

Statewide Biological Database

Florida Department of Environmental Protection

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Introduction

Statewide system introduction

The statewide biological database application (BioDB) contains ecological information related to samples of aquatic flora (periphyton and phytoplankton) and fauna (macrobenthos and zooplankton). The database also handles associated physical/chemical information and toxicity bioassay data. Data is stored in Oracle tables on a server in Tallahassee and accessed by a relational database program called 4th Dimension.

The database administrator is responsible for maintenance of the information in the master taxonomic list. The reference tables and data uploads to BIOS are the responsibility of the assistant database administrator. Other laboratories or offices will have a group administrator who will be able to mark samples from his lab or office “complete” (i.e., available for retrieval), and add permanent information to the station, survey, and waterbody reference tables. People who need access to the information in this database will be given “retrieve only” permission, and may not add, edit, or delete any data.

How to get a user name and password

User names and passwords are added by the biological database administrator.

Getting started

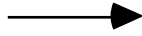
Starting BioDB

How to get the data base running:

- 1) Double-click on the database file to start 4D. On the Macintosh the file name will be named something like BiolDBxxx.x.x; Windows users will see a file called BLDBxxx.4DB (the x's represent the version number and will vary). The login screen shows an option for logging on to the “real” database or the “test” database. The test database is used for training and programming, and is only available at higher access levels. For most users, the “test” option will be grayed out and you will log in to the real database. Enter your username and password (case sensitive), and hit the Enter/Return key or click the **Login** button.
- 2) As login proceeds, a white message box will appear that will indicate what is being done.
- 3) If there is a new version of the Florida list (animal or plant, or both), you will be asked if you want to download it. You must select “Yes” to continue logging into the database, otherwise, the program will automatically quit.
- 4) After the Florida list status is checked or downloaded, the procedure checks for changes in the other reference tables. If changes are detected, those tables are automatically downloaded.
- 5) After everything is loaded, the white message box will disappear and you are ready to begin.

Deciding what to do next

Once you have successfully started the program, the screen will be gray with a logo in the middle and a menu bar at the top. We call this the “splash screen”.



If you have a small screen on your computer, you can click the “zoom box” (the small box in the upper right corner on the same line with the words “Florida Department of Environmental Protection”) and it will resize the window to fit in your screen. Or, click on the bottom right corner of the display frame and drag the window to the appropriate size



Selecting the various drop-down menu items on the top menu bar allows the user to navigate through the many functions of the program.

How to shut down the data base:

- 1) Quit out of 4D (File pulldown menu, select Quit). Windows users must be sure to use the Quit command and not the “X” in the upper right corner! Closing the program **does not** properly log out users from the database!
- 2) You will see a message box indicating that 4D is emptying work areas. At the end of this process, a dialog box will say that you are logged off of Oracle. Click **OK**.

Quitting BioDB

Conventions used in this manual and by the database

Buttons and Keyboard Equivalents

This manual assumes the user has a basic understanding of the Macintosh or Windows 95 operating system and is able to navigate through the fundamental operations.

Most of the windows displayed by this program have on-screen buttons. Here is a sample window:

Find Data for:

STORET Sta Name:

or

Station Nickname:

Date: ☐ > ☒ = ☐ <

Survey:

☐ **Restrict to Group...** 0

For wildcard search:

1) Underline character matches any single character

2) Percent sign matches a string of any length

Example: _R% would load all station codes of any length that have the letter R as the 2nd character.

Cancel **Find**

There are two buttons in the window above, one says **Cancel** and one says **Find**. Notice that the one labeled “**Find**” has a dark line around it. This means that if you press the “Enter” key on your keyboard, it is the same thing as clicking on the “**Find**” button. Please notice that you have both an “Enter” and a “Return” key on your keyboard. Pressing “Return” is not always the same thing as pressing “Enter”. As with all buttons, you may also click the button with your mouse.

Many of the buttons have keyboard equivalents. These key commands are different for the Mac and Windows versions of the database.



Mac



Windows

When you see the “⌘” or the “|” with a letter on a button, this means that Mac users can hold down the command key (that is the key with ⌘ on it) and Windows users can press the Ctrl key along with the letter to execute the button. This is the same thing as clicking on that button.

If you get stuck or confused and you want to put things back the way they were when you started, click on the “**Cancel**” button. “Cancel” means “ignore the changes I made in this window”. Most windows have a “**Cancel**” button. Even though it is not displayed on the key itself, pressing ⌘. (Mac) or |. (Windows) is the same thing as pressing on the “**Cancel**” button.

Searching using Wildcards

Throughout the program, you may need to search for a variety of items (STORET station codes, water body names, etc.). The “%” character can be used as a wild card, to substitute for any part of a text string. For example, to call up a list of all STORET station codes starting with “200”, type in “200%” and press “Enter/Return”. A select box will appear containing a list of the associated codes from which to choose.

For some modules in the program, the “@” sign is used as the wildcard. There will always be a message box on screen that will state which wild card character to use.

Station Nicknames

When this database was started, we loaded 5,280 STORET station codes into the station reference table. This database identifies a station by its STORET number, by a nickname, and by a DEP ID number. The latter two have nothing to do with STORET. For the 5,280 stations initially loaded, the computer assigned a nickname that has the first 5 characters of the county name followed by a sequential number. So the nickname for the first STORET station in Pinellas county that the computer found became “PINEL1”. For this reason, counties with 4 or fewer letters (like Lee and Leon) have a space in their nicknames (“LEE 1”).

Since that initial station loading, approximately 1500 additional stations have been entered into the station reference table. When a new station is entered, the user can choose a nickname, up to 10 characters. Often the nickname becomes useful when searching for a group of stations that were sampled for a particular project. For example, the user may give several stations that were sampled for “Project XYZ” nicknames like “XYZSta1”, “XYZSta2”, and “XYZSta3”. A single search can be performed where all of the stations with nickname “XYZ%” will bring up all of the stations for the project.

Because of this usefulness in grouping stations used for different sampling goals, station nicknames are often changed. The same station is often used for different projects over time, and it is not unusual to change the nickname to correspond with its most current use. It is not a good idea to change the STORET station code, however, since it must match with an existing station in the federal database.

All the data are stored with DEP ID numbers. Stations, taxa names, gear types, and many other things have these ID's. These ID's are sequentially assigned by the computer and cannot be edited by anyone using this database program. This means that you can change nicknames and regular names and not affect the data that use them. These “long” names are stored in a place where the computer can look them up when they are needed. If this is confusing to you, don't worry about it. This is just to let you know that you can correct misspellings without harming any data already entered.

How to enter and edit data – Biological Database

Query the Database for Stations

- 1) Before a sample can be set up in the database, its STORET station location must be established in the station reference table. The splash screen should be displayed on the screen (look on page 7 to see what a splash screen looks like). Go to the Reference Info menu:

Reference Info
Stations
Surveys
Sample Gear
Feeding Groups
Collectors
Identifiers
County Lat/Lon
Station Levels
Water Bodies

- 2) Select Stations. The following **Station Information** screen will be displayed:

Florida Department of Environmental Protection			
Station Information			
STORET Station	Nickname	Station Description	DEP ID
25020056		SADDLE CK CANAL @ OLD W'NTR HVN BT'W HW'Y	6461
25020011		Whidden Creek @ Old Bowling Green Rd	6457
25020038		BEARS BR @ US HW'Y 17	6460
25020047		Peace Creek Canal @ Gandy Bridge	6458
25020235		LAKE LENA RUN @ THORNHILL RD	6459
24030057	ZEPHYRTST	Zephyrhills River, TP38	5898
WCA124	Z4	WCA1, 6.38 km E-SE of S-6 Pump Station	6363
WCA123	Z3	WCA1, 4.0 km E-SE of S-6 Pump Station	6362
WCA122	Z2	WCA1, 1.94 km E-SE of S-6 Pump Station	6361
WCA121	Z1	WCA1, 0.69 km E-SE of S-6 Pump Station	6360
WCA120	Z0	WCA1, .69 km ESE of S6 Pump Station in L39 Canal	6380
19020060	YULEETST	Unnamed tributary to Lumber Creek	6776
19020059	YULEEREF	Unnamed tributary to Nassau River	6775
22020017	YONCKREF	Yon Creek @ SR12	7056

Number of stations displayed above = 6826			
Find by criteria %F	Show selected stations	Sort %S	Done %D
Add new station %N	Show all stations	Print %P	
Download entire station table			

One way to find out if the station of interest has been established would be to scroll through the nearly 7,000 entries, but this is rather labor intensive. Another option is to use the **Sort** key to arrange the stations in a more easily viewed order. It is usually faster to click on the **Find by Criteria** button (or use the **Ctrl-F** or **⌘-F** key sequence), which will display the following screen:

Criteria for Finding Stations

STORET Station Code Station Nickname Water Body	County Station Level Type Survey	
Water Bodies that match	Water Bodies to retrieve	Surveys that match
Cancel	Find stations by lat/lon	Find Stations by criteria above

- 3) You can select stations based on several criteria: STORET station code, station nickname, waterbody, county, station level type, or survey.
 - a) To retrieve by STORET station number or station nickname, enter the item in the appropriate field. You can also enter the first part of the STORET number or nickname; in this case no wildcard is required. Click the **Find Stations by criteria above** button.
 - b) If you are searching by water body and aren't sure of the entire name of the water body, you can search by entering in a partial string. For example, if searching for the water body "Bear Creek", you only need to type in "Bear" and hit the "Enter/Return" key to bring up a listing of all water bodies beginning with "bear". Double click on the water body of interest to place it in the "Water Bodies to retrieve" box. (You can search for multiple water bodies, adding each one to the retrieval box by double clicking on the water body.) Click the **Find Stations by criteria above** button.
 - c) To search by county, enter the first few letters of the county. If there is more than one county to choose from, a box will be displayed which allows a choice. If only one county matches the string entered, that county will be placed in the field. Click the **Find Stations by criteria above** button.
 - d) Clicking on the search by Station Level Type will bring up a pull-down menu containing the station attributes corresponding to the STORET system. Make a choice and click the **Find Stations by criteria above** button.
 - e) If a previous sample has been established at a station then it was associated with a survey. Enter the first few letters of a survey in the survey field. This will fill in the box below it with any surveys that match your entry. Select the one you want and click the **Find Stations by criteria above** button.
 - f) The above criteria can be combined, resulting in a more restricted search with a shorter list of stations. **When the search combines STORET station or nickname with survey, it is necessary to use a wildcard (%) when entering only part of the STORET number or nickname.** This search is different because the database must query the sample table in Oracle, which is now downloaded during login.

- g) Another option for creating a list of stations is to define a rectangle on a map using latitude and longitude coordinates. Click the **Find Stations by lat/lon** button to view the screen at right. If you know the coordinates for the upper left and lower right corners you can type the degrees and minutes in the appropriate fields. To select an area on the map, click the box labeled “Selecting Lat/Lon on Map”. The area directly below this tells you whether you are to click on the upper left or lower right corner of the rectangle. Once you have defined the geographic range by clicking on the lower right, you must deselect the checkbox, which will make the OK and Cancel buttons available again. Click OK and the program will find the stations located within the specified area.

The image shows a map of Florida titled "Drainage Basins" with various watershed boundaries. Overlaid on the map is a dialog box for selecting coordinates. The dialog box has two sections for coordinates, each with "Degrees" and "Minutes" input fields for both Latitude and Longitude. Below these is a checkbox labeled "Selecting Lat/Lon on Map". When this checkbox is selected, a message states "The next point you click will be the upper left" and provides "X" and "Y" input fields. At the bottom of the dialog are "Cancel" and "OK" buttons.

Upper Left Coordinates			
	Degrees	Minutes	
Latitude	0	0	
Longitude	0	0	

Lower Right Coordinates			
	Degrees	Minutes	
Latitude	0	0	
Longitude	0	0	

☐ Selecting Lat/Lon on Map

The next point you click will be the upper left

X 0 Y 0

Cancel OK

- 4) One of two things will happen at this point.

- a) If the station does not exist in the database, you will see a message that says “No stations were found that matched your search request”. People with “DataEntry” only permission cannot add a new station. Contact your group database administrator for assistance in having the station added to the database. You cannot proceed further with the entry of this data sheet. Put it in a “problem” stack and move on to the next data sheet. Press Done to exit from this screen.

- b) If the station(s) does exist in the database, a screen will appear listing the selected sites(s).
- c) By double clicking on the station of interest, a detailed information screen like the one at right will display:

Florida Department of Environmental Protection

Station Information DEP ID: 6039

STORET station code 22030024 (15 chars)

Station nickname WAKRB066V (10 chars)

Station Description WAKULLA RIVER 100YDS BELOW BOGGY BRANCH (48 chars)

Water Body WAKULLA RIVER 1214

County 129 Wakulla (50 chars) % for wildcard

latitude degrees 30 mins 9 secs 48.5

longitude degrees 84 mins 13 secs 25.9

HUC Code 03120001 (8 chars) 108588.5 303205.9

Subbasin 0 (not required)

This section is not required

EPA reach (20 chars)

☐ On ☐ Off reach

Reach miles 0 (number xxxxx.xxx)

Check digit (2 chars)

Station Type

Level 1 (required)

Stream

Level 2a (required)

Ambient

Levels 2b, 3, & 4 are required for PIPE;

Level 2b

Level 3

Level 4

Level 5 (optional)

What's been sampled?

Delete this station **Done** **Cancel** **Save & Next**

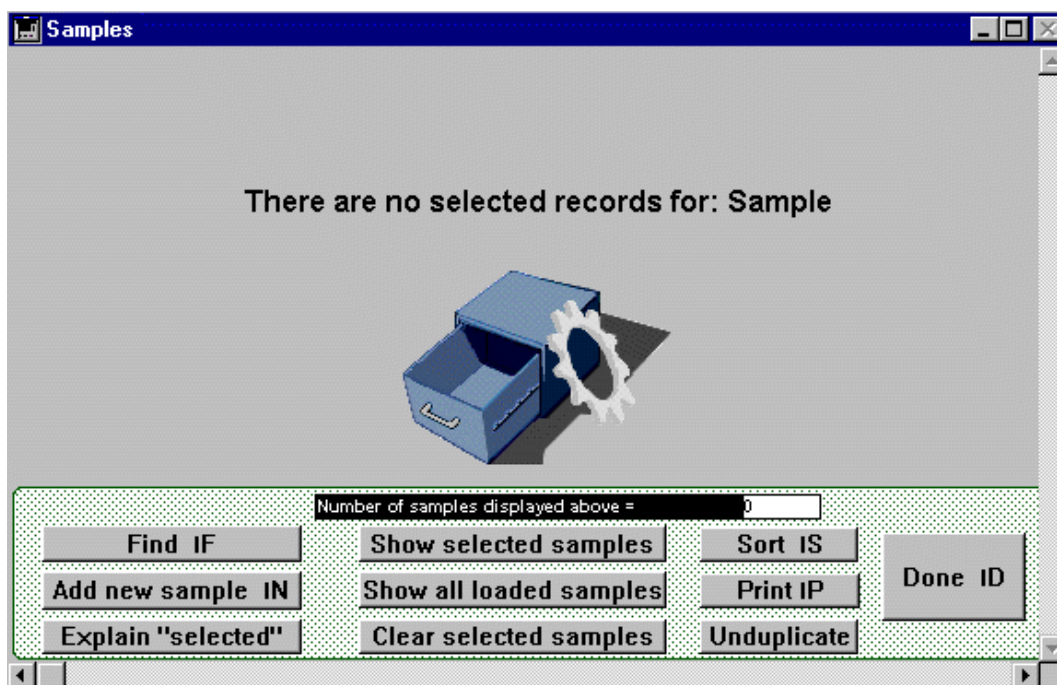
Compare the station information on your data sheet with the information on the screen to see if they are indeed the same station. If you are unsure, contact your database administrator for assistance. If you are sure the stations are the same, proceed to the next section, Data Entry. Press Cancel to exit from this screen, then Done to exit from the main “Station Information” screen and return to the splash screen.

Sample Data Entry

Find Samples

You are back at the splash screen. Go to the Samples menu and select Samples.

a) You will see a screen like this:



- 1) Click on Find.
- 2) Choose the search criteria that will be most useful. You can search by STORET station number, station nickname, sample date, or survey.

You can also restrict the search to a particular collector or to a user group, or find samples that contain data from particular biological communities. If you know the SampleID (assigned by the computer when the sample is created), you can use that to find a sample.

Make sure **Incomplete** is selected, and click on Find.

- 3) If the sample was not found, you will see a blank screen with a message reading: "There are no selected records for: Sample".

You will need to create a new sample, covered in the next section.

Add New Sample

- 1) From the screen with the message listed above, click on the button that reads "Add New Sample". The following screen will be displayed:

Enter Station and Date for the new sample

STORET code

Station Nickname

Sample Date

If you put an "@" in the Storet name, it will be used as a wildcard. For example: 200@ will look for all stations that start with a Storet code of 200. If you omit the "@" it will look to see if there is a Storet station code "200" in the station table.

- 2) Enter the STORET station code and the sampling date. You can enter either the STORET name or the station nickname and the program will automatically fill in the other name. (Note that you can do a wild card search here for the STORET code if you don't remember the entire code, using the "@" sign; check out the message box that appears on this screen for guidance.). Click OK and the program will search to see if this sample has already been entered. If a sample with that particular sampling

date already exists, a warning message will display: "A sample for this station has already been entered. Do you still want to enter this new sample?" Don't click on Yes unless you are very sure that this is a second sample taken on the same day at the same station. It is best to check with your database administrator before doing this. If you do set up a second sample for a particular station and date, take note of the SampleID that the computer has assigned. It will be useful for keeping track of which data corresponds with which sample.

- 3) Next you will see the sample information screen. Notice that the station and date information have been inserted for you.

Samples

Sample Information

Survey

Station Nickname

STORET code

Sample Date

Time

Physical/Chemical

Benthos

Zooplankton

Periphyton

Phytoplankton

All data entered & verified?

Comments

Collected by

Abad, Rick
Abate, Glen
Armstrong, Randall
Banks, E. Lee
Barber, Ed
Barge, Christy

Entered by Group:

Sample ID

Sent to BIOS on:

- 4) Enter the survey (click on the entry box and select a survey name from the drop-down list), sample time, comments, and collector. If the collector's name does not appear in the scrollable list, contact your database administrator to have it added.

- 5) Notice the box in the lower right corner of the sample information screen. It lists the group that the user belongs to, as well as the Sample ID (which will be assigned when the sample is saved for the first time), and the date that the data are sent to BIOS. The group is particularly important, as only members of the group that created the sample may enter or modify the data. However, all groups may retrieve data from any other group.
- 6) Use the pop-up menu next to the appropriate data type name(s) (e.g., benthos) to show which data were sampled. For each data type you will be asked for this information.

- 6a) First, enter the number of gears used to collect samples from each biological community type.

- 6b) Next, you will need to choose the particular gear(s) used. Use the drop-down lists shown on the left to do this, and click OK.

- 6c) You will now be prompted for specific details for each gear chosen.

- 6d) Enter the number of replicates.
- 6e) Enter the gear factor. The gear factor is used to define the sampling effort required to get one replicate.

For example, a data sheet shows that one “replicate” was accumulated with two ponar grabs and another “replicate” with three grabs. Assume that no other gear types were used. On the sample screen, you mark that benthos was sampled. When asked how many gear types, enter “2”. Next you are asked to select each gear type sampled. Select ponar two times. The box that

asks you the number of replicates, qualitative or quantitative, etc., has a box where you may enter a gear factor. In this example, you would enter one replicate and a gear factor of two for the first ponar and one replicate and a gear factor of three for the second. In retrieval, these will be counted as two separate samples. Assume the following data:

Taxon	2 rep grab # indiv/m ²	3 rep grab # indiv/m ²
<i>Mediomastus ambiseta</i>	15	25
<i>Streblospio benedicti</i>	43	0

Retrieval of number of samples, number of individuals/m² and number of taxa for this station/date would be: Number of samples=2, Number of individuals/m²=83 (pooled) or =42 (averaged), Number of taxa=2. You can change the gear factor on the benthos screen and the program will recalculate the number of individuals per unit area for the taxa that have already been entered.

A second example is the use of the gear factor to accommodate subsampling. When the entire contents of a sample are not processed, the gear factor equals the proportion of the sample material analyzed. When quantitative gears are used, the gear factor is used in the calculation of the number of individuals/m². When subsampling is performed with qualitative gears the gear factor may be used to adjust the organism counts. This is an optional feature of data retrievals that is rarely used.

Another use of the gear factor is to adjust for surface area differences in sampling equipment. For example, the Petite Ponar dredge is defined in the database as having a standard surface area of 240 cm². A slightly smaller dredge of the same type (ponar) may have a surface area of 215 cm², approximately 90% of the standard. The value, 0.90 may be entered in the gear factor field to resolve the difference.

Here is an example of the use of the three conditions above. A sample was collected using a ponar dredge with a surface area of 215 cm². Six replicated were collected and composited, and half of the sample was processed. The gear factor in this case would be:

$$\text{Gear Factor} = (\# \text{ of gear uses}) \times (\% \text{ of sample processed}) \times (\% \text{ of standard gear})$$

$$\text{Gear Factor} = (6) \times (.50) \times (.90) = 2.7$$

If you have any questions about what to enter in the gear factor field, it is best to talk with your database administrator.

- 6f) Choose Qualitative or Quantitative as the sample type. You will not be permitted to choose quantitative for a gear that is defined as qualitative.
- 6g) There are four choices in the drop-down menu for Confidence in ID's: 99.9%, 99%, 90%, and Unknown. This is a required field for upload to BIOS. Since it applies to the entire sample and different organisms may be identified with varying degrees of confidence, the default entry is "Unknown". If you feel that one of the other choices applies to every organism in the sample, you may select one of them.

- 7) Click on “Done” when all the sample information has been entered. (If you changed your mind and don’t really want to enter this sample, click on “Cancel”.) If you forgot to enter some piece of information, the computer will beep and show a message describing what is missing.

Note: If you need to delete an entire sample, use the Delete this Sample button on this screen. However, if data have already been entered for any of the community types, you will not be allowed to delete the sample until the data has been deleted.

- 8) After saving the sample information, you will be back at the screen listing the samples that were found or set up. Click on “Done”, and answer “Yes” to “Do you want to clear the selection?”.

Modify Existing Sample

There will be occasions where you will need to modify the information that was entered at the time the sample was created. You may have to change the survey or collector, add a sample time, or add a gear. Note that you may not change the station or date after the sample is created. If either of these are wrong you must delete the sample and its contents and start all over again.

- 1) To change sample attributes you must first “find” the sample as described earlier in this section (page 14). After you successfully find the sample to change, you will see the following screen:

The screenshot shows a window titled "Samples" with a "Sample Information" header. Below the header is a table with the following data:

Done?	Station Nickname	Station STORET Name	Sample Date	Survey	Owner	SampleID	Ben	Zoo	Per	Phy	PC	BIOS	BIOS Date
N	HILLS29	24010294	09/22/98	BIORECON	1	13344	1	2	2	1	2	0	00/00/00

Below the table, there is a section with buttons and a text field:

- Number of samples displayed above = 1
- Buttons: Find IF, Show selected samples, Sort IS, Add new sample IN, Show all loaded samples, Print IP, Done ID, Explain "selected", Clear selected samples, Unduplicate.

Legend in the top right corner:

- 3= Sampled, Done
- 2= Not sampled
- 1= Sampled, Not Done

- 2) Double-click on the line with the sample information and you will see the detailed information for this sample. For example:

Samples

Sample Information

Survey **BIORECON**

Station Nickname **HILLS29**

STORET code **24010294**

Physical/Chemical D **Not sampled**

Benthos **Sampled**

Zooplankton **Not sampled**

Periphyton **Not sampled**

Phytoplankton **Sampled**

Show gear types

 Delete this sample

 Cancel

 Done

All data entered & verified? **No**

Mark this sample complete

Sample Date **09/22/98**

Time **00:00**

Comments

Collected by

Boler, Richard

Borer, Robert

Bouman, Ruth

Brown, Kenton L.

Bruno, Nick

Bulgrin, Scott J.

Entered by Group: **1**

Sample ID **13344**

Sent to BIOS on: **00/00/00** **0**

- 3) Check the sample time to be sure it matches (or is very close) to the sample time on your data sheet. It is possible to have two different samples taken at the same station on the same day. In this situation the samples are identified by a unique Sample ID, which is computer-generated when the sample is created. If you know the Sample ID, compare it to the one listed in the lower right corner of the screen.
- 4) Look at the data type section of the screen to see if the type of data you need to enter has been marked as "Sampled". For example, on the screen displayed above, both the Phytoplankton and Benthos parameters have been marked as "Sampled". You can change the status from "Not Sampled" to "Sampled" by clicking on the entry box next to the parameter of interest and selecting the appropriate choice from the drop-down list box. You may change the status of a data type from "Sampled" to "Not Sampled" only if no data have been entered.
- 4) To change the survey, simply choose another option from the drop-down menu. You may change the date and time by entering the amended values in the appropriate fields.

Physical/Chemical D **Not sampled**

Benthos **Sampled**

Zooplankton **Not sampled**

Periphyton **Not sampled**

Phytoplankton **Sampled**

Show gear types

- 5) To add a gear type, click on the Show gear types button. A screen similar to the one at right will display.

Change the number of gears to the next highest number (in this case, 2). Click OK.

You will be asked to confirm the addition of a gear type. Click on NO if you really don't want to add a new gear, otherwise, click on Yes

You will see a series of pop-up menus for you to select the gear type. Since in this example you are adding one gear, use the first of the four boxes to select your gear, then click on OK:

Next you will be asked for the details of the sample:
Fill in the boxes and click on OK.

If necessary, review the section on “Gear Factor”, page 17.

There will be a short delay while the program adds the gear information and then you will see:

The screenshot shows a software window titled "Samples". Inside, there's a section titled "Gear Types Sampled" which is divided into four quadrants:

- Benthos**: Shows "# Gear Types" as 2. Below this are three input fields containing "Dipnet", "Dipnet X20", and an empty field.
- Zooplankton**: Shows "# Gear Types" as 0. Below this are three empty input fields.
- Periphyton**: Shows "# Gear Types" as 0. Below this are four empty input fields.
- Phytoplankton**: Shows "# Gear Types" as 1. Below this are four input fields, with the first one containing "WaterBottl" and the others empty.

At the bottom center of the window is an "OK" button.

You can see that your gear has been added. Click on OK and you will be back at the main sample screen. Click on **Done** and then **Done** again. You can answer “Yes” or “No” to the question about clearing the sample information. If you think you may want to look at it again, click on “No”, otherwise, click on “Yes”.

Analysis Results Entry

Data resulting from field or laboratory analyses may only be entered into a sample by a user assigned to the same “group” as the person who added/created the sample. For example, if John Doe is assigned to “group 11”, he cannot enter data into a sample which was created by Sally Smith who is in group 2. If you try to enter data into a sample and notice that you can’t access many of the screens, check to see which group the sample belongs to. You can check on the group you are in by going to the main start-up screen of the 4D program, clicking on the “User Info” menu item, then clicking on “Show my Info”.

The method of entering data is similar for macrobenthos, zooplankton, phytoplankton, and periphyton. To step through the method, we will use macrobenthos as an example.

- 1) From the splash screen, pull down the **Sample** menu and select the appropriate data type. For this example, we will select **Benthos**. The resulting screen displays the message “There are no selected records for: Benthos”. After insuring that the **Incomplete** button is selected on the lower left side of the screen, click on **Find**.
- 2) Enter the search criteria (STORET Name, Nickname, Sample Date, Survey or some combination), then click on **Find**.

- 3) The benthos data screen will be displayed with the pertinent sample information loaded:

4th Dimension

File Edit Help

[Benthos]

Benthos Data for Samples Marked Incomplete Your group is: 1

Station Nickname	STORET Name	Date	Gear	Nreps	Gear Factor	BenthID	SampleID	Owner Group	1=Quan 2=Qual
CALMREF	24040058	08/19/96	Bkman	1	1	12014	10734	2	1
HIAWATHREF	24040057	08/12/96	Bkman	1	1	12013	10519	2	1
MIDDLETST	24040028	04/11/96	Bkman	1	1	10614	9846	6	1

Restrict "Find" to data that are:
☒ Incomplete
☐ Complete

Number of samples displayed above = 3

Find IF Show selected samples Sort IS
 Show Stats Show all loaded samples Print IP Done ID
 Explain "selected" Print Reps Clear selected samples Unduplicate
 Find Samples with lost scientific names

The data for the other data types (zooplankton, periphyton, etc.) are loaded exactly the same way.

- 4) Double-click on the sample information, and you will see the detailed benthos information screen:

[Benthos]

Benthos

Station 31020040
TENMILREF

Date 02/07/95

BIOS status

SampleID 6023
BenthID 7077
Owned by your group? N

Number of replicates 1 Gear factor 0.01

Sample type Qualitative
Gear used Dipnet X20
Confidence in ID's 90.0%
Identified by Perez, Francisco J.
Petrovits, Andrea
Pluchino, Eric S.
Quintana, Urania
Ray, Donald H.

Go to Taxa Data %G

Delete this gear Done Cancel Save

The information at the top of the screen cannot be edited, it is displayed for reference. The information in the middle of the screen can be edited. You will notice that this is the same information you entered when a new sample was created and marked that benthos was sampled. Modifications to the number of replicates, gear factor, sample type, etc., which were made from the sample information screen may be modified from this screen. Select the name of the person who performed the taxonomic identification. Only one identifier can be associated with each sample. If the name of the identifier does not appear in the scrollable area, contact the Database Administrator or the Assistant Database Administrator

to have that individual added.

- 5) To enter the taxa data, click on Go to Taxa Data. If you have made any changes to the sample detail screen, you will be prompted to save them before you can proceed to the taxa data area. If there is more than one replicate, you will be asked which replicate you want to enter. You will see this screen if no data have been entered for the requested replicate:



If taxa have been entered, you will see them listed on a screen similar to the one below.

[Benthos]

Benthos Sample Taxonomic Information

BenthID	12016	Date	08/06/96
Station	25020143	Gear	Ekman
CANNONREF		Rep No.	1

Number of entries =	16
Total individuals counted	118
Total individuals/m2=	7,691.77

TaxaID	Scientific Name	No. counted	No. per m2
68854	Naididae	1	65.18
68639	Limnodrilus hoffmeisteri	5	325.92
70493	Hydrobiidae	1	65.18
70343	Pomacea paludosa	2	130.37
76668	Planorbella scalaris	4	260.74
117695	Eoparygyractus	1	65.18
10000684	Desserobdella phalera	2	130.37
10000573	Gloiobdella elongata	12	782.22
129581	Parachironomus monochromus	1	65.18
129873	Cladotanytarsus	1	65.18
10000081	Polypedilum halterale grp.	3	195.55
10000075	Phaenopsectra obediens grp.	1	65.18
128277	Procladius	1	65.18
10000062	Glyptotendipes sp. b epler	2	130.37
129494	Glyptotendipes paripes	73	4,758.49
10000018	Palpomyia/bezzia grp.	8	521.48

Add new taxa data %N
Sort %S
Print %P
Done %D

- 6) In either case, to add taxa, click on Add new taxa data. To edit an existing taxon, double-click on the line you want to modify. Both choices will take you to the taxon entry screen:

As with the benthos information screen, the information in the top box is not editable, but the middle box is.

With the “Search Master List” box unchecked, enter part of the scientific name and press the tab or the enter/return key:

Scientific name tanyt

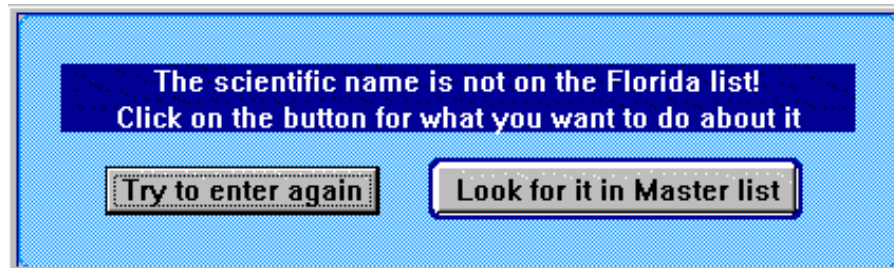
All the names on the Florida list that start with those letters will be displayed:

36 Records	
Tanytarsus	129978
Tanytarsus buckleyi	129983
Tanytarsus coffmani	129977
Tanytarsus confusus	129984
Tanytarsus dendyi	129988
Tanytarsus dissimilis	129990
Tanytarsus glabrescens	130030
Tanytarsus...	130034

Scroll through the list and find the name that matches, then click once on that name. The fewer letters you type, the longer the list in the box. It is best to enter at least 4-5 letters to keep the list relatively short. You can type the entire scientific name. If you enter the entire name and it is on the

Florida list, the scroll box will not appear and the cursor will move to the number of individuals counted box.

- 7) If you do not see the name you want on the list click the Cancel button. You will see:



Check the spelling of your entry, and if it was misspelled, click on Try to enter again. If you are sure you spelled your entry correctly, click on Look for it Master List.

Note on the Master and Florida Taxa Lists

There are two lists of scientific names in this database: the *Master* list and the *Florida* list. The master list has the names of plants and animals found throughout the entire United States. It was originally loaded from a copy of the BIOS list as it was in 1994. (BIOS is a federal database of plant and animal data that is tied to the STORET system.) The Florida list is a subset of this master list and contains only those plants and animals found in Florida.

The Florida BioDB will allow the entry of scientific names that appear on the Florida list. If you try to enter a name that is not on the Florida list, the program will let you check to see if it appears on the master list. If the name is found on the master list, you are given the option to move it to the Florida list.

Sometimes a species name appears on the Florida list, but its genus name does not. If you try to use only the genus name, the program will automatically enter the species name in the entry box. To get around this, check the box "Search master list only" to bypass the Florida list and search only the master list. Under most circumstances, you will not need to check this box. Keep in mind that the Florida list is stored on your computer. The master list is stored in Tallahassee on the server. Since this involves accessing a network, the master list search can be much slower than the usual Florida list search. So don't check the box unless absolutely necessary! To search the master list, check the box BEFORE you enter the scientific name; otherwise the default Florida list will be searched

- 7a) The master list is very large (over 200,000 entries). If you only typed a few letters of the name, there may be many names that match. The more letters you type in, the shorter the list and the shorter the time it takes to search. The matches will be displayed in a window like this:

Names found on the master list

Taaningichthys

Taaningichthys bathyphilus

Taaningichthys minimus

Taaningichthys paurolychus

Tabanidae

Tabanus

Tabanus aar

Tabanus abactor

Tabanus abditus

Tabanus abdominalis

Tabanus actaeon

Tabanus acutus

Tabanus aegrotus

Tabanus affinis

Tabanus allynii

Tabanus americanus

Tabanus amplifrons

Tabanus annularis

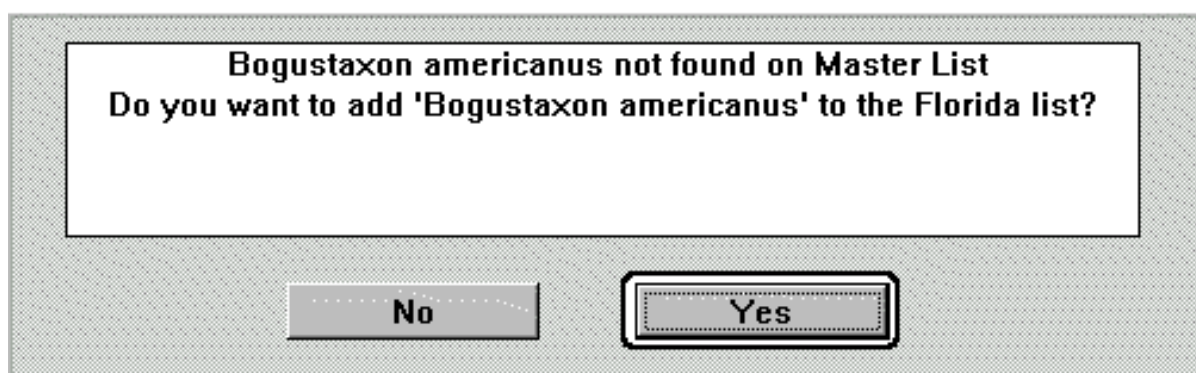
Tabanus annulatus

None of these

Select

Click one time on the name you want and then click Select.

7b) If you don't see the name you want, click on None of these. You will then see:

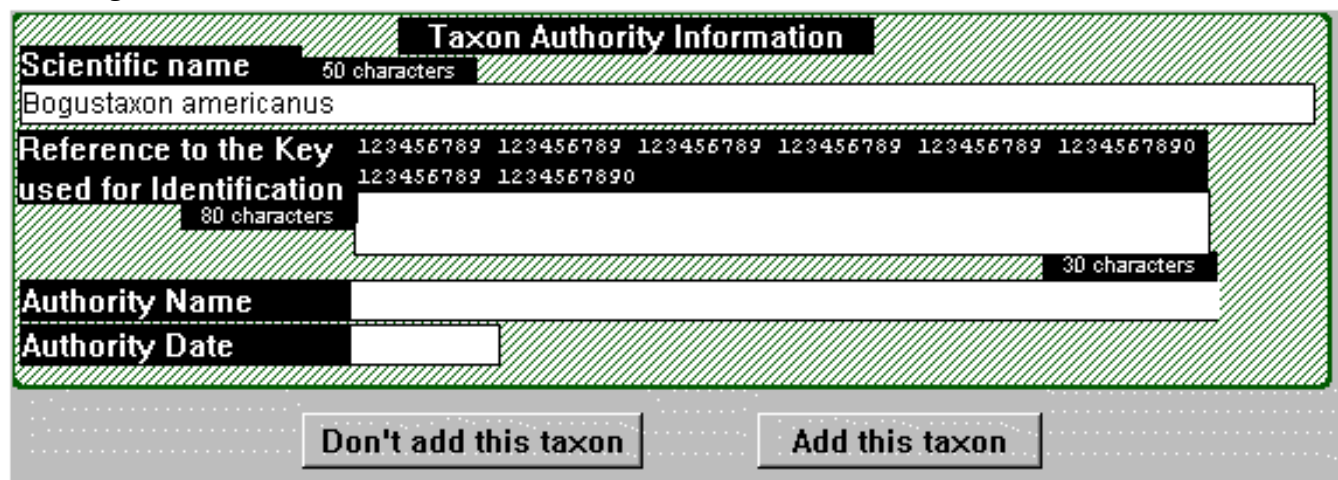


You should only click on Yes if you have checked possible alternative spellings. Otherwise, click on No, then click on Cancel when you get back to the taxon entry screen.

Adding Taxa to the Florida Taxa List

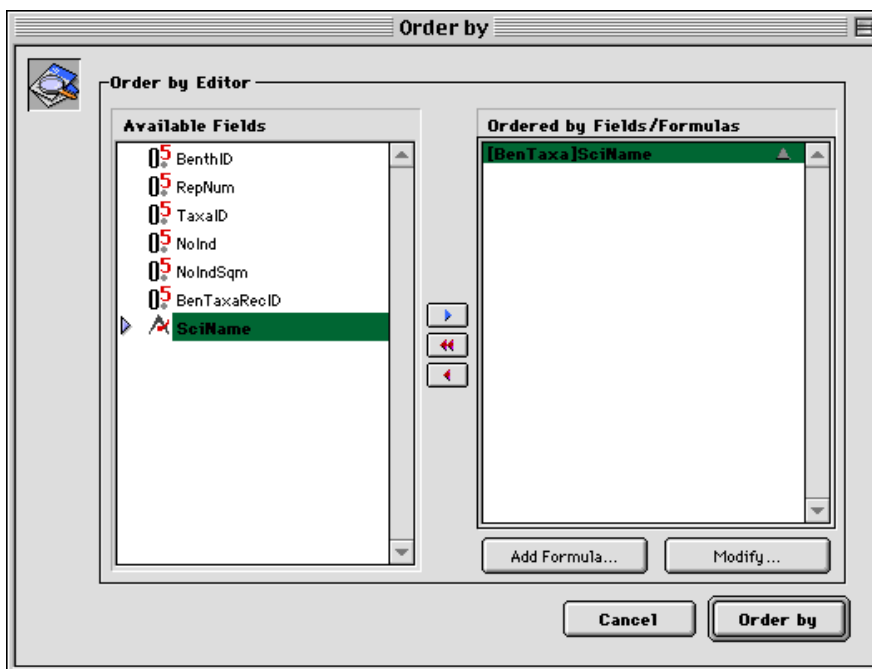
- 8) Any user with data entry permission may add taxa to the Florida list, provided you have specific information regarding the person who named the taxon, the year it was named, and the taxonomic key used to identify it. These newly added taxa are flagged as ‘temporarily’ on the Florida list until the Database Administrator adds them permanently. Samples cannot be marked “complete” (discussed in the next section) until all taxa have been permanently placed on the Florida list.

If you answered Yes to adding a taxon to the Florida list, you will be presented with a screen for entering the information mentioned above.



Enter the Authority name and date, that is, the name of the person who named the taxon and the year it was named. The box above this is for the reference to the key used to identify the organism, which may or may not be the same. The taxon cannot be added to the Florida list without this information. When you are finished, click on Add this taxon. If you find that you do not have the necessary information, click on Don't add this taxon, and try again after you have collected it.

- 9) If you successfully entered a taxon name, enter the number counted. If the sample is quantitative, the computer will automatically calculate the number of individuals per unit area based on the gear factor and replicate information (used for phytoplankton, periphyton, and zooplankton samples). Qualitative data may be added with or without counts (i.e., leave it as zero), and there is no calculation of the number per unit area. If you know the number per unit area (or volume for plankton), check this number against the number on your data sheet. If it is not the same value, be sure you entered the number counted correctly. If that is ok, check the gear type since it has a number associated with it used to calculate the number per unit area. Other sources of problems could be an incorrect gear factor and for periphyton, zooplankton, or phytoplankton data, the replicate information (dilution factor, number of grids counted, etc) could have an error. Do not proceed until you have resolved the problem. Click on **Cancel** to get back to the benthos detail screen, then on **Cancel** again if the problem is not there. If you have trouble figuring out what to do, ask your database administrator.
- 10) If the number per unit area is correct, you can do one of three things.
 - a) This was the last taxon for the replicate — click on **Done**. The program will ask “Do you want to save your changes?”— click on **OK**.
 - b) You have more taxa to enter for this replicate - click on **Save and next** (or press the **Enter** key).
 - c) You don’t want what you have entered on this screen to be saved — click on **Cancel**.
- 11) Once you return to the taxa list for the current replicate, you can print the screen by clicking on **Print**. It is sometimes helpful to sort the data in a particular order before printing. To do this, click on **Sort**. A window like the following will display:



Click on time on the name of variable on which to sort the data. (If you want them sorted into the same order as you entered them, click on “BenTaxaRecID”.) Click on **Sort**. The taxa will stay in sorted order as long as you are on that screen; if you enter more data, they will go back to the presorted order.

- 12) When you are finished with the current replicate, click on **Done**. You will be back at the benthos detail screen. If you want to enter data for another replicate, click on **Go to Taxa Data** and enter the number of the next replicate. Click on **Done** when finished.
- 13) Click on **Done** to get back to the splash screen when you are finished entering benthos data.

Replicate Information

- 1) Replicate information describes how the sample was handled during the analysis, and is used to calculate the number of individuals per unit area or volume for each taxon entered. From the splash screen, go to the **Samples** drop-down menu and choose **Phytoplankton**, **Periphyton**, or **Zooplankton**. Follow the steps for loading data as described for basic data entry through step 4. These three data types will have a button on the sample detail screen labeled **Go to Replicate Info**:

Phytoplankton

Station: 20010010
Date: 08/06/96
SampleID: 10511
PhytoID: 1936
Gear factor: 1
Owned by your group? Y
BIOS status:

Number of replicates: 1
Sample type: Quantitative
Gear used: WaterBottl
Confidence in ID's: 99.0%
Identified by: Stafford, Heather
Stetler, Robert
Strom, Douglas G.
Stuckey, Mark
Tamburello, Lisa
Diatom Status: Diatoms never entered

Go to Replicate Info
Recalc All Unit Area
Go to Taxa Data %G
Incorporate Diatoms

Delete this sample Done Cancel Save

- 2) Click on **Go to Replicate Info** and you will see a screen that will let you enter information for each replicate. If the sample has more than one replicate, you will be asked which replicate you want to enter; otherwise, it will go directly to one of these screens depending on the type of data you are entering. An example of the replicate information screen for each data type is displayed on the next page.

Request

What replicate?
1

Cancel OK

Periphyton Replicate Detail

Station	NONSTORET108	SampleID	13676
	MES01-8	PeriID	2295
Date	11/24/98	PeriRepID	2421
Gear	PeriAS-C11		

Help in case you don't remember how to convert mls to liters or vice-versa. Enter a number in one of the boxes and its converted value will display in the other

Replicate 1

1000mls =
1liters

Replicate Information		Counting Cell Information	
Area scraped (mm2)	0	Grid Length (mm)	.00
Sample volume (mls)	0.0	Cell Depth (mm)	.0
Dilution factor (1-100)	0	No. grids counted	0

You can use this section to help you calculate the area scraped. The numbers entered in these boxes are just for doing the calculation and are not saved.

Area of one slide in mm2	3750	Calculate area scraped
Number of slides	4	

Phytoplankton Replicate Detail

Station	25020143	SampleID	10505
	CANNONREF	PhytoID	1934
Date	08/06/96	PhytoRep	2002
Gear	WaterBottl		

Help in case you don't remember how to convert mls to liters or vice-versa. Enter a number in one of the boxes and its converted value will display in the other

Replicate 1

1000mls =
1liters

Replicate Information		Counting Cell Information	
Volume collected/filtered (mls)	200	Grid Length (mm)	.23
Sample volume (mls)	75.0	Cell Depth (mm)	4.5
Dilution factor (1-100)	1	No. grids counted	14

You can use this section to help you calculate the volume filtered. The numbers entered in these boxes are just for doing the calculation and are not saved.

For tow samples:

Area of mouth of net in cm2	0	Calculate volume filtered
Depth of body of water in meters	0	

Zooplankton Replicate Detail

Station	33040050	SampleID	9784
	CRES1	ZooID	32
Date	11/13/84	ZooRepID	32
Gear	PlankNet		

Help in case you don't remember how to convert mls to liters or vice-versa. Enter a number in one of the boxes and its converted value will display in the other one.

Replicate 1

1000mls =
1liters

Replicate Information	
Volume collected/filtered (mls)	0.0
Sample volume (mls)	0.0
Volume of sample examined (mls)	0

You can use this section to help you calculate the volume filtered. The numbers entered in these boxes are just for doing the calculation and are not saved.

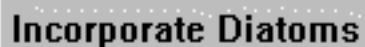
For tow samples:

Area of mouth of net in cm2	0	Calculate volume filtered
Depth of body of water in meters	0	

- 3) Enter the information. Be sure that the numbers you enter are in the appropriate units, converting from the value on your data sheet if necessary. There is conversion helper on the upper right side of the screen (see page 30, above). For example, if you want to know how many milliliters are in 4 liters, double-click on the “1” in front of the word liters, type the number 4, then press the tab key.
- 4) Sometimes for a tow (or scraped) sample you do not have the volume filtered (or area scraped). You can calculate that value by entering the information in the bottom part of the box, then clicking on **Calculate volume filtered**. The answer will be put in the box next to **Sample volume** (or **Area scraped**). The values in the bottom box are not saved, but are just used to calculate the sample volume (or area scraped).
- 5) When all the data have been entered, click on **Done** and you will be returned to the detail screen in step 1. If there were taxa data already entered for the replicate whose sample volume or area information you edited, the number of individuals per unit area will be recalculated for each taxon entered using the new replicate information.

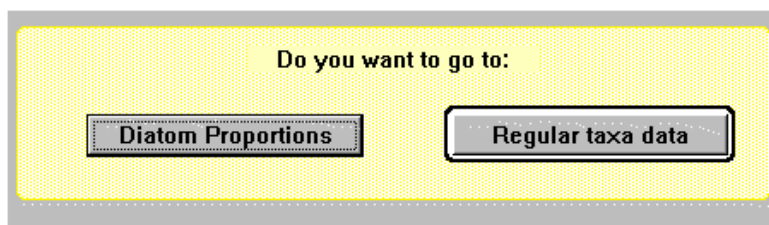
Diatom Proportions

When periphyton (and occasionally phytoplankton) data are identified, a portion of the sample is removed for diatom analysis. This material is processed differently and counted separately. The percentages of each diatom taxon are applied to a “grand total” of diatoms derived when the “wet periphyton” or “regular taxa” are counted. You can enter the subsample identifications using “Diatom Proportions”. After the diatom proportions are calculated they are merged into the counts of wet periphyton using a button on the detail screen called “Incorporate Diatoms” (see below). There is also a bar that tells you the current status of the diatom data (never entered, entered but not incorporated, or incorporated).

A rectangular button with a green border and a light green background. The text "Incorporate Diatoms" is centered in a bold, black, sans-serif font.

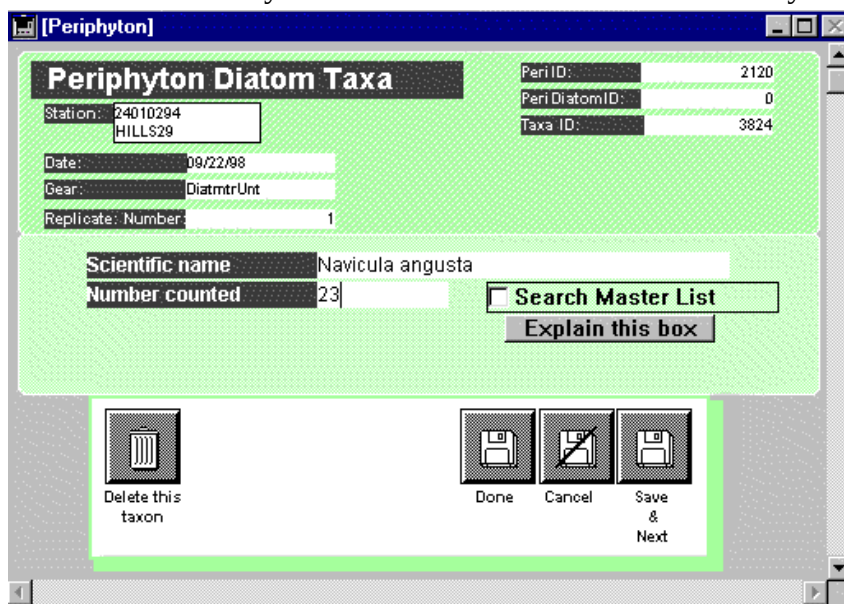
Entering Diatom Proportions

- 1) When you click on Go to Taxa Data for phytoplankton or periphyton data, you will be given a choice box like the one displayed below. If the sample contains replicates, you will be prompted for the replicate number first.

A yellow rectangular dialog box with a black border. At the top, it says "Do you want to go to:". Below this, there are two buttons: "Diatom Proportions" on the left and "Regular taxa data" on the right. Both buttons have a black border and a light gray background.

Regular taxa data are entered as described in the “Analysis Results Entry” section of this manual. Do not enter the grand total of diatoms counted, however. That will be done in the Incorporate Diatoms operation. For Diatom Proportions, follow these steps.

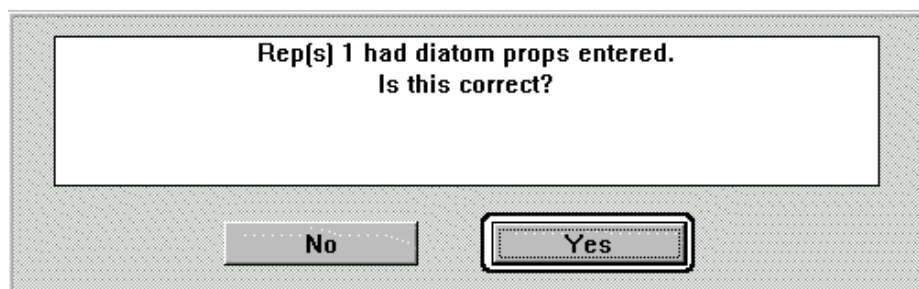
- 2) A screen similar to the one for the regular taxa data will appear, letting you know that there are no selected records for: PeriTaxa.
- 3) Click on Add new taxa data and you will see the “Diatom Taxa” data entry screen:

A screenshot of a software window titled "[Periphyton]". The main title is "Periphyton Diatom Taxa". The form contains several input fields: "Station:" with "24010294" and "HILLS29" below it; "Date:" with "09/22/98"; "Gear:" with "DiatmtrUnt"; "Replicate: Number:" with "1". On the right, there are three fields: "Peri ID:" with "2120", "Peri Diatom ID:" with "0", and "Taxa ID:" with "3824". Below these, there is a "Scientific name" field with "Navicula angusta" and a "Number counted" field with "23". There are two buttons: "Search Master List" and "Explain this box". At the bottom, there are three icons: a trash can labeled "Delete this taxon", a floppy disk labeled "Done", a crossed-out floppy disk labeled "Cancel", and a floppy disk labeled "Save & Next".

Enter the taxa information. The data entry process works just like that for regular taxa data except that there is no “number of individuals per unit area”. Click Done when finished.

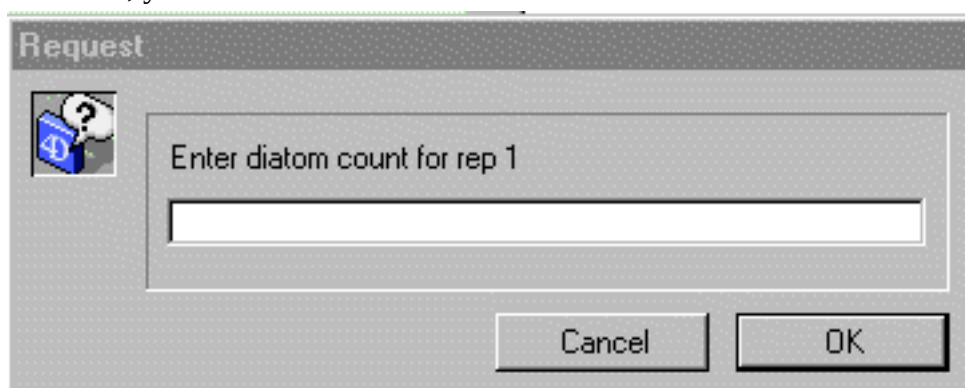
Incorporating Diatoms

- 1) Click on the Incorporate Diatoms button (see screens under “Diatom Proportions”).
- 2) You will see a choice box like this:



The computer scans all the replicates and tells you how many had separate diatoms entered (there may have been replicates with no diatoms).

- 3) Click on YES if the message is correct; if not, click on NO. If the message is incorrect, diatom data may have been entered for the wrong sample. Investigate this possibility before proceeding, as this operation cannot be undone.
- 4) If you click on Yes, you will see:



In this box you enter the actual number of diatoms entered for the replicate. The computer will calculate the number of individuals by adding up the counts for all the diatom taxa entered for the replicate. That total is used as the denominator to figure out the proportion that each taxon is of all the diatom taxa that were entered. That proportion is multiplied by the number entered in the box above to get the actual number of each taxon to insert in the database.

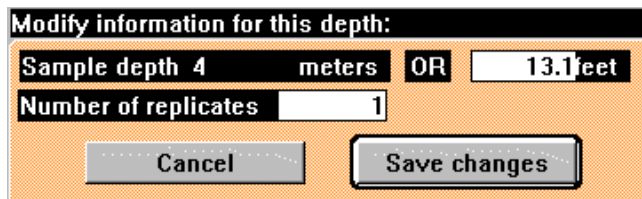
Physical/Chemical Data Entry

- 1) From the main screen, go to the Samples drop-down menu and select PhysChem. Load the sample of interest as described in “Analysis Results Entry” on page 22. Double-click on the sample you want to enter/edit. A screen like this will appear:

- 2) For each physical/chemical parameter, a “-9” will appear in the box (when the cursor is in it) when no data value was entered for it. This “-9” is actually stored as a null value in the Oracle database; however, 4th Dimension has this quirk that converts null values to zeros when they are loaded from Oracle. Since zero is a valid value for most of these parameters, a switch has been set to convert null values to -9’s when they are displayed and back to null values when they are stored.
- 3) First, enter the station depth and Secchi depth, if applicable. You can enter depth in meters or feet depending on what was written on your data sheet. Both feet and meters will be displayed on the screen, but the metric value will be stored in the Oracle database.
- 4) Next, enter the depth(s) at which the phys/chem parameters were measured.
 - a) To add a sampled depth, click on Add New Sampled Depth. You will see:

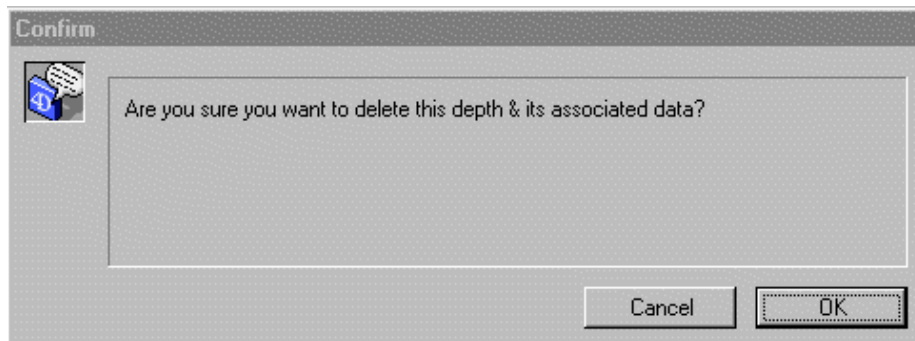
- b) Select “meters” or “feet”, depending on the units in which depth was measured, then enter the depth that was sampled. If it is a surface sample, enter zero as the depth. You also need to enter the number of replicate physical/chemical samples taken at this depth. Usually only one replicate was taken, but you can have more than one if more than one was sampled. This is not depth profile where each replicate is taken at a different depth. At this level, a replicate is more than one sample taken at the same depth. (Note that if you enter a sampled depth that is deeper than the station depth entered on the previous screen, an error message will be generated.

- c) Click on Add this depth, which will add the depth data and return you to the main Physical/Chemical data screen above, where you will see the new sampled depth displayed in the scroll box
- 5) To edit a sampled depth, click one time on the depth to edit, then click on the button labeled Edit Selected Depth. The following screen will appear. Click on Save changes when you are finished editing.



The screenshot shows a dialog box titled "Modify information for this depth:". It contains two rows of input fields. The first row has "Sample depth 4" in a black box, followed by "meters" in a black box, "OR" in a black box, and "13.1 feet" in a white box. The second row has "Number of replicates" in a black box, followed by a white box containing the number "1". At the bottom of the dialog box are two buttons: "Cancel" and "Save changes".

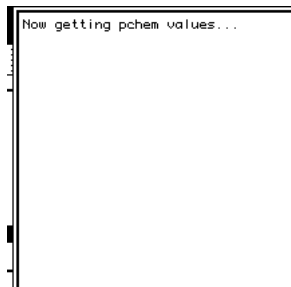
- a) If you want to delete a sampled depth, click one time on the depth you want to remove, then click on the button labeled Delete this depth. You will be given a chance to change your mind:



The screenshot shows a dialog box titled "Confirm". It contains a message box with the text "Are you sure you want to delete this depth & its associated data?". At the bottom of the dialog box are two buttons: "Cancel" and "OK".

If data values (like DO, pH, turbidity, etc) were entered for that sample depth, they will be deleted.

- 6) To enter the actual data values, click on **Enter/Edit Data**. There is no need to highlight a sampled depth as all data for this sample will be loaded. You will see:



followed by:

Physical/Chemical Replicate Information	
Station Nickname	BIGGANTTST
STORET Name	23010411
Sample Date	10/01/98

Sample Depth (m)	Replicate
3.0	1
6.0	1
8.0	1

Done ID

Each individual replicate is displayed. Double-click on the one you want. The program will load around 100 variables, then the following screen will be displayed:

Station	32020108	Date	04/25/97	SampleID	12112	PchemDepthID	11519
DOUBLEREF		Depth	0.0	PchemID	9923	PchemRepID	11908
Replicate	1						

Physical/Chemical Replicate Detail	
Alkalinity (mg/l CaCO3)	-9
Conductivity, lab (µmho/cm)	
Conductivity, field (µmho/cm)	
DO, non-probe (mg/l)	
DO, probe (mg/l)	
Hardness (mg/l CaCO3)	
pH (standard units)	
Salinity (ppt)	
Temperature (°C)	
Turbidity (NTU)	

Go to:
Nutrients %N
Microbiology %M
Other Pchem %O
Sediments %S
Pigments %A
Done
Cancel
Help

Notice that the boxes are empty except the highlighted one and it has a -9 in it. Remember that -9 means missing (i.e., this parameter was not measured). The missing values will appear blank except when the cursor is in that field when it will be -9. Type in the values that were measured. Be sure the value you enter is in the same units displayed on the screen. For example, DO should be entered as mg/l. If you want further information about a parameter, hold the cursor in the entry field. A box will appear that gives the name of the parameter, the STORET code, a range of “normal” values, and the units. If your measurement is beyond the “normal” range, an alert box will ask you to confirm that this is the value you intended.

Confirm	
	!!!Warning!!! This is greater than the usual limit of 10! Enter it anyway?
Cancel OK	

Macintosh users have a second option. They can turn on “Balloon Help” by choosing “Show Balloons” from the Help menu, the last toolbar menu on the right.

Now when you hold the cursor over the white box next to a parameter name, you will see a description of that parameter, with the same information listed above. Be sure to turn “Balloon

Help” off when you are finished as it can be annoying to have these boxes popping up all the time. You turn it off the same way you turned it on.

Use the buttons on the right side of the screen to move to other parameters (i.e., Nutrients, Microbiology, etc.). Do not click on Done until all the parameters on all the different screens have been entered.

When entering Microbiological data, you will see a screen like this:

	Check if TNTC
Enterococci, membrane filter (no./100 ml)	☐ Yes
Escherichia coli, membrane filter (no./100 ml)	☐ Yes
Fecal coliforms, membrane filter (no./100 ml)	☐ Yes
Fecal coliforms, multiple tube (no./100 ml)	☐ Yes
Fecal Streptococcus, membrane filter (no./100 ml)	☐ Yes
Coliforms, total, membrane filter (no./100 ml)	☐ Yes
Coliforms, multiple tube (no./100 ml)	☐ Yes
Plate count, total (no./ml)	☐ Yes

The check boxes to the left are to be used if the count for the parameter was “too numerous to count”. When data are retrieved and each sample is retrieved separately, the letters TNTC will appear for the parameter value in the output. If the sample is part of an averaged value, the number (if not a missing value) entered in the box will be included in the average. Be sure you think about this when you enter a value in the box; it can be left empty.

Go to:

Nutrients IN

Microbiology IM

Other Pchem IO

Sediments IS

Pigments IA

Done

Cancel

Help

In some data entry screens (Nutrients and Pigments), you will see check boxes that allow the user to indicate the selected parameter cannot be measured below a detection limit. It works the same way in retrieval as TNTC, except you will see the letters BDL when individual samples are retrieved.

Nitrite+Nitrate, dissolved	☐ < detection limit
Nitrite+Nitrate, total	☐ < detection limit
Nitrogen, total (mg/L N)	☐ < detection limit
Nitrogen, total Kjeldahl (mg/L N)	☐ < detection limit
Orthophosphate, dissolved (mg/L P)	☐ < detection limit
Orthophosphate, total (mg/L P)	☐ < detection limit

- 7) Click on Done when all the data have been entered. You will see:

Save changes?

Cancel

OK

Click on OK to save the modifications you made. You will return to the “Physical/Chemical Replicate Information” screen, where you can select another depth or replicate to edit, or click Done if finished. Click Done again, then OK to save changes. Continue clicking on Done to return to the splash screen.

Marking Samples Complete

Marking samples complete

When a new sample is created, it is automatically marked “incomplete”. This means that if someone is retrieving data, the data for this sample will not be retrieved. Once all the data that were taken for the sample have been entered and verified, a person with “group administrator” access can mark the sample “complete” (and therefore available for access by others) by following these steps.

- 1) Follow steps 1a-d of the “Sample Data Entry” to load the sample information. The screen will look like this:

Sample Information													
Done?	Station Nickname	Station STORET Name	Sample Date	Survey	Owner	SampleID	Ben	Zoo	Per	Phy	PC	BIOS	BIOS Date
N	DIXIE1	21020031	05/05/98	IMPOUNDMENT STUDY	1	13224	1	2	1	2	2	0	00/00/1010
N	HILLS29	24010294	09/22/98	BIORECON	1	13344	1	2	1	1	1	0	00/00/1010

3=Sampled, Done
2=Not sampled
1=Sampled, Not Done

Number of samples displayed above = 2

Find IF Show selected samples Sort IS Done ID

Add new sample IN Show all loaded samples Print IP

Explain "selected" Clear selected samples Unduplicate

- 2) Double-click on the sample you want to mark complete.
- 3) The screen will look like this:

Samples

Sample Information

Survey: **IMPOUNDMENT STUDY**

Station Nickname: **DIXIE1**

STORET code: **21020031**

Physical/Chemical D: **Not sampled**

Benthos: **Sampled**

Zooplankton: **Not sampled**

Periphyton: **Sampled**

Phytoplankton: **Not sampled**

Show gear types

Sample Date: **05/05/98**

Time: **00:00**

Comments:

Collected by: **Woodbridge, Robert**
Wright, James O.
Wynn, J. Greg
Young, David
Young, William T.
Zenas, Martin

Entered by Group: **1**

Sample ID: **13224**

Sent to BIOS on: **00/00/1010** **0**

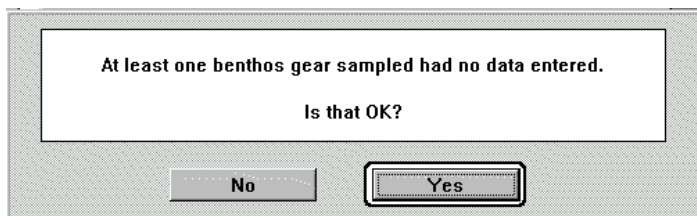
Mark this sample complete

Delete this sample Cancel Done

Click once on “Mark this sample complete”.

- 4) You will see a box in the middle of the screen that will keep you informed about what the computer is doing. —————→

The first thing it does is make sure that data were entered for each data type that was marked “Sampled”. If it finds a data type with no taxonomic data entered, you will see a screen like this:

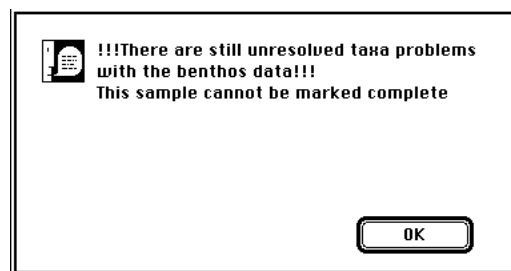


each biological sample. It will give an alert, and take you back to the sample information screen. You must enter the identifier before the sample can be marked complete.

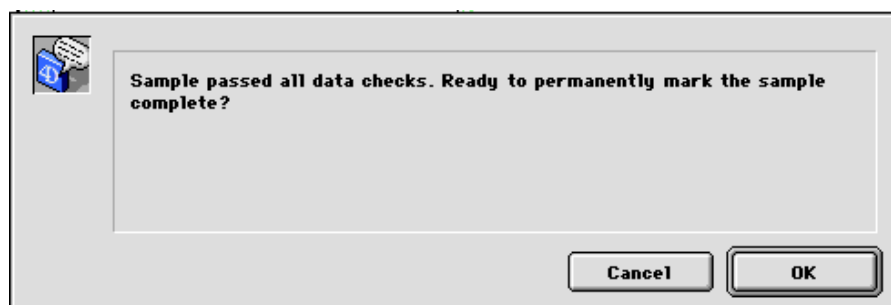
The computer checks all the taxa that were entered for this sample and makes sure that these taxa are marked as Florida taxa. If they are not, you will see a screen like the one at right and you will be returned to the screen in step 3.

If it really was a sample with nothing in it, click on “Yes”; if there really were data entered, click on “No” and then enter the missing data.

The computer also checks to see if an identifier has been entered for



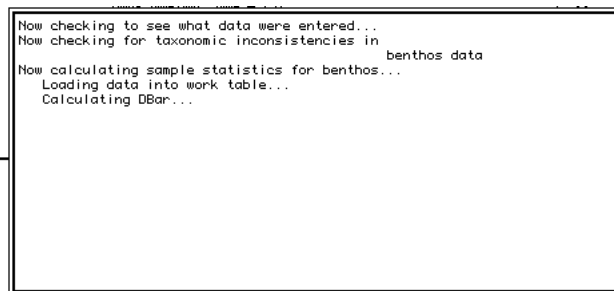
The biological database administrator is responsible for resolving the taxonomic inconsistencies. Tell your group administrator about the problem so s/he can help investigate. Often, new taxa were added to the Florida list during data entry, and the Database Administrator has not yet updated it. If there were no taxonomic inconsistencies, you will see a message like the one on the left.



If you click on OK, the computer will calculate the number of individuals counted, number of individuals per unit area, number of taxa, DBar, and, if appropriate, Florida Index and Lake Condition Index. These numbers are stored with the sample data to make retrievals work faster.

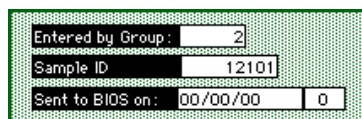
- 5) While the computer is calculating the statistics, you will see:

When it is finished you will be returned to the window as shown in step 1 except that a “Y” appears under the column labeled “Done?” rather than an “N”. The sample is now available for retrieval by a member of any group.



Marking samples incomplete

You must have “group administrator” access to do this, and must be a member of the group that created, or “owns” the sample. Once a sample is marked “complete”, it is available to be retrieved. There may be an occasion when you realize that some of the data entered need to be changed. If the data have not been sent to BIOS (the federal biological database) yet, you can mark the sample “incomplete” and change the data. You can tell that a sample has been sent to BIOS by looking for a date in the lower right corner of the sample information screen:



The date will be all zeros if the data have not gone to BIOS. In addition, if the data have been sent to BIOS, the “**Mark sample incomplete**” button will be grayed-out.

Click on the “**Mark sample incomplete**” button. There will be a delay and then you will be returned to a screen that looks like the one in step 1 of “Marking samples complete”. There will be an “N” under “Done?” where there was a “Y” before. The data can now be modified.

If the data have been uploaded to BIOS, they cannot be edited; however, a comment may be added to the sample information detail screen in the comments box.

How to enter and edit data – Toxicological Database

Query the Database for Facilities

- 1) Most samples processed for toxicity analyses were collected from some type of facility that discharges into surface water. Before an effluent sample can be set up in the database, its facility must be established in the facility reference table. With the splash screen displayed, go to the Bioassay menu and choose Facilities.

Bioassay	User Info	Hel
Samples		
Facilities		
Facility types		
NPDES sites		
DEP Districts		
Sample types		
Diluents		
Test organisms		
Calculation methods		
Causes of toxicity		
Maintenance		

The following Facility Information screen will be displayed:

- 2) As was described for the Biological Database, there are a few ways to determine if the facility of interest has been established. The user can scroll through the entries or use the **Sort** key to arrange

the facilities in a more easily viewed order. It is usually faster to click on the Find by Criteria button (or use the Ctrl-F or ⌘-F key sequence), which will display the following screen:

Find Facility:

District:

Facility Name:

alton

Cancel

Find

All synonyms of the facilities that match will be included.

Note:

You can use "@" as a wildcard character in the facility name.

Example: "@WWTP" would find all facility names that end with WWTP.

If you also picked a district, you would find all the WWTP in the that district.

Enter the first few letters of the facility name. The program inserts a wildcard character after the text that is typed by the user, so all facilities with names beginning with that string will be found. You can use two criteria to further restrict the search by choosing a district from the popup menu.

- unknown
Tallahassee
Southwest Distr
Southeast Distr
South Distr
Northwest Distr
Northeast Distr
Central Distr

Facility names can change over time, and the database has a mechanism for keeping track of these “synonyms”, as well as the most current name for the facility. Please see the notes in the Data Dictionary for details on the relationship between current and former facility names. When a search is performed, all synonyms of the facilities that match are displayed.

- 3) One of two things will happen at this point.
- a) If the facility does not exist in the database, you will see a message that says “No facilities found”. If you have “Data Entry” permission, you will not be allowed to enter a new facility. Contact your group database administrator for assistance in having the facility added to the database. You cannot proceed further with the entry of this data. Press DONE to exit from this screen.

b) If the station(s) does exist in the database, a screen will appear listing the selected sites(s). For the query pictured above, the program will return a list of five facilities:

Florida Department of Environmental Protection

Facility Information

DEP ID	Current	Facility Name	District	Status
18	256	Alton Box Board Company	UK	0
19	256	Alton Packaging Company	UK	0
102	256	Container Corporation of America	UK	0
51	256	Jefferson Smurfit	NE	0
256	256	Jefferson Smurfit, Fernandina	UK	0

Number of facilities displayed above = 5

You are in group 1.

You have permission to enter/edit data.

Find by criteria ⌘F

Show pending

Sort ⌘S

Done ⌘D

Add new facility ⌘N

Show all

Print ⌘P

DEP State

version

c) By double clicking on the facility of interest, a detailed information screen like the one at right will display:

d) Compare the facility information on your data sheet with the information on the screen to see if they are indeed the same facility. If you are unsure, contact your database administrator for assistance. If you are sure the stations are the same, proceed to the next section, Data Entry. Press Cancel to exit from this screen, then Done to exit from the main “Facility Information” screen and return to the splash screen.

Florida Department of Environmental Protection

Facility Information

Site status0Parent ID256

ID for this name18 (computer-generated)

Facility NameAlton Box Board Company

District IDNENortheast Distr(50 chars)

Address1234 Industrial Highway(30 chars)

CityJacksonville(30 chars)

StateFLZip Code32222-0000

☐ Most current name for facility

☒ Check if this name is acceptable

If you are adding a new facility, you can't assign a synonym name until you have saved the name (click done, then double-click the new name)

Show all names for this facility

Pick a synonym for this name

Delete this facility

Done ⌘D

Cancel ⌘.

Save & Next (Enter key)

Sample Data Entry

The sample data entry portion of the toxicological database is still in the design phase, but close to completion. The next version of this manual will document this section in detail.

DEP Statewide Biological Database

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99 January 26 version

Reference Tables – Biological Database

The “Reference Info” pull-down menu on the splash screen allows the user to view the Reference Tables in the Biological Database. Reference tables are really “look up tables”. This means that they contain information that the computer needs to make reports and screens that make sense. For example, a station is known by its DEP ID number, its STORET number, or by its station nickname. In addition, you may need to know its latitude/longitude, the county where it is found, its HUC code, among other things.

Three of the reference tables (Stations, Counties, and Waterbodies) have an extra button that searches the database and creates a list of associated samples. This function will be discussed in detail later in this section.

Stations

There are nearly 7,000 stations in the database (Fall, 1998). When you choose Stations from the Reference Info pull-down menu, all of the stations are listed, as displayed below. While this list may be scrolled through to find the station of interest, it is more efficient to use the database’s “Find by Criteria” function. This was explained in detail in the section “Query the Database for Stations”, beginning on page 11

STORET Station	Nickname	Station Description	DEP ID
25020056		SADDLE CK CANAL @ OLD W'NTR HVN BT'W HW'Y	6461
25020011		Whidden Creek @ Old Bowling Green Rd	6457
25020038		BEARS BR @ US HW'Y 17	6460
25020047		Peace Creek Canal @ Gandy Bridge	6458
25020235		LAKE LENA RUN @ THORNHILL RD	6459
24030057	ZEPHYRTST	Zephyrhills River, TP38	5898
WCA124	Z4	WCA1, 6.38 km E-SE of S-6 Pump Station	6363
WCA123	Z3	WCA1, 4.0 km E-SE of S-6 Pump Station	6362
WCA122	Z2	WCA1, 1.94 km E-SE of S-6 Pump Station	6361
WCA121	Z1	WCA1, 0.69 km E-SE of S-6 Pump Station	6360
WCA120	Z0	WCA1, .69 km ESE of S6 Pump Station in L39 Canal	6380
19020060	YULEETST	Unnamed tributary to Lumber Creek	6776
19020059	YULEEREF	Unnamed tributary to Nassau River	6775
22020017	YONCKREF	Yon Creek @ SR12	7056

Number of stations displayed above = 6826

Find by criteria %F Show selected stations Sort %S Done %D

Add new station %N Show all stations Print %P

Download entire station table

When the station of interest is found, double-click on it to display the Station Information detail screen. If the station does not yet exist in the database, it may be added by clicking on the Add New Station button.

Anyone with Group Administrator access and above may enter a new station in the database, and should follow these guidelines:

- 1) The STORET station code may have 15 characters, and must be unique. Make sure it is a valid station in the STORET system as well, since these data are uploaded to the federal database (BIOS) on a regular basis.
- 2) The station nickname must also be unique, and may only have 10 characters. Remember that nicknames are subject to change as the stations are used for different purposes.
- 3) The waterbody name must be listed in the Waterbody reference table. To help determine

Florida Department of Environmental Protection

Station Information DEP ID: 6039

STORET station code: 22030024 (15 chars)

Station nickname: WAKRBOGGY (10 chars)

Station Description: WAKULLA RIVER 100YDS BELOW BOGGY BRANCH (48 chars)

Water Body: WAKULLA RIVER (50 chars)

County: 129 Wakulla (50 chars, % for wildcard)

Latitude degrees: 30 mins: 9 secs: 48.5

Longitude degrees: 84 mins: 13 secs: 25.9

HUC Code: 03120001 (8 chars) 108588.5 303205.9

Subbasin: 0 (not required)

This section is not required

EPA reach: (20 chars)

Reach miles: 0 (number xxxx.xxx)

Check digit: (2 chars)

Station Type

Level 1 (required): Stream

Level 2a (required): Ambient

Levels 2b, 3, & 4 are required for PIPE;

Level 2b:

Level 3:

Level 4:

Level 5 (optional):

What's been sampled?

Buttons: Delete this station, Done, Cancel, Save & Next

- if it is present, you may type the first few letters of the waterbody name, and a box will appear with matching waterbodies to choose from. If it is not on the list, you must exit the station entry area and add the waterbody. Anyone with Group Administrator access and above may enter new waterbodies.
- 4) Latitude and longitude are expressed as “degrees, minutes, seconds”. Make sure you enter the correct latitude and longitude for the station location. As the program saves the information you enter, it checks them against the county selected in the pull-down menu, and gives an alert if the coordinate(s) are outside defined boundaries.
 - 5) The Hydrologic Unit Code (HUC) is a required field, but the USGS subbasin and EPA reach information is optional.
 - 6) Station levels 1 and 2a are required. If the level 1 chosen is “pipe”, then levels 2b, 3, and 4 are required. Station level 5 is optional.

What's Been Sampled?

There is a button below the Station Level 5 pull-down menu at the lower right of the screen called What's been sampled?. This function which allows the user to obtain a list of all of the samples collected at that station, including the gear used, county, waterbody name, and the types of data collected

Florida Department of Environmental Protection

Sampled	STORET Station Code	Nickname	Sample Date	Gear Name	County Name	Benthos?	Periphy?	Phyto?	Zoo?	Pchem?	Waterbody Name
8280	22030024	WAKRBOGGY	01/19/78	PetitePonr	WAKULLA	Y	N	N	N	N	WAKULLA RIVER
8277	22030024	WAKRBOGGY	07/13/87	PetitePonr	WAKULLA	Y	N	N	N	N	WAKULLA RIVER
11646	22030024	WAKRBOGGY	03/04/97	PetitePonr	WAKULLA	Y	N	N	N	Y	WAKULLA RIVER

Number of samples displayed above = 3

Buttons: Save as file, Sort %S, Print %P, Done %D

Surveys

Each sample entered into the database must be associated with a survey in order for it to be uploaded to BIOS. During sample creation, the elements from the survey table populate the pull-down menu that is used to assign a survey to a sample. All surveys must have a BIOS ID Number, which is issued by STORET. If a new survey needs to be entered, you must contact the Database Administrator or Assistant Database Administrator and provide the following information:

- 1) the starting date of the survey;
- 2) the survey name; and
- 3) the purpose of the survey. The survey purpose must be one of the following: Baseline, Enforcement, Monitoring, Research, Screening, or Use Attainability.

Choose Surveys from the Reference Info menu to see the following listing.

Florida Department of Environmental Protection				
Survey Information				
DEP ID	BIOS ID	Start Date	Survey Name	Survey Purpose
2	1	3/17/50	FLORIDA AMBIENT	Monitoring
6	2	8/1/78	KISSIMMEE R STUDY	Use Attainability
3	3	2/1/82	SUWANNEE R BASELINE	Baseline
7	4	10/13/84	IMPOUNDMENT STUDY	Use Attainability
8	5	10/21/85	OCHLOCKONEE R STUDY	Use Attainability
9	6	11/17/86	LAKE MUNSON STUDY	Use Attainability

Number of surveys displayed above = 24

Double click on an entry, or click the Add new survey button to view the Survey Information Detail screen.

Survey Information	
DEP ID	17 (computer-generated)
BIOS ID	15 (5 digits)
Start Date	07/01/95 (mm/dd/yyyy)
Survey Name	BIORECON (20 chars)
Purpose	Screening (20 chars)



Delete this survey



Done



Cancel



Save & Next

Sample Gear

The sample gear table describes the various tools used for collecting biological samples and observations. Choose **Sample Gear** from the **Reference Info** pull-down menu to get a listing similar to those displayed for the Station and Survey tables.

Double click on a gear entry to see the Sample Gear Information Detail screen. Each gear has a BIOS ID for storage in STORET, a nickname for general use in the database, and a description field for extra details. Gear types can be designated as Regular, Part of a Group, or the Group Title. Gear groups are used to associate “like gears”. During retrievals, the gear group may be chosen to pool samples from all gears in the group, or the individual gears may chosen to keep the data separate. A more detailed example of this is given in the “Retrieval Details” on page 73.

Certain gears used to collect macrobenthos data are designed to collect a quantitative sample, that is, of known surface area. There is a field for entering the surface area of the gear, which is used for calculating the density of organisms in quantitative samples.

Only the Database Administrator can add new sampling gears; you must contact him(her) if you feel your gear is not represented by those in the table.

Functional Feeding Groups

Many of the Florida macrobenthos taxa in the database have had functional feeding groups assigned to them. Select Feeding Groups from the Reference Info menu to see the list below.

Functional Feeding Groups		
Group Code	Group Description	Type
0	Unknown	1
5	Sub col-gthr/dep fdr	2
12	Shredder (macr) (fw)	2
41	Sh + sr	3
11	Scraper (peri) (fw)	2
10	Scavenger (animals)	2
9	Predator/carnivore	2
8	Plant piercer	2
61	Pl + sh	3
20	Pc + sv	3
19	Pc + sh	3
62	Pc + sf	3
28	Pc + pl	3
7	Parasite	2
17	Pa + pc	3
6	Epi col-gthr/dep fdr	2
42	Da + sv	3
15	Da + sr	3
16	Da + sh	3
13	Da + sf	3
18	Da + pl	3
14	Da + pc	3
4	Col-fltr/susp fdr	2
3	Brower-grazer (mar)	2
26	Bg + sv	3

For information displayed above

Add new FF Code %N

Sort %S

Print %P

Done %D

There are two categories of feeding group: single and multiple, represented by Types 2 and 3 at left, respectively. A single feeding strategy is something like “predator/carnivore” or “suspension feeder”. This means that the animal has only one method of feeding. Multiple strategies are made up of several single strategies; for example, “Pc + sh”, which stands for “predator/carnivore” and “shredder”. When multiple feeding strategies are defined, each single feeding strategy used to define it is assigned a percent (see screen below). The percents always sum to 100%.

Functional Feeding Groups

Feeding Code **13** (computer-generated)

Description **Da + sf** (20 chars)

Strategy type **Multiple Strategies**

Group	Percent
Col-fltr/susp fdr	.50
Epi col-gthr/dep fdr	.50

Percents sum to: **1**

Delete this feeding group

Done Cancel

Taxa that use this feeding group
Click once here to write the displayed taxa to file "FFTaxa"

- Spionidae
- Polydora
- Polydora socialis
- Polydora plena
- Polydora caulleryi
- Polydora ciliata
- Polydora commensalis
- Polydora ligni
- Polydora websteri
- Polydora tetrabranchia
- Polydora aggregata
- Polydora hartmanae
- Prionospio
- Prionospio heterobranchia
- Prionospio pinnata
- Prionospio steenstrupi
- Prionospio pygmaea
- Prionospio cristata
- Prionospio fallax
- Prionospio treadwelli
- Spio
- Spio setosa

Show 1st 1,000 taxa

Show next 1,000 taxa

To delete a group, change its percent to zero and click the "Delete groups" button.

Add feeding group

Delete groups

The functional feeding group detail screen allows the user to search the database and generate a list of all taxa assigned to that particular strategy. Click on the **Show 1st 1,000 Taxa** button. An alert box will appear, asking if you want to restrict the search.

Do you want to restrict it to a specific phylo code?

If you click Yes, the program will ask you for a numeric phylogenetic code that corresponds to the taxonomic level of interest. For example, you may be interested in all Dipterans that are suspension feeders. The phylogenetic code for Dipterans is '460530', which you can get from the View taxon info items under the Taxa menu. This is discussed in detail later in this manual.

If you click No, the database will search the entire Florida List for taxa with that feeding strategy. The resulting list will appear in the box at right. A small box in the lower right corner of the screen tells how many taxa are in the list. If there are more than 1,000 taxa, the Show next 1,000 taxa button will be available.

There is a small box at the top of the taxa list, which is actually a button. Click once and the list of taxa will be written to a file named 'FFTaxa', located in the same folder as the database. Every time you write to FFTaxa, the organism names are appended to those already present, so it is best to empty the file occasionally. It can also be renamed or discarded, as the database will automatically make a new one the next time you need to write taxa to it.

Taxa that use this feeding group
Click once here to write the
displayed taxa to file "FFTaxa"

Only the Database Administrator can add or edit functional feeding groups information.

Collectors

All samples must be associated with a collector before they can be stored in BIOS. The Assistant Database Administrator is responsible for maintaining the collector list in the Biological Database and in the STORET reference table. Contact him(her) to have new personnel added to the list.

Choose **Collectors** from the **Reference Info** menu to see the list of collectors, along with their agency affiliations and phone numbers during the time they collected samples.

Sample Collectors				
DEP ID	BIOS ID	Collector's Name	Address	Phone
202	157	Abad, Rick	FL DEP, NW District	904-436-8340
93	93	Abate, Glen	FL DER, NE Dist.	904-448-4300
2	29	Armstrong, Randall	FL DER, Tallahassee	unknown
3	39	Banks, E. Lee	FL DEP, NE District	904-448-4340
4	43	Barber, Ed	FL DER, NE District	904-396-6959
76	16	Barge, Christy	FL DEP, Tallahassee	904-487-2245

For collector information displayed above			
Add new collector IN	Sort IS	Print IP	Done ID

Identifiers

Each biological sample must have an associated identifier before it can be uploaded to BIOS. The Assistant Database Administrator is responsible for maintaining the identifier list in the Biological Database and in the STORET reference table. Contact him(her) to have new personnel added to the list.

Choose Identifiers from the Reference Info menu to see the list of taxonomic identifiers, along with their agency affiliations and phone numbers during the time they identified samples.

Sample Identifiers				
DEP ID	BIOSID	Identifier Name	Identifier Address	Identifier Phone
59	53	Young, William T.	FL DER, NW District	904-436-8340
69	11	Young, David	FL DEP, Tallahassee	904-487-2245
58	6	Wynn, J. Greg	FL DEP, Tallahassee	904-487-2245
84	76	Wright, James, O.	FL DEP, NE Dist.	904-448-4300
95	86	Whiting, Vicki	FL DEP, Tallahassee	904-487-2245
88	79	White, Conrad	Brevard Co., Dept. of Nat. Res.	407-633-2016
56	71	Walton, Albert S.	FL DEP, S District	813-639-4967
126	120	Walker, Jack	FL DER, NW District	904-444-8300

For sample information displayed above

Add new identifier %N
Sort %S
Print %P
Done %D

County LatLon

Select County LatLon from the Reference Info menu to get a listing of all of the Florida counties, as well as generic entries for a county in Georgia or Alabama. Double clicking on a county displays the screen at right.

This table stores the FIPS County Code, as well as latitude and longitude coordinates that describe a box that completely encloses the county. These coordinates are used to verify that those entered for a station are within the county the user assigns to the station.

The “What’s been sampled?” button retrieves a list of samples in the database that have been collected in the selected county. The “What’s been sampled?” function was described earlier in this section.

County Lat/Lon

County 39 Gadsden

What's been sampled?

Latitude

Minimum

30

23

03

degrees

minutes

seconds

Maximum

31

43

03

degrees

minutes

seconds

Longitude

Minimum

84

16

36

degrees

minutes

seconds

Maximum

85

56

10

degrees

minutes

seconds

**Delete
this
county**

Done

Cancel

**Save
&
Next**

Station Levels

The Station Level table lists characteristics of the sampling stations that correspond to those used in the STORET system. Choose **Station Levels** from the Reference Info menu to display this list. Level 1 describes different types of natural and man-made locations. Levels 2 through 5 allow the user to describe the intended uses of the sampling stations, some of which are appropriate only for particular Level 1 attributes (i.e., “pipe”). These station level attributes are assigned during the creation of a new station, and can be altered for an individual station on the station information detail screen.

Station Level Information			
Level 1-5	Level ID	PopUp Name	BIOS name
1	2	Canal	CANAL
1	3	Lake	LAKE
1	4	Reservoir	RESERV
1	5	Spring	SPRING
1	6	Well	WELL
1	7	FreshWetLand	FWTLND
1	8	SaltWetLand	SWTLND
1	9	Estuary	ESTURY
1	10	Ocean	OCEAN
1	11	Land	LND
1	12	Pipe	PIPE
1	1	Stream	STREAM
2a	2	Non-Ambient	NONAMB
2a	1	Ambient	AMBNT
2b	1	No pollute abatement	NTRTMT
2b	2	Some pollute abatement	PTRTMT
2b	3	All pollute abatement	TREATD
2b	4	Combined treatment	CMBTRT
2b	5	Sewer	SEWER
2b	6	In treat facility	INPLNT
3	2	Industrial	IND
3	3	Combined	CMBMI
3	4	Agricultural	AGRI
3	5	Residential	DOMEST
3	6	Abandoned site	ABANDN
3	1	Municipal	MUN
4	2	Outfall/dischg/effluent	OUTFL

For information displayed above

Add new category IN

Sort IS

Print IP

Done ID

Station Level	
Station Level ID	7 computer-assigned
Level [1,2a,2b,3,4,5]	1
PopUp menu name	FreshWetLand
BIOS Name	FWTLND
What's been sampled?	

Double click on a station level to see the Station Level Detail Screen. The “What’s been sampled?” button retrieves a list of samples in the database that have been collected at all stations having the selected attribute. The “What’s been sampled?” function was described earlier in this section.

Water Bodies

All stations in the database must be associated with a waterbody, which are listed in this reference table. Choose Water Bodies from the Reference Info menu to display the waterbody list, where you can sort or print the list, find specific waterbodies, or add a new one if you have Group Administrator access.

DEP ID	STORET ID	Water Body Name
1231		A.J. HENRY LAKE
700		ADA LAKE
346		AINGER (ROCK) CREEK
59		AIRPORT BAYOU

Number of water bodies displayed above = 1595

Find by criteria %F Show selected water bodies Sort %S Done %D

Add new water body %N Show all water bodies Print %P

Presently, there are nearly 1600 waterbodies in the database so scrolling through the list to see if a particular waterbody is there would be rather cumbersome. To use the “Find” function, Click on the Find by criteria button. The following screen will be displayed:

Criteria for Waterbodies

Waterbody Name

STORET Station Code

Waterbody DEP ID

Cancel Find waterbodies by criteria above

Hint:
 You can use "@" as a wildcard character in Waterbody name & STORET boxes. For example:
 a@river
 will find all rivers that start with the letter "a".
 You can only enter one DEP ID at a time (no > or < at this time).

The black box on the right of the screen gives hints for using wildcard searches. Once you have located your waterbody, double click on the line to reveal the Waterbody Information Detail screen.

Water Bodies

DEP ID (computer-generated)

STORET Code (25 chars)

Water Body Name Required (50 chars)

What's been sampled?

Delete this water body Done Cancel Save & Next

The “What’s been sampled?” button retrieves a list of samples in the database that have been collected at all stations in or on the selected waterbody. The “What’s been sampled?” function was described in detail earlier in this section

Reference Tables – Toxicological Database

The reference tables that are unique to the toxicological portion of the database are accessed via the Bioassay pull-down menu. Two tables are used by both the biological and toxicological sections: the County Location Table and the Waterbody Table, described earlier.

Bioassay	User Info	Hel
Samples		
Facilities		
Facility types		
NPDES sites		
DEP Districts		
Sample types		
Diluents		
Test organisms		
Calculation methods		
Causes of toxicity		
Maintenance		

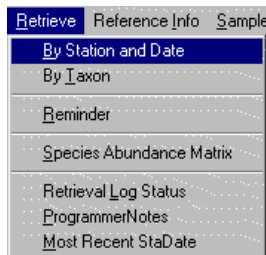
The tables associated with each menu item are:

Facilities:	Oracle table name: MT\$FACILITY_TOX 4D table name: [ToxFacility]
Facility Types:	Oracle table name: MT\$FACILITYTYPE_TOX 4D table name: [FacilityTypeTox]
NPDES Sites:	Oracle table name: MT\$NPDES_TOX 4D table name: [NPDESTox]
DEP Districts:	Oracle table name: MT\$DISTRICT_TOX 4D table name: [District_Tox]
Sample Types:	Oracle table name: MT\$SAMPLETYPE_TOX 4D table name: [ToxSampType]
Diluents:	Oracle table name: MT\$DILUENT_TOX 4D table name: [Diluent_Tox]
Test Organisms:	Oracle table name: MT\$TESTORG 4D table name: [TestOrg]
Calculation Methods:	Oracle table name: MT\$CALC_TOX 4D table name: [Calc_Tox]
Causes of Toxicity:	Oracle table name: MT\$CAUSE_TOX 4D table name: [Cause_Tox]

A detailed description of each of these reference tables will be available in the next version of the database manual

Retrieve Data

Types of Retrieval



There are two ways to retrieve data from this database. For retrievals “By Station and Date” locations and time periods are specified and information about the plants, animals, and physical/chemical parameters is returned. For retrievals “By Taxon”, you specify a taxon (or group of taxa) and you get the locations and time periods where it was found. Both methods will only retrieve data from samples marked “complete”, i.e., all data for the sample have been entered and verified, and all taxonomic inconsistencies have been resolved.

If you select “Reminder” from the above menu, the displayed message will be:

Retrieval By Station and Date

For this type of retrieval, you must specify locations (stations), dates (time periods), and variables (like number of taxa, Florida Index) to include. The results are displayed on the screen in a spreadsheet format which can be manipulated prior to saving as a tab-delimited text file. When the retrieval is finished, the following screen will be displayed:

To view the retrieval results click on the button that indicates the type of retrieval you requested.

If you do not wish to view the retrieval results before saving the file, you may just click “Done” when the retrieval is finished. This will take you back to the splash screen.

The program saves the retrieval results to default text files, located in the same folder as the program. The files are named according to the type of retrieval (see white box on screen at left). You can make a copy of these files and rename them for use in another software package. The program reuses these files (they are overwritten during each retrieval) so it is important that they be left in the 4th Dimension folder.

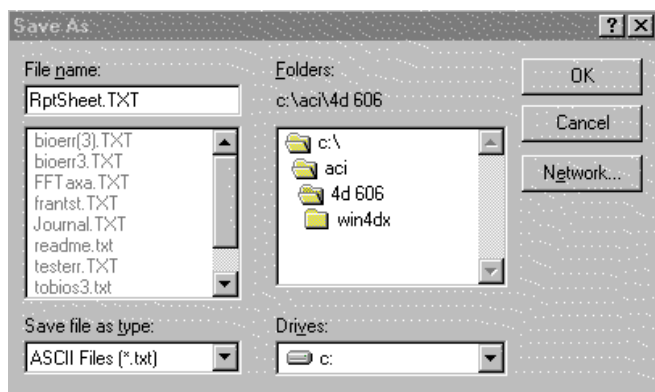
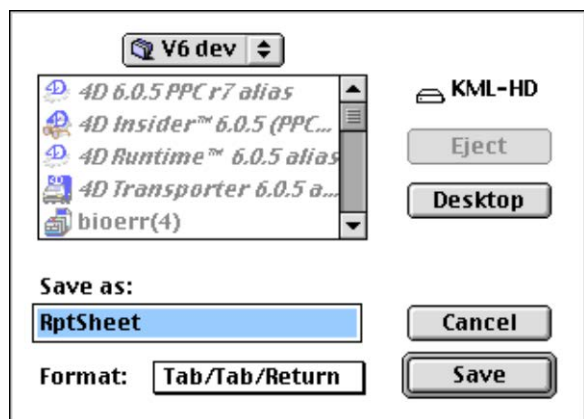
In this example both calculated variables and a taxa list “as entered” were retrieved for station “DPL2” for all sample dates between October 1990 and September 1991. The “CalcVars” spreadsheet is shown below.

Notice that there is a second row of menus just beneath the black message box on the left side of the screen. This row of menus has items that allow a limited amount of data manipulation, mainly related to sorting, printing, and saving. You can use these menus from here or you can “zoom” the spreadsheet so that it covers the entire screen.

The screenshot shows a software window titled "Florida Department of Environmental Protection". It has a menu bar with "File", "Edit", "Retrieve", "Reference Info", "Samples", "Taxa", "Bioassay", "User Info", and "Help". Below the menu bar is a black message box with the text: "If you zoom the spreadsheet, click on the close box in the upper left corner when you are done." To the right of the message box is a "Done" button. Below the message box is a row of menus: "File", "Edit", "Cells", "General Database". The main area is a spreadsheet with columns A through I. The data is as follows:

	A	B	C	D	E	F	G	H	I
1	StaNickName	DPL2	DPL2	DPL2	DPL2	DPL2	DPL2	DPL2	DPL2
2	StoretCode	32030E17	32030E17	32030E17	32030E17	32030E17	32030E17	32030E17	32030E17
3	Date	10/23/90	11/20/90	12/18/90	01/15/91	02/12/91	04/09/91	05/07/91	06/04/91
4	NSamplesBENHesterDend	1	1	1	1	1	1	1	1
5	NindCountedBENHesterDend	199	223	338	189	157	89	258	49
6	Nind/UnitAreaBENHesterDend	526.48	590.04	670.74	375.1	311.67	176.71	512	980.3
7	NTaxaBENHesterDend	20	38	21	26	39	26	27	4
8	DBarBENHesterDend	3.49	3.85	1.44	3.53	4.24	3.93	2.96	2.8
9	FlaIndexBENHesterDend	11	21	7	14	15	14	12	2
10	ID	10295	10309	10306	10335	10387	10424	10459	1049
11									
12									

While the spreadsheet is “zoomed” the regular database menus will be replaced by this row of spreadsheet menus. When you are finished with spreadsheet manipulations, click on the close box in the upper left corner to return to the display above.



If you want to save this output to a file that can be opened in a spreadsheet or word processing program, select “Save as...” from File menu (the lower File menu unless the spreadsheet is zoomed; then it would be the only File menu). When saving the file, **it is very important** to choose the format

option Tab/Tab/Return (Mac) or ASCII Files(*.txt) (Windows), located just under the field used to name the new file. **You will have to manually select this, as the default condition is to save the file as a 4D Calc document** (the 4D plug-in that creates the spreadsheet). **The 4D Calc document will not be able to be opened in your other software programs.**

Along with the calculated variables, you can request taxa lists for each station/date/gear combination. One choice will report the taxa with the names as they were entered; the second choice shows the taxa as they were when the variables were calculated (i.e., synonyms collapsed, indefinite taxa “collapsed upward”—this is discussed in detail in the section named “Upward collapsing of taxa” and in Appendix 2). Here is an example of a taxa list:

If you zoom the spreadsheet, click on the close box in the upper left corner when you are done.

Done

Click here to "zoom" the spreadsheet

File
Edit
Cells
General Database

☒ Station nickname:

	A	B	C	D	E	F
1	Station nickname:	DPL2				
2	STORET name:	32030E17				
3	Sample date:	10/23/90				
4	Benthos gear:	HesterDend				
5	Quantitative data as entered.					
6						
7	Phylum: Arthropoda					
8	Leptophlebiidae	3	7.94			
9	Choroterpes hubbelli	1	2.65			
10	Habrophlebiodes brunneipennis	2	5.29			
11	Caenis	2	5.29			
12	Leuctra	1	2.65			
13	Hydroporus	1	2.65			
14	Palpomyia/bezzia grp.	2	5.29			
15	Chironomidae	12	31.75			
16	Ablabesmyia mallochi	33	87.30			
17	Ablabesmyia rhamphe grp.	27	71.43			
18	Conchapelopia	13	34.39			
19	Helopelopia	1	2.65			
20	Meropelopia	6	15.87			
21	Corynoneura	1	2.65			
22	Thienemanniella fusca	2	5.29			

Retrieval By Taxon

You specify a taxon and the stations, dates, counties, and geographic coordinates where that taxon or that taxon and all subordinate taxa were found are displayed in a spreadsheet like this:

RptSheet										
☒	FLRATTREF									
	Sta Nickname	STORET Name	Sample Date	Station Description	Latitude	Longitude	County	Sample ID	Station ID	General Info
1	FLRATTREF	22020001	11/12/1996	ATTAPULGUS CR FLA 159 NW JAMISON	30 39 17	84 27 42	Gadsden	10940	1678	Labiobaetis propinquus
2	ORNGREF	28020148	08/27/1997	ORANGE RIVER HENDRY PROPERTY	26 39 42	81 42 56	Lee	12895	2460	Macrobrachium Data
3	MONSANTST	33020031	06/25/1996	ESCAM R BELD MONSANTO NEW OUTFA	30 35 43	87 09 31	Santa Rosa	10165	1372	
4	ECONFINREF	22050078	04/17/1997	Econfin River Forestry BMP Study Ref Site C	30 09 54	83 50 13	Taylor	11737	6607	
5	SIHOSTST	31010233	08/12/1997	South Mosquito Ck @ Branch Rd	30 41 30	84 43 34	Gadsden	12760	7058	
6	FLRQUINTST	22020046	11/12/1996	QUINCY CREEK BELOW FLORIDIN	30 35 50	84 34 30	Gadsden	10945	1693	
7	MOSESCK02	27010135	12/11/1996	Moses CK 1mi N of SR206 & 0.7mi W of US1	29 46 10	81 19 43	St Johns	12368	6873	
8	BARCLUNK	28020240	08/13/1997	Barron WCD C-2 Canal above SR80	26 46 02	81 19 26	Hendry	12910	7283	
9	MONSANREF	33020009	06/25/1996	ESCAMBIA R AT UPPER BLUFFS, ref for Monsanto FYI	30 36 38	87 15 30	Escambia	10158	1353	

If you want to save the results to a file, you can choose **Save as...** from the spreadsheet **File** menu. You must remember to choose the format option **tab/tab/return** if you want to use this file in another software package.

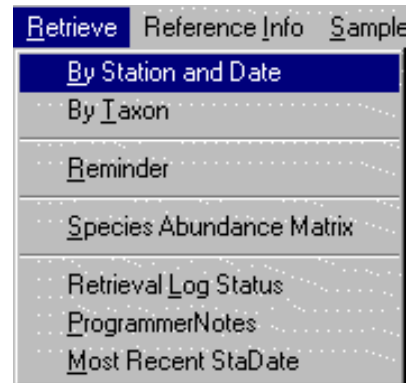
Reminder

All data displayed in this manual are made-up. Real station names may have been used, but any associated data was completely fabricated. Do not try to make any biological inferences from what you see in this document.

Basics of Retrieve by Station and Date

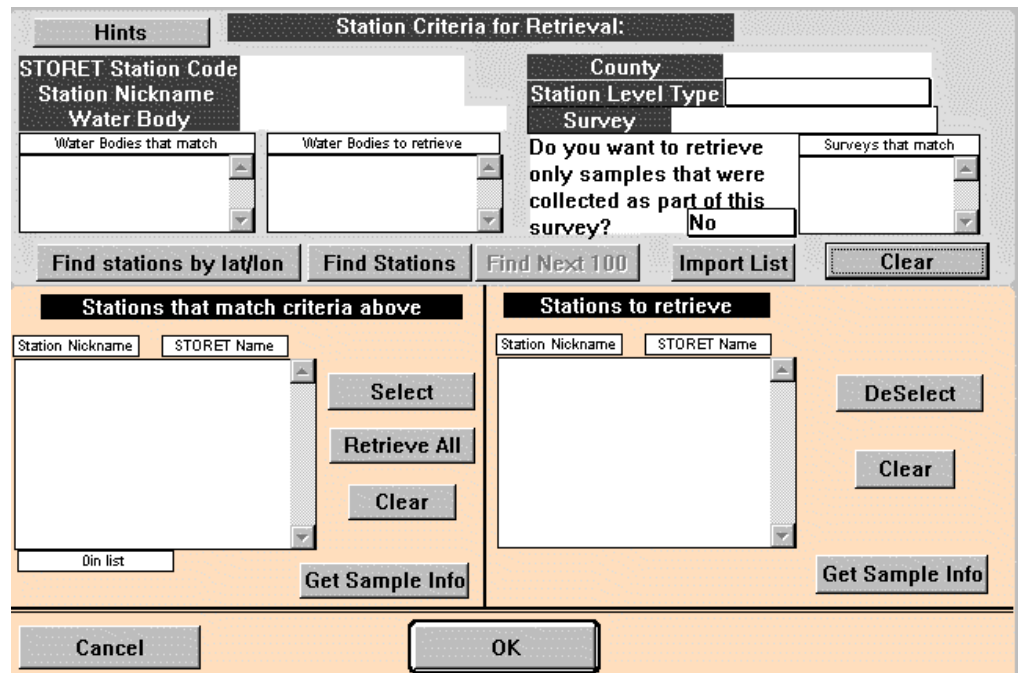
For this type of data retrieval, you will specify what locations (stations), time periods (dates), and parameters (variables) you want to include. The following steps will describe how to do a basic data retrieval. This part will give you the “how”; the “Details” section will give you the “why”. You can choose to write the criteria you to a file named “RetrievalLog” that is stored in your 4th Dimension folder by selecting Retrieval Log Status from the Retrieve menu and telling the program to do so. That way, if you forget what you specified, you can open this file in a word processing program. It is a good idea to occasionally empty this file as information is stored in it every time someone runs a retrieval and it can grow to be rather large. When you empty it, be sure to save it as a text file so 4th Dimension can still use it.

- 1) Use the Retrieve menu and select Retrieve by Station and Date



- 2) There will be a slight delay and then a large station selection screen will be displayed:

If your screen is too small to display the entire view at once, you will have to use the scroll bars to the left and bottom of the screen to position yourself. There are two main parts to this Station Criteria screen. The upper third of the screen is for entering the location, station level, or associated survey information



for the station(s) you want retrieve. This area works the same way as that used for querying the Station reference table, and is described in detail in the section titled “**Query the Database for Stations**”, beginning on page 11.

The Find Stations button will put all the stations that meet the specified criteria in the left scroll box. Double click on each station of interest, or click Retrieve All to get data from all of the listed stations.

- 3) Another way to load stations into the “Stations that match criteria” scroll box is to import a station list. Click on the Import List button. An alert box will appear that will let you know that the list must be in the form of a text file with one station nickname on each line. Navigate to the file, open it, and the list will be loaded. One way that this list may be created is through the “What’s Been Sampled?” function, described on page 46. The results from this query can be saved to a file and opened in a spreadsheet. Then, the column containing nicknames can be copied and pasted into a new file and saved as text. This can be a real timesaver if you have many stations to retrieve.
- 4) To see what data are available for the stations in either scroll box, click on Get Sample Info. There may be a delay before the following screen will be displayed:

2	Physical/chemical samples from	01/20/76	through	08/30/95
2	Benthos samples from	01/20/76	through	08/30/95
0	Periphyton samples from	99/99/99	through	00/00/00
1	Phytoplankton samples from	08/30/95	through	08/30/95
0	Zooplankton samples from	99/99/99	through	00/00/00

Done

This gives you the opportunity to “cancel” if the time period or data type of interest to you are not in the database. . If you want to start over with your station selections, click on Clear; if you don't want to do the retrieval, click on Cancel.

5) Once all the stations you want are in the “Stations to retrieve” box, click on OK. The next entry screen will display:

6) Now you select the time periods to include in the retrieval from this screen: I strongly suggest that you click the button in front of the type of date you want BEFORE you enter the starting and ending dates. This is not essential, but it can save you from having to reenter the dates depending on what you select. Assume that you selected two stations on the previous station screen, SUW1 and SUW2. Station SUW01 was sampled on 4/1/85 (10 individuals counted), 4/21/85 (15 individuals) and 5/10/85 (20 individuals). Station SUW02 was sampled on 4/15/85 (30 individuals) and 5/15/85 (35 individuals). Suppose you entered a retrieval range of “04/01/85” through “05/31/85”.

7) The following examples demonstrate the differences in the results when you choose the various date combining options:

Keep each date separate

The dates on all samples found within the range specified for the stations you previously selected will be reported separately. The resulting file will have rows like this:

StaNickName	STOREName	SampleDate	NumberSamples	NumberCounted
SUW1	31030003	850401	1	10
SUW1	31030003	850421	1	15
SUW1	31030003	850510	1	20
SUW2	31030004	850415	1	30
SUW2	31030004	850515	1	35

Combine by month

All the samples taken within each calendar month are “pooled” before the variables are calculated.

StaNickName	STOREName	SampleDate	NumberSamples	NumberCounted
SUW1	31030003	8504	2	25
SUW1	31030003	8505	1	20
SUW2	31030004	8504	1	30
SUW2	31030004	8505	1	35

Combine by year

All the samples taken within each calendar year are “pooled” before the variables are calculated. The starting and ending dates would be changed to “01/01/85” through “12/31/85” and any other samples taken in that year would be included. If there were no other samples in 1985 for these two stations you would get:

StaNickName	STOREName	SampleDate	NumberSamples	NumberCounted
SUW1	31030003	1985	3	45
SUW2	31030004	1985	2	65

Combine all dates All the samples taken within the date range you specify are “pooled” before the variables are calculated.

StaNickName	STORETname	SampleDate	NumberSamples	NumberCounted
SUW1	31030003	1985	3	45
SUW2	31030004	1985	2	65

Custom Combining This option allows you to pool all samples taken in groups of months. This feature is explained in the “Advanced features” section.

- 8) After you have selected the appropriate date option, click on OK to continue or Cancel to get out of the retrieval and back to the splash screen.

- 9) Select all the kinds of data you want to retrieve on this screen: There are three columns of boxes: Calculated variables — Variables like “number of individuals counted”, “number of taxa”, “DBar “(Shannon-Weaver diversity), etc. Taxa List A — A list of all the taxa for each date/station combination as the data entry person typed them. This means synonyms remain separate and no “upward collapsing” of taxa (i.e., the taxa will appear exactly as entered).

Taxa List B — A list of all the taxa for each date/station as they

are when prepared for calculation of variables. This means synonyms have been collapsed and non-distinct taxa have been collapsed “upward” (explained in the “Retrieval Details” section).

If you select a box under Taxa List A or B, select “Names only” or “Names and counts” in the box titled “For Taxa List(s)”. This tells the program whether or not you want the “number counted” printed next to each taxon’s name. There are two other options in this area: “No spaces in front of names” and “No phylum labels”. These have to do with the output formatting, and do not affect the results.

- 10) You have to decide if you want data that were collected and identified quantitatively or qualitatively. If you select “qualitative” or “both” some variables will be not be available for calculation and will be grayed-out on the next screen that is displayed. (“Both” means pool qualitative and quantitative and treat as if all of it was qualitative).
- 11) If you selected “Keep each date separate” for the dates, you can choose between “Combine replicates” and “Keep replicates separate”. If you chose any kind of grouping, you can only “Combine replicates”. “Keep replicates separate” means that variables will be calculated for each replicate of each sample. “Combine replicates” means all replicates within a sample are combined before the variables are calculated.

- 12) When retrieving “calculated variables” with reps combined, you can get physical/chemical data, if some was entered, by clicking in the box in front of **Get associated pchem**. If all you want is physical/chemical data, click in front of **Physical/Chemical only**. If the replicates for biological community samples were kept separate, you may not retrieve associated pchem.
- 13) Click on **OK** when you have finished making your report selections. If you selected any “Calculated variables”, proceed to step 14; if you chose “Physical/chemical only”, go to step 19; if you only selected taxa lists you can skip to step 20.

- 14) For each data type (macrobenthos, zooplankton, phytoplankton, and periphyton) you selected, you will be presented with a screen like this. The top of the screen identifies the type of data to be retrieved. If you selected “quantitative” data, all the boxes will be available; if you chose “qualitative” or “both”, some of them will be “grayed-out” which means that those variables cannot be calculated. “Number of samples” is always checked and cannot be “unchecked”. The “Retrieval Details” section has a description of the difference between “pool” and “average”, as does the information box at the right of the screen. Click in the box in front of each variable you want to have calculated.

Macrobenthos Data

☒ Number of samples (always done)
☐ Number of individuals/unit area
Number of individuals counted
☐ Pool ☐ Average
Number of taxa
☐ Pool ☐ Average
DBar (Shannon-Weaver Diversity)
☐ Pool ☐ Average
Florida Index
☐ Pool ☐ Average
Benthos Component of Lake Condition Index
☐ Pool ☐ Average
 Select all Clear

Available Gear Types
 [Dropdown menu]
Gear to Retrieve
 [List box] Clear %R
☐ Adjust sampling effort
 !!! Warning !!! "Adjust sampling effort" is NOT intended to be used on quantitative samples (except under unusual circumstances). It is primarily designed for use on dip net samples to compare the relative (yet qualitative) abundance between stations.

Individual Taxa to Retrieve
 [List box]
 Double-click on a name to remove it from the list
☐ Include dominant taxon
 Pick Taxa to retrieve
☐ # Individuals/unit area
☐ # Individuals counted (Pool)
☐ # Taxa in selected group
☐ Percent of sample (Pool)

Feeding Groups to Retrieve
 [List box]
 Double-Click on a name to remove it from the list
 Pick All Feeding Groups
 Pick Feeding Groups
☐ Number of individuals/unit area
☐ # Individuals counted (Pool)
☐ # Taxa in selected group
☐ Percent of sample (Pool)

What do 'Pool' and 'Average' mean?
 These terms refer to the way the taxa and counts are combined before the values (DBar, Fla Index, etc.) are calculated.
 POOL means that the data from all the samples in a station/date group are assembled into one grand taxa list BEFORE any values are calculated.
 AVERAGE means that the values are calculated separately for each sample in a station/date group and are then averaged to give the final value.
 When you have only one sample, pool and average give the same value. If multiple samples are combined to get a value, pool and average will give different results.
 If you are retrieving individual samples, (i.e., no station groups, keep dates separate), the retrieval will run much faster if you select 'Average'. This is because sample values are already calculated and stored in the database. The pooling option triggers the computer to calculate the numbers from scratch.

OK, I'm done picking variables
 Cancel

- 15) The statistics for individual taxa of interest can be calculated by clicking on the button that says Pick Taxa to retrieve. A small screen will display, allowing you to enter the individual taxa to retrieve. Select either “Only entries with this name” or “All entries in this taxonomic group”, depending on your criteria. To retrieve only those entries with the exact name as entered, select the

Enter individual taxa to retrieve:

[Text input field]

☒ Only entries with this name
☐ All entries in this taxonomic group

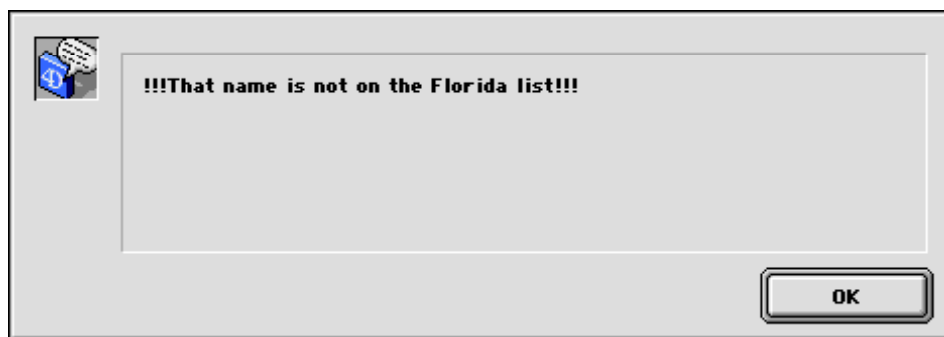
Cancel OK & Next
 OK & Done

If the scientific name has synonyms, occurrences of the synonyms will be included in this retrieval.

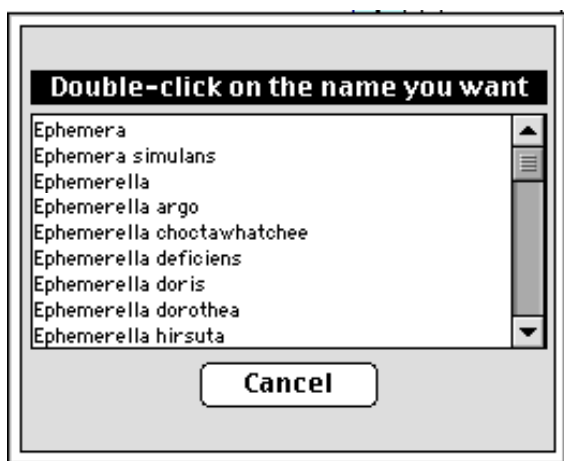
first option. To retrieve all names under the taxonomic entry, e.g., all the Pelecypods, select the second option. If you select the latter, an asterisk (“*”) will appear in front of the name. Leave the asterisk there; that is how the program

knows which option to choose.

Next, type in the name of the taxon of interest, or part of the name, and either tab out of the box or hit the “Enter/Return” key. The computer checks the Florida master list. If the name you typed is not on the Florida list, the following alert box will be displayed:



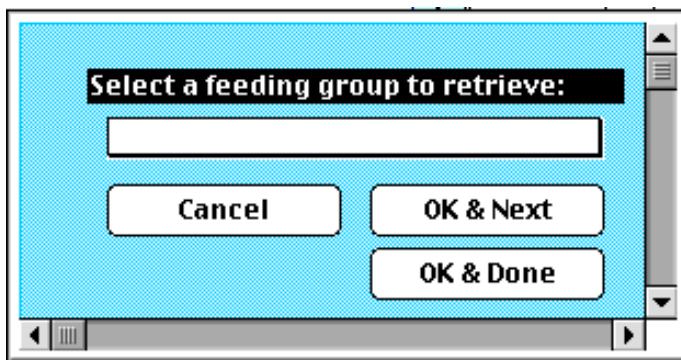
If only one name on the list matches what was entered, that name appears in the box; otherwise, a scrollable list with all the possible names will appear. Double-click on the name you want. You can only select names that are on the Florida master taxa list because those are the only names that appear in the database. Click on OK&Next if you want to select another taxon or on OK&Done if this is the last name you want to select. Click on Cancel if you changed your mind and don't want to select this taxon, or if the name you want is not on the list. The names you selected will appear in the scrolling box on the main screen when you are done. If you later decide you don't want a taxon, just double-click on it in the scrollable box and it will disappear. Now click in the boxes in front of the variables you want for the taxa you selected, i.e., # Individuals/unit area, # Individuals Counted, # Taxa in Selected Group, or Percent of Sample. If you want to retrieve the name of the most abundant taxon, click in the box labeled Include Dominant Taxon.



Important Note! There are some taxonomic anomalies associated with the Master Taxa list used in the Federal database, STORET (BIOS). This affects some of the most commonly retrieved phylogenetic groups, and must be taken into consideration when retrieving and tabulating data from this database.

- a) When retrieving members of the Dipteran family Chironomidae, you must ask for the family Chironomidae and the subfamily Orthocladiinae and add the results. Don't forget to click the radio button “All entries in this taxonomic group” when you pick the taxon or group to retrieve.
- b) To retrieve members of the order Odonata, you must ask for Odonata and the suborder Zygoptera. Add the two to calculate the number or percent of Odonates.

- 16) If the data type is “macrobenthos data”, you will be able to select functional feeding groups. There are two ways to do this. Click on the Pick Feeding Groups button and you will see the following screen:



There is a popup menu (shown below) with all the single feeding strategies. Select the feeding group of interest to you, then click on OK&Next if you want another feeding group; click on OK&Done if the current group is the last one you want. Click in the boxes in front of the

Sub col-gthr/dep fdr
Shredder (macr) (fw)
Scraper (peri) (fw)
Scavenger (animals)
Predator/carnivore
Plant piercer
Parasite
Epi col-gthr/dep fdr
Col-filtr/susp fdr
Browser-grazer (mar)

variables you want calculated for the feeding groups you selected. You will always be given the statistics for feeding group “unknown” so you can gage the reliability of the numbers for the other strategies. Be sure you read (in the “Details” section) how the numbers are accumulated for feeding groups before using these values.

Another method of choosing feeding groups for retrieval allows you to display all of the feeding



groups and remove those that don't apply. Click on Pick all Feeding Groups. When you double click on the groups you don't want they will be removed, leaving only those feeding groups of interest.

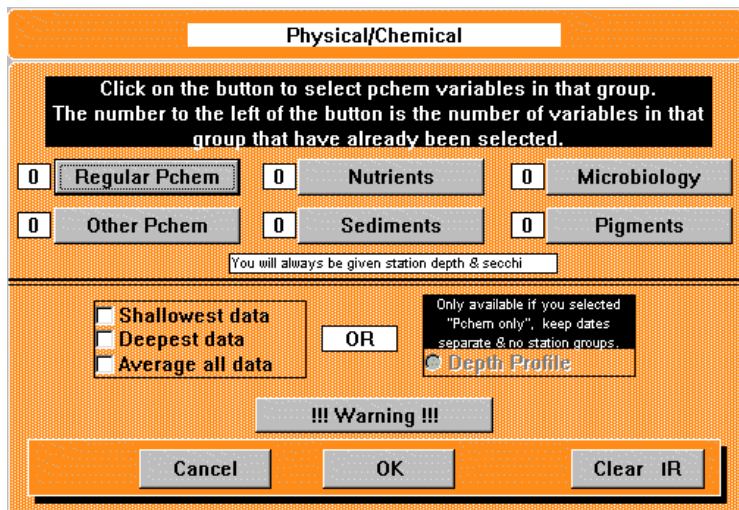
After selecting the feeding groups to retrieve, click in the boxes in front of the variables you want, i.e., # Individuals/unit area, # Individuals Counted, # Taxa in Selected Group, or Percent of Sample.

- 17) Next, select what gear types to retrieve. Click in the field below “Available Gear Types” in the upper right corner of the screen, holding down the mouse button to display a drop-down menu containing the gear types. Select the one(s) of interest to add them to the “Gear to Retrieve” box. If you change your mind about a gear, click on the Clear button to remove all of the selected gear types. You must then start over with the gear type selection. Each variable you select will be calculated for each gear type selected, separately. You cannot pool data for more than one gear type (except for “group gear type” -see “Details Section”). For example, if you choose “number of samples (NSamp)”, “number of individuals/unit area (NbrUnit)”, and “Florida Index (FlaIdx)” as the variables and “HesterDend”



and “PetitePonr” as the gear types, your spreadsheet file will have six columns: HesterDendNSamp, HesterDendNbrUnit, HesterDendFlaIndx, PetitePonr NSamp, PetitePonr NbrUnit, and PetitePonr FlaIndx.

- 18) Once all your selections are made, click on OK, I'm done picking variables. If there is another data type (i.e., periphyton, phytoplankton, etc.), you will be presented with another screen to select the variables for it. If you also selected “Get associated pchem”, you will see the physical/chemical screen described in step 19 will appear, after the screens for all the plant and animal data types.
- 19) There are 63 physical/chemical variables and they are selected through the screen below.

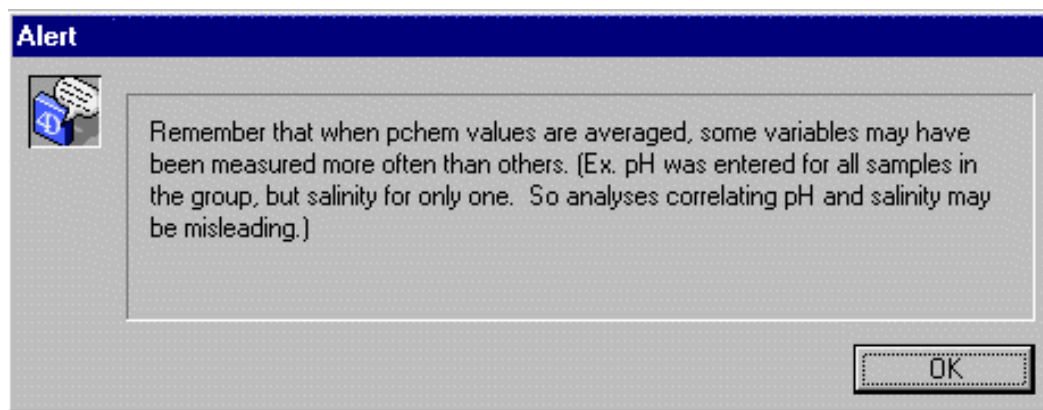


The screen is titled "Physical/Chemical" and has an orange background. At the top, it says "Click on the button to select pchem variables in that group. The number to the left of the button is the number of variables in that group that have already been selected." Below this, there are six buttons arranged in two rows of three. Each button has a number "0" to its left. The buttons are: "Regular Pchem", "Nutrients", "Microbiology", "Other Pchem", "Sediments", and "Pigments". Below the buttons, there is a text box that says "You will always be given station depth & secchi". At the bottom, there are three checkboxes: "Shallowest data", "Deepest data", and "Average all data". To the right of these checkboxes is a button labeled "OR". Further right is a button labeled "Depth Profile" with a small icon. Above the "Depth Profile" button is a text box that says "Only available if you selected 'Pchem only', keep dates separate & no station groups." At the bottom of the screen, there is a button labeled "!!! Warning !!!". At the very bottom, there are three buttons: "Cancel", "OK", and "Clear IR".

The six buttons on the screen (i.e., “Regular Pchem”, “Nutrients”, etc.) represent functional groups of variables. The number next to each button tells you how many variables from that group you have chosen (in this case, none). The station depth and secchi reading are automatically included in the retrieval file, so there is no need to specifically select these. If you chose “Physical/chemical only” and “Keep each date separate”, you can select “depth profile” which will give you a file with a row with the values of the variables you selected for every depth sampled for every station/date

combination. This option will be grayed-out if you selected “Get associated pchem”, and are also retrieving biological community data.

You can check all or some of “shallowest data”, “deepest data”, and “average all data”. Your choice will be dependent on the type of plant and animal data you previously selected. For many station/date combinations in this database, there was only one set of physical/chemical data taken, so if “shallowest” and “deepest” depths are selected, those columns will have the same values (since the shallowest reading was also the deepest). If you click on **!!!Warning!!!** you will see:



The next page has a diagram with an example of the screen you will see for each of the six buttons. The screen called “Less-Used Pchem Variables” is displayed when you click on “Other Pchem”. The rest of the screens have the same name as the button you click.

Florida Department of Environmental Protection

Regular Physical/Chemical Variables

- ☐ Alkalinity (mg/l CaCO₃)
- ☐ Conductivity, lab (µmho/cm)
- ☒ Conductivity, field (µmho/cm)
- ☐ DO, non-probe (mg/l)
- ☒ DO, probe (mg/l)
- ☐ Hardness (mg/l CaCO₃)
- ☐ pH (standard units)
- ☐ Salinity (ppt)
- ☒ Temperature (°C)
- ☐ Turbidity (NTU)

[Return to Main Screen](#)

Florida Department of Environmental Protection

Nutrient Variables

- ☐ Limiting Nutrient
- ☐ Ammonia, dissolved (mg/L N)
- ☒ Ammonia, total (mg/L N)
- ☐ Ammonia, unionized (mg/L NH₃)
- ☐ Nitrate, dissolved (mg/L N)
- ☐ Nitrate, total (mg/L N)
- ☐ Nitrite, dissolved (mg/L N)
- ☐ Nitrite, total (mg/L N)
- ☐ Nitrite+Nitrate, dissolved
- ☒ Nitrite+Nitrate, total
- ☐ Nitrogen, total (mg/L N)
- ☐ Nitrogen, total Kjeldahl (mg/L N)
- ☐ Orthophosphate, dissolved (mg/L P)
- ☐ Orthophosphate, total (mg/L P)
- ☒ Phosphorus, total (mg/L P)

[Return to Main Screen](#)

Florida Department of Environmental Protection

Algal Growth Variables

- ☒ Algal growth potential (mg dry wt/L)
- ☐ Chlorophyll-a, monochromatic, periphyton (mg/m²)
- ☒ Chlorophyll-a, monochromatic, water (µg/L)
- ☐ Phaeophyton, monochromatic, periphyton (mg/m²)
- ☒ Phaeophyton, monochromatic, water (µg/L)

[Return to Main Screen](#)

Florida Department of Environmental Protection

"Less-Used" Pchem Variables

- ☐ Carbon, total organic (mg/L C)
- ☐ Chloride, dissolved (mg/L)
- ☐ Chloride, total (mg/L)
- ☐ Residue, dissolved (TDS) (mg/L)
- ☐ Residue, total (mg/L)
- ☒ Residue, total nonfilterable (TSS) (mg/L)
- ☐ Residue, total volatile (mg/L)
- ☐ Residue, volatile nonfilterable (mg/L)
- ☐ Silica, dissolved (mg/L SiO₃)
- ☐ Silica, total (mg/L SiO₃)
- ☐ Sulfate, dissolved (mg/L SO₄)
- ☐ Sulfate, total (mg/L SO₄)
- ☐ Velocity, stream (ft/sec)

[Return to Main Screen](#)

Florida Department of Environmental Protection

Sediment Variables

Particle Size

- ☐ Less than 0.063 mm
- ☐ 0.063-0.125 mm
- ☐ 0.125-0.25 mm
- ☐ 0.25-0.5 mm
- ☐ 0.5-2.0 mm
- ☐ Greater than 2.0 mm
- ☒ Organic fraction

[Return to Main Screen](#)

Florida Department of Environmental Protection

Microbiology Variables

- ☐ BOD, 5-day (mg/L)
- ☐ BOD, 20-day (mg/L)
- ☐ Enterococci, membrane filter (no./100 ml)
- ☐ Escherichia coli, membrane filter (no./100 ml)
- ☐ Fecal coliforms, membrane filter (no./100 ml)
- ☐ Fecal coliforms, multiple tube (no./100 ml)
- ☐ Fecal Streptococcus, membrane filter (no./100 ml)
- ☐ Coliforms, total, membrane filter (no./100 ml)
- ☐ Coliforms, multiple tube (no./100 ml)
- ☐ Plate count, total (no./ml)

[Return to Main Screen](#)

Once you have selected everything you want, click on OK. The Clear button will mark all the physical/chemical variables to “not selected” and all the numbers next to the buttons will be changed to zero. If you don’t want to continue with the retrieval, click on Cancel and you will be returned to the splash screen.

- 20) If you chose to have a taxa list report, you will get a list for each station/date/gear combination you specified. If you selected a taxa list, but no calculated variables, you will see a screen like this:

You can restrict the taxa list to data collected with just one or several gear types. If you selected a taxa list with “Names only” instead of “Names and counts”, you can click on No Gear Restriction. This option will give you a taxa list of all plants or animals taken at each station/date combination regardless of how it was sampled (it will pay attention to what you marked for “quantitative/qualitative/both” so if you want everything, select “both”).

- 21) The computer will now do the actual retrieval. A box will appear in the middle of the screen that will tell you what station/date/gear it is currently calculating.

- 22) When the retrieval is finished, the following screen will be displayed.

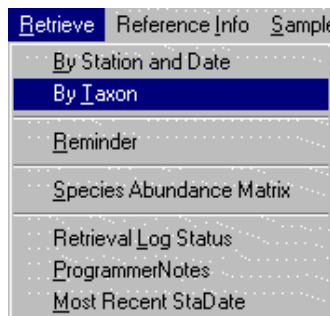
Depending on the retrieval options selected, one to three retrieval files will be generated containing the results. If you chose to have variables calculated (biological and/or pchem), you can click on the Show Calc Vars button to view the results. If you chose to retrieve a taxa list, click on Show Taxa “as entered” or Show Taxa “as calculated”, whichever is appropriate.

This file is viewed as a “4D Calc spreadsheet”. Please review the section on using this internal spreadsheet and saving files for other applications, beginning on page 56. When you are finished viewing the retrieval results, click on **Done** to return to the splash screen.

Basics of Retrieve by Taxon

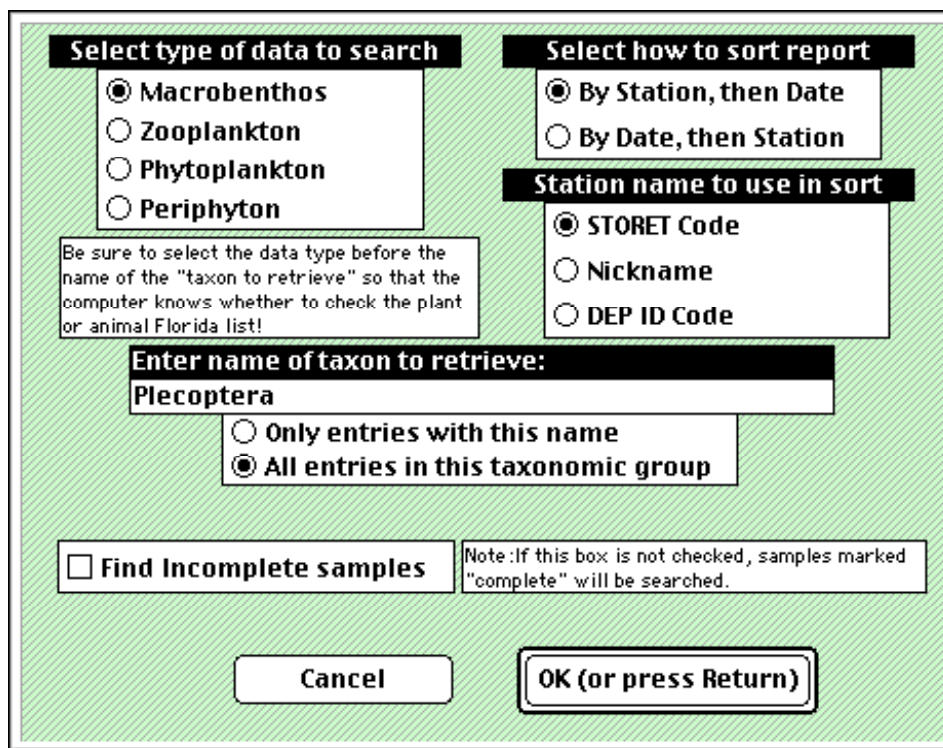
For this type of data retrieval, a taxon is specified and the computer will display stations, dates, and other details (of complete samples) where that taxon was found.

- 1) Use the Retrieve menu and select:

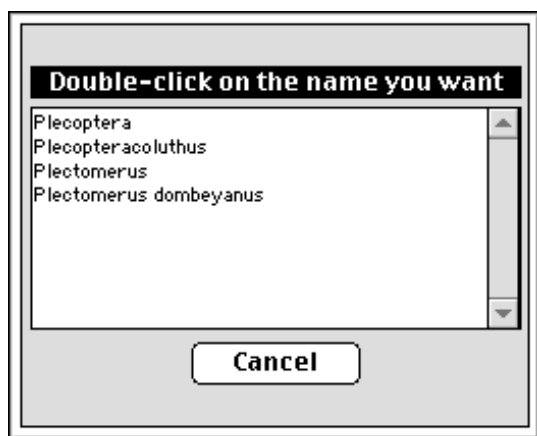


- 2) You will be presented with a screen to make your taxa selection:

- 3) First select the type of data (macrobenthos, periphyton, etc). Be sure this is done before selecting any of the other options so the program will know whether to use the plant or animal table when it goes to check the taxon name entered.

A screenshot of a dialog box titled 'Select type of data to search'. The dialog box has a light green background with a black border. It contains several sections: 'Select type of data to search' with radio buttons for 'Macroinvertebrates' (selected), 'Zooplankton', 'Phytoplankton', and 'Periphyton'; 'Select how to sort report' with radio buttons for 'By Station, then Date' (selected) and 'By Date, then Station'; 'Station name to use in sort' with radio buttons for 'STORET Code' (selected), 'Nickname', and 'DEP ID Code'; 'Enter name of taxon to retrieve:' with a text box containing 'Plecoptera'; and two radio buttons for 'Only entries with this name' and 'All entries in this taxonomic group' (selected). There is also a checkbox for 'Find Incomplete samples' and a note: 'Note: If this box is not checked, samples marked "complete" will be searched.' At the bottom are 'Cancel' and 'OK (or press Return)' buttons.

- 4) The report generated can be sorted by station and then date or vice-versa. The sort will only use one of the three station identifiers (STORET code, nickname, DEP ID code), so select one of these three options.



- 5) Enter part or all of the name of the taxon of interest. In the example, the first part of the name for “Plecoptera” is entered. After typing part of the name, press either the tab or Enter/Return key. The program will check the master plant or animal list and look for all names that start with the letters you entered. If only one match is found, that name will appear in the box. If more than one name matches, you will see a list like that displayed at left. Double-click on the name that you want. If you don’t see the name of the taxon, click the **Cancel** button and try to enter it again, just in case you misspelled it. The name will appear on the list if it occurs in the

samples marked “complete” in this data base.

- 6) Decide if you want the computer to look for all samples that have the name you selected entered exactly as you typed it (all entries identified with the scientific name “Plecoptera” – not identified to a lower level) or if you want it to find all entries in that taxonomic group, all plecopterans, for example. If you choose “All entries in this taxonomic group”, an asterisk “*” will appear in front of the name. Leave it there, that is how the program knows which option was selected.
- 7) Once all your choices have been made, click on **OK**. There will be a delay while the program conducts the search, then a screen will display the results as a “4D Calc spreadsheet”. Please review the section on using this internal spreadsheet and saving files for other applications, beginning on page 56.
- 8) When you are finished with the 4D Calc spreadsheet, click on **Done** to go back to the “Retrieve by Taxon” screen. Click **Cancel** to return to the splash screen.

Retrieval Details

Sample data

Qualitative/Quantitative/Both

When taxonomically-oriented data are entered, each gear's data are marked as qualitatively or quantitatively sampled. The gear type itself is not marked as qualitative or quantitative, but the actual sample is marked. Quantitative counts are converted to numbers per unit area (or unit volume, according to the community sampled); qualitative counts are not. At retrieval time, you must specify what kind of data you want. This choice affects the variables that can be calculated. Diversity and numbers per unit area are only available if you select quantitative data. You can specify that you want both quantitative and qualitative samples for the gear type of interest. When you do that all data are treated as if they were qualitative. This category has no effect on physical/chemical data.

Adjust Sampling Effort

Some analyses methods, particularly those for the processing of qualitative dip net samples, call for subsampling. The proportion of the sample processed is accommodated by the gear factor, discussed on page 17. During retrieval, you may choose to apply this gear factor to the counts so that you may compare the relative (yet qualitative) abundance between stations. However, the usual suite of measurements used to interpret qualitative macrobenthos data are not dependent on relative abundance but on the relative proportions of individuals from different taxonomic groups.

Keep replicates separate/combine replicates

When data are taken, there are usually multiple replicates that comprise a representative sample. In most retrievals, all the replicates are combined prior to calculating sample statistics. In some cases you may need to see statistics based on individual replicates. You can do this by selecting stations without grouping anything and "keep dates separate". If you choose this option, you may only retrieve one type of biological data and you may not get associated physical/chemical data in the same retrieval.

Pool/Average

When samples are combined to get one number for the "pooled" retrieval option, the computer builds a list of all the taxa found for the station and date group, accumulates the counts, and then calculates the statistics. When you want "averages", the computer calculates the statistics for each individual station/date and then averages them. For retrievals with one sample for each station and date group, "pool" and "average" give the same result.

Functional Feeding Groups

Many of the Florida macrobenthos taxa in the database have had functional feeding groups assigned to them. There are two categories of feeding group: single and multiple. A single feeding strategy is something like "parasite", "carnivore", "collector/gatherer", or "suspension feeder". This means that the animal has only one method of feeding. Multiple strategies are made up of several single strategies; for example, "collector/gatherer" and "shredder". When multiple feeding strategies are defined, each single feeding strategy used to define it is assigned a percent (see screen below). The values always sum to 100%.

Assume a retrieval has asked for the number of "Epi col-gthr/dep fdrs" (above

DEP Statewide Biological Database

Group	Percent
Col-fitr/susp fdr	.50
Epi col-gthr/dep fdr	.50

surface deposit feeders) in a sample. The search found 45 individuals whose feeding group was “Epi col-
gthr/dep fdr” and 67 who were “Da + sf”, which represents the multiple strategy of above surface deposit
feeding and suspension, or filter feeding (“Col-fltr/susp fdr”). The number of deposit feeders reported
would be $(45 + (.50 \times 67)) = 79$ (it always rounds to a whole integer value). The program finds all the taxa
with multiple strategies that use the requested single method and multiplies the number of individuals
for each taxon by the percent of the single strategy component.

It is also important to remember that not all macrobenthos taxa have had a functional feeding group
assigned. Assume the following sample data:

Taxon	Feeding group assigned in database	Number of individuals	Actual (but unknown) feeding group
1	Parasite	25	Parasite
2	Unknown	75	Deposit feeder
3	Deposit feeder	30	Deposit feeder

A retrieval has requested the percent of deposit feeders in the sample. The computer will give that
percent as $(30/130) \times 100 = 23.1\%$. But for 58% of the sample, the feeding group is unknown. The true
number of collectors is $((30 + 75)/130) = 81\%$. For that reason, every time a retrieval requests even one
feeding group, the number and percent of individuals with feeding group “unknown” is also reported for
each sample. Be sure you pay attention to these numbers so you can get a feel for how good the numbers
are for your requested feeding group.

Gear types/Gear levels

In general you cannot pool data taken with different gear types. The exception is if the gear of

The screenshot shows the 'Sampling Gear' form with the following fields and values:

- DEP ID: 4 (computer-generated)
- BIOS ID: (empty)
- Gear Nickname: SweepGrp (10 chars) (30 chars)
- Description: Group of sweep nets
- This gear is a: Group title (20 chars)
- Data Type: Macrobenthos
- Surface Area: 14.0000 (cm2, Macrobenthos only)

At the bottom, there are four buttons: 'Delete this gear' (trash icon), 'Cancel' (X icon), 'Done' (checkmark icon), and 'Save & Next' (floppy disk icon).

The screenshot shows the 'Sampling Gear' form with the following fields and values:

- DEP ID: 5 (computer-generated)
- BIOS ID: 123
- Gear Nickname: Sweep1 (10 chars) (30 chars)
- Description: Sweeps through snags
- This gear is a: Part of a group (20 chars)
- Group title for this gear is: SweepGrp
- Data Type: Macrobenthos
- Surface Area: 35.0000 (cm2, Macrobenthos only)

At the bottom, there are four buttons: 'Delete this gear' (trash icon), 'Cancel' (X icon), 'Done' (checkmark icon), and 'Save & Next' (floppy disk icon).

interest is a “gear group”. For example, suppose
there are different kinds of sweep nets entered in the database as separate gear types: sweep1, sweep2,
and sweep3. They were entered this way because someone may want to retrieve only the data taken with
one type of sweep net. Another gear type named “SweepGrp” is created as a “group title”. This is not an
actual gear but a name for a group of gears. The reference screen for each are shown below.

When doing a retrieval, if you select the gear type “SweepGrp”, you will get all the data taken with gear that are part of the “SweepGrp” group pooled. Only the Database Administrator status can add new gear types to the database.

“Upward collapsing” of taxa (i.e., Prepare for retrieval calculations)

When biological data (taxa and counts) are combined, the number of taxa may become artificially inflated by the incorporation of the same taxon under different names, and by counting high level identifications (family or genus) caused, for example, by immature or damaged specimens, as different taxa from more precise identifications (species) of better material. An erroneously high taxa count creates additional anomalies among statistics involving these counts, such as the Shannon-Weaver diversity index. As an arbitrary example, one might wish to combine these two replicates:

rep. 1	<i>Helopelopia</i> sp.	4	
	<i>Dicrotendipes simpsoni</i>	21	
	<i>Dicrotendipes modestus</i>	1	
	<i>Hyaella azteca</i>	11	
			4 taxa and 37 individuals

rep. 1	<i>Conchapelopia</i> sp.	2	
	<i>Dicrotendipes</i> sp.	20	
	<i>Hyaella azteca</i>	9	
	<i>Planorbella</i> sp.	1	
			4 taxa and 32 individuals

Simple combining would give:

total	<i>Conchapelopia</i> sp.	2	
	<i>Helopelopia</i> sp.	4	
	<i>Dicrotendipes simpsoni</i>	21	
	<i>Dicrotendipes modestus</i>	1	
	<i>Dicrotendipes</i> sp.	20	
	<i>Hyaella azteca</i>	20	
	<i>Planorbella</i> sp.	1	
			7 taxa and 69 individuals

Upward collapsing, however, will combine *Conchapelopia* and *Helopelopia* as synonyms, and will apportion the individuals from *Dicrotendipes* sp. to the two identified species of that genus, resulting in:

total	<i>Conchapelopia</i> sp.	6	
	<i>Dicrotendipes simpsoni</i>	40	
	<i>Dicrotendipes modestus</i>	2	
	<i>Hyaella azteca</i>	20	
	<i>Planorbella</i> sp.	1	
			5 taxa and 69 individuals

Note that if “*Dicrotendipes* sp.” had represented a distinct species level entity with no available or known name, it would have properly been entered as “*Dicrotendipes* sp. 14 Epler” or a similar name, and would then not have been combined. Collapsing will also take place at other taxonomic levels: family level i.d.’s will combine with generic level i.d.’s, species will combine with subspecies, etc.

See Appendix 2 for a detailed example of how data are prepared and the calculations done.

Programmer Notes

There is an item (Programmer Notes) in the retrieval pull-down menu that will ask you if you want all SQL statements generated in a station/date retrieval to be written to a file named LoriNote. Normally you want to click **Cancel**, but if there is a retrieval problem, you can answer **OK**. After the retrieval runs, turn it off and give a copy of the file LoriNote to the programmer maintaining this program. It will let him/her see exactly what was going on during your retrieval. It does generate a large amount of code and the file is never automatically overwritten, so LoriNote can grow to be rather large file. When you log on, it is automatically set to **Cancel**.

Advanced Retrieval Functions

Date Groups

A date group is a definition of one of more time periods that will be accumulated for each station before statistics are calculated. For example, you may want to get the number of taxa found in all Januaries from 1990 through 1992 for station 9. For example, suppose you have these data:

Station	Date	Taxon	Number of individuals
1	1/15/90	1	23
1	1/15/90	2	3
1	1/23/91	1	12
2	1/23/91	3	14
2	1/18/92	1	29

The computer will first make a table like this:

Taxon	Number of individuals
1	64
2	3
3	14

and then calculate the number of individuals, diversity, etc. The program will only allow you to group whole calendar months of data.

Defining a new date group

- 1) Click the button in front of Custom combining, then enter the starting and ending date of the range of interest, then click on Load Dates. To continue our example of all Januaries from 1990 through 1992, the screen would look like this:

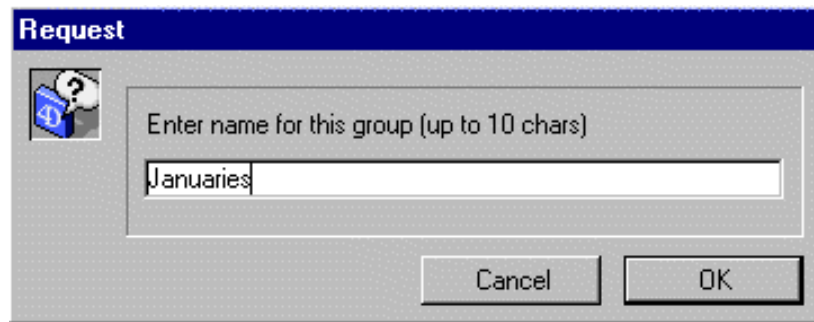
The screenshot shows a software window for defining a date group. At the top, there are five radio button options: 'Keep each date separate', 'Combine by month', 'Combine by year', 'Combine all dates', and 'Custom combining'. The 'Custom combining' option is selected. To the right of these options are two text input fields: 'Choose dates starting with:' containing '01/01/90' and 'through:' containing '12/31/93'. Below these fields are 'Cancel' and 'OK' buttons. A 'Load Dates' button is located below the radio buttons, with a small tooltip that says 'This button is for use with "Custom combining" only.' Below the 'Load Dates' button is a section with four list boxes: 'Available Dates' (containing dates from 90/01 to 90/12), 'Dates to Combine' (empty), 'Groups to retrieve' (empty), and 'Dates in Group' (empty). Below the 'Available Dates' list is a 'Select All' button. Below the 'Dates to Combine' list are 'Combine these' and 'Clear All' buttons. Below the 'Groups to retrieve' list is a 'Show Dates' button.

The computer loads all the months between the starting and ending date into the box labeled "Available Dates".

- 2) Double-click on the dates you want to include in the group. They will appear under the box labeled "Dates to Combine". When you have all the dates for one group in the box, click on Combine these. For the example, you would scroll through the "Available Dates" and double-click on "90/01", "91/01", and "92/01". The box will look like this:

This is a close-up of the 'Dates to Combine' list box. It contains three entries: '90/01', '91/01', and '92/01'. Below the list box are two buttons: 'Combine these' and 'Clear All'.

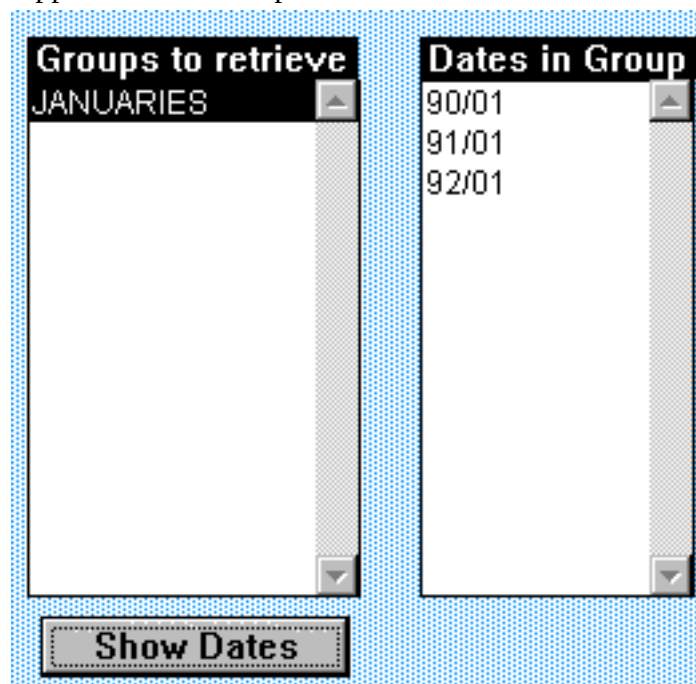
- 3) When you click on **Combine these**, you will be asked to name the group.



A dialog box titled "Request" with a blue header bar. It contains a text input field with the placeholder text "Enter name for this group (up to 10 chars)". The field contains the text "Januaries". Below the field are two buttons: "Cancel" and "OK".

This name will appear in the file and reports created by this retrieval. You cannot save date groups, so each time you run a retrieval and want to use date groups, you will have to define the groups.

- 4) The group name will appear under “Groups to retrieve” like this:



The interface shows two side-by-side list boxes. The left list box is titled "Groups to retrieve" and contains the text "JANUARIES". The right list box is titled "Dates in Group" and contains the dates "90/01", "91/01", and "92/01". Below the list boxes is a button labeled "Show Dates".

If you forget what is in a particular group, click once on the name of the group, then on **Show Dates**. You will see the months in the group under “Dates in group” as displayed above.

- 5) You can select another date group if necessary (like all Februaries). When you have defined all your groups, click on **OK**. You will see a message that tells you the program is building date clauses for each of your groups. The program is generating a SQL phrase it needs to do the retrieval for each date group. When all the phrases have been created, you will be taken to the report selection screen.

Species Abundance Matrix

Overview

The DEP Biology section has a program named Ordana that was written by Stephen A. Bloom of the University of Florida to do classification (cluster analysis) and ordination on benthic community data. In order to use this program, the data must be put into a matrix of species and stations in a very specific format. More often this matrix itself is useful in data analysis, so we call this routine "Species Abundance Matrix".

The Biological Database can prepare a matrix file that is suitable to use as input to Ordana from a taxa list file that was created by Retrieve-By station and date. It can also produce a version of the matrix that is tab-delimited with full scientific names and station name labels that can be used in a spreadsheet or word processing program.

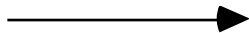
Basics

In order to use Species Abundance Matrix, you must have a "taxa list with counts" that you created in Retrieve - By Station and Date. It will convert the taxa list into a matrix with the taxa names in the first column followed by a column for each station/date combination with the number of individuals for each taxon. For example, assume you have a "taxa list with counts" file with four stations like this:

Species Abundance Matrix will produce a file like

Station nickname: COLUM4 STORET name: 21030003 Sample date: 08/13/84 Benthos gear: PetitPonar Quantitative data as prepared for calculations. Phylum: Annelida Placobdella phalera 299 Phylum: Arthropoda Pseudochironomus 1 Total number of individuals 300 *** End of List *** ----- Station nickname: COLUM5 STORET name: 21030003 Sample date: 08/13/84 Benthos gear: PetitPonar Quantitative data as prepared for calculations. Phylum: Annelida Placobdella phalera 23 Phylum: Arthropoda Tribelos fuscicornis 51 Pseudochironomus 109 Cladotanytarsus 789 Enallagma cardenium 32 DEP Statewide Biological Database	Station nickname: COLUM6 STORET name: 21030003 Sample date: 08/13/84 Benthos gear: PetitPonar Quantitative data as prepared for calculations. Phylum: Annelida Placobdella phalera 98 Phylum: Arthropoda Epicordulia regina 14 Total number of individuals 112 *** End of List *** ----- Station nickname: COLUM7 STORET name: 21030003 Sample date: 08/13/84 Benthos gear: PetitPonar Quantitative data as prepared for calculations. Phylum: Annelida Placobdella phalera 299 Phylum: Arthropoda Epicordulia regina 10 88
--	---

this:



Scientific Name	COLUM4	COLUM5	COLUM6	COLUM7
Cladotanytarsus	0	789	0	0
Placobdella phalera	299	23	98	299
Pseudochironomus	1	109	0	0
Abedus immaculatus	0	0	0	0
Enallagma cardenium	0	32	0	0
Epicordulia regina	0	0	14	10
Tribelos fuscicornis	0	51	0	0

Steps to follow:

- 1) Select Retrieve – Species Abundance Matrix.

- 2) This screen will be displayed:



- 3) Decide if you want to restrict which taxa are included in your matrix. The choices are:

- a) All taxa

Every taxon that is in the original taxa list file is included in the matrix.

- b) Top n taxa where n=

The program makes a list of all the taxa found in the original taxa list file and sums the number of individuals for those taxa over all stations. You enter a number in the box after “... where n=“ to indicate how many of the most abundant taxa you want to include. Assume the original taxa list file had the following data:

Station 1

<i>Placobdella phalera</i>	10
<i>Limnodrilus hoffmeisteri</i>	12
<i>Hyaella azteca</i>	123

Station 2

<i>Limnodrilus hoffmeisteri</i>	47
---------------------------------	----

Station 3

<i>Placobdella phalera</i>	5
<i>Polypedilum illinoense</i>	34

The computer will make a list of all the taxa that occurred and the number of individuals in each, then sort them from most to least abundant:

<i>Hyaella azteca</i>	123
<i>Limnodrilus hoffmeisteri</i>	59
<i>Polypedilum illinoense</i>	34

What taxa do you want to include in the matrix?

☒ All taxa

☐ Top n taxa where n = 0

☐ Taxa that occur at least n times where n = 0

What kind of file do you want?

☒ Tab-delimited file

☐ Ordana input file

How to sort tab-delimited file?

☐ By number of occurrences

☒ By taxon hierarchical no.

Do you want to use:

☒ Counts as entered

☐ Numbers per unit area

Check this box if you want to:

☒ Average counts

Buttons: Describe, Help, Cancel, OK

If you want to get the “top 2 taxa”, the resulting matrix file would look like this:

Scientific name	Station 1	Station 2	Station 3
<i>Hyaella azteca</i>	123	0	0
<i>Limnodrilus hoffmeisteri</i>	12	47	0

c) Taxa that occur at least n times where n=

The program makes a list of all the taxa found in the original taxa list file and sums the number of individuals for those taxa over all stations, just as in (b). You enter a number in the box after “...where n=“ to indicate many individuals the taxa must have (over all stations) to be included in the matrix file. Using the example above, if you enter the number 25 (i.e., a taxa must have at least 25 individuals to be included), the resulting matrix file would look like this:

Scientific name	Station 1	Station 2	Station 3
<i>Hyaella azteca</i>	123	0	0
<i>Limnodrilus hoffmeisteri</i>	12	47	0
<i>Polypedilum illinoense</i>	0	0	34

4) Decide on the file format for your matrix file. The choices are:

a) Tab-delimited file

The data will be stored in columns with tabs between the numbers. The first line of the file will have column labels. This file can easily be used in a spreadsheet or statistics program. For example, the matrix in 3c will look like this as a tab-delimited file:

Scientific name tab Station 1 tab Station 2 tab Station 3

Hyaella azteca tab 123 tab 0 tab 0

Limnodrilus hoffmeisteri tab 12 tab 47 tab 0

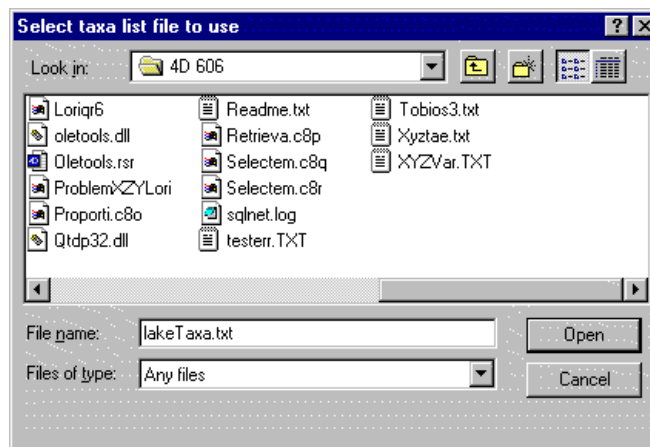
Polypedilum illinoense tab 0 tab 0 tab 34

b) Ordana input file

The data are stored in the format needed for the Ordana program. This format is not useful for anything but the Ordana program. Only the first 9 characters of the scientific name can be included in the file. This is not a problem since Ordana ignores the first 10 characters anyway. The first line of the file has the number of taxa followed by the number of stations. The matrix in 3c will look like this as an Ordana input file:

```
00003 00003
Hyaella 00123 00000 00000
Limnodril 00012 00047 00000
Polypedil 00000 00000 00034
```

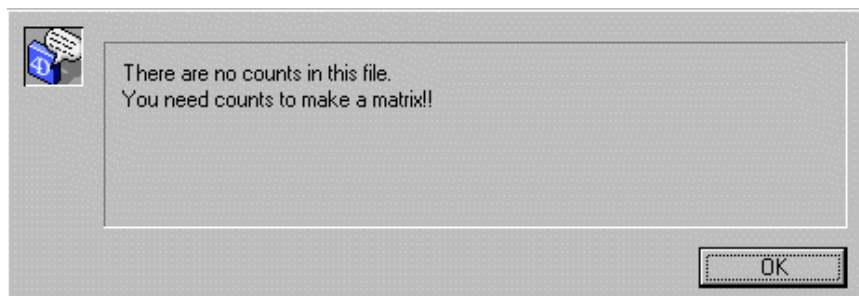
5) Next you will see a dialog box for picking the taxa list file to use:



You can get out of the Species Abundance Matrix routine by clicking on Cancel. Otherwise, choose a taxa list file and click on Open.

- 6) In this example, the taxa list was saved in a file named “LakeTaxa.txt”. If you selected a taxa list that does not have counts, you will see:

which means that the taxa list file you selected had only the scientific names and no counts (or maybe it wasn’t a taxa list file at all). The program can only make a matrix file from a taxa list file with counts, so when you click on OK, the program will quit Species Abundance Matrix and take you back to the splash screen .



- 7) If a taxa file with counts was successfully chosen, the program starts to do the calculations. A window will appear that will tell you the progress of those calculations.
- 8) When the program is ready to save the matrix information, you will see a box for entering the name and location of the new matrix file.



Enter the file name and click on Save. If you don’t want to save the file, click on Cancel. A progress box will indicate that the program is saving the file. Once the file is saved, the program returns to the splash screen. For best viewing, you should use a spreadsheet program like Excel to look at a tab-delimited matrix file, but you can also use a word processing program like Word. If you made a file for Ordana, you can exit 4D and run it in the usual way at this point.

How to maintain the master taxonomy table

Overview

The master taxonomy table is a list of over 200,000 plants and animals found in the United States. It was originally built from the master taxa list of the federal biological database, BIOS, which is a part of the STORET system. There is information stored about each taxon including whether or not it is found in Florida. The subset of the master taxa table that is marked as being in Florida is called the Florida list. Most of the taxa on the master list are marked as not being found in Florida. Since no one went through the entire list looking for Florida taxa, there are taxa on the list that are found in Florida but are not yet marked as Florida taxa.

The database administrator (DBA) is in charge of the scientific maintenance of the information in this table. A person doing data entry can enter any scientific name s/he wants. The computer checks to see if the name is a Florida taxon. If it is, the entry is accepted. If it is not, the computer warns the person and asks if s/he wants to retry entering the name (in the case of misspelling) or if the master list should be scanned. When the master list is scanned and the name is found, the taxon is marked as “temporarily” on the Florida list. If the name was not found anywhere on the master list, the data entry person can add it anyway and it will also be marked as “temporarily” on the Florida list. At a later time, the DBA can use Problems under Taxa to see what names have been temporarily added and who added them. The DBA can then decide to permanently add the name to the Florida list or to change the entries bearing that name to a different name.

All users have access to Taxa List Reports, View Taxon Info, and Show Fla List Date under the Taxa pulldown menu. Only the DBA has access to Problems and Maintenance.

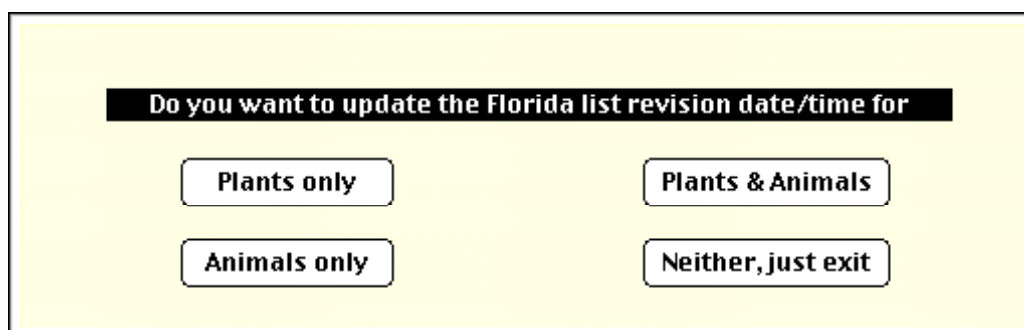
Data Storage and Download of Reference Lists

The data are stored in an Oracle database in Tallahassee. Each client has a 4th Dimension database program. These individual 4th Dimension databases are kept empty (i.e., do not permanently keep any data) with the following exceptions: the list of Florida plants and animals, reference lists used by the biological database (stations, waterbodies, counties, collectors, identifiers, gear types, surveys, etc.), and the reference lists used by the toxicity module (facilities, test organisms, NPDES sites, and others). The date these lists were downloaded to each client is stored in each 4th Dimension database.

Each of the lists mentioned above has a revision date that gives the date and time that the biological database administrator (DBA) last made changes to the Florida plants or animals, or when another user added or deleted information from another list. These revision dates are stored in the table MT\$SysMaint in the Oracle database. When you log on, the program checks the dates attached to the Oracle (master) version and if it is newer than the date attached to the list in 4th Dimension, it will download a new version of any file that has changed.

Items on these lists, particularly the scientific names, are used frequently by the program and it is better to have them on your client machine. This dramatically decreases the network traffic because you don't have to wait for information to be loaded from Oracle, and the amount of time you have to wait while executing the procedures that use them.

When the DBA is finished using either Problems or Maintenance under the Taxa pulldown menu, he/she will see this message:

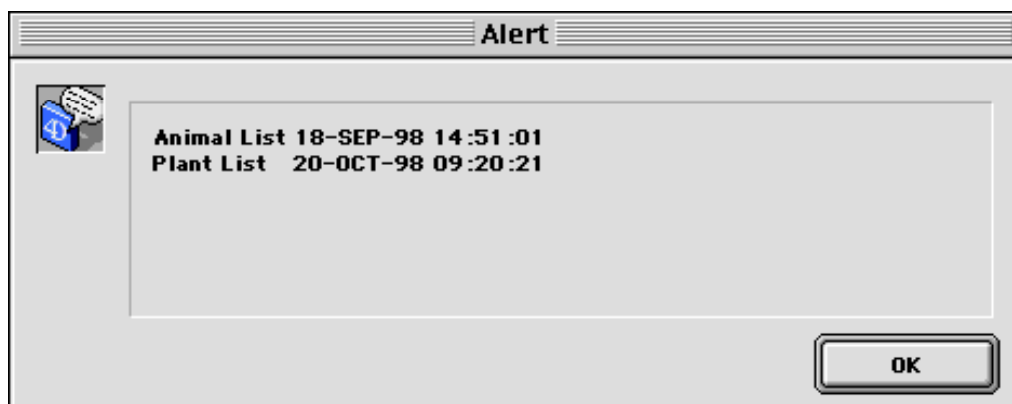


The DBA will have the option to update the Plant list, animal list, both lists, or neither. If a list is updated, the date and time stored in the main Oracle database will be changed to the current date and time on your computer's internal clock. This will mean that the next time anyone logs on the database, they will have to download a new version of that list. If Neither list is updated, the Oracle date will not be changed. The lists should be updated only after all changes have been made.

Show Fla List Date (Revision Date/Time)

This will show you the revision dates and times associated with the Florida plant and animal taxa lists that reside in your local 4th Dimension database. Refer to "Data Storage and Download of Reference Lists" for a complete description of revision dates and times.

- 1) Select View Show Fla List Date under the Taxa pulldown menu.
- 2) A display box will show the version of the plant and the animal list that have been downloaded into your 4th Dimension database. It will look like this:

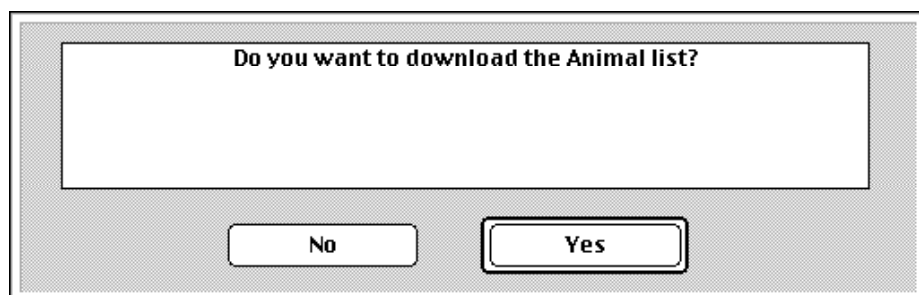


- 3) Click on OK when you are finished looking at the screen. You will be returned to the splash screen.

Download Fla List

This menu option allows the user to download the complete Florida plant and animal lists while logged on to the database. Although the list is downloaded during the logon procedure, there may occasionally be network interference that can cause an interruption in the download process. This may not be apparent to the user unless he(he) tries to enter a taxon that should have been included in a former list update. Downloading a new Florida list can be done any time there is a question about whether the most current list is being used.

- 1) Choose Download Fla List from the Taxa menu. A screen will display, asking if you want to download the animal list. If you select Yes, the program will begin the download,



displaying a message box to show the progress:

```
Preparing to download the Animal info
Reordering currently loaded Florida Animal taxa...
Deleting currently loaded Florida Animal taxa-
Please wait...
Searching master list for Florida Animal taxa...
Loading next 1000 taxa...
Loading next 1000 taxa...
```

When the download is complete, a message box will indicate the number of animal taxa on the current Florida list:



- 2) If you want to download the plant list, answer **NO**, you do not want to download the animal list. The next screen will ask if you want to download the plant list. Answer **YES**, and the program will execute a similar routine as that for the animal list. If you answer **NO**, you do not want to download the plant list, you will be returned to the splash screen.

Adding new taxa

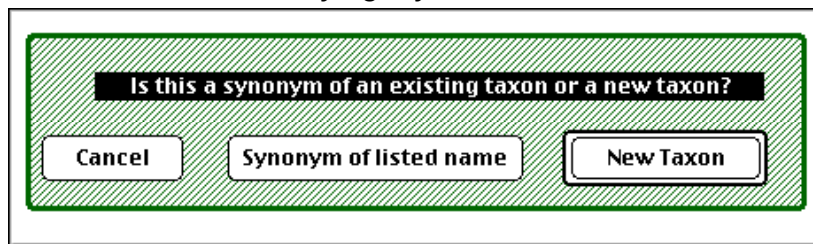
- 1) Under the Taxa pulldown menu, select Maintenance.
- 2) You will see a screen like this:

Click on Add new taxon.

- 3) You will see a screen like this:

You enter the scientific name and any of the other information that you know. You are required to add the phylogeny. For a description of the information on this screen, look in Appendix 5 (Data Dictionary) “Master Taxa Table”.

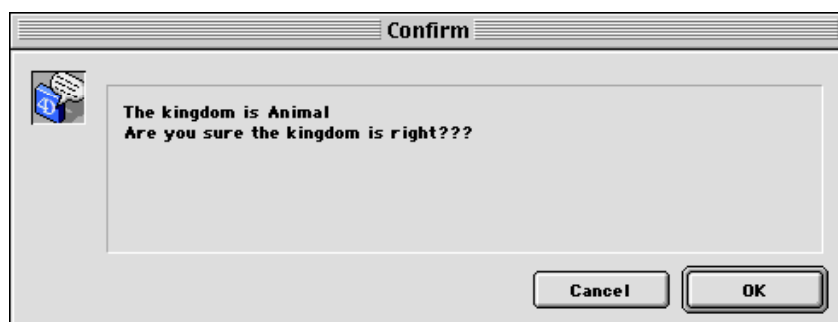
- 4) To add the phylogeny, be sure to select the appropriate “Phylogenetic Category” and “Kingdom”, then click on the button labeled Add Phylogeny. You will see:



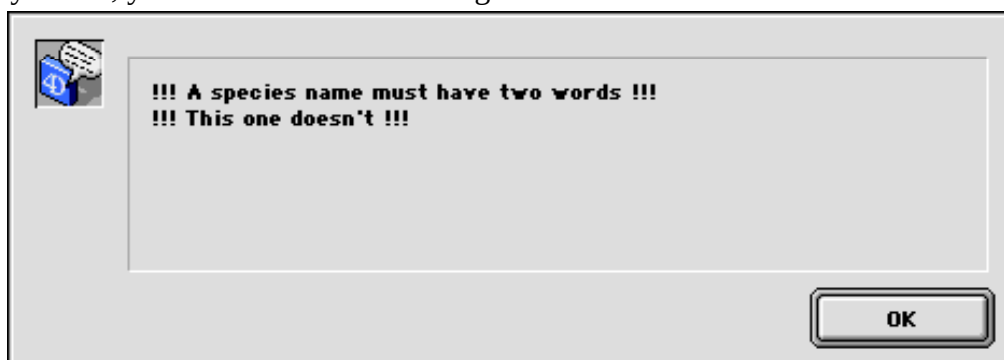
a) New Taxon

- i) First you will see:

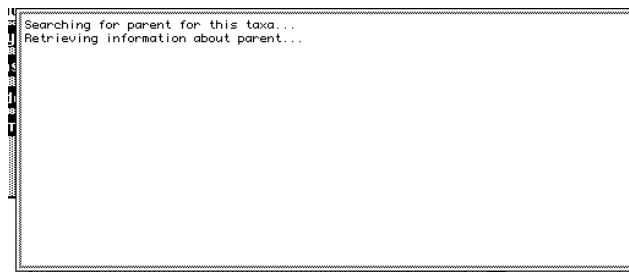
→ and have a chance to change the kingdom if you forgot to set it properly. Click on OK if the kingdom is correct. Otherwise, click on Cancel. You will be returned to the maintenance screen. Change the kingdom and start over with Add Phylogeny.



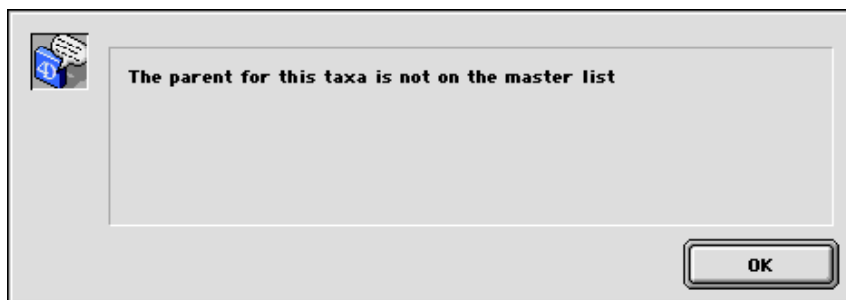
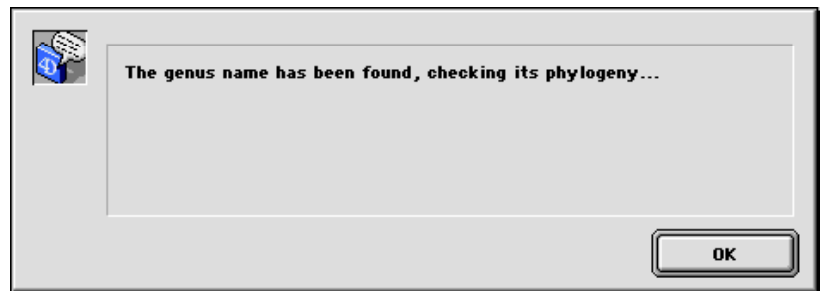
- ii) If the taxon you have added is a species or variety, the program will look for its parent. But first it will make sure that the scientific name for a species is two words and three words for a variety. If not, you will see an error message like this:



If the correct number of words are present, it will look for the parent. If you were adding the species *Lagodon rhomboides* to the list, the parent would be the genus *Lagodon*. It will not let you enter a species for a genus that is not on the master taxa list, nor a variety that does not have its species. If it is a species or variety you are adding, you will see a message like this:

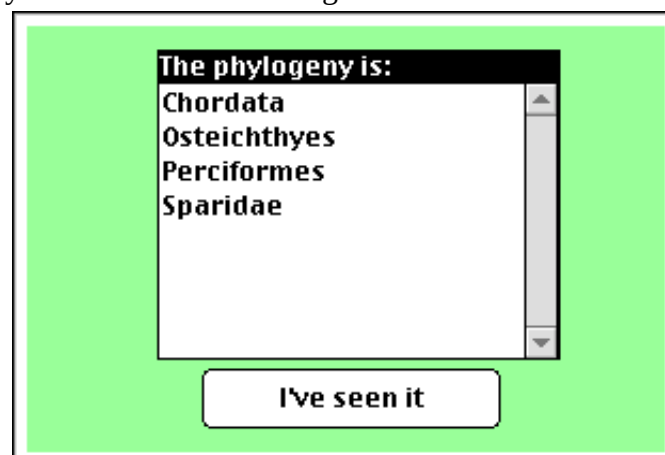


followed by this if the name is found:

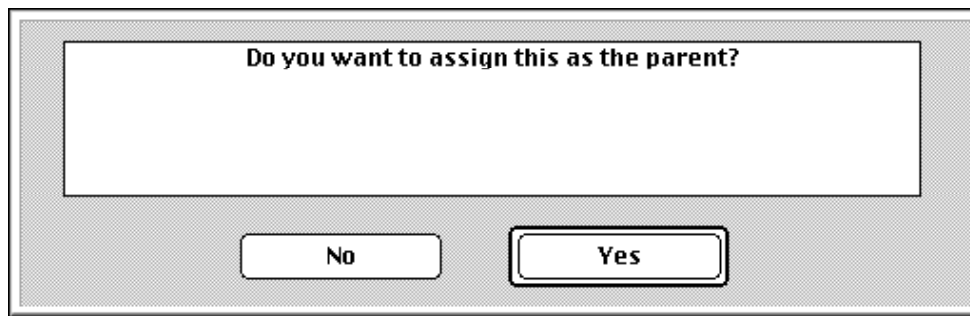


or this if the parent is not found:

If the parent is found, you will see the following information:



There are a few cases of plants or animal names that are legitimately used more than once and can mean two different organisms. You need to see the phylogeny to be sure that you have the correct parent. When you click on I've seen it, you are not accepting this as the parent. The next screen lets you decide what to do:



Regardless of which answer you select, you will be returned to the maintenance screen.

- iii) If the phylogenetic category is genus or higher level, you will see a screen like this:

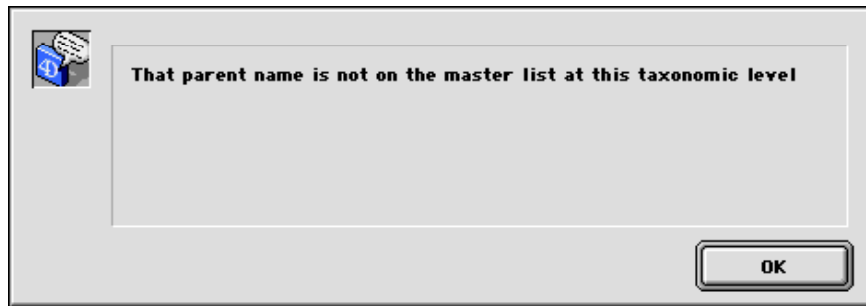
 A software window with a gray background. On the left, there are four radio buttons labeled "Phylum", "Class", "Order", and "Family". The "Phylum" radio button is selected. To the right of these buttons is a button labeled "Show all classes for this phylum". Below the radio buttons is a white text input box containing the text "Lagodon". To the left of this box is a "Cancel" button. To the right of the box is a button labeled "Use this as the immediate parent for:". On the right side of the window is a large white scrollable area. Below the scrollable area are two buttons: "Use selected name as parent" and "Put selected name in box".

This screen will help you select the phylogeny. Click in the button in front of the lowest level of the phylogeny for this category that you know. If you click on Phylum, you will be able to step through the entire phylogeny; however, if you know the Order, you can save the time of stepping through the higher level categories. At the minimum, you must know the name of the phylum.

In this example, the genus *Lagodon* is being added. The phylum name "Chordata" is entered in the white box and then the button Show all classes for this phylum is clicked.

 This screenshot shows the same software window as the previous one, but with more content. The scrollable area on the right now displays a list of taxonomic classes: Agnatha, Amphibia, Appendicularia, Ascidiacea, Aves, Cephalochordata, Chondrichthyes, Mammalia, Osteichthyes, Reptilia, and Thaliacea. The "Osteichthyes" class is currently selected and highlighted. The text input box on the left still contains "Lagodon", and the "Show all classes for this phylum" button is still present.

All the classes in the phylum Chordata are displayed in the scrollable box to the left. If you double-click on a name, it is put into the white box and the button label changes to Show all orders for this class. When you have the immediate parent name in the box, select on the button Use this as immediate parent for:. You do not need to go through the entire phylogeny. If you know that the family for this genus is Sparidae, you can just enter the name in the box. Be sure to click in front of family to tell the computer that the name you entered is for a family. The computer will search the master taxa list for a family name that matches what you entered. If it does not find one, it will display this message:

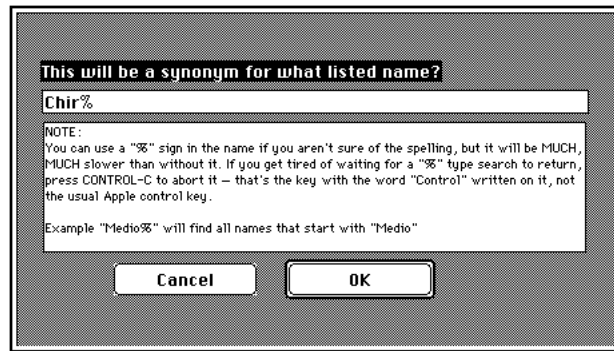


Double check to be sure that you spelled the name properly and if that does not work try stepping through the phylogeny starting at the phylum level. If it still is not on the master list, you will have to add it before you can add the taxon you are trying to add. This means you will have to **Cancel** out of the taxon you are adding and use **Add new taxon** to add the parent.

If the parent name is found, you will be returned to the maintenance screen. Click on the **View Phylogeny** button to verify that the phylogeny is correct.

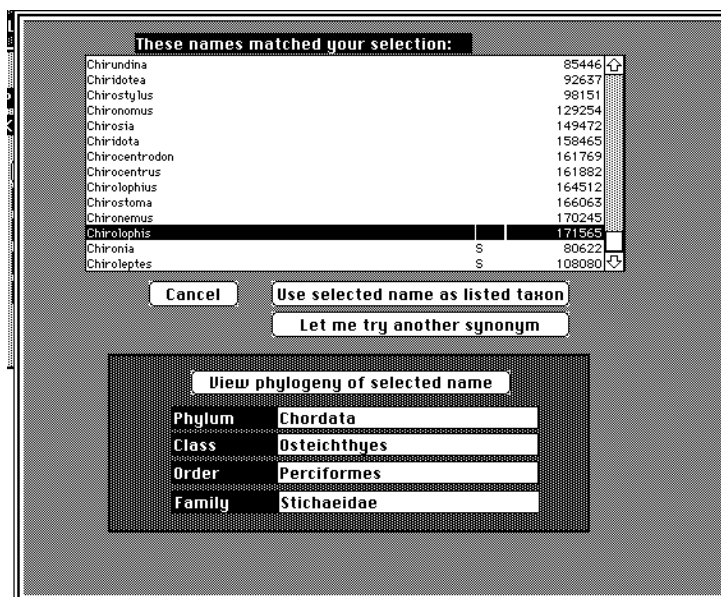
b) **Synonym of listed name**

i) You will see a screen like this:

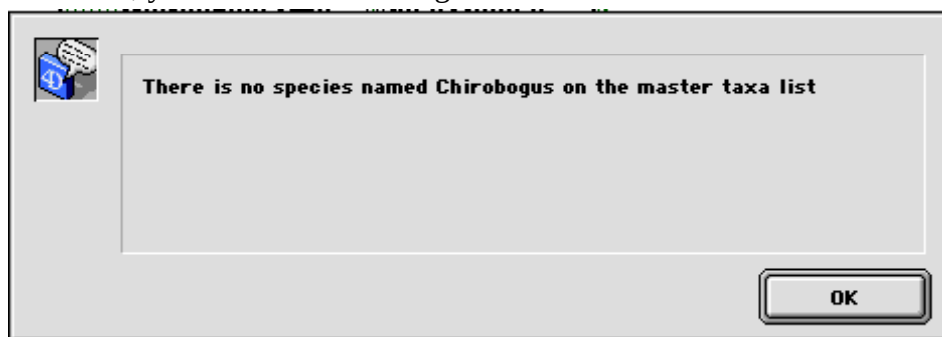


You should enter the scientific name for which your new name is a synonym. It is much, much faster to type in the entire scientific name; however, if you can't remember how to spell it, you can use a "%" as a wildcard. For example, "Chir%" will find all scientific names that start with "Chir" and are at the same phylogenetic level as your new taxon. This can take a long time (multiple minutes), especially for a species.

ii) All the names that match the name you entered are displayed on the screen like this:



You can highlight (click once on) the name of the synonym and then click on View phylogeny of selected name. The phylogeny of the highlighted name will be shown in the boxes below. It is important to do this to be sure that you have the right name. Many scientific names can look similar but be spelled slightly different. If nothing is found for the name you entered, you will see the message:

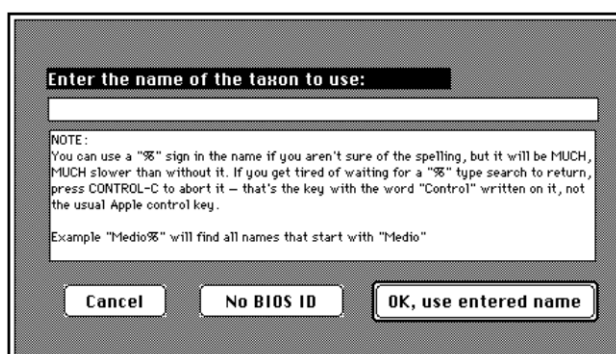


When you click on OK, you will be returned to the screen to try to enter another name.

- iii) When you are sure you have the correct name highlighted, click on Use selected name as listed taxon. This means that the new taxon on the maintenance screen will be considered a synonym of the highlighted name. If none of the names are right and you want to enter another name, click on Let me try another synonym and you will be returned to the previous screen. There will be an "S" next to the word "Synonym".

5) BIOS-related items

- a) If you know that the taxon is on the BIOS list, type a "Y" next to On BIOS?; otherwise, leave it "U" (for unknown/no).
- b) When the data are reformatted for BIOS, the scientific name is used (not the taxaID). If the scientific name is not on the BIOS system, the data record will be rejected by BIOS. Some of the names used by DEP will never be on the BIOS taxonomy list. In these cases you must decide what BIOS-acceptable name should be used when the data are reformatted. You do this by clicking on Add/Change BIOS ID. You will see a screen like this:



Enter the scientific name of the taxon you want to use. If there was a BIOS name already assigned and you want to remove it, click on No BIOS ID. The name entry works like the one in (4b,i) above. If more than one name matches, you will see a screen that works like the one in (4b,ii) above. Once you have selected the name you want, you will be returned to the maintenance screen. There is a box that displays the BIOS Taxon ID. This is a display only—you cannot edit it. The box under Show Name for BIOS ID is also display only.

- 6) Once you have selected all the information, click on Done. The program will ask if you want to save the changes. Click OK to save, click Cancel if you have changed your mind about adding the taxon. The program will check to be sure that you have provided all the required information. If you missed something (like the phylogeny or scientific name), it will tell you and then put you back on the maintenance screen so that you can correct the problem.

Editing existing taxa

- 1) Under the Taxa pulldown menu, select Maintenance.
- 2) You will see a screen like this:



- 3) There are several methods for finding taxa needing maintenance. They will be described below.
 - a) Click on Find by Name or ID. A selection window will be displayed:

Find Master Taxa for:

Scientific name:

or TaxonID*: ☐ < ☒ = ☐ > ☐ Range

0

Lower limit 0
Upper limit 0

Cancel **Find**

For wildcard search on name:
 1) Underline character matches any single character
 2) Percent sign matches a string of any length
 Example: R% would load all taxa codes of any length that have the letter R as the 2nd character.

* Reminder: The TaxonID is the sequential number assigned when a name is added to the master list. It is a different number than the phylogeny code which is used for phylogenetic searches.

An individual taxon can be selected by its scientific name or by its taxon ID number. Sometimes you will have one of these pieces of information, but not the other. The section “Using scientific name search boxes” under “Operation basics” explains how to most effectively search for a scientific name or group of names. If you know the taxon id number, enter it in the box, click in the button in front of the “=” sign, then click on Find. You **cannot** use wildcard characters when specifying taxon ID’s. If you want to load a range of taxon ID’s, click on the button in front of **Range**. A series of two boxes will be displayed for you to enter the lower and upper limits of the range of ID’s of interest to you.

Enter lower limit of range

1010

Cancel **OK**

Enter upper limit of range

1025

Cancel **OK**

Your choices will be displayed in the selection box like this:

Lower limit	1010
Upper limit	1025

You can edit these numbers by selecting the numbers and editing them just like regular text—you do not have to reselect range. Click on Find when the range is the way you want it. The taxa that match your choices will be displayed on the screen like this:

Florida Department of Environmental Protection

Master Taxa List Information 16

Taxald	Scientific Name	Phylogeny
1010	Phormidium angustissimum	030103001006018
1011	Phormidium autumale	030103001006019
1012	Phormidium corium	030103001006020
1013	Phormidium crouani	030103001006021
1014	Phormidium fragile	030103001006022
1015	Phormidium molle	030103001006023
1016	Phormidium truncatum	030103001006024
1017	Phormidium subfuscum	030103001006025
1018	Phormidium tinctorium	030103001006026
1019	Phormidium valderianum	030103001006027
1020	Phormidium africanum	030103001006028
1021	Phormidium bigranulatum	030103001006029
1022	Phormidium bohneri	030103001006030
1023	Phormidium frigidum	030103001006031
1024	Phormidium jenkelianum	030103001006032
1025	Phormidium laminosum	030103001006033

Find by Name or ID %F

Get next 100

Find immediate children

Get next 100

Add new taxon %N

Find by Phylogeny code

Get next 100

Write to file

Show all taxa

Show selected taxa

Find space runs

Find leading spaces

Find trailing spaces

Clear all %R

Sort %S

Print %P

Done %D

If there are no taxa that meet your selection criteria, you will see:

Florida Department of Environmental Protection

There are no selected records for: MasterTaxa

Find by Name or ID ⌘F Find by Phylogeny code Find space runs
Get next 100 Get next 100 Find leading spaces
Find immediate children Write to file Find trailing spaces
Get next 100 Show all taxa Clear all ⌘R Sort ⌘S Done ⌘D
Add new taxon ⌘N Show selected taxa Clear selected Print ⌘P

To edit or view the information for a particular taxon in the list, double-click on the name and you will see the main maintenance screen:

Florida Department of Environmental Protection

Master Taxa List Information

Scientific name 50 characters Taxa Id Number 1025
Phormidium laminosum
Entered in FlaBioIDB by: BIOS 30 characters
Authority Name GOMONT
Authority Date
Authority Reference 80 characters
Range Not assigned Florida Index 0 Not assigned
Functional Feeding Unknown Lake Index 0 Not assigned

Phylogenetic Information

Phylogenetic Category Species
Kingdom Plant
Add Phylogeny View Phylogeny
Phylum
Class
Order
Family
Synonym

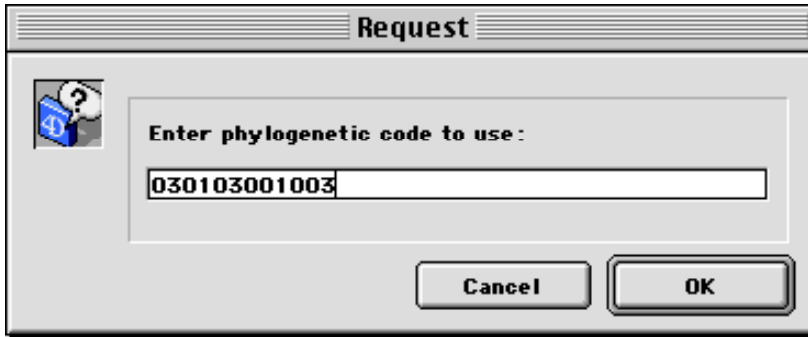
Other Taxonomic Lists

On Florida list? No
On BIOS? Y
BIOS Taxon ID
Add/Change BIOS ID
Show Name for BIOS ID
030103001006033 992

Delete this taxon Done Cancel

The section “Adding new taxa” covers how to use this screen.

- b) Click on Find by Phylogeny code. The following box will appear. Entering the entire phylogenetic code for a single taxon will retrieve only that individual. You can also enter the code other taxonomic levels. In the example at left, the phylogenetic code has been entered for the genus *Lyngbya*. Click on OK to view the search results.



The image shows a 'Request' dialog box with a title bar. Inside the dialog, there is a question mark icon in a blue box. The text 'Enter phylogenetic code to use :' is followed by a text input field containing '030103001003'. At the bottom are 'Cancel' and 'OK' buttons.

The box in the upper right corner of the screen indicates that 74 taxa were found that have the phylogeny code 030103001003. If more than 100 were found, the first 100 would be shown on the screen and the Get next 100 button would be available to show the next set.

Florida Department of Environmental Protection

Master Taxa List Information
74

Taxaid	Scientific Name	Phylogeny
870	Lyngbya	030103001003
871	Lyngbya aerugineo-caerulea	030103001003001
872	Lyngbya aestuarii	030103001003002
873	Lyngbya confervoides	030103001003003
874	Lyngbya gracilis	030103001003004
875	Lyngbya lutea	030103001003005
876	Lyngbya semiplena	030103001003006
877	Lyngbya majuscula	030103001003007
878	Lyngbya martensiana	030103001003008
879	Lyngbya subtilis	030103001003009
880	Lyngbya rivulariarum	030103001003010
881	Lyngbya kuetzingii	030103001003011
882	Lyngbya contorta	030103001003012
883	Lyngbya birgei	030103001003013

Find by Name or ID ⌘F

Find by Phylogeny code

Find space runs

Get next 100

Get next 100

Find leading spaces

Find immediate children

Write to file

Find trailing spaces

Get next 100

Show all taxa

Clear all ⌘R

Sort ⌘S

Done ⌘D

Add new taxon ⌘N

Show selected taxa

Clear selected

Print ⌘P

c) Sometimes there is a need to find the species for a particular genus, or the varieties for a species. In the example below, *Micromenetus dilatatus* has been found.

Taxald	Scientific Name	Phylogeny
76648	Micromenetus dilatatus	450108012012005

Buttons: Find by Name or ID %F, Find by Phylogeny code, Find space runs, Get next 100, Find immediate children, Write to file, Find leading spaces, Find trailing spaces, Show all taxa, Clear all %R, Sort %S, Done %D, Add new taxon %N, Show selected taxa, Clear selected, Print %P.

Select the taxon name and click on Find immediate children. The program will look for any taxa for which the selected taxon was assigned as a parent. In this example, the search resulted in one child, shown below:

Taxald	Scientific Name	Phylogeny
76648	Micromenetus dilatatus	450108012012005
10000624	Micromenetus dilatatus avus	45010801201200501

Buttons: Find by Name or ID %F, Find by Phylogeny code, Find space runs, Get next 100, Find immediate children, Write to file, Find leading spaces, Find trailing spaces, Show all taxa, Clear all %R, Sort %S, Done %D, Add new taxon %N, Show selected taxa, Clear selected, Print %P.

d) When the user enters a new name for the Master Taxa list, typing errors involving spaces occur occasionally. These errors are not easily seen, and can interfere with the ability to use the “Find” routines in the taxa maintenance area and the data entry routines. The next three buttons are designed to find taxa with extra spaces somewhere in the name so they can be fixed.

Find space runs looks for taxa that has more than one space between parts of the name. The message at right displays.

```
Now searching the entire master list for any name that has  
a space run. This may take awhile as  
this kind of search does not use the indexes efficiently.  
Please wait...
```

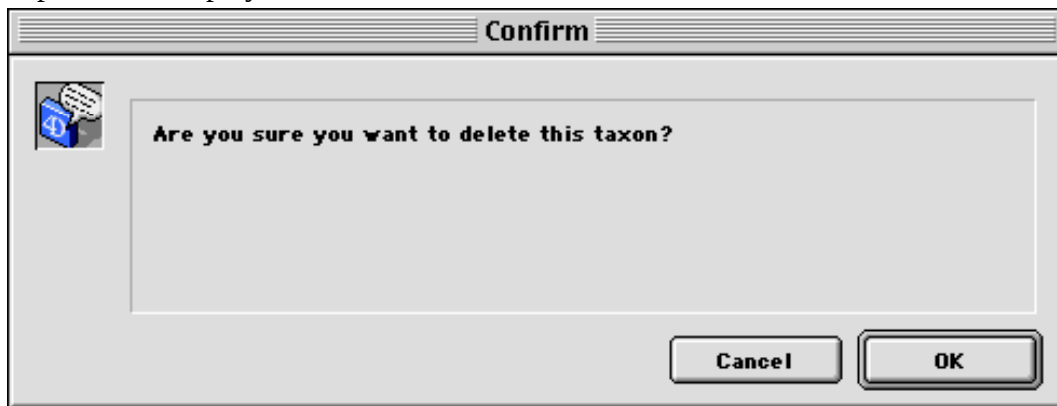
Find leading spaces
finds stray spaces in front
of the taxon name.

Find trailing spaces
looks for stray spaces at
the end of the taxon name.

If no problems with extra spaces in taxon names were found, you are returned to the main taxa maintenance screen.

Deleting taxa

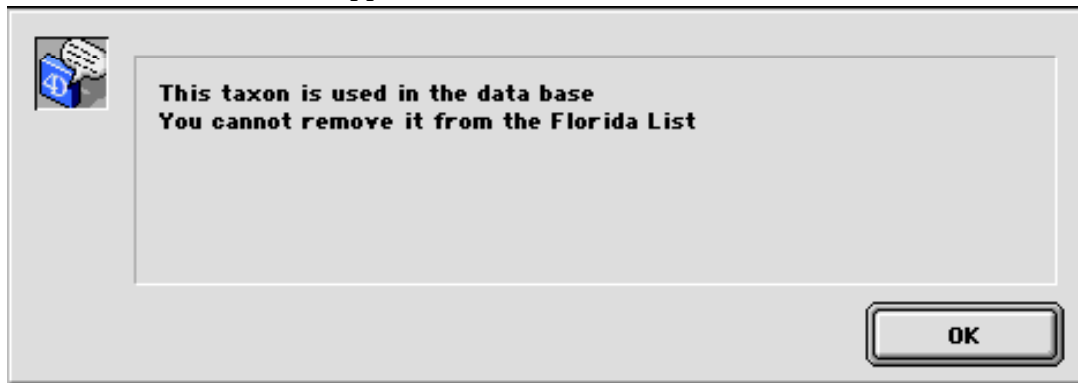
- 1) Use the instructions under “Editing existing taxa” to load the taxon you want to delete on the screen.
- 2) Click on the button labeled **Delete this taxon** on the bottom left side of the maintenance screen.
- 3) The computer will display this screen:



This is to give you a chance to change your mind. If you do not want to delete the taxon, click on **Cancel**; otherwise, click on **OK** to continue with the delete.

- 4) The computer will search the data tables (benthos and zooplankton for an animal, phytoplankton and periphyton for a plant) to be sure that the taxon does not occur there.

a) If it does, this screen will appear:



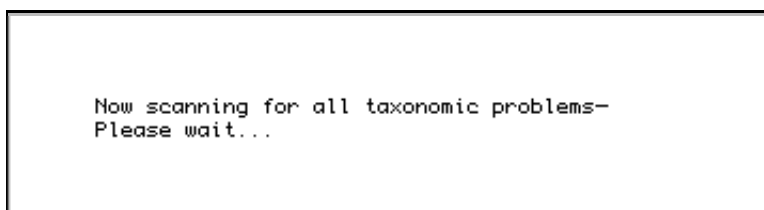
When you click on OK, you will be taken back to the maintenance screen. You cannot delete a taxon that is used in the data tables. If you want to find out where the taxon is used, get back to the splash screen (click on Done or Cancel), then select By Taxon from the Retrieve pulldown menu.

- b) If the taxon is not found in the data tables, it will be deleted from the master taxa list and you will be returned to the taxa maintenance screen, which may or may not have other taxa listed depending on what you loaded from the Find button.

Handling data entry-related problems

The database administrator (DBA) is the only person who has access to this function.

- 1) Select Problems from the Taxa pulldown menu. You will see this screen:

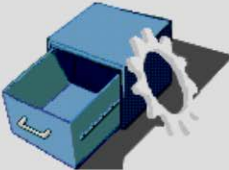


while the computer searches the master taxa list for taxa that have been temporarily added to the list or moved to the Florida list by data entry.

- 2) When the search is complete, you will see a screen like the one shown on the next page:

Florida Department of Environmental Protection

There are no selected records for: TaxaWork



Problems found during scan

4 Animal taxa on master, not on Fla list
1 Animal taxa not on master list

1 Plant taxa on master, not on Fla list
0 Plant taxa not on master list

ReScan for all problems Search based on criteria below Done %D

Find the following taxa: ☒ On master list, not on Fla list
☐ Taxa not on master list

Currently working on: ☒ Animals
☐ Plants

There are two kinds of problems:

- a) a taxon on the master list needs to be marked as one found in Florida;
- b) a new taxon needs to be added to the master taxa list.

Notice that the screen says “There are no records for: TaxaWork”. The computer does not automatically load any of the problem taxa. There is a summary of the problems found immediately below the white space. You need to handle each type of problem separately. Decide what you want to do first by clicking in front of “Animals” or “Plants”, then in front of the type of problem you want to resolve, and then on Search based on criteria below. The program will load taxa involved in the problem at the top of the screen like this:

Florida Department of Environmental Protection

Problems with Taxonomy

EntBy	SciName	TaxaID
Northup_R	Tracheliidae	46290
Northup_R	Ephelota coronata	46555
Northup_R	Edmondsonia montana	68848
Northup_R	Ephemera blanda	101528

Problems found during scan

4 Animal taxa on master, not on Fla list
1 Animal taxa not on master list

1 Plant taxa on master, not on Fla list
0 Plant taxa not on master list

ReScan for all problems Search based on criteria below Done %D

Find the following taxa: ☒ On master list, not on Fla list
☐ Taxa not on master list

Currently working on: ☒ Animals
☐ Plants

You have to double-click on each taxon to resolve its problem individually. You will see a screen like this:

The top reminds you of the type of problem, the name of the taxon, and the user name of the person who triggered the problem. None of these things can be edited. You have to use the buttons at the bottom of the screen to decide what to do. If you want to see what (or how many) samples are involved, click on *Which samples?*. If the taxon is an animal you will see a choice like this:

For plants you have the choice of phytoplankton or periphyton. After you make your choice, the program searches the appropriate table and then displays the samples that have the taxon of interest entered.

Florida Department of Environmental Protection				
Station Codes		Date	Gear	Rep
Storet	Nickname			
SUW01	SUW01	10/5/93	HesterDend	2

Print %P Done %D

You cannot edit this information and if you double-click on a line, it shows you the same screen with only one line. This information is here to help you decide what to do. Click on *Print* if you want a hardcopy of what you see on the screen. Click on *Done* when you are finished looking at the list. You will be returned to the screen with the choice buttons. Depending on the problem you have several choices to resolve it:

- a) Change to another taxon - The name is entered in error and it should be something else. You will see taxon name selection box like this:

Enter the new name. Refer to “Using scientific name search boxes” under “Operation basics” if you are unsure how to enter a name. If you enter a name using a wildcard, all names that meet the criteria will be displayed on a screen like the one shown at left.

Phylum	Arthropoda
Class	Insecta
Order	Diptera
Family	Tabanidae

Sometimes a scientific name may really be in the master list more than once. For example, *Gundlachia* is the genus name for both a plant and an animal. Click once on a name and then on View phylogeny of selected number to be sure that you selected the right one. Click on OK when the name you want is highlighted. The computer will change **all occurrences** of that name in the database, so be sure you have the right name before clicking on OK. If the name was used in more than one sample and you want to use a different name for each sample, edit the individual samples like you do for data entry.

- b) Add to Florida List - The name was on the master list, but was not marked as a taxon found in Florida. When you select this, the computer marks it as a Florida taxon and the data (benthos, zooplankton, etc) are not modified in any way. You will see:

- c) Add to Master List - The name was not on the master taxa list and you have decided to add it. You will be taken to a master taxa maintenance screen for this name:

The screenshot shows a web-based form titled "Florida Department of Environmental Protection" with a sub-header "Master Taxa List Information". The form is divided into several sections:

- Scientific name**: 50 characters, value: *Polypedilum floridensis*
- Taxa Id Number**: 10001378
- Entered in FlaBioIDB by:** AsstAdmin (30 characters)
- Authority Name**: Lurding
- Authority Date**: 1998
- Authority Reference**: 80 characters, value: "this is a fake taxon added to get the screen shots for the manual update"
- Range**: Range includes Fla
- Florida Index**: 0, Not assigned
- Functional Feeding**: Unknown
- Lake Index**: 0, Not assigned
- Phylogenetic Information**:
 - Phylogenetic Category**: Species
 - Kingdom**: Animal
 - Add Phylogeny** and **View Phylogeny** buttons
 - Phylum**: Arthropoda
 - Class**: Insecta
 - Order**: Diptera
 - Family**: Orthoclaadiinae
 - Synonym**: (empty field)
- Other Taxonomic Lists**:
 - On Florida list?**: Yes
 - On BIOS?**: U
 - BIOS Taxon ID**: 0
 - Add/Change BIOS ID** button
 - Show Name for BIOS ID** button
 - BIOS ID values: 460530033112056 and 1296570

At the bottom of the form are **Cancel** and **Done** buttons.

You need to fill in the information for the taxon (see "Adding new taxa") and click on Done. If you change your mind, click on Cancel. The data (benthos, zooplankton, etc) are not modified in any way. When you click on Done you will see a message indicating that the taxon has been added to the Master List as a Florida taxon. When you are finished resolving the taxonomic problems, click on Done. You will be asked if you want to update the revision dates. See the section titled "Revision Date/Time for Animals and Plants" if you are unsure how to answer.

Taxa List Reports

A taxa list report looks like this:

TaxaId	SciName	Phylo	Re	Ph	FlaList
601	Cyanophycota	03			1 1
602	Cyanophyceae	0301			2 1
603	Chroococcales	030101			3 1
604	Chroococcaceae	030101001			4 1
625	Aphanocapsa	030101001003			5 1
636	Aphanothece	030101001004			5 1
644	Aphanothece stagnina	030101001004006			6 1
646	Aphanothece clathrata	030101001004007			6 1
654	Chroococcus	030101001005			5 1
671	Chroococcus minutus	030101001005009			6 1
682	Gloeocapsa	030101001007			5 1
703	Gloeothece	030101001008			5 1
714	Gomphosphaeria	030101001009			5 1
727	Merismopedia	030101001011			5 1
728	Merismopedia glauca	030101001011001			6 1
729	Merismopedia convoluta	030101001011002			6 1
739	Merismopedia tenuissima	030101001011009			6 1

Cancel Show next 100

- 1) Select Taxa List Reports under the Taxa pulldown menu.
- 2) A selection box will be displayed:

Master Taxa Report

☐ Entire master list
☒ Florida list only

☒ Animals
☐ Plants

☐ On BIOS
☐ Not on BIOS
☒ All

Restrict search to names like:

Cancel

OK

There are three decisions to make.

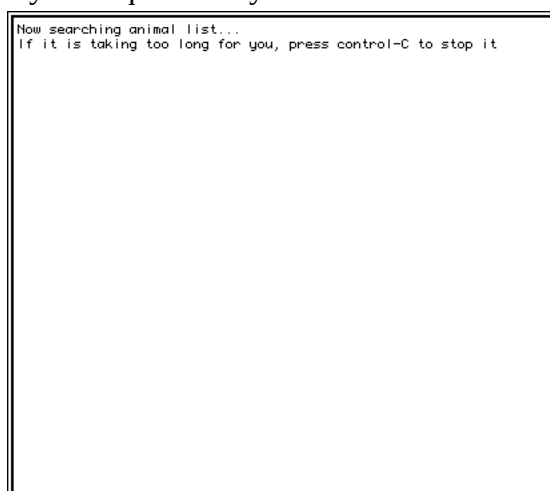
- a) Do you want the entire master list or only those that are found in Florida? Click in the button in front of your choice.
- b) You have to select either “Animals” or “Plants”. You cannot get both in the same list.
- c) You can restrict the list to those taxa that are on BIOS, those that are marked with “unknown” BIOS status (Not on BIOS), or ignore the BIOS status (All).

The list can be further restricted by entering a name in the box labeled Restrict search to names like. For example, if you entered “Chiron”, you would get all the taxa names that start with those letters:

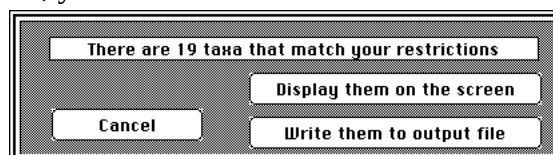
Florida Department of Environmental Protection					
Taxaid	SciName	Phylo	Re	Ph	FlaList
127917	Chironomidae	460530032		4	1
129254	Chironomus	460530033082		5	1
129278	Chironomus crassicaudatus	460530033082013		6	1
129280	Chironomus decorus	460530033082015		6	1
129296	Chironomus ochreatus	460530033082027		6	1
129303	Chironomus plumosus	460530033082030		6	1
129311	Chironomus pungens	460530033082032		6	1
129313	Chironomus riparius	460530033082033		6	1
129320	Chironomus staegeri	460530033082035		6	1
129322	Chironomus stigmaterus	460530033082036		6	1
129329	Chironomus tuxis	460530033082041		6	1
129839	Chironomus xenolabis	460530033121001	S	6	1

Cancel Show next 100

- 3) Click on OK when all your choices have been made.
- 4) The computer will work on your request and you will see these messages:



- 5) When the search is complete, you will see a box like this:



You will be told how many taxa were found that met your criteria. You have to decide how you want to view them. If you click on **Display them on the screen** and there are more than 100, you will see the first 100, then you can click on a button to view the next 100. If you click on **Write them to output file**, they will all be written to a tab-delimited text file that can be opened in a program like Word or Excel. Regardless of which you choose the list will be sorted in phylogenetic order. Click on **Cancel**, if you do not want to see them.

- 6) When the program does the search in step 4, it does not retrieve the actual taxa names but just gets the count. The count can be done much more quickly than the actual retrieval, so the computer gives you a chance to decide if you really want to see the names before making you wait for them. So after you click on either "Display..." or "Write...", you will see the message box in 4 again while it retrieves the actual names.

- 7) If you selected “Write them to output file”, you will see the standard “Save as” file box so you can name the file that will be written.
- 8) You will be taken back to the splash screen when the file is written or you click on “Cancel” on the display screen.

View Taxon Info

This will show the phylogeny of a plant or animal if you provide a scientific name or a taxon ID number.

- 1) Select View Taxon Info under the Taxa pulldown menu.
- 2) A selection box will be displayed:

Scientific name You can use the "%" as a wildcard

labiobaetis%

Taxa Id Number 0

Cancel View Info

You can enter either the scientific name or the taxon ID. If you enter a taxon ID and then enter a scientific name, the taxon ID will be erased. You can use the wildcard character to load more than one scientific name; you cannot use a wildcard character with a taxon ID. Click on View Info to continue.

- 3) All the scientific names that match your criteria will be loaded into a screen like this:

Names matching your request		Number of names in list
Labiobaetis	10001006	4
Labiobaetis ephippiatus	10001287	
Labiobaetis frondalis	10001286	
Labiobaetis propinquus	10001068	

Cancel Next ID View info of selected taxon

Click once on a name and then click on View info of selected taxon. A screen displaying all available information for that taxon will appear.

Master Taxa List Information			
Scientific name	50 characters	Taxa Id Number	10001068
Labiobaetis propinquus			
Entered in FlaBioIDB by:	Lurding_K	30 characters	
Authority Name	Walsh		
Authority Date	1863		
Authority Reference	80 characters McCafferty & Waltz. 1995. Labiobaetis, Baetidae, new status, new N American spp.		
Range	Range includes Fla	Florida Index	0 Not assigned
Functional Feeding	Unknown	Lake Index	0 Not assigned

Phylogenetic Information	Other Taxonomic Lists
Phylogenetic Category	Species
Kingdom	Animal
Show synonyms	View Phylogeny
Phylum	
Class	
Order	
Family	
Synonym	S
On Florida list?	Yes
On BIOS?	U
BIOS Taxon ID	0
Show Name for BIOS ID	
	460504002004054
	0
	100860

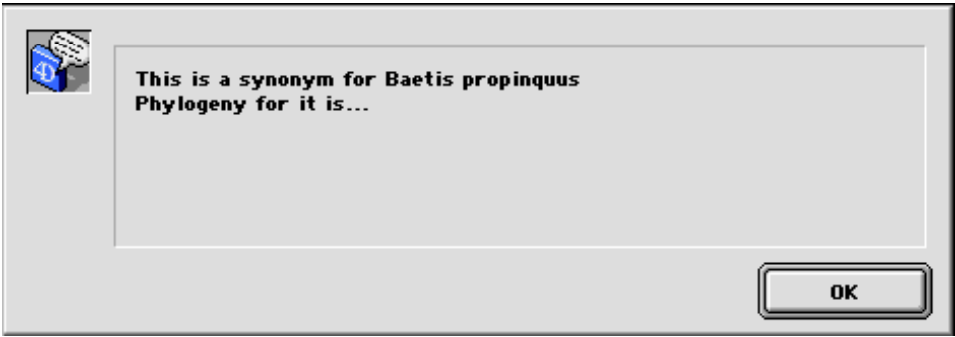
Cancel

If the taxon is a synonym of another name, you will see a "S" in the box at the bottom of the screen. Click on Show synonyms to see all of the names assigned to this phylogenetic code.

All synonyms for phylo code: 460504002004054		
Baetis propinquus	100860	
Labiobaetis propinquus	10001068	S

OK

To see the phylogeny of this taxon, click on View Phylogeny. Since this organism has a synonym, you see the following alert:



After you click OK, the phylogeny appears at the bottom left of the screen.

Phylogenetic Information	
Phylogenetic Category	Species
Kingdom	Animal
Show synonyms View Phylogeny	
Phylum	Arthropoda
Class	Insecta
Order	Ephemeroptera
Family	Baetidae
Synonym	S

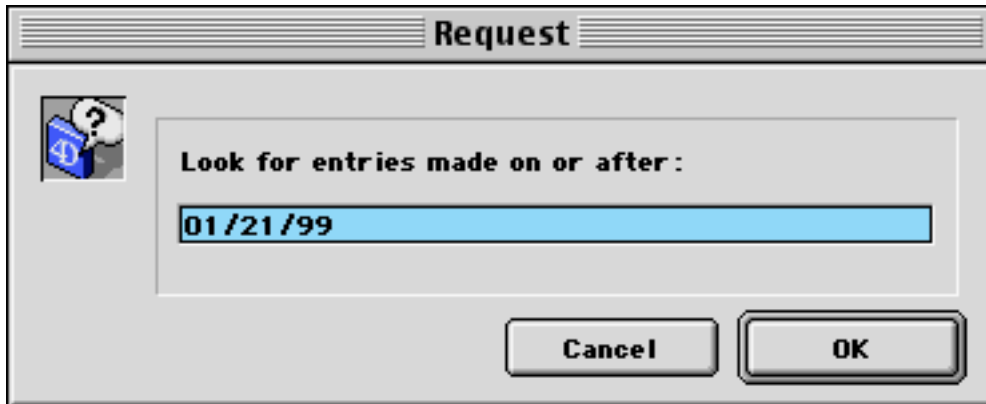
- 4) When you are finished with the taxa on the screen, click on Cancel and you will be returned to the selection box described in step 2. You can enter another name or click on Cancel if you are finished. You will be returned to the splash screen.

Administrative Reports

DBA Sample Report

The Database Administrator (DBA) may use this routine to obtain the number of entries in selected Oracle tables by User Name. This gives a good indication of the kinds of data entered from a specified date to the present.

- 1) Select DBA Sample Info from the Samples menu. A request box will appear with a prompt to enter the sample date to begin with in the query:



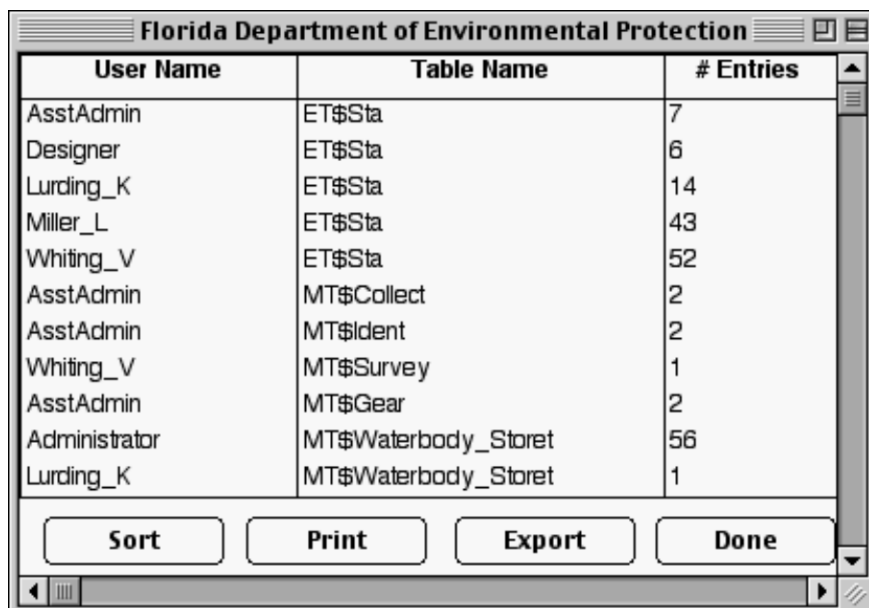
The program will search the tables from the date entered to the present date. It must be entered with the format XX/XX/XX. If it is entered incorrectly, an alert box will

remind the user of this.

```
Now working on table:
ET$Sta
MT$Collect
MT$Ident
MT$Survey
MT$Gear
MT$Waterbody_Storet
ET$TaxaMstr
DT$Sample
DT$Benthos
DT$BenTaxa
```

- 2) While the search is performed, the following message will inform the user of its progress.

3) The search results are displayed in a window listing the user name, table, and number of table entries for the requested time period. From here they can be sorted, printed, or exported to a tab-delimited text file. Click on Done to return to the splash screen.



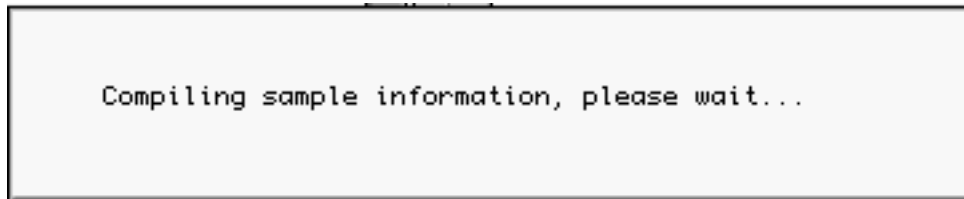
User Name	Table Name	# Entries
AsstAdmin	ET\$Sta	7
Designer	ET\$Sta	6
Lurding_K	ET\$Sta	14
Miller_L	ET\$Sta	43
Whiting_V	ET\$Sta	52
AsstAdmin	MT\$Collect	2
AsstAdmin	MT\$Ident	2
Whiting_V	MT\$Survey	1
AsstAdmin	MT\$Gear	2
Administrator	MT\$Waterbody_Storet	56
Lurding_K	MT\$Waterbody_Storet	1

Buttons: Sort, Print, Export, Done

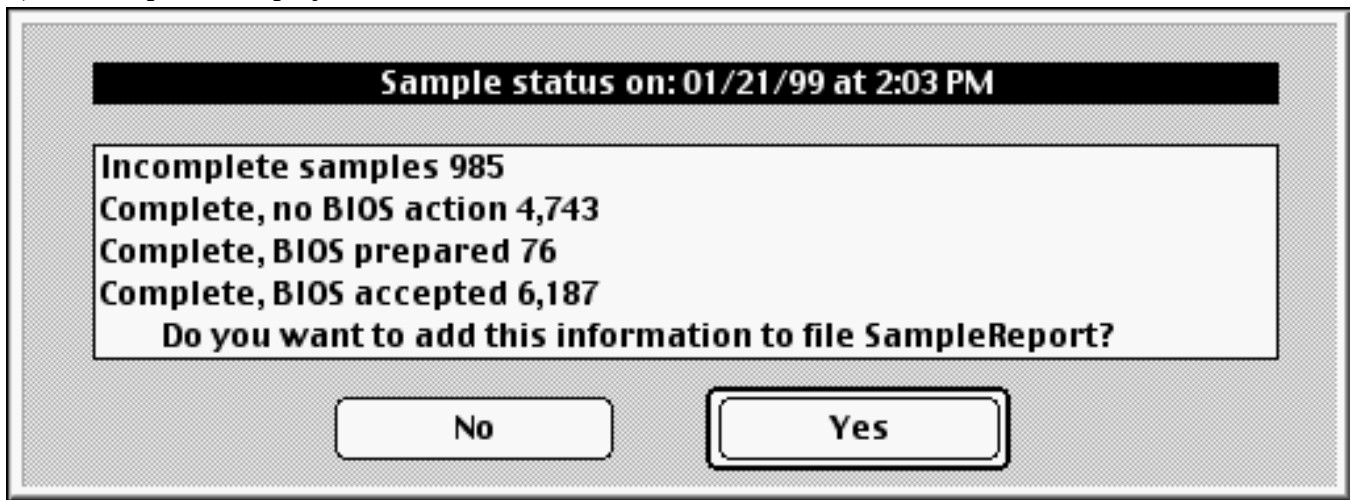
Sample Status Report

This report allows the Database Administrator to retrieve the number of samples in the Biological Database within each status category.

- 1) Choose **Sample Status Report** from the **Samples Menu**. The following message box appears as the program executes the procedure:



- 2) The report is displayed on the screen.



If the DBA clicks **Yes**, the results are written to a file called "SampleReport" located in the 4th Dimension folder. If the file does not exist, the program will create it. If the file is already present, the routine will append these results to any others in the file. If the DBA clicks **No**, he or she will be returned to the splash screen.

Access levels/User Info

Overview

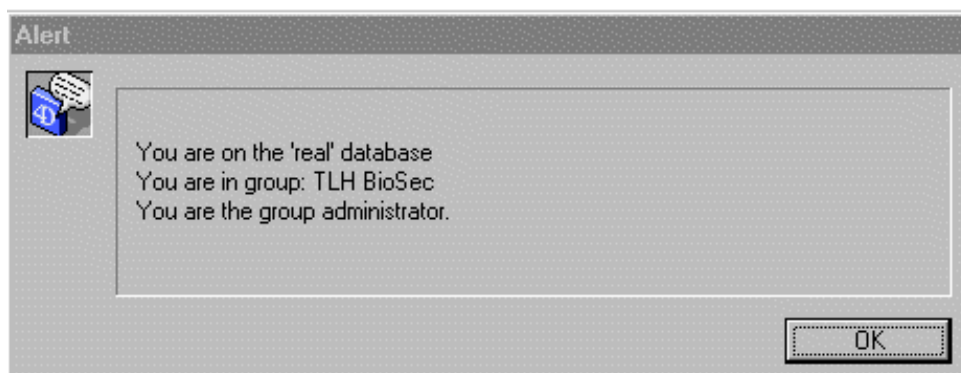
When a new user is added to the system, s/he is assigned one or more access levels. These give the user access to different parts of the system. This database has six access levels at this time. A graphic display of group permissions is on the following pages. They are:

- **DesignerGrp** Has access to everything, including Design mode which allows program modification. Only one person can have this and it is a special userID that cannot be modified.
- **BioDBA** Has access to everything except Design mode. Only one person can have this and it is a special userID that cannot be modified.
- **AsstAdmin** Has edit access to all reference tables except Sample Gear, Feeding Groups, and County and Station Level Types; has access to everything else except the Taxa Problems and Maintenance, and User Functions.
- **GroupAdmin** Has edit access to Station and Waterbody reference tables and view access to the rest; no access to any taxa file maintenance function; can mark samples “complete”.
- **DataEntryGrp** Has view access to all reference; no access to any taxa file maintenance function; cannot mark samples “complete”.
- **RetrieveGrp** Only has access to the Retrieve pulldown menu and report-oriented items in the Taxa pulldown menu; all other items will be grayed-out.

In addition, each user is assigned to a group. You can edit information entered into the system by your group only, however, you may view incomplete sample information entered by any group. Retrieval of complete data ignores group for all users.

Show my Info

By selecting Show my info under the User Info pulldown menu, you will see all the access/user group information for your user ID. Only the DesignerGrp and BioDBA can add or edit userID information.



Group = BioDBA (Biological Database Administrator)

File	Edit	Retrieve	Ref	Reference Info	San	Samples	Taxa	Bioassay
Force StartUp				Stations		Samples	%S	
Set LogSW				Surveys		Benthos	%B	
Logon Oracle	%L			Sample Gear		Periphyton	%R	
Logoff Oracle	%O			Feeding Groups		Phytoplankton	%K	
Change my password				Collectors		Zooplankton	%Z	
Quit 4D	%Q			Identifiers		PhysChem	%C	
				County LatLon		PhysChem Report		
				Station Levels		Sample Status Report		
				Water Bodies		DBA Sample Report		

Taxa	Bioassay	User Info	Hel
Problems			
Maintenance			
Taxa List Reports			
View Taxon Info			
Show Fla List Date			
Download Fla List			
Prepare for BIOS			
Mark BIOS upload results			
Make BIOS corrections			

Bioassay	User Info	Hel
Samples		
Facilities		
Facility types		
NPDES sites		
DEP Districts		
Sample types		
Diluents		
Test organisms		
Calculation methods		
Causes of toxicity		
Maintenance		

User Info	Help
Quit to design	%U
Show my info	
Users	
User Groups	
ImportPCVars	
ExportImportFileInfo	
Menu Tester-Lori	
AACallProcToTes	
Import LIMS info	
Export LIMS info	

Group = AsstAdmin (Assistant Database Administrator)

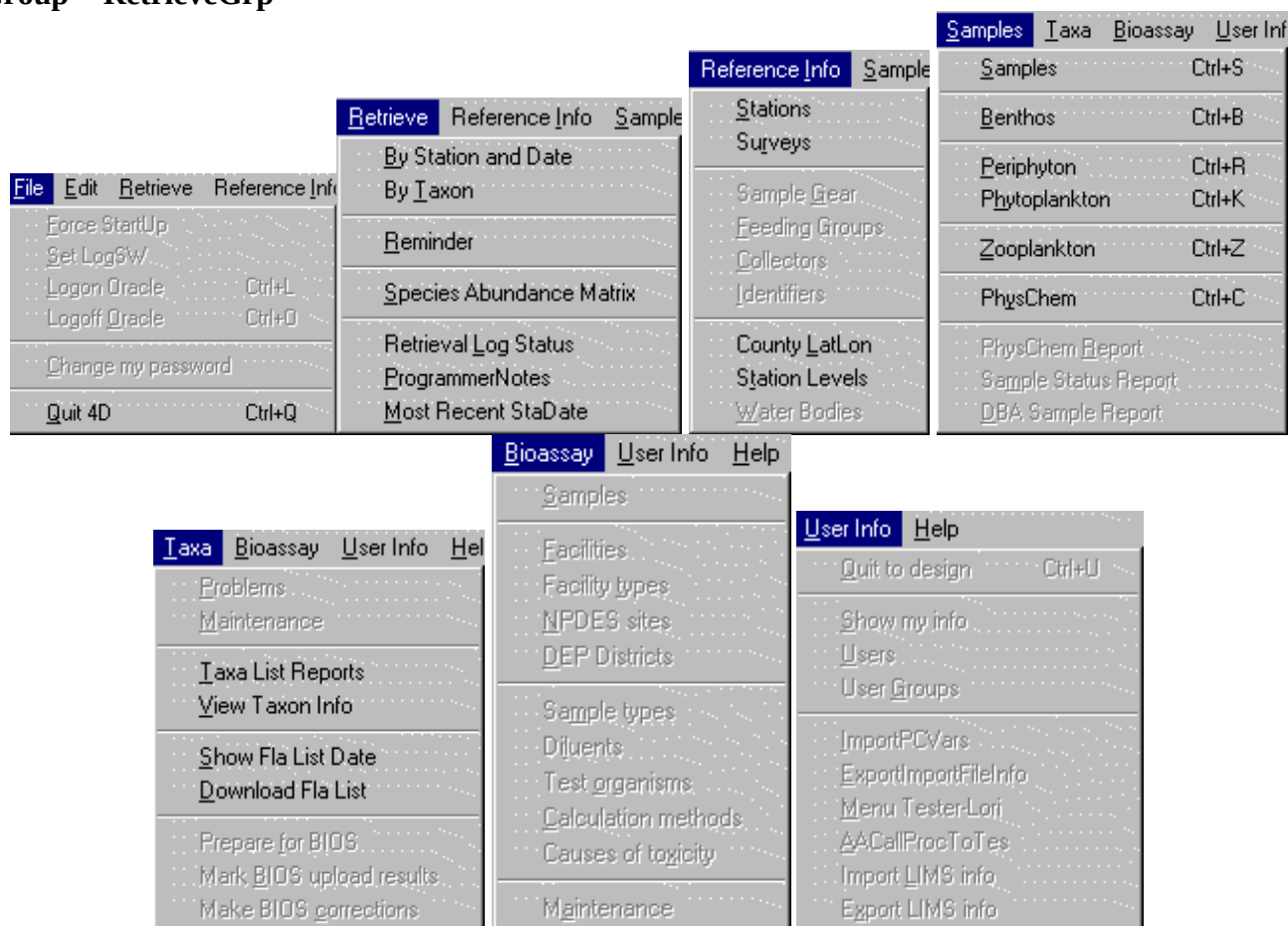
File	Edit	Retrieve	Reference Info	Sample	Reference Info	Sample	Samples	Taxa	Bioassay	User Info
Force StartUp			By Station and Date		Stations		Samples			Ctrl+S
Set LogSW			By Taxon		Surveys		Benthos			Ctrl+B
Logon Oracle			Reminder		Sample Gear		Periphyton			Ctrl+R
Logoff Oracle			Species Abundance Matrix		Feeding Groups		Phytoplankton			Ctrl+K
Change my password			Retrieval Log Status		Collectors		Zooplankton			Ctrl+Z
Quit 4D			ProgrammerNotes		Identifiers		PhysChem			Ctrl+C
			Most Recent StaDate		County LatLon		PhysChem Report			
					Station Levels		Sample Status Report			
					Water Bodies		DBA Sample Report			

Taxa	Bioassay	User Info	Hel
Problems			
Maintenance			
Taxa List Reports			
View Taxon Info			
Show Fla List Date			
Download Fla List			
Prepare for BIOS			
Mark BIOS upload results			
Make BIOS corrections			

Bioassay	User Info	Help
Samples		
Facilities		
Facility types		
NPDES sites		
DEP Districts		
Sample types		
Diluents		
Test organisms		
Calculation methods		
Causes of toxicity		
Maintenance		

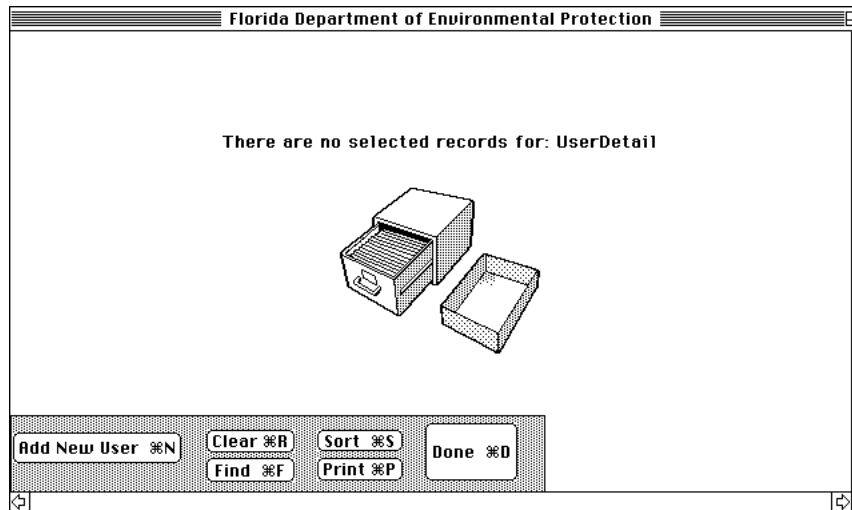
User Info	Help
Quit to design	Ctrl+U
Show my info	
Users	
User Groups	
ImportPCVars	
ExportImportFileInfo	
Menu Tester-Lori	
AACallProcToTes	
Import LIMS info	
Export LIMS info	

Group = RetrieveGrp



Adding New Users

- 1) Select Users under the User Info pulldown menu.
- 2) You will see a screen like this:



Click on Add new user.

- 3) You will see the user maintenance screen:

User Information

User Name
(up to 15 characters for both)

Password

Group ID **TLH BioSec**

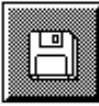
User Status 1=Logged on; 0=Not logged on

☐ Group administrator permission?

☒ Data Entry Permission?

☐ Tox Data Entry Permission?

 **Delete this user**

 **Done**  **Cancel**  **Save & Next**

DBA

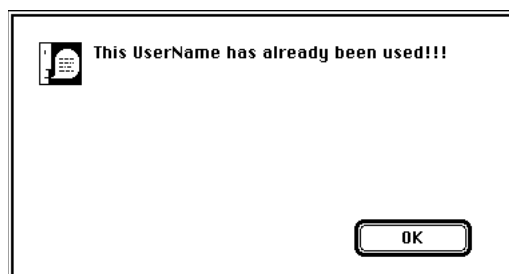
TLH BioSec
JAX BioLab
PNS BioLab
ORL BioLab
TPA BioLab
PG BioLab
WPB BioLab
Visitors
TLH Bssy
TLH BurLab

Enter a user name and a password, each one should have a maximum of 15 characters (case is important, i.e., “Password” is different than “password”). The default sets the group ID to

“TLHBioSec” and gives data entry permission. If this user should be different, make the necessary changes by selecting another group from the pop-up menu or clicking in a different permission category. When a check box has an “x”, it means that permission is granted.

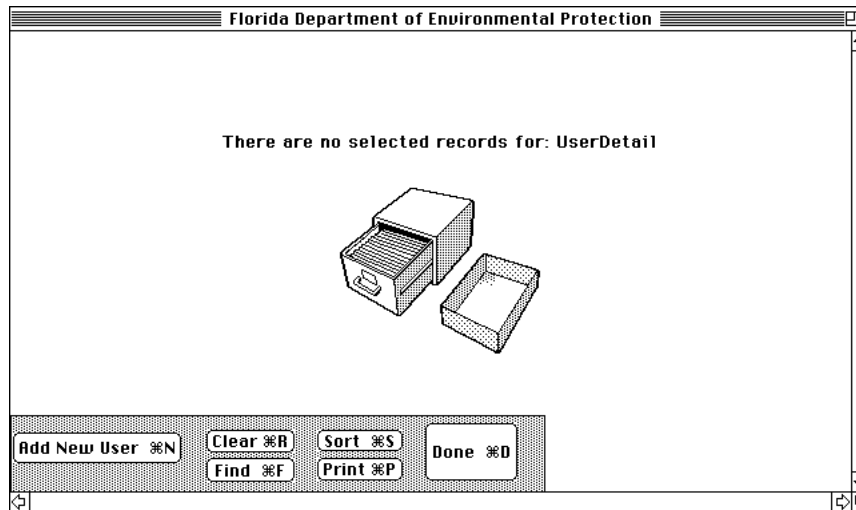
- 4) Click on **Done** when you are finished (or on **Save & Next** if you have another user to add). The computer will check the user name that you added. If it already exists, you will see:

and you will be returned to the maintenance screen.



Editing/Deleting Existing Users

- 1) Select Users under the User Info pulldown menu.
- 2) You will see a screen like this:



Click on Find.

- 3) You will see a user selection box:

There are three ways to load user names:

- a) Enter a specific user name.
- b) Use the popup menu next to “or all users in group” to select a group.

- c) Use the radio buttons to load users with or without certain permissions.

These three choices are mutually exclusive. For example, if you enter a user name and then click in front of With, the user name will be erased.

- 4) Click on Load.
5) The computer will load the user names that meet your criteria like this:

Florida Department of Environmental Protection

DataBase User Information 0=No, 1=Yes

UserName	Group ID	GroupAdmin?	Data Entry?	Tox Entry?	User Status
Jackson_J	2	0	1	0	0
McPherson_C	2	0	1	0	0
Quintana_U	2	1	1	0	0
Whiting_V	2	1	1	0	1
EspyK	2	0	1	0	0
Tamburello_L	2	1	1	0	1
Richardson_U	2	0	1	0	0
Wolfe_S	2	1	1	0	0
Baughman_U	2	0	1	0	0
Miller_EA	2	0	1	0	0
Lashbrook_S	2	0	1	0	0
Hua_M	2	0	1	0	0
Richardson_C	2	0	1	0	0

Add New User %N Clear %R Sort %S Done %D
 Find %F Print %P

- 6) Double-click on the name you want to edit or delete. You will be taken to the user maintenance screen:

User Information

User Name Wolfe_S
(up to 15 characters for both)

Password *****

Group ID 2 TLH BioSec

User Status 0 1=Logged on; 0=Not logged on

☒ Group administrator permission?
☒ Data Entry Permission?
☐ Tox Data Entry Permission?

 **Delete this user**
  **Done**
  **Cancel**
  **Save & Next**

The user name is locked (i.e., you cannot edit it). If you want the user name to be different, you have to delete this user and add a new one. The password can be edited.

- 7) If you need to change something, make the changes and click on Done. You will see:

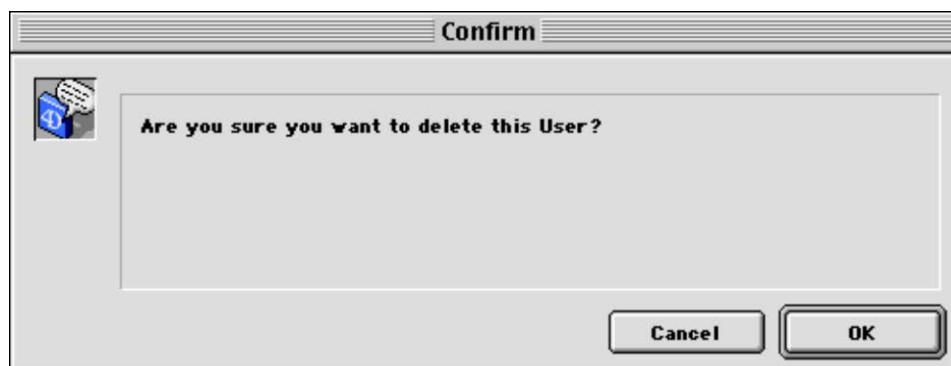
Confirm

Save changes?

Cancel OK

Click on OK if you want to save the changes, click on Cancel if you want to put the information back the way it was before you edited it.

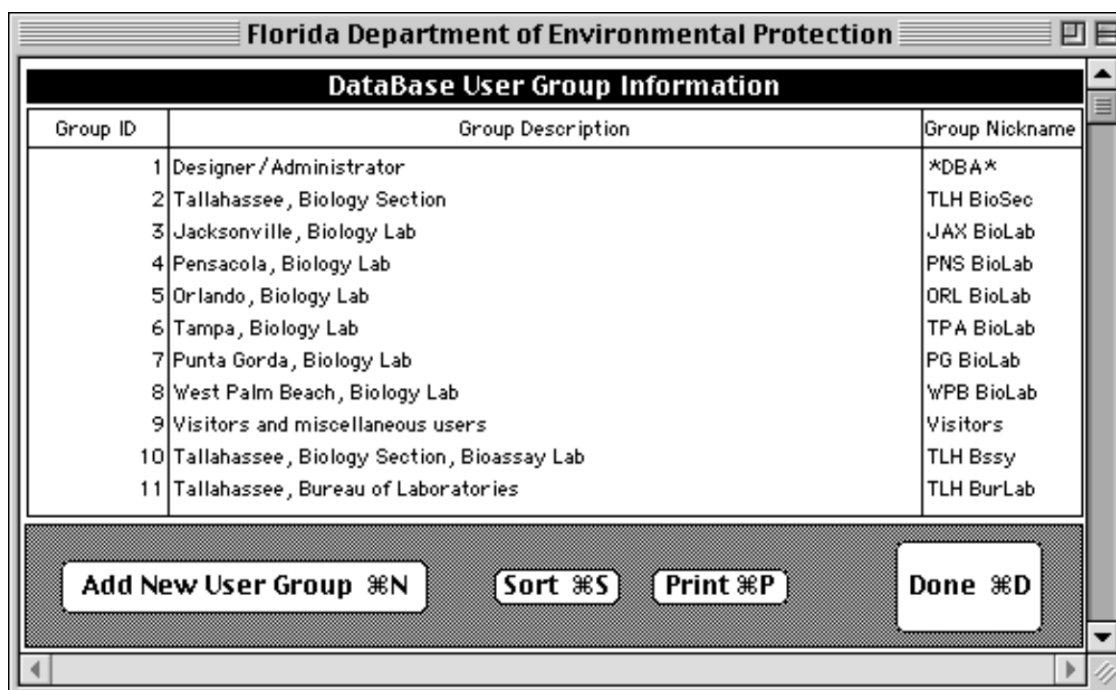
- 8) If you want to delete the user, click on Delete this user. You be given one last chance to change your mind:



- 9) You will be taken back to the screen displayed in step 5. You can edit another user, load different users, or click on Done if you are finished. You will be taken back to the splash screen.

Adding New User Groups

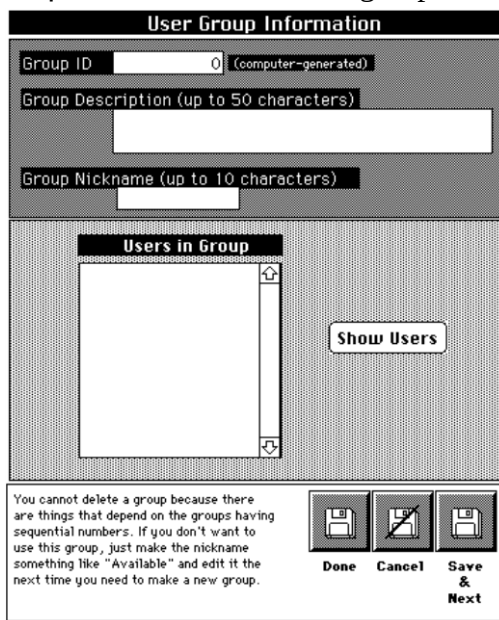
- 1) Select User Groups under the User Info pulldown menu.
- 2) You will see a screen like this:



All the existing user groups will be listed.

- 3) Once a user group has been added, it cannot be deleted. This is because there are several program-related functions that count on the group numbers being sequential. If there is a group that you do not need anymore, rename it to something like "Available" and then reuse it the next time you need a new group.

- 4) Click on Add New User Group. You will see the user group maintenance screen:



User Group Information

Group ID (computer-generated)

Group Description (up to 50 characters)

Group Nickname (up to 10 characters)

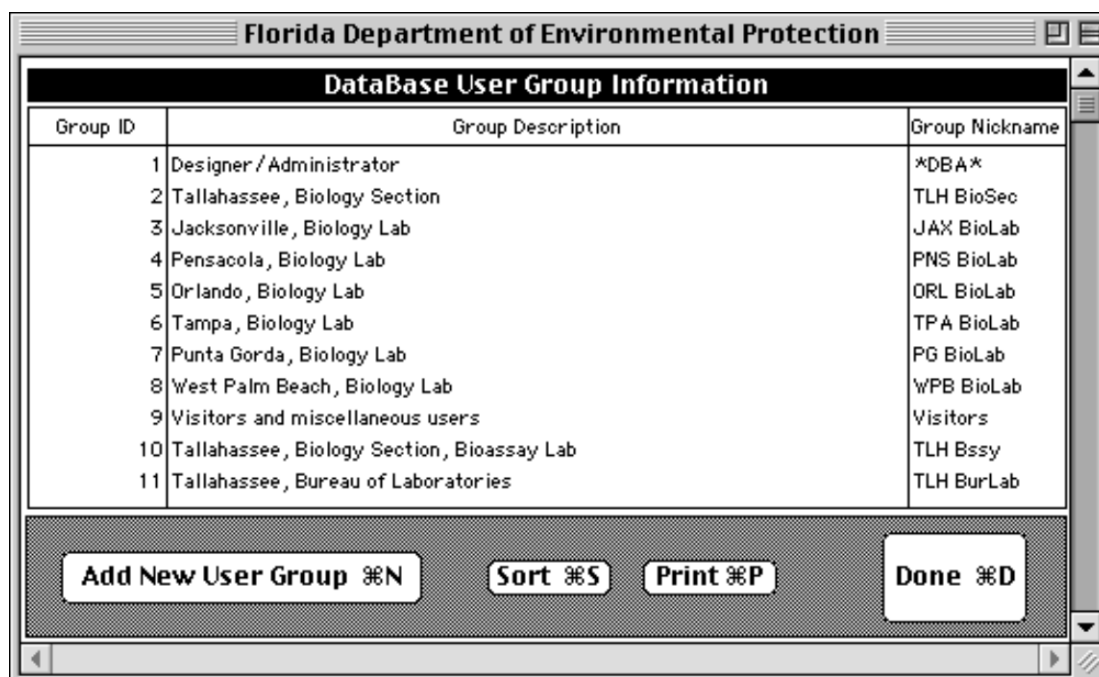
Users in Group

You cannot delete a group because there are things that depend on the groups having sequential numbers. If you don't want to use this group, just make the nickname something like "Available" and edit it the next time you need to make a new group.

Enter a description of the group (up to 50 characters) and the nickname for the group (up to 10 characters). The nickname will be used in popup menus for selecting groups. The Show Users button does nothing when you are adding a new group since there can't be any users for a non-existent group. Click on Done or Save & Next when finished.

Editing User Groups

- 1) Select User Groups under the User Info pulldown menu.
- 2) You will see a screen like this:



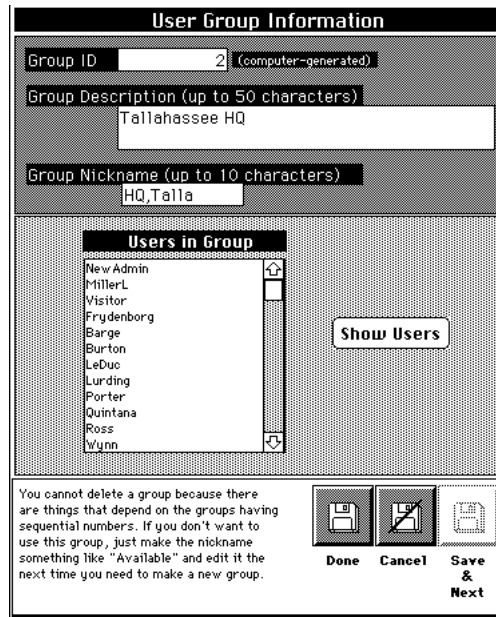
Florida Department of Environmental Protection

DataBase User Group Information

Group ID	Group Description	Group Nickname
1	Designer / Administrator	*DBA*
2	Tallahassee, Biology Section	TLH BioSec
3	Jacksonville, Biology Lab	JAX BioLab
4	Pensacola, Biology Lab	PNS BioLab
5	Orlando, Biology Lab	ORL BioLab
6	Tampa, Biology Lab	TPA BioLab
7	Punta Gorda, Biology Lab	PG BioLab
8	West Palm Beach, Biology Lab	WPB BioLab
9	Visitors and miscellaneous users	Visitors
10	Tallahassee, Biology Section, Bioassay Lab	TLH Bssy
11	Tallahassee, Bureau of Laboratories	TLH BurLab

All the existing user groups will be listed.

- 3) Double-click on the user group that you want to edit. You will see the user group maintenance screen for it:



The screenshot shows a 'User Group Information' window. It has three input fields: 'Group ID' with the value '2' and '(computer-generated)' text; 'Group Description (up to 50 characters)' with the value 'Tallahassee HQ'; and 'Group Nickname (up to 10 characters)' with the value 'HQ,Talla'. Below these is a 'Users in Group' section with a scrollable list of names: New Admin, MillerL, Visitor, Frydenborg, Barge, Burton, LeDuc, Lunding, Porter, Quintana, Ross, and Wynn. To the right of the list is a 'Show Users' button. At the bottom, there is a message: 'You cannot delete a group because there are things that depend on the groups having sequential numbers. If you don't want to use this group, just make the nickname something like "Available" and edit it the next time you need to make a new group.' Below the message are three buttons: 'Done', 'Cancel', and 'Save & Next'.

- 4) Make the changes you want. If you want to see what user names have been assigned to this group, click on **Show Users** and they will be displayed in the scrollable box. You cannot change the users assigned to the group here. You have to edit each user individually.
- 5) Click on **Done** when the changes are finished, click on **Cancel** if you want the group put back the way it was before you edited it. You will be back at the screen displayed in step 2. You can edit another group or click on **Done** if you are finished. You will be taken back to the splash screen.

Deleting User Groups

You cannot delete a user group. This is because there are several program-related functions that count on the group numbers being sequential. If there is a group that you do not need anymore, rename it to something like "Available" and then reuse it the next time you need a new group.

Sending data to BIOS

BIOS is the biological part of the federal STORET system. The benthos, zooplankton, periphyton, and phytoplankton data entered in this database are uploaded to the BIOS system. Before these data can be uploaded, they have to be converted into the proper format and have acceptable BIOS ID's for part of the information. For example, the station has to have a STORET name that is currently in the STORET system, the scientific name has to be on the BIOS master taxonomic list, the sampling gear has to have an acceptable BIOS name, and the collectors and identifiers associated with samples must be listed in a reference table in STORET. You will notice that many of the reference tables have a field called "BIOS ID". These are ID's assigned by the STORET User Support and are to be used on data uploaded to BIOS. A DEP ID is only used in this database and is never uploaded to BIOS. There is a routine called Prepare for BIOS under the Taxa pulldown menu that finds data ready to go to BIOS, scans it for possible incompatibilities with BIOS, and writes a file suitable to upload to BIOS.

Who can do it

Only the database administrator and assistant administrator can prepare and upload data to BIOS.

Prepare data for BIOS

- 1) Select Prepare for BIOS under the Taxa pulldown menu. The screen below will be displayed and a menu called BIOS sets will be available.

BIOS sets	Help
Show all set numbers in use	Show applicable set numbers
Count samples prepared	Find more samples to prepare
Show samples in a set	Show samples not in a set
	Clear a set

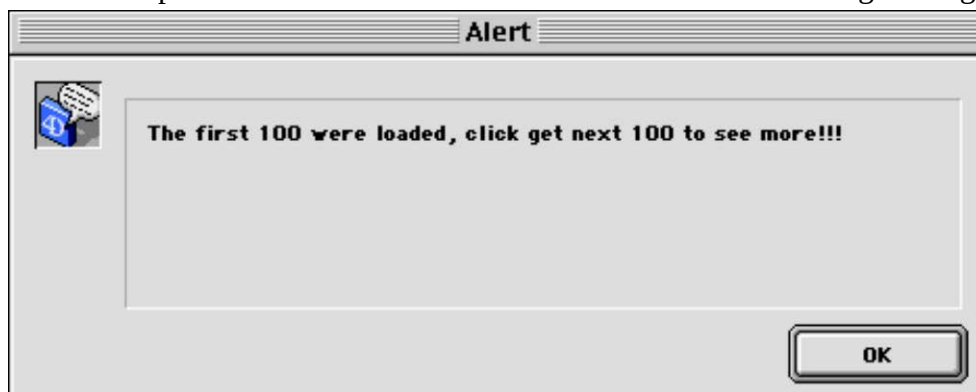
To retrieve a list of samples to prepare for BIOS, choose Find more samples to prepare from the BIOS sets menu. A message box will display:

Looking for samples eligible to go to BIOS...

Samples that are eligible to go to BIOS must meet the following criteria:

- a) they have been marked "complete";

- b) they have a value of zero for the field BIOSSTAT, and BIOSDATE will be "00/00/00", meaning it has not been prepared or accepted for BIOS. Look at the description of the field BIOSSTAT in table DT\$Sample to understand how this field keeps track of BIOS data;
 - c) they contain biological data (samples with pchem data only are not stored in BIOS); and
 - d) the survey may not be "unknown".
- 2) If more than 100 samples that meet the above criteria are found the following message will display.



Click OK to view the first 100 samples.

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Samples to go to BIOS

If you only want to send some of these samples to BIOS, select them (hold down the command key to select more than one), then click the "Show selected samples" button.

3=Sampled
2=Not sampled

Done?	Sta NickName	Station STORET Name	Sample Date	Survey	GroupID	SampleID	BIOS	Set	BIOS Date	Ben	Zoo	Per	Phy	PC
Y	STMR125REF	19010041	08/03/94	ECOREG REF STREAMS	2	3956	0		00/00/00	3	2	2	2	2
Y	STMR125REF	19010041	01/25/95	ECOREG REF STREAMS	2	6825	0		00/00/00	3	2	2	2	2
Y	STMR125REF	19010041	07/11/95	ECOREG REF STREAMS	2	7167	0		00/00/00	3	2	2	2	3
Y	STMR125REF	19010041	01/03/96	ECOREG REF STREAMS	2	9192	0		00/00/00	3	2	2	2	3
Y	PALSTSOREF	19010043	02/23/94	LAKE BIOASSESSMENTS	2	5220	0		00/00/00	3	2	2	3	3
Y	PALSTSOREF	19010043	08/08/94	LAKE BIOASSESSMENTS	2	9293	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	03/03/93	ECOREG REF STREAMS	2	4281	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	08/17/93	ECOREG REF STREAMS	2	4275	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	03/07/94	ECOREG REF STREAMS	2	4296	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	07/25/94	ECOREG REF STREAMS	2	3965	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	03/06/95	ECOREG REF STREAMS	2	6829	0		00/00/00	3	2	2	2	2
Y	PIGEONREF	19010099	07/09/96	ECOREG REF STREAMS	2	10591	0		00/00/00	3	2	2	2	3

Buttons: Make set of samples, Show selected samples, Show all, Done %D, Send all these to BIOS, Get next 100, Clear all, Sort %S, Print %P

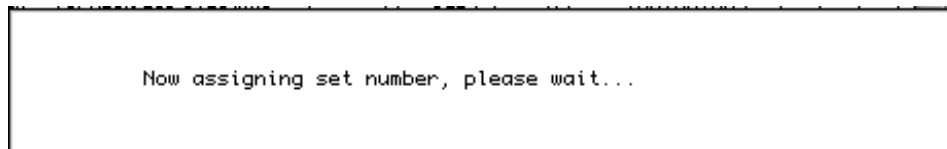
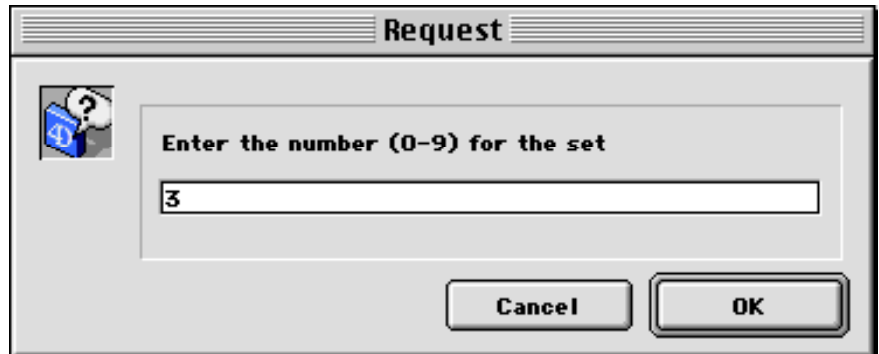
If you want to prepare more than 100 samples, click on Get next 100. You may load 100 samples at a time until you have loaded all of the samples eligible to go to BIOS.

You have three options at this point:

- 1) If you don't want to prepare any of the samples for BIOS, click on Done.
- 2) If you want to prepare all the samples displayed for BIOS, click on Send all these to BIOS.
- 3) You want to send some of the displayed samples, but not others. Click once on the first sample you want to send, then hold down the command key (the one with the apple on it) and select the other samples you want. When you have selected all the ones you want, click on Show selected samples. Only the samples you selected will be displayed on the screen.

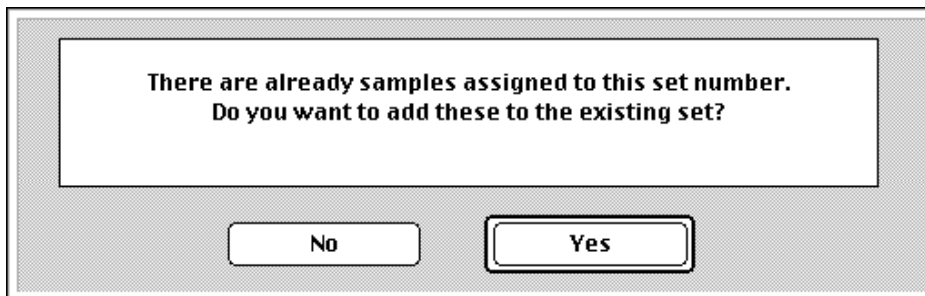
The samples you did not pick will be listed the next time you run “Find more samples to prepare”.

- 3) Once you have displayed eligible samples, you may place them in a “set”. The **Send all these to BIOS** routine generates an error report (described in detail below). This is useful for retrieving the same collection of samples once you leave the “Prepare for BIOS” area and then return. To create a set of samples using those displayed, click on **Make a set of samples**. You will be prompted for a set number between 0 and 9. If there is no set already defined for the number you entered, the program will assign the set number. You will see the following message:



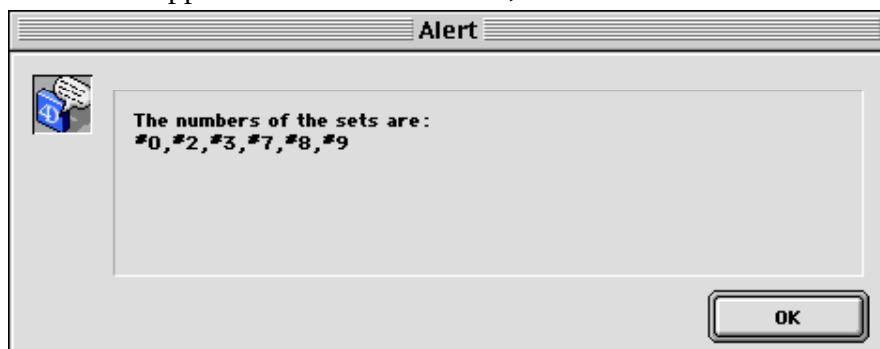
You will then be returned to the screen shown in step 2, and the “Set” column will display the assigned number.

If there are samples already assigned to the number you entered, the program will display the

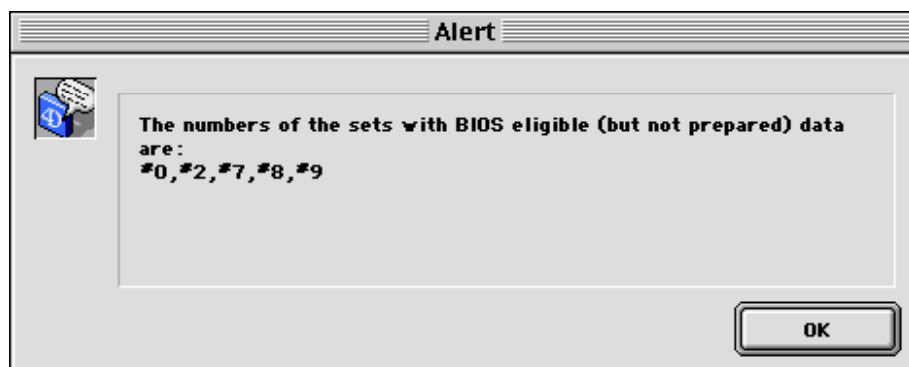


message shown below. Click on **Yes** if you want to add the displayed samples to the set, or **NO** if you don't. The program will return to the screen shown in step 2.

To see which set numbers have been used and contain samples to be prepared or those that have already been prepared, select **Show all set numbers in use** from the BIOS sets pull down menu. The message below will appear. To create a new set, choose a number that has not been used.

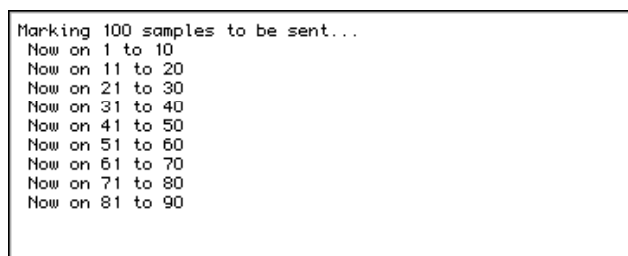


To see which sets contain samples waiting to be prepared (and so could be added to), select Show applicable set numbers from the BIOS sets pull down menu. The following message will be shown:

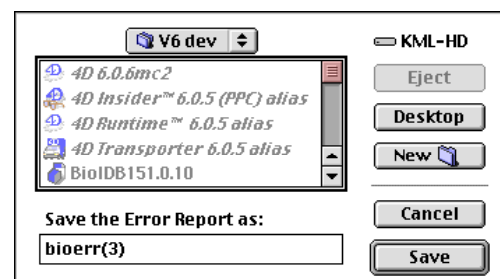


If you have already defined a set but have not displayed it, choose Show samples in a set from the BIOS sets pull down menu. The program will prompt you for the set number and then retrieve all of the samples in that set. If the set contains more than 100 samples, you will get an alert like the one shown in step 2, and can load the rest 100 at a time by clicking the Show next 100 button.

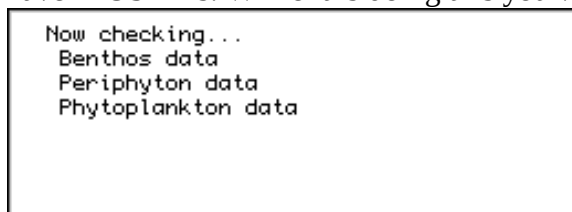
- 4) Once you have displayed the samples to be prepared for BIOS upload (whether or not they are in a set), click on Send all these to BIOS. You will see:



followed by

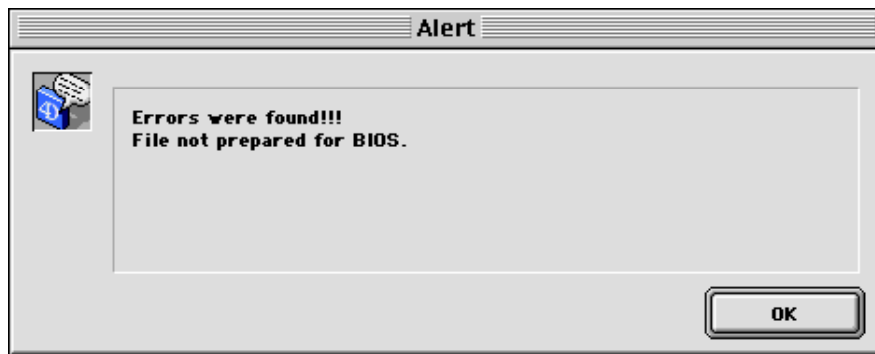


The computer will scan the samples that are to be prepared and make sure that they have taxon ID's that are either on BIOS or have had an alternate BIOS ID assigned and that all other BIOS-related fields have BIOS ID's. While it is doing this you will see:



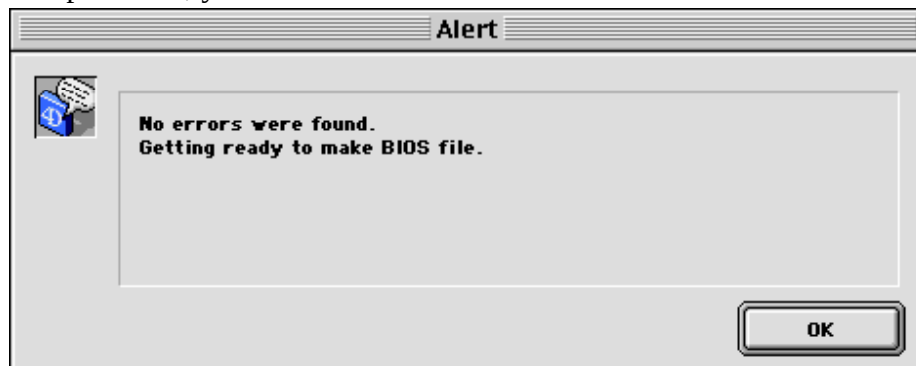
All the problems that are found will be written to the file you specified in the box above. An example of the error file is shown later in this section

- 5) If the error scan found problems, you will see:

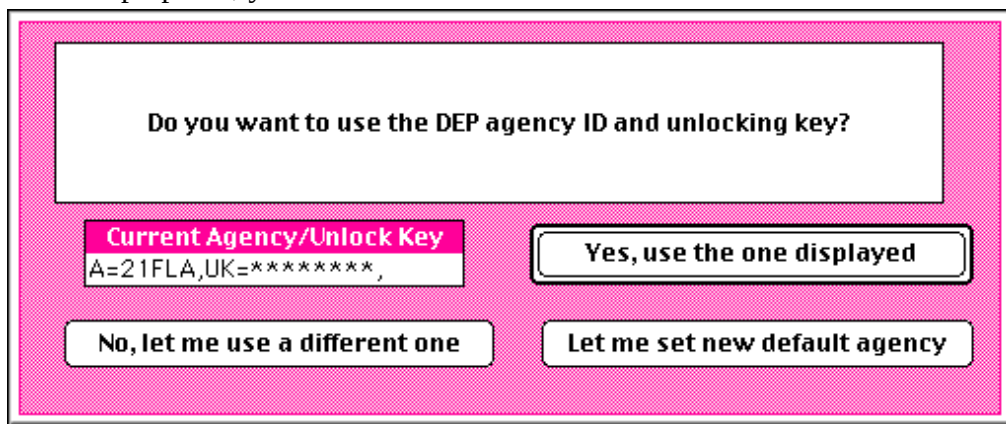


and you will be returned to the splash screen.

If there were no problems, you will see:

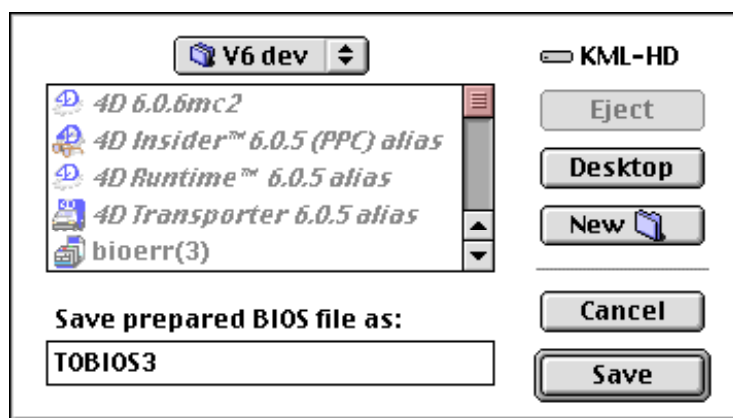


6) Before the file is prepared, you will see

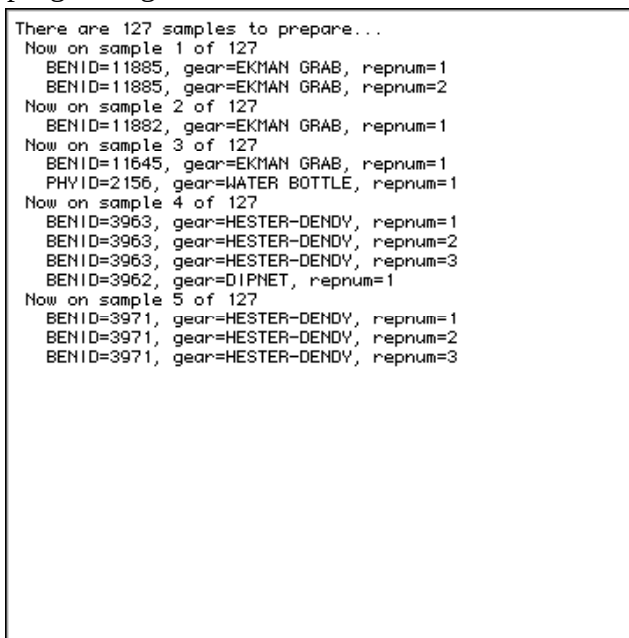


The first line of file that is sent to BIOS must contain the agency ID and unlocking key. The default values appear in the box. If you want to use those, click on Yes, use the one displayed. You can change the values for a particular batch of data by clicking No, let me use a different one. If you want a different agency code and unlocking key to appear in the box the next time you prepare samples for BIOS, click on Let me set new default agency.

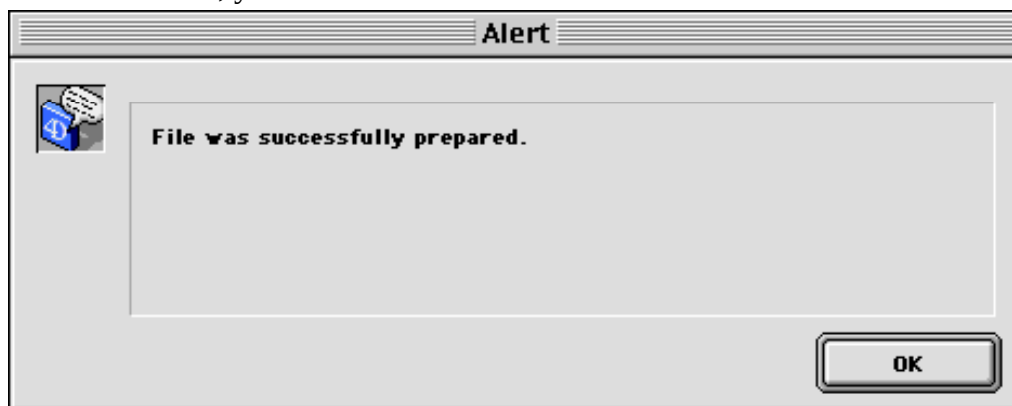
7) Next you will be asked to name the file for the reformatted data:



- 8) The program will then prepare a file suitable to upload to BIOS. The amount of time it takes to do this depends on how many samples you are converting. You will see a message box like this so you can see how things are progressing:



- 9) When the file is finished, you will see:



After you click on OK, you will be returned to the splash screen.

- 10) If errors were found while attempting to make the BIOS upload file (step 5 above), they must either be resolved or the sample(s) must be removed from the batch to be prepared. During the “Send all these to BIOS” procedure, an error file was named. This file can be opened in any text editor (SimpleText, NotePad) or word processing (Microsoft Word) program.. The contents of the file will look like this example:

```
SurveyID 101 (TMDL STUDIES) does not have a BIOS ID.
-----
*****
Problems found in benthos data:
GearID 5 (Lori1) does not have a BIOS ID.
IdentifierID 337 (Baughman, Julie) does not have a BIOS ID
-----
Taxa that are not on BIOS and have no alternate BIOSID:
10000906 Neoporus
10001006 Labiobaetis
*****
Problems found in periphyton data:
Taxa that are not on BIOS and have no alternate BIOSID:
10000857 Fragilaria pinnata trigona
*****
Problems found in phytoplankton data:
*****
Problems found in zooplankton data:
*****
```

It will always put a heading for each data type; if no problems were found with that data type there will be nothing listed below it.

The example above lists several types of errors that may be encountered. Samples with errors must be must be removed from the batch to be prepared. It is useful to define a “set” (see step 3 above) to hold the samples with problems to resolve so that they do not appear as eligible. When the program looks for eligible samples, it finds those that are not yet assigned to a set.

- a) The survey does not have a BIOS ID. All surveys in the database must also be listed in the STORET(BIOS) reference tables and be issued a BIOS ID. This error would occur if the BIOS ID number was not entered in the biological database (set at zero). The DBA or Assistant DBA may be in the process of obtaining the BIOS ID assignment.
- b) The gear does not have a BIOS ID. There is a great deal of flexibility in the way that the database handles different gear types and groups, but each gear must be uploaded with a name that corresponds exactly with one in the BIOS gear reference table. If the DBA has not yet entered the BIOS ID for the gear, this error will result.
- c) The identifier does not have a BIOS ID. Similar to the surveys, biological sample identifiers must be listed in the STORET reference tables and be issued a BIOS ID number. This error would be encountered if the BIOS ID was still set at zero for an identifier. You must find the sample(s) associated with that identifier and remove them until the BIOS ID has been entered.
- d) Taxa that are not on BIOS and have no alternate BIOSID. These samples contain taxa that have been added to the Florida list but did not appear on the BIOS master list. The samples have been marked complete and data can be retrieved and used locally, but the samples cannot be uploaded until the names are added to the federal master list. The DBA and assistant DBA periodically send requests to BIOS, along with taxonomic references, to have new taxa added

to the master list. To determine which samples contain the “problem” taxa, do a “Retrieve by taxon” and compare the results with the “samples to go to BIOS” list. Remove those samples with problem taxa.

Uploading to BIOS

After the BIOSPrep file is created by the database, it is uploaded via ftp to STORET. Commands for data storage are issued in the STORET environment, and a process of error checking follows. None of the data are stored until all of the errors are resolved or the samples with errors are deleted from the upload file. Several of these errors are similar to those described above.

Handling BIOS error reports

- 1) Station not valid for agency code. Most stations in DEP are associated with the agency code “21FLA”, but there may be biological sampling stations stored under a different code. In this case, the unlocking key (UK) will be unique for that agency code. The District/Section STORET coordinator who set up the station will know what agency code is associated with it. A new file must be created with the proper agency code and unlocking key to store data for those stations.
- 2) Station does not have “BIO” as an attribute. Not only must all stations have been stored in the STORET system, they also need to have “BIO” listed as an attribute in STORET before biological data can be uploaded to BIOS. Note that this is a BIOS requirement and not a database requirement, as “BIO” is not an attribute that is chosen in the “add new station” procedure. To resolve this problem, the STORET coordinator can run a simple program that will add “BIO” to the station attribute list. Following the weekend update cycle, the station will be valid for storage of biological data
- 3) Survey, collector, and/or identifier numbers have not been assigned to this agency code. Following a written request to STORET User Support, reference numbers are assigned by BIOS to surveys, collectors, and identifiers. To obtain reference numbers for surveys the following information must be provided: survey name, date survey began, and purpose of survey (baseline, enforcement, monitoring, research, screening, or use attainability). Information needed for collectors and identifiers includes name, organization (during the time the individual collected or identified samples), address, telephone number, and an alternate telephone number if applicable. Requests to BIOS for these numbers are initiated by the assistant DBA. This error should only occur rarely, as the “Prepare for BIOS” routine will catch those reference table entries of zero for BIOSID. If an incorrect BIOS ID was added (one not corresponding to an entry in the BIOS reference tables), this error will result.
- 4) Gear type not expressed properly. BIOS has a list of valid gear types and abbreviations, and they must be expressed **exactly** as they are listed. This problem should only arise when any new gear types are added to the reference table in the database, without the proper BIOS ID.
- 5) Taxon name invalid. Although the “Prepare for BIOS” routine checks for taxonomic names that are not listed on the BIOS master list, some names may be flagged in the database as being acceptable when they really are not. During storage, taxonomic entries are validated by comparison with the BIOS master list, and those which do not match are rejected.

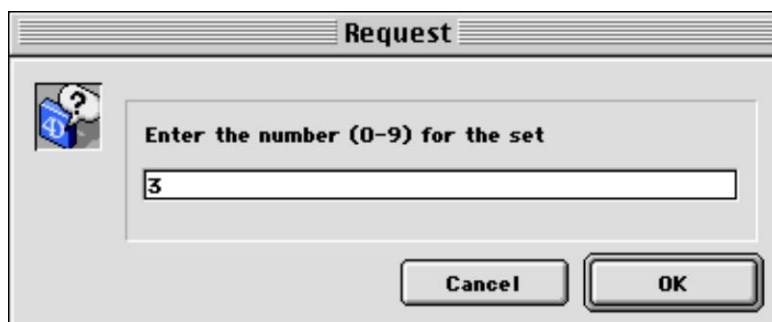
Finalizing BIOS results in BioDB

Once some samples have been “prepared for BIOS”, their BIOS status field is set to a value of “1” which means that it was sent to BIOS but we don’t know if it was accepted by BIOS or not. This routine is used to reset that status to “accepted” or back to “unprepared” (not accepted by BIOS).

- 1) Select Mark BIOS upload results from the Taxa pulldown menu. You will see this screen:

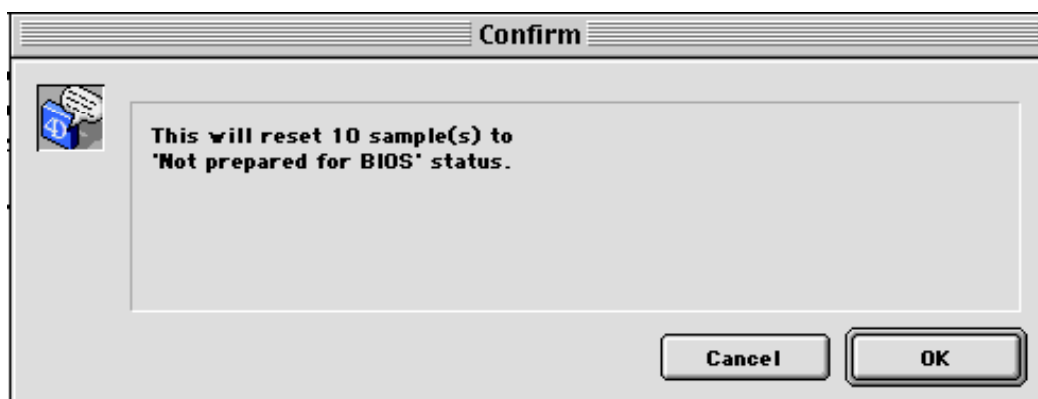


- 2) You must now display the samples to be marked “accepted” or “unprepared”. If the samples were never assigned to a set, choose Show samples not in a set from the BIOS sets pulldown menu. The program will load all samples that have been prepared for upload but not in a set. If the batch of samples were assigned to a set, choose Show samples in a set. You will be asked to enter the set number:

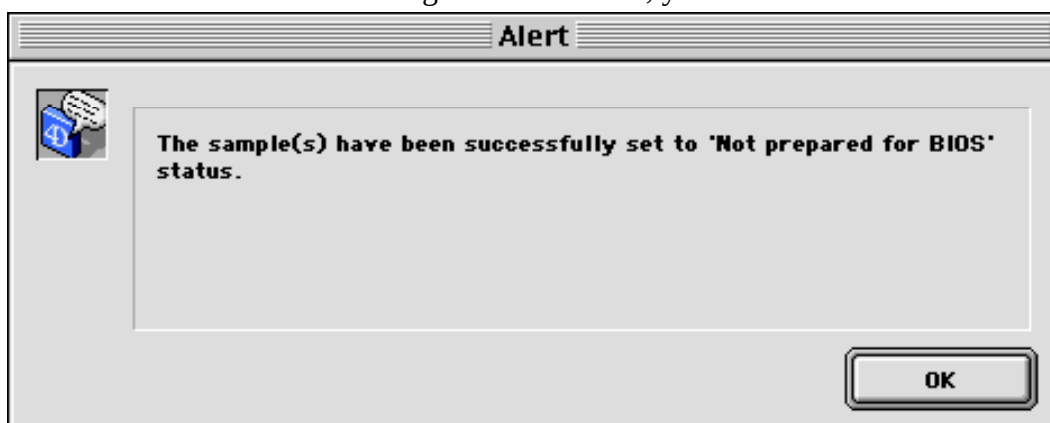


A screen like the one shown in step 2 will display, listing all samples that were prepared and assigned to the set you entered.

- 3) If BIOS found errors, you need to reset these samples to “never sent to BIOS” status. Select the samples with errors. You may need to command-click (Mac) or cntrl-click (Windows) to select discontinuous samples. When you have selected all of the samples that had BIOS errors, click on Show selected samples, and then on Mark these “unprepared”. You will see this screen:

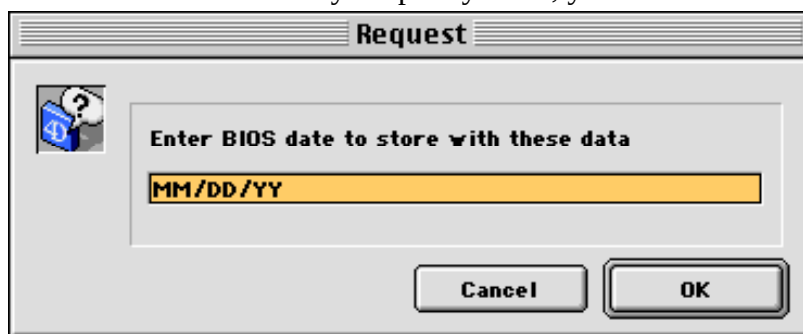


If you have change your mind and do not want to reset the BIOS status, click Cancel, otherwise click OK. When it has finished resetting the BIOS status, you will see:



Click on OK to return to the “Mark BIOS upload results” screen.

- 4) If there are samples left in the set that were accepted by the BIOS system, click on Mark these BIOS accepted. This will set the BIOS status to “accepted by BIOS” and the BIOS date associated with this sample will be set to a date that you specify. First, you will see:



and you enter the date that you want marked on each sample as the date it was accepted by BIOS. Be sure you type the date with the slashes, i.e., “05/03/94”. If you don’t want to mark the samples as accepted, click on Cancel. After you click on OK, the computer updates the sample table. When it is finished you will see:



After you click on OK, you will be returned to the “Mark BIOS upload results” screen. If there are samples from another set to mark, begin again with step 2. When you are finished, click on Done to return to the splash screen.

Make BIOS Corrections

Once a sample has a BIOS status of 2 (data successfully sent to BIOS), it cannot be marked incomplete. The only change that can be made is to add or alter the comments box on the main sample screen. Occasionally, however, some type of error is discovered, such as a mistake in a taxonomic identification or some other sample information. To make a correction in a sample that has been sent to BIOS, the BIOS status must be changed to status 0 (never sent to BIOS) and then marked incomplete. After the changes are made, it is important to make sure that the change is also made to the sample in the federal database. There are two ways to do this:

- a) Use the routines in the STORET environment to change the sample that was stored. The sample in the database could then be set back to status 2 and the BIOS date reassigned.
- b) Use the routines in the STORET environment to delete the sample with the error. The sample in the database would remain at status 0 and be re-uploaded at some time in the future, when a new BIOS date would be assigned.

Samples may also need a change in status if something unforeseen happens during the “Prepare for BIOS” routine. During this procedure, samples are set to BIOS status of -1, and then set to 1 when the routine ends. If the computer crashes during the procedure, the samples may stay set to this value and must be changed to 0 or 1.

Only the database administrator (DBA) may make BIOS corrections.

- 1) Choose Make BIOS corrections from the Taxa pulldown menu. The following screen will be displayed.

Sample ID to correct: 0

Date BIOS Accepted: 00/00/00

Cancel Update

Samples to be corrected must be identified by the sample ID, the unique number that was assigned when the sample was created. Enter the sample ID and press return.

- 2) The BIOS status will be selected in the pop-up menu. If the sample has been accepted by BIOS, the BIOS date will appear below the status.

Sample ID to correct: 2868

Accepted by BIOS: 2

Date BIOS Accepted: 01/22/96

Cancel Update

The three choices in the pop-up menu appear below. If the samples are changed from "Accepted by BIOS" to either of the other two, the BIOS date is set to 00/00/00.

Never sent to BIOS
Prepared for BIOS
Accepted by BIOS

Choose the appropriate BIOS status option and click on Update.

- 3) An alert box appears, telling you the sample has been corrected.

Successfully updated! Do you want to do another?

Cancel OK

Click on OK if you have more samples to correct, and you will return to a blank sample correction screen. If you are finished correcting samples, click on Cancel and you will be returned to the splash screen.

Technical Information

It is not the intention of this manual to teach you how to program in 4th Dimension or Oracle. If you want to make changes, you will need some knowledge of the how to get around in 4th Dimension and of Oracle SQL syntax. You are strongly encouraged to read the 4D Oracle Manual before making any programming changes to this system. You need to know how these programs interact before making changes or additions.

Oracle and 4th Dimension

Oracle and 4th Dimension are two database programs sold by different companies, Oracle and ACI, respectively. The data are stored in an Oracle database that resides on a server in Tallahassee. 4th Dimension is a database program that can be used without Oracle; however, for this database it is used as way of having a familiar Macintosh or PC interface to access data stored in an Oracle database. The 4th Dimension database is nearly empty, except for several reference tables (listed below). When you request a function like “Retrieve by Station and Date”, 4th Dimension sends a SQL command to the Oracle database to get the data. Oracle returns the data and it is stored in 4th Dimension while you work with it. When you log off the database, most of the files (exceptions explained below) in the 4th Dimension database are emptied. If there are two computers logged on the system at the same time, their 4th Dimension databases are completely independent of each other and each will have different data loaded into them depending on what data requests have been made by each user. The Oracle database is what they have in common; the data are retrieved and updated to the same Oracle database. Each version of 4th Dimension acts as a single-user version.

There is an external procedure called 4D Oracle (a 4th Dimension product) that has been attached to the database program file that does the actual communication between 4th Dimension and Oracle. For a complete description of how Oracle and 4th Dimension interact, read the 4D Oracle documentation (from ACI) that accompanies the software.

There are several files in each 4th Dimension database that are not emptied each time you log off. The animal, plant, station, waterbody, collector, identifier, survey, and county tables are not emptied because most are relatively large and have information that is not changed frequently. This saves the time of reloading them every time you log on, as the program only does this when a change has been made to the Oracle (master) table. Also, having the information in these tables resident on each client computer results in increased performance, as the program does not have to send a SQL command to the Oracle database to query them. Global procedure EmptyAll does the emptying in case you need to keep other tables from being emptied. The tables that are saved are:

- | | |
|-------------|--|
| Animal | - The Florida animal taxa names and ID's (usually 7,000+ records) |
| Plant | - The Florida plant taxa names and ID's (usually 2,000+ records) |
| Station | - The stations, along with geographic locations and station attributes (nearly 7,000 records) |
| Waterbody | - Bodies of water to which stations can be assigned (currently 1600 records) |
| Collectors | - Individuals associated with the field collection of samples (currently 187 records) |
| Identifiers | - Individuals associated with the taxonomic identification of biological samples (currently 142 records) |
| Survey | - Survey names, purposes, and start dates (currently 24 records) |
| CtyLatLon | - The Florida county information (69 records) |

- UserInfo - Holds the revision date and time and maximum number of records ever loaded into the Florida plant and animal tables, and for any other table not emptied when you log off. There is only one record in this file.
- PCOracle - Keeps the name of the physical/chemical variables. If this table becomes corrupted or is inadvertently emptied, it can be reloaded by a user from the "Database Administrator" group. Under pulldown menu User Info select ImportPCVars. It will use file PCVars.txt to reload the table. When it has been loaded you should see this message:



Important 4th Dimension Information

The 4th Dimension application itself (not the biological database program) exists in two forms. One is a full version that allows certain users access to the programming environment. The other form is a “run-time” version which means that it will run the biological database program, but does not allow anyone any access to the programming environment. The latter is the version that is on most of the computers on the network (it is cheaper to buy and takes less RAM to run). For Mac users who can allocate RAM to the 4D Runtime application, you will need to give it at least 8 MB of RAM to run. The more RAM you can give it, the faster it will run. The size of a retrieval that you can display is also dependent on how much RAM you give 4D.

The files and folders needed to run the biological database system are:

Structure Files

One structure file is needed for the Mac version of the database. It will be named something like **BiolDB151.0.10** - The version numbers may be different since each time the program is updated, the number is incremented, but it will start with “BiolDB”. This is the file with the actual biological database program in it. When you want to use a new version of the program file, put it in the folder and rename the existing “.data” file to the new name.

The windows version of the database uses two files for the structure. They will have names similar to **Bldb151.4db** and **Bldb151.4rsr**.

Data Files

The 4th Dimension data file for the Mac version will have the same name as the structure file above with “.data” attached to the end (**BiolDB151.0.10.data**). It will hold the information in the tables that are not emptied and hold the information downloaded from Oracle while you are working. If this file becomes corrupted, you can easily make a new one. Just get rid of the corrupted version, double-click on “BiolDB151.0.10” and it will ask you for the name of the data file to use. One of the choices is a button labeled “New data file”. Click on that button. It will tell you that you need to load new Florida lists, so say OK. It will automatically reload the county information. You need to manually reload the physical/chemical variable name file as described in the previous section, “Oracle and 4th Dimension”.

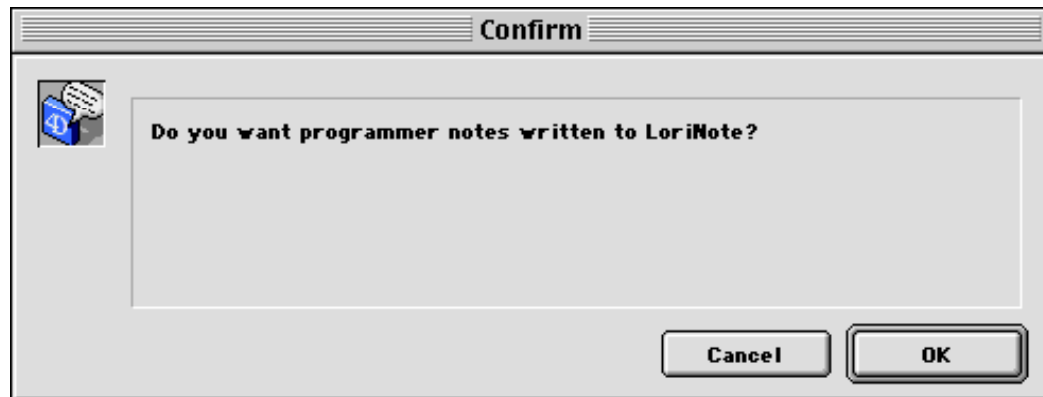
The PC version requires two data files. They will be named something like **Bldb151.4dd** and **Bldb151.4dr**.

4th Dimension 6.0.6 or **4D Runtime** (the version numbers may be different) - The database application program. This is the engine that drives the program in the structure file.

Mac4DX or WIN4DX Folder

This folder must be located in the same folder as the structure and data files. It contains “plug-ins” that expand the capabilities of 4th Dimension. If all of the necessary items are not present in the folder, or if the folder gets moved to a different location, the procedures will not run properly, or will not run at all.

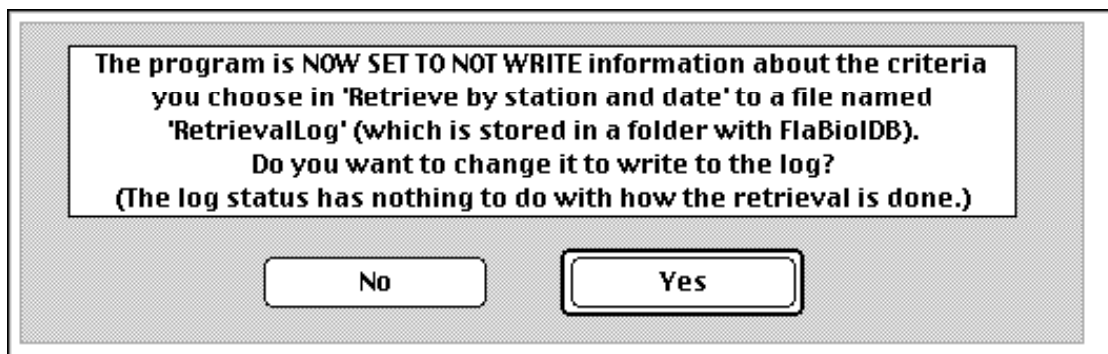
LoriNote - Under the Retrieve pulldown menu there is an item named Programmer Notes. When you select this item, you will see this box:



If you click on OK and run Retrieve - By Station and Date, all the SQL calls are written to file LoriNote in the 4th Dimension folder. If you click on Cancel, it will not do that anymore. This is for a programmer who is trying to debug a retrieval problem. LoriNote is a text file and should be left empty unless it is being used for debugging.

RetrievalLog - When Retrieve - By Station and Date is run, the user can choose to have the retrieval options selected written to a text file named RetrievalLog.

Choose Retrieval Log Status from the Retrieve menu. The following screen will display.



If you click Yes, the program will write to the log. Here is an example of what would be in this file:

```
File opened on 11/16/98 at 10:48:00

*****
Retrieval started on 11/16/98 at 10:48:03 by AsstAdmin
Field: vSrchStoret - value = 33040014
Button: Retrieve All (stations match criteria)
Button: StationRetrieveLayout - OK
Restrict retrieval to samples that are in the survey above?=No
Stations selected:
BIGHORSREF 33040014
-----
Open DateRetrieve Screen
Date selections: vStartDate=2/16/94
                 vEndDate=2/16/94
Date Option = 1
Layout: ReportRetrieve
Button: ckBenVar
Button: OK
Layout: Variable selection for Macroenthos Data
Button: Nind/unit area
Button: Nind counted, pooled
Button: No. taxa, pooled
Button: DBar, pooled
```

```

Button: Fla Index, pooled
Button: LC Index, pooled
Button: OK
Gear types selected:
HesterDend
Individual taxa selected:
Feeding groups selected:

End of user selections, starting retrieval...
Station nickname: BIGHORSREF
STORET name:      33040014
Sample date:      02/16/94
Benthos gear:     HesterDend
Quantitative
-----
Retrieval complete 11/16/98 at 10:48:35
*****

```

File closed on 11/16/98 at 10:49:55

When you want to stop writing to RetrievalLog, choose Retrieval Log Status from the Retrieve menu again. A similar screen will display, only this time clicking on Yes will tell the program to stop writing to the log file. Otherwise, when you log off and log on again, the program will reset and stop writing to RetrievalLog.

This file needs to be emptied from time to time so it doesn't get too large. You can do that by opening the file in Word (or other text editing program), selecting everything and deleting it. Be sure to save the file as text and not as a Word file.

PCVars.txt - The text file with the physical/chemical variable names and associated information that are loaded into 4D through User Info - ImportPCVars. The first column is the variable number, then the variable name, the third column is set to true if it is to be included in a retrieval and false otherwise (i.e., initial value does not matter because the program resets it), the fourth column is set to true if this variable can have counts that are TNTC (too numerous to count), and the last column is set to true if the variable can have values BDL (below detection limits). This is the current contents of this tab-delimited text file:

1	ALKALINITY	False	False	False
2	CONDLAB	False	False	False
3	CONDFLD	False	False	False
4	DONON	False	False	False
5	DOPROBE	False	False	False
6	HARDNESS	False	False	False
7	PH	True	False	False
8	SALINITY	True	False	False
9	TEMP	False	False	False
10	TURBIDITY	False	False	False
11	NH3DISS	False	False	True
12	NH3TOT	False	False	True
13	NH3UNION	False	False	True
14	NO3DISS	False	False	True
15	NO3TOT	False	False	True
16	NO2DISS	False	False	True
17	NO2TOT	False	False	True
18	NO3NO2DISS	False	False	True
19	NO3NO2TOT	False	False	True

20	TOTN	False	False	True
21	TKN	False	False	True
22	OPDISS	False	False	True
23	OPTOT	False	False	True
24	PHOSPTOT	False	False	True
25	BOD5	False	False	False
26	BOD20	False	False	False
27	ENTEROC	True	True	False
28	ECOLI	True	True	False
29	FECALMEM	True	True	False
30	FECALTUBE	False	True	False
31	FECALSTREP	False	True	False
32	COLIMEM	False	True	False
33	COLITUBE	False	True	False
34	PLATE	False	True	False
35	TOC	False	False	False
36	CLDISS	False	False	False
37	CLTOT	False	False	False
38	RESIDISS	False	False	False
39	RESIDTOT	False	False	False
40	TSS	False	False	False
41	RESIDVOL	False	False	False
42	RESIDVNON	False	False	False
43	SILICATOT	False	False	False
44	SILICATOT	False	False	False
45	SO4DISS	False	False	False
46	SO4TOT	False	False	False
47	VELOCITY	False	False	False
48	SEDS1	False	False	False
49	SEDS2	False	False	False
50	SEDS3	False	False	False
51	SEDS4	False	False	False
52	SEDS5	False	False	False
53	SEDS6	False	False	False
54	SEDORG	False	False	False
55	ALGGROW	False	False	False
56	CLAPERI	True	False	True
57	CLAH20	True	False	True
58	PHAEOPERI	False	False	True
59	PHAEOH20	False	False	True
60	LIMNUTRIENT	False	False	False

Important Oracle Information

The Bureau of Information Systems (BIS) takes care of the Oracle part of the database. They keep backups and monitor it to optimize its speed of operation. They do not do any program changes or bug fixes.

If it is necessary to change the logon string that is programmed into the 4th Dimension database operation you will need to find someone with the full programmable version of 4th Dimension and who has access to the programming environment. Once you are in “Design” mode, you will need to edit the global procedure named “Script_Login”. You will see the logon string and you can change it to whatever it needs to be.

How to get out of the database if you think it has frozen

The current process of the database could be in one of two places at any given time: 1) in 4th Dimension or 2) in Oracle. I have tried to display message boxes when a procedure that takes a long time is running; however, I may have missed one or two. If it has gone to Oracle (like in a long retrieval) pressing Control-C will stop it. This is dangerous to do in functions are updating the database, as you may leave something partially updated. If Control-C works, you will probably see an Oracle error message box and when you click OK, everything that was partially done will be “undone”. To be safe, Cancel out of everything and clear selections if asked until you get back to the splash screen and quit 4D. If you were doing something that updates data, reload those data and make sure of how they were left.

If Control-C doesn't work, look at your hard disk. Some hard disks have a light that flashes while the computer is writing to it. If that is your case and you see the light flashing, 4th Dimension is writing something and it is best to leave it alone. If you absolutely must stop it, there is something you can do but you should really only do this as a last resort. Press Command- (that is the Apple command key and the period key). It is unpredictable what will happen. It may stop what it is running and take you back to the startup screen, it may cause the program to quit, or it may do nothing at all. If you end up at the splash screen, quit 4th Dimension, and then restart the computer. If the 4th Dimension quits, you must restart the computer. It may look like everything is fine, but in my experience it is not. Parts of memory get corrupted and strange things happen. Restart the computer even if you are frustrated and decide not to try 4th Dimension again. I have used this method to get out of 4th Dimension and then tried to run it again immediately without restarting. Every time, 4th Dimension will freeze before the logon box and then you have to press command-option-esc to get out.

The key commands described above are only appropriate for the Mac operating system. No corresponding commands are available for the Windows operating system.

Last Resort - Mac

If all else fails, press command-option-esc (Mac) and then you will see a box that asks if you want to force quit 4th Dimension. Click on OK and then restart the machine. Sometimes OK does not work. In that case the only thing you can do is turn off the machine. If you are not sure how to do this, please find someone who does. Just turning off a computer that can be writing to a disk can cause you to lose things on your hard disk. If you are not sure what to do, ask for help. Sometimes it takes a complete machine shutdown (not just restart) to get the memory back the way it should be.

Last Resort – Windows

If the program does not appear to be responding, pressing control-alt-delete one time should allow you to end the task. Once you are back at the Windows desktop, it is a good idea to restart the computer. If you are not able to successfully end the 4th Dimension task, you will need to press control-alt-delete a second time to reboot the computer.

Appendices

Appendix 1. Installation

What you need to install

You need to have version 6 of either 4th Dimension or 4D Runtime installed on your computer. In addition you will need these files:

The most recent version of the database (structure file) usually named like this: BiolDB151.0.10 (Mac) or Bldb151.1db and Bldb151.rsr (Windows) (the numbers change).

Create two empty text files using a word processing program like Word named LoriNote and RetrievalLog.

This file are also needed:

PCVars.txt

Installing

You must give 4D Runtime at least 8 mb of RAM to run properly. If you will be using the full version of 4th Dimension, you will need to give it at least 10 MB of RAM. If you can give the application more RAM, it will run faster.

The database file should have the stack size set to a larger than default value. If you want to check it do the following:

- 1) Be sure 4th Dimension or 4D Runtime are not running.
- 2) In the Utilities folder (in the 4th Dimension folder) there is a program called “Customizer Plus”, double-click on it.
- 3) You will just see a menu bar at the top, select **File - Open** and you select the name of the 4th Dimension database (like BiolDB151.0.10).
- 4) Some choices will appear on the screen, double-click on “Preferences”.
- 5) Another window will appear and there will be a box next to “Stack size”. The number should be at least 250.
- 6) Click in the close box and then choose **File - Quit**.

You are ready to start running the database for the first time. Double-click on “BiolDB151.0.10” (or whatever the current numbered version is) and it will ask you for the name of the data file to use. One of the choices is a button labeled “New data file”. Click on that button. You want your data file to have the same name as the database file, but with “.data” at the end. The correct name is usually suggested by 4th Dimension. The program will proceed with the startup procedures. It will tell you that you need to load new Florida lists, so say OK. It will automatically load the reference table information. You need to manually load the physical/chemical variable name file as described in “Oracle and 4th Dimension”. When these steps are done, you should be ready to go to work.

Appendix 2. Detailed example of “Upward collapsing” of taxa

The purpose of this section is to explain how the taxa are prepared for the “retrieve by station/date” calculations and for “Mark sample complete” when the sample statistics are calculated. When you see the abbreviation “DD” it means the Data Dictionary which is at the end of this manual (look in the table of contents for the page number).

The tables involved in this process are:

Benthos table (DT\$Benthos) - fields used for retrieval are:

PK\$BenthID - there is a unique number for each station/date/gear sampled
Number of replicates

Benthos Taxa table (DT\$BenTaxa) - fields used for retrieval are:

FK\$BenthID - ties this entry to the appropriate information in the benthos table
Replicate
FK\$TaxaID - ties this entry to the taxon information stored in Master Taxa table
Number of individuals counted
Number of individuals per unit area

Master Taxa table (ET\$Taxamstr) - fields used for retrieval are:

PK\$TaxaID - there is unique number for every taxon in the table
Phylo - A 17-character phylogenetic code for this taxon (see page 182 for a full description of this code.)
Phylcat - phylogenetic level (see page 181)

For this example, there are two samples with BenthID's 295 (2 reps) and 296 (4 reps) with data entered as follows:

BenthID 295, replicate 1

Benthos Sample Taxonomic Information			
BenthID	295	Date	12/17/93
Station	UNKNOWN	Gear	HesterDend
	SUW01	Rep No.	1
Number of entries =		8	
Total individuals counted =		167	
Total individuals/m2 =		139,168.00	
TaxaID	Scientific Name	No. counted	No. per m2
96221	Macrobrachium ohione	2	1,667.00
96227	Macrobrachium carcinus	2	1,667.00
96225	Macrobrachium acanthurus	2	1,667.00
96220	Macrobrachium	2	1,667.00
67459	Dasybranchus lumbricoides	4	3,333.00
92695	Caecidotea racovitzai australis	21	17,500.00
101495	Baetisca obesa	78	65,000.00
128079	Ablabesmyia	56	46,667.00

BenthID 295, replicate 2

Benthos Sample Taxonomic Information			
BenthID	295	Date	12/17/93
Station	UNKNOWN	Gear	HesterDend
	SUW01	Rep No.	2
Number of entries =		3	
Total individuals counted =		57	
Total individuals/m2=		47,501.00	

TaxaID	Scientific Name	No. counted	No. per m2
128178	Labrundinia pilosella	2	1,667.00
129935	Paratanytarsus	32	26,667.00
97654	Justitia longimanus	23	19,167.00

BenthID 296, replicate 1

BenthID 296, replicate 2

Benthos Sample Taxonomic Information			
BenthID	296	Date	02/01/94
Station	UNKNOWN	Gear	HesterDend
	SUW11	Rep No.	2
Number of entries =		12	
Total individuals counted =		127	
Total individuals/m2=		1,057.00	

TaxalD	Scientific Name	No. counted	No. per m2
10000042	Dicrotendipes simpsoni	2	17.00
129708	Polypedilum scalaenum	14	117.00
129949	Tanytarsus similatus	1	8.00
128236	Thienemannimyia	1	8.00
129452	Dicrotendipes nervosus	16	133.00
129428	Dicrotendipes	14	117.00
128583	Cricotopus bicinctus	63	525.00
128131	Helopelopia	7	58.00
128130	Conchapelopia	3	25.00
115408	Cheumatopsyche	4	33.00
76698	Physella	1	8.00
68623	Tubifex tubifex	1	8.00

BenthID 296, replicate 3

Benthos Sample Taxonomic Information			
BenthID	296	Date	02/01/94
Station	UNKNOWN	Gear	HesterDend
	SUW11	Rep No.	3
Number of entries =		12	
Total individuals counted =		87	
Total individuals/m2=		723.00	

TaxalD	Scientific Name	No. counted	No. per m2
129708	Polypedilum scalaenum	3	25.00
129452	Dicrotendipes nervosus	7	58.00
129428	Dicrotendipes	2	17.00
128585	Cricotopus brunnicans	1	8.00
128583	Cricotopus bicinctus	58	483.00
128575	Cricotopus	1	8.00
128237	Hayesomyia	1	8.00
128171	Krenopelopia hudsoni	1	8.00
128131	Helopelopia	5	42.00
128130	Conchapelopia	6	50.00
128097	Ablabesmyia mallochi	1	8.00
68856	Slavina appendiculata	1	8.00

BenthID 296, replicate 4

Benthos Sample Taxonomic Information			
BenthID	296	Date	02/01/94
Station	UNKNOWN	Gear	HesterDend
	SUW11	Rep No.	4
Number of entries =		10	
Total individuals counted =		99	
Total individuals/m2=		824.00	

TaxaID	Scientific Name	No. counted	No. per m2
129708	Polypedilum scalaenum	4	33.00
129936	Paratanytarsus dubius	1	8.00
129452	Dicrotendipes nervosus	4	33.00
129428	Dicrotendipes	6	50.00
128583	Cricotopus bicinctus	71	592.00
128171	Krenopelopia hudsoni	1	8.00
128131	Helopelopia	3	25.00
128130	Conchapelopia	3	25.00
115408	Cheumatopsyche	5	42.00
68856	Slavina appendiculata	1	8.00

These data look like this in the Oracle table DT\$Benthos along with phylogenetic information from the master taxa table. These data have been sorted by BenthID, phylo, and repnum to help you follow the steps. The column labeled "RE" is the revision code which is an "S" if the taxaID is a synonym.

FK\$BENTHID	FK\$TAXAID	PHYLO	RE	REPNUM	NOIND	NOINDSQM
295	67459	440100060009003		1	4	3333
295	92695	46043101900300202		1	21	17500
295	96220	460434015002		1	2	1667
295	96221	460434015002001		1	2	1667
295	96225	460434015002002		1	2	1667
295	96227	460434015002003		1	2	1667
295	97654	460434035002001		2	23	19167
295	101495	460504012001001		1	78	65000
295	128079	460530032017		1	56	46667
295	128178	460530032024005		2	2	1667
295	129935	460530033132		2	32	26667
296	68623	440203004004001		2	1	8
296	68639	440203004005001		1	1	8
296	68856	440203005001001		1	1	8
296	68856	440203005001001		3	1	8
296	68856	440203005001001		4	1	8
296	68898	440203005006		1	1	8
296	68950	440203005008003		1	2	17
296	76698	450108013003		2	1	8
296	115408	460528004002		1	2	17
296	115408	460528004002		2	4	33
296	115408	460528004002		4	5	42
296	128097	460530032017010		3	1	8
296	128131	460530032020	S	1	4	33
296	128130	460530032020		2	3	25
296	128131	460530032020	S	2	7	58
296	128130	460530032020		3	6	50
296	128131	460530032020	S	3	5	42
296	128130	460530032020		4	3	25
296	128131	460530032020	S	4	3	25
296	128171	460530032023001		3	1	8
296	128171	460530032023001		4	1	8
296	128236	460530032032		2	1	8
296	128237	460530032032	S	3	1	8
296	128575	460530033016		3	1	8
296	128583	460530033016006		1	14	117
296	128583	460530033016006		2	63	525
296	128583	460530033016006		3	58	483
296	128583	460530033016006		4	71	592
296	128585	460530033016007		3	1	8
296	129428	460530033089		1	20	167
296	129428	460530033089		2	14	117
296	129428	460530033089		3	2	17
296	129428	460530033089		4	6	50
296	129452	460530033089012		1	8	67
296	129452	460530033089012		2	16	133
296	129452	460530033089012		3	7	58
296	129452	460530033089012		4	4	33
296	10000042	460530033089013		1	3	25
296	10000042	460530033089013		2	2	17
296	129708	460530033112033		1	9	75
296	129708	460530033112033		2	14	117
296	129708	460530033112033		3	3	25
296	129708	460530033112033		4	4	33
296	129827	460530033119004		1	1	8
296	129935	460530033132		1	1	8
296	129936	460530033132001		4	1	8
296	129949	460530033132007	S	2	1	8
296	10000043	460530033132009		1	1	8
296	10000041	460530033137046		1	1	8

60 rows selected.

Assume that the two samples are to have their statistics calculated separately (as in “Mark this sample complete”). The steps in preparing the taxa to do the calculations appear below. Appendix 3 has all the SQL statements generated in this preparation, just in case you are interested. You do not have to look at Appendix 3 to make sense of what is happening, in fact don’t look at it the first time through.

Step 1.

Select all phylo codes for the taxaID's found in DT\$BenTaxa for each BenthID and put the results in a work table (ET\$Rnetwork). There will only be one line for each BenthID/Phylo (i.e., sum over reps for number counted, average over reps for number per unit area). This will cause synonyms to be pooled because all synonyms have the same phylo code, but each “true” taxon has a unique phylo code. Also get the phylogenetic category (phylcat, page 181) for each taxaID from the master taxa table and insert it into the work table.

The data end up in the work table like the one below (it has been sorted by BenthID and phylo code). Groups that need to be “proportioned” have been marked with symbols. Each group has a unique symbol.

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
	295	6	440100060009003	4	1666.5
	295	7	46043101900300202	21	8750
*	295	5	460434015002	2	833.5
*	295	6	460434015002001	2	833.5
*	295	6	460434015002002	2	833.5
*	295	6	460434015002003	2	833.5
	295	6	460434035002001	23	9583.5
	295	6	460504012001001	78	32500
	295	5	460530032017	56	23333.5
	295	6	460530032024005	2	833.5
	295	5	460530033132	32	13333.5
	296	6	440203004004001	1	2
	296	6	440203004005001	1	2
	296	6	440203005001001	3	6
	296	5	440203005006	1	2
	296	6	440203005008003	2	4.25
	296	5	450108013003	1	2
	296	5	460528004002	11	23
	296	6	460530032017010	1	2
@	296	5	460530032020	31	64.5
	296	6	460530032023001	2	4
	296	5	460530032032	2	4
\$	296	5	460530033016	1	2
\$	296	6	460530033016006	206	429.25
\$	296	6	460530033016007	1	2
!	296	5	460530033089	42	87.75
!	296	6	460530033089012	35	72.75
!	296	6	460530033089013	5	10.5
	296	6	460530033112033	30	62.5
	296	6	460530033119004	1	2
%	296	5	460530033132	1	2
%	296	6	460530033132001	1	2
%	296	6	460530033132007	1	2
%	296	6	460530033132009	1	2
	296	6	460530033137046	1	2

35 rows selected.

You will note that it is not possible to keep taxaID at this point since synonyms may have been combined in this accumulation. Let's look at phylo code 460530032020 for BenthID 296. The data were entered like this:

FK\$BENTHID	FK\$TAXAID	PHYLO	RE	REPNUM	NOIND	NOINDSQM
296	128131	460530032020	S	1	4	33
296	128130	460530032020		2	3	25
296	128131	460530032020	S	2	7	58
296	128130	460530032020		3	6	50
296	128131	460530032020	S	3	5	42
296	128130	460530032020		4	3	25
296	128131	460530032020	S	4	3	25

You will note that some entries were made with the synonym name and some with the “currently accepted” name (e.g., *Conchapelopia* and *Helopelopia* which are synonyms in my version of the master taxa table). The line with the “@” symbol above shows how these data were accumulated after step 1. The number counted is just a sum of noind. The number per unit area, however, is an average. Rep 1 has 33, rep 2 has (25+58)=83, rep 3 has (50+42)=92, and rep 4 has (25+25)=50 per unit area. $(33+83+92+50)/4 \text{ reps} = 64.5 \text{ per unit area per rep}$.

Step 2.

Get a list of all the distinct BenthID's in the work table. You **never** proportion over samples; said another way, you only adjust numbers within one sample (where sample means a unique station/date/gear which is represented by a unique BenthID). Now do the rest of the steps for each BenthID separately. In the example, there are two BenthID's, 295 and 296.

Start loop for each BenthID

Step 3.

Get a list of all the distinct phylcats in the work table for this BenthID. For BenthID 295 that would be 5, 6, and 7; for 296, 5 and 6.

Start loop for each phylcat except the largest. (For 295, it will be done for phylcat 6, then 5; for 296 for 5 only)

Step 4.

We are starting at the bottom of the phylogenetic scale, doing the necessary proportions, then moving up one level. Another way of saying this is that we proportion the species over varieties, then genera over species and varieties, families over genera, species, and varieties, etc.

This step is a complicated statement. The command tells Oracle to get phylo codes (and their noind and noindunit, now called pnind and punit respectively) where there are phylo codes that start with this code and have a phylcat that is larger than this phylcat. That being clear as mud, the example will show what we want. The line with the symbol “@” will be the one returned by the command for BenthID 295.

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
@	295	5	460434015002	2	833.5
*	295	6	460434015002001	2	833.5
*	295	6	460434015002002	2	833.5
*	295	6	460434015002003	2	833.5

You can see that the first line has a phylo code like the beginning of the ones below it, and that the ones below it have a larger phylcat. This means that the first line is a genus level entry and the next three are species under that genus. If Oracle doesn't find any relationships like this, it jumps out of the loop because there is nothing to “proportion” at this level.

Start loop for each phylo to be “proportioned”

Step 5.

Get the sum of number counted (denom1) and number per unit area (denom2) over all entries for this phylo with a larger phylcat (i.e., add up everything phylogenetically under this phylo code). In the case of the example in step 4, that would be $6=(2+2+2)$ and $2500.5=(833.5+833.5+833.5)$, respectively.

Step 6.

One update command is given to update all entries under the current phylo (lines 2-4 in step 4):

1) set $\text{noind}=\text{noind}+\text{round}(((\text{noind}/\text{denom1})*\text{pnind}),0)$

where noind is the current number counted for this entry, denom1 from step 5 and pnind from step 4, and round it to zero decimal places. So noind for line 2 in step 4 becomes $2 + ((2/6)*2)=2.6667$ which rounds to 3.

2) set $\text{noindunit}=\text{noindunit}+\text{round}(((\text{noindunit}/\text{denom2})*\text{punit}),2)$

where noindunit is the current number per unit area for this entry, denom2 from step 5 and punit from step 4, and round it to two decimal places. So noindunit for line 2 in step 4 becomes $833.5+((833.5/2500.5)*833.5)=1111.33334$ which rounds to 1111.33.

So now we have:

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
*	295		6 460434015002001	3	1111.33
*	295		6 460434015002002	3	1111.33
*	295		6 460434015002003	3	1111.33

Step 7.

Get the sum of the noind (call it newtot) and noindunit (call it newunit) entries that just received the update. In our example, newtot would = 9 (should be 8) and newunit = 3333.99 (should be 3334).

Step 8.

If $\text{denom1}+\text{pnind}$ is not equal newtot (that is the old total is not equal to the new total), make the adjustment to the entry with the most individuals. In the case of our example, the number of individuals is the same for all entries, so the first one entered is adjusted. Then do the same for $\text{denom2}+\text{punit}$ if not equal to newunit. Now we have:

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
*	295		6 460434015002001	2	1111.34
*	295		6 460434015002002	3	1111.33
*	295		6 460434015002003	3	1111.33

Step 9.

Delete the entry that had its numbers proportioned. In the example, it would be this entry:

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
@	295		5 460434015002	2	833.5

end phylo loop

end phylcat loop

end benthID loop

Now, to calculate the number of taxa for each benthID, just count how many phylo codes there are (11 for 295 and 24 for 296). For number counted and unit area, just sum the columns for each benthID. This “prepared” table will be used to calculate DBar (uses number counted), Florida Index, Lake Condition Index, individual taxa and feeding group statistics (percents based on denominator of numbers per unit area for quantitative data, on number counted for qualitative data with counts entered).

This is what the data look like after proportioning. They have been sorted by BenthID and phylo.

FK\$BENTHID	FK\$TAXAID	PHYLCAT	PHYLO	NOIND	NOINDUNIT
295		6	440100060009003	4	1666.5
295		7	46043101900300202	21	8750
295		5	460434015002	2	833.5
295		6	460434015002001	2	833.5
295		6	460434015002002	2	833.5
295		6	460434015002003	2	833.5
295		6	460434035002001	23	9583.5
295		6	460504012001001	78	32500
295		5	460530032017	56	23333.5
295		6	460530032024005	2	833.5
295		5	460530033132	32	13333.5
296		6	440203004004001	1	2
296		6	440203004005001	1	2
296		6	440203005001001	3	6
296		5	440203005006	1	2
296		6	440203005008003	2	4.25
296		5	450108013003	1	2
296		5	460528004002	11	23
296		6	460530032017010	1	2
296		5	460530032020	31	64.5
296		6	460530032023001	2	4
296		5	460530032032	2	4
296		5	460530033016	1	2
296		6	460530033016006	206	429.25
296		6	460530033016007	1	2
296		5	460530033089	42	87.75
296		6	460530033089012	35	72.75
296		6	460530033089013	5	10.5
296		6	460530033112033	30	62.5
296		6	460530033119004	1	2
296		5	460530033132	1	2
296		6	460530033132001	1	2
296		6	460530033132007	1	2
296		6	460530033132009	1	2
296		6	460530033137046	1	2

35 rows selected.

Appendix 3. SQL statements generated by retrieval by station and date.

These are the SQL statements generated by the retrieval routine to prepare the sample data for calculation of sample statistics. The name of the procedure that generated the statement appears just before each SQL statement.

File opened on 2/17/94 at 14:04:49

RetrStep1

```
insert into et$network (fk$benthid,noind,noindunit,phylo,phylcat,uname) select
fk$benthid,sum(noind),(sum(noindsqm)/avg(nreps)), phylo,phylcat,'Designer' from
dt$bentaxa,dt$benthos,dt$sample,et$taxamstr where pk$taxaid=fk$taxaid and fk$benthid=pk$benthid and
fk$sampleid=pk$sampleid and fk$gear=1 and qualquan=1 and (ak$sta=2 or ak$sta=12) and
sampdate>to_date('01-DEC-93:00:00','dd-mon-yy:hh24:mi') group by fk$benthid,phylcat,phylo
```

RetrStep2

```
select distinct(fk$benthid) into :currID: from et$network where uname=:tUserName: with :cursorThree:
```

RetrStep2

```
select distinct(phylcat) into :ArrTCat: from et$network where fk$benthid=:currID: and uname=:tUserName: order by
phylcat desc
```

RetrStep2A

```
select phylo,noind,noindunit into :currphylo:,:pnind:,:punit: from et$network where phylo in (select
distinct(substr(phylo,1,15)) from et$network where phylcat>6 and fk$benthid=:currID: and uname=:tUserName:)
and phylcat=:currPCat: and fk$benthid=:currID: and uname=:tUserName: with :cursorOne:
```

RetrStep2A

```
select phylo,noind,noindunit into :currphylo:,:pnind:,:punit: from et$network where phylo in (select
distinct(substr(phylo,1,12)) from et$network where phylcat>5 and fk$benthid=:currID: and uname=:tUserName:)
and phylcat=:currPCat: and fk$benthid=:currID: and uname=:tUserName: with :cursorOne:
```

460434015002,2,833.5

RetrStep2B-select

```
select sum(noind),sum(noindunit) into :denom1:,:denom2: from et$network where phylcat > :currPCat: and phylo
like '460434015002%' and fk$benthid=:currID: and uname=:tUserName: with :cursorTwo:
```

RetrStep2B-update

```
update et$network set
noind=noind+round(((noind/6)*2),0),noindunit=noindunit+round(((noindunit/2500.5)*833.5),2) where phylcat >
:currPCat: and phylo like '460434015002%' and fk$benthid=:currID: and uname=:tUserName:
```

RetrStep2C

```
select sum(noind),sum(noindunit),count(*) into :newtot:,:newunit:,:ctaxa: from et$network where phylcat >
:currPCat: and phylo like '460434015002%' and fk$benthid=:currID: and uname=:tUserName:
```

RetrStep2C1

```
select max(noind) from et$network where phylcat > :currPCat: and phylo like '460434015002%' and
fk$benthid=:currID: and uname=:tUserName:
```

RetrStep2C1

```
select rowid from et$network where phylcat > :currPCat: and phylo like '460434015002%' and fk$benthid=:currID:
and uname=:tUserName: and noind=:Tmax:
```

RetrStep2C1

```
update et$network set noind=round(noind-1,0) where rowid=:rowid
```

RetrStep2C2

select max(noindunit) from et\$network where phylcat > :currPCat: and phylo like '460434015002%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C2

select rowid from et\$network where phylcat > :currPCat: and phylo like '460434015002%' and fk\$benthid=:currID: and uname=:tUserName: and noindunit=:Tmax:

RetrStep2C2

update et\$network set noindunit=round(noindunit+0.01000000000000000888,2) where rowid=:rowid

RetrStep2D

delete from et\$network where phylo='460434015002' and fk\$benthid=:currID:

RetrStep2

select distinct(phylcat) into :ArrTCat: from et\$network where fk\$benthid=:currID: and uname=:tUserName: order by phylcat desc

RetrStep2A

select phylo,noind,noindunit into :currphylo:,:pnind:,:punit: from et\$network where phylo in (select distinct(substr(phylo,1,12)) from et\$network where phylcat>5 and fk\$benthid=:currID: and uname=:tUserName:) and phylcat=:currPCat: and fk\$benthid=:currID: and uname=:tUserName: with :cursorOne:

460530033016,1,2

RetrStep2B-select

select sum(noind),sum(noindunit) into :denom1:,:denom2: from et\$network where phylcat > :currPCat: and phylo like '460530033016%' and fk\$benthid=:currID: and uname=:tUserName: with :cursorTwo:

RetrStep2B-update

update et\$network set noind=noind+round(((noind/207)*1),0),noindunit=noindunit+round(((noindunit/431.25)*2),2) where phylcat > :currPCat: and phylo like '460530033016%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C

select sum(noind),sum(noindunit),count(*) into :newtot:,:newunit:,:ctaxa: from et\$network where phylcat > :currPCat: and phylo like '460530033016%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2D

delete from et\$network where phylo='460530033016' and fk\$benthid=:currID:

460530033089,42,87.75

RetrStep2B-select

select sum(noind),sum(noindunit) into :denom1:,:denom2: from et\$network where phylcat > :currPCat: and phylo like '460530033089%' and fk\$benthid=:currID: and uname=:tUserName: with :cursorTwo:

RetrStep2B-update

update et\$network set noind=noind+round(((noind/40)*42),0),noindunit=noindunit+round(((noindunit/83.25)*87.75),2) where phylcat > :currPCat: and phylo like '460530033089%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C

select sum(noind),sum(noindunit),count(*) into :newtot:,:newunit:,:ctaxa: from et\$network where phylcat > :currPCat: and phylo like '460530033089%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2D

delete from et\$network where phylo='460530033089' and fk\$benthid=:currID:

460530033132,1,2

RetrStep2B-select
select sum(noind),sum(noindunit) into :denom1,:denom2: from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName: with :cursorTwo:

RetrStep2B-update
update et\$network set noind=noind+round(((noind/3)*1),0),noindunit=noindunit+round(((noindunit/6)*2),2) where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C
select sum(noind),sum(noindunit),count(*) into :newtot,:newunit,:ctaxa: from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C1
select max(noind) from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C1
select rowid from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName: and noind=:Tmax:

RetrStep2C1
update et\$network set noind=round(noind+1,0) where rowid=:rowid

RetrStep2C2
select max(noindunit) from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName:

RetrStep2C2
select rowid from et\$network where phylcat > :currPCat: and phylo like '460530033132%' and fk\$benthid=:currID: and uname=:tUserName: and noindunit=:Tmax:

RetrStep2C2
update et\$network set noindunit=round(noindunit-0.01,2) where rowid=:rowid

RetrStep2D
delete from et\$network where phylo='460530033132' and fk\$benthid=:currID:

Appendix 4. Physical/Chemical variable description

Parameters	Oracle Name	STORET No.	Significant Decimals	Min	Max	Units
algal growth potential	ALGGROW	85209	6.1	0	0200.0	mg dry wt/L
alkalinity, total	ALKALINITY	00410	4.0	0	300.	mg/LCaCO3
ammonia, dissolved	NH3DISS	00608	7.3	0	010.000	mg/LN
ammonia, total	NH3TOT	00610	7.3	0	010.000	mg/LN
ammonia, unionized	NH3UNION	00619	7.3	0	010.000	mg/LNH3
BOD, 5-day	BOD5	00310	6.1	0	0100.0	mg/L
BOD, 20-day	BOD20	00324	6.1	0	0100.0	mg/L
carbon, total organic	TOC	00680	5.1	0	100.0	mg/L C
chloride,dissolved	CLDISS	82295	9.3	0	50000.000	mg/L
chloride, total	CLTOT	00940	9.0	0	50000.	mg/L
chlorophyll-a,monochromatic,periphyton	CLAPERI	32223	6.2	0	060.00	mg/m2
chlorophyll-a, monochromatic, water	CLAH20	32211	6.2	0	050.00	µg/L
conductivity, field	CONDFLD	00094	6.0	0	50000.	µmho/cm
conductivity, lab	CONDLAB	00095	6.0	0	50000.	µmho/cm
D.O., non-probe	DONON	00300	4.1	0	10.0	mg/L
D.O., probe	DOPROBE	00299	4.1	0	10.0	mg/L
enterococci, membrane filter	ENTEROC	02361	7.0	0	050000.	no./100ml
Escherichia coli, membrane filter	ECOLI	02360	7.0	0	050000.	no./100ml
fecal coliforms, membrane filter	FECALMEM	31616	7.0	0	050000.	no./100ml
fecal coliforms, multiple tube	FECALTUBE	31615	7.0	0	050000.	no./100ml
fecal Streptococcus, membrane filter	FECALSTREP	31673	7.0	0	050000.	no./100ml
hardness, total	HARDNESS	00900	6.0	0	10000.	mg/LCaCO3
nitrate, dissolved	NO3DISS	00618	6.2	0	030.00	mg/L N
nitrate, total	NO3TOT	00620	7.3	0	030.000	mg/LN
nitrite + nitrate, dissolved	NO3NO2DISS	00631	5.1	0	030.0	mg/LN
nitrite + nitrate, total	NO3NO2TOT	00630	6.2	0	030.00	mg/L N
nitrite, dissolved	NO2DISS	00613	7.3	0	010.000	mg/LN
nitrite, total	NO2TOT	00615	7.3	0	010.000	mg/LN
nitrogen, total (TKN+N02+N03)	TOTN	00600	6.2	0	030.00	mg/L N
nitrogen, total Kjeldahl	TKN	00625	7.3	0	030.000	mg/L N
orthophosphate, dissolved	OPDISS	00671	6.3	0	01.000	mg/L P
orthophosphate, total	OPTOT	70507	6.3	0	01.000	mg/L P
pH	PH	00400	5.2	0	12.00	su
phaeophyton-a, monochromatic, periphyton	PHAEOPERI	32224	6.2	0	060.00	mg/m2
phaeophyton-a, monochromatic, water	PHAEOH20	32218	6.2	0	050.00	µg/L
phosphorus, total	PHOSPTOT	00665	6.3	0	01.000	mg/L P
plate count, total	PLATE	31751	8.0	0	0100000.	no./ml
residue, dissolved	RESIDISS	70300	6.0	0	50000.	mg/L
residue, total	RESIDTOT	00500	6.0	0	50000.	mg/L
residue, total nonfiltrable (TSS)	TSS	00530	5.0	0	0100.	mg/L
residue,total volatile	RESIDVOL	00505	5.0	0	0100.	mg/L
residue, volatile nonfiltrable	RESIDVNON	00535	5.0	0	0100.	mg/L
salinity	SALINITY	00480	4.1	0	35.0	ppt
sediment prtcl size, 0.063-0.125mm	SEDS1	80251	6.2	0	100.00	%
sediment prtcl size, 0.125-0.25mm	SEDS2	80252	6.2	0	100.00	%
sediment prtcl size, 0.25-0.5mm	SEDS3	80253	6.2	0	100.00	%
sediment prtcl size, 0.5-2.0mm	SEDS4	80254	6.2	0	100.00	%
sediment prtcl size, <0.063mm	SEDS5	80250	6.2	0	100.00	%
sediment prtcl size, >2.0mm	SEDS6	80256	6.2	0	100.00	%
sediment, organic fraction	SEDORG	80096	6.2	0	100.00	%
silica, dissolved	SILICADISS	00955	5.1	0	020.0	mg/L SiO3
silica, total	SILICATOT	00956	5.1	0	020.0	mg/L SiO3
sulfate, dissolved	SO4DISS	00946	7.1	0	05000.0	mg/L SO4
sulfate, total	SO4TOT	00945	6.0	0	05000.	mg/L SO4
water temperature	TEMP	00010	4.1	0	40.0	°C

tidal stage (high or low)	TIDE	70211	character 2 H=High tide, L=Low tide,			
U=Unknown						
tidal shift(before or after)	TIDEPHASE	70211	character 2 B=Before tide, A=After tide,			
Parameters	Name	No.	Decimals	Min	Max	Units
U=Unknown						
tidal time adjustment	TIDEHRS	70211	2.0HH (hours, before or after, high or low tide)			
	TIDEMINS	70211	2.0MM (minutes, before or after, high or low tide)			
total coliforms, membrane filter	COLIMEM	31501	7.0	0	050000.	no./100ml
total coliforms, multiple tube	COLITUBE	31505	7.0	0	050000.	no./100ml
turbidity	TURBIDITY	82079	6.1	0	0200.0	ntu
velocity, stream	VELOCITY	00055	3.1	0	1.0	ft/sec

These fields have been removed from the parameter table as they are covered by the taxonomy tables:

diversity, macroinvert., art. sub.	82251
diversity, macroinvert., nat. sub.	82246
no. taxa, macroinvert., qualitative	71498
no. taxa, macroinvert., quantitative, art. sub.	82255
no. taxa, macroinvert., quantitative, nat. sub.	82250
no. taxa, periphyton	71483
no. taxa, phytoplankton	71260

Appendix 5. Using scientific name search boxes

Many selection screens (like the one below) ask you to enter a scientific name.

Load Master Taxa for:

Scientific name:

or TaxonID: ☐ < ☐ = ☐ > ☒ Range

0

Lower limit 0
Upper limit 0

Cancel Load

For wildcard search on name:
1) Underline character matches any single character
2) Percent sign matches a string of any length
Example: _R% would load all taxa codes of any length that have the letter R as the 2nd character.

This section will describe the most efficient way to do this. The fastest search is to type the exact scientific name. There is something called an index that has been created for scientific names. When you type the exact scientific name, the computer can go straight to the information for that name. If you cannot remember the exact spelling or if you want to find a group of similar scientific names, you can use a “wildcard” search. You can enter an underline character to match any single character. For example, “_era” means find all scientific names that are four letter long and the last three letters are “era”. A percent sign in a name means to match a string of any length. For example, “Chiro%us” means find all scientific names that start with “Chiro” and end with “us”. It doesn't matter how many letters are in between; however, “Chiro_us” means find all scientific names that are eight letters long, start with “Chiro” and end with “us”. You can start the string with a percent sign or underline character, like “%decoru”. This is the least efficient way to search for a name. The more starting characters you can specify, the better the index can work. “%decorus” means that the computer has to scan the entire taxa list, “C%decorus” means it only has to scan the names that start with “C”. Of course, if “%decorus” is what you need, you can do it, just be prepared to wait while the search is done. If the search is taking too long, you can try typing control-C (Mac Users) and you may be able to stop it. It often stops the search, but not always.

Appendix 6. STORET Station Levels

These are the STORET station levels to describe a water body being sampled and other characteristics of the sampling site. There are 5 levels: 1, 2a, 2b, 3, 4, 5. Levels 1 and 2a or 2b are required (exceptions for “Pipe”). Each level is separated by a “/” and no embedded blanks are allowed. STORET help file contains all valid station types. Example: STREAM/AMBNT/BIO. Valid station types as defined by STORET are:

Level 1 (required) Oracle name=STALEV1

STREAM	Station samples from a stream. A naturally occurring, freshwater, free-flowing, channeled body of surfacewater, with regular or seasonal flow, that empties into an ocean, lake, reservoir, or another stream. Includes rivers.
CANAL	Station samples from a canal. An artificial, channeled waterway used for navigation, drainage, land irrigation, etc. Includes drainage ditches.
LAKE	Station samples from a lake. An inland body of water, naturally formed. Includes ponds.
RESERV	Station samples from a reservoir. A man-made body of water formed by damming or obstructing a stream or river (many “lakes” are actually reservoirs).
SPRING	Station samples from a spring. A natural flow of groundwater from the earth, which feeds into a stream or body of water on the surface.
WELL	Station samples from a well. An artificial excavation from which groundwater is drawn or through which liquid waste is disposed of by injection.
FWTLND	Station samples from a freshwater wetland. A tract of soft, wet land saturated and sometimes partially covered with freshwater (where the water table is at or near the surface of the land) or where the surface is covered by shallow freshwater due to seasonal flooding or tidal conditions. Includes swamps and freshwater marshes.
SWTLND	Station samples from a saltwater wetland. A tract of soft, wet land saturated and sometimes partially covered with salt, brackish or estuarine waters or where the surface of the land is covered by shallow saltwater due to tidal conditions. Includes saltmarshes and coastal areas.
ESTURY	Station samples from an estuary. That part of a river or stream or other natural body of water having un-impaired connection with the open sea, where the sea water is measurably diluted with freshwater derived from land drainage. Includes lagoons, bays, inlets, and harbors.
OCEAN	Station samples from an ocean. The open sea.
LND	Station is not located within a body of water and samples soil, air, precip, etc.
PIPE	Station samples at or within a man-made facility. Includes water supply, wastewater treatment and industrial sites, and sewers.

Level 2a (required) Oracle name=STALEV2A

AMBNT	Monitoring ambient conditions of the environment. Includes facility intakes pulling directly from an ambient source (Ex.- STREAM/AMBNT/MUN/INTAKE).
NONAMB	Monitoring at or within a man-made facility. Compliance monitoring falls into this category. Includes sites where facility discharge has directly influenced or impacted, though not necessarily polluted, the environment.

Level 2b (required for PIPE †; otherwise, optional) Oracle name=STALEV2B

NTRTMT	No pollution abatement has been performed.
PTRTMT	Some, but not all, of the intended pollution abatement has been performed.
TREATD	All of the intended pollution abatement has been performed.
CMBTRT	Combined treatment, where treatment status does not clearly fall into one of the categories defined above. Includes unknown treatment status.
SEWER	Monitoring within a sewer (see level 5 for further identification).
INPLNT	Inside a treatment facility. This type is used in conjunction with plant location codes defined within the STORET User Handbook.

Level 3 (Required for PIPE †; otherwise, optional) Oracle name=STALEV3

MUN	Municipal (incorporated). Includes water supply or wastewater treatment facilities.
IND	Industrial facility.
CMBMI	Combined MUN and IND.
AGRI	Agricultural site. Includes raw crops, feedlots, grazing and silviculture (forestry).
DOMEST	Domestic (residential) domicile or facility. Includes water supplies and on-lot septic systems for private dwellings.
ABANDN	The site from which samples are gathered is abandoned.

Level 4 (Required for PIPE †; otherwise, optional) Oracle name=STALEV4

INTAKE	Intake or influent.
OUTFL	Outfall, discharge, or effluent.
CMBSRC	Combined source (INTAKE and OUTFL).

Level 5 (one or more; optional for all) Oracle name=STALEV5

SPRAY	Site where water has been sprayed on the surface of the land for purposes of irrigation.
SBSOIL	Subsoil - a drain tile system or other points just below the surface of the land.
HRZTL	Horizontal well.
TUNNEL	Tunnel - an underground corridor.
GALLERY	Gallery - an artificial, underground structure implanted to collect groundwater.
PRECIP	Wet atmospheric deposition (precipitation) due to the condensation of water vapor. Includes mist, rain, sleet, snow, and hail.
NRSHRE	Near shore - less than 3 kilometers (approximately 1.9 miles) from a major shore.

OFSHRE	Off shore - from 3 to 8 kilometers (approximately 1.9 to 5 miles) from a major shore.
OPENLK	Open water - greater than 8 kilometers (approximately 5 miles) from a major shore.
RUNOFF	Stormwater runoff.
STMSWR	Stormwater sewer.
SANSWR	Sanitary sewer.
CMBSWR	Combined STMSWR and SANSWR.
SUPPLY	Water supply storage or treatment facility.
NET	Fixed site network station.
MONITR	Source monitoring site, which monitors a known problem or to detect a specific problem.
HAZARD	Site of hazardous or toxic wastes or substances.
BACK	Monitoring for background (baseline) water quality. Opposite of DOWN.
DOWN	Down (i.e., within a potentially polluted area) from a facility which has a potential to pollute. See also DOWNGR and UPGR.
MET	Site where sampling is performed to describe scientific phenomena related to meteorological conditions, such as temperature, solar radiation, winds and the quantity and quality of atmospheric deposition.
LNDTRT	Land treatment area.
UPGR	Upgradient of a well or spring. Only valid for use with WELL or SPRING (groundwater sites).
DOWNGR	Downgradient of a well or spring. Only valid for use with WELL or SPRING (groundwater sites).
RCRA	RCRA monitoring site.
CERCLA	CERCLA (Superfund) monitoring site.
BASSAY	Bioassay site.
IMPDMT	Impoundment. Includes waste pits, treatment lagoons and settling and evaporation ponds.
LNDFL	Landfill.
INJECT	Site where liquid waste has been injected underground as a means of disposal.
NONPNT	Nonpoint source pollution. Includes eutrophication, acidification, thermal change, organic nutrients, sedimentation, and hydromodification.
DEVLMT	Development site. Includes construction.
MINE	Mine or site of mining activities. Includes reclaimed land areas and coal mining.
DISTR	Water supply distribution system.
BIO	Biological monitoring site (for BIOS Field Survey System).
FISH	Fish tissue sampling site.
TISSUE	Plant or animal matter sampling site.
SOLIDS	Sludge or sediment sampling site.
SLUDGE	Sludge spreading site.
POLLUT	Site of pollution incident.
RANNEY	Ranney collector (usually associated with level 1 code WELL).
ONLOT	On-lot septic system.

ECOREG Reference station where sampling is performed to characterize water quality at nonimpacted or least impacted sites in an ecoregion.

† Entries from Levels 2b, 3 and 4 are NOT required for sites sampling from storm sewers, e.g., PIPE/NONAMB/RUNOFF/STMSWR, or from a water supply system's distribution system, e.g., PIPE/NONAMB/DISTR.

Appendix 7. Programmer Notes

Note 1: Relationship between PK\$Facility_Used and FK\$Facility_ToX

These columns appear in tables MT\$Facility_ToX (Oracle) and [ToxFacility] (4D). PK\$Facility_Used is the primary key for this table; no PK\$Facility_Used will appear more than once in this column.

FK\$Facility_ToX is used to determine the most current name for a facility. There are two scenarios:

- PK\$Facility_Used = FK\$Facility_ToX This means that this row is the current name for the facility
- PK\$Facility_Used != FK\$Facility_ToX This row is an old name for the facility; FK\$Facility_ToX has the PK\$Facility_Used value to the current name (!= means “not equal”)

Example:

PK\$FACILITY_USED	FK\$FACILITY_TOX	FACILITYNAME
533	534	Joe's Box Company
532	534	Joe's Container Company
534	534	Joe's Packaging Company

These are three names for the same company. The current name is Joe's Packaging Company (because PK\$Facility_Used = FK\$Facility_ToX).

Note 2: Tox Facility Synonym - entering “None”

[ToxFacility] Input Form - button “Pick a Synonym for this Name”

If the gCurrEnv is “New”, there is no concern that this ID may be used as the current ID for another facility since it does not exist, yet. If editing an existing facility (**gCurrEnv=“Edit”**), the situation is one of the following:

(Assume PK\$Facility_Used = 19 is the ID being edited)

<i>PK\$Facility_Used</i>	<i>FK\$Facility_ToX</i>	
19	19	Changing 19 to 19 has no affect.
19	~~18~~ 19	If FK\$Facility_ToX is changed to 19, it just means that it is no longer a synonym of the others.
18	18	
17	18	
19	19	If “None” is selected, it just changes the 19 to 19 - it affects nothing.
18	19	
17	19	

Note 3: Tox Facility Synonym - entering something other than “None”

[ToxFacility] Input Form - button “Pick a Synonym for this Name”
and global procedure *SaveFacilityChg*

See Flow Chart following for a graphic overview.

If the **gCurrEnv** is “New” the situation is one of the following:

(Assume PK\$Facility_Used = 19 is the new ID)

PK\$Facility_Used *FK\$Facility_Tox*

19	19	No other record could have FK\$Facility_Tox=19 as this is a new name (and PK\$Facility_Used was just assigned); changing 19 to 19 has no affect.
----	----	--

19	18	If FK\$Facility_Tox is something other than the ID assigned, it means “Pick a synonym” button was used to assign 18 as a synonym. You need to know if the name you added is the new current name. So program asks if it is a new name when <i>SaveFacilityChg</i> runs. If it is the new current name, all FK\$Facility_Tox that are 18 are changed to 19; otherwise they are left alone.
----	----	---

18	18
17	18

If the **gCurrEnv** is “Edit” the situation is one of the following:

(Assume PK\$Facility_Used = 19 is the ID being edited)

PK\$Facility_Used *FK\$Facility_Tox*

19	19	Changing 19 to 19 has no affect.
----	----	----------------------------------

19	~~19~~ 21	If you pick the name for PK\$Facility_Used=16, the program will insert its FK\$Facility_Tox (which in the example is 21), NOT the 16. The program does an update statement to change all occurrences of FK\$Facility_Tox=19 to 21. Then it asks if 19 is the new current name (in <i>SaveFacilityChg</i> if NewSynonym=1). If the user says “yes”, all the 21’s are changed to 19; otherwise, they are left alone.
----	------------------	--

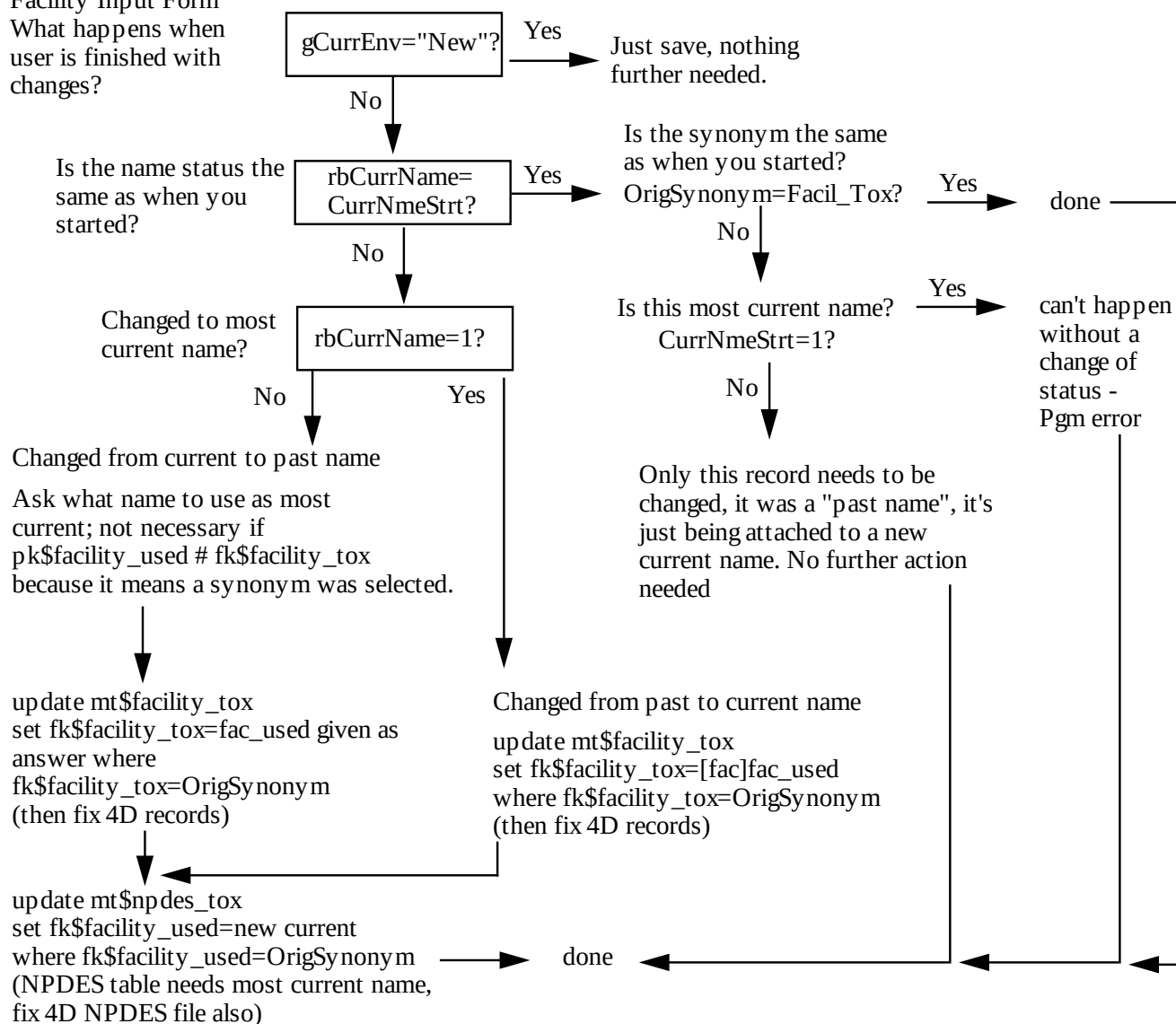
18	~~19~~ 21
17	~~19~~ 21
16	21
21	21

19	~~18~~ 19	If FK\$Facility_Tox is changed from something else to 19, it just means that 19 is no longer a synonym of the others.
----	------------------	---

18	18
17	18

Facility Edit Flow Chart

Facility Input Form
What happens when
user is finished with
changes?



Be sure if you change [ToxFacility]Facility_Tox that you also update [ToxFacility]OtherName
Do not change facility ID's used in ToxSample table. A sample is attached to the name as it was
when the sample was taken. NPDES table must have most recent name attached to it.

Variables used (note: "#" means not equal)

rbCurrName = check box that tells whether or not this is the
most current name for this facility (0=No, 1=Yes)

CurrNmeStrt = variable set when input layout starts that tells
status of current name for this facility
0 = no, it wasn't current name when edit started
1 = yes, it was current name when edit started

OrigSynonym = zero or the ID of the most current name for
the facility when input layout started.

Data Dictionary

Note: All references to STORET are to the old, or Legacy STORET system. STORET has since been modernized and is the initial implementation stage. In the future, there are likely to be revised requirements for upload of biological data to the federal database (which may also have a new name).

There are two fields that are present in nearly every Oracle table. Since there is no real need for users to access these fields, there are no corresponding fields in the 4D tables.

User Name	USERNAME	Varchar2(30)
	The name of the user who added a row to the table.	
Time Stamp	TIME_STAMP	Date
	The date and time the row was added to the table, except for the Station table where it is the user and date of the “last change”.	

Reference Tables (needed for compatibility with BIOS)

Biological Database

The reference tables contain primarily “look-up” information. Some of the information in these tables is required for compatibility with STORET and its biological component, BIOS. The reference information for the biological portion of the database is maintained via the Reference Info pulldown menu:

The tables associated with each menu item are:

Station:	ET\$STA
Surveys:	MT\$SURVEY
Sample Gear:	MT\$GEAR
Feeding Groups:	MT\$FFTABLE
Collectors:	MT\$COLLECT
Identifiers:	MT\$IDENT
County LatLon:	MT\$COUNTY_LOC
Station Types:	MT\$STALEV1, MT\$STALEV2A, MT\$STALEV2B, MT\$STALEV3, MT\$STALEV4, MT\$STALEV5
Water Bodies:	MT\$WATERBODY_STORET

A detailed description of each table follows.

Station Table (ET\$STA; [Station])

Oracle table name: ET\$STA

4D table name: [Station]

This table holds all the descriptive information for a station.

Y = required by STORET

N = optional for STORET

This system will not create transactions to create new STORET stations. You will have to contact the DEP STORET administrator to add a new station to STORET and get a STORET number for it.

Field	Required?	Description
DEP ID	Y	PK\$STAID [Station]DERID Number(7) Real A computer-generated, sequential number for the station (Oracle sequence S\$STA). This is the primary key for this file.
STORET station code	Y	PK\$STA [Station]Sta Varchar2(15) Alpha(15) The STORET station code for the location. Originally it was to be the primary key (thus the PK\$ name), but did not end up that way as not all stations have STORET names.
Station nickname	Y	STANICKNAME [Station]StaNickName Varchar2(10) Alpha(10) A ten-character "nickname" for the station. Currently many station nicknames start with the first five characters of the county name.
Station type	Y	STALEV1 [Station]Level1 Number(2) Real Describes the type of waterbody, e.g., stream, lake, canal, pipe.
		STALEV2A [Station]Level2a Number(2) Real Indicates whether monitoring takes place under ambient environmental conditions (AMBNT) or within a man-made facility (NONAMB).
		STALEV2B [Station]Level2b Number(2) Real Required if Level1 = "pipe", otherwise optional. Describes attributes related to level of pollution abatement.
		STALEV3 [Station]Level3 Number(2) Real

Required if Level1 = “pipe”, otherwise optional. Describes the type of non-ambient site, e.g., industrial, agricultural, municipal.

STALEV4	Number(2)
[Station]Level4	Real

Required if Level1 = “pipe”, otherwise optional. Indicates whether the site represents an intake, outfall, or a combined source.

LONSEC	Number(4,1)
[Station]lonsec	Real

The individual degrees, minutes, and seconds of latitude and longitude.

Latitude		LATITUDE [Station]Latitude	Number(9,1) Real	This is a value used in search routines so that degrees, minutes, and seconds do not have to be evaluated individually. It is calculated as follows: $(\text{LatDeg} * 3600) + (\text{LatMin} * 60) + \text{LatSec}$
Longitude		LONGITUDE [Station]Longitude	Number(9,1) Real	This is a value used in search routines so that degrees, minutes, and seconds do not have to be evaluated individually. It is calculated as follows: $(\text{LonDeg} * 3600) + (\text{LonMin} * 60) + \text{LonSec}$
Station Loc Description	Y	STADESC [Station]stadesc	Varchar2(48) Alpha(48)	A brief description of the site location. It should be as informative as room allows. (48 characters)
USGS cata- log number	Y	USGSNBR [Station]usgsnbr	Varchar2(8) Alpha(8)	The U.S.G.S cataloging unit number, or Hydrologic Unit Code (HUC) in which the station is located.
Sub-basin code	N	SUBBASIN [Station]subbasin	Number(2) Real	EPA sub-basin code - EPA has not defined sub-basins and if nothing is entered, two zeros are assumed.
EPA reach number	N	EPAREACH [Station]epareach	Varchar2(20) Alpha(20)	The EPA reach number on which the station is located or the reach that receives the drainage from the stream where the station is located.
On reach?		ONREACH [Station]onreach	Varchar2(3) Alpha(3)	If a reach number is entered, this field must be completed. "ON" indicates that a station is located on the reach, and "OFF" is used if the station is on a stream whose water enters the indicated reach directly or through one or more tributaries.
Miles		MILES [Station]rmiles	Number(8,3) Real	The miles from the downstream end of the reach to the point where the station is located or where the water enters the reach if the station is not on the reach.
Check digit		CKDIGIT [Station]ckdigit	Varchar2(2) Alpha(2)	A check digit is entered which is used by an algorithm to verify that the 11 digit reach data is correct. The check digit is shown in the river reach file directory.

Water body	N	AK\$WATERBODY	Number(5)
		[Station]WaterID	Real
		The code for the water body for this station.	

The following field is included in the 4D table:

Water body

[Station]Waterbody

Alpha(50)

A 50-character description of the waterbody for this station. When station information is downloaded from Oracle, the waterbody name comes along even though it is stored in the Oracle table MT\$Waterbody_STORET. This makes searches in 4D work more efficiently.

Station Level Tables

These are tables used in the station table for STALEV1, STALEV2A, etc. These categories can be used as retrieval criteria. For example, retrieve all stations where level 1 is “Canal”. The entries do not have to be valid STORET codes since this system does not generate new station transactions for STORET at this time.

The MT\$StaLev series has six tables in Oracle, but only one table in 4D [DummyStaLev]. The 4D table has a field “StaLevel” that tells you which Oracle table it came from. These are lookup tables that store information about a station.

MT\$STALEV1

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV1 Number(2) Computer-assigned sequential number for this name (Oracle sequence S\$STALEV1).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

MT\$STALEV2A

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV2A Number(2) Computer-assigned sequential number for this name Oracle sequence S\$STALEV2A).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

MT\$STALEV2B

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV2B Number(2) Computer-assigned sequential number for this name (Oracle sequence S\$STALEV2B).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

MT\$STALEV3

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV3 Number(2) Computer-assigned sequential number for this name (Oracle sequence S\$STALEV3).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

MT\$STALEV4

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV4 Number(2) Computer-assigned sequential number for this name (Oracle sequence S\$STALEV4).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

MT\$STALEV5

Field	Required?	Description
DEP-assigned ID	Y	PK\$STALEV5 Number(2) Computer-assigned sequential number for this name (Oracle sequence S\$STALEV5).
Popup Menu Name	Y	POPUPNAME Varchar2(25) A 10-character version of this name to use in popup menus.
BIOS Name	N	BIOSNAME Varchar2(6) The BIOS code for this name. If it is not a BIOS code, leave it empty.

Collector Table (MT\$COLLECT; [Collector])

This table contains the names of the people who were in charge of sampling field trips. This table is required for compatibility with the BIOS system. A collector is selected for each sample taken.

Oracle table name: MT\$COLLECT

4D table name: [Collector]

Field	Required?	Description
DEP-assigned Collector Ref Code	Y	PK\$COLLECT [Collector]DERID Real A code for each person who collects biological samples for the agency (Oracle sequence S\$COLLECT). This number is assigned by EPA after a written request by the assistant data base administrator. BIOS requires that each sample stored for an agency contain the reference number of at least one collector. Since the data need to be entered while waiting for a response, we will maintain a DEP-assigned code. When BIOS does assign a number, it will be included in this table, but the data will be stored with the DEP-assigned number. When the data are reformatted to be sent to BIOS, the Storet code will be put in place of the DEP-assigned code.
BIOS-assigned Collector Ref Number	Y	BIOSID [Collector]BIOSID Real An integer (unique for the agency) for each person who collects biological samples for the agency. Each sample stored for an agency is required to contain the reference number of at least one collector.
Name	Y	COLLNAME [Collector]CollName Collector's name
Address	Y	COLLADDRESS [Collector]CollAddress Collector's address
Phone	Y	COLLPHONE [Collector]CollPhone Collector's phone number

Identifier Table (MT\$IDENT; [Identifier])

This table contains the names of the people who were in charge of identifying the plants or animals found in the samples. This table is required for compatibility with the BIOS system. An identifier is selected for each sample/data type/gear taken.

Oracle table name: MT\$IDENT

4D table name: [Identifier]

Field	Required?	Description
DEP-assigned Identifier Ref Code	Y	PK\$IDENT [Identifier]DERID A code for each person who identifies organisms collected by the agency (Oracle sequence S\$IDENT). This is to be done the same way as Collector Reference Numbers, so please read that description above for details.
BIOS-assigned Identifier Ref Number	Y	BIOSID [Identifier]BIOSID An integer (unique for the agency) for each person who identifies organisms collected by the agency. Each sample stored for an agency is required to contain the reference number of at least one identifier.
Name	Y	IDNAME [Identifier>IDName Identifier's name
Address	Y	IDADDRESS [Identifier>IDAddress Identifier's address
Phone	Y	IDPHONE [Identifier>IDPhone Identifier's phone number

Survey Table (MT\$SURVEY; [Survey])

Many samples are taken as part a of project. This table contains the names of projects that have data included in the database. This table is required for compatibility with the BIOS system. A survey is selected for each sample taken. There are entries for “Unknown” for the samples that are not part of a project, but these may not be uploaded to BIOS.

Oracle table name: MT\$SURVEY

4D table name: [Survey]

Field	Required?	Description
DEP-assigned Survey Code	Y	PK\$SURVEY Number(5) [Survey]DERID Real A code for each survey conducted by the agency (Oracle sequence S\$SURVEY). This is to be done the same way as Collector Reference Numbers, so please read that description above for details.
BIOS-assigned Survey Number	Y	BIOSID Number(5) [Survey]BIOSID Real A unique (for the agency) number for each survey conducted by the agency. Each sample sent to BIOS is required to begin with the reference number of the survey of which it is a part.
Start Date	Y	STARTDATE Date [Survey]StartDate Date Date survey started
Name	Y	SVYNAME Varchar2(20) [Survey]SvyName Alpha(20) Name of the survey
Purpose	Y	SVYPURPOSE Varchar2(20) [Survey]SvyPurpose Alpha(20) The purposes must be: Enforcement, Research, Use Attainability, Monitoring, Screening or Baseline (definitions are in BIOS manual).

Sample Gear Table (MT\$GEAR; [Gear])

This table contains the names of the types of gear used to take samples. This table is required for compatibility with the BIOS system. A gear is selected for each sample/data type taken. If the gear is used to sample quantitative benthos data, the surface area of the gear is included.

Oracle table name: MT\$GEAR

4D table name: [Gear]

Field	Required?	Description
DEP-assigned Gear Code	Y	PK\$GEAR [Gear]DERID Number(3) Real A sequentially-assigned number for each gear (Oracle sequence S\$GEAR). This number is computer generated when a new gear is added.
BIOS Code	Y	BIOSID [Gear]BIOSID Varchar2(30) Alpha(30) BIOS code for this sampling gear. If there is no BIOS code, leave blank. The BIOS codes are only specific to type of sampling gear without size restrictions. (Ex. all Hester-Dendy samplers would have a BIOS code of Hester-Dendy).
Gear Descrip	Y	GDESC [Gear]GDesc Varchar2(50) Alpha(50) Full name for the sampling gear. (Ex., "Hester-Dendy sampler with 4 plates of 12 cms each")
Data Type	Y	GDATA TYPE [Gear]GDataType Varchar2(2) Alpha(2) Type of data this sampler collects: B=Macrobenthos, K=Plankton (zoo or phyto), A=Attached plants (periphyton).
Surface area	Y	GSURFAREA [Gear]GSurfArea Number(11,4) Real For benthos samplers, the total surface area of the sampler in square centimeters. For all other data types and qualitative benthos samplers, leave blank.
Gear Nickname	Y	GNICKNAME [Gear]GearNickName Varchar2(10) Alpha(10) A ten-character alphanumeric code to represent a particular sampling gear. This code is used in popup menus that refer to gear.
Gear Level	Y	GEARLEVEL [Gear]GearLevel Number(1) Real Takes a value of: 1 = Regular gear; 2 = Group title; 3 = Part of a group.
Level 1 GearID	Y	AK\$GEARLEV1 [Gear]Level1ID Number(3) Real If GearLevel = 3, the PK\$Gear ID of its group title; zero otherwise.

County Location Table (MT\$COUNTY_LOC; [CtyLatLon])

This table gives a county number and the latitude and longitude coordinates that describe a box that completely encloses the county. They are used to verify that the coordinates entered for a station are within the county the user assigns to the station.

Oracle table name: MT\$COUNTY

4D table name: [CtyLatLon]

Field	Required?	Description	
FIPS County Code	Y	PK\$CTYNO [CtyLatLon]County Odd number between 1 and 133 for the county. The counties are numbered in alphabetical order, so Alachua=1, Bay=2, etc. Numbers 133 and 135 are generic county designations for Alabama and Georgia, respectively.	Number(3) Real
County Name	Y	CTYLOC_NAME [CtyLatLon]CtyName Alphanumeric name of the county.	Varchar2(15) Alpha(20)
Minimum Latitude Coordinates	Y	MINLATDEG [CtyLatLon]MinLatDeg minimum latitude degree	Number(3) Real
	Y	MINLATMIN [CtyLatLon]MinLatMin minimum latitude minutes	Number(3) Real
	Y	MINLATSEC [CtyLatLon]MinLatSec minimum latitude seconds	Number(3) Real
Maximum Latitude Coordinates	Y	MAXLATDEG [CtyLatLon]MaxLatDeg maximum latitude degree	Number(3) Real
	Y	MAXLATMIN [CtyLatLon]MaxLatMin maximum latitude minutes	Number(3) Real
	Y	MAXLATSEC [CtyLatLon]MaxLatSec maximum latitude seconds	Number(3) Real
Minimum Longitude Coordinates	Y	MINLONDEG [CtyLatLon]MinLonDeg minimum longitude degree	Number(3) Real
	Y	MINLONMIN [CtyLatLon]MinLonMin	Number(3) Real

minimum longitude minutes

	Y	MINLONSEC [CtyLatLon]MinLonSec minimum longitude seconds	Number(3) Real
Maximum Longitude Coordinates	Y	MAXLONDEG [CtyLatLon]MaxLonDeg maximum longitude degree	Number(3) Real
	Y	MAXLONMIN [CtyLatLon]MaxLonMin maximum longitude minutes	Number(3) Real
	Y	MAXLONSEC [CtyLatLon]MaxLonSec maximum longitude seconds	Number(3) Real

Waterbody Table (MT\$WATERBODY_STORET; [WaterBody])

This table contains the names of the waterbodies in the state of Florida. This table is required for compatibility with the BIOS system. A waterbody is selected for each station defined.

Oracle table name: MT\$WATERBODY_STORET

4D table name: [WaterBody]

Field	Required?	Description
DEP-assigned Waterbody Code	Y	PK\$WATERBODY [WaterBody]DERID A sequential computer-generated identifier for a body of water (Oracle sequence S\$WATERBODY). Number(5) Real
STORET- assigned ID	N	STORETID [WaterBody]StoretID A unique code exists in the STORET system for each waterbody. If that number exists and is known for this waterbody, it is entered here. Varchar2(25) Alpha(25)
Waterbody name	Y	WATERNAME [WaterBody]WaterName A 50-character description of the waterbody (like "Wekiva River"). Varchar2(50) Alpha(50)

Toxicological Database

Some of the reference tables used for the biological portion of the database are also used for the toxicological functions. These are the waterbody table (MT\$WATERBODY_STORET; [Waterbody]) and the county location table (MT\$COUNTY_LOC; [CtyLatLon]). Those tables that are unique to the toxicology area are described in this section. The reference information for the toxicological portion of the database is maintained via the second and third sections of the Bioassay pulldown menu:

Bioassay	User Info	Hel
Samples		
Facilities		
Facility types		
NPDES sites		
DEP Districts		
Sample types		
Diluents		
Test organisms		
Calculation methods		
Causes of toxicity		
Maintenance		

Note: Changes to tables only temporary until approved by the database administrator.

Facility Names Table (MT\$FACILITY_TOX; [ToxFacility])

This table contains the names of the facilities that have toxicological data in the database.

Oracle table name: MT\$FACILITY_TOX

4D table name: [ToxFacility]

Field	Required?	Description
DEP-assigned Facility Name Code	C	PK\$FACILITY_USED [ToxFacility]Facility_Used A unique, sequential number assigned to one particular name for one particular facility (Oracle sequence S\$FACILITY_TOX). Number(7) Real
DEP-assigned Facility Code	C	FK\$FACILITY_TOX [ToxFacility]Facility_Tox The number for a particular facility; a given facility may be known by several names (PK\$Facility_Used) (see Programmer Notes in Appendix 7). Number(7) Real
Name	Y	FACILITYNAME [ToxFacility]FacilityName One of the names that the facility has been known by. Varchar2(50) Alpha(50)
District	N	AK\$DISTRICT [ToxFacility]District Varchar2(2) Alpha(2)

The code for the district handling permitting for this facility.

Street Address	N	FCADDRESS [ToxFacility]FCAddress Mailing address for this facility.	Varchar2(30) Alpha(30)
City	N	FCCITY [ToxFacility]FCCity City for the mailing address for this facility.	Varchar2(30) Alpha(30)
State	N	FCSTATE [ToxFacility]FCState State for the mailing address for this facility (2 characters).	Varchar2(2) Alpha(2)
Zip Code	N	FCZIP [ToxFacility]FCZip Zip code for the mailing address for this facility in the form “#####-####” (dash not stored).	Number(9) Real
Row Status	C	ROWSTATUS [ToxFacility]RowStatus If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.	Number(1) Real

The following field is included in the 4D table:

Other Facility Name	Y	[ToxFacility]OtherName Another name that the facility is known by, usually a “parent” name.	Alpha(30)
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Facility Types Table (MT\$FACILITYTYPE_TOX; [FacilityTypeTox])

This table contains the types of facilities that have toxicological data in the database.

Oracle table name: MT\$FACILITYTYPE_TOX
4D table name: [FacilityTypeTox]

Field	Required?	Description	
DEP-assigned Facility Type Code	C	PK\$FACILITY_TYPE [FacilityTypeTox]Facility_Type A unique, sequential number assigned when facility type is added to the table (Oracle sequence S\$FACILITYTYPE_TOX).	Number(2) Longint
Facility Type	Y	FACILITY_TYPE [FacilityTypeTox]FacilityTypeNam A description of facility type; types known at this time are: Agriculture Chemical Processing Drinking Water Treatment Electrical Power Generation Food Processing	Varchar2(30) Alpha(30) Mining None Other Pulp and Paper Sewage Treatment

Hospital/Medical

Row Status	C	ROWSTATUS	Number(1)
		[FacilityTypeTox]RowStatus	Real
		If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.	

NPDES Table (MT\$NPDES_TOX; [NPDESTox])

This table contains the information about the NPDES discharges of facilities in the database.

Oracle table name: MT\$NPDES_TOX

4D table name: [NPDES_ToX]

Field	Required?	Description	
NPDES Number	Y	PK\$NPDES [NPDES_ToX]NPDESnum The NPDES number for a site.	Varchar2(9) Alpha(9)
Facility Used	N	FK\$FACILITY_USED [NPDES_ToX]Facility_Used Key to the name of the facility whose has this NPDES site.	Number(7) Real
County	N	FK\$CTYNO [NPDES_ToX]County County where the site is found.	Number(3) Real
Sample location detail	N	SAMPLOC [NPDES_ToX]SampLoc 80 character description of this site.	VarChar2(80) Alpha(80)
Receiving Water	N	AK\$WATERBODY [NPDES_ToX]WaterbodyID Code for the first named waterbody that receives flow from sample site.	Number(5) Real
Row Status	C	ROWSTATUS [NPDES_ToX]RowStatus If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.	Number(1) Real

The following fields are included in the 4D table:

Facility Name	Y	[NPDES_ToX]FacilityName	Alpha(50)
		The facility name associated with the NPDES site. It is stored in the Oracle table MT\$FACILITY_TOX.	
Waterbody Name	Y	[NPDES_ToX]FacilityName	Alpha(50)
		The name of the receiving waterbody associated with the NPDES site. It is stored in the Oracle table MT\$WATERBODY_STORET.	

District Names Table (MT\$DISTRICT_TOX; [District_ToX])

This table lists the DEP districts.

Oracle table name: MT\$DISTRICT_TOX

4D table name: [District_ToX]

Field	Required?	Description
District Code	C	PK\$DISTRICT [District_ToX]District Varchar2(2) Alpha(2) A 2-character code to identify a district.
District Name	Y	DISTRICT_NAME [District_ToX]District_Name Varchar2(15) Alpha(15) The full name of the district (like Northwest).
Row Status	C	ROWSTATUS [District_ToX]RowStatus Number(1) Real If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.

Toxicity Sample Type Table (MT\$SAMPTYPE_TOX; [ToxSampType])

This table contains attribute information about the discharge sample.

Oracle table name: MT\$SAMPTYPE_TOX

4D table name: [ToxSampType]

Field	Required?	Description
Sample Type Code	C	PK\$TOXSAMPTYPE [ToxSampType]ToxSampTypeID Number(3) Real A unique, sequential number assigned when sample type is added to the table (Oracle sequence S\$SAMPTYPE_TOX).
Sample Type	Y	TOXTYPE_NAME [ToxSampType]ToxSampTypeName Varchar2(30) Alpha(30) A description of sample type; types known at this time are: Effluent Process water Ground water Pure chemical Landfill leachate Sanitary sewage Membrane concentrate Sediment None Surface water Other
Row Status	C	ROWSTATUS [ToxSampType]RowStatus Number(1) Real If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.

Diluent Type Table (MT\$DILUENT_TOX; [Diluent_Tox])

This table lists the diluents used in toxicological assays.

Oracle table name: MT\$DILUENT_TOX

4D table name: [Diluent_Tox]

Field	Required?	Description
Diluent Type Code	C	PK\$DILUENT [Diluent_Tox]Diluent Number(2) Real A unique, sequential number assigned to a diluent name when it is added to the table (Oracle sequence S\$DILUENT_TOX).
Name	Y	DILUENT_NAME [Diluent_Tox]Diluent_Name Varchar2(20) Alpha(20) The name of diluent - types known at this time are: Well water NSW (natural seawater) ASW (artificial seawater) 20% MW (mineral water) Other
Row Status	C	ROWSTATUS [Diluent_Tox]RowStatus Number(1) Real If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.

Bioassay Organism Table (MT\$TESTORG; [TestOrg])

This table lists the test organisms used in toxicological assays.

Oracle table name: MT\$TESTORG

4D table name: [TestOrg]

Field	Required?	Description
Test Organism Code	C	PK\$TESTORG [TestOrg]TestOrgID Number(3) Real A unique, sequential number assigned to a test organism when it is added to the table (Oracle sequence S\$TESTORG_TOX).
Name	Y	TESTORGNAME [TestOrg]TestOrgName Varchar2(30) Alpha(30) The full scientific name of the animal or plant.
Row Status	C	ROWSTATUS [TestOrg]RowStatus Number(1) Real If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.

The following fields are included in the Oracle table. They were added to accommodate a function that has not been implemented.

Test Organism Synonym	TESTORGSYN	Varchar2(2)
	Two character code to represent an additional name(s) that the test organism may be known by. It is intended to be null if the name represents the current version and "S" if it is an older name.	
Synonym Code	FK\$TESTORG	Number(3)
	The code for the synonym of this taxon as listed in the primary key for this table, PK\$TESTORG.	

Calculation Method Table (MT\$CALC_TOX; [Calc_Tox])

This table lists methods for calculating the results of toxicological assays.

Oracle table name: MT\$CALC_TOX
4D table name: [Calc_Tox]

Field	Required?	Description	
Calculation Method Code	C	PK\$CALCMETHOD	Number(2)
		[Calc_Tox]CalcMethod	Real
		A unique, sequential number assigned to a calculation method when it is added to the table (Oracle sequence S\$CALC_TOX).	
Name	Y	CALCNAME	Varchar2(30)
		[Calc_Tox]Calc_Name	Alpha(30)
		A description of the calculation method - types known at this time are: Noncalculated (LC50 only) Probit (LC50 only) Spearman-Karber (LC50 only) Trimmed Spearman-Karber (LC50 only) Binomial (LC50 only) Moving average (LC50 only) Dunnett's (NOEC/LOEC only) Steele's Many-One-Rank (NOEC/LOEC only)	
Calculation Type	Y	CALC_TEST	Number(1)
		[Calc_Tox]Calc_Test	Real
		The type of calculation this is appropriate for: 1=LC50 only, 2=NOEC/LOEC only, 3=Both.	
Row Status	C	ROWSTATUS	Number(1)
		[Calc_Tox]RowStatus	Real
		If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.	

Toxicity Causes Table (MT\$CAUSE_TOX; [Cause_Tox])

This table lists causes for toxicity.

Oracle table name: MT\$CAUSE_TOX

4D table name: [Cause_Tox]

Field	Required?	Description
Toxicity Cause Code	C	PK\$TOXCAUSE [Cause_Tox]ToxCause Number(2) Real A unique, sequential number assigned to a cause when it is added to the table (Oracle sequence S\$CAUSE_TOX).
Causes of Toxicity	Y	CAUSE_NAME [Cause_Tox]Cause_Name Varchar2(40) Alpha(20) A description of the possible causes of toxicity in a sample; causes known at this time are: Cl ₂ NH ₃ pH
Row Status	C	ROWSTATUS [Cause_Tox]RowStatus Number(1) Real If value is 1, the row is waiting for database administrator approval; if value is null, the row has been approved.

The following tables are included in 4D, or both 4D and Oracle. While they have no menu access for editing, they provide “lookup” information within the context of certain forms, or store codes for items defined in 4D lists.

LIMS Codes Table ([LIMS_Codes])

This is a lookup table that holds the full text corresponding to the DEP Bureau of Laboratories LIMS data qualifier codes.

4D table name: [LIMS_Codes]

Field	Required?	Description
LIMS Code	Y	[LIMS_Codes]LIMS_Code Alpha(2) Letter codes that are used to qualify measurements in the LIMS.
Code Meaning	Y	[LIMS_Codes]Meaning Text The meaning of the code.

Test Unit Names Table ([TestUnitNames])

This table holds codes and names to indicate the duration of a toxicity bioassay.

4D table name: [TestUnitNames]

Field	Required?	Description
Unit Code	Y	[TestUnitNames]TestUnitID Integer A numeric code entered by the user when a new unit is added to the table.
Unit Name	Y	[TestUnitNames]TestUnitName Alpha(7) The name of the unit, e.g., minutes, hours, days.

Chlorination Status Table ([ToxChlorinate])

This table holds codes and names to indicate whether a toxicity bioassay was chlorinated, unchlorinated, or dechlorinated.

4D table name: [ToxChlorinate]

Field	Required?	Description
Chlorination Code	Y	[ToxChlorinate]TestChlorID Integer A numeric code entered by the user when a new chlorination status is added to the table.
Chlorination Status Name	Y	[ToxChlorinate]ToxChlorName Alpha(13) The name of the chlorination status, e.g., chlorinated, unchlorinated, dechlorinated.

Toxicity Parameter Table (MT\$PARAM_BIO; [ToxParam])

This table lists physical/chemical parameters used in the toxicological section of the database, along with units and a name to display in pop-up menus.

Oracle table name: MT\$PARAM_BIO

4D table name: [ToxParam]

Field	Required?	Description
Parameter Code	C	PK\$PARAMID Number(3) [ToxParam]ParamID Real A unique, sequential number assigned to a parameter when it is added to the table (Oracle sequence S\$PARAM_BIO).
Parameter Units	Y	AK\$UNIT Number(3) [ToxParam]ParamUnitID Real The units of measurements for the parameter.

Parameter Name	Y	PARAMNAME [ToxParam]ParamName The full name of the parameter.	Varchar2(50) Alpha(50)
Display Name	Y	PARAMDISPLAY [ToxParam]ParamDisplay A shorter name for the parameter to be used in pop-up menus.	Varchar2(15) Alpha(50)

Toxicity Parameter Unit Table (MT\$UNIT_BIO; [ToxParamUnit])

This table lists units for the physical/chemical parameters used in the toxicological section of the database.

Oracle table name: MT\$UNIT_BIO
4D table name: [ToxParamUnit]

Field	Required?	Description
Unit Code	C	PK\$UNIT [ToxParamUnit]ParamUnitID Real A unique, sequential number assigned to a unit when it is added to the table (Oracle sequence S\$UNIT_BIO).
Unit Name	Y	UNITNAME [ToxParamUnit]UnitName Alpha(20) The full name of the unit.
Unit Display	Y	UNITDISPLAY Varchar2(15) A shorter name for the unit to be used in pop-up menus.

Taxa-related Tables

Master Taxa Table (ET\$TAXAMSTR; [MasterTaxa])

This table holds the names and information about taxa. The original table was loaded from the BIOS taxonomic list of plants and animals in the United States (i.e., not just Florida) in 1992.

Oracle table name: ET\$TAXAMSTR

4D table name: [MasterTaxa]

Field	Required?	Description
The TaxaID code fields are used exactly as they are in the BIOS system.		
TaxaID Code	Y	PK\$TAXAID [MasterTaxa]TaxaId Number(10) Real A sequential computer-generated identifier for this scientific name (Oracle sequence S\$TAXAMSTR). Any name < 10,000,000 came from the BIOS system meaning that the name came on the original BIOS taxonomic list; any number larger was generated at DEP. It has nothing to do with the phylogeny of the organism.
Parent TaxaID	Y	PTAXAID [MasterTaxa]PTaxaid Number(10) Real The PK\$TAXAID of the immediate parent of this entry. The parent must be in a major taxonomic category like phylum, class, order, family, genus, or species.
Immediate Parent TaxaID	N	IPTAXAID [MasterTaxa]IPTaxaid Number(10) Real Not used now. BIOS is in the process of adding more phylogenetic categories to their taxa system. There is no programming in this system that uses this column at this time. It will be used to store the PK\$TAXAID of the most immediate parent which may be a suborder, superfamily, etc.
Synonym TaxaID	N	SYNTAXAID [MasterTaxa]SynTaxaID Number(10) Real If this name is a synonym of one in the table, the PK\$TAXAID of that name appears here.
Phylogenetic Category	Y	PHYLCAT [MasterTaxa]PhylCat Number(2) Real 1=Phylum; 2=Class; 3=Order; 4=Family; 5=Genus; 6=Species; 7=Variety.
Kingdom	Y	KINGDOM [MasterTaxa]Kingdom Number(1) Real 1 = Plant; 2 = Animal.

Phylogenetic Code	Y	PHYLO [MasterTaxa]Phylo	Varchar2(17) Alpha(18)	A 17-character code that describes the phylogeny of the organism according to: <u>Characters</u> <u>Description</u> 1-2 Phylum 3-4 Class 5-6 Order 7-9 Family 10-12 Genus 13-15 Species 16-17 Variety
Revision Status	Y	REVISION [MasterTaxa]Revision	Varchar2(2) Alpha(2)	May be an "S" or null. "S" means that this is a synonym for another name on the list . A null in this field means that this is the most accepted version of this name. A synonym and its more accepted name will have identical values in PHYLO.
Scientific name	Y	SCINAME [MasterTaxa]SciName	Varchar2(45) Alpha(50)	Full, spelled-out scientific name (e.g. <i>Mediomastus ambiseta</i>). This is the way BIOS wants to receive taxonomic information, not by taxonomic code.
Authority Name	N	AUTHORITY [MasterTaxa]Authority	Varchar2(30) Alpha(30)	The source of the original description of this scientific name.
Authority Date	N	AUTHDATE [MasterTaxa]AuthDate	Varchar2(4) Alpha(4)	The date of the original description of this scientific name.
Authority Ref	N	AUTHREF [MasterTaxa]AuthRef	Varchar2(80) Alpha(80)	The bibliographic citation of the taxonomic key used to identify the taxon.
Entered in System by	Y	ENTBY [MasterTaxa]EntBy	Varchar2(15) Alpha(15)	Location and username of the person who initially made this entry into the table. For example, HQLondon would be headquarters, Landon Ross; BIOS would be entered for those that came from the BIOS list.
BIOS?	Y	BIOS [MasterTaxa]BIOS	Varchar2(2) Alpha(2)	Y= This scientific name is on the BIOS list; N = not on BIOS list; U = don't know (it could have been added at DEP, but was added to BIOS after the most recent list we have).

Alternate	N	BIOSID	Number(10)
BIOS ID		[MasterTaxa]BIOSID	Real
		The PK\$TAXAID of the scientific name to use for this taxon if its own scientific name is not to be used when data are prepared for BIOS	

Florida List	Y	FLALIST [MasterTaxa]FlaList 1=Yes, on Florida list (i.e., this is a taxon found in Florida); 0=No, not on Florida list.	Number(2) Real
Attribute Codes	Y	(each is stored as a separate field, but searches may be done for a combination of attribute codes)	
Range		TRANGE [MasterTaxa]Range	Varchar2(2) Alpha(2)
		1 = Range unchecked, authoritatively checked taxa 2 = Range not in Florida, authoritatively checked taxa 3 = Range includes Florida, authoritatively checked taxa 4 = Range may include Florida, authoritatively checked taxa 5 = Unchecked taxa (will never be on BIOS) 6 = Numbered taxa (will never be on BIOS) 7 = Not in Florida, but needs to be on Florida list	
Florida Index		FLAINDX [MasterTaxa]FlaIndex	Varchar2(2) Alpha(2)
		The value entered in the Oracle table is the number of points for the class. These points are summed for all taxa in a sample to get the Florida Index value for that sample. 0 =Non-Class One or Two, including marine invertebrates, non-invertebrates, & plants 1 =Class 2 2 =Class 1	
Lake Condition Index		LAKEINDX [MasterTaxa]LakeIndx	Varchar2(2) Alpha(2)
		The value entered in the Oracle table is the number of points for the class. These points are summed for all taxa in a sample to get the Lake Condition Index value for that sample. 0 =Non-Class One or Two, including marine invertebrates, non-invertebrates, & plants 1 =Class B 2 =Class A	
Functional Feeding Group		AK\$FFID	Number(3)

The functional feeding group code from MT\$FFID describes the method of feeding for this taxon. This field is left null if the taxon has no functional feeding group determined or if the taxon is a non-invertebrate or plant.

Functional Feeding Tables (MT\$FFID; [FFID])

This table describes the different methods of feeding employed by invertebrates.

Oracle table name: MT\$FFID

4D table name: [FFID]

Field	Required?	Description
Feeding Group Code	Y	PK\$FFID [FFID]FFID Number(3) Real The primary key for this table (Oracle sequence S\$FFID).
Description	Y	FFDESC [FFID]FFDesc Varchar2(20) Alpha(20) Up to 20 characters to describe the feeding group. This field is used in scrollable areas that show all the feeding group choices.
Group type	Y	FFTYPE [FFID]FFType Number(1) Real 1=Feeding method unknown, 2=single feeding strategy, 3=multiple feeding strategies.

Functional Feeding Tables (MT\$FFGroup; [FFGroup])

If the a feeding group uses “multiple feeding strategies”, this table is used to describe it. The percent fields of all rows with the same FK\$FFID1 must sum to 100.

Oracle table name: MT\$FFGROUP

4D table name: [FFGroup]

Field	Required?	Description
Feeding Group Code	Y	PK\$FFID1 [FFGroup]FFID1 Number(3) Real The feeding group that is being described.
Feeding Group Code	Y	PK\$FFID2 [FFGroup]FFID2 Number(3) Real One of the feeding groups that comprise feeding strategy FK\$FFID1.
Percent	Y	FFPercent [FFGroup]FFPercent Number(6,2) Real The percent that FK\$FFID2 is of feeding group FK\$FFID1

The following field is included in the 4D table:

Description	Y	[FFGroup]FFDesc Alpha(20) Alphanumeric description of the feeding group. This field is used in scrollable areas that show all the feeding group choices. This information is stored in Oracle table MT\$FFID.
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Sample-related Tables

Biological Database

Sample Table (DT\$SAMPLE; [Sample])

This table describes a sample, i.e., what was sampled at a particular location (station) on a specific date, at a specific time.

Oracle table name: DT\$SAMPLE

4D table name: [Sample]

Y = required field

N = optional field

C = computer will keep track of this field

Field	Required?	Description
DEP-assigned sample ID	C	PK\$SAMPLEID [Sample]SampleID Number(9) Real Computer-generated sequential number to uniquely identify this sample (station/date/time/survey/collector) (Oracle sequence S\$SAMPLE).
STORET station code	Y	AK\$STA [Sample]Sta Number(7) Real DEP-assigned station code (PK\$STAID in station table)
Date sampled	Y	SAMPDATE [Sample]SampDate Date Date Date a sample was taken.
Time sampled	N	SAMPTIME [Sample]SampTime Varchar2(5) Time Time a sample was taken. Time may be sent to BIOS, but is not required.
DEP-assigned Survey Code	Y	AK\$SURVEY [Sample]Survey Number(5) Real BIOS requires a survey identification number (1-99999) be attached to each sample. The base information for this survey is stored in the survey reference table and includes the date, time, name and purpose of the field survey.
DEP-assigned Collector Code	Y	AK\$COLLECT [Sample]Collector Number(5) Real The collector reference code for the person in charge of the sampling trip.
Group ID	C	AK\$GROUPID [Sample]OwnGroup Number(2) Real The number of the group that entered these data.
Comments	N	COMMENTS Varchar2(80)

[Sample]Comments

Alpha(80)

A brief description of anything special noted during sampling, e.g.,
“Station was flooded”. Allow up to 50 characters . This is not a BIOS-
related field.

Complete?	C	SAMPCOMPLETE [Sample]SampComplete	Varchar2(2) Alpha(2)	Are all the data entered and verified for this sample? This means that all taxonomic discrepancies have been resolved and all codes in the data files are on the Florida list. If the value is “Y”, the data for this station/date are available for retrieval and analysis as well as ready to be sent to BIOS.
BIOS date	Y	BIOSDATE [Sample]BIOSDate	Date Date	The date the data were uploaded to BIOS. If the data have not gone to BIOS, the date will be blank (00/00/00). All data for all community types must be complete and verified before any of it is sent to BIOS. The system will add only complete, verified samples to BIOS. After the data are sent to BIOS, the only field that can be edited is “Comments”.
BIOS status	Y	BIOSSTAT [Sample]BIOSStat	Number(2) Real	The status of this sample relative to BIOS 0 = Never sent to BIOS. 1 = Data file with this sample was prepared to send to BIOS. 2 = Data were successfully sent to BIOS. -1 = During prepare for BIOS routine, samples are set to this value and then set to 1 when the routine ends. If routine bombs, values may stay set to this value.
BIOS Set	N	BIOSET [Sample]BIOSet	Number(1) Alpha(2)	During the “Prepare for BIOS” routine, the sample may be assigned to a set. This field holds the set number, from 0 to 9.
Community status fields	Y	The following fields will contain one of three values: 1 = Sampled - This type of data was sampled and data entry/verification is not complete. 2 = Not sampled - This type of data was not sampled at this station at this date and time. 3 = Done - This type of data was sampled and all data have been entered and verified. These data are ready for retrieval.		
Benthos status		STBENTHOS [Sample]StBenthos	Number(1) Real	Macrobenthos community sample status.
No. of benthos gear		NBRBENTHOS [Sample]NbrBenthos	Number(2) Real	Number of different sample gear types used to collect macroinvertebrates.
Zooplankton status		STZOO [Sample]StZoo	Number(1) Real	Zooplankton community sample status.

No. of zooplankton gear	NBRZOO [Sample]NbrZoo Number of different sample gear types used to collect zooplankton.	Number(2) Real
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Periphyton status	STPERI [Sample]StPeri Periphyton community sample status.	Number(1) Real
No. of periphyton gear	NBRPERI [Sample]NbrPeri Number of different sample gear types used to collect periphyton.	Number(2) Real
Phytoplankton status	STPHYTO [Sample]StPhyto Phytoplankton community sample status.	Number(1) Real
No. of phytoplankton gear	NBRPHYTO [Sample]NbrPhyto Number of different sample gear types used to collect phytoplankton.	Number(2) Real
Parameter status	STPARAM [Sample]StParam Physical/chemical information status.	Number(1) Real

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, survey, time, or gear) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them here makes 4D run more efficiently.

STORET Station Name	[Sample]StoretName The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.	Alpha(15)
Station Nickname	[Sample]StaNickname The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.	Alpha(10)
Station Description	[Sample]StaDesc Brief description of the site location. It is stored in the Oracle table ET\$Sta.	Text
Station Latitude	[Sample]Latitude The value equivalent to the station latitude in seconds, used for searches and calculations. It is stored in the Oracle table ET\$Sta.	Real
Station Longitude	[Sample]Longitude The value equivalent to the station longitude in seconds, used for searches and calculations. It is stored in the Oracle table ET\$Sta.	Real
Latitude degrees	[Sample]LatDeg Degrees portion of the station latitude. It is stored in the Oracle table ET\$Sta.	Real
Latitude	[Sample]LatMin	Real

minutes	Minutes portion of the station latitude. It is stored in the Oracle table ET\$Sta.
Latitude seconds	[Sample]LatSec Real Seconds portion of the station latitude. It is stored in the Oracle table ET\$Sta.
Longitude degrees	[Sample]LonDeg Real Degrees portion of the station longitude. It is stored in the Oracle table ET\$Sta.
Longitude minutes	[Sample]LonMin Real Minutes portion of the station longitude. It is stored in the Oracle table ET\$Sta.
Longitude seconds	[Sample]LonSec Real Seconds portion of the station longitude. is stored in the Oracle table ET\$Sta.
Survey Name	[Sample]SvyName Alpha(20) The name of the survey associated with the sample. It is stored in Oracle table MT\$Survey.
Time	[Sample]TextTime Alpha(5) A field to hold the text form of the time sampled.
First benthos gear	[Sample]BGear1 Real Number of the first sample gear type used to collect macroinvertebrates.
Second benthos gear	[Sample]BGear2 Real Number of the second sample gear type used to collect macroinvertebrates.
Third benthos gear	[Sample]BGear3 Real Number of the third sample gear type used to collect macroinvertebrates.
Fourth benthos gear	[Sample]BGear4 Real Number of the fourth sample gear type used to collect macroinvertebrates.
First peri- phyton gear	[Sample]PrGear1 Real Number of the first sample gear type used to collect periphyton.
Second peri- phyton gear	[Sample]PrGear2 Real Number of the second sample gear type used to collect periphyton.
Third peri- phyton gear	[Sample]PrGear3 Real Number of the third sample gear type used to collect periphyton.
Fourth peri- phyton gear	[Sample]PrGear4 Real Number of the fourth sample gear type used to collect periphyton.
First phyto-	[Sample]PhGear1 Real

plankton gear	Number of the first sample gear type used to collect phytoplankton.
Second phyto- plankton gear	[Sample]PhGear2 Real Number of the second sample gear type used to collect phytoplankton.
Third phyto- plankton gear	[Sample]PhGear3 Real Number of the third sample gear type used to collect phytoplankton.
Fourth phyto- plankton gear	[Sample]PhGear4 Real Number of the fourth sample gear type used to collect phytoplankton.

First zoo-plankton gear	[Sample]ZGear1	Real	Number of the first sample gear type used to collect zooplankton.
Second zoo-plankton gear	[Sample]ZGear2	Real	Number of the second sample gear type used to collect zooplankton.
Third zoo-plankton gear	[Sample]ZGear3	Real	Number of the third sample gear type used to collect zooplankton.
Fourth zoo-plankton gear	[Sample]ZGear4	Real	Number of the fourth sample gear type used to collect zooplankton.

Benthos Table (DT\$BENTHOS; [Benthos])

This table holds the information about a sample taken by a particular gear. More than one gear may have been used to collect information at a particular station on a specific date and time. It is also possible that the same gear type was used more than once (i.e., a ponar was used to take a quantitative sample and was used again to take a qualitative sample). There is one row entered in this table for each gear/qualquan that comprises an individual sample.

Oracle table name: DT\$BENTHOS

4D table name: [Benthos]

Field	Required?	Description
BenthID	C	PK\$BENTHID [Benthos]BenthID System-generated code to represent this station/date/time/survey/collector/gear/qual (Oracle sequence S\$BENTHOS). Number(9) Real
SampleID	C	FK\$SAMPLEID [Benthos]SampleID Represents the station/date/time/survey/collector for these data. Number(9) Real
DEP-assigned gear code	Y	FK\$GEAR [Benthos]Gear The type of gear used to capture these animals (DEP-assigned code in sample gear reference table). Number(3) Real
Identifier	Y	AK\$IDENT [Benthos]Ident The DEP code for the name in MT\$IDENT that was in charge of identifying the benthos in the sample. Number(5) Real
Qualitative or Quantitative	Y	QUALQUAN [Benthos]QualQuan 1 = sample was processed as quantitative sample 2 = sample was processed as qualitative sample Number(2) Real
Number of replicates	Y	NREPS [Benthos]Nreps If replicate samplers were used, enter the number of replicates sampled; otherwise, enter the number 1. Number(2) Real
ID confidence level	Y	IDCONF [Benthos]IDConf The level of confidence in the taxonomic identifications for this BenthID. This field is required by BIOS for every ID, but our system will assign a sample-specific level of confidence. The letter codes are what BIOS uses. Your entry screen will let you pick the level of confidence and will automatically insert the correct letter for it. The values are: 1 = 99.9 percent confidence (1 chance in 1000 of making an error); Number(2) Real

2 =	99.0	“	“	(1 chance in 100 of making an error);
3 =	90.0	“	“	(1 chance in 10 of making an error);
4 =	Percent confidence unknown.			

Gear Factor	Y	GEARFACTOR [Benthos]GearFactor	Number(7,4) Real
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The gear factor is used to account for differences in the use and size of quantitative gears, or in sample processing techniques. It can be any one or combination of the following three components, as appropriate:

- (1) the number of times the sampling gear was deployed to collect one replicate (quantitative gears);
- (2) the proportion of the sample processed (quantitative or qualitative gears); and
- (3) the proportion of the gear deployed to the standard gear, as defined in MT\$Gear (quantitative gears).

BIOS status	C	BIOSTAT [Benthos]BIOSStat	Number(2) Real
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!!!These fields in these tables are unused. Their functions are addressed in dt\$sample and [Sample]!!!

The following fields are calculated after the sample is marked complete. They are calculated by pooling all the replicates for this PK\$BENTHID, thus these are sample-specific values. There are no corresponding 4D fields in [Benthos] for these pooled values. They are the variables most often requested in a retrieval and saving them here will result in faster retrievals.

Number of individuals counted in the sample	NINDC	Number(9)
Number of individuals per meter squared	NINDU	Number(14,2)
Number of taxa in this sample	NTAXA	Number(5)
Florida Index	FLINDEX	Number(5)
Lake Condition Index	LCINDEX	Number(5)
Shannon-Weaver Diversity Index	DBAR	Number(6,2)

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, date, owner group) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them in this table makes 4D run more efficiently.

STORET Station Name	[Benthos]StoretName	Alpha(15) The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.
Station Nickname	[Benthos]StaNickname	Alpha(10) The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.
Sample Date	[Benthos]SampDate	Date The date the sample was collected. It is stored in the Oracle table DT\$Sample.
Owner Group	[Benthos]OwnGroup	Real

The number of the group that enters these data. It is stored in the Oracle table DT\$Sample.

Benthos Taxa Table (DT\$BENTAXA; [BenTaxa])

This table stores the individual taxa information for each replicate of each pk\$benthid.

Oracle table name: DT\$BENTAXA

4D table name: [BenTaxa]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$BENTAXARECID Number(9) [BenTaxa]BenTaxaRecID Real Computer-generated sequential number for this fk\$benthid/replicate/taxaID (Oracle sequence S\$BENTAXA).
BenthID	C	FK\$BENTHID Number(9) [BenTaxa]BenthID Real Represents the station/date/time/survey/collector/gear/qual for these data.
Replicate No.	Y	REPNUM Number(2) [BenTaxa]RepNum Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Taxa Code.	Y	FK\$TAXAID Number(10) [BenTaxa]TaxaID Real The taxa code for this animal.
No. Individuals.	Y	NOIND Number(6) [BenTaxa]NoInd Real The number of animals of this taxa code that were counted in this replicate.
No. Individuals. per m ²	Y	NOINDSQM Number(12,2) [BenTaxa]NoIndSqm Real For quantitative samples only, computer calculates the number of individuals per m ² of sampler area by: no. individuals counted / (sampler area in cm ² * .0001 m ² /cm ²)

The following field is included in the 4D table.

Taxon Scientific Name	[BenTaxa]SciName Alpha(50) Full, spelled-out scientific name. These names correspond to the values in the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr.
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Zooplankton Table (DT\$ZOOPL; [Zooplankton])

This table holds the information about a sample taken by a particular gear. More than one gear may have been used to collect information at a particular station on a specific date and time. It is also possible that the same gear type was used more than once (i.e., a plankton net was used to take a quantitative sample and was used again to take a qualitative sample). There is one row entered in this table for each gear/qualquan that comprises an individual sample.

Oracle table name: DT\$ZOOPL

4D table name: [Zooplankton]

Field	Required?	Description
ZOOID	C	PK\$ZOOID [Zooplankton]ZooID Number(9) Real System-generated code to represent this station/date/time/survey/collector/gear/qual (Oracle sequence S\$ZOOPL).
SampleID	C	FK\$SAMPLEID [Zooplankton]SampleID Number(9) Real Represents the station/date/time/survey/collector for these data.
DEP-assigned gear code	C	FK\$GEAR [Zooplankton]Gear Number(3) Real The type of gear used to capture these animals (DEP-assigned code in sample gear reference table).
Identifier	Y	AK\$IDENT [Zooplankton]Ident Number(5) Real The DEP code for the name in MT\$IDENT that was in charge of identifying the zooplankton in the sample.
Qualitative or Quantitative	Y	QUALQUAN [Zooplankton]QualQuan Number(2) Real 1 = sample was processed as quantitative sample 2 = sample was processed as qualitative sample
Number of replicates	Y	NREPS [Zooplankton]Nreps Number(2) Real If replicate samplers were used, enter the number of replicates sampled; otherwise, enter the number 1.
ID confidence level	Y	IDCONF [Zooplankton>IDConf Number(2) Real The level of confidence in the taxonomic identifications for this BenthID. This field is required by BIOS for every ID, but our system will assign a sample-specific level of confidence. The letter codes are what BIOS uses. Your entry screen will let you pick the level of confidence and will automatically insert the correct letter for it. The values are: 1 = 99.9 percent confidence (1 chance in 1000 of making an error);

2 = 99.0 “ “ (1 chance in 100 of making an error);
3 = 90.0 “ “ (1 chance in 10 of making an error);
4 = Percent confidence unknown.

Gear Factor	Y	GEARFACTOR [Zooplankton]GearFactor The number of times the sampling gear was deployed to collect one replicate.	Number(7,4) Real
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BIOS status	C	BIOSSTAT [Zooplankton]BIOSStat !!!These fields in these tables are unused. Their functions are addressed in dt\$sample and [Sample]!!!	Number(2) Real
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The following fields are calculated after the sample is marked complete. They are calculated by pooling all the replicates for this PK\$ZOOID, thus these are sample-specific values. There are no corresponding 4D fields in [Zooplankton] for these pooled values. They are the variables most often requested in a retrieval and saving them here will result in faster retrievals. Note: Fields with an asterisk(*) are present but not calculated, as they are not appropriate for this data type.

Number of individuals counted in the sample	NINDC	Number(9)
Number of individuals per ml	NINDU	Number(14,2)
Number of taxa in this sample	NTAXA	Number(5)
*Florida Index	FLINDEX	Number(5)
*Lake Condition Index	LCINDEX	Number(5)
Shannon-Weaver Diversity Index	DBAR	Number(6,2)

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, date, owner group) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them in this table makes 4D run more efficiently.

STORET Station Name	[Zooplankton]StoretName The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.	Alpha(15)
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Station Nickname	[Zooplankton]StaNickname The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.	Alpha(10)
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Sample Date	[Zooplankton]SampDate The date the sample was collected. It is stored in the Oracle table DT\$Sample.	Date
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Owner Group	[Zooplankton]OwnGroup The number of the group that enters these data. It is stored in the Oracle table DT\$Sample.	Real
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Zooplankton Replicate Information Table (DT\$ZOOEPS; [ZooReps])

This is information needed to calculate the number of individuals per ml in DT\$ZooTaxa. There is one row in this table for each replicate of each pk\$zooid.

Oracle table name: DT\$ZOOEPS

4D table name: [ZooReps]

Field	Required?	Description
Unique ID for this rep	C	PK\$ZOOEPID Number(9) [ZooReps]ZooRepID Real Computer-generated sequential number for this fk\$zooid/replicate (Oracle sequence S\$ZOOEPS).
ZooID	C	FK\$ZOOID Number(9) [ZooReps]ZooID Real Represents the station/date/time/survey/collector/gear/qual for these data.
Replicate No.	Y	REPNUM Number(2) [ZooReps]RepNum Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Volume of water filtered or grabbed (mLs)	Y	VOLCOLLECT Number(8,1) [ZooReps]VolCollect Real The amount of water that passed through the net or in the grab sample. If it was a tow, have to calculate how much water went through the net according to the flowmeter directions or whatever is appropriate to the way the tow was done and the size of the net.
Sample volume	Y	SAMPVOL Number(7,1) [ZooReps]SampVol Real The volume of the sample in the bottle in mls.
Sample volume	Y	SAMPVOL Number(7,1) [ZooReps]SampVol Real The volume of the sample in the bottle in mls.
Dilution factor	Y	DILFACT Number(7,1) [ZooReps]DilutFactor Real A value used in the equation to account for the dilution or concentration of sample material. For example, if you took 1 mL of the original sample and added 3 mLs of DI water to it, the dilution factor to enter is 4 which came from 1 mL/(1 mL + 3 mLs), or a 1 in 4 solution.
Counting cell information		
Grid length	Y	GRIDLEN Number(5,2) [ZooReps]GridLen Real Length of one side of counting grid in mm.

Cell depth	Y	CELLDEPTH [ZooReps]CellDepth Depth of counting cell in mm.	Number(4,1) Real
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No. grids	Y	NBRGRIDS	Number(3)
		[ZooReps]NbrGrids	Real
		Number of grids counted.	

Zooplankton Taxa Table (DT\$ZOOTAXA; [ZooTaxa])

This table stores the individual taxa information for each replicate of each pk\$zooid.

Oracle table name: DT\$ZOOTAXA
4D table name: [ZooTaxa]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$ZOOTAXARECID [ZooTaxa]ZooTaxaRecID Computer-generated sequential number for this fk\$zooid/replicate/taxon (Oracle sequence S\$ZOOTAXA). Number(9) Real
ZooID	C	FK\$ZOOID [ZooTaxa]ZooID Represents the station/date/time/survey/collector/gear/qual for these data. Number(9) Real
Replicate No.	Y	REPNUM [ZooTaxa]RepNum If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1. Number(2) Real
Taxa Code	Y	FK\$TAXAID [ZooTaxa]TaxaID The taxa code for this animal. Number(10) Real
No. Individuals	Y	NOIND [ZooTaxa]Noind The number of animals of this taxa code that were counted in the subsample of this replicate. Number(6) Real
No. Individuals per mL	Y	NOINDCM2 [ZooTaxa]NoIndSqCm For quantitative samples only, computer calculates this number of individuals/mL by: <u>$(1000 \text{ mm}^3/\text{ml} * \text{no. indiv counted} * \text{sample vol} * \text{dilution})$</u> $\text{grid}^2 * \text{cell depth} * \text{no. flds counted} * \text{vol filtered or grabbed}$ Number(12,2) Real

The following field is included in the 4D table.

Taxon	[ZooTaxa]SciName	Alpha(50)
Scientific	Full, spelled-out scientific name. These names correspond to the values in	

Name the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr.

Periphyton Table (DT\$PERIPHY; [Periphyton])

This table holds the information about a sample taken by a particular gear. More than one gear may have been used to collect information at a particular station on a specific date and time. It is also possible that the same gear type was used more than once. There is one row entered in this table for each gear/qualquan that comprises an individual sample.

Oracle table name: DT\$PERIPHY

4D table name: [Periphyton]

Field	Required?	Description
PERIID	C	PK\$PERIID [Periphyton]PeriID System-generated code to represent this station/date/time/survey/collector/gear/qual (Oracle sequence S\$PERIPHY). Number(9) Real
SampleID	C	FK\$SAMPLEID [Periphyton]SampleID Represents the station/date/time/survey/collector for these data. Number(9) Real
DEP-assigned gear code	Y	FK\$GEAR [Periphyton]Gear The type of gear used to collect these periphyton (DEP-assigned code in sample gear reference table). Number(3) Real
Identifier	Y	AK\$IDENT [Periphyton]Ident The DEP code for the name in MT\$IDENT that was in charge of identifying the periphyton in the sample. Number(5) Real
Qualitative or Quantitative	Y	QUALQUAN [Periphyton]QualQuan 1 = sample was processed as quantitative sample 2 = sample was processed as qualitative sample Number(2) Real
Number of replicates	Y	NREPS [Periphyton]Nreps If replicate samplers were used, enter the number of replicates sampled; otherwise, enter the number 1. Number(2) Real
ID confidence level	Y	IDCONF [Periphyton]IDConf The level of confidence in the taxonomic identifications for this BenthID. This field is required by BIOS for every ID, but our system will assign a sample-specific level of confidence. The letter codes are what BIOS uses. Your entry screen will let you pick the level of confidence and will automatically insert the correct letter for it. The values are: 1 = 99.9 percent confidence (1 chance in 1000 of making an error); Number(2) Real

2 =	99.0	“	“	(1 chance in 100 of making an error);
3 =	90.0	“	“	(1 chance in 10 of making an error);
4 =	Percent confidence unknown.			

Gear Factor	Y	GEARFACTOR [Periphyton]GearFactor	Number(7,4) Real	The number of times the sampling gear was deployed to collect one replicate.
Diatom Proportion Status	Y	DIATOM [Periphyton]DiatomStatus	Number(2) Real	1 = no diatom proportions have ever been entered for this sample 2 = diatom proportions have been entered, but have not been incorporated 3 = diatom proportions were entered, and they have been incorporated
BIOS status	C	BIOSTAT [Periphyton]BIOSat	Number(2) Real	!!!These fields in these tables are unused. Their functions are addressed in dt\$sample and [Sample]!!!

The following fields are calculated after the sample is marked complete. They are calculated by pooling all the replicates for this PK\$PERIID, thus these are sample-specific values. There are no corresponding 4D fields in [Periphyton] for these pooled values. They are the variables most often requested in a retrieval and saving them here will result in faster retrievals. Note: Fields with an asterisk(*) are present but not calculated, as they are not appropriate for this data type.

Number of individuals counted in the sample	NINDC	Number(9)
Number of individuals per cm ²	NINDU	Number(14,2)
Number of taxa in this sample	NTAXA	Number(5)
*Florida Index	FLINDEX	Number(5)
*Lake Condition Index	LCINDEX	Number(5)
Shannon-Weaver Diversity Index	DBAR	Number(6,2)

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, date, owner group) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them in this table makes 4D run more efficiently.

STORET Station Name	[Periphyton]StoretName	Alpha(15)	The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.
Station Nickname	[Periphyton]StaNickname	Alpha(10)	The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.
Sample Date	[Periphyton]SampDate	Date	The date the sample was collected. It is stored in the Oracle table DT\$Sample.
Owner Group	[Periphyton]OwnGroup	Real	

The number of the group that enters these data. It is stored in the Oracle table DT\$Sample.

Periphyton Replicate Information Table (DT\$PERIREPS; [PeriReps])

This is information needed to calculate the number of individuals per cm² in DT\$PeriTaxa. There is one row in this table for each replicate of each pk\$periid.

Oracle table name: DT\$PERIREPS

4D table name: [PeriReps]

Field	Required?	Description
Unique ID for this rep	C	PK\$PERIREPID [PeriReps]PeriRepID Number(9) Real Computer-generated sequential number for this fk\$periid/replicate (Oracle sequence S\$PERIREPS).
PERIID	C	FK\$PERIID [PeriReps]PeriID Number(9) Real Represents the station/date/time/survey/collector/gear/qual for these data.
Replicate No.	Y	REPNUM [PeriReps]PeriID Number(2) Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Area scraped	Y	AREASCRAPE [PeriReps]AreaScraped Number(6) Real The area in mm ² of all slides (or other surface) scraped into this sample bottle.
Sample volume	Y	SAMPVOL [PeriReps]SampVol Number(7,1) Real The volume of sample resulting from scraping and rinsing of slides (or other collection material) and the original collection container, in mLs.
Dilution factor	Y	DILFACT [PeriReps]DilFact Number(3) Real A value used in the equation to account for the dilution of sample material. For example, if you took 1 mL of the original sample and added 3 mLs of DI water to it, the dilution factor to enter is 4 which came from 1 mL/(1 mL + 3 mLs), or a 1 in 4 solution.
Counting cell information		
Grid length	Y	GRIDLEN [PeriReps]GridLen Number(5,2) Real Length of one side of counting grid in mm.
Cell depth	Y	CELLDEPTH [PeriReps]CellDepth Number(4,1) Real Depth of counting cell in mm.

No. grids	Y	NBRGRIDS [PeriReps]NbrGrids Number of grids counted.	Number(3) Real
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Periphyton Taxa Table (DT\$PERITAXA; [PeriTaxa])

This table stores the individual taxa information for each replicate of each pk\$periid.

Oracle table name: DT\$PERITAXA

4D table name: [PeriTaxa]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$PERITAXARECID Number(9) [PeriTaxa]PeriTaxaRecID Real Computer-generated sequential number for this fk\$periid/replicate/taxon (Oracle sequence S\$PERITAXA).
PeriID	C	FK\$PERIID Number(9) [PeriTaxa]PeriID Real Represents the station/date/time/survey/collector/gear/qual for these data.
Replicate No.	Y	REPNUM Number(2) [PeriTaxa]RepNum Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Taxa Code	Y	FK\$TAXAID Number(10) [PeriTaxa]TaxaID Real The taxa code for this plant.
No. Cells	Y	NOIND Number(6) [PeriTaxa]NoInd Real The number of individual units of this taxa code that were counted.
No. Cells per cm ²	Y	NOINDCM2 Number(12,2) [PeriTaxa] NoIndSqCm Real For quantitative samples only, computer calculates this number of cells per cm ² by: <u>$(1000 \text{ mm}^3/\text{ml} * 100 \text{ mm}^2/\text{cm}^2 * \text{no. cells counted} * \text{sample vol} * \text{dilution})$</u> grid ² * cell depth * no. flds counted * area scraped

The following field is included in the 4D table.

Taxon Scientific Name	[PeriTaxa]SciName Alpha(50) Full, spelled-out scientific name. These names correspond to the values in the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr.
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Periphyton Diatom Proportion Table* (DT\$PERIDIATOM; [PeriDiatom])

Oracle table name: DT\$PERIDIATOM

4D table name: [PeriDiatom]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$PERIDIATOMID [PeriDiatom]PeriDiatomID Computer-generated sequential number for this fk\$periid/replicate/taxon (Oracle sequence S\$PERITAXA). Number(9) Real
PeriID	C	FK\$PERIID [PeriDiatom]PeriID System-generated code to represent this station/date/time/survey/collector/gear/qual. Number(9) Real
Replicate No.	Y	REPNUM [PeriDiatom]RepNum If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1. Number(2) Real
Taxa Code	Y	FK\$TAXAID [PeriDiatom]TaxaID The taxa code for this diatom. Number(10) Real
No. Cells	Y	NOIND [PeriDiatom]NoInd The number of diatoms of this taxa code that were counted. Number(6) Real

The following field is included in the 4D table.

Taxon Scientific Name	[PeriDiatom]SciName Full, spelled-out scientific name. These names correspond to the values in the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr. Alpha(50)
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* Data are stored in this table temporarily, and are deleted from here after they have been incorporated into the periphyton taxa table

Phytoplankton Table (DT\$PHYTOPL; [Phytoplankton])

This table holds the information about a sample taken by a particular gear. More than one gear may have been used to collect information at a particular station on a specific date and time. It is also possible that the same gear type was used more than once. There is one row entered in this table for each gear/qualquan that comprises an individual sample.

Oracle table name: DT\$PHYTOPL

4D table name: [Phytoplankton]

Field	Required?	Description
PHYTOID	C	PK\$PHYTOID [Phytoplankton]PhytoID System-generated code to represent this station/date/time/survey/collector/gear/qual (Oracle sequence S\$PHYTOPL). Number(9) Real
SampleID	C	FK\$SAMPLEID [Phytoplankton]SampleID Represents the station/date/time/survey/collector for these data. Number(9) Real
DEP-assigned gear code	Y	FK\$GEAR [Phytoplankton]Gear The type of gear used to collect these periphyton (DEP-assigned code in sample gear reference table). Number(3) Real
Identifier	Y	AK\$IDENT [Phytoplankton]Ident The DEP code for the name in MT\$IDENT that was in charge of identifying the phytoplankton in the sample. Number(5) Real
Qualitative or Quantitative	Y	QUALQUAN [Phytoplankton]QualQuan 1 = sample was processed as quantitative sample 2 = sample was processed as qualitative sample Number(2) Real
Number of replicates	Y	NREPS [Phytoplankton]Nreps If replicate samplers were used, enter the number of replicates sampled; otherwise, enter the number 1. Number(2) Real
ID confidence level	Y	IDCONF [Phytoplankton]IDConf The level of confidence in the taxonomic identifications for this BenthID. This field is required by BIOS for every ID, but our system will assign a sample-specific level of confidence. The letter codes are what BIOS uses. Your entry screen will let you pick the level of confidence and will automatically insert the correct letter for it. The values are: 1 = 99.9 percent confidence (1 chance in 1000 of making an error); 2 = 99.0 “ “ (1 chance in 100 of making an error); Number(2) Real

3 = 90.0 “ “ (1 chance in 10 of making an error);
4 = Percent confidence unknown.

Gear Factor	Y	GEARFACTOR [Phytoplankton]GearFactor	Number(7,4) Real	The number of times the sampling gear was deployed to collect one replicate.
Diatom Proportion Status	Y	DIATOM [Phytoplankton]DiatomStatus	Number(2) Real	1 = no diatom proportions have ever been entered for this sample 2 = diatom proportions have been entered, but have not been incorporated 3 = diatom proportions were entered, and they have been incorporated
BIOS status	C	BIOSAT [Phytoplankton]BIOSat	Number(2) Real	!!!These fields in these tables are unused. Their functions are addressed in dt\$sample and [Sample]!!!

The following fields are calculated after the sample is marked complete. They are calculated by pooling all the replicates for this PK\$PHYTOID, thus these are sample-specific values. There are no corresponding 4D fields in [Phytoplankton] for these pooled values. They are the variables most often requested in a retrieval and saving them here will result in faster retrievals. Note: Fields with an asterisk(*) are present but not calculated, as they are not appropriate for this data type.

Number of individuals counted in the sample	NINDC	Number(9)
Number of individuals per mL	NINDU	Number(14,2)
Number of taxa in this sample	NTAXA	Number(5)
*Florida Index	FLINDEX	Number(5)
*Lake Condition Index	LCINDEX	Number(5)
Shannon-Weaver Diversity Index	DBAR	Number(6,2)

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, date, owner group) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them in this table makes 4D run more efficiently.

STORET Station Name	[Phytoplankton]StoretName	Alpha(15)	The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.
Station Nickname	[Phytoplankton]StaNickname	Alpha(10)	The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.
Sample Date	[Phytoplankton]SampDate	Date	The date the sample was collected. It is stored in the Oracle table DT\$Sample.
Owner Group	[Phytoplankton]OwnGroup	Real	

The number of the group that enters these data. It is stored in the Oracle table DT\$Sample.

Phytoplankton Replicate Information Table (DT\$PHYTOREPS; [PhytoReps])

This is information needed to calculate the number of individuals per cm² in DT\$PhytoTaxa. There is one row in this table for each replicate of each pk\$phytoid.

Oracle table name: DT\$PHYTOREPS

4D table name: [PhytoReps]

Field	Required?	Description	
Unique ID for this rep	C	PK\$PHYTOREPID	Number(9)
		[PhytoReps]PhytoRepID	Real
		Computer-generated sequential number for this fk\$phytoid/replicate (Oracle sequence S\$PHYTOREPS).	
PHYTOID	C	FK\$PHYTOID	Number(9)
		[PhytoReps]PhytoID	Real
		Represents the station/date/time/survey/collector/gear/qual for these data.	
Replicate No.	Y	REPNUM	Number(2)
		[PhytoReps]RepNum	Real
		If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.	
Volume of water filtered or grabbed (mls)	Y	VOLCOLLECT	Number(8,1)
		[PhytoReps]VolCollect	Real
		The amount of water that passed through the net or in the grab sample. If it was a tow, have to calculate how much water went through the net according to the flowmeter directions or whatever is appropriate to the way the tow was done and the size of the net.	
Sample volume	Y	SAMPVOL	Number(7,1)
		[PhytoReps]SampVol	Real
		The volume of the sample after filtering (net samples) or concentrating (grab samples) in mLs.	
Dilution factor	Y	DILFACT	Number(3)
		[PhytoReps]DilFact	Real
		A value used in the equation to account for the dilution of sample material. For example, if you took 1 mL of the original sample and added 3 mLs of DI water to it, the dilution factor to enter is 4 which came from 1 mL/(1 mL + 3 mLs), or a 1 in 4 solution.	
Counting cell information			
Grid length	Y	GRIDLEN	Number(5,2)
		[PhytoReps]GridLen	Real
		Length of one side of counting grid in mm.	

Cell depth	Y	CELLDEPTH [PhytoReps]CellDepth Depth of counting cell in mm.	Number(4,1) Real
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No. grids	Y	NBRGRIDS	Number(3)
		NbrGrids	Real
		Number of grids counted.	

Phytoplankton Taxa Table (DT\$PHYTOTAXA; [PhytoTaxa])

This table stores the individual taxa information for each replicate of each pk\$PhytoId.

Oracle table name: DT\$PHYTOTAXA

4D table name: [PhytoTaxa]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$PHYTOTAXARECID Number(9) [PhytoTaxa]PhytoTaxaRecID Real Computer-generated sequential number for this fk\$phytoid/replicate/taxon (Oracle sequence S\$PHYTOTAXA).
PhytoID	C	FK\$PHYTOID Number(9) [PhytoTaxa]PhytoID Real Represents the station/date/time/survey/collector/gear/qual for these data.
Replicate No.	Y	REPNUM Number(2) [PhytoTaxa]RepNum Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Taxa Code	Y	FK\$TAXAID Number(10) [PhytoTaxa]TaxaID Real The taxa code for this plant.
No. Cells	Y	NOIND Number(6) [PhytoTaxa]TaxaID Real The number of cells of this taxa code that were counted in the subsample of this replicate.
No. Cells per mL	Y	NOINDCM2 Number(12,2) [PhytoTaxa]NoIndSqCm Real For quantitative samples only, computer calculates this number of cells per ml by: <u>(1000 mm³/ml * no. indiv counted * sample vol * dilution)</u> grid ² * cell depth * no. flds counted * vol filtered or grabbed

The following field is included in the 4D table.

Taxon Scientific Name	[PhytoTaxa]SciName Alpha(50) Full, spelled-out scientific name. These names correspond to the values in the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr.
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Phytoplankton Diatom Proportion Table (DT\$PHYTODIATOM; [PhytoDiatom])*

Oracle table name: DT\$PHYTODIATOM

4D table name: [PhytoDiatom]

Field	Required?	Description
Unique ID for this taxa entry	C	PK\$PHYTODIATOMID Number(9) PhytoDiatom]PhytoDiatomID Real Computer-generated sequential number for this fk\$phytoid/replicate/taxon (Oracle sequence S\$PHYTOTAXA).
PhytoID	C	FK\$PHYTOID Number(9) PhytoDiatom]PhytoID Real System-generated code to represent this station/date/time/survey/collector/gear/qual.
Replicate No.	Y	REPNUM Number(2) PhytoDiatom]RepNum Real If replicate samplers were used, enter the number of this replicate; otherwise, enter the number 1.
Taxa Code	Y	FK\$TAXAID Number(10) PhytoDiatom]TaxaID Real The taxa code for this diatom.
No. Cells	Y	NOIND Number(6) PhytoDiatom]NoInd Real The number of diatoms of this taxa code that were counted.

The following field is included in the 4D table.

Taxon Scientific Name	PhytoDiatom]SciName Alpha(50) Full, spelled-out scientific name. These names correspond to the values in the 4D field TaxaID. Scientific names are stored in the Oracle table ET\$TaxaMstr.
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* Data are stored in this table temporarily, and are deleted from here after they have been incorporated into the phytoplankton taxa table

Physical/Chemical Table (DT\$PCHEM; [Pchem])

This table holds the information about a physical/chemical samples taken at the same time and station as flora and/or fauna samples. There is one row entered in this table for each pk\$sampleid that had physical/chemical data recorded.

Oracle table name: DT\$PCHEM

4D table name: [Pchem]

Field	Required?	Description
PCHEMID	C	PK\$PCHEMID [Pchem]PchemID Number(9) Real System-generated code to represent this station/date/time/survey/collector/gear/qual (Oracle sequence S\$PCHEM).
SampleID	C	FK\$SAMPLEID [Pchem]SampleID Number(9) Real Represents the station/date/time/survey/collector for these data.
Number of depths sampled	Y	NBRDEPTHS [Pchem]NbrDepths Number(2) Real The number of different water depths where samples were taken.
BIOS status	C	BIOSSTAT [Pchem]BIOSStat Number(2) Real !!!These fields in these tables are unused. Their functions are addressed in dt\$sample and [Sample]!!!
Station water depth	N	STADEPTH [Pchem]StaDepth Number(5,1) Real Depth of the water in meters at this station.
Secchi	N	SECCHI [Pchem]Secchi Number(7,1) Real The secchi depth reading taken at this station, in meters.

The following fields are included in the 4D table. They represent attributes of components associated with the sample (station, date, owner group) and are displayed in various forms and spreadsheets within the 4D environment. They are also used in searches, so including them in this table makes 4D run more efficiently.

STORET Station Name	[Pchem]StoretName The STORET station code for the sample location. It is stored in the Oracle table ET\$Sta.	Alpha(15)
Station Nickname	[Pchem]StaNickname The ten character nickname for the station. It is stored in the Oracle table ET\$Sta.	Alpha(10)

Sample Date	[Pchem]SampDate	Date	The date the sample was collected. It is stored in the Oracle table DT\$Sample.
Owner Group	[Pchem]OwnGroup	Real	The number of the group that enters these data. It is stored in the Oracle table DT\$Sample.

Physical/Chemical Depth Table (DT\$PCHEMDEPTH; [PchemDepths])

This table describes each physical/chemical depth sampled.

Oracle table name: DT\$PCHEMDEPTH

4D table name: [PchemDepths]

Field	Required?	Description
Unique ID for this sample depth	C	PK\$PCDEPTHID [PchemDepths]PCDepthID Number(9) Real Computer-generated sequential number for this fk\$pchemid/replicate/sample depth (Oracle sequence S\$PCDEPTH).
PCHEMID	C	FK\$PCHEMID [PchemDepths]PchemID Number(9) Real Represents the station/date/time/survey/collector for these data.
Number of reps taken at this depth	Y	NBRREPS [PchemDepths]NbrReps Number(2) Real Number of replicate samples taken at this depth.
Depth	Y	SAMPDEPTH [PchemDepths]SampDepth Number(5,1) Real The depth (in meters) where this sample was taken. Enter zero for surface.

Physical/Chemical Depth Replicate Table (DT\$PCHEMREPS; [PchemReps])

These are parameters that may be stored for each station, date, and depth sampled.

Oracle table name: DT\$PCHEMREPS

4D table name: [PchemReps]

Field	Required?	Description
Unique ID for this sample depth	C	PK\$PCREPID [PchemReps]PCRepID Number(9) Real Computer-generated sequential number for this fk\$pchemid/replicate/sample depth (Oracle sequence S\$PCREPS).
PCDEPTHID	C	FK\$PCDEPTHID [PchemReps]PCDepthID Number(9) Real Represents the station/date/time/survey/collector/depth for these data.
Replicate No.	Y	REPNUM [PchemReps]RepNum Number(2) Real If replicates were done, enter the number of this replicate; otherwise, enter the number 1.

Parameters	4D Name	Oracle Name	STORET For- No.	mat	Min	Max	Units
algal growth potential	AlgGrow	ALGGROW	85209	6.1	0	0200.0	mg dry wt/L
alkalinity, total	Alkalinity	ALKALINITY	00410	4.0	0	300.	mg/L CaCO3
ammonia, dissolved	NH3Diss	NH3DISS	00608	7.3	0	010.000	mg/LN
ammonia, total	NH3Tot	NH3TOT	00610	7.3	0	010.000	mg/LN
ammonia, unionized	NH3Union	NH3UNION	00619	7.3	0	010.000	mg/LNH3
BOD, 5-day	BOD5	BOD5	00310	6.1	0	0100.0	mg/L
BOD, 20-day	BOD20	BOD20	00324	6.1	0	0100.0	mg/L
carbon, total organic	TOC	TOC	00680	5.1	0	100.0	mg/L C
chloride,dissolved	CLDiss	CLDISS	82295	9.3	0	50000.000	mg/L
chloride, total	CLTOT	CLTOT	00940	9.0	0	50000.	mg/L
chlorophyll-a,monochromatic, periphyton	CLaPeri	CLAPERI	32223	6.2	0	060.00	mg/m2
chlorophyll-a, monochromatic, water	CLaH2O	CLAH20	32211	6.2	0	050.00	µg/L
conductivity, field	CondFld	CONDFLD	00094	6.0	0	50000.	µmho/cm
conductivity, lab	CondLab	CONDLAB	00095	6.0	0	50000.	µmho/cm
D.O., non-probe	DOnon	DONON	00300	4.1	0	10.0	mg/L
D.O., probe	DOProbe	DOPROBE	00299	4.1	0	10.0	mg/L
enterococci, membrane filter	Enteroc	ENTEROC	02361	7.0	0	050000.	no./100ml
Escherichia coli, membrane filter	EColi	ECOLI	02360	7.0	0	050000.	no./100ml
fecal coliforms, membrane filter	FecalMem	FECALMEM	31616	7.0	0	050000.	no./100ml
fecal coliforms, multiple tube	FecalTube	FECALTUBE	31615	7.0	0	050000.	no./100ml
fecal Streptococcus, membrane filter	FecalStrep	FECALSTREP	31673	7.0	0	050000.	no./100ml
hardness, total	Hardness	HARDNESS	00900	6.0	0	10000.	mg/L CaCO3
nitrate, dissolved	NO3Diss	NO3DISS	00618	6.2	0	030.00	mg/L N
nitrate, total	NO3Tot	NO3TOT	00620	7.3	0	030.000	mg/LN
nitrite + nitrate, dissolved	NO3NO2Diss	NO3NO2DISS	00631	5.1	0	030.0	mg/LN
nitrite + nitrate, total	NO3NO2Tos	NO3NO2TOT	00630	6.2	0	030.00	mg/L N
nitrite, dissolved	NO2Diss	NO2DISS	00613	7.3	0	010.000	mg/LN
nitrite, total	NO2Tot	NO2TOT	00615	7.3	0	010.000	mg/LN
nitrogen, total (TKN+N02+N03)	TOTN	TOTN	00600	6.2	0	030.00	mg/L N
nitrogen, total Kjeldahl	TKN	TKN	00625	7.3	0	030.000	mg/L N
orthophosphate, dissolved	OPDiss	OPDISS	00671	6.3	0	01.000	mg/L P
orthophosphate, total	OPTot	OPTOT	70507	6.3	0	01.000	mg/L P
pH	pH	PH	00400	5.2	0	12.00	su
phaeophyton-a, monochromatic, periphyton	PhaeoPeri	PHAEOPERI	32224	6.2	0	060.00	mg/m2
phaeophyton-a, monochromatic, water	PhaeoH2O	PHAEOH20	32218	6.2	0	050.00	µg/L
phosphorus, total	PhosphTos	PHOSPTOT	00665	6.3	0	01.000	mg/L P
plate count, total	Plate	PLATE	31751	8.0	0	0100000.	no./ml
residue, dissolved	ResiDiss	RESIDISS	70300	6.0	0	50000.	mg/L
residue, total	ResidTot	RESIDTOT	00500	6.0	0	50000.	mg/L
residue, total nonfiltrable (TSS)	TSS	TSS	00530	5.0	0	0100.	mg/L
residue,total volatile	ResidVol	RESIDVOL	00505	5.0	0	0100.	mg/L
residue, volatile nonfiltrable	ResidVNon	RESIDVNON	00535	5.0	0	0100.	mg/L
salinity	Salinity	SALINITY	00480	4.1	0	35.0	ppt
sediment prtcl size, 0.063-0.125mm	Seds1	SEDS1	80251	6.2	0	100.00	%
sediment prtcl size, 0.125-0.25mm	Seds2	SEDS2	80252	6.2	0	100.00	%
sediment prtcl size, 0.25-0.5mm	Seds3	SEDS3	80253	6.2	0	100.00	%
sediment prtcl size, 0.5-2.0mm	Seds4	SEDS4	80254	6.2	0	100.00	%
sediment prtcl size, <0.063mm	Seds5	SEDS5	80250	6.2	0	100.00	%
sediment prtcl size, >2.0mm	Seds6	SEDS6	80256	6.2	0	100.00	%
sediment, organic fraction	SedOrg	SEDORG	80096	6.2	0	100.00	%
silica, dissolved	SilicaDiss	SILICADISS	00955	5.1	0	020.0	mg/L SiO3
silica, total	SilicaTot	SILICATOT	00956	5.1	0	020.0	mg/L SiO3
sulfate, dissolved	SO4Diss	SO4DISS	00946	7.1	0	05000.0	mg/L SO4
sulfate, total	SO4Tot	SO4TOT	00945	6.0	0	05000.	mg/L SO4

water temperature	Temp	TEMP	00010	4.1	0	40.0	°C
tidal stage (high or low)	Tide	TIDE	70211char 2	H=High tide, L=Low tide, U=Unknown			

Parameters	4D Name	Oracle Name	STORET For- No.	mat	Min	Max	Units
tidal shift(before or after)	TidePhase	TIDEPHASE	70211char 2	B=Before tide, A=After tide, U=Unknown			
tidal time adjustment	TideHours	TIDEHRS	70211	2.0HH	(hours, before or after, high or low tide)		
	TideMins	TIDEMINS	70211	2.0MM	(minutes, before or after, high or low)		
total coliforms, membrane filter	ColiMem	COLIMEM	31501	7.0	0	050000.	no./100ml
total coliforms, multiple tube	ColiTube	COLITUBE	31505	7.0	0	050000.	no./100ml
turbidity	Turbidity	TURBIDITY	82079	6.1	0	0200.0	ntu
velocity, stream	Velocity	VELOCITY	00055	3.1	0	1.0	ft/sec

The following variables are 1 if the variable is below detection limit; 0 otherwise. They are not STORET parameters, so do not have a STORET parameter number.

Parameters	4D Name	Oracle Name	For- mat	Min	Max
ammonia, dissolved	BDLNH3Diss	BDLNH3DISS	F1	0	1
ammonia, total	BDLNH3Tot	BDLNH3TOT	F1	0	1
ammonia, unionized	BDLNH3Union	BDLNH3UNION	F1	0	1
nitrate, dissolved	BDLNO3Diss	BDLNO3DISS	F1	0	1
nitrate, total	BDLNO3Tot	BDLNO3TOT	F1	0	1
nitrite, dissolved	BDLNO2Diss	BDLNO2DISS	F1	0	1
nitrite, total	BDLNO2Tot	BDLNO2TOT	F1	0	1
nitrite + nitrate, dissolved	BDLNO3NO2Diss	BDLNO3NO2DISS	F1	0	1
nitrite + nitrate, total	BDLNO3NO2Tot	BDLNO3NO2TOT	F1	0	1
nitrogen, total (TKN+N02+N03)	BDLTotN	BDLTOTN	F1	0	1
nitrogen, total Kjeldahl	BDLTKN	BDLTKN	F1	0	1
orthophosphate, dissolved	BDLOPDiss	BDLOPDISS	F1	0	1
orthophosphate, total	BDLOPTot	BDLOPTOT	F1	0	1
phosphorus, total	BDLPhospTot	BDLPHOSPOT	F1	0	1
chlorophyll-a,monochromatic, periphyton	BDLCLaPeri	BDLCLAPERI	F1	0	1
chlorophyll-a, monochromatic, water	BDLCLaH2O	BDLCLAH2O	F1	0	1
phaeophyton-a, monochromatic, periphyton	BDLhaeoPeri	BDLPHAEOPERI	F1	0	1
phaeophyton-a, monochromatic, water	BDLPHAEOH2O	BDLPhaeoH2O	F1	0	1

The following variables are 1 if the variable is too numerous to count; 0 otherwise. They are not STORET parameters, so do not have a STORET parameter number.

Parameters	4D Name	Oracle Name	For- mat	Min	Max
enterococci, membrane filter	TNTCEnteroc	TNTCENTEROC	F1	0	1
Escherichia coli, membrane filter	TNTCEColi	TNTCECOLI	F1	0	1
fecal coliforms, membrane filter	TNTCFecalMem	TNTCFECALMEM	F1	0	1
fecal coliforms, multiple tube	TNTCFecalTube	TNTCFECALTUBE	F1	0	1
fecal Streptococcus, membrane filter	TNTCFecalStrep	TNTCFECALSTREP	F1	0	1
total coliforms, membrane filter	TNTCColeMem	TNTCCOLIMEM	F1	0	1
total coliforms, multiple tube	TNTCColiTube	TNTCCOLITUBE	F1	0	1
plate count, total	TNTCPlate	TNTCPLATE	F1	0	1

The following field is included in the 4D table.

Sample Depth	[PchemReps]SampDepth	Real
	The depth where this sample was collected. It is stored in the Oracle table DT\$PCHEMDEPTH.	

The following field is included in the Oracle table.

Tide Time	TIDETIME	Varchar2(5)
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The time (HH:MM) of occurrence of the tidal stage entered. This text version of the time is built from the [TideHours] and [TimeMins] fields.

Toxicological Database

Toxicity Sample Table (T\$TOXSAMPLE; [ToxSample])

This table describes a sample collected for toxicological assays, i.e., what was sampled at a particular location (station) on a specific date, at a specific time. Note: **bolded** items in the table make up the primary key.

Oracle table name: T\$TOXSAMPLE

4D table name: [ToxSample]

Y = required field

N = optional field

C = computer will keep track of this field

Field	Required?	Description
DEP-assigned Tox sample ID	C	PK\$TOXID [ToxSample]ToxID Number(7) Real A unique, sequential number assigned when the sample is added to the database. This number is the primary key for this table, created by Oracle sequence S\$ID_TOX.
Facility Used Code	C	FK\$FACILITY_USED [ToxSample]FacilityID Number(7) Real The sequential number assigned to a particular name of a facility. A facility (FK\$Facility) may have more than one name (FK\$Facility_Used) in table MT\$Facility_Tox.
Sample Date	Y	SAMPDATE [ToxSample]SampDate Date Date The date (month/day/year) the sample was collected.
Sample Time	Y	SAMPTIME [ToxSample]SampTime Varchar2(5) Time The time (hour and minutes) the sample was collected.
Sample Complete?	C	SAMPCOMPLETE [ToxSample]SampComplete Varchar2(2) Alpha(2) Are all data entered & verified for this sample? If the value is "Y", the data are available for retrieval and may not be edited; if "N", the data may still be edited. A sample cannot be marked complete if any of the fields that refer to reference tables have values that have not been "accepted" by the database administrator. A complete sample can be marked "N" by the database administrator if later editing is needed.
Group ID	C	AK\$GROUPID [ToxSample]OwnGroup Number(2) Real The user group that entered (and owns) this sample. The groups are stored in table MT\$UserGroup.

Sample Type 1	Y	FK\$TOXSAMPTYPE [ToxSample]ToxSampTypeID	Number(3) Real
Sample Type 2	N	FK\$TOXSAMPTYPE2 [ToxSample]ToxSampTypeID2	Number(3) Longint
Sample Type 3	N	FK\$TOXSAMPTYPE3 [ToxSample]ToxSampTypeID3	Number(3) Longint Describes the sample's physical characteristics (effluent, sediment, surface water, etc) and the type of sample (sanitary sewage, landfill leachate, process water); allow up to 3 choices per sample. The lookup table for the names of the sample types is MT\$SampType_Tox (key is PK\$ToxSampType).
Facility Type	Y	FK\$FACILITY_TYPE [ToxSample]Facility_type	Number(2) Longint Describes the type of facility (chemical plant, power plant, etc.); only one choice per sample. The lookup table for the names of the facility types is MT\$FacilityType_Tox (key is PK\$Facility_Type).
NPDES Number	Y	FK\$NPDES [ToxSample]NPDESnum	Varchar2(9) Alpha(9) NPDES number (9 chars) for a sampling point. If you know an NPDES number, you know the waterbody, sample loc detail, sample county. The lookup table for the NPDES information is MT\$NPDES_Tox (key is PK\$NPDES).
Sample County	C*	FK\$\$CTYNO County [ToxSample]CountyName	Number(3) Real Alpha(20) The county where the sample was taken. The lookup table for county information is MT\$County_Loc (key is PK\$Ctyno). * If "No NPDES Number" is entered, the user must enter the county information.
Station	N	FK\$\$STAID [ToxSample] [StaID] [ToxSample]StoretName [ToxSample]StaNickName	Number(7) Real Alpha(20) Alpha(20) The ID of the station in ET\$STA (key is PK\$StaID); allows access to STORET number (PK\$STA), Station nickname (STANICKNAME) and other station information for sample site.
Contact Person	Y	CONTACT_PERSON [ToxSample]Contact_Person	Varchar2(20) Alpha(20) The person who knows how the sample was taken.
Waterbody	C*	AK\$WATERBODY [ToxSample]WaterbodyID [ToxSample]WaterName	Number(5) Real Alpha(50)

Receiving waterbody - First named waterbody that receives flow from sample site (see note about NPDES numbers). The lookup table for waterbody information is MT\$Waterbody_Storet (key is PK\$Waterbody).
 * If “No NPDES Number” is entered, the user must enter the county information.

Sample location detail	N	SAMPLOC [ToxSample]SampLoc	Varchar2(80) Alpha(80)	80 character description of the site where the sample was taken.
Sample comment	N	SAMP_COMMENT [ToxSample]Samp_Comment	Varchar2(80) Alpha(80)	80 characters for any other comments regarding the taking of the sample.
Toxicity?	Y	TOX_FOUND [ToxSample]Tox_Found	Varchar2(1) Alpha(2)	Was toxicity found? Values are “Y”, “N”, “D” for Yes, No, “Don’t know” (when sample is marked complete, this field must be yes or no).
Toxicity Cause	N	FK\$TOXCAUSE [ToxSample]Tox_Cause	Number(2) Real	Possible causes of toxicity (scroll field that shows stock choices, but need to allow additions to the stock list (MT\$ToxCause); a given sample may have more than one cause - allow for 5).
LIMS Sample/ Job Number	Y	LIMSNUM [ToxSample]LIMSnum	Varchar2(17) Alpha(17)	LIMS sample/job number in this format: “94-NOV-23-###-###”. It will probably be changed to the 6 digit sample ID used in LIMS. The work is in progress.

The following fields are included in the 4D table.

Facility Name	[ToxSample]FacilityName	Alpha(50)	The name of the facility associated with FK\$FACILITY_USED. It is filled automatically when the user enters the NPDES number.
Time (text)	[ToxSample]TextTime	Alpha(5)	The sample time in text form.

Bioassay Table (DT\$BIOASSAY; [Bioassay])

This table contains information on individual bioassays associated with a toxicological sample, described in T\$TOXSAMPLE. Note: **bolded** items in the table make up the primary key.

Oracle table name: DT\$BIOASSAY

4D table name: [Bioassay]

Y = required field

N = optional field

C = computer will keep track of this field

Field	Required?	Description
DEP-assigned test ID	C	PK\$TOXTEST Number(7) [Bioassay]ToxTestID Real A unique, sequential number assigned when the test is added to the database. This number is the primary key for an individual test; created by Oracle sequence S\$ID_TOXTEST.
Toxicity Sample ID	C	FK\$TOXID Number(7) [Bioassay]ToxID Real Foreign key that points to the appropriate PK\$ToxID in T\$ToxSample for this test.
Test Organism Code	Y	AK\$TESTORG Number(3) [Bioassay]TestOrgID Real Test organism - the primary key of the scientific name of the animal or plant used in the test.
Test type part 1	Y	TEST_PT1 Number(1) [Bioassay]Test_Pt1 Real Static nonrenewal, Static renewal, Flowthrough
Test type part 2	Y	TEST_PT2 Number(1) [Bioassay]Test_Pt2 Real Acute, Chronic
Test unit	Y	TESTUNIT Number(1) [Bioassay]TestUnit Integer The units for the amount of time the test lasted (hours, days, weeks).
Test duration	Y	TESTDURATION Number(3) [Bioassay]TestDuration Real The number of units that the test lasted (24,48,72,96).
Test type part 3	Y	TEST_PT3 Number(1) [Bioassay]Test_Pt3 Real Definitive, Screen
Chlorination	Y	CHLORINATION Number(1)

[Bioassay]Chlorination Integer
Chlorinated, Dechlorinated, Unchlorinated (display in this order)

Result category	Y	RESULT_CAT [Bioassay]Result_Cat 1=st, 2=nt, 3=tox; Pick from popup but show definitions. st = ">20% & ≤ 50% mortality" nt = "LC50 > 300 or < 20% mortality" tox = "LC50 <100% or mortality > 50%"	Number(1) Integer
Percent mortality	Y	PCT_MORT [Bioassay]Pct_Mort The percent mortality in highest concentration.	Number(5,1) Real
Salinity adjusted	Y	SAL_ADJ [Bioassay]Sal_Adj Was the sample salinity adjusted?(Y=yes, N=no, P=not applicable).	Varchar2(1) Integer
pH- adjusted	Y	PH_ADJ [Bioassay]pH_Adj Was the sample pH adjusted?(Y=yes, N=no, P=not applicable).	Varchar2(1) Integer
LC50	N	LC50 [Bioassay]LC50 The calculated LC50 for the test (format _ _ _).	Number(5,1) Real
LC50 Calc Method	N	LC50_CALC [Bioassay]LC50_Calc The calculation method used for the LC50.	Number(2) Real
IC20	N	IC20 [Bioassay]IC20 The calculated IC20 for the test (format _ _ _ . _).	Number(5,1) Real
NOEC	N	NOEC [Bioassay]NOEC The calculated NOEC for the test (format _ _ _ . _).	Number(6,2) Real
LOEC	N	LOEC [Bioassay]LOEC The calculated LOEC for the test (format _ _ _ . _).	Number(6,2) Real
NOEC/LOEC Calc Method	N	NLOEC_CALC [Bioassay]NLOEC_Calc The calculation method used for the NOEC or LOEC.	Number(2) Real
Diluent	Y	DILUENT [Bioassay]Diluent Well water, NSW (natural seawater), ASW (artificial seawater), 20% MW (mineral water), DEP well water, and receiving body water. More diluents may be added to this list.	Number(2) Real
Test	N	TEST_COMMENT	Varchar2(250)

Comments

[Bioassay]Test_Comment

Text

A 250 character field for any comments about the actual test.

The following fields are chemistry values for the sample as it was at the beginning of the test (i.e., after adjustments were made). LIMS comment codes are used for these pchem “code” fields.

pH	Y	PH [Bioassay]pH	Number(4,1) Real	The pH of the sample as it was at the beginning of the test (only one number allowed; can be blank; no >, <, or other symbols).
pH codes	N	PH_CODE [Bioassay]pH	Varchar2(15) Alpha(15)	Comment codes for the pH as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).
Conductivity (µmhos/cm)	Y	COND [Bioassay]Cond	Number(6) Real	The conductivity of the sample as it was at the beginning of the test.
Conductivity codes	N	COND_CODE [Bioassay]Cond_Code	Varchar2(15) Alpha(15)	Comment codes for the conductivity as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).
Alkalinity (mg/L)	Y	ALKALINITY [Bioassay]Alkalinity	Number(4) Real	The alkalinity of the sample as it was at the beginning of the test.
Alkalinity codes	N	ALKALINITY_CODE [Bioassay]Alkalinity_Code	Varchar2(15) Alpha(15)	Comment codes for the alkalinity as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).
Hardness (mg/L)	N	HARDNESS [Bioassay]Cond	Number(6) Real	The hardness of the sample as it was at the beginning of the test (should just be a number; will have to remove letters and “>”).
Hardness codes	N	HARDNESS_CODE [Bioassay]Hardness_Code	Varchar2(15) Alpha(15)	Comment codes for the hardness as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).
Total Ammonia (mg/L NH ₃)	Y	NH3TOT [Bioassay]NH3TOT	Number(7,3) Real	The total ammonia in a sample as it was at the beginning of the test (need to remove “<”).
Total Ammonia codes	N	NH3TOT_CODE [Bioassay]NH3TOT_Code	Varchar2(15) Alpha(15)	

Comment codes for the total ammonia as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).

Unionized Ammonia (mg/L N)	Y	NH3UNION [Bioassay]NH3Union	Number(7,3) Real	The unionized ammonia in the sample as it was at the beginning of the test (need to remove "<").
Unionized Ammonia codes	N	NH3UNION_CODE [Bioassay]NH3Union_Code	Varchar2(15) Alpha(15)	Comment codes for the unionized ammonia as it was at the beginning of the test; up to 5 codes may be entered, separated by commas (15 chars).

The following fields are included in the 4D table. They are the alphanumeric expressions associated with numeric codes in other fields and are used to populate various pull-down menus.

pH Adjustment		[Bioassay]pHAdjName	Alpha(3)	The choice list to indicate whether the sample was pH adjusted. The corresponding code is stored in the Oracle field PH_ADJ.
Salinity Adjustment		[Bioassay]SalAdjName	Alpha(3)	The choice list to indicate whether the sample was salinity adjusted. The corresponding code is stored in the Oracle field SAL_ADJ.
LC50 Calc Method Name		[Bioassay]LC50_CalcName	Alpha(30)	The choice list to indicate method of LC50 calculation. The corresponding code is stored in the Oracle field LC50_CALC.
NLOEC Calc Method Name		[Bioassay]NLOEC_CalcName	Alpha(30)	The choice list to indicate method of NOEC or LOEC calculation. The corresponding code is stored in the Oracle field NLOEC_CALC.
Test Name		[Bioassay]TestName	Alpha(50)	This field represents a list of test names, formed by the concatenation of test type parts 1, 2, and 3 above. It is used for a display on the toxicity sample setup form.
Test Unit Name		[Bioassay]TestUnitName	Alpha(7)	The choice list to indicate the units for the amount of time the test lasted (hours, days, weeks). The corresponding code is stored in the Oracle table TESTUNIT.
Chlorination		[Bioassay]ChlorName	Alpha(13)	The choice list to indicate whether the test was chlorinated, dechlorinated, or unchlorinated. The corresponding code is stored in the Oracle table CHLORINATION.

Toxicity Sample Phys/Chem Table (DT\$TOXSAMPCHEM; [ToxChem])

This table contains information on the physical/chemical parameters associated with a toxicological sample, described in T\$TOXSAMPLE.

Oracle table name: DT\$TOXSAMPCHEM

4D table name: [ToxChem]

Field	Required?	Description
Phys/Chem Value ID	C	PK\$TOXCHEMID Number(7) [ToxChem]ToxChemID Real A unique, sequential number assigned when the phys/chem measurement is added to the database (Oracle sequence S\$TOXSAMPCHEM). This number identifies the sample/bioassay/value.
Toxicity Sample ID	C	FK\$TOXID Number(7) [ToxChem]ToxID Real Foreign key that points to the appropriate PK\$TOXID in T\$TOXSAMPLE for this test.
Toxicity Parameter ID	C	FK\$TOXID Number(3) [ToxChem]ParamID Real Foreign key that points to the appropriate PK\$PARAMID in MT\$PARAM_BIO for this parameter.
Parameter Value	Y	PARAMVALUE Float(63) [ToxChem]ParamValue Real The actual measurement of the parameter.
Data Qualifier Code	N	LIMSQUAL Varchar2(15) [ToxChem]LIMSQual Alpha(15) The data qualifier code for the measurement, if any. There can be up to 5 qualifier codes, separated by commas.

Work Tables

These are tables used during retrieval and other maintenance activities. The contents of many of the tables (ET\$RETNWORK, ET\$RETNWORK1, ET\$PCWORK, ET\$DBAR, [DBAInfo], [RetrInfo], [TaxaFileStats], [TaxaList], and [TaxaWork]) are emptied when the retrieval is done. Some tables ([DateGrps], [DatePhrase]) are not emptied, but overwritten when they are used again in a subsequent retrieval. MT\$LOGTABLE holds log, ln, and log₂ values to use during diversity calculations. This is necessary because Oracle does not have a log function.

Animal Table ([Animal])

This table holds the current version of the Florida animal taxa list. The table contents are updated (downloaded from Oracle) at logon if the revision date has been changed by the database administrator, or at the user's request. Taxa related functions (data entry and taxa maintenance) use the information in this 4D table instead of the master taxa table in Oracle (ET\$TAXAMSTR), which makes the program more efficient.

4D table name: [Animal]

Field	Description	
TaxaID Code	[Animal]TaxaId	Real
	A sequential computer-generated identifier for this scientific name. Any name < 10,000,000 came from the BIOS system meaning that the name came on the original BIOS taxonomic list; any number larger was generated at DEP. It has nothing to do with the phylogeny of the organism.	
Phylum	[Animal]Phylum	Alpha(2)
	The phylum of the taxon.	
Class	[Animal]Class	Alpha(2)
	The class of the taxon.	
Order	[Animal]Order	Alpha(2)
	The order of the taxon.	
Family	[Animal]Family	Alpha(3)
	The family of the taxon.	
Genus	[Animal]Genus	Alpha(3)
	The genus of the taxon.	
Species	[Animal]Species	Alpha(3)
	The species of the taxon.	
Variety	[Animal]Variety	Alpha(2)
	The variety of the taxon.	
Scientific name	[Animal]SciName	Alpha(50)

Full, spelled-out scientific name (e.g. *Mediomastus ambiseta*).

Entered in System by	[Animal]EntBy	Alpha(5)	Username of the person who initially made this entry into the table (up to 5 characters).
On BIOS?	[Animal]Bios	Alpha(2)	Y= This scientific name is on the BIOS list; N = not on BIOS list; U = don't know (it could have been added at DEP, but was added to BIOS after the most recent list we have)
Range	[Animal]Range	Alpha(2)	1 = Range unchecked, authoritatively checked taxa 2 = Range not in Florida, authoritatively checked taxa 3 = Range includes Florida, authoritatively checked taxa 4 = Range may include Florida, authoritatively checked taxa 5 = Unchecked taxa (will never be on BIOS) 6 = Numbered taxa (will never be on BIOS) 7 = Not in Florida, but needs to be on Florida list
Florida Index	[Animal]FlaIndex	Alpha(2)	The number of Florida Index points for the taxon.
Lake Condition Index	[Animal]LakeIndx	Alpha(2)	The number of Lake Condition Index points for the taxon.
FFG Code	[Animal]FFGrp	Alpha(2)	The code for the taxon's feeding strategy.
Phylogenetic Category	[Animal]PhylCat	Real	1=Phylum; 2=Class; 3=Order; 4=Family; 5=Genus; 6=Species; 7=Variety.
Revision Status	[Animal]Revision	Alpha(2)	May be an "S" or null. "S" means that this is a synonym for another name on the list . A null in this field means that this is the most accepted version of this name. A synonym and its more accepted name will have identical values in PHYLO.
Master List Status?	[Animal]MstrStatus	Real	1=Yes, on master list; 0=No, not on master list
Florida List	[Animal]FlaList	Real	1=Yes, on Florida list (i.e., this is a taxon found in Florida); 0=No, not on Florida list.
Parent TaxaID	[Animal]PTaxaid	Real	The TaxaID of the immediate parent of this entry. The parent must be in a major taxonomic category like phylum, class, order, family, genus, or species.

Immediate Parent TaxaID	[Animal]IPTaxaid Not used now. See note for this field in the description for 4D table [MasterTaxa].	Real
Kingdom	[Animal]Kingdom 1 = Plant; 2 = Animal.	Real

Database Administrator Information Table ([DBAInfo])

This table holds information about the number of changes to selected Oracle tables and which users made the changes. It is used by the “DBA Sample Report” routine.

4D table name: [DBAInfo]

Field	Description
User Name	[DBAInfo]UserName Alpha(15) The name of the user updating the table.
Table Name	[DBAInfo]TableName Alpha(20) The name of the table updated.
Number of Changes	[DBAInfo]Count Real The number of changes made to a table by a particular user for the time period entered in the “DBA Sample Report” routine.

Date Group Table ([DateGrps])

This table is used to define custom date groups during the “Retrieve by Station and Date” routine.

4D table name: [DateGrps]

Field	Description
Group Name	[DateGrps]GroupName Alpha(10) The name of the group.
Date	[DateGrps]MonYr Alpha(5) The individual dates in the group (MM/YY).

Date Phrase Table ([DatePhrase])

When custom date groups are defined during the “Retrieve by Station and Date” routine, this table holds information used by the program to construct a date phrase to be inserted into the “where” portion of the sql statement to Oracle.

4D table name: [DatePhrase]

Field	Description
Date Index	[DatePhrase]DateIndex Integer A number assigned to the date phrase when it is created.
Date Phrase	[DatePhrase]DateWhere Text The actual date phrase.
Date Group	[DatePhrase]DateLabel Alpha(20)

Name

The name of the custom date group.

Table Information Table ([FileInfo])

This table holds information about 4D tables (called files in a previous version of 4D). This information is used for various select, insert, and update commands for moving data from 4D to Oracle tables, and for import and export of table information.

4D table name: [FileInfo]

Field	Description	
4D Table Name	[FileInfo]TableName4D The name of the 4D table.	Alpha(15)
Oracle Table Name	[FileInfo]TableNameOra The name of the Oracle table. If there is no corresponding Oracle table, “not used for oracle” is indicated.	Alpha(25)
Column Information	[FileInfo]ColumnInfo This field is a subtable with the following subfields:	Subtable
4D Column Name	ColumnName4D The name of the 4D column in [FileInfo]TableName4D	Alpha(15)
Oracle Column Name	ColumnNameOra The name of the Oracle column in [FileInfo]TableNameOra. If there is no corresponding Oracle table, the name of the 4D column is repeated in this subfield.	Alpha(15)
Include Column?	IncludeColumn Used in the PhysChem section in the biological database, for the building of sql statements in generic routines. If the column name can appear “as is” in a sql statement, it is marked “Y” in this column.	Boolean
Key Column?	KeyColumn Indicates whether or not the column is the primary key in the Oracle table.	Boolean
Empty on Quit?	EmptyOnQuit Indicates whether or not the table should be emptied when the user logs off.	Boolean

Log Table (MT\$LOGTABLE)

This table is needed since Oracle does not have any kind of log function and logs of proportions between 0 and 1.0 are needed to calculate diversity. At this time (January 1999) there are 10,000 entries in this table with log values for numbers from .0001 to 1.0000.

Oracle table name: MT\$LOGTABLE

Field	Description	
Proportion	FINDNBR	Number(8,6)
	The proportion for which a log value is needed.	
Natural log	LN	Number(9,6)
	The natural logarithm (log base e) of FINDNBR.	
Log ₁₀	LOG	Number(9,6)
	Log base 10 of FINDNBR.	
Log ₂	LOG2	Number(9,6)
	Log base 2 of FINDNBR.	

Physical/Chemical Calculation Work Table (ET\$PCWork)

This table is defined exactly like DT\$PCHEMREPS and is used during retrieval to store data during interim calculations.

Oracle table name: DT\$PCWork

Physical/Chemical Variable Work Table ([PCOracle])

This table holds information on which physical/chemical measurements have been selected for a retrieval, and whether a measurement may be labeled “BDL” (Below Detection Limit) or “TNTC” (Too Numerous to Count). It is used by routines in “Retrieve by Station and Date”, as well as import and maintenance functions.

4D table name: [PCOracle]

Field	Required?	Description
Variable Number		VarNum Integer A sequential number assigned to a phys/chem variable when it is entered in the table.
Variable Name		VarName Alpha(20) The name of the variable.
Included?		VarCk Boolean Indicates whether the variable was selected in the last retrieval.
TNTC		TNTC Boolean Indicates whether the variable can be labeled TNTC (too numerous to count).
BDL		BDL Boolean Indicates whether the variable can be labeled BDL (below detection limit).

Plant Table ([Plant])

This table holds the current version of the Florida plant taxa list. The table contents are updated (downloaded from Oracle) at logon if the revision date has been changed by the database administrator, or at the user's request. Taxa related functions (data entry and taxa maintenance) use the information in this 4D table instead of the master taxa table in Oracle (ET\$TAXAMSTR), which makes the program more efficient.

4D table name: [Plant]

Field	Description	
TaxaID Code	[Plant]TaxaId	Real
	A sequential computer-generated identifier for this scientific name. Any name < 10,000,000 came from the BIOS system meaning that the name came on the original BIOS taxonomic list; any number larger was generated at DEP. It has nothing to do with the phylogeny of the organism.	
Phylum	[Plant]Phylum	Alpha(2)
	The phylum of the taxon.	
Class	[Plant]Class	Alpha(2)
	The class of the taxon.	
Order	[Plant]Order	Alpha(2)
	The order of the taxon.	
Family	[Plant]Family	Alpha(3)
	The family of the taxon.	
Genus	[Plant]Genus	Alpha(3)
	The genus of the taxon.	
Species	[Plant]Species	Alpha(3)
	The species of the taxon.	
Variety	[Plant]Variety	Alpha(2)
	The variety of the taxon.	
Scientific name	[Plant]SciName	Alpha(50)
	Full, spelled-out scientific name (e.g. <i>Gomphonema parvulum</i>).	
Entered in System by	[Plant]EntBy	Alpha(5)
	Username of the person who initially made this entry into the table (up to 5 characters).	
On BIOS?	[Plant]Bios	Alpha(2)
	Y= This scientific name is on the BIOS list; N = not on BIOS list; U = don't know (it could have been added at DEP, but was added to BIOS after the most recent list we have)	

Range	[Plant]Range	Alpha(2)	1 = Range unchecked, authoritatively checked taxa 2 = Range not in Florida, authoritatively checked taxa 3 = Range includes Florida, authoritatively checked taxa 4 = Range may include Florida, authoritatively checked taxa 5 = Unchecked taxa (will never be on BIOS) 6 = Numbered taxa (will never be on BIOS) 7 = Not in Florida, but needs to be on Florida list
Florida Index	[Plant]FlaIndex	Alpha(2)	The number of Florida Index points for the taxon.
Lake Condition Index	[Plant]LakeIndx	Alpha(2)	The number of Lake Condition Index points for the taxon.
FFG Code	[Plant]FFGrp	Alpha(2)	The code for the taxon's feeding strategy.
Phylogenetic Category	[Plant]PhylCat	Real	1=Phylum; 2=Class; 3=Order; 4=Family; 5=Genus; 6=Species; 7=Variety.
Revision Status	[Plant]Revision	Alpha(2)	May be an "S" or null. "S" means that this is a synonym for another name on the list . A null in this field means that this is the most accepted version of this name. A synonym and its more accepted name will have identical values in PHYLO.
Master List Status?	[Plant]MstrStatus	Real	1=Yes, on master list; 0=No, not on master list
Florida List	[Plant]FlaList	Real	1=Yes, on Florida list (i.e., this is a taxon found in Florida); 0=No, not on Florida list.
Parent TaxaID	[Plant]PTaxaid	Real	The TaxaID of the immediate parent of this entry. The parent must be in a major taxonomic category like phylum, class, order, family, genus, or species.
Immediate Parent TaxaID	[Plant]IPTaxaid	Real	Not used now. See note for this field in the description for 4D table [MasterTaxa].
Kingdom	[Plant]Kingdom	Real	1 = Plant; 2 = Animal.

Retrieval Information Table ([RetrInfo])

This table holds biological sample information. It is used by the routines that execute the “What’s Been Sampled?” function that allows the user to retrieve a list of samples in the biological database by county, station level (waterbody type), station, and waterbody name.

4D table name: [RetrInfo]

Field	Required?	Description
Sample ID		[RetrInfo]Sampleid Longint Computer-generated sequential number to uniquely identify the sample (station/date/time/survey/collector).
Storet Station Name		[RetrInfo]StaStoret Alpha(15) STORET station code for the sample location.
Station Nickname		[RetrInfo]StaNickname Alpha(10) 10 character “nickname” for the station.
Sample Date		[RetrInfo]SampDate Date Date the sample was taken.
Sample Gear		[RetrInfo]GearName Alpha(10) Name of the gear used to collect the sample.
County		[RetrInfo]CountyName Alpha(15) County where the sample was collected.
Benthos Status		[RetrInfo]StBen Real Indicates whether benthos data were collected.
Periphyton Status		[RetrInfo]StPeri Real Indicates whether periphyton data were collected.
Phytoplankton Status		[RetrInfo]StPhyto Real Indicates whether phytoplankton data were collected.
Zooplankton Status		[RetrInfo]StZoo Real Indicates whether zooplankton data were collected.
Phys/Chem Status		[RetrInfo]StPC Real Indicates whether physical/chemical data were collected.
Waterbody		[RetrInfo]WaterName Alpha(50) The name of the waterbody where the sample was collected.
Benthos Status Display		[RetrInfo]DispBen Alpha(2) Displays “Y” or “N”, depending on the benthos status.
Periphyton Status Display		[RetrInfo]DispPeri Alpha(2) Displays “Y” or “N”, depending on the periphyton status.

Phytoplankton Status Display	[RetrInfo]DispPhyto	Alpha(2) Displays “Y” or “N”, depending on the phytoplankton status.
Zooplankton Status Display	[RetrInfo]DispZoo	Alpha(2) Displays “Y” or “N”, depending on the zooplankton status.
Phys/Chem Status Display	[RetrInfo]DispZoo	Alpha(2) Displays “Y” or “N”, depending on the physical/chemical status.

Report Sheets Table ([Rpt_Sheets])

This table is used to hold a 4D Calc spreadsheet (or “picture”). It is used by the routines that display retrieval results. The methods attached to the input form contain the program code to prepare and display data.

4D table name: [Rpt_Sheet]

Field	Description
Report Name	[Rpt_Sheet]Rpt_Name Text Name of the retrieval report.
Report “picture”	[RetrInfo]RptSheet_ Picture A picture field used to display the 4D Calc spreadsheet created by a retrieval method.

Retrieval Work Table (ET\$RETNWORK)

This table is used primarily to accumulate all entries for each TaxaID into one number and to get some information for it from the master taxa list. This table is used for retrievals of benthos, periphyton, phytoplankton, and zooplankton and is used by more than one PL/SQL program.

Oracle table name: ET\$RETNWORK

Field	Required?	Description
TaxaID		FK\$TAXAID TaxaID of the organism. Number(10)
No. of individuals		NOIND Number of individuals counted. Number(12,2)
No. of indiv/unit area		NOINDUNIT Number of individuals per unit area. This unit varies with the data type. Number(12,2)
Username		UNAME Varchar2(15)

The user name of the person doing this retrieval. This is to accommodate network operation where more than one user may be doing retrievals at the same time.

Functional feeding type	FFTYPE	Number(2)	Type of functional feeding group (single or multiple or none) for this taxon. If it is a multiple strategy and there is a retrieval by feeding group, multiple feeding strategies must be accumulated differently.
SampleID	FK\$SAMPLEID	Number(10)	Sample ID of the sample being processed.
No. of samples	NSAMPS	Number(5)	Number of samples that went into this accumulation.
BenthID	FK\$BENTHID	Number(9)	BenthID or PeriID or PhytoID or ZooID being processed.
No. of replicates	NREPS	Number(3)	Total number of replicates that went into this accumulation.

Retrieval Work Table 1 (ET\$RETNWORK1)

This table is used primarily to accumulate all entries for a given TaxaID for a given username into one number and to get some information for it from the master taxa list. This table is used for retrievals of benthos, periphyton, phytoplankton, and zooplankton and is used by more than one PL/SQL program. This table does not have a counterpart in 4D. The programs that use this table will send some kind of cumulative SQL statement and return the result into a 4D variable.

Oracle table name: ET\$RETNWORK1

Field	Required?	Description
TaxaID		FK\$TAXAID TaxaID of the organism.
SampleID		FK\$SAMPLEID The ID of the sample being processed.
BenthID		FK\$BENTHID The ID of the benthos, periphyton, phytoplankton, or zooplankton sample being processed. It is called "Benth" instead of peri or phyto or zoo only because benthos was the only thing in the database when this table was created.
No. of individuals		NOIND Number of individuals counted.
No. of		NOINDUNIT Number(12,2)

Username	UNAME	Varchar2(15)	The user name of the person doing this retrieval. This is to accommodate network operation where more than one user may be doing retrievals at the same time. There will be multiple users doing retrievals at the same time, this allows the program to get only those rows appropriate for a particular username.
Functional feeding type	FFTYPE	Number(2)	Type of functional feeding group (single or multiple or none) for this taxon.
Functional feeding ID	AK\$FFID	Number(3)	The functional feeding group assignment for the taxon in this row.
Phylogenetic category	PHYLCAT	Number(2)	1=Phylum, 2=Class, 3=Order, 4=Family, 5=Genus, 6=Species, 7=Variety
Phylogenetic code	PHYLO	Varchar2(17)	A 17-character code that describes the phylogeny of the organism. See “Master Taxa Table” for a full description of this code.
Florida Index	FLAINDX	Varchar2(2)	Holds the Florida Index value calculated.
Lake Conditon Index	LAKEINDX	Varchar2(2)	Holds the Lake Condition Index value calculated.

Taxa File Stats Table ([TaxaFileStats])

This table is used primarily to hold biological sample information and selected calculated retrieval results. It is used by the routines that create a 4D Calc spreadsheet for display of retrieval results. It is used by the “Show Stats” button for benthos, periphyton, phytoplankton, and periphyton.

4D table name: [TaxaFileStats]

Field	Description	
Number of individuals counted	[TaxaFileStats]NindC	Real Number of individuals counted in the sample.
Number of individuals per unit area	[TaxaFileStats]NindU	Real Number of individuals per unit area (or volume).
Number of taxa	[TaxaFileStats]NTaxa	Real Number of taxa in the sample.
Diversity	[TaxaFileStats]DBar	Real Shannon-Weaver Diversity Index.

Florida Index	[TaxaFileStats]FLIndex Florida Index value.	Real
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Lake Condition Index	[TaxaFileStats]LCIndx	Real	Lake Condition Index value.
Station Nickname	[TaxaFileStats]StaNickName	Alpha(10)	10 character “nickname” assigned to the station where the sample was collected.
Storet Station Name	[TaxaFileStats]StoretName	Alpha(15)	The STORET station name assigned to the station where the sample was collected.
Sample Date	[TaxaFileStats]SampDate	Date	The data that the sample was collected.
BenthID	[TaxaFileStats]BenthID	Real	BenthID or PeriID or PhytoID or ZooID component of the sample being processed.
Sample Gear	[TaxaFileStats]GearName	Alpha(10)	The name of the gear type used to collect the sample.
Qual or Quan?	[TaxaFileStats]QualQuan	Alpha(15)	Indicates whether the sample was processed as qualitative or quantitative.
Number of replicates	[TaxaFileStats]NReps	Real	If replicate samplers were used, the number of replicates sampled; otherwise, 1.

Taxa List Table ([TaxaList])

This table is to hold the results of the “Retrieve by Taxon” routine.

4D table name: [TaxaList]

Field	Description		
Scientific Name	[TaxaList]SciName	Alpha(45)	Full, spelled out scientific name of the organism.
Phylogenetic Code	[TaxaList]Phylo	Alpha(17)	A 17-character code that describes the phylogeny of the organism.
Number of individuals	[TaxaList]Noind	Real	Number of individuals of the organism counted in the sample.
Number of individuals per unit	[TaxaList]Noindunit	Real	Number of individuals per unit area (or volume) of the organisms in the sample.
TaxaID Code	[TaxaList]TaxID	Real	

A computer-generated identifier for this scientific name.

Taxa Work Table ([TaxaWork])

This table names and other information about selected organisms. It is used by the taxa maintenance routines

4D table name: [TaxaWork]

Field	Description
TaxaID Code	[TaxaWork]TaxaId Real A sequential computer-generated identifier for this scientific name. Any name < 10,000,000 came from the BIOS system meaning that the name came on the original BIOS taxonomic list; any number larger was generated at DEP. It has nothing to do with the phylogeny of the organism.
Phylum	[TaxaWork]Phylum Alpha(2) The phylum of the taxon.
Class	[TaxaWork]Class Alpha(2) The class of the taxon.
Order	[TaxaWork]Order Alpha(2) The order of the taxon.
Family	[TaxaWork]Family Alpha(3) The family of the taxon.
Genus	[TaxaWork]Genus Alpha(3) The genus of the taxon.
Species	[TaxaWork]Species Alpha(3) The species of the taxon.
Variety	[TaxaWork]Variety Alpha(2) The variety of the taxon.
Scientific name	[TaxaWork]SciName Alpha(50) Full, spelled-out scientific name (e.g. <i>Mediomastus ambiseta</i>).
Entered in System by	[TaxaWork]EntBy Alpha(5) Username of the person who initially made this entry into the table (up to 5 characters).
On BIOS?	[TaxaWork]Bios Alpha(2) Y= This scientific name is on the BIOS list; N = not on BIOS list; U = don't know (it could have been added at DEP, but was added to BIOS after the most recent list we have)
Range	[TaxaWork]Range Alpha(2) 1 = Range unchecked, authoritatively checked taxa 2 = Range not in Florida, authoritatively checked taxa

- 3 = Range includes Florida, authoritatively checked taxa
- 4 = Range may include Florida, authoritatively checked taxa
- 5 = Unchecked taxa (will never be on BIOS)
- 6 = Numbered taxa (will never be on BIOS)
- 7 = Not in Florida, but needs to be on Florida list

Florida Index	[TaxaWork]FlaIndex	Alpha(2)	The number of Florida Index points for the taxon.
Lake Condition Index	[TaxaWork]LakeIndx	Alpha(2)	The number of Lake Condition Index points for the taxon.
FFG Code	[TaxaWork]FFGGrp	Alpha(2)	The code for the taxon's feeding strategy.
Phylogenetic Category	[TaxaWork]PhylCat	Real	1=Phylum; 2=Class; 3=Order; 4=Family; 5=Genus; 6=Species; 7=Variety.
Revision Status	[TaxaWork]Revision	Alpha(2)	May be an "S" or null. "S" means that this is a synonym for another name on the list . A null in this field means that this is the most accepted version of this name. A synonym and its more accepted name will have identical values in PHYLO.
Master List Status?	[TaxaWork]MstrStatus	Real	1=Yes, on master list; 0=No, not on master list
Florida List	[TaxaWork]FlaList	Real	1=Yes, on Florida list (i.e., this is a taxon found in Florida); 0=No, not on Florida list.
Authority	[TaxaWork]Authority	Alpha(30)	The source of the original description of this scientific name.
Authority Date	[TaxaWork]AuthDate	Alpha(4)	The date of the original description of this scientific name.
Authority Ref	[TaxaWork]AuthRef	Alpha(80)	The bibliographic citation of the taxonomic key used to identify the taxon.

User Maintenance Tables

These tables keep track of the user names and user groups. Each DEP district and Tallahassee are a separate user group. Users may only edit and delete data that were added by their group. There is an administrative level that has full access to all the data regardless of the owner group.

User Group Table (MT\$USERGROUP; [UserGroup])

Oracle table name: MT\$USERGROUP

4D table name: [UserGroup]

Field	Required?	Description
Group ID	Y	PK\$GROUPID [UserGroup]GroupID Number(2) Real A sequential number assigned by the computer to identify this group.
Group description		GROUPDESC [UserGroup]GroupDesc Varchar2(50) Alpha(50) Up to 50 characters to describe the group.
Group nickname		GROUPNICK [UserGroup]GroupNick Varchar2(10) Alpha(10) A 10-character nickname for the group. This is the name that will appear in popup menus.

User Detail Table (MT\$USERDETAIL; [UserDetail])

Oracle table name: MT\$USERDETAIL

4D table name: [UserDetail]

Field	Required?	Description
Username		PK\$USERNAME [UserDetail]UDusername Varchar2(15) Alpha(15) A username of up to 15 characters. This is the name entered at logon.
Password		UPASSWORD [UserDetail]UDPassword Varchar2(15) Alpha(15) The password for this username to be entered at logon.
GroupID		FK\$GROUPID [UserDetail]GroupID Number(2) Real The ID of the group (PK\$GROUPID in MT\$USERGROUP) for this username.
Administrative?		GPADMIN [UserDetail]GpAdmin Number(1) Real A value of 1 is entered if this username has group administrator permission. That means this username can mark samples complete/incomplete.
Data Entry?		DATAENTRY Number(1)

[UserDetail]DataEntry Real

A value of 1 is entered if this username has permission to enter data. If not, the username has “retrieve only” permission.

User Status?	USERSTATUS [UserDetail]UserStatus	Number(1) Real
	A value of 1 means this username is currently logged on the system; it is zero otherwise. This variable is checked at logon to make sure that there are not two people logged on to the same username at the same time. This is important because retrieve by station and date uses a work table that stores the username which is used to count the proper rows. If the computer crashes, UserStatus is the same as it was before the crash, so the logon procedure asks if you are restarting after a crash. If there is a normal logoff, this value is set to zero.	
Tox Entry Status?	TOXENTRY [UserDetail]ToxEntry	Number(1) Real
	A value of 1 is entered if this username has permission to enter toxicity data. If not, the username has "retrieve only" permission.	

System Maintenance Tables

System Maintenance Table (MT\$SYSMAINT; [UserInfo])

Oracle table name: MT\$SYSMAINT

4D table name: [UserInfo]

This table is maintained by the computer system itself for internal program needs. There is only one row in both the Oracle table and the 4D file. There are several fields that only occur in the 4D file to monitor progress of long downloads.

The date information is read from Oracle into some 4D variables at startup, then compared with the values in [UserInfo]. If the date is different (no direction to the difference), the appropriate table in 4D is emptied and reloaded from Oracle. The date in 4D is then updated to be the same as the one in Oracle. Project method *FlaListStatus* and *StartUpLoads* handle this loading process.

Programmer note: In the beginning, the 4D table had a field for both the date and the time for each table that was being monitored. Later, it was more efficient to just store the Oracle date (which has date and time) as a text field in the field labeled as "date". Since 4D won't let you delete fields that you don't need, the old time fields are still there but unused. These unused 4D fields are:

[UserInfo]CtyListTime
[UserInfo]ColListTime
[UserInfo]IDListTime
[UserInfo]SvyListTime
[UserInfo]GearListTime
[UserInfo]FFListTime
[UserInfo]StaLevTime
[UserInfo]FacilTime
[UserInfo]STypeToxTime
[UserInfo]DistTime
[UserInfo]TestOrgTime
[UserInfo]DilTime
[UserInfo]CalcToxTime

[UserInfo]CauseToxTime
 [UserInfo]FacTypeTime
 [UserInfo]NPDESTime
 [UserInfo]WaterTime
 [UserInfo]StaTime

These fields only exist in [UserInfo] and not in the Oracle table MT\$SysMaint.

[UserInfo]AgencyUnlockKey	This is the current default agency key for use in BIOS routines. The user may edit this. At this time only one person sends data to BIOS. In the future, if there is more than one person, each one can select what code they want as a default.
[UserInfo]LoadInProgress	Set to "AN" when it starts a Florida list animal download or "PL" when it starts a plant list. It is empty otherwise. If the program bombs or something goes wrong with the network, the program can pick up where it left off in the download.
[UserInfo]Last1000	Number of the last successfully downloaded and saved animal or plant row. It is used with LoadInProgress to pick up where it left off.
[UserInfo]MaxRecsAnimal	The maximum number of rows that were ever in 4D file [Animal].
[UserInfo]MaxRecsPlant	The maximum number of rows that were ever in 4D file [Plant].

These two numbers are used when emptying the 4D animal or plant table before reloading. 4D does not physically remove a deleted record. The next time a record is added, it will use an existing "deleted" record. This number allows the program to calculate how many deleted records there are and to delete them in descending record number order so that the record numbers will be reassigned in ascending order - ie, so things appear in alphabetical order without having to sort all the time.

These fields exist in both [UserInfo] and the Oracle table MT\$SysMaint.

Database version	DBVERSION	Varchar2(6) - created, but not used yet [UserInfo] - field doesn't exist, yet Will be used to keep track of the user's current version of the database. If it does not match the Oracle version, it will trigger a message that tells the user that a newer version of the database program exists. The intention is to have an automatic updater in the future.
Animal	LASTFLADATE [UserInfo]DateFlaAList	Date Alpha(18) The last time modifications were made to the Florida animal taxa list.
Plant	LASTFLAPDATE [UserInfo]DateFlaPList	Date Alpha(18) The last time modifications were made to the Florida animal taxa list.
County	LASTCTYDATE [UserInfo]CtyListDate	Date Alpha(18)

The last time modifications were made to MT\$CTYLATLON (county reference table).

Collector	LASTCOLDATE [UserInfo]ColListDate The last time modifications were made to MT\$Collect (collector reference table).	Date Alpha(18)
Identifier	LASTIDDATE [UserInfo]IDListDate The last time modifications were made to MT\$Ident (identifier reference table).	Date Alpha(18)
Survey	LASTSVYDATE [UserInfo]SvyListDate The last time modifications were made to MT\$Survey (survey reference table).	Date Alpha(18)
Gear	LASTGEARDATE [UserInfo]GearListDate The last time modifications were made to MT\$Gear (gear reference table).	Date Alpha(18)
Functional feeding groups	LASTFFDATE [UserInfo]FFListDate The last time modifications were made to MT\$FFID and/or MT\$FFGroup (functional feeding group reference tables).	Date Alpha(18)
Station Levels	LASTSTALEV [UserInfo]StaLevDate The last time modifications were made to any of MT\$StaLev1, MT\$StaLev2A, MT\$StaLev2B, MT\$StaLev3, MT\$StaLev4, MT\$StaLev5 (station level name reference tables).	Date Alpha(18)
Facility Information	LASTFACIL [UserInfo]FacilDate The last time modifications were made to MT\$Facility_Tox (toxicity database facility information reference table).	Date Alpha(18)
Tox Sample Types	LASTSTYPETOX [UserInfo]STypeToxDate The last time modifications were made to MT\$SampType_Tox (toxicity database sample type reference table).	Date Alpha(18)
DEP Districts	LASTDIST [UserInfo]DistDate The last time modifications were made to MT\$District_Tox (toxicity database DEP District information reference table).	Date Alpha(18)
Test Organisms	LASTTESTORG [UserInfo]TestOrgDate	Date Alpha(18)

The last time modifications were made to MT\$TestOrg (toxicity test organism information reference table).

Diluent	LASTDIL	Date
	[UserInfo]DilDate	Alpha(18)
The last time modifications were made to MT\$Diluent_Tox (toxicity database diluent information reference table).		

Calculation Methods (Tox)	LASTCALCTOX	Date
	[UserInfo]CalcToxDate	Alpha(18)
The last time modifications were made to MT\$Calc_Tox (toxicity database calculation information reference table).		

Causes of Toxicity	LASTCAUSETOX	Date
	[UserInfo]CauseToxDate	Alpha(18)
The last time modifications were made to MT\$Cause_Tox (toxicity database causes of toxicity information reference table).		

Facility Type	LASTFACTYPE [UserInfo]FacTypeDate The last time modifications were made to MT\$FacilityType_ToX (toxicity database facility type informaton reference table).	Date Alpha(18)
NPDES	LASTNPDES [UserInfo]NPDESDate The last time modifications were made to MT\$NPDES_ToX (toxicity database NPDES information reference table).	Date Alpha(18)
Waterbodies	LASTWATERDATE [UserInfo]WaterDate The last time modifications were made to MT\$Waterbody_Storet (waterbody information reference table).	Date Alpha(18)
Stations	LASTSTADATE [UserInfo]StaDate The last time modifications were made to ET\$Sta (station information reference table).	Date Alpha(18)

Update Tracking Table (MT\$BIO_DELETES)

During the logon routine, the program looks to see if certain reference tables (Station) have been updated since the user last logged on. If table has been updated, a new version is downloaded. The information stored in this table is used in this process.

Oracle table name: MT\$BIO_DELETES

Field	Required?	Description
Table Name		TABLERNAME Varchar2(80) The name of the Oracle table.
Primary Key		KEYID Number(10) The primary key of the item that was changed in TABLERNAME.
When Changed?		TIME_STAMP Date The date that TABLERNAME was changed.
Who Changed?		USERNAME Varchar2(15) The user who updated TABLERNAME.

Glossary

Parent (taxonomic)

The taxonomic entry in the master list phylogenetically “above” another. For example, phylum Annelida is the “parent” of class Polychaeta.

Child (taxonomic)

The taxonomic entry in the master list phylogenetically “below” another. For example, class Gastropoda is the “child” of phylum Mollusca.

Number of individuals counted (nickname=RawCount)

This number is the raw count entered from a data entry sheet. A sampling factor, sample volume, or other information may have been used to calculate numbers/unit area from the raw counts, so raw counts are not always comparable from one sample, or even one replicate, to the next.

Number of individuals per unit area (nickname=NindArea)

This is calculated from the raw count and various other factors depending on the data type.

Number of individuals per unit area, proportioned (nickname=RawProp)

If a taxonomic entry has “children” in any replicate of the sample, the higher level entry's RawProp is zero and its RawCount number of individuals is added to the “children” based on what proportion each child is of all the children. The number of taxa and DBar are calculated from nindprop.

Bibliography

Bloom, S.A., S.L. Santos, and J.G. Field. A package of computer programs for benthic community analyses. Bull. Mar. Sci. 27(3):577-580. 1977.

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