cell on the Data view pane will be grey and the **Samples dialog** will be blank.



Sample	Top Depth	Base Depth	Type	Label
150.0m LOG		150.00	LOG	
155.0m LOG		155.00	LOG	
170m CU		170.00	CU	
176.9m LOG		176.90	LOG	
177.0m LOG		177.00	LOG	
177.1m LOG		177.10	LOG	
180m CU		180.00	CU	
200.0m SC		200.00	SC	
230m CU		230.00	CU	
243.84m CO		243.84	CO	
246.89m CO		246.89	CO	
249.94m CO		249.94	CO	
250m CU		250.00	CU	
252.98m CO		252.98	CO	
256.03m CO		256.03	CO	
259.08m CO		259.08	CO	
260m CU		260.00	CU	
262.13m CO		262.13	CO	
265.17m CO		265.17	CO	
268.22m CO		268.22	CO	
270m CU		270.00	CU	
271.27m CO		271.27	CO	
274.32m CO		274.32	CO	
300.0m SC		300.00	SC	
310m CU		310.00	CU	
360m CU		360.00	CU	

By default details for all the samples from a data file will be displayed in a table. To display the samples in a well press the **Load all** button.

The first table column displays the depth of each **Sample** (together with depth units and sample type).

> ***Note:*** The sample depths are rounded according to a StrataBugs convention for sample types (i.e. nearest whole number for cuttings, one decimal place for sidewall cores and two decimal places for cores).

The second and third columns show the actual values of the sample **Top Depth** and **Base Depth** as recorded. Samples with a single depth value will display in the Base Depth column [or the Top Depth column depending on the default set].

The next column displays the sample **Type** and **Label** (if there is one).

You can edit the attributes of an individual sample by highlighting it on the list and then pressing the **Edit...** button. The **Edit sample dialog** appears. Any editorial changes you make will aply only to the selected sample.

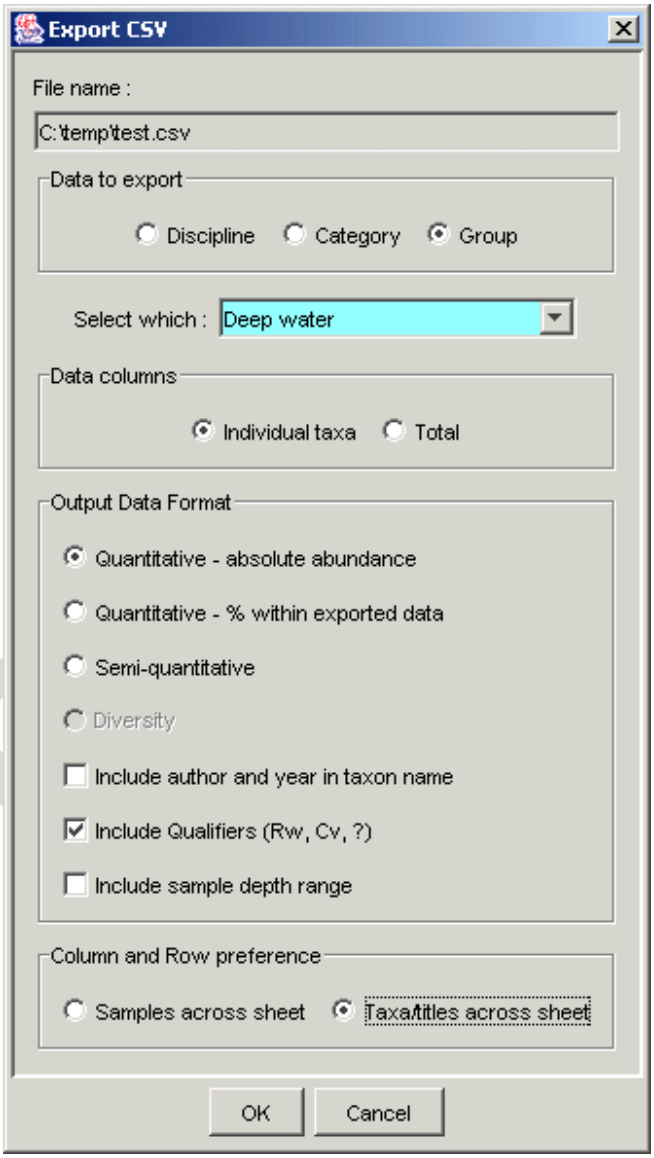
To exclude samples from the list highlight them and press the **Exclude** button.

To select all of the samples press the **Select all** button.

To clear a previous selection press the **Clear selection** button.

To edit a number of samples at once, highlight the samples on the list and then press the **Edit Selection** button. The **Edit sample dialog** appears. Any editorial changes you make will apply to all the samples selected.

Press the **Save as...** button to save all the data for samples which have not been explicitely excluded as a CSV file. Enter a suitable filename when prompted to do so. Press **OK**. The **Export CSV dialog** appears.



This will enable you to select the content and style of the data which you export.

First decide if you want to export the entire **Discipline**, a single **Category** or a single **Group** and select the appropriate option button.

If you select the Category or Group option you will be prompted to **Select which** category or Group from a drop list.

You must then select one of the options to export the data either for **Individual taxa** or as a (Group or Category) **Total**.

There are a number of Output data format options - select one from **Quantitative - absolute abundance, Quantitative - % of exported data, Semiquantitative** or **Diversity**. You can then choose whether to **Include author and year, Include qualifiers (Rw, Cv, ?)** and **Include sample depth range** by selecting the appropriate checkboxes.

Finally, you should choose whether you want to plot the **Samples across sheet** or **Taxa/titles across sheet**. This refers to the orientation of the data matrix on a spread sheet which can be generated from the CSV file. Your choice will be governed by your requirements or those of other software.

Press **OK** to save the data to a CSV file.

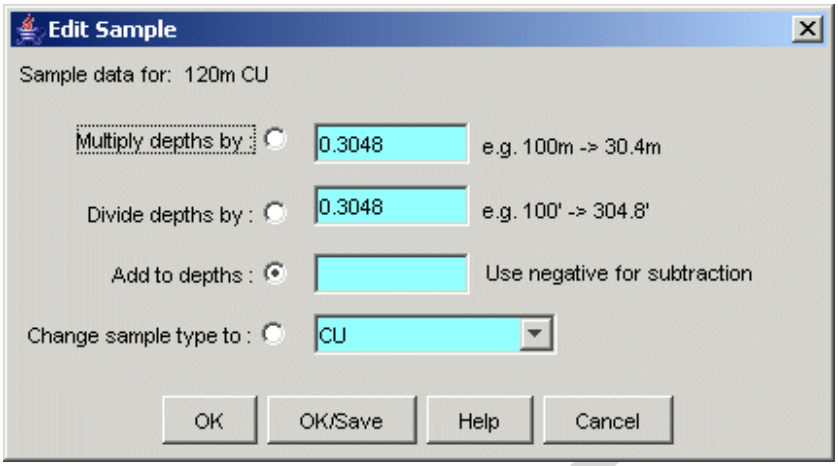
For wells in your database you can assign ages from an IGD scheme to the samples in a well. Press **Ages...**to open the **Sample Age dialog** .

To view sample lithologies or import them from a cuttings log file press the **Lithologies** button to open the **Sample Lithology dialog.**

When you have finished with the Samples dialog press the **Close** button when you have finished.

Edit sample dialog

The **Edit Sample dialog** enables you to edit the depth and type of a sample in a data file or in your database.



You can convert depths which have been incorrectly entered into your database. The default value of 0.3048 will correctly convert metres to feet using the **Multiply depths by** option. To convert feet into metres select the **Divide depths by** option. Of course, you can enter any other number as you wish for whatever purpose.

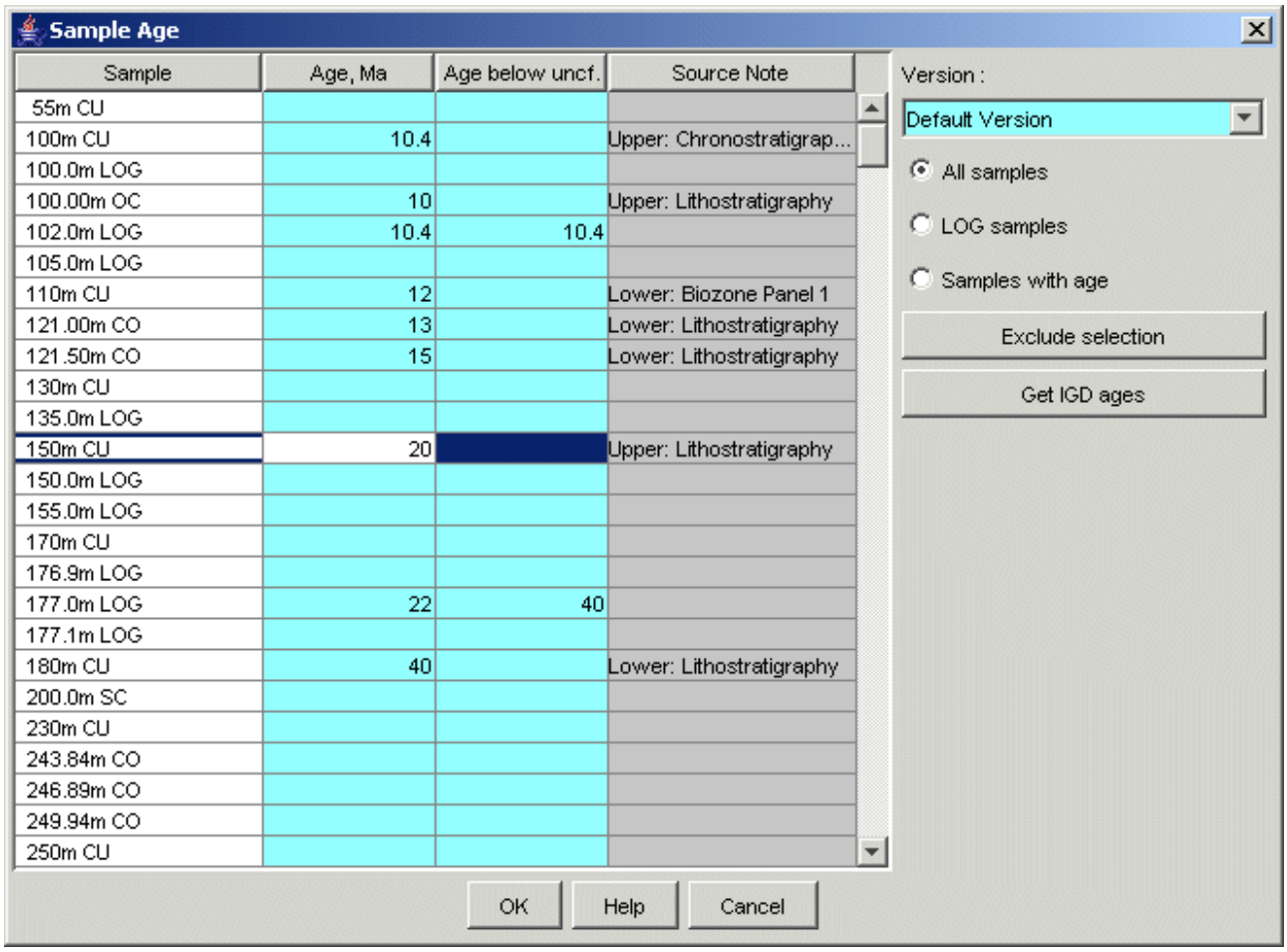
To correct depths from subsea to BRT, for instance you can use the **Add to depths** option to increase the value of the selected sample. To reduce the depth value enter a numeral preceded by a minus sign.

To change a sample type, select the **Change sample type to** option and select the correct sample type from the drop down list.

When you have finished editing the sample press OK, OK/Save or Cancel to return to the **Samples dialog**.

Sample Age dialog

The **Sample Age dialog** enables you to add or edit the ages assigned to specific samples. You would want to do this if you are planning to plot a chart on an age scale or draw a chronostratigraphic diagram. In addition, for wells in your database you can assign ages from an IGD scheme to the samples in a well. If you have identified IGD units in a well and these units have ages assigned to them in an IGD Scheme, the boundary ages from the Scheme can be automatically assigned to the samples on which the IGD interpretations have been made. The assignment is not made if the IGD boundary has been defined as an Unconformity, ?Unconformity or Fault in the well. Press the **Ages...** button and the **Sample Age dialog** will appear. Initially it will be blank.



Select the version (for the IGD) from the drop down list attached to the **Version** field then select one of the option buttons to display **All samples**, **LOG samples** only or **Samples with age** already assigned.

A list of samples in the current well will be displayed. The ages of any samples previously dated will be displayed in Ma. For identified stratigraphic breaks (Unconformity, ?Unconformity, Fault or ?Fault) ages already assigned in the database will show with the age above and below the break separately.

Ages are editable, so if you see an inconsistency you can change it here. Double click on the age you want to edit and type over the existing text.

> ***Note:*** *editing the ages in this dialog will only affect the dates in the well not the ages assigned to the IGD unit boundaries in a Scheme.*

To exclude samples from the assignment process, highlight them on the list and press the **Exclude selection** button.

To assign IGD boundary ages to samples in the list press the **Get IGD ages** button. The ages derived form IGD interpretations will be added to the list. **Source Notes** identify the IGD type on which the age assignment is based.

> ***Note:*** *the addition of IGD boundary ages will not overwrite any existing ages assigned to samples.*

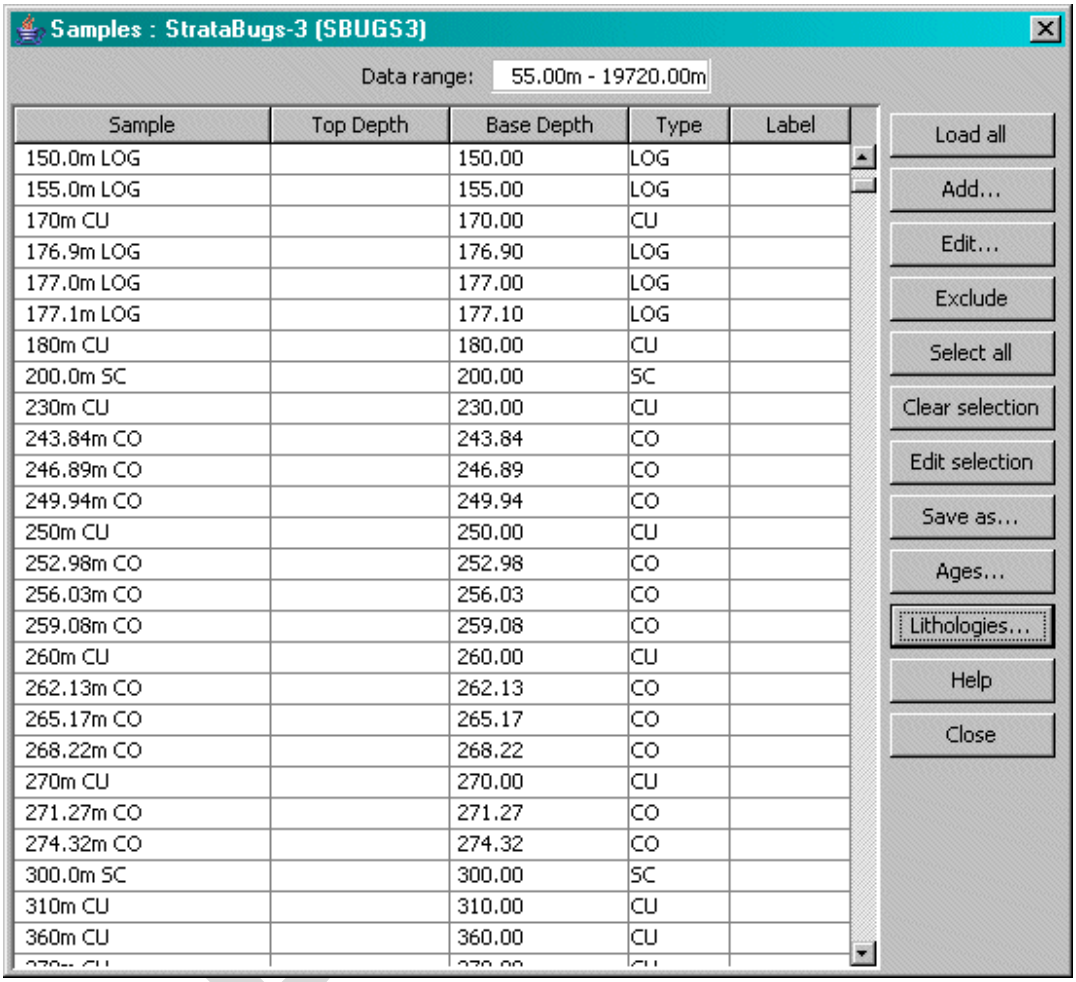
When you have finished it is a good idea to select the **Samples with age** option button to review the revised list of dated samples for the current well.

Press **OK** to save the newly dated samples to your database or Cancel to return to the Samples dialog without saving the changes.

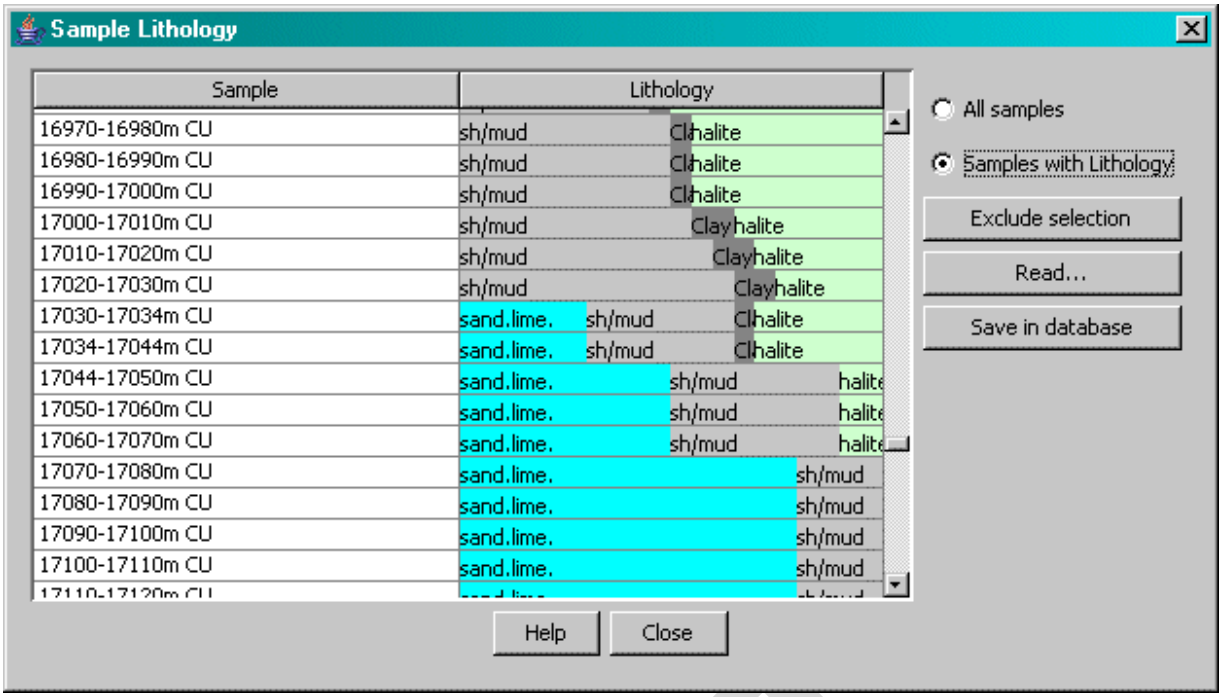
Sample Lithology import

Sample lithology is entered sample by sample in the **Samples Application**. (See Help in Samples application). If you want to import sample lithologies from a file you can do from the **Samples dialog** in Organiser.

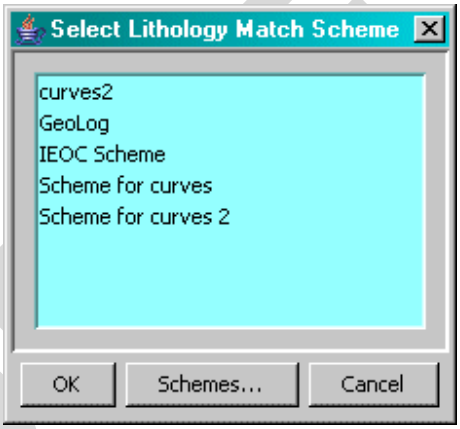
First Open a well in the Main Organiser Window. Then select **Samples** data type. The **Samples dialog** appears. (Press **Load** all to display existing samples)



Press the **Lithologies** button. The **Sample Lithology dialog** appears. The Lithology column will be blank.

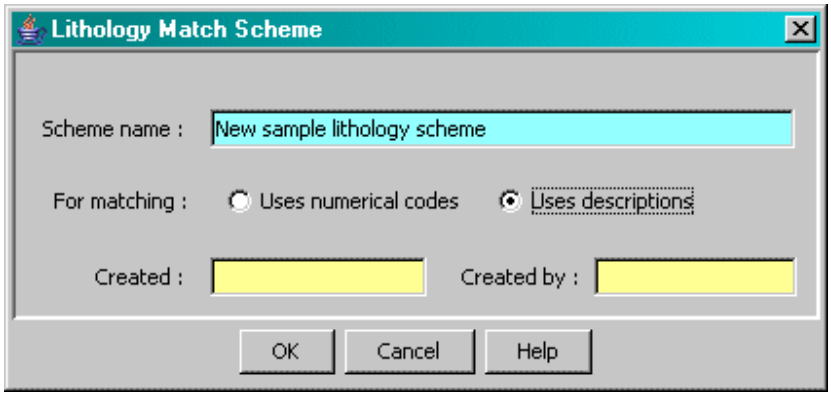


Press the **Read** button. If you select Sample lithology data file the **Select Lithology Match Scheme** appears.

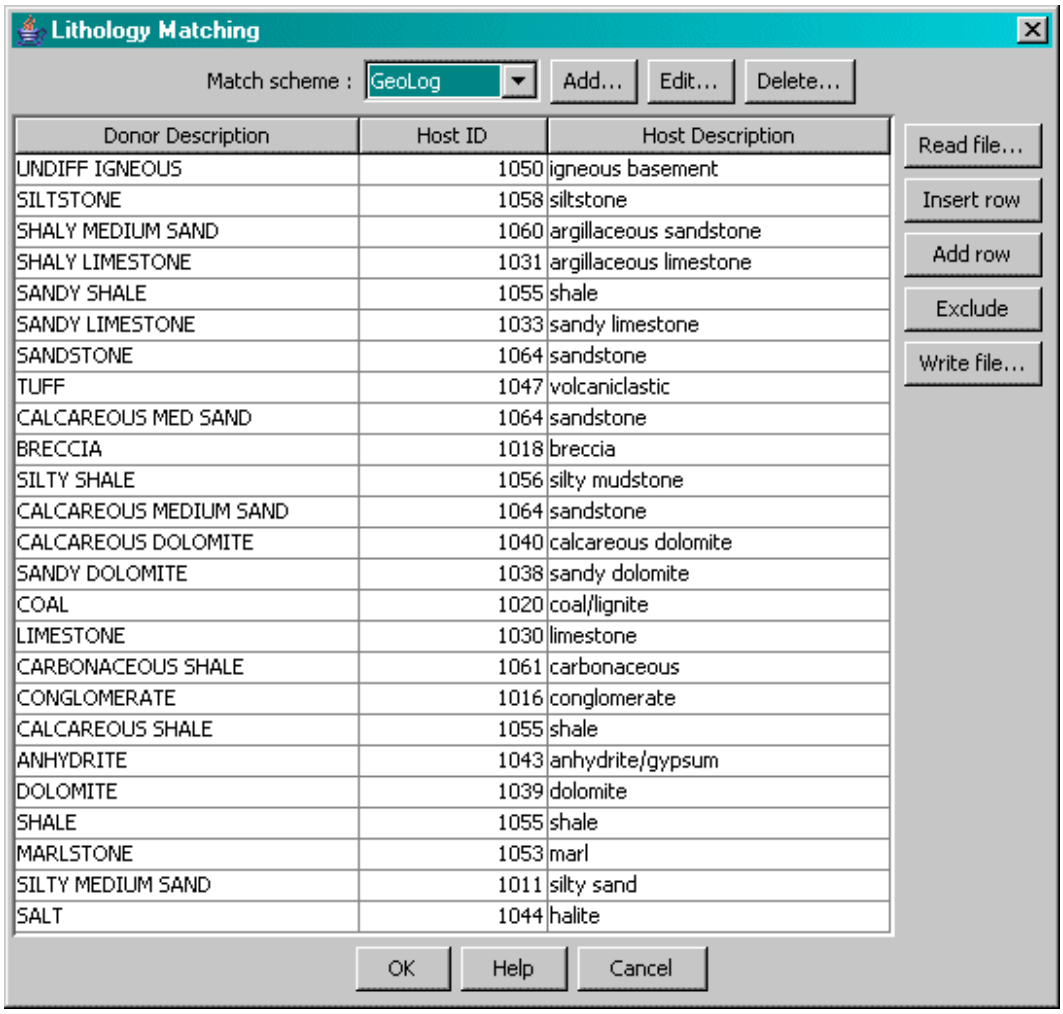


Select a scheme from the list and press **OK**.

If there is no suitable matching scheme press **Schemes** to open the **Lithology Match Scheme dialog**.



Press **Add** and enter the name of the new scheme in the **Lithology Match Scheme dialog**. Select the **Uses descriptions** option and press **OK**. The **Lithology Matching dialog** is blanked and the name of the new scheme is displayed in the **Match scheme** field.



Donor Description	Host ID	Host Description
UNDIFF IGNEOUS	1050	igneous basement
SILTSTONE	1058	siltstone
SHALY MEDIUM SAND	1060	argillaceous sandstone
SHALY LIMESTONE	1031	argillaceous limestone
SANDY SHALE	1055	shale
SANDY LIMESTONE	1033	sandy limestone
SANDSTONE	1064	sandstone
TUFF	1047	volcaniclastic
CALCAREOUS MED SAND	1064	sandstone
BRECCIA	1018	breccia
SILTY SHALE	1056	silty mudstone
CALCAREOUS MEDIUM SAND	1064	sandstone
CALCAREOUS DOLOMITE	1040	calcareous dolomite
SANDY DOLOMITE	1038	sandy dolomite
COAL	1020	coal/lignite
LIMESTONE	1030	limestone
CARBONACEOUS SHALE	1061	carbonaceous
CONGLOMERATE	1016	conglomerate
CALCAREOUS SHALE	1055	shale
ANHYDRITE	1043	anhydrite/gypsum
DOLOMITE	1039	dolomite
SHALE	1055	shale
MARLSTONE	1053	marl
SILTY MEDIUM SAND	1011	silty sand
SALT	1044	halite

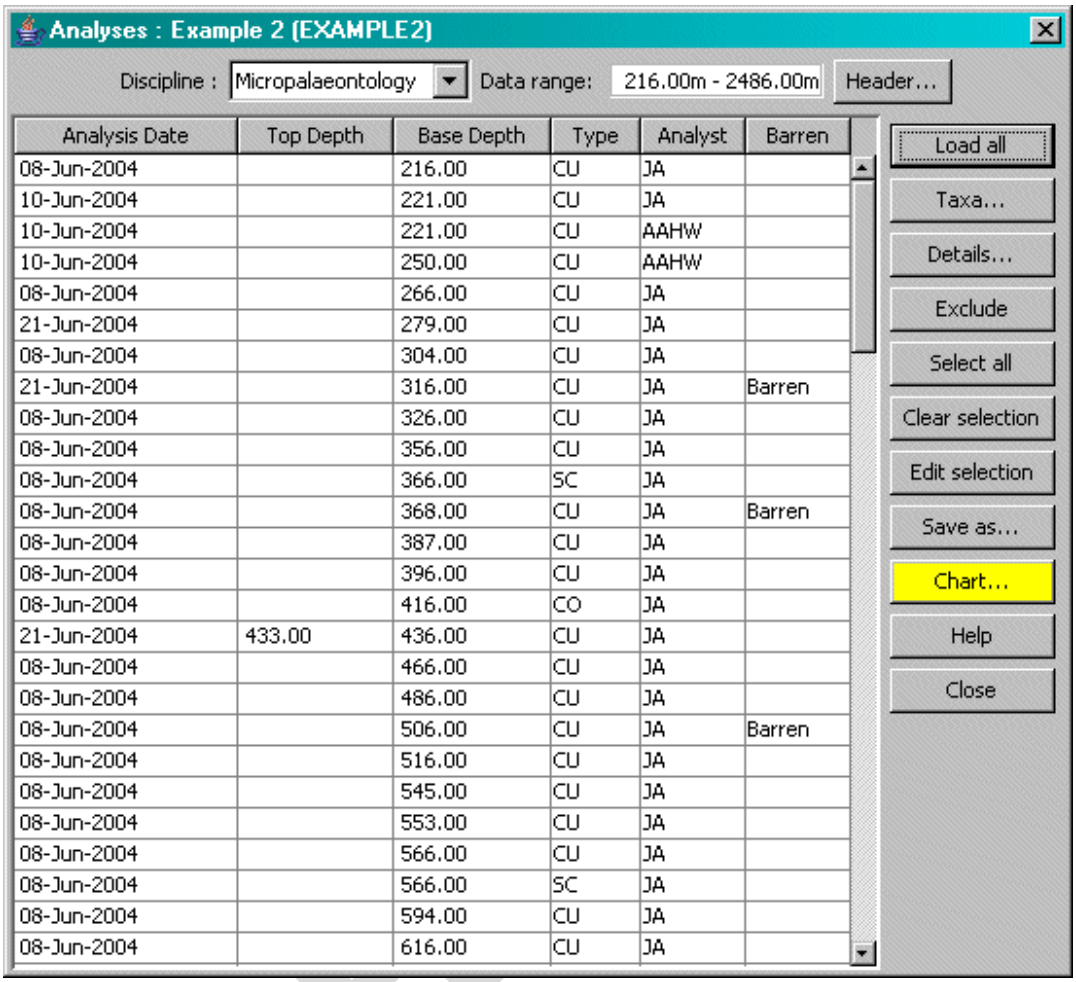
You can enter the Donor - Host translations row by row. Enter the Donor description and select the Host description from the drop down list. This will automatically selectthe correct Host ID. Alternatively, you can press the **Read file** button to read the sample lithology

scheme from a CSV Lithology Index file and populate the **Lithology Matching dialog**. Press **OK** and you will be asked to confirm that you wish to save these data to the database.

The **Sample Lithology dialog** will then be populated with the data from the datafile. If no data appear select either **All samples** or **Samples with Lithology**.

To save the data press **Save in database**.

Analyses dialog



Analysis Date	Top Depth	Base Depth	Type	Analyst	Barren
08-Jun-2004		216.00	CU	JA	
10-Jun-2004		221.00	CU	JA	
10-Jun-2004		221.00	CU	AAHW	
10-Jun-2004		250.00	CU	AAHW	
08-Jun-2004		266.00	CU	JA	
21-Jun-2004		279.00	CU	JA	
08-Jun-2004		304.00	CU	JA	
21-Jun-2004		316.00	CU	JA	Barren
08-Jun-2004		326.00	CU	JA	
08-Jun-2004		356.00	CU	JA	
08-Jun-2004		366.00	SC	JA	
08-Jun-2004		368.00	CU	JA	Barren
08-Jun-2004		387.00	CU	JA	
08-Jun-2004		396.00	CU	JA	
08-Jun-2004		416.00	CO	JA	
21-Jun-2004	433.00	436.00	CU	JA	
08-Jun-2004		466.00	CU	JA	
08-Jun-2004		486.00	CU	JA	
08-Jun-2004		506.00	CU	JA	Barren
08-Jun-2004		516.00	CU	JA	
08-Jun-2004		545.00	CU	JA	
08-Jun-2004		553.00	CU	JA	
08-Jun-2004		566.00	CU	JA	
08-Jun-2004		566.00	SC	JA	
08-Jun-2004		594.00	CU	JA	
08-Jun-2004		616.00	CU	JA	

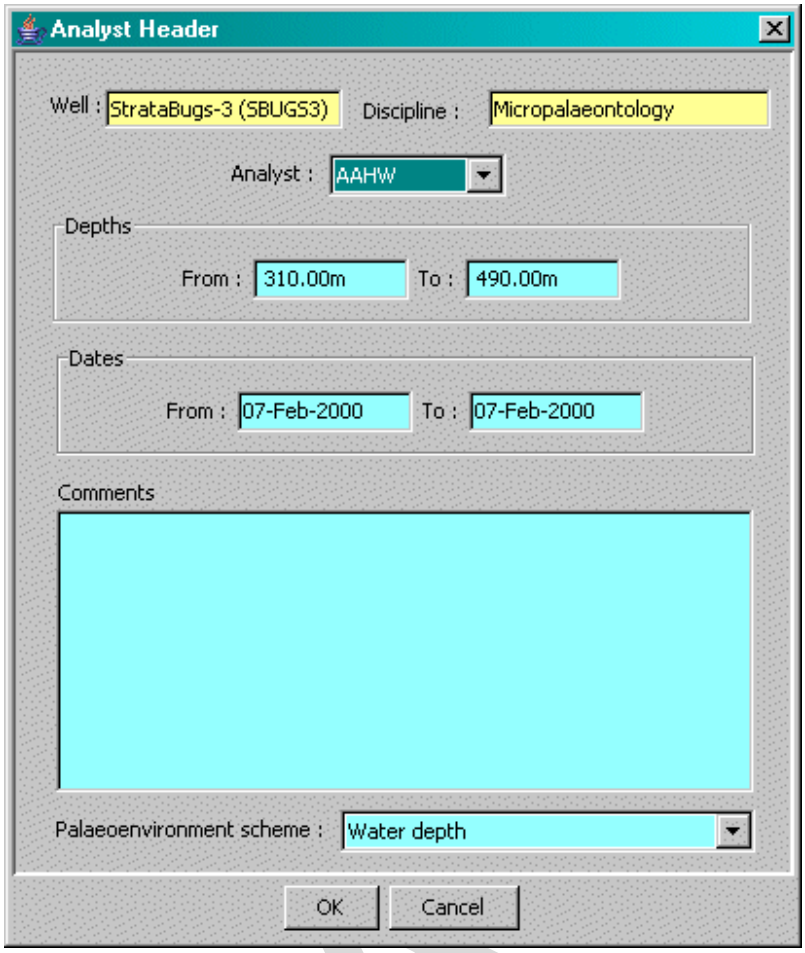
To access the **Analyses dialog** first highlight the dataset for a particular discipline and well in the Data view panel, and select **View | Selected data**. Alternatively, you can double click on the dataset name in one of the discipline columns to select it. The **Analyses dialog** will appear.

By default details for all the samples from a data file will be displayed in a table. To display the samples in a well press the **Load all** button.

To display analyses for another discipline other than the default selectone from the drop downlist on the **Discipline** field. You will have to reload for each discipline selected.

To view and edit details of the analyst for any particular analysis press the **Header...** button. The **Analyst Header dialog** appears.

> ***Note:*** *The* ***Header...*** *button is only present if you have extended your database for it using* ***Tools | Create database objects | Create analyst table header****.*



From here you can select a **Palaeoenvironment Scheme** if you are going to record palaeoenvironments on a sample by sample basis.

The first table column in the **Analyses dialog** displays the **Analysis Date** of each sample.

The second and third columns show the actual values of the sample **Top Depth** and **Base Depth**. Samples with a single depth value will display in the Base Depth column [or the Top Depth column depending on the default set].

The next column displays the sample **Type** and **Analyst**.

The final column shows which samples are **Barren**.

To see the recorded taxa for an individual sample highlight a sample on the list to select it and press the **Taxa...** button. The **Occurrences dialog** will appear. Alternatively, you can double click on the sample in the list. Sample data from a data file are shown in the upper pane.

To see the details for an individual sample highlight it on the list to select it and press the **Details...** button. The **Sample Details dialog** will appear. Alternatively, you can double click on the sample in the list.

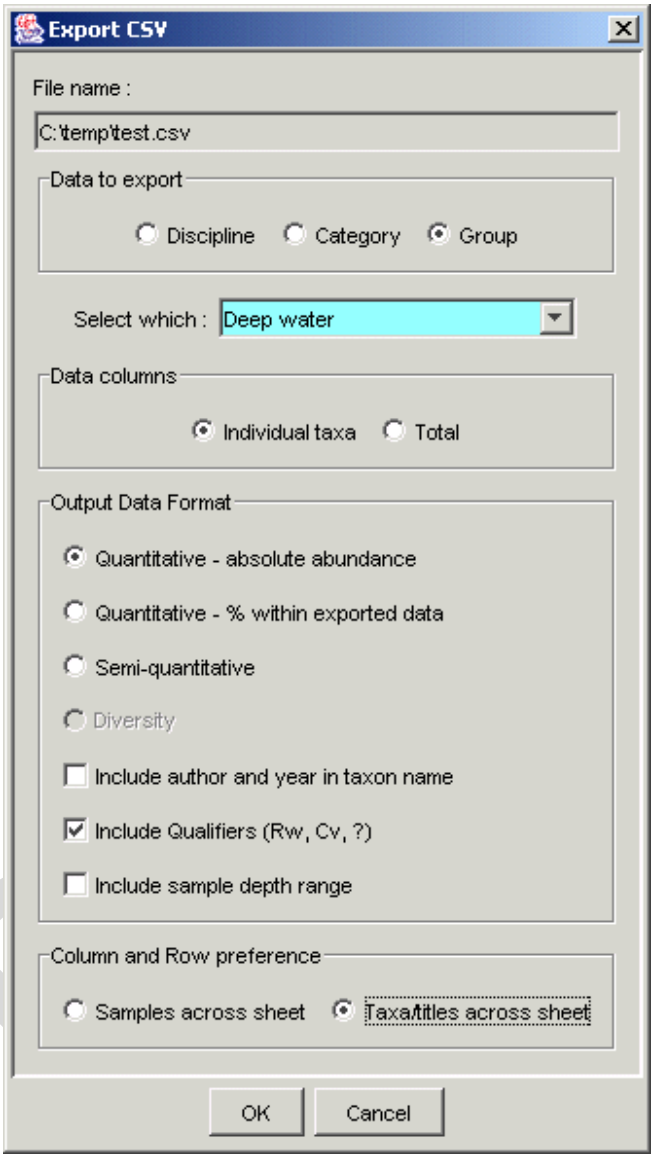
To exclude samples from the list highlight them and press the **Exclude** button.

To select all of the samples press the **Select all** button.

To clear a previous selection press the **Clear selection** button.

To edit the analysis date or analyst for one or more samples, highlight the sample(s) on the list and then press the **Edit selection** button. The **Edit Analyses dialog** appears. Any editorial changes you make will apply to all the samples selected.

Press the **Save as...** button to save all the data for samples which have not been explicitely excluded as a CSV file. Enter a suitable filename when prompted to do so. Press **OK**. The **Export CSV dialog** appears. This will enable you to select the content and style of the data which you export.



First decide if you want to export the entire **Discipline**, a single **Category** or a single **Group** and select the appropriate option button.

If you select the Category or Group option you will be prompted to **Select which** category or Group from a drop list.

You must then select one of the options to export the data either for **Individual taxa** or as a (Group or Category) **Total**.

There are a number of Output data format options - select one from **Quantitative - absolute abundance, Quantitative - % of exported data, Semiquantitative** or **Diversity**. You can then choose whether to **Include author and year, Include qualifiers (Rw, Cv, ?)** and **Include sample depth range** by selecting the appropriate checkboxes.

Finally, you should choose whether you want to plot the **Samples across sheet** or **Taxa/titles across sheet**. This refers to the orientation of the data matrix on a spread sheet which can be generated from the CSV file. Your choice will be governed by your requirements or those of other software.

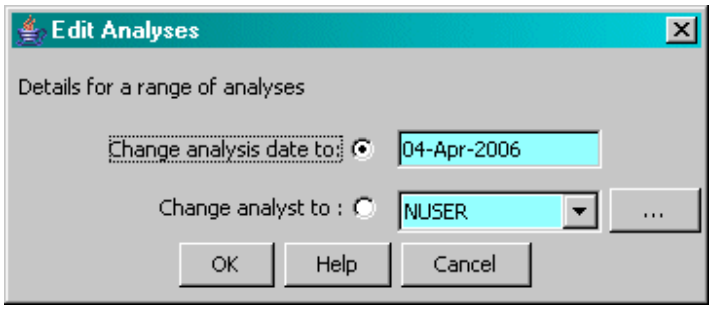
Press **OK** to save the data to a CSV file.

Chart - you will only see this option if you are testing the application.

When you have finished with the Samples dialog press the **Close** button when you have finished.

Edit Analyses dialog

The **Edit analyses dialog** enables you to edit the analysis date and analyst of a sample. You may wish to do this to update historical data for which analysts were originally not known or to correct data assigned to the wrong analyst.

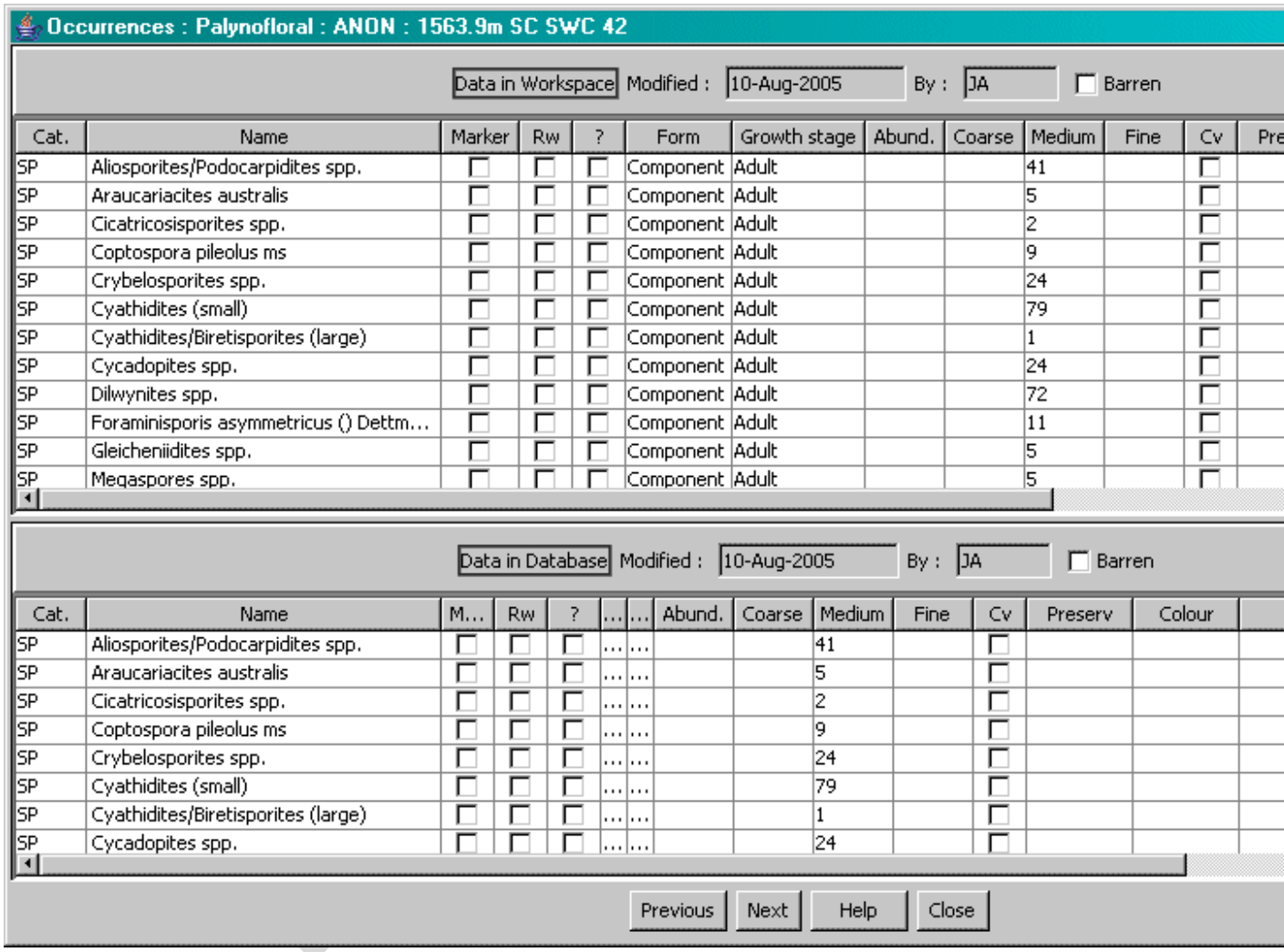


First select one or more samples on the list in the Analyses dialog, then select in the **Edit Analyses dialog** either the **Change analyst date to** or the **Change analyst to** option button. To edit the date just type in a date in the same format as the existing one. To change the analyst select one from the drop down list which will display all the analysts who have data assigned to them in the current well. If the analyst you require is not listed here push the ellipsis (**...**) button to display a list of all analysts in the database.

When you have made the changes press the **OK** button.

Occurrences dialog

To access the **Occurrences dialog** first highlight the dataset for a particular discipline and well in the Data view panel, and select **View | Selected data**. Alternatively, you can double click on the dataset name in one of the discipline columns to select it. This will open the **Analyses dialog** listing all the sample analyses for the well. Highlight a sample on the list and press the **Taxa** button.



If there are data in the database for the same sample/discipline this will be displayed in a lower pane, otherwise the pane will not appear. The data are arranged in columns displaying Category, taxon name and abundance and other details about the occurrence of individual taxa in the selected sample. The date of the last data modification and the analyst responsible are shown at the top of the dialog. The example dialog displays Microfaunal data. Dialogs for other disciplines are identical.

By default the taxa will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order).

If the sample is barren, no taxon names will appear in the upper pane and the **Barren** check box will be selected on.

Edit any of the data in any of the fields.

To remove taxa in the current sample from the workspace first highlight one or more on the list in the upper pane and then press the **Exclude** button. Press the **Show...** button to display a list of any taxa which you have excluded.

To delete all the taxa of the current discipline in the current sample from the database press the **Delete all** button.

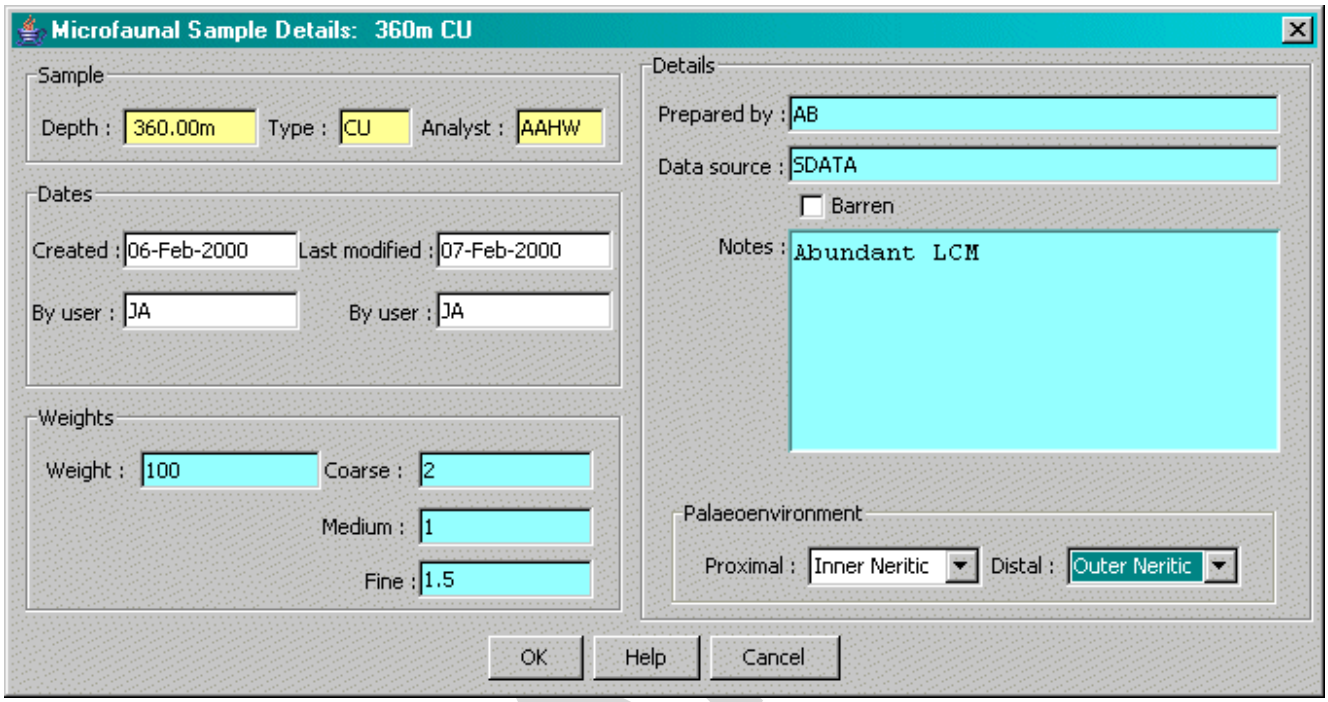
If there are conflicts between the displayed data for the current sample and the data already in the database edit the data in the current sample so that it is correct and pressing the **Merge** button.

The **Previous/Next** buttons enable you to scroll through the list of samples and view the taxa recorded for each sample.

Press the **Close** button when you have finished.

Sample Details dialog

The **Sample Details dialog** displays details about individual samples. To see the details of a sample first select it on the sample list in the **Analyses dialog** and then press the **Details...** button.



The sample **Depth**, **Type** and **Analyst** are displayed with dates of when the sample was **Created** and when each was **Last modified** and by whom.

If you wish to normalise your samples to a specific weight, type in the weight in the **Weight** field. (To enable the normalised distributions to be plotted correctly you should set the normalised weight in the Options tab of the Taxon Distribution Panel in the Chart application.)

If you analyse only a fraction of a sample you can enter the amount (as the denominator of a fraction). You can do this for three different fractions of the sample (labelled **Coarse** , **Medium** and **Fine**).

You can enter information here about who the samples were **Prepared by** or what was the **Data source**.

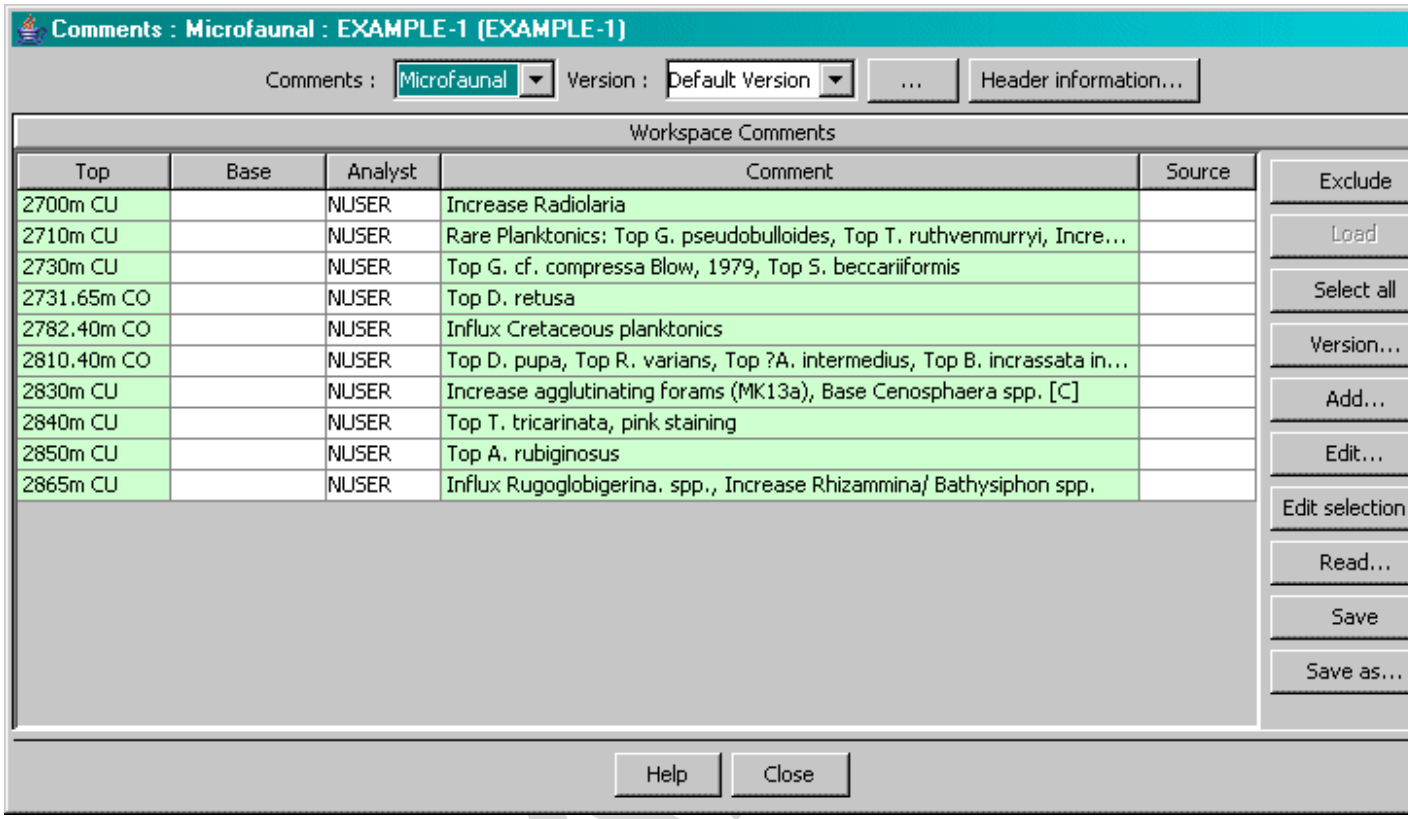
If the sample has been analysed (opening and closing the sample will do this) but no taxa recorded the **Barren** checkbox will be checked on. If you wish to override this you can.

There is also space for **Notes**.

Below this are two drop down lists to enable you to record the interpreted **Palaeoenvironment** for the current sample. Enter Proximal and Distal values from the default Palaeoenvironment scheme to provide a "sample by sample" palaeoenvironmental curve in Charts application. The default palaeoenvironment can be set in the **Analyses dialog**. The data collected in this way can be displayed in the Charts application by selecting the Plot samples option in the Palaeoenvironment Panel dialog.

When have finished press **OK** to save any changes or **Cancel** to quit without saving changes.

Comments dialog



To access the **Comments dialog** highlight the dataset for a well in the Data view panel and select **View | Selected data**. Alternatively, you can double click on the dataset to select it. By default comments for the discipline you selected in the Data view panel will be displayed in an upper workspace pane. If Comments for the selected well exist in the database they will be displayed in a lower database pane, otherwise the pane will not appear. By default the comments will be sorted in depth order. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order). The example is for a well where there is no existing data in the database.

By default details for all the samples from a data file will be displayed in a table. To display the samples in a well press the **Load all** button.

The **Comments** drop down list enables you to switch between comments for the selected discipline and those for other disciplines without having to close the dialog and reselect one from the Data view panel.

The drop down list on the **Version** field at the top of the dialog enables you to switch to different versions of the selected well. If the version name you require is not on the list push the elipsis and select one or add a new one using the **Select version dialog.**

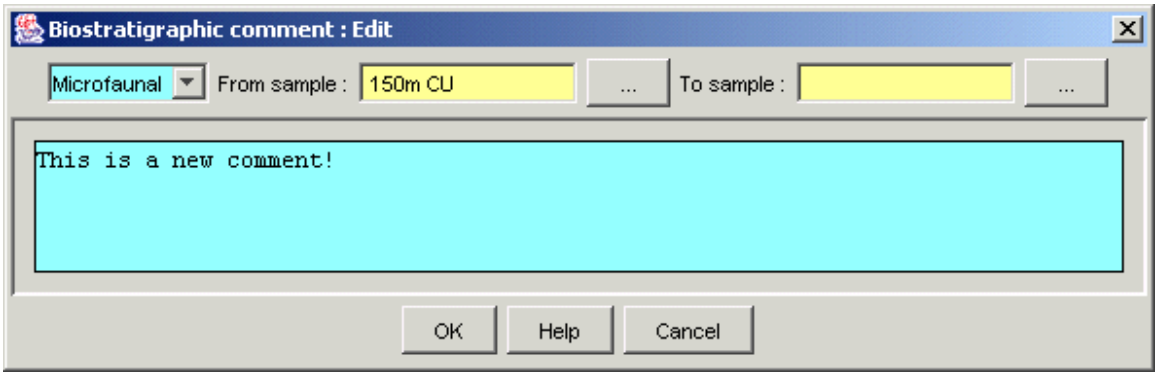
Press **Header information** to see existing information about this data type.

To exclude a Comment from the list highlight it and press the **Exclude** button.

To select all the comments on the list press the **Select all** button. You can then use the **Exclude** button to remove all the comments at once.

Press the **Version** button on the right hand side of the dialog to select a version in the host well.

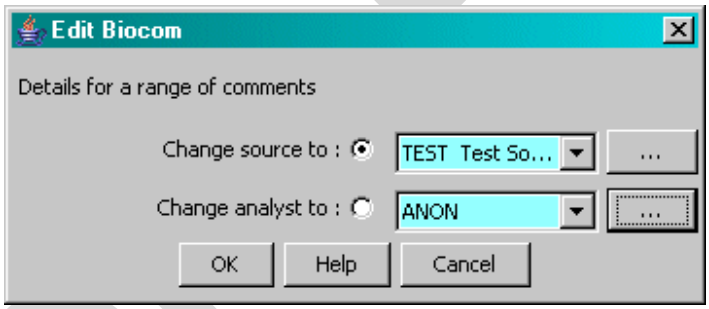
To add a comment for a particular depth press the **Add...** button. The **Biostratigraphic comment dialog** appears.



Select the correct discipline and use the ellipsis buttons(**...**) to select a depth (or a depth range) for the comment. Enter the comment in the text box below. When you have finished entering your comment press **OK** to save the comment in your workspace or **Cancel** to close the dialog without saving the comment.

To edit an existing comment, first highlight it on the list and then press the **Edit...** button and follow the procedure for adding a comment (above).

To make similar changes to a number of comments, highlight a selection of comments and then press the **Edit selection** button. The **Edit Biocom dialog** appears.



Read

Save

Save as

Press the **Close** button when you have finished.

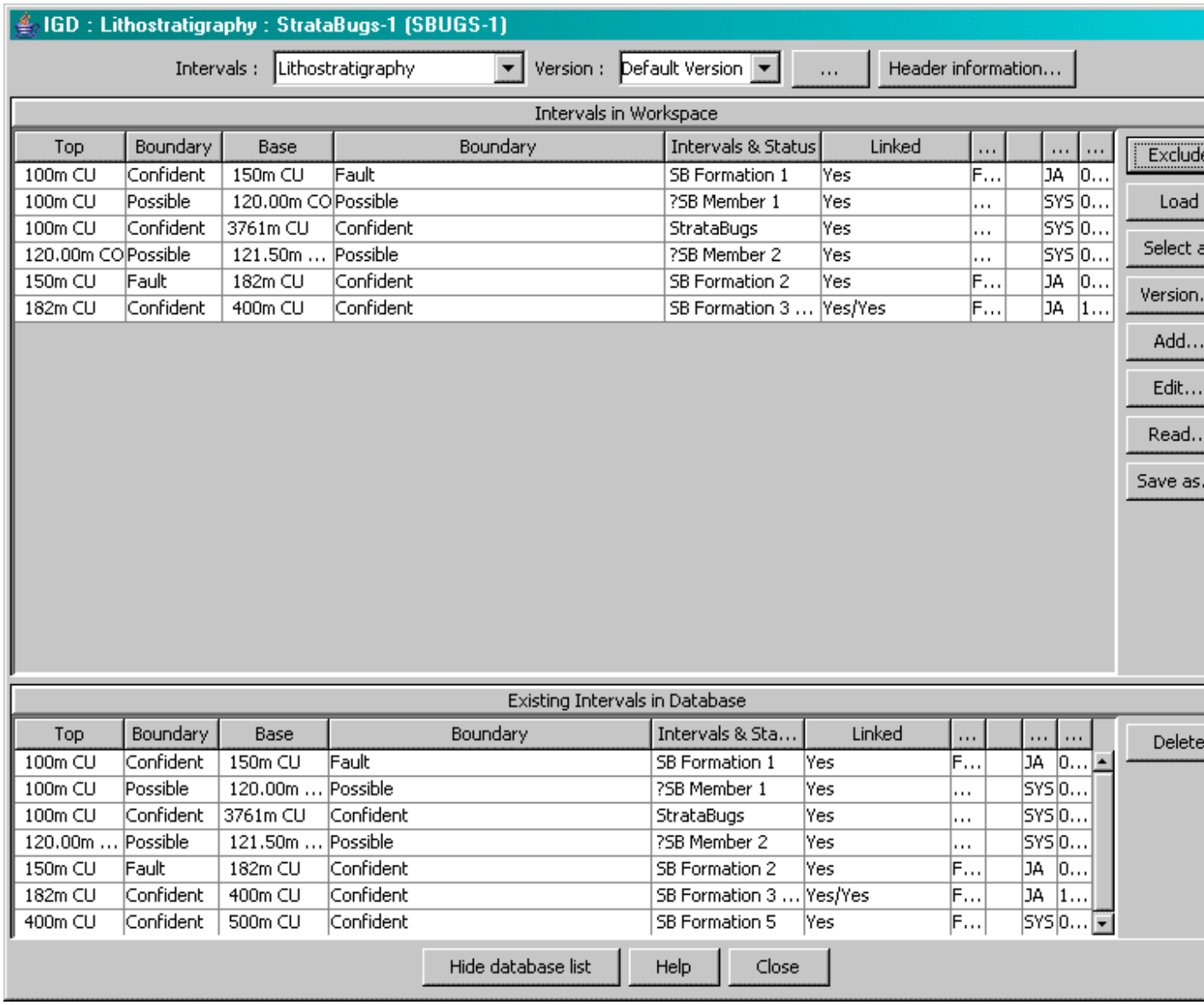
IGD dialog

To access the **IGD dialog** highlight the dataset for a well in the **Data view panel** and select **View | Selected data...** Alternatively, you can double click on the dataset to select it.

The IGD data dialog displays all the IGD units for the selected well and data type, either from your database or from a datafile. Data from a datafile will appear in a single pane. Data from the database will be displayed in a lower pane, with a blank upper pane.

At this point you can edit the dataset before you import it to the database or modify a dataset from your database before you export it.

You may wish to compare a dataset in a datafile with data for well already in your database. To do this you must first Match the data in the datafile and the wellname with the database. First **Match taxa** then **Match IGD**, followed by **Match well.** When you have done this the two datasets will appear in their respective panes in your workspace (datafile data in the upper pane, database data in the lower pane).

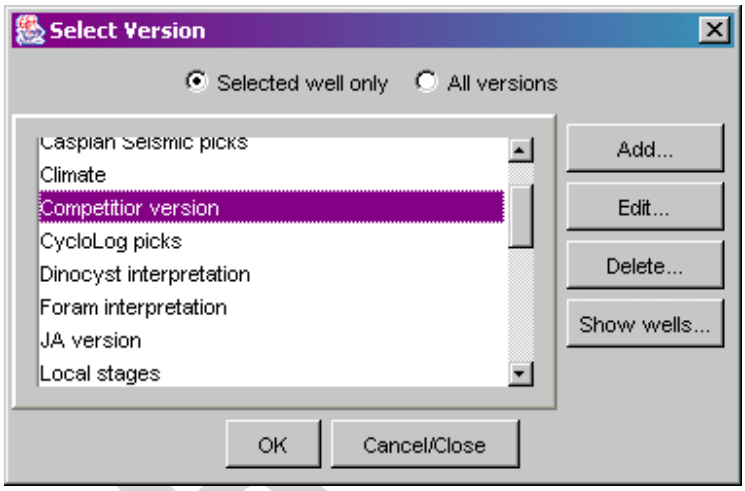


The example is for Lithostratigraphic units. The layout is similar for Chronostratigraphy, Biozones, Sequences and Palaeoenvironments. Select the IGD type from the drop down listat the top of the dialog.

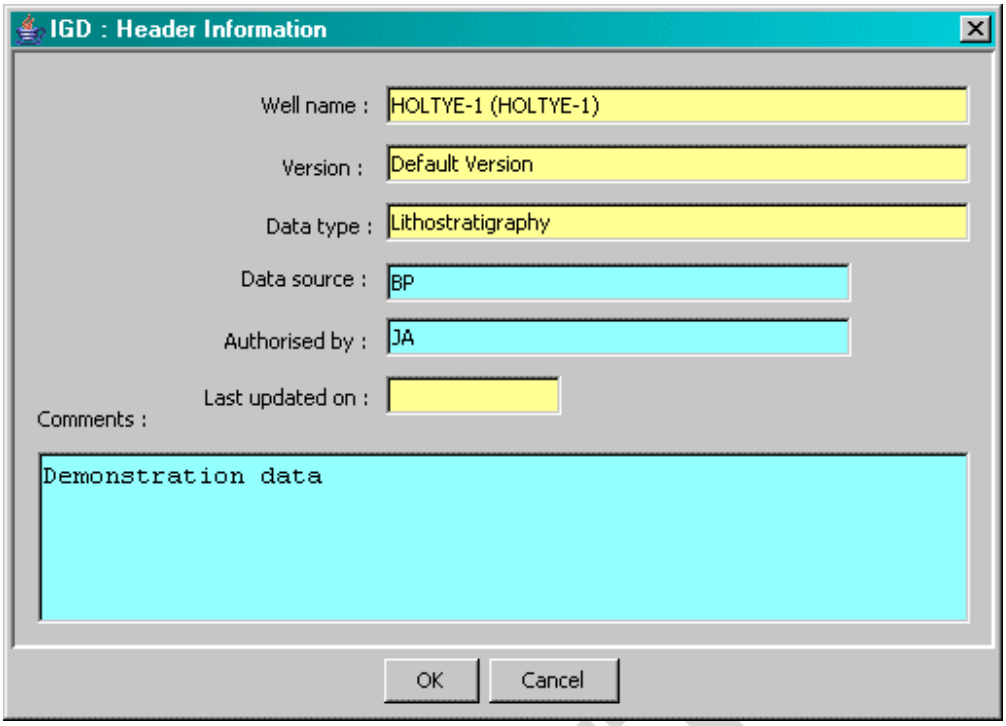
Toggle the **Hide database list/Show database list** button to hide/display the units in the database in a separate pane at the bottom of the dialog.

To edit an IGD unit, select one from the list and press the **Edit...** button. Alternatively, you can double click on the sample in the list.

The data are arranged in columns displaying top and base boundaries together with the boundary type, unit name, whether linked to a scheme or not, column selected for display and the date of the last data modification and the analyst responsible. By default the IGD units will be sorted in depth order. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order). The **Intervals** drop down menu enables you to switch between the selected IGD type and other IGD types without having to close the dialog and reselect from the Data view panel. To select a specific version of the IGD to display select one from the drop down list on the **Version** field. To add or edit a version press the ellipsis **(...)** button to the right of the Version field. The **Select version dialog** appears.



To add or edit Header informationfor this IGD type press the **Header information** button at the top of the dialog. The **IGD: Header Information dialog** will appear.



Add or edit the information in the blue fields. Press OK when you have finished.

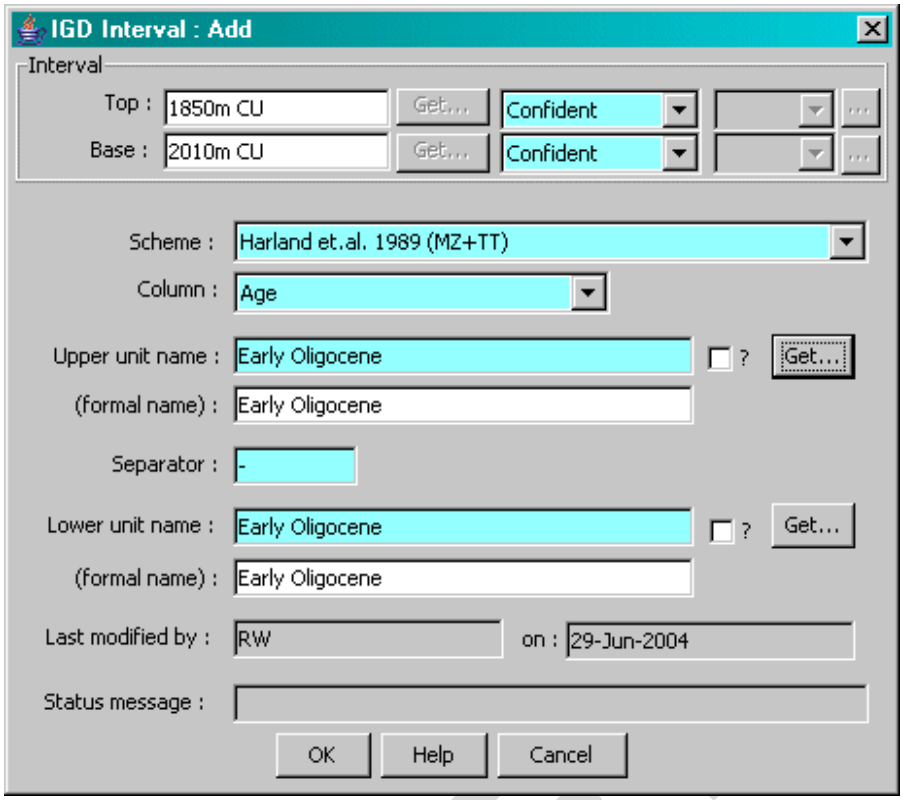
To exclude an IGD unit from the list highlight it on the list and press the **Exclude** button on the IGD dialog.

To load data for the selected well to the workspace from your database press the **Load** button.

To select all the items on the list press the **Select all** button.

To change the version for an individual item on the list press the **Version...** button. The **Select version dialog** appears.

To add a new unit to the list press the **Add...** button. The **IGD Interval dialog** appears.



To edit the details of an individual unit highlight it and then press the **Edit...** button. The **IGD Interval dialog** appears.

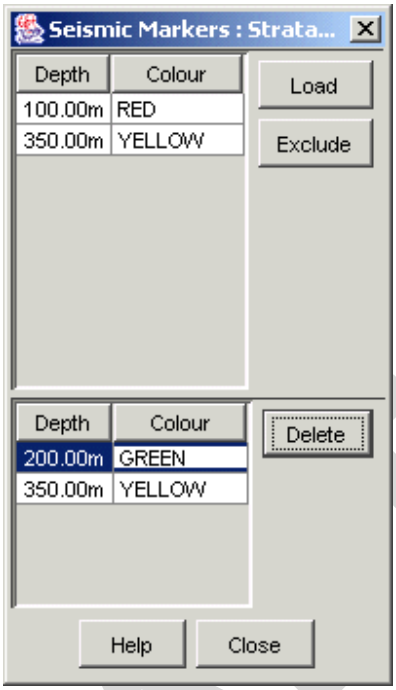
To read the contents of a file to import IGD data from a list of "surfaces", press the **Read** button and select a file. The format of the file must be in CSV format with data arranged in in the order: well name,surface_name,pick_depth,age,data source.

To delete an existing unit from the database, highlight it in the lower (database) pane and press the **Delete** button. You will be asked to confirm that you want to delete the unit.

Press the **Close** button when you have finished.

Seismic markers dialog

To access the **Seismic markers dialog** highlight the dataset for a well in the **Data view panel** and select **View | Selected data...** Alternatively, you can double click on the dataset to select it.



The **Seismic markers dialog** displays all the seismic markers and their depths for the selected well. Data from files will be displayed in the upper pane. If there are data in the database for the same well this will be displayed in a lower pane, otherwise the pane will not appear.

> ***Note:*** You must **Match Wells** first for the database data to appear.

To load markers for the selected well to the workspace from your database press the **Load** button.

To exclude a seismic marker from the list highlight it on the list and press the **Exclude** button.

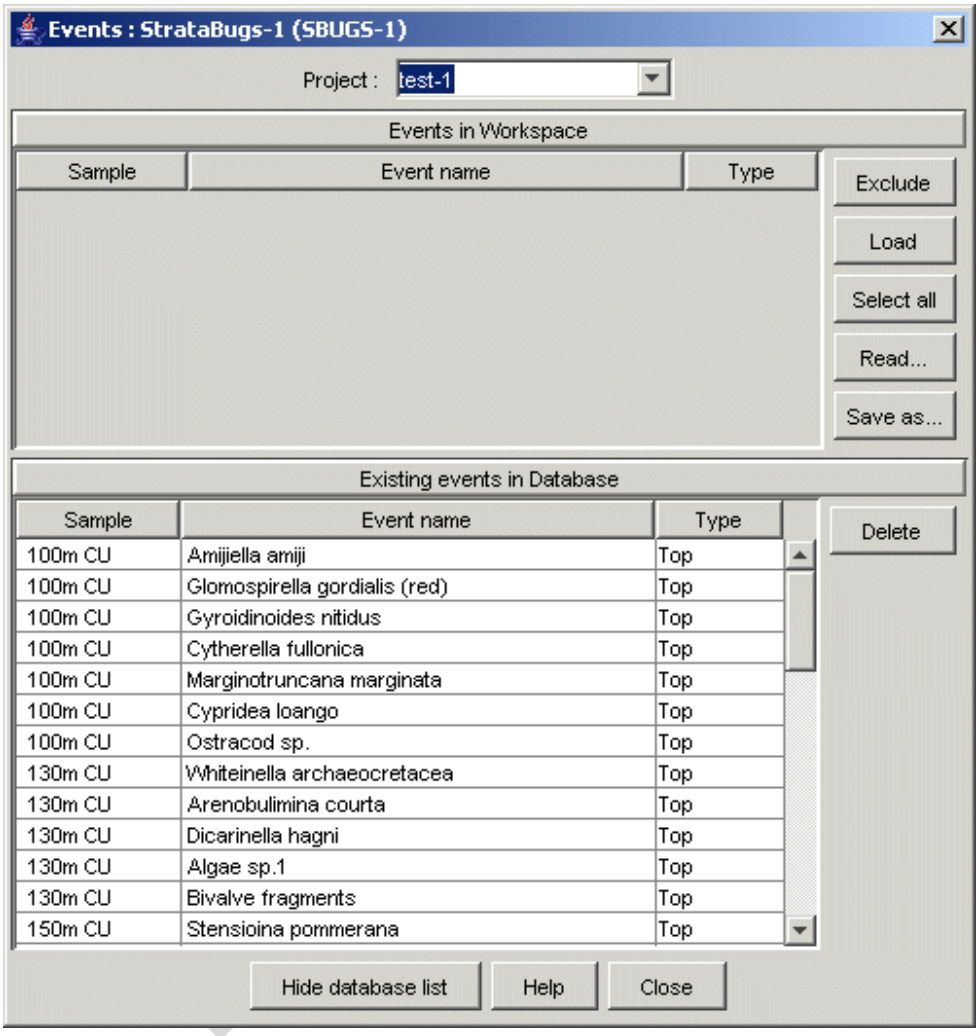
To delete an existing marker from the database, highlight it in the lower (database) pane and press the **Delete** button. You will be asked to confirm that you want to delete it.

Press the **Close** button when you have finished.

Events dialog

[under development]

To access the **Events dialog** highlight the dataset for a well in the **Data view panel** and select **View | Selected data...** Alternatively, you can double click on the dataset to select it. The Events dialog allows you to see what events are in the database. It also allows you to Read a list of events from an Openworks file, and to write out the events in the workspace into a file.



For data from the database, from the drop down menu at the top of the dialog, select the **Project** from which events are to be Loaded, Read into, or written from.

The Events data dialog displays all the events for the selected well, either from your database or from a datafile. Data from a datafile will appear in a single pane. Data from the database will be displayed in a lower pane, with a blank upper pane.

At this point you can edit the dataset before you import it to the database or modify a dataset from your database before you export it.

You may wish to compare a dataset in a datafile with data for well already in your database. To do this you must first Match the data in the datafile and the wellname with the database.

First **Match taxa** then **Match IGD**, followed by **Match well.** When you have done this the two datasets will appear in their respective panes in your workspace (datafile data in the upper pane, database data in the lower pane) - Is this correct.

Toggle the **Hide database list/Show database list** button to hide/display the units in the database in a separate pane at the bottom of the dialog.

To exclude an event from the list highlight it on the list and press the **Exclude** button.

To load events for the selected well to the workspace from your database press the **Load** button.

To select all the items on the list press the **Select all** button.

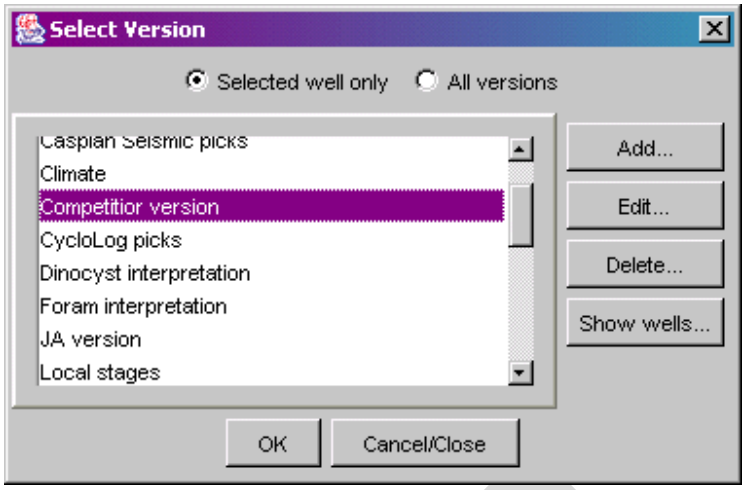
To delete an existing unit from the database, highlight it in the lower (database) pane and press the **Delete** button. You will be asked to confirm that you want to delete the unit.

Press the **Close** button when you have finished.

Select version dialog

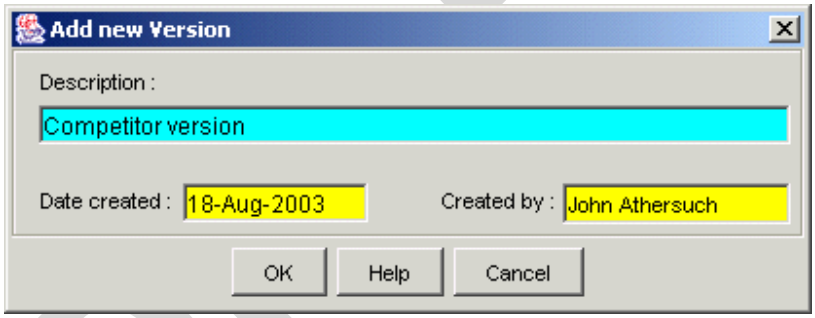
To access this dialog highlight an IGD dataset in the Data view panel and select **Version...** from the **IGD data dialog**.

The **Select version dialog** displays a list of versions for IGD well data.



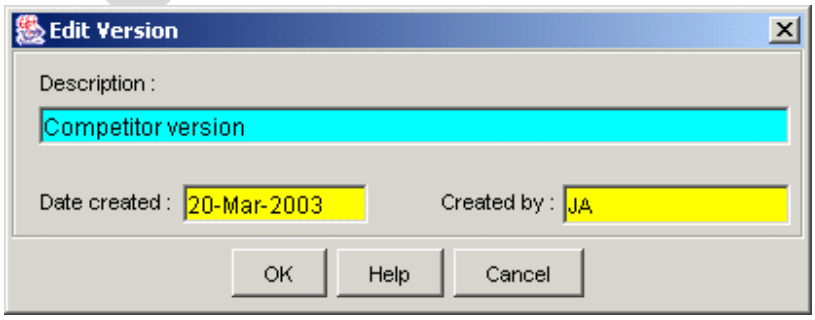
Use the radio buttons to select to display a list all versions previously used for the **Selected well only** or **All versions** for all wells.

Select a version from the list or if you need to add a new version press the **Add...** button. The **Add new version dialog** will appear.



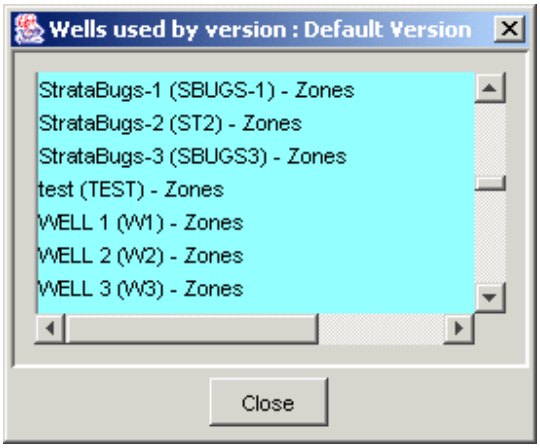
Enter a description for the new version and press **OK**.

To edit a version, select it on the list and press the **Edit...** button. The **Edit version dialog** will appear. Edit the description and press **OK**.



To delete a version, select it on the list and press the **Delete...** button.

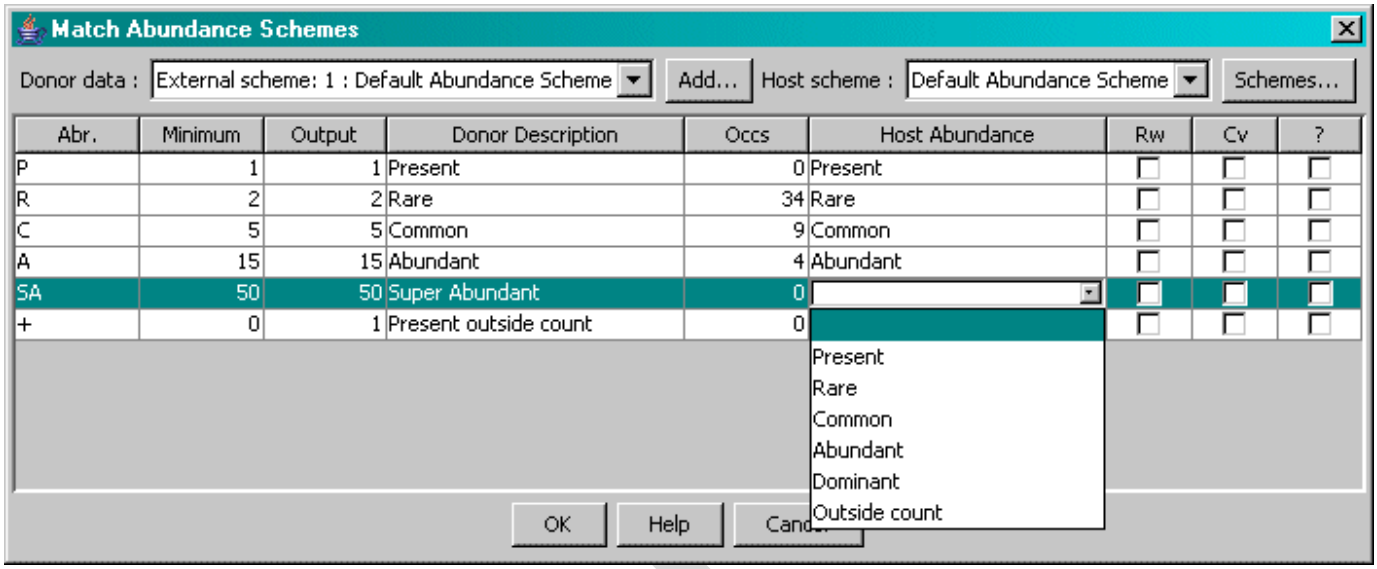
To display a list of wells in which this version has been applied select a version from the list and press the **Show wells...** button. A list of wells and the IGD type that has been assigned to the selected version are displayed in the **Version Usage dialog**.



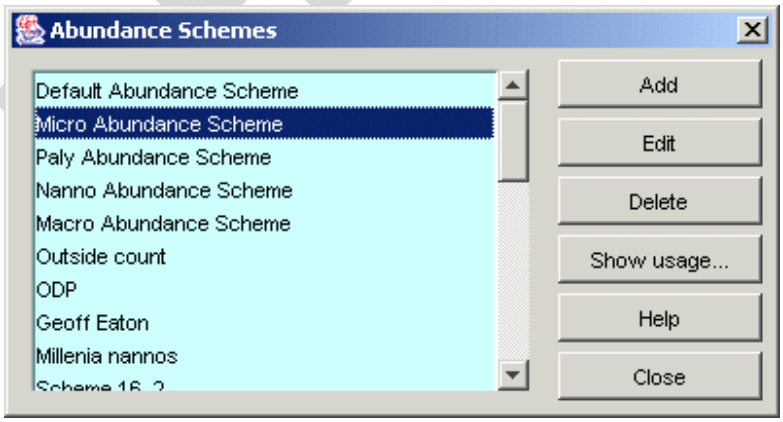
Press **OK** or **Cancel/Close** when you have finished.

Match abundance schemes dialog

Data can be recorded and stored numerically or semiquantitatively. Semiquantitative data must be matched against an equivalent numerical scale in an Abundance scheme. Abundance schemes can have up to 12 ranks including a special one for "outside the count" records. (There is a Config | Database option to increase the earlier maximum 10 ranks to 12).



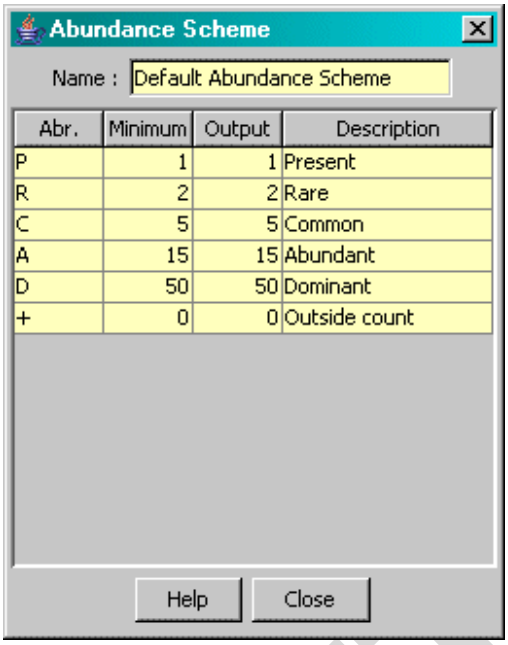
This dialog displays the donor abundance scheme name (if there is one). You will need to add this scheme to your database or match it with an existing scheme so that the numerical equivalence of semiquantitative ranks is maintained if data are imported. If there is no donor scheme you may match the donor data against an existing one in your database. If there is no appropriate abundance scheme you can add one. To see the details of all of the available schemes in your database press the **Schemes...** button. The **Abundance schemes dialog** will appear.



From here you can add a new scheme, or edit or delete an existing one.

Select a scheme which will match the donor data from the drop down menu attached to the **Host scheme** field. When a scheme has been selected the ranks which match will be posted

in the Host abundance fields and the complete scheme will be displayed in an **Abundance scheme dialog** which will appear.



Use this display to match the terms in the Donor scheme with the Host scheme. Each of the rows in the Host Abundance column will provide a drop down menu of terms from the selected abundance scheme from which you can select equivalent terms. You can qualify those occurrences which should be Reworked, Caved or Questionable.

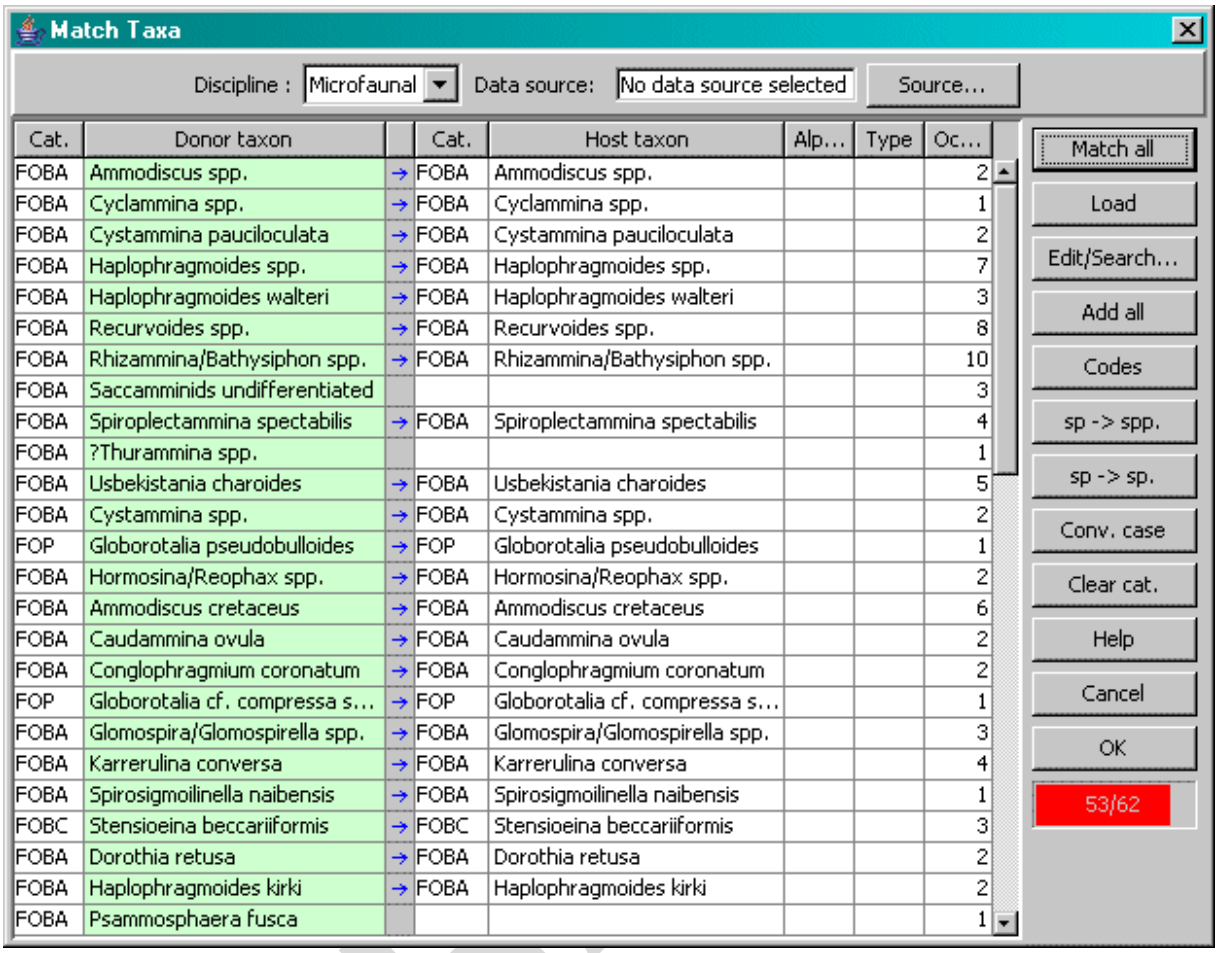
The **Occs** (Occurrences) column displays the number of times the rank occurs in the workspace dataset.

To add the abundance scheme from the donor data file to the database press the **Add...** button. The **Abundance scheme dialog** will appear.

You can add the scheme or modify it before it is added.

For more information on abundance schemes go to **Abundance schemes**

Match taxa dialog



Cat.	Donor taxon		Cat.	Host taxon	Alp...	Type	Oc...
FOBA	Ammodiscus spp.	→	FOBA	Ammodiscus spp.			2
FOBA	Cyclammina spp.	→	FOBA	Cyclammina spp.			1
FOBA	Cystammina pauciloculata	→	FOBA	Cystammina pauciloculata			2
FOBA	Haplophragmoides spp.	→	FOBA	Haplophragmoides spp.			7
FOBA	Haplophragmoides walteri	→	FOBA	Haplophragmoides walteri			3
FOBA	Recurvoides spp.	→	FOBA	Recurvoides spp.			8
FOBA	Rhizammina/Bathysiphon spp.	→	FOBA	Rhizammina/Bathysiphon spp.			10
FOBA	Saccamminids undifferentiated						3
FOBA	Spiroplectammina spectabilis	→	FOBA	Spiroplectammina spectabilis			4
FOBA	?Thurammina spp.						1
FOBA	Usbekistania charoides	→	FOBA	Usbekistania charoides			5
FOBA	Cystammina spp.	→	FOBA	Cystammina spp.			2
FOP	Globorotalia pseudobulloides	→	FOP	Globorotalia pseudobulloides			1
FOBA	Hormosina/Reophax spp.	→	FOBA	Hormosina/Reophax spp.			2
FOBA	Ammodiscus cretaceus	→	FOBA	Ammodiscus cretaceus			6
FOBA	Caudammina ovula	→	FOBA	Caudammina ovula			2
FOBA	Conglophragmium coronatum	→	FOBA	Conglophragmium coronatum			2
FOP	Globorotalia cf. compressa s...	→	FOP	Globorotalia cf. compressa s...			1
FOBA	Glomospira/Glomospirella spp.	→	FOBA	Glomospira/Glomospirella spp.			3
FOBA	Karrerulina conversa	→	FOBA	Karrerulina conversa			4
FOBA	Spirosigmoilinella naibensis	→	FOBA	Spirosigmoilinella naibensis			1
FOBC	Stensioeina beccariiformis	→	FOBC	Stensioeina beccariiformis			3
FOBA	Dorothia retusa	→	FOBA	Dorothia retusa			2
FOBA	Haplophragmoides kirki	→	FOBA	Haplophragmoides kirki			2
FOBA	Psammosphaera fusca						1

The **Match taxa dialog** enables you to match the taxon names in a data file with those in your database. Taxa in the data file are displayed in the "Donor" taxa column. If Category codes are available for any of the taxa these will be shown in the left hand column. Matching taxa in the database will be displayed in the "Host" taxon column. If a match for a particular taxon cannot be found the relevant Host taxon field will be blank. You can translate the unrecognised name to one which is in the database or add it to the database as a new species. Unmatched taxa often result from spelling and formatting errors so bear this in mind when matching taxa. The number of occurrences of each taxon in the dataset are displayed in the right hand column. You can use this information to form an opinion as to how important it may be to translate a particular taxon name.

By default the taxa will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order).

Typically you would match as many taxa as possible against your database, and then edit names in the data file which are incorrectly spelt or formatted, and then add genuinely new taxa to the database. There are a number of options which you select from buttons on the right hand side of the dialog as follows:

Source... A data Source is usually an organisation or individual from whom you receive data. If you have previously received data from the source that provided the data file you are currently working with you can press the **Load** button to match the taxa in the data file against a translation table created in a previous session from the same source. Press the **Source...** button and the **Select source dialog** appears.

Match all. To match names against all the names in the database press the **Match all** button. Any names recognised as already present in your StrataBugs database will be added to the Host taxon column on the right hand side of the dialog box. This avoids using any previous taxa translations

> ***Note:*** The number of taxa currently matched is recorded in a counter on the right hand side of the dialog box.
>
> ***Note:*** If any taxa have been assigned to Categories in the source data which do not match the ones designated in your database the global search will not retrieve them and you will have to add them individually and assign the correct Category.

Load. If you press the **Load** button any names found in a translation table created in a previous session from the same source will be translated and appear on the right hand side of the dialog box.

Note: If you press the **Load** button first previous taxon translations will take priority. If you press the **Match all** button first taxa will be match against the database as a priority. So for a particular data source, if taxon *Alpha beta* has previously been translated as Alpha gamma, if both taxon names are in your database you can choose to import either name. Selecting **Match all** first will match *A. beta* to *A.beta*, pressing **Load** first will translate *A.beta* to *A.gamma.*

Edit/Search... Select any remaining names that have not been matched or which you wish to edit, one at a time, and push the **Edit/Search...** button. The **Select taxa dialog** appears displaying the selected name.

Add all. If you wish to add all the taxa from the source file irrespective of whether they are matched in the database or not push the **Add all** button. This will not overwrite previous selections made using Load or Global commands but may add incorrect names to your database. It is dangerous to do this if you are less than certain about the quality of the data in the data file, particularly spelling and formatting styles.

> ***Hint:*** To import a long list of taxa which are not recognised by the database quickly and safely, scan the list by eye and provide translations for all the names which have more than two parts (i.e. more than genus and species names). Then scan the rest of the list looking for any obvious errors (eg sub-species and species epithets together in the same field, cf. and ? included in the species field, etc.). Next use **Add all**. All the taxa for which the genus name can be recognised are automatically added. Then edit the first species of each remaining genus, providing the correct category assignment and add it. Repeat **Add all**. Repeat the last steps if there are any left.

Codes. By default taxa are matched using their full taxonomic names. If you select the **Codes** button the taxa will be matched by alphanumeric codes. These are convenient abbreviations (e.g. Mel pomp or Ammobac 1) which you may wish to use. There are options in the Chart plotting application to display these taxa either by their full names or alphanumeric codes.

Sp -> Spp. If you wish to switch all terms sp., Sp., sp, SP ,spp, Spp, etc. to spp. to consistently record un-identified taxa as part of a generic group of species press the **Sp -> Spp.** button.

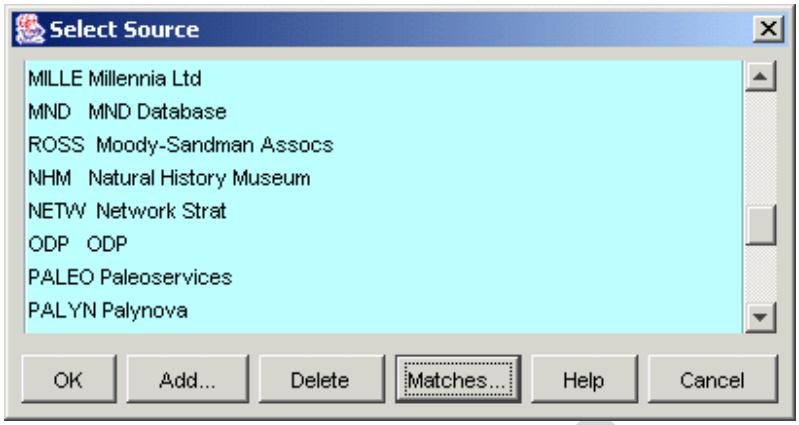
Conv. case. To capitalise taxon names of unmatched taxa which are not in the proper case press the **Conv.case** button. For instance names appearing all in uppercase will be changed so that only the initial letter of the genus (and sub-genus if present) will be capitalised. This will not affect any text following the term sp.

Press the **OK** button to close the dialog. The changes you have made will be saved to the workspace and can be saved to the daabase if required, later.

Press the **Cancel** button to close the dialog but not save any of the changes you may have made.

Select source dialog

The **Select source dialog** enables you to select a data source for the data file. Typically this will be the name of an organisation or individual who supplied you with the data.



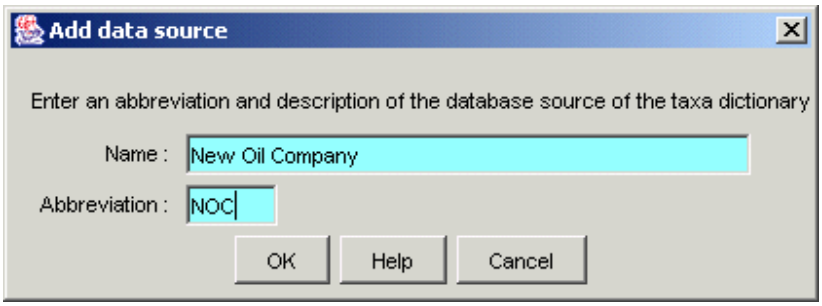
You may add a source to the list by pressing the **Add...** button and typing the name of the source organisation and a suitable abbreviation in the fields provided in the **Add data source dialog**.

To delete a source first highilght it on the list of sources and then press the **Delete** button.

To view the translations which have previously been created for a particular source press matches **Matches...**. The **Source matches dialog** appears.

When you have finished press the **OK** or **Cancel** button.

Add data source dialog



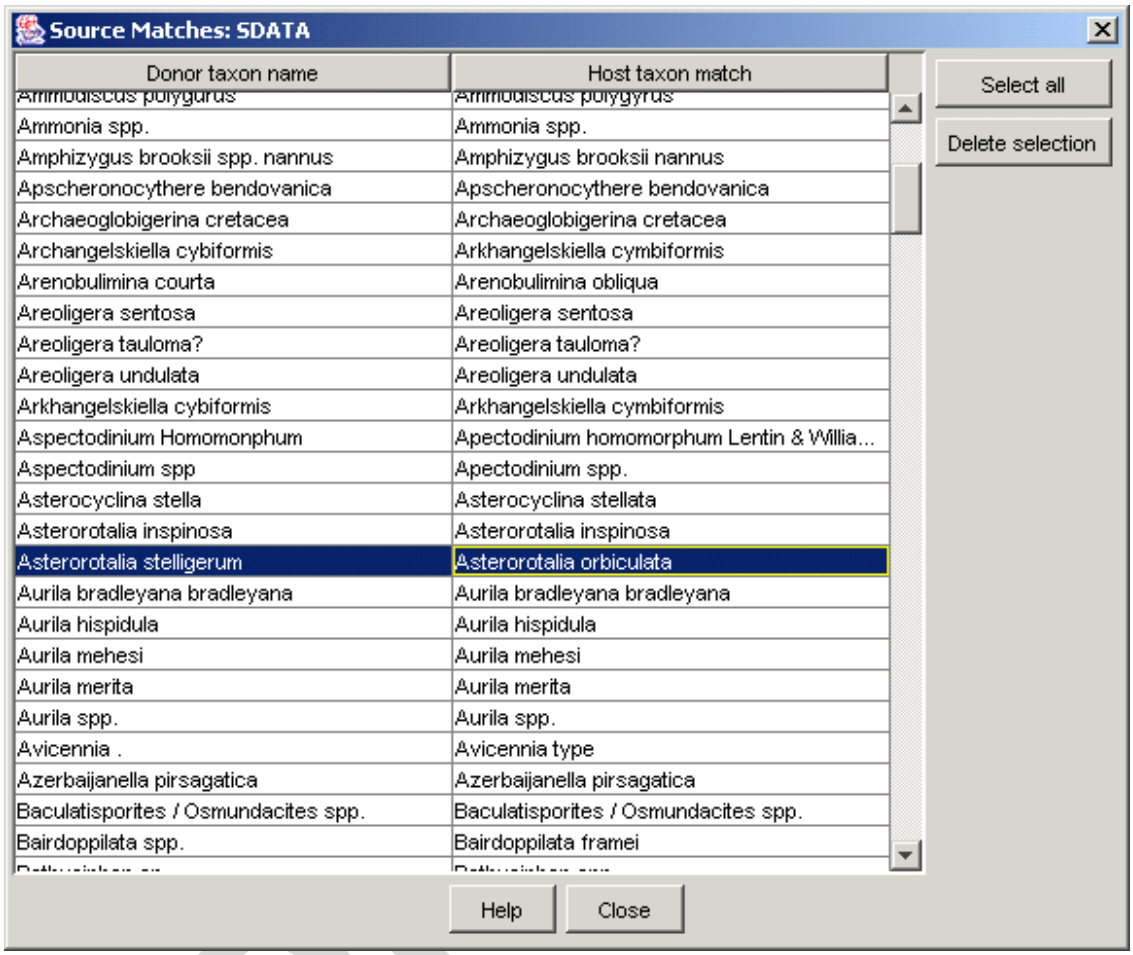
The **Add data source dialog** enables you to add a new source. You will need to do this each time you receive data from a different organisation or individual so that the data from each soure can be identified separately in the database.

Enter the name of the new organisation and an abbreviation.

Push **OK** to return to the **Select Source dialog**.

Source matches dialog

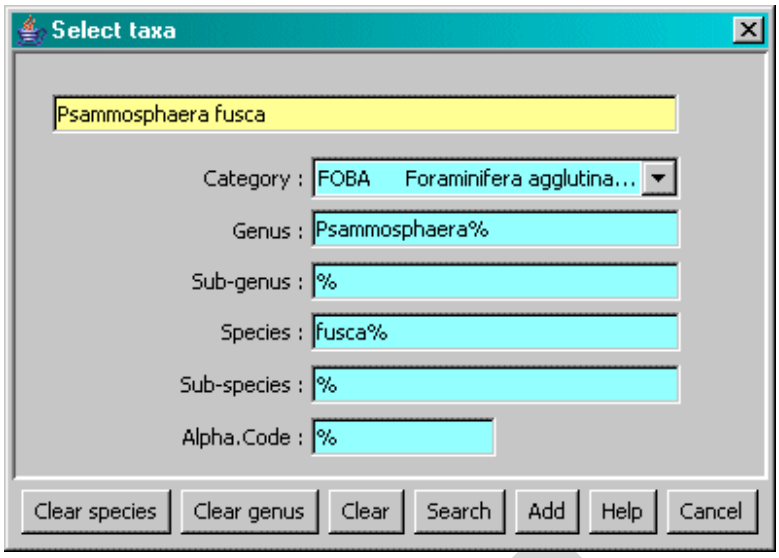
The **Source matches dialog** displays the Donor taxa and the matching Host taxon names for the selected Source. You may use this as a reference or delete translations which you may have created in error or no longer require.



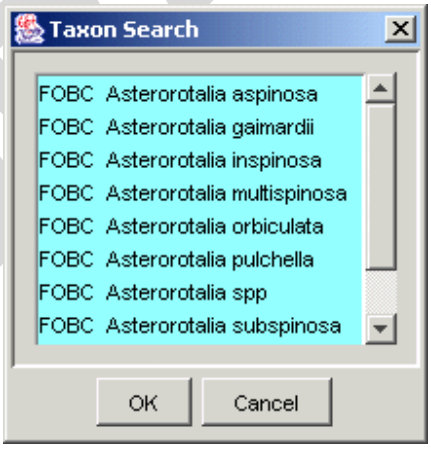
To delete items from the list, first highlight one or more items on the list and then press the **Delete selection** button. To delete all the translations you can press the **Select all** button followed by the **Delete selection** button.

Press the **Close** button to return to the **Select source dialog**.

Select taxa dialog



Using the **Select taxa dialog** you may add an unmatched taxon name to the database or edit it so that it matches a name already in the database. When the dialog opens it will display the name of the selected taxon in the yellow field at the top of the dialog. This field cannot be edited. Below this are a number of blue, editable fields each containing a component part of the selected taxon name. Check the contents of each field for spelling and formatting errors. Commonly you will have to edit the fields so that the various components of the name are in the correct fields. You can use the **Clear species**, **Clear genus** and **Clear** buttons to speed up this process. When you have made these changes you can press the **Search** button to search the database for the revised name and display a list of taxon names matching your search criteria in the **Taxon Search dialog**.



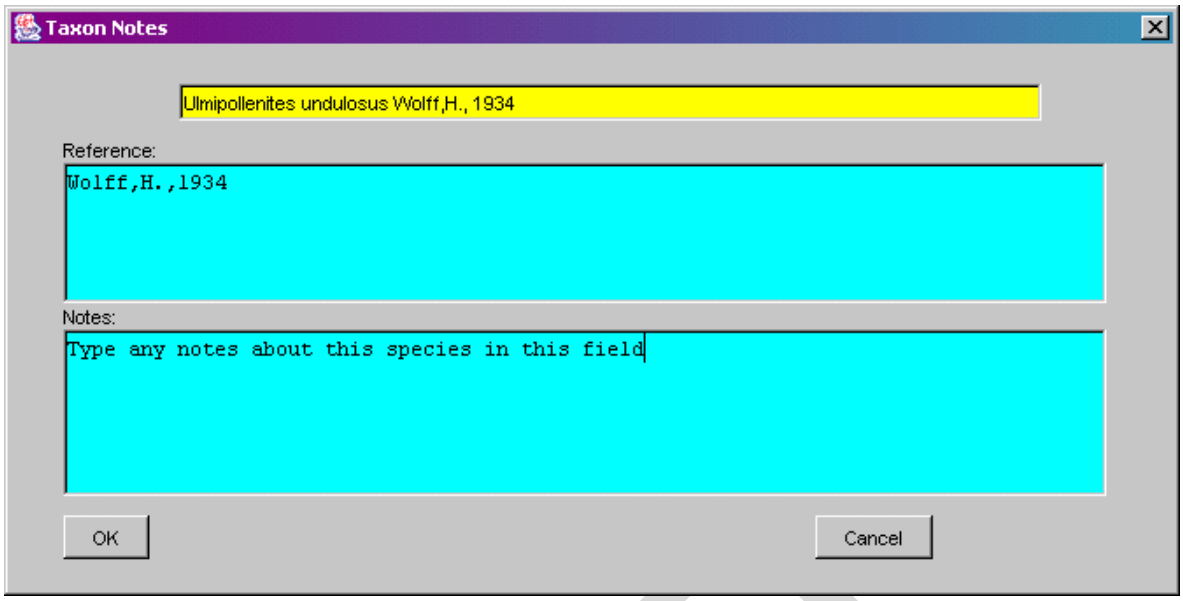
Hint: *Make sure that the wildcard (%) is positioned correctly within each field to allow a search. In addition, if you are not sure how a name is spelt, you may find it useful to remove all or part of the name and search the database again.*

If the taxon you are searching for is on the list, select it and press **OK**. The name will be inserted as the Host taxon. If the taxon you are searching for is **not** on the list, you must add it to the database. To do this press the **Add** button on the **Select taxa dialog** to open the **Add/edit taxon details dialog**.

To exit without saving any changes press the **Cancel** button.

Taxon notes dialog

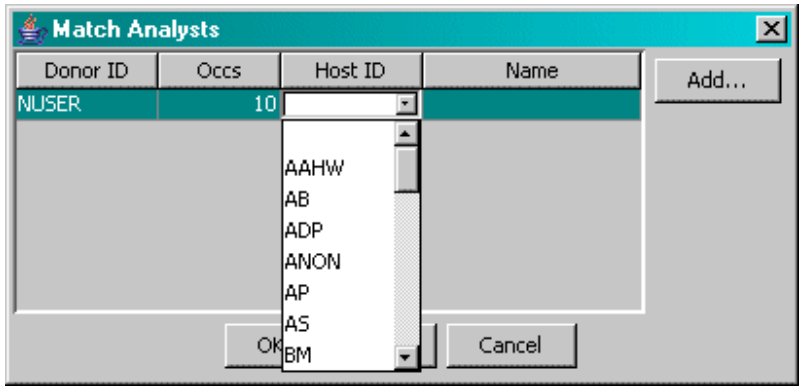
Add references and make notes about a taxon in the **Taxon notes dialog**.



Type freestyle text in the **Reference** and **Notes** fields and press **OK** to save the data, or exit the dialog without saving the notes by pressing **Cancel**.

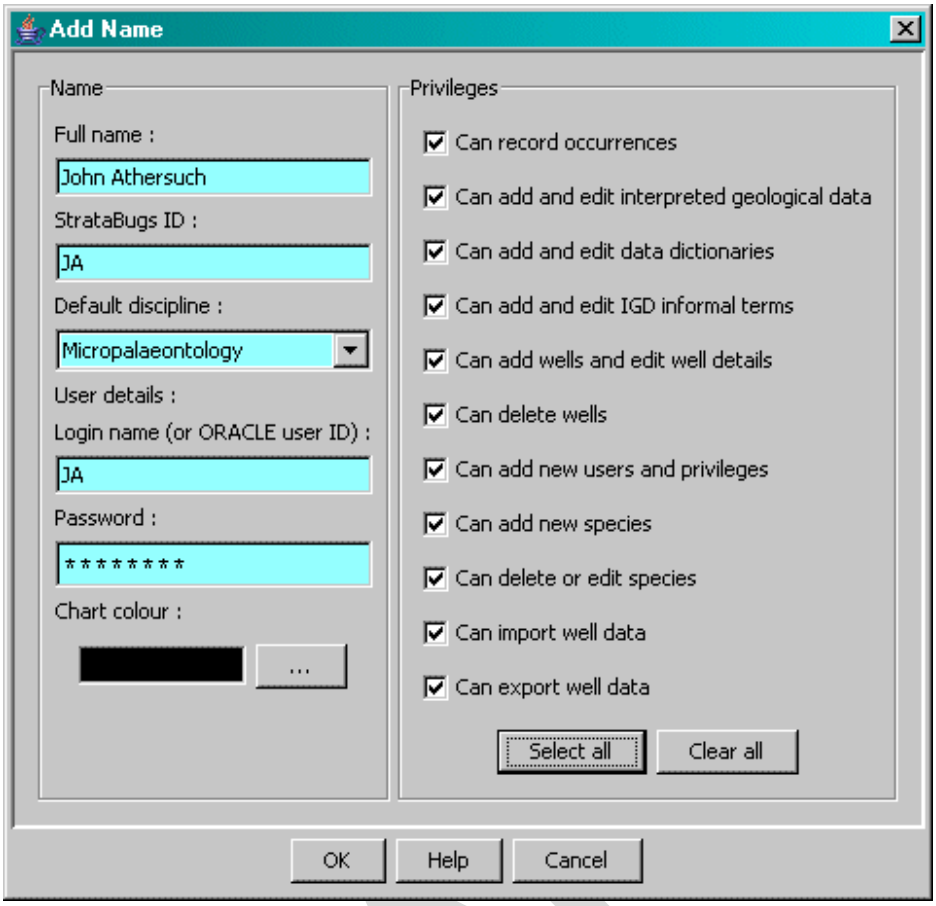
Match analysts dialog

The **Match analysts dialog** enables you to match the analyst of an incoming sample with a StrataBugs Name in your database. You can also edit the analyst assigned to any sample(s).



Select the **Analysts...** item on the Match menu. The **Match analysts dialog** will appear displaying a list of the analysts recorded in the dataset in your workspace. Each Donor ID and the number of occurrences in the dataset is recorded on the left and the matching StrataBugs ID and Name is shown on the right. If there is no match the StrataBugs ID and Name fields will be blank. To change or make a matching StrataBugs ID and Name pull down the menu attached to the StrataBugs ID field and select one from the list.

If there is no matching Host ID available press the **Add** button. This will open the **Add Name dialog**.



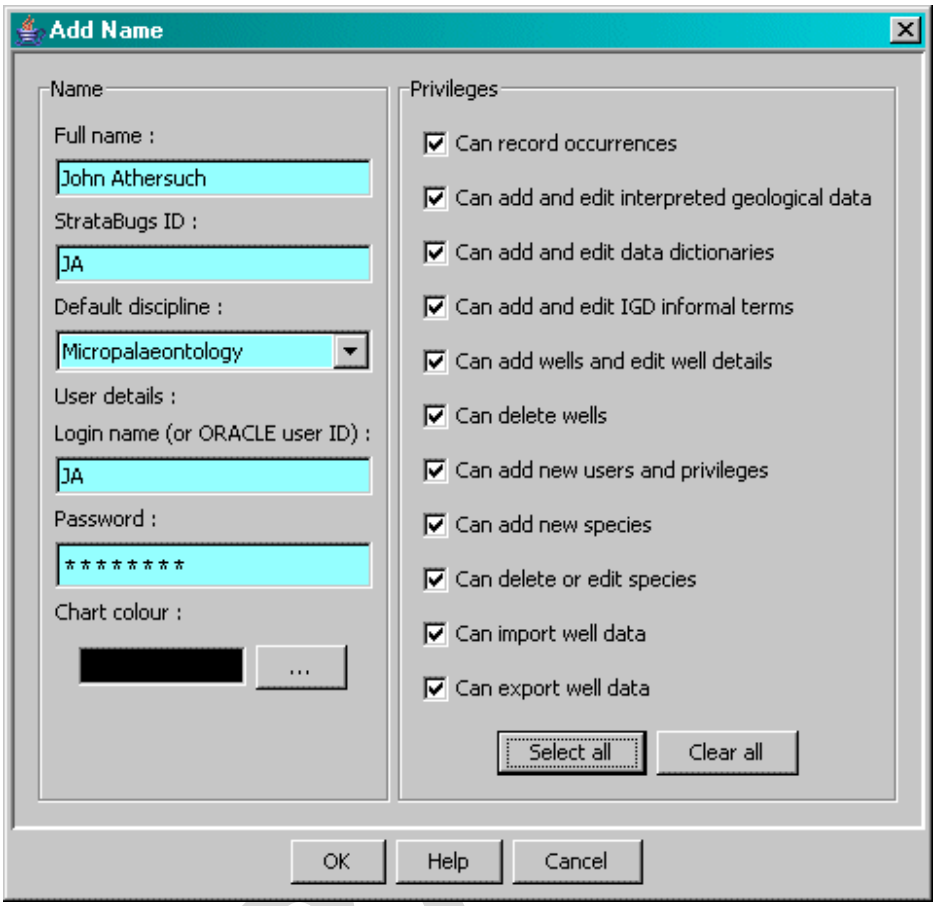
Complete the Full name, StrataBugs ID and Default discipline fields on the lefthand side. There is no need to complete the User details (Login name and Password) or to select any of the Privileges checkboxes if the analyst is not going to be a user of your StrataBugs database. For further details see **Name dialog**.

Press the **OK** button. The new StrataBugs Name will be displayed in the Match analysts dialog.

Press the **OK** button to close the dialog.

Press the **Cancel** button to close the dialog but not save any of the changes you may have made.

Name dialog



To register a new StrataBugs Name or edit an existing one fill in the details on the lefthand side of the dialog. The first field should contain the **Full name**. Next enter a StrataBugs user ID, typically this will be the user's initials. Set the **Default discipline** by selecting one from the drop down menu.

If the person you are registering is to be a user of your StrataBugs database you need to complete the following User details fields.

Enter a **Login name** (or Oracle user ID if appropriate).

Enter a **Password** (and ensure that the user will remember it!). You will not be able to refer back to this dialog if the password is forgotten as they are encrypted once the details are saved.

You can display the analyses of each user in a different colour on a chart. To set a user colour select **Chart colour** by pressing the ellipsis (**...**) button to the right of the **Chart colour** field.

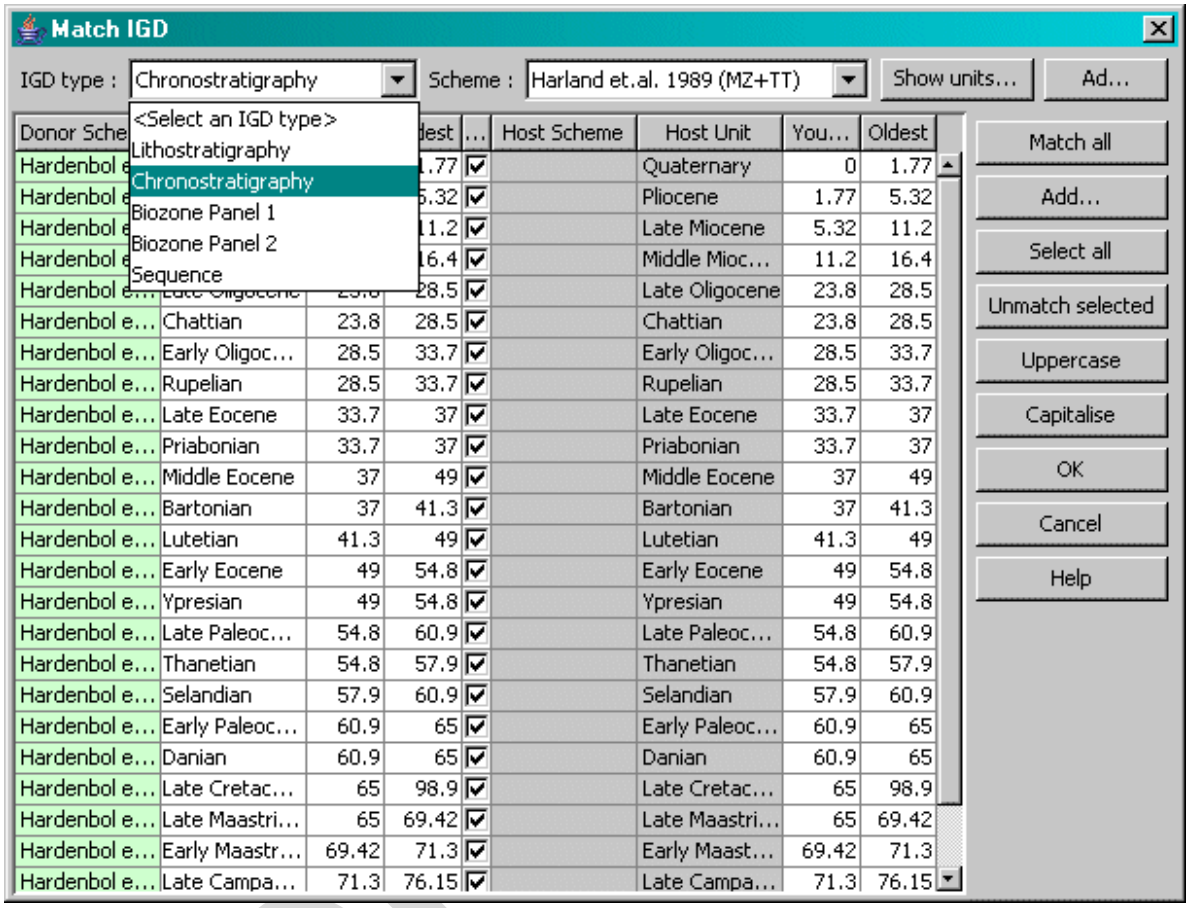
On the right hand side of the dialog is a list of **Privileges**. Check the items which you wish the new user to access. For instance you may wish to restrict a temporary assistant from deleting wells and adding new user privileges!

Note: *If a User ceases to be a User you should delete the Login name and Password.*

When you have completed the registration process press **OK** to save the new user's details of **Cancel**.

Match IGD dialog

The **Match IGD dialog** enables you to match IGD Schemes and Units in the data file with those already in your database. Note that the display will show all units in all wells in the dataset selected in the Data view pane.



Donor Sche					Host Scheme	Host Unit	You...	Oldest
Hardenbol e...			1.77	☑		Quaternary	0	1.77
Hardenbol e...			5.32	☑		Pliocene	1.77	5.32
Hardenbol e...			11.2	☑		Late Miocene	5.32	11.2
Hardenbol e...			16.4	☑		Middle Mioc...	11.2	16.4
Hardenbol e...			28.5	☑		Late Oligocene	23.8	28.5
Hardenbol e...	Chattian	23.8	28.5	☑		Chattian	23.8	28.5
Hardenbol e...	Early Oligoc...	28.5	33.7	☑		Early Oligoc...	28.5	33.7
Hardenbol e...	Rupelian	28.5	33.7	☑		Rupelian	28.5	33.7
Hardenbol e...	Late Eocene	33.7	37	☑		Late Eocene	33.7	37
Hardenbol e...	Priabonian	33.7	37	☑		Priabonian	33.7	37
Hardenbol e...	Middle Eocene	37	49	☑		Middle Eocene	37	49
Hardenbol e...	Bartonian	37	41.3	☑		Bartonian	37	41.3
Hardenbol e...	Lutetian	41.3	49	☑		Lutetian	41.3	49
Hardenbol e...	Early Eocene	49	54.8	☑		Early Eocene	49	54.8
Hardenbol e...	Ypresian	49	54.8	☑		Ypresian	49	54.8
Hardenbol e...	Late Paleoc...	54.8	60.9	☑		Late Paleoc...	54.8	60.9
Hardenbol e...	Thanetian	54.8	57.9	☑		Thanetian	54.8	57.9
Hardenbol e...	Selandian	57.9	60.9	☑		Selandian	57.9	60.9
Hardenbol e...	Early Paleoc...	60.9	65	☑		Early Paleoc...	60.9	65
Hardenbol e...	Danian	60.9	65	☑		Danian	60.9	65
Hardenbol e...	Late Cretac...	65	98.9	☑		Late Cretac...	65	98.9
Hardenbol e...	Late Maastri...	65	69.42	☑		Late Maastri...	65	69.42
Hardenbol e...	Early Maastr...	69.42	71.3	☑		Early Maast...	69.42	71.3
Hardenbol e...	Late Campa...	71.3	76.15	☑		Late Campa...	71.3	76.15

When the dialog first opens it will be blank. Select an IGD type from the drop down menu on the **IGD type** field and data of that type will appear. By default the IGD units will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order). If the units are linked to a scheme its name will appear in the **Donor Scheme column** and the **Keep informal term** checkbox (minimised by default) will not be checked.

To match these IGD units to a Scheme in your database select one from the drop down menu on the **Scheme** field at the top of the dialog.

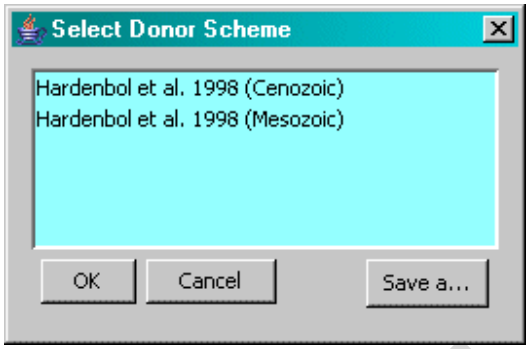
If you want to see the make up of the Scheme you have selected press the **Show units...** button. This will open the **IGD Scheme dialog**.

Having selected a suitable scheme press the **Match all** button to match the donor units in the data file.

If you do not have a suitable matching scheme for the donor data you can add the donor scheme if there is one in datafile. Press the **Add...** button to the right of the **Show Units...**

button. If the IGD units are associated with a donor scheme the **Select Donor Scheme dialog** will appear.

> ***Note:*** *The* ***Keep informal term*** *checkbox will by default be selected off for matched items. Units which you cannot, or do not wish to link to a Scheme in the database may be entered as "informal terms". You can either leave them like this or link them to a scheme at a later date. Unmatched intervals will not be discarded, just not linked to a scheme.*



Select a scheme name from the list and press **OK**.

If there is no donor scheme in the datafile and you are unable to match the donor units against an existing scheme, you can proceed and import the donor units as informal terms and link them later. Alternatively, cancel the import and create a new scheme then restart the import and select the new scheme. Highlight each unit in turn and press the **Add...** button. This will open the **IGD Scheme dialog** and the **IGD Unit dialog** simultaneously. Complete the fields in the **IGD Unit dialog** and press **OK**. The new unit will be added to the scheme in the **IGD Scheme dialog**. When you have entered all the units press the **Close** button.

The **Select all** button will select all the items on the list.

Unmatch selected will reverse any matches which you have made.

If you prefer your IGD terms to be entirely in uppercase, first highlight one or more units on the list and then press the **Uppercase** button.

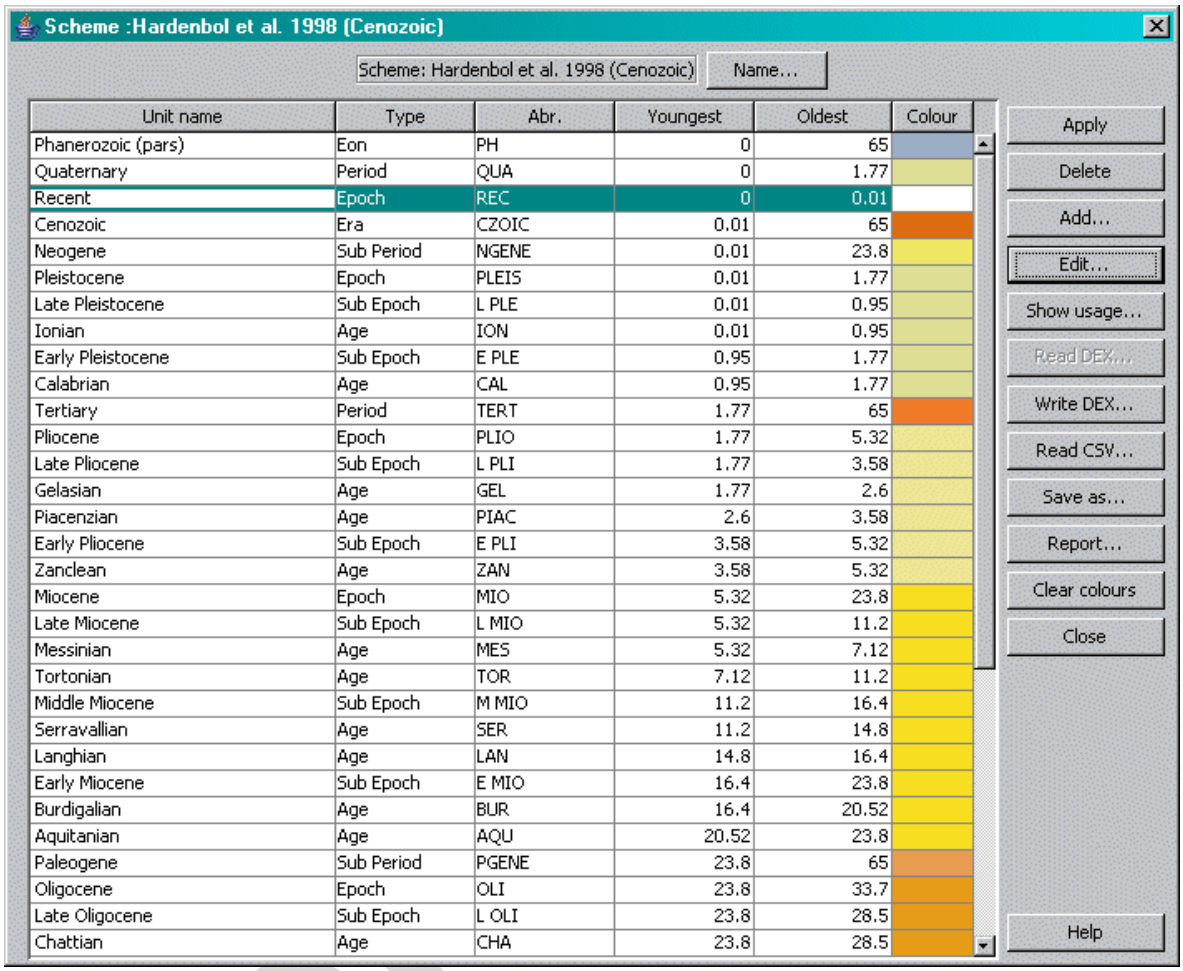
If you prefer your IGD terms to be capitalised (i.e. first letter of the first word is a capital letter, others are all lower case), first highlight one or more units on the list and then press the **Captalise** button.

Press the **OK** button to close the dialog. The changes you have made can later be saved.

Press the **Cancel** button to close the dialog but not save any of the changes you may have made.

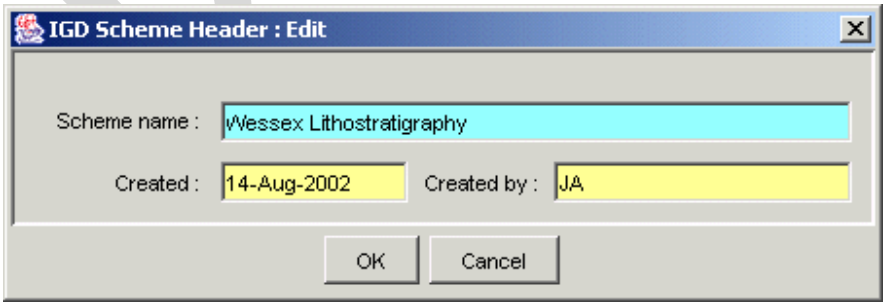
Scheme dialog

The selected IGD scheme name is displayed at the top of the **Scheme dialog**.



Unit name	Type	Abr.	Youngest	Oldest	Colour
Phanerozoic (pars)	Eon	PH	0	65	
Quaternary	Period	QUA	0	1.77	
Recent	Epoch	REC	0	0.01	
Cenozoic	Era	CZOIC	0.01	65	
Neogene	Sub Period	NGENE	0.01	23.8	
Pleistocene	Epoch	PLEIS	0.01	1.77	
Late Pleistocene	Sub Epoch	L PLE	0.01	0.95	
Ionian	Age	ION	0.01	0.95	
Early Pleistocene	Sub Epoch	E PLE	0.95	1.77	
Calabrian	Age	CAL	0.95	1.77	
Tertiary	Period	TERT	1.77	65	
Pliocene	Epoch	PLIO	1.77	5.32	
Late Pliocene	Sub Epoch	L PLI	1.77	3.58	
Gelasian	Age	GEL	1.77	2.6	
Piacenzian	Age	PIAC	2.6	3.58	
Early Pliocene	Sub Epoch	E PLI	3.58	5.32	
Zanclean	Age	ZAN	3.58	5.32	
Miocene	Epoch	MIO	5.32	23.8	
Late Miocene	Sub Epoch	L MIO	5.32	11.2	
Messinian	Age	MES	5.32	7.12	
Tortonian	Age	TOR	7.12	11.2	
Middle Miocene	Sub Epoch	M MIO	11.2	16.4	
Serravallian	Age	SER	11.2	14.8	
Langhian	Age	LAN	14.8	16.4	
Early Miocene	Sub Epoch	E MIO	16.4	23.8	
Burdigalian	Age	BUR	16.4	20.52	
Aquitanian	Age	AQU	20.52	23.8	
Paleogene	Sub Period	PGENE	23.8	65	
Oligocene	Epoch	OLI	23.8	33.7	
Late Oligocene	Sub Epoch	L OLI	23.8	28.5	
Chattian	Age	CHA	23.8	28.5	

Press the **Name...** button to the right of the Scheme name if you want to edit the Scheme name in the **IGD Scheme Header dialog**.



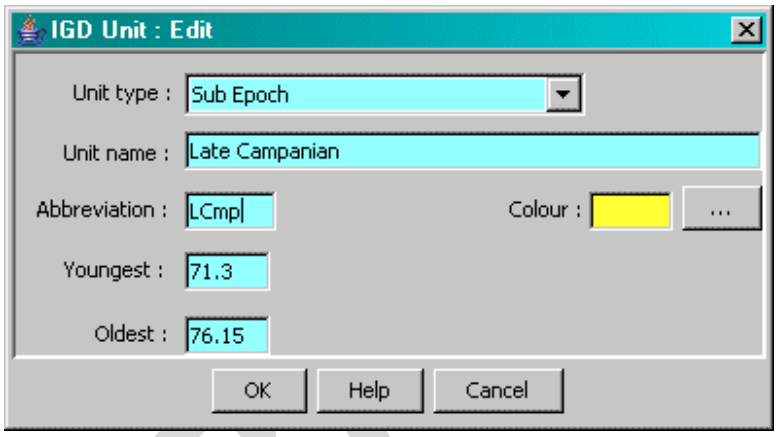
The main part of the Scheme dialog displays the units for a selected IGD data type and Scheme. By default the units will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order).

To match units in a datafile which have not been automatically matched to terms in your database using **Match all**, first highlight a unit in the dataset in the Match IGD dialog and then highlight one which you wish to match it with in the Scheme dialog and finally press the **Apply** button.

If you want to delete a unit, first highlight it and then press the **Delete** button. You will be asked to confirm your request.

To add a unit to a scheme first highlight a unit and then press the **Add...** button. The **IGD Unit dialog** will appear. Select the Unit type from the drop down list attached to the **Unit type** field. Type in a **Unit name** and an **Abbreviation** (this can be displayed as an alternative to the full name on charts if required). Enter boundary ages in the **Youngest** and **Oldest** fields. For Chronostratigraphic schemes these will probably be precise numerical values. For other types of scheme (e.g. biozones, lithostratigraphic units) where boundaries are likely to be diachronous, you should select an approximate numerical age. To add a colour for a unit press the ellipsis (**...**) button next to the **Colour** field and select a colour from the colour palette which appears.

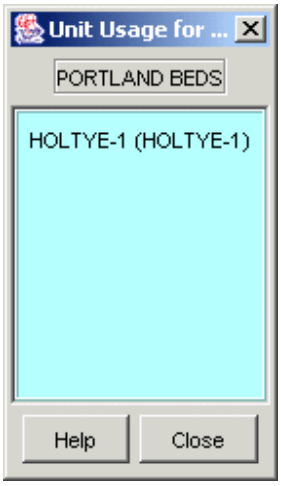
To edit a unit in a scheme first highlight a unit and then press the **Edit...** button. The **IGD Unit dialog** will appear displaying the details of the selected unit.



Edit the unit as you require. To edit a colour for a unit press the ellipsis (**...**) button next to the Colour field and select a colour from the colour palette which appears. Press the **OK** button to save the changes.

> ***Note:*** *Uniqueness of unit names, abbreviations and overlaps of units of the same type are checked at this point and you will be advised about any errors. The Scheme cannot be saved until any errors have been corrected.*

If you need to know in which wells in your database a particular unit has been used press the **Show usage...** button. This will open the **Unit Usage dialog** displaying a list of the wells in which the unit has previously been used.



To read data directly from a DEX file prepared for this purpose by another user of StrataBugs press the **Read DEX...** button and select the appropriate DEX data file. You cannot use this process to add new units to an existing. If unit colour definitions exist in the DEX file only those matching existing unit names in the scheme will be imported. Any existing colours will be overwritten. You can download schemes from the StrataData website and import them in the same way.

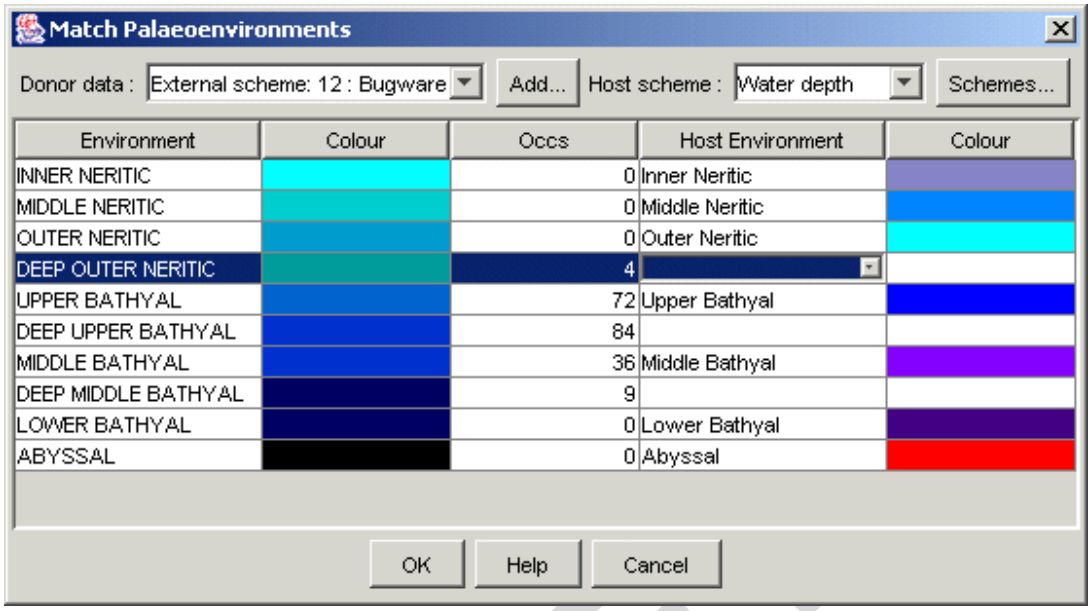
To save the Scheme information as a DEX file press the **Write DEX...** button and Save to an appropriately named data file. This can be read by another StrataBugs user.

To clear the colours for all the units in the scheme press the **Clear colours** button. You will be asked to confirm your request. You may wish to do this if you have used one scheme (by Writing and then Reading a DEX file) as the basis for another.

Press the **Close** button to close the dialog without losing the data which can be saved later.

Match palaeoenvironments dialog

The **Match palaeoenvironments dialog** enables you to match Palaeoenvironment Schemes and Units in the data file with those already in your database. Note that the display will show all units in all wells in the dataset selected in the Data view pane.



Display a dataset containing palaeoenvironmental data in your workspace and select **Palaeoenvironments** from the **Match** menu. The palaeoenvironmental scheme for the wells(s) in the workspace will be compared on the left while any matches will be displayed on the right. The matches are made on the basis of unit names.

If you have more than one Palaeoenvironmental scheme in your dataset, you need to match each in turn using the drop down list attached to the **Donor data** field.

If you want to add the new scheme to your database press the **Add...** button. The **Palaeoenvironmental scheme dialog** appears.

Press **OK** to add the scheme to your database. If you do this, of course all the units in the scheme will be matched. To read the contents of a file press the **Read...** button. To save the Palaeoenvironment scheme as a DEX file press **Save as...**.

To change the scheme to which the Donor data are matched select a scheme from the drop down menu on the **Host Scheme** field in the Match Palaeoenvironments dialog.

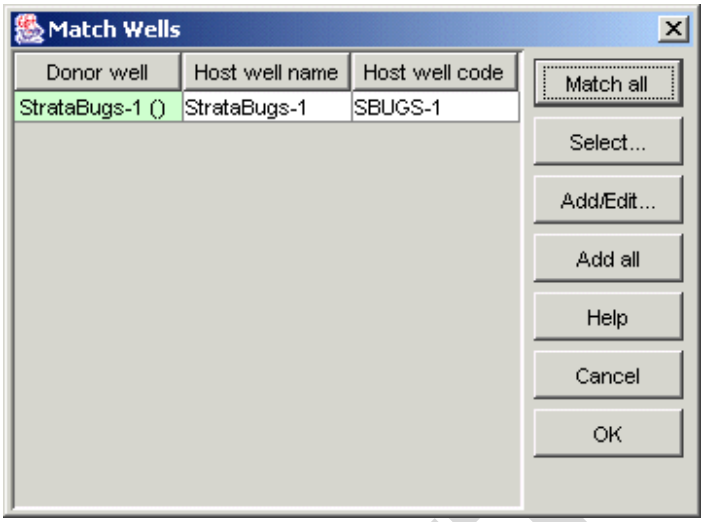
To check the units in a scheme, to edit an existing scheme or to add a new one to accomodate the Donor data press the **Schemes...** button. This will open the **Palaeoenvironment schemes dialog**.

Press the **OK** button to close the dialog. The changes you have made can later be saved.

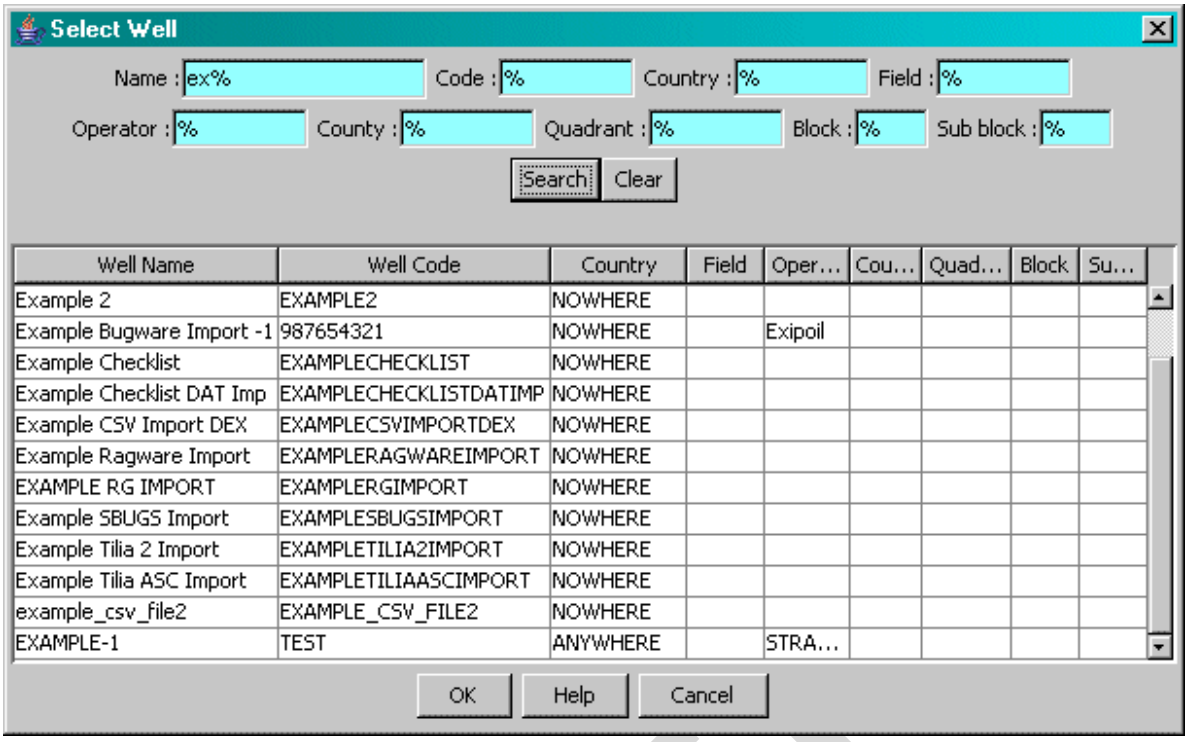
Press the **Cancel** button to close the dialog but not save any of the changes you may have made.

Match wells dialog

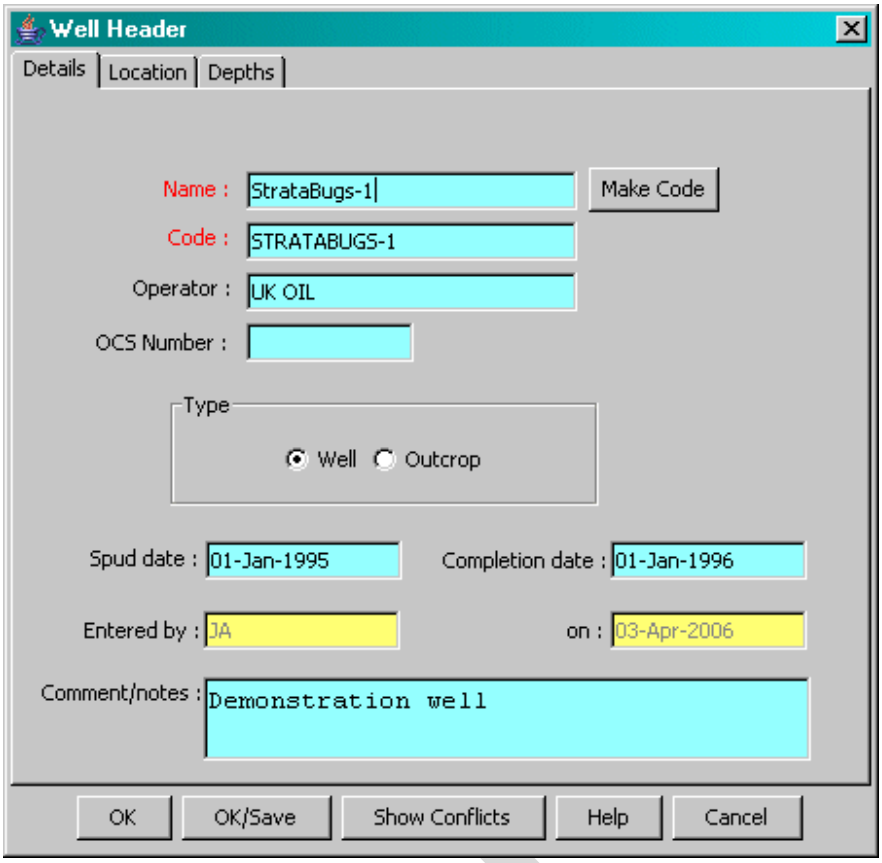
The Match wells dialog enables you to match wells in a data file with those in your database.



Press the **Match all** button and automatically the database will be searched for a matching well name for each Donor well (based on well codes) The matching Host well name and Host well code will be displayed. By default the IGD units will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order). Highlight the well name on the list and press the **Select...** button to search the database for a well with which you wish to match the well data in the data file. This does not have to be same name or code. The **Select Well dialog** appears.



If the well you require is not in your database you may add it. Highlight the well name on the list and press the **Add/Edit...** button to add a well to the database or to edit the details of an existing one. The **Well Header dialog** appears.



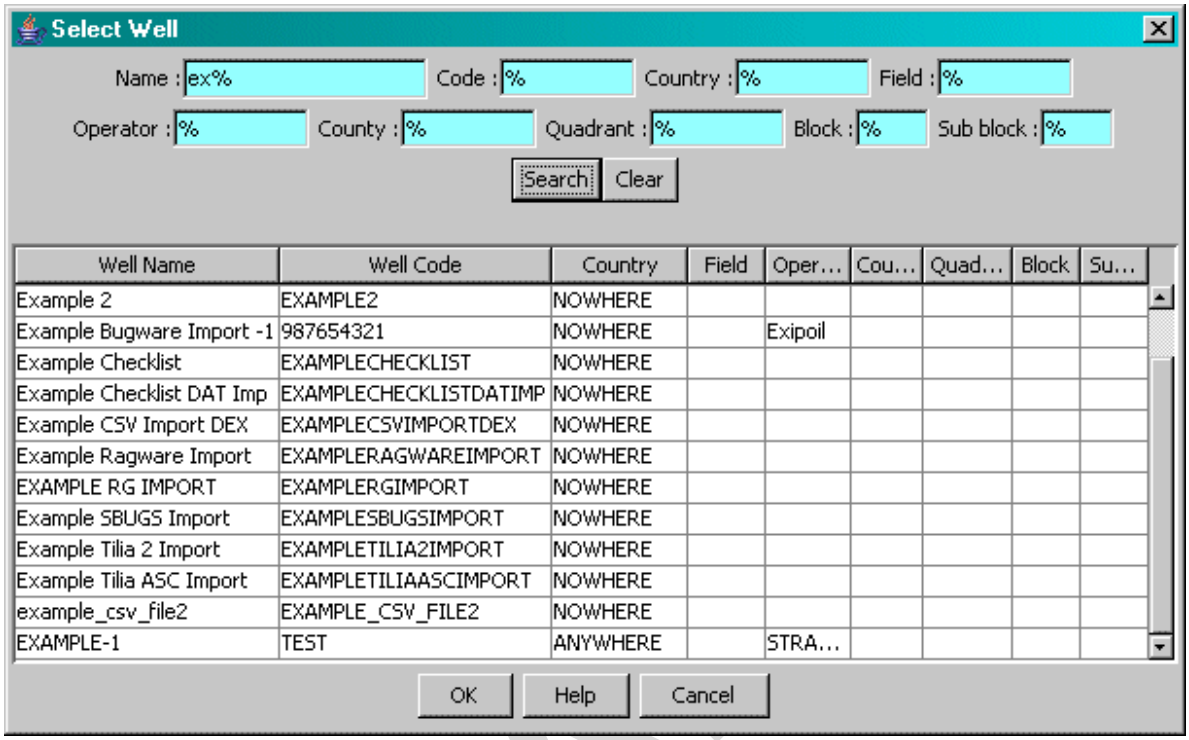
Press the **Add all** button to automatically add all unmatched Donor well names/codes to Host well name/code list.

> ***Note:*** *Donor well names will be matched against existing wells with identical well codes, others will be added as new wells.*

Press **OK** to save your selection, or exit the dialog without making a selection by pressing **Cancel**.

Select well dialog

The **Select well dialog** enables you to search for wells in your database. Use text strings and wildcards (%) in the Name, Code and Country fields to refine your search if necessary.



Press the **Search** button on this dialog to search the database for wells matching the search criteria. By default the well names will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order). If there is no suitable Host well in the database you may add one from the **Match wells dialog**.

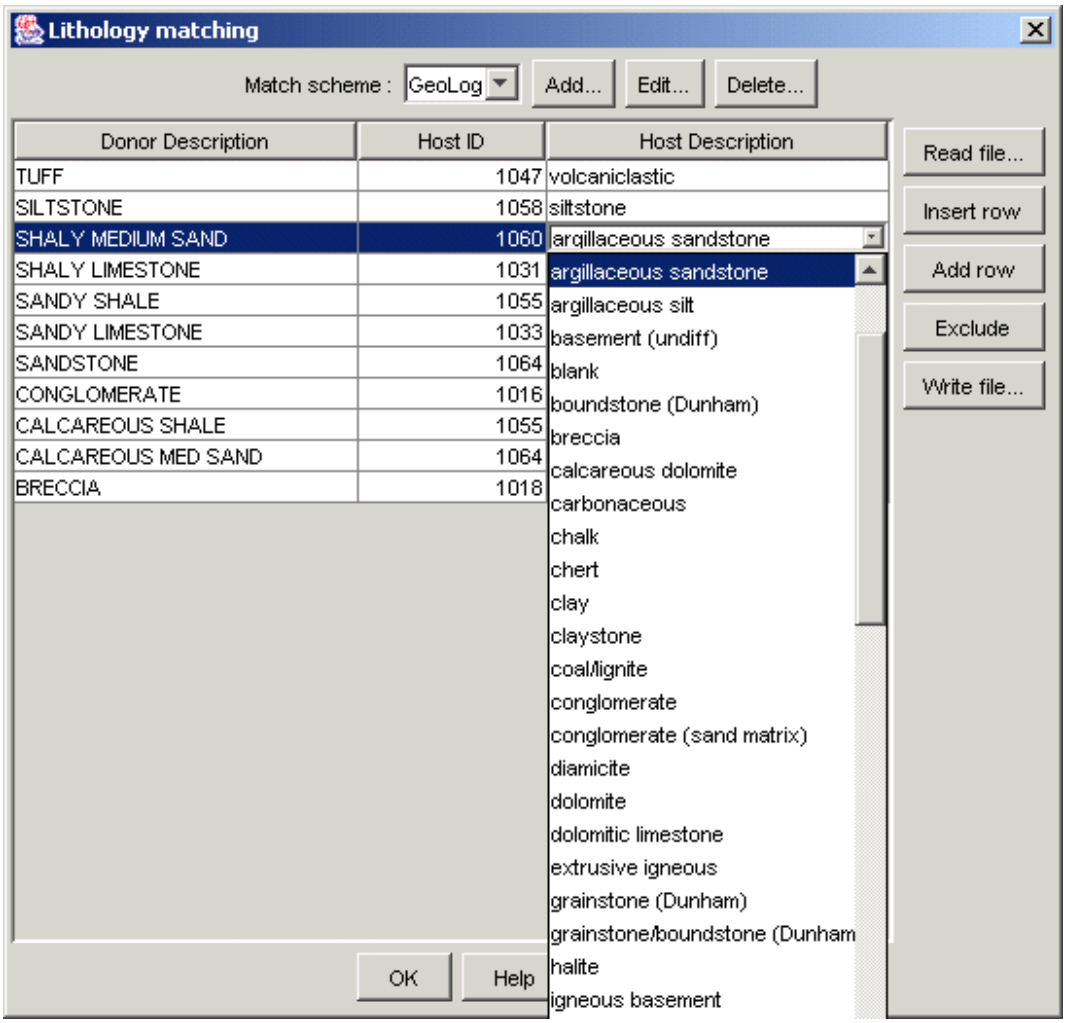
Press the **Clear** button to remove any previous search strings.

Press **OK** to save your selection, or exit the dialog without making a selection by pressing **Cancel.**

Lithology matching dialog

You may wish to use lithology data from sources other than other StrataBugs users. If you want to display lithology data from a datafile in your workspace so that your can later save it to your database or to a datafile, you must first create a match between the "Donor" lithotype dictionary and the "Host" StrataBugs lithologies. This is called a Lithology match scheme and you can create one by reading an existing dictionary from a datafile or from scratch. In either case the Lithology match scheme provides a "translation" of the terms in a Lithology datafile to terms recognised by your database.

To create a Lithology match scheme, select **Tools | Lithology matching** to open the **Lithology matching dialog**.



This dialog will be blank unless you have previously used **Index | File | Import lithology file...** in which case it will display the Donor and Host IDs and descriptions from the last import you made.

To read the contents of a previously created lithology dictionary file, press the **Read file...** button. The **Open dialog** appears. You have a choice to select OpenWorks lithology index files (.txt):

```
LANDMARK NAME STRING    ID

CONGLOMERATE    82
BRECCIA 83
GLACIAL TILL      110
COARSE SAND      63
BEDDED SAND      73
CROSS BEDDED SAND       74
SANDSTONE MC    141
MEDIUM SAND      52
FINE SAND        43
LITHIC COARSE SAND       40
LITHIC FINE SAND 41
LITHIC MEDIUM SAND       53

SILTY COARSE SAND        69
SILTY MEDIUM SAND        59
SILTY FINE SAND  48

CHERTY COARSE SAND       65
CHERTY MEDIUM SAND       55
CHERTY FINE SAND         44
CALCAREOUS CRS SAND      71
CALCAREOUS MED SAND      61
CALCAREOUS FINE SAND     50
DOLOMITIC COARSE SND     68
DOLOMITIC FINE SD        47
DOLOMITIC MED SAND       58
```

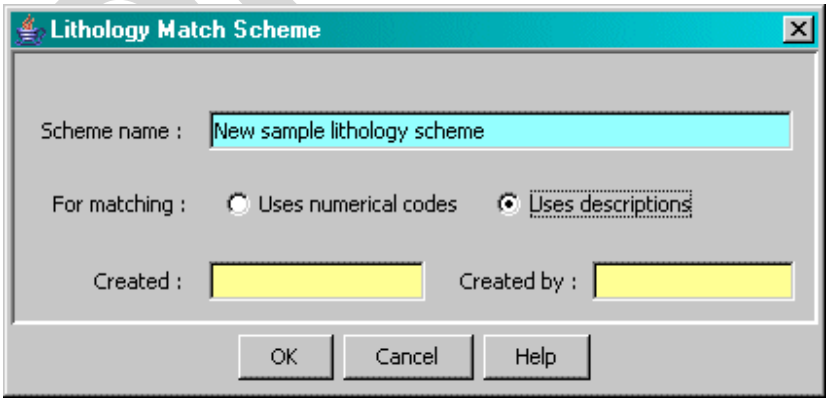
or CSV lithology index files(.csv):

EXAMPLE LITHOLOGY INDEX FILE

Navigate to the appropriate file and press **Open**. This will populate the **Donor ID** and **Donor Description** columns.

To select an appropriate match for each of the Donor descriptions click on the **Host description** field to activate a drop down menu of terms from the StrataBugs lithology dictionary. Select one which best matches the datafile abbreviation. The Host ID and Host Description fields will then be filled.

To construct a lithology match scheme from scratch you must first add a new scheme. To do this press the **Add...** button at the top of the dialog. The **Lithology match scheme dialog** appears.



Add the name of the new scheme and whether terms are to be matched on the basis of numerical codes or descriptions and press **OK** to return to the **Lithology matching dialog**.

To provide matching descriptions press the **Add row** button to activate the first row of a table. Type in the code (numerical matching only) and abbreviation of one of the datatypes from the datafile in the Donor descriptions field (this may be an abbreviation such as SST for "Sandstone"). To select an appropriate match for each of the Donor descriptions click on the **Host description** field to activate a drop down menu of terms from the StrataBugs lithology dictionary. Select one which best matches the datafile abbreviation.

To insert a row of data, first highlight the row immediately beneath the insertion point and then press the **Insert row** button and proceed as for **Add row**. If you want to remove a row of data from the matching process press the **Exclude** button.

Press the **OK** button to commit the changes to your database. You will be told how many values you have entered and asked if you want to commit these to yourdatabase. If you answer "yes" , the values in table you have just created will be saved in the selected scheme. Then from the **Data view pane**, highlight the Lithology data type for the current well, select **View | Selected data...** and press the **Read...** button. The **Open dialog** appears. Navigate to the appropriate lithology datafile and press **Open**.

This will read the contents of a lithology datafile, translate the terms and display them in your workspace. You can then save the data to your database or to a datafile.

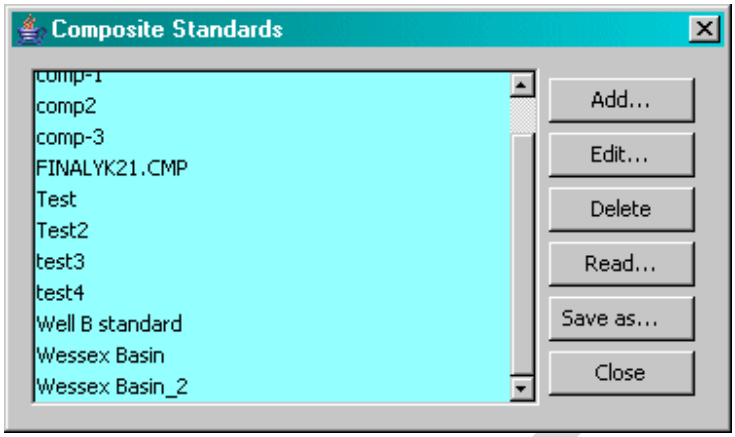
To edit the name and details of the selected scheme press **Edit...** to open the **Lithology match scheme dialog**. Edit the details and press **OK** to save the changes.

To delete the selected scheme press **Delete...**. You will be asked to confirm that you wiant to delete the scheme.

When you have finished entering your matches press the **Write file...** button if you want to create a text file of your translations which can be shared with other StrataBugs users.

Composite standards dialog

Composites Standards dialog displays a list of the existing composite sections in your database.



The **Add** button opens the **Composite Standard dialog.** Enter a name for the new composite section and a range of values in the **Section top** and **Section Base** fields. These can be in any units (Ma, CSU, etc). Enter the unit type in the **Units** field.

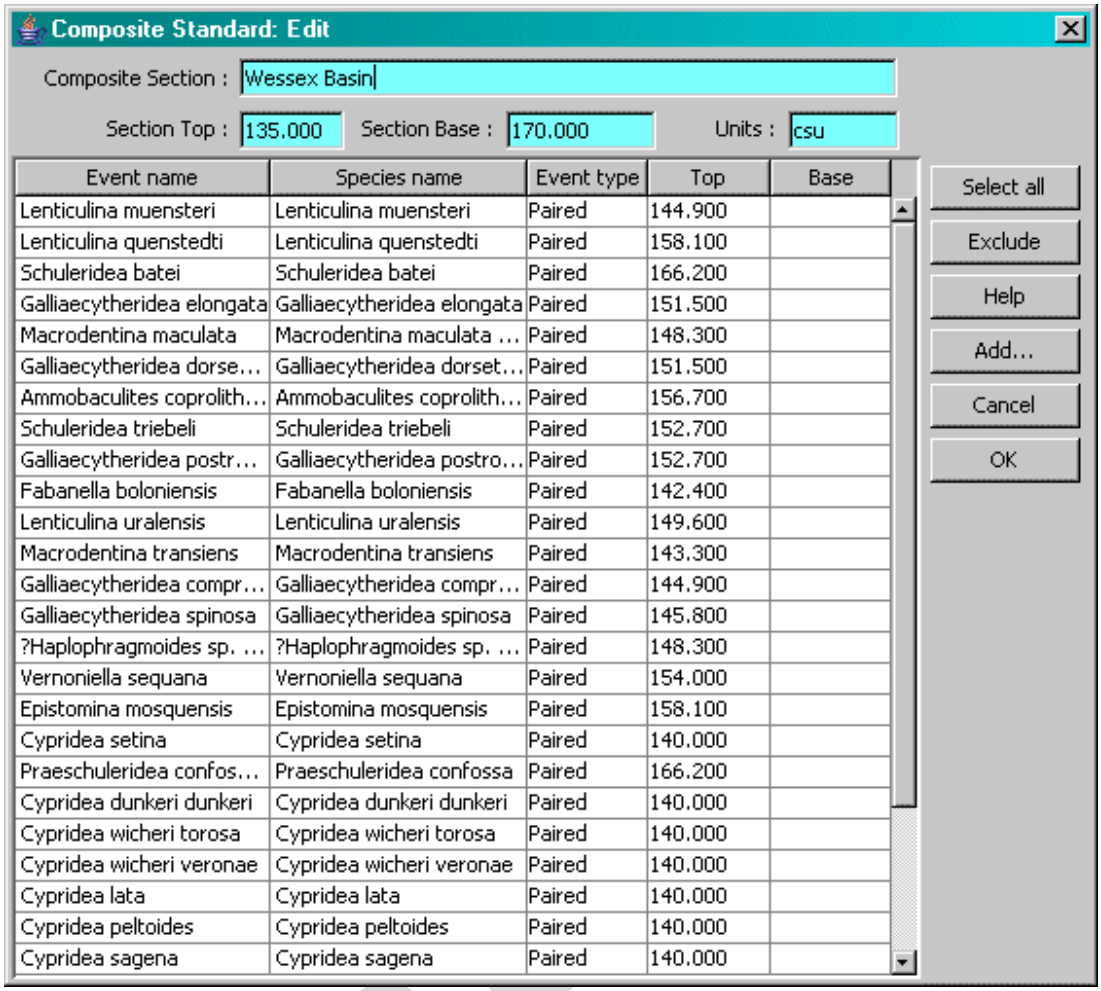
Edit also opens the **Composite Standard dialog** and enables you to edit an exisiting composite standard.

Highlight a composite standard on the list and press **Delete** to delete it from the database.

Read enables you to read a composite section from a DEX file. You will be required to match the taxa in the datafile against those in the database in the usual way (see **Match taxa dialog**). You will then be required to match events against those in your database using the **Match Events dialog**.

Press **Save as** to save the composite as a DEX file.

Press **Close** to close the **Composite Standards dialog**.

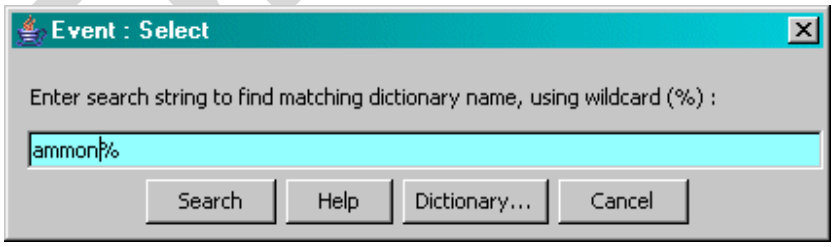


Select all will highlight all the events on the list.

Exclude to exclude selected taxa from the list.

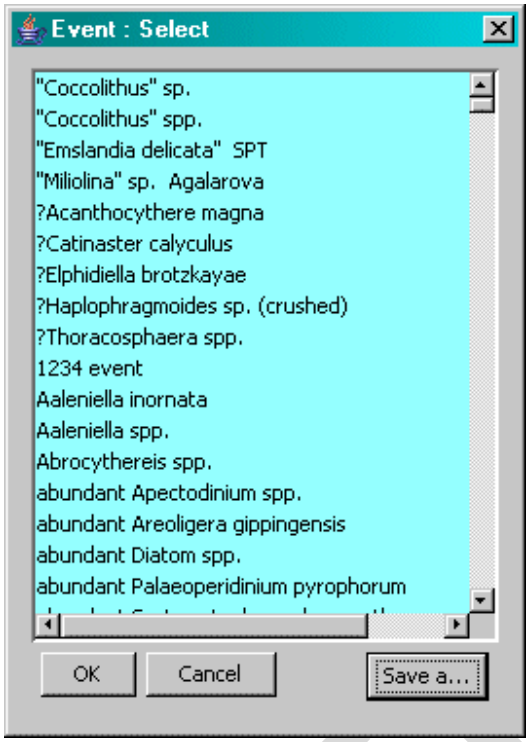
Add to open the **Event dialog** to add a new event to the composite.

OK or **Cancel**



Enter a string to find a taxon in your database and then press **Search** to open the **Select Event dialog**.

[these two dialogs have the same title - will be changed]



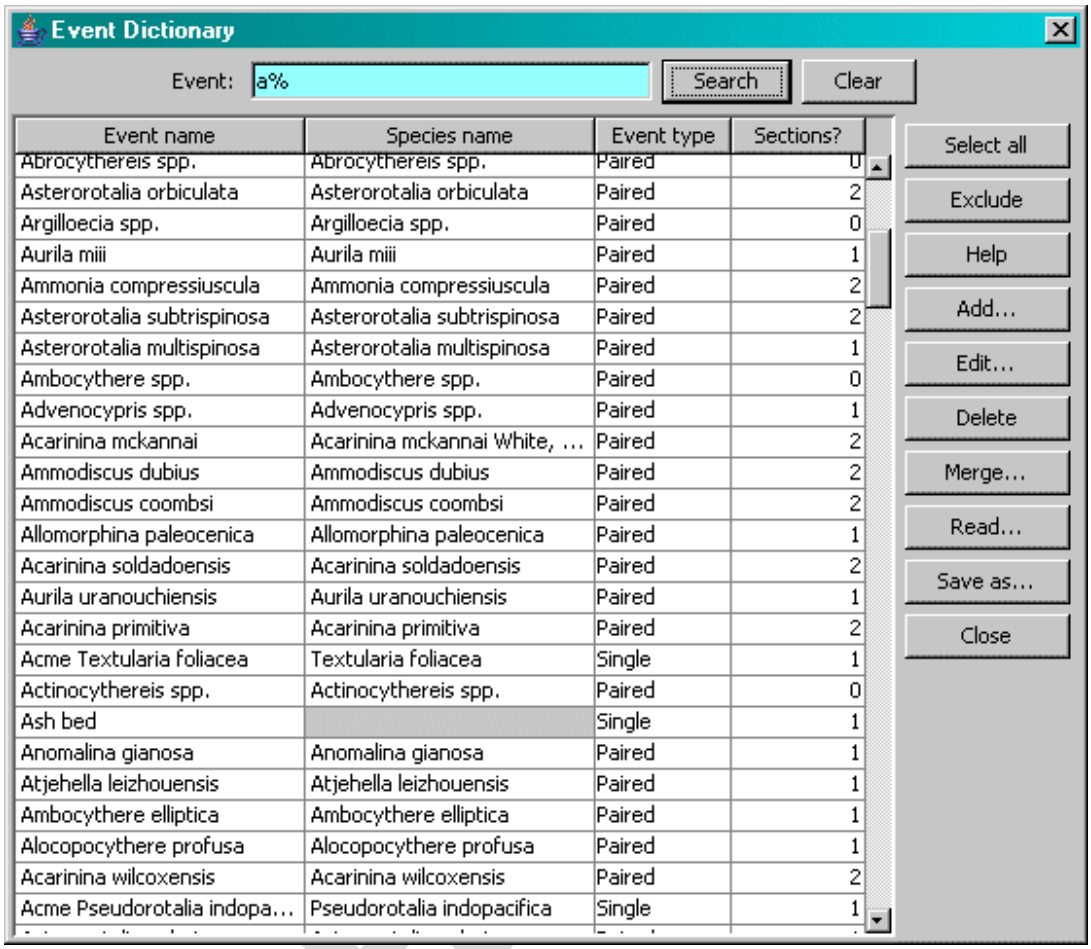
Save as... saves the contents of the list as a text file.

OK or **Cancel**

The **Dictionary** button opens the **Event Dictionary dialog**.

Event Dictionary dialog

Select the **Event dictionary...** item from the Tools menu and the **Event Dictionary** dialog appears.



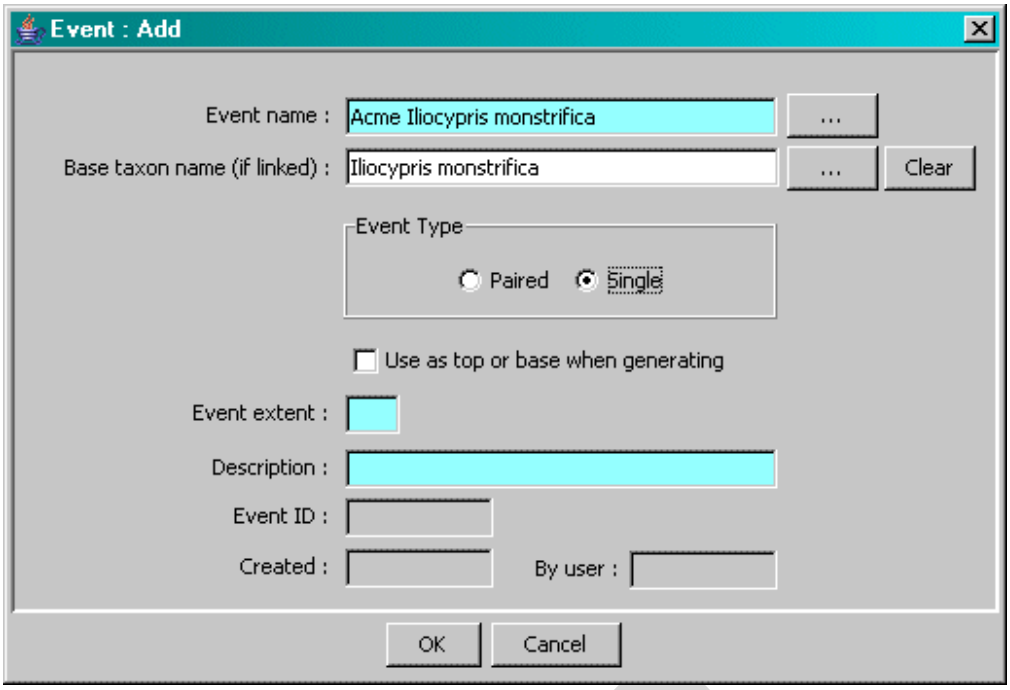
To display one or more event names in the **Event Dictionary dialog** enter a search string (partial text string with wildcard, %) in the **Event Dictionary** field. Press the **Search** to retrieve the event names. The event names will be displayed alongside the names of the species on which each of the events is based (if there is one), the event type (paired, single) and the number of sections in which each event occurs. By default the events will be sorted alphabetically. To sort them based on other columns in the table, select the appropriate table column header (Shift + select to reverse order).

To clear the search string in the Event Dictionary field press the **Clear** button.

Select all will automatically highlight all the events on the list.

To remove events from your workspace highlight selected events on the list and press **Exclude**.

Press **Add...** to open the **Event: Add dialog**. This enables you to add new events to the list and to the event dictionary.



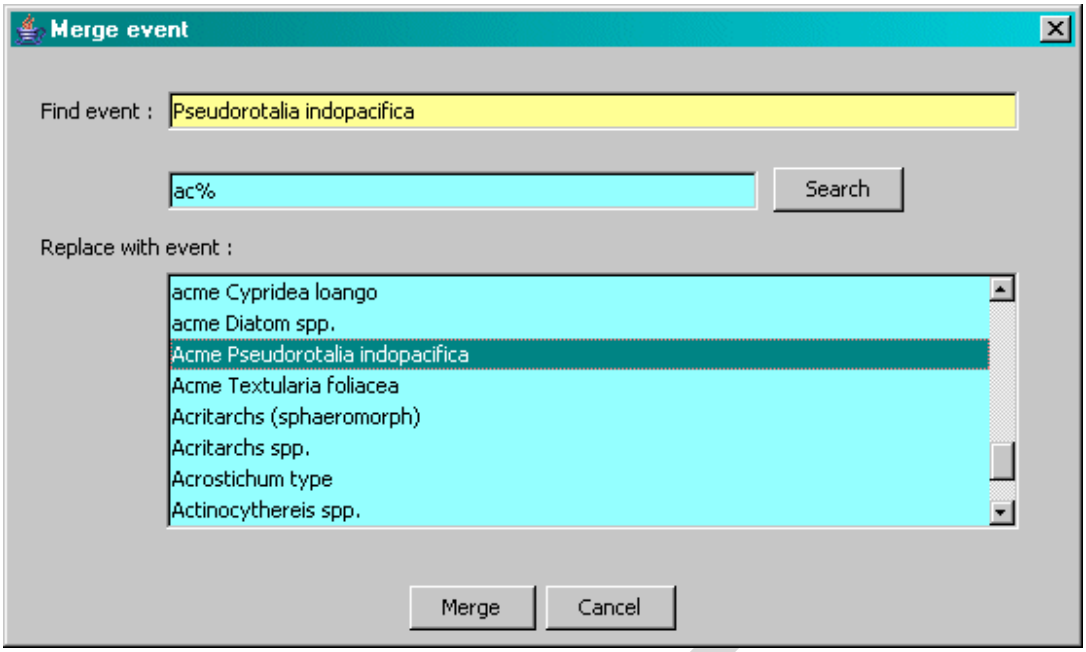
Use the ellipsis buttons (**...**) to the right hand side of the **Event name** and **Base Taxon name** (if appropriate) to create an event. These open the **Event: Select dialog** and **Select Taxa dialog**, respectively.

Press **Edit...** to open the **Event: Edit dialog**. This enables you to edit selected events on the list.

To delete an event from the dictionary first highlight it on the list and then press the **Delete** button.

> ***Note:*** *You will receive a warning if the event you have selected has been used in in any sections or composites. Once deleted the event is irretrievably lost.*

Select an event from the list and press **Merge** to open the **Merge Event dialog** which enables you to replace one event by another.



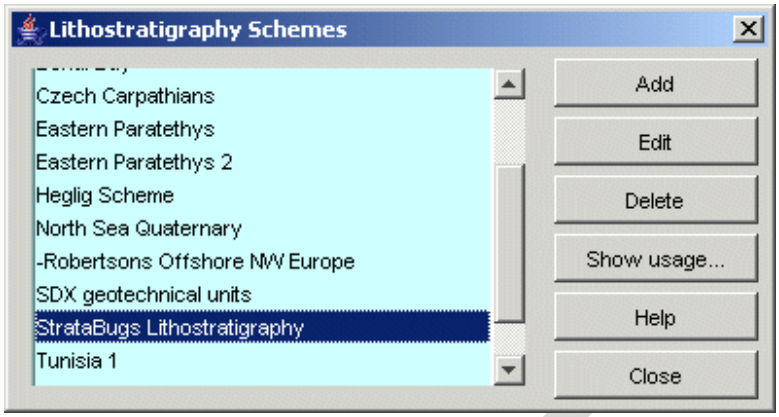
Press **Read...** to read a list of events from a DEX file and display them in your workspace.

Press **Save as...** to save the listed events in a DEX file.

When you have finished press the **Close** button.

IGD Schemes dialog

The **IGD schemes dialog** enables you to add an IGD scheme, or to edit or delete an existing scheme. To add a new IGD scheme press the **Add** button. The **IGD scheme dialog** appears. The example here is for the Lithostratigraphy IGD type.



To edit an existing scheme, first highlight it on the list and then press the **Edit** button.

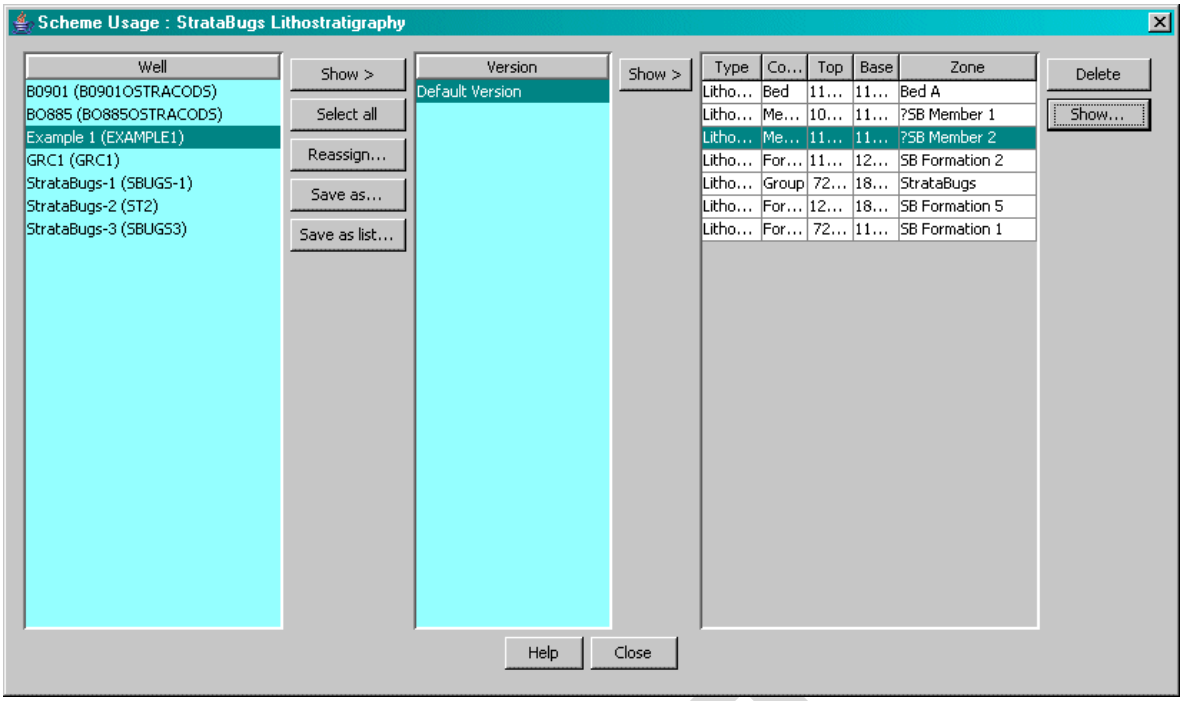
To delete a scheme, first highlight it on the list and then press the **Delete** button. If the scheme has been used in wells you will be warned that you cannot delete the scheme until you have reassigned data in these wells to other schemes.

To see how a scheme has been used in database wells press the **Show usage...** button. The **IGD Scheme Usage dialog** appears displaying a list of wells in which the selected IGD scheme has previously been used.

Press the **Reassign** button to change the assignments of all the IGD units in the selected well(s) to another scheme.

Press the **Save as...** button to save all the selected well(s) and well codes as a CSV file.

Press the **Save as list** to save all the selected wells as a **Well list**.



You can select a well and press the **Show>** button to the right of the well list to the see the versions of data available. Select a version and press the **Show>** button to the right of the version list to see the IGD units for that well and version. Press the **Show...** button to the right of the IGD units list to go to the **Show interval dialog**.

Press **Close** when you have finished with this dialog.

When you have finished with IGD schemes press **Close**.

Chart manager dialog

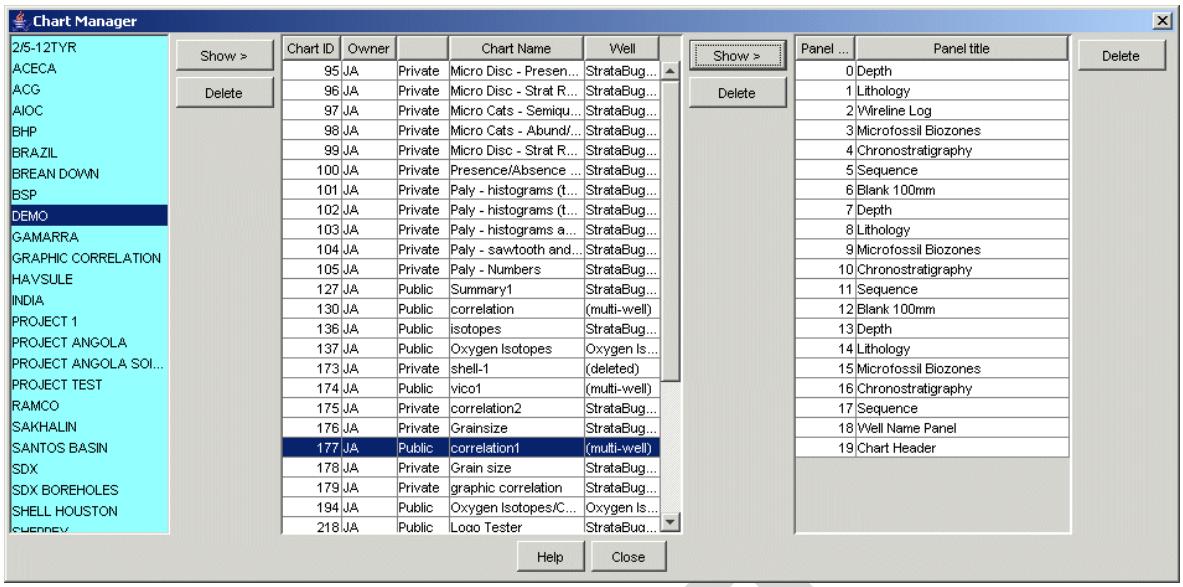


Chart Manager enables you to edit existing charts. You may wish to do this if you want to delete a number of charts or wish to remove a large number of panels from an existing chart. If a chart fails to load due to a corruption of a panel you can check which panel may be causing the problem from the information dialog which displays while the chart is opening and then delete it here.

To delete an entire project highlight the Project in the list on the lefthand side of the dialog and then press the lefthand **Delete** button.

To delete an entire chart from your database, first, highlight the Project in the list on the lefthand side of the dialog. Then press the lefthand **Show>** button to display a list of all the charts currently in the selected project. Press the centre **Delete** button to delete the chart.

To delete one or more panels from a chart, select the chart on the list and press the righthand **Show>** button to diplay a list of panels in the selected chart. Then press the righthand **Delete** button to delete the selected panel from the chart.

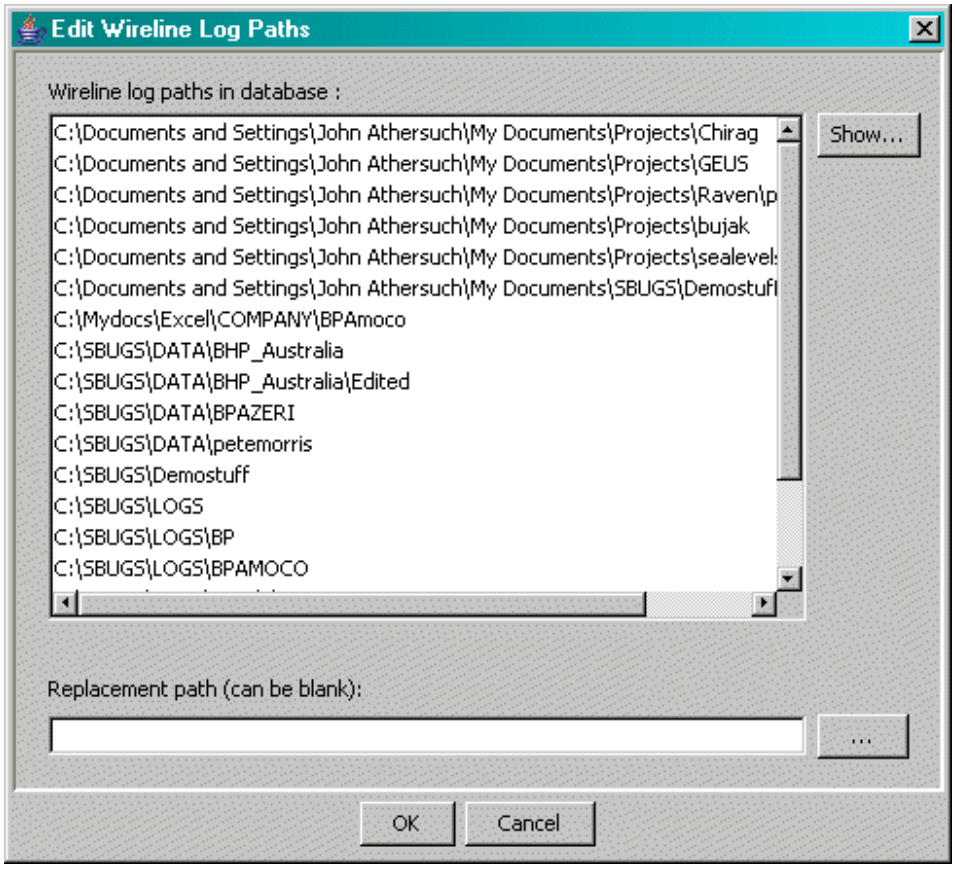
Edit Wireline Log Paths Dialog

The **Edit Wireline Log Paths Dialog** lists all the locations where logs in your charts are located. You can use this dialog to switch between locations if your logs reside in different folders.

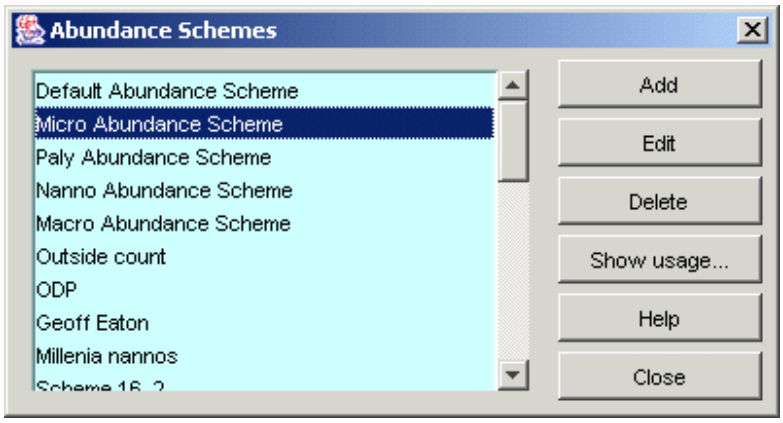
Select one or more to change them to the replacement path in the **Replacement path** field. You can browse for a suitable replacement folder by pressing the ellipsis button (**...**) next to the **Replacement path** field.

Select one and press **Show** (or double click on the item) to browse the folder that it points to. Selecting an item without providing a replacement path will result in the path being deleted from the list.

Note: *If the folder has been deleted since you originally selected it in Charts, the location will display your default Home location.*



Abundance Schemes dialog

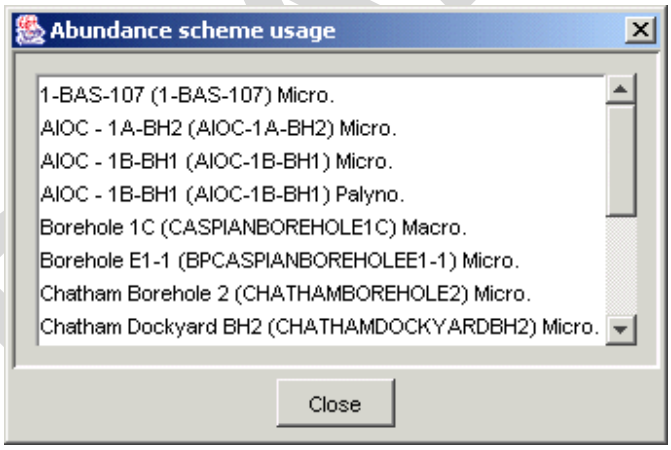


The **Abundance schemes dialog** enables you to add an abundance scheme, or to edit or delete an existing scheme. To add a new abundance scheme press the **Add** button. The **Abundance scheme dialog** appears.

To edit an existing scheme, first highlight it on the list and then press the **Edit** button.

To delete a scheme, first highlight it on the list and then press the **Delete** button. If the scheme has been used in wells you will be warned that you cannot delete the scheme until you have reassigned data in these wells to other schemes.

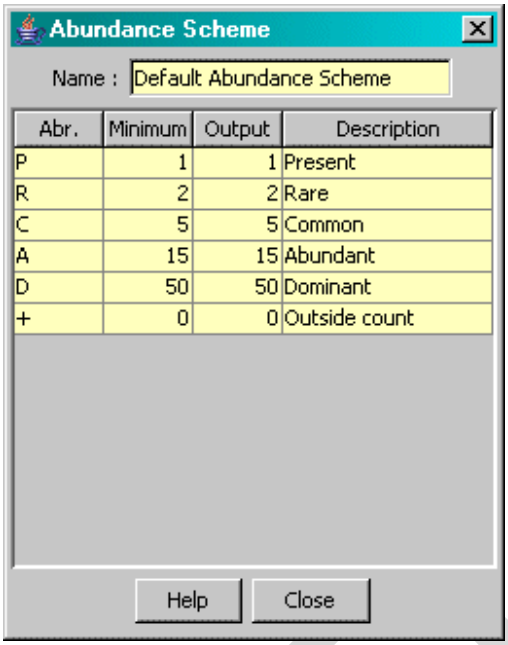
To see how a scheme has been used in database wells press the **Show usage...** button. The **Abundance Scheme Usage dialog** appears displaying a list of wells in which the selected abundance scheme has previously been used.



Press **Close** when you have finished with this dialog.

When you have finished with abundance schemes press **Close**.

Abundance Scheme dialog



The **Abundance scheme dialog** enables you to add new abundance schemes and to edit existing ones.

To add a new abundance scheme enter a name for the new scheme in the Name field then press the **Add** button to activate the first row of data fields. For each rank in the new scheme, enter an abbreviation, a minimum value, an output value and a text description in the appropriate fields. Press the **Add** button again to add the details of the next rank. To insert a row, first highlight the row beneath the insertion point and then press the **Insert** button. To remove a row, first highlight the row and then press the **Remove** button. When you have finished press **OK** to save the new scheme or **Cancel** to exit without saving the scheme.

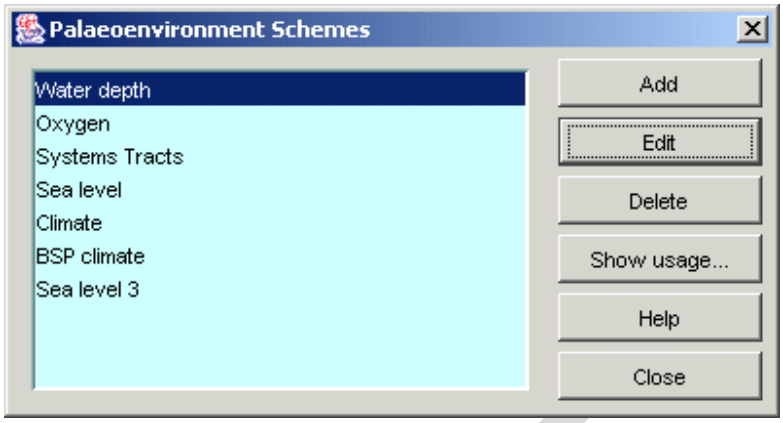
To edit an existing abundance scheme edit any of the data items following the same procedure as for adding a new scheme (see above). If the scheme you edit is in use you will be asked to confirm that you want to edit it.

To delete a row from a scheme, first highlight it on the list and then press the **Remove** button. If the scheme has been used in wells you will be warned that you cannot edit it until you have reassigned data in these wells to other schemes.

Palaeoenvironment Schemes dialog

The **Palaeoenvironment Schemes dialog** enables you to add a palaeoenvironment scheme, or to edit or delete an existing scheme.

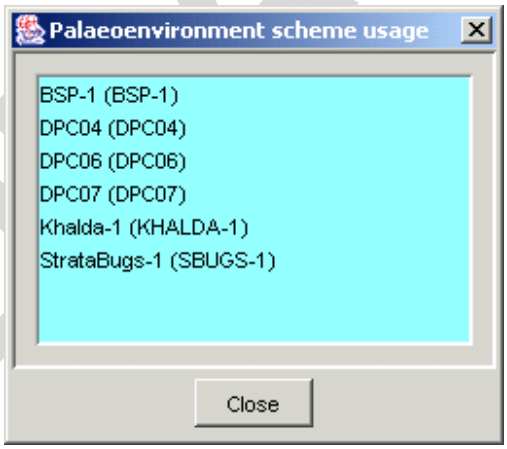
To add a new palaeoenvironment scheme press the **Add** button. The **Palaeoenvironment Scheme dialog** appears.



To edit an exiting scheme, first highlight the name of the scheme on the list and then press the **Edit** button. The **Palaeoenvironment Scheme dialog** appears.

To delete an exiting scheme, first highlight the name of the scheme on the list and then press the **Delete** button.

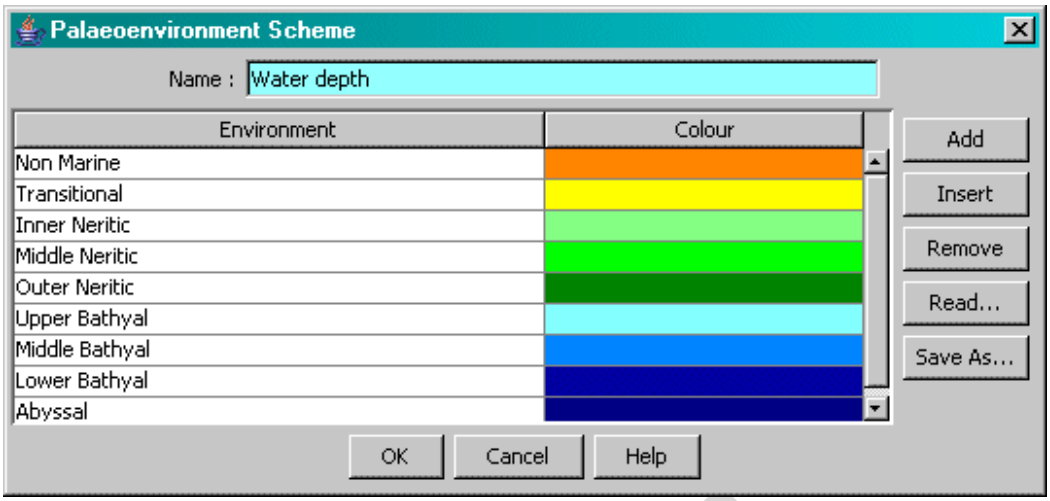
To see if the Scheme has been previously used and if so, in which wells, first highlight the name of the scheme on the list and then press the **Show usage...** button. The **Palaeoenvironment Scheme Usage dialog** will appear displaying a list of wells in which the selected schemes have previously been used.



Press **Close** when you have finished with this dialog.

When you have finished with palaeonvironment schemes press **Close**.

Palaeoenvironment scheme dialog



The **Palaeoenvironment Scheme dialog** enables you to add palaeoenvironment schemes. Any scheme can contain up to 15 units. These should be arranged in order on the list starting with the most proximal and ending with the most distal. These will appear in order from left to right on a chart.

To create a new palaeoenvironment scheme, first enter the name of the new scheme in the **Name** field. Then, press the **Add** button to create the first unit in the palaeoenvironment scheme. This should be the most proximal unit in your scheme. Enter the name of the unit in the **Unit name** field. Double click on the **Colour** field to the right and select a colour for this unit (default is cyan).

To insert a unit before an existing unit, highlight the unit below it on the list and press the **Insert** button.

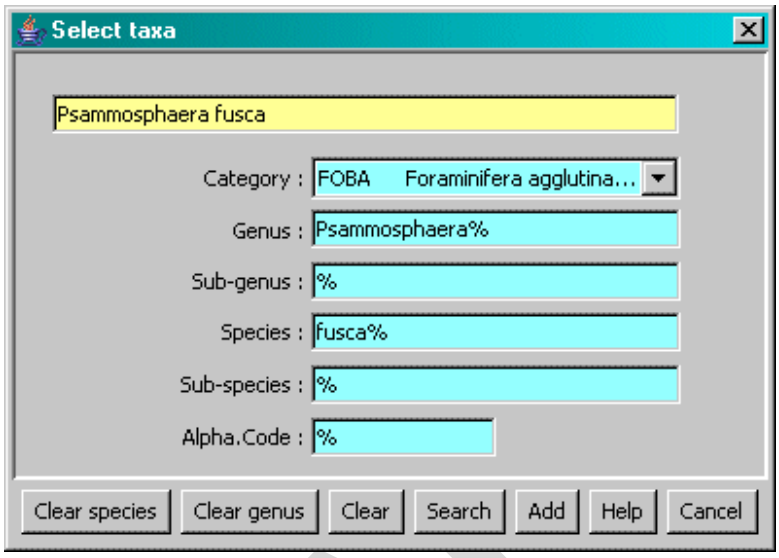
Press **Remove** to delete a unit from the scheme. If the scheme has been used in wells you will be warned that you cannot delete the scheme until you have reassigned data in these wells to other schemes.

When you have finished press **OK** or **Cancel**.

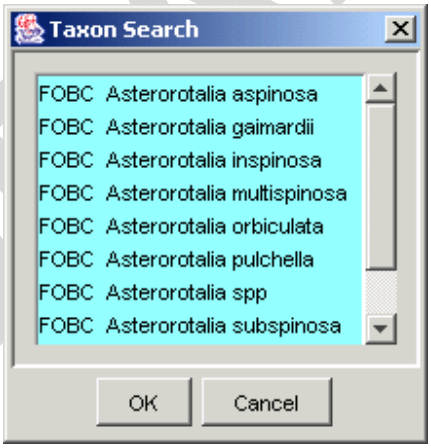
Taxon Dictionary

The **Taxon dictionary** enables you to add and edit taxon names in your workspace. First activate the Taxon browser by selecting **View | Browser panes** from the main menu. Then select the **Taxon dictionary** item from the **Tools** menu.

There are several ways of populating the Taxon browser pane. If you open a data file containing taxon names these will be automatically posted in the browser. To select individual taxa you should choose **Tools | Taxon dictionary | Select taxon...** and then search for the taxon using the **Select taxa dialog**.



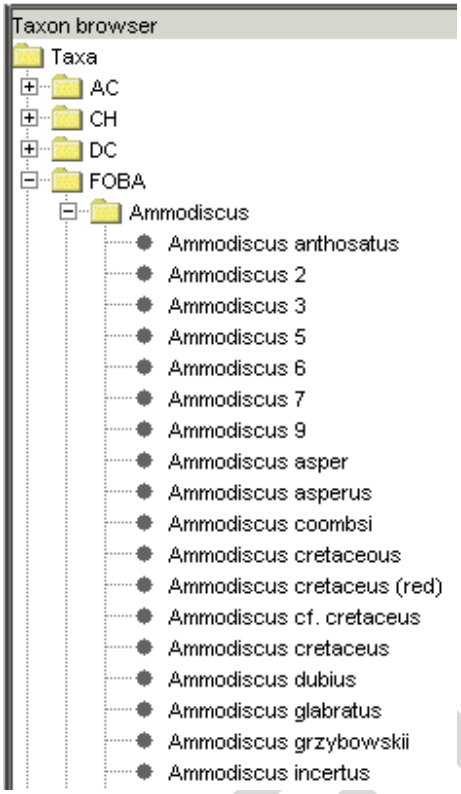
Select a name from the list in the **Taxon search dialog** and press **OK**.



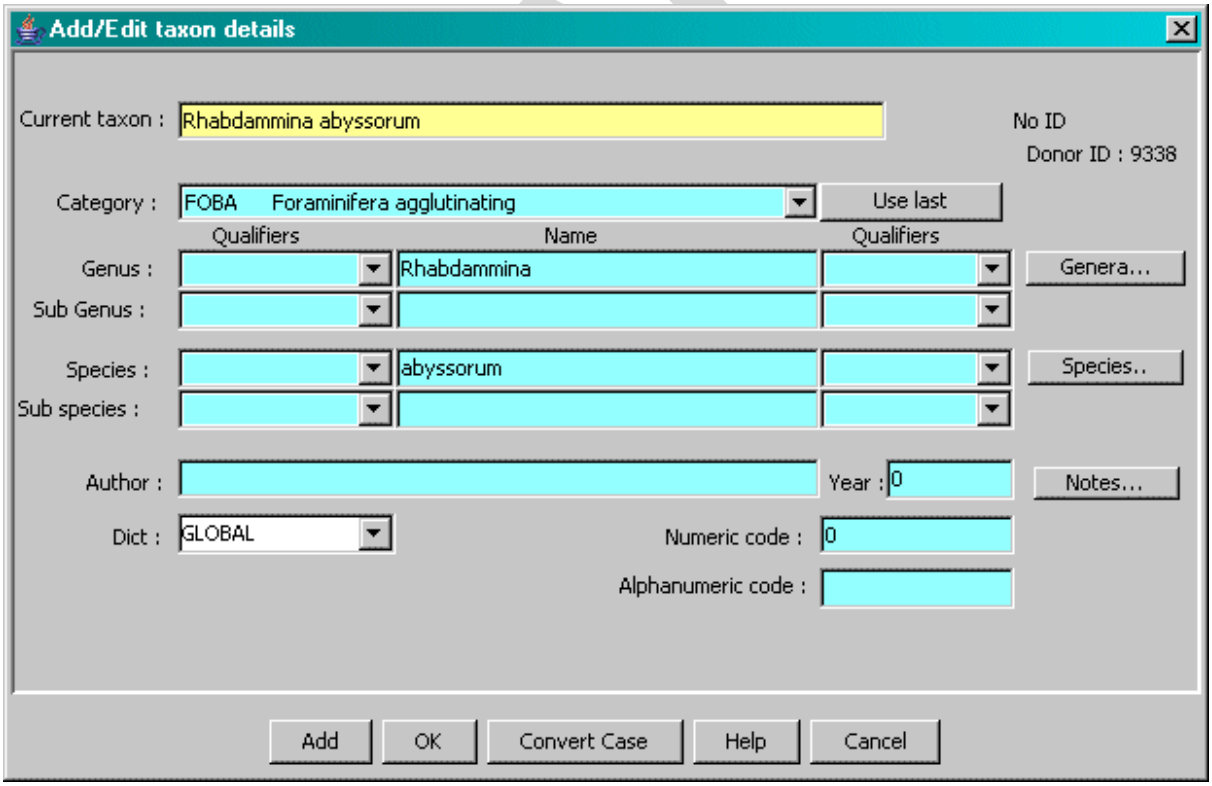
To display all of the taxa in your database select **Tools | Taxon dictionary | Load all taxa**.

> ***Note:*** *This may take several minutes if you have a lot of taxa in your database).*

Whichever method you use the selected taxa will appear arranged hierachically in the **Taxon browser**.



You can drill down to individual species names and view or edit them in the **Add/Edit Taxon details dialog**.



You can save the taxon names in your workspace in a number of different ways using other options on the **Tools | Taxon dictionary menu**.

Save in database will save the taxa displayed in your workspace to the database.

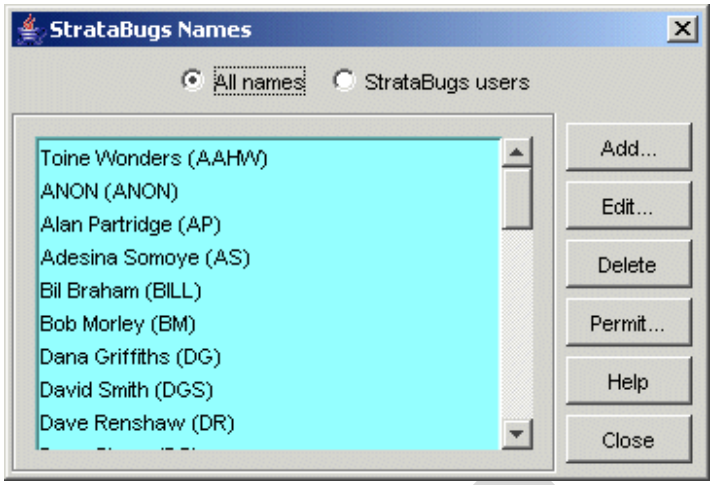
Save as enables you to save a list of taxa in a text file ordered by **Genus, Species, Category, ID number** or **Numeric code**.

Fix data

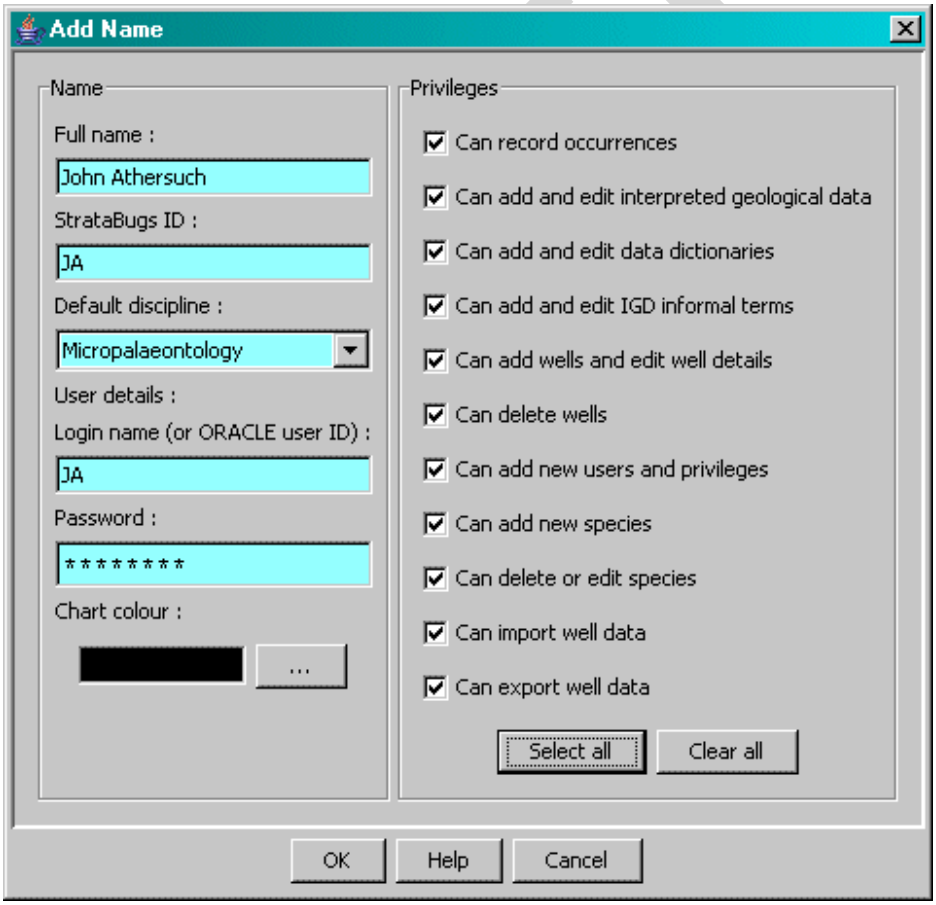
Create database objects

StrataBugs Names dialog

The **StrataBugs Names dialog** displays a list of the registered analysts users of your StrataBugs system.



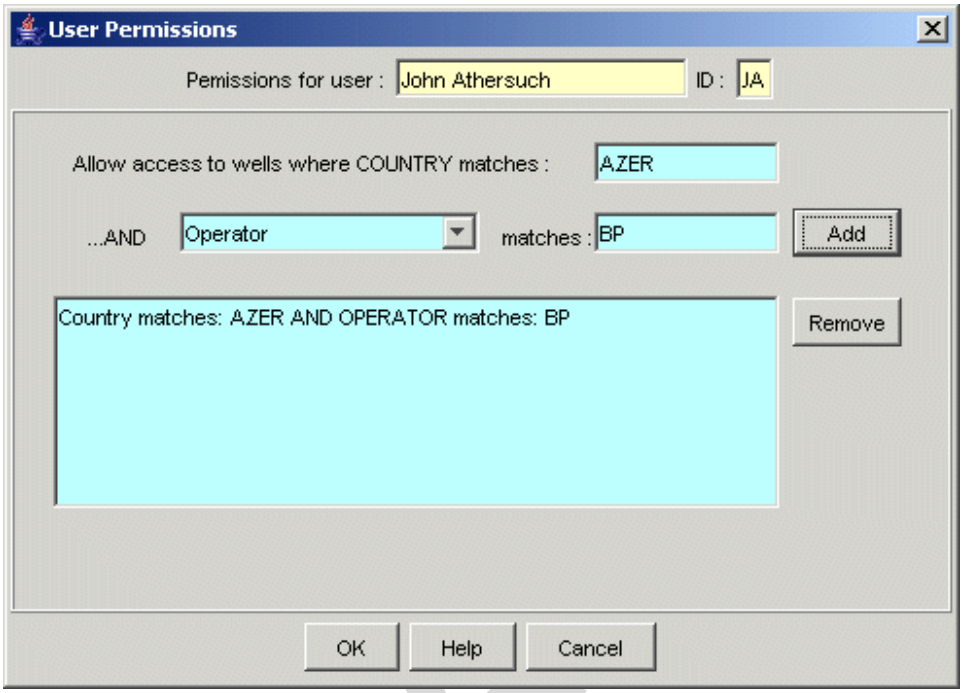
To add a new name press the **Add...** button to open the **Name dialog**.



To edit the details of an existing user first select a name from the list and then press the **Edit...** button. This will also open the **Name dialog** and display the current details of the selected user. The user's password will be encrypted.

To delete an existing user from the system first select a name from the list and then press the **Delete** button. Press **Close** when you have finished.

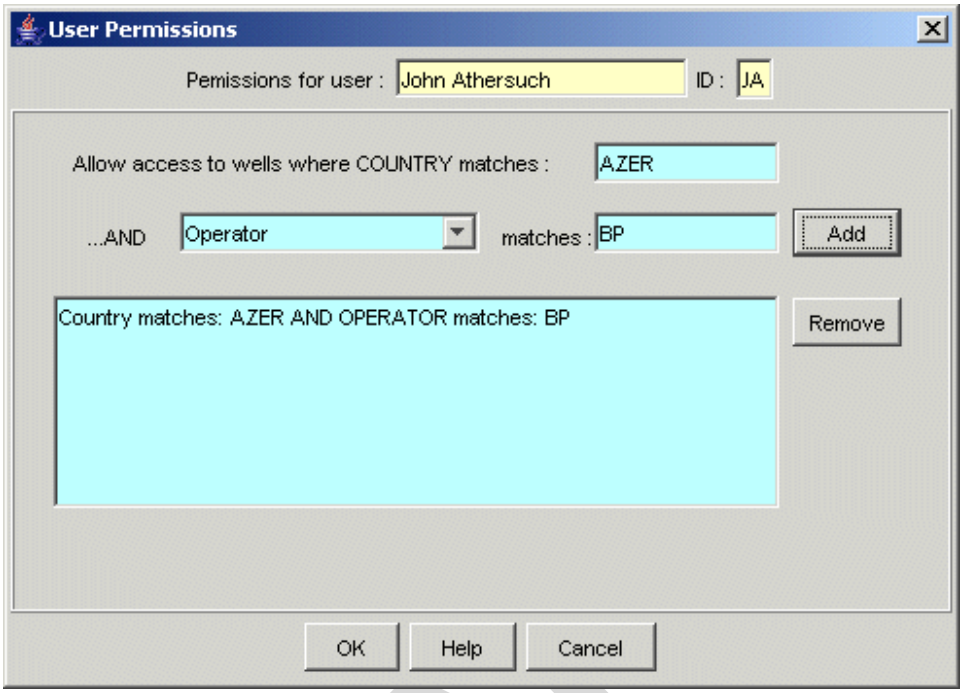
To restrict access of specific users to particular wells press the **Permit...** button to open the **User Permissions dialog.**



Enter criteria in the fields to define which wells a user can have access to.

User permissions dialog

To restrict access of specific users to particular wells press the **Permit...** button to open the **User Permissions dialog**.



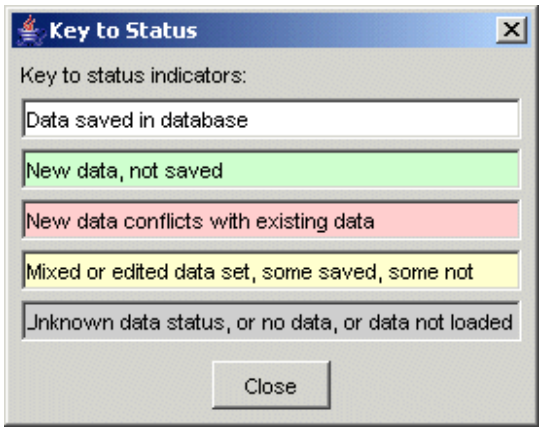
Enter criteria in the fields to define which wells a user can have access to. These should be a combination of a text string from a country name and the Field or Operator.

Database

Preferences

SQL tracing

Key to status dialog



In the main window of Organiser and in many of the dialogs data items are colour coded to indicate their current status. You can access this **Key to status dialog** from the Help menu at any time to check the status colours.

White - indicates that the data displayed in the workspace have been saved in the database.

Green - indicates that the data in the workspace have not been matched with data in the database and are regarded as "new".

Red - indicates a conflict between the data in the workspace and the data in the database. The data cannot be saved until the conflicts are resolved.

Yellow - indicates that some data items in a dataset have been saved and some not.

Grey - indicates that there are no data of that type available or that the status of the data is unknown or that the data have not been loaded to the workspace.

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