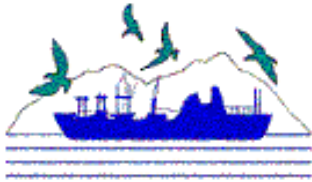


Dredging Data Entry Guide

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1.1 The Dredged Material Data Entry Utility

This Access file was generated during the CSTF SQD project to aid in entering a large volume of dredged material characterization reports. It was included as part of the project as a potential useful utility for including other hard copy reports into the CSTF SQD. The program is not intended for public distribution and is not bug-free. After entering the data, we recommend that a data manager upload the data into the database, as there are a series of steps that must be conducted (e.g., population of the Sample Master table, see Technical Reference Manual). This guide was modified from original instructions given to those entering the data, and was meant for junior level scientists who understand the basic chemistry and biological testing.

1.2 Entering Data from Hard-Copy Reports

The file provided in the Templates folder on the SQD Version 1.0 CD-ROM is a copy of the master database (empty data tables, with Lookup Lists). This file (Dredging Data Entry.mdb) includes a series of linked forms for entering dredged material characterization data from hard-copy reports. This section provides step-by-step instructions to use these forms to enter dredging data.

To avoid the frustration of editing or re-entering previously entered data, we recommend that you thoroughly review the originating study before you begin. In particular, use the originating report's Table of Contents to see whether you will be entering some or all of the following types of data:

- ❑ Sediment Chemistry – Generally listed as “Chemical Testing” or “Chemical and Physical Characteristics of Sediments;”
- ❑ Subsurface Sediment Chemistry - Includes samples collected below one foot of depth;
- ❑ Sediment Toxicity – Generally listed as “Biological Testing”, “Suspended-Particulate Phase Testing”, “Solid Phase Testing;”
- ❑ Bioaccumulation – Look for “Bioaccumulation Test” or “Bioaccumulation Tissue Chemistry” as part of the biological testing;
- ❑ Elutriate Chemistry – Generally listed as such.
- ❑ Infaunal Data – Generally listed as such.

1.2.1 Create a MetaManager Record

The first step in entering new data should be to enter the study overview into the MetaManager, which will give the study a unique identifier and shortened Study Name.

1.2.2 Entering Sediment Data/Setup Stations



Figure 1-1. Dredging data entry opening screen.

After you've created your MetaManager record, open the Dredging Data Entry template database to begin entering data. First, copy the database onto your local hard drive from the CD-ROM, and re-set the properties from read-only. At the Welcome screen, you have three options: Set Up Stations, Enter Data, or QA Data. The first step in data entry is to set up stations, which correspond to the locations where the sediment samples were collected. You cannot enter data without first setting up the stations.

Click the Set up Stations button on the Welcome screen. If you are entering a new study, select New Study from the upper right corner of the 'SCCWRP Study Information' form. To update station information for a previously entered study, select from the "Find a Study..." drop-down list. Then enter the following general study information.

- ❑ Dataset ID – This number was generated when you filled out the MetaManager report;
- ❑ Study type – For this application, you should choose dredging;
- ❑ Study name – This should match the Metadata Dataset name from the metadata record;
- ❑ Agency – The funding entity behind the report;
- ❑ Comments – An optional field for any relevant information;
- ❑ Initials – Noting who entered the data;
- ❑ Date – Noting when data entry was initiated.

The next step is to define the stations, beginning with the Station ID.

EXAMPLE: Table from the Dredged Materials Characterization Report

Area	Depth (m MLLW)	Number of Locations	Sample Compositing
1	Mudline to – 5.5	8 upper	1 Composite
1	-5.5 to –9.6	8 lower	1 Composite
2	Mudline to – 5.5	8 upper	1 Composite
2	-5.5 to –9.6	8 lower	1 Composite
3	Mudline to – 7.6	8	1 Composite
Reference	NA	1	1 grab
Control	NA	NA	1

Station IDs: Area 1, Area 2, Area 3, LA 2 Reference, and Tomales Bay – Control

Station ID

The Station ID or name can generally be found in the “Methods” section of the report being entered, in a table of samples taken from the entire region. Each area sampled must be included as a Station ID, including the reference or control area, which may be listed separately in the originating report. For elutriate data, enter the location where seawater was collected for analysis. Enter only one area per row. Enter each area only once as a Station ID, even if more than one sample was collected there.

A table showing an example of several areas that were sampled is shown above, along with the names of the StationIDs selected for this report.

SCCWRP: Study Information

Dataset ID: 115 Study Type: Dredging Find a Study... POLA Berth 240B Final Report

Study Name: POLA Berth 240B Final Report

Agency: Port of Los Angeles

Comments:

Initials: JAF Date: 4/21/2002

Data Types

Sediment Chemistry Yes

Subsurface Sed Chemistry Yes

Sediment Toxicity Yes

Bioaccumulation Yes

Butriate Chemistry No

Infaunal Data No

Station Information Core Composites Coring Event Dredge Date Station Occupation

Enter StationIDs here: NOTE: If the cores were composited over an area, then StationID = AreaID

StationID	Latitude	Longitude	Study Type
Berth 240B	0	0	Dredging
LA-2 Ref	33.55333333	-118.18	Dredging
Control	-99	-99	Dredging
Control 1	-99	-99	Dredging
Control 2	-99	-99	Dredging
*			

Move through Studies Other Options

Study Reference Preview and Print CompositeID

CLOSE

Figure 1-2. Dredging data entry study information and station setup screen.



Latitude/Longitude



The latitudinal and longitudinal coordinates for each station generally can be found in either the Methods/Sample Collection or Data Appendix of the report being entered. If the coordinates are not provided in the text or a table, they can later be determined with GIS using from figures in the report. If the 'station' is actually a laboratory control (which must also have an assigned Station ID), then enter 0 for the coordinates. If there are no coordinates provided, use the standard convention of -99 for missing data in numeric fields.

As you can see in Figure 1-2, some stations that are not control samples will have 0 or -99 for their latitude and longitude coordinates. Zero is used when several cores have been collected over an area and then composited to generate a single set of data for that area. In such cases, the coordinates for the specific coring locations in that station will be entered in the Core Event section.

All coordinates must be in latitude/longitude datum=NAD 83. With the advent of GPS, this is generally the norm. However, it is possible that data

will be reported in NAD 27, or even in a different coordinate system (most commonly, California State Plane). If such cases, the coordinates must be converted to datum=NAD 83 before being entered.

 **TROUBLE SHOOTING** : If you get an error message with the options to “End” or “Debug” press “End” and then hit the “Previous Study” button.

 **NOTE** : You can navigate between the stations by using the record navigation arrows above the study navigation buttons.

1.2.3 Study Reference



Once you have completed the station information, open the forms for study reference. Click on the study reference button at the bottom of your screen and enter the year, author, title, authors, and source (funding agency) for the report. You should be able to find these fields on the title page.

1.2.4 Core Composites

The next step is to set up the Composite IDs specifying where composite samples were taken. First, click on the tab labeled ‘Core Composites’ next to the Station Information tab.

CompositeIDs

From the Station Name pull-down menu just below the tab, select the previously entered StationID for the coring locations you will now be entering. Then you can begin entering CompositeIDs or names for the sub locations where cores were taken. You will probably find the CompositeID names in the originating report in the same place where you found the Station Names. If no unique names have been assigned to the composite coring locations you can create them from the station and strata information. An example for selection of CompositeIDs is shown below.

 **NOTE** : The CompositeID field gives you flexibility to use dashes, spaces (or no spaces) in the names as you choose.

EXAMPLE: Table from the Dredged Materials Characterization Report
Core Composite Ids using the example table shown above:

Area 1 TOP
Area 1 BOT
Area 2 TOP
Area 2 BOT
Area 3
LA-2 Reference
Control

SCCWRP: Study Information

Dataset ID: 114 Study Type: Dredging Find a Study... Berth 121, 122-124 Final Report

Study Name: Berth 121, 122-124 Final Report

Agency: Port of Los Angeles

Comments:

Initials: JAF Date: 5/8/2002

Data Types

Sediment Chemistry Yes

Subsurface Sed Chemistry Yes

Sediment Toxicity Yes

Bioaccumulation Yes

Elutriate Chemistry No

Infaunal Data No

Station Information Core Composites Coring Event Station Occupation

Station Name: Berth 121-2

StationID	CompositeID	Horizon	AnalysisType	Comments
Berth 121-2	Berth 121-2 A	1:1	Tier III	
Berth 121-2	Berth 121-2 B	1:1	Tier III	
Berth 121-2	Berth 121-2 Bot	2:2	Tier III	
Berth 121-2	Berth 121-2 C	1:1	Tier III	
Berth 121-2	Berth 121-2 D	1:1	Tier III	
Berth 121-2	Berth 121-2 E	1:1	Tier III	
Berth 121-2	Berth 121-2 Top	1:2	Tier III	
Berth 121-2				

Move through Studies Other Options

Study Reference Preview and Print CompositeID

CLOSE

Figure 1-3. Dredging data entry core composite screen.

There are several scenarios for which you will need to create additional Composite IDs beyond the obvious ones for coring sub locations. Ideally, you should review the originating report for these now, so they don't get missed in the data entry process.

- ❑ You will need to add CompositeIDs for any duplicate samples analyzed in the lab. For example, if the sample "Berth-121-B" was duplicated and analyzed again, you would add a CompositeID such as "Berth-121-B DUP".
- ❑ You will need to enter separate CompositeIDs for each bioassay control sample shown in the report. (The other bioassay results will be captured under the CompositeID where the sample originated.)
- ❑ You will need to create separate CompositeIDs for up to 5 bioaccumulation test replicates, if such testing was performed.

Horizon

The next data to enter is the Horizon. The horizon or horizontal layer data can usually be found from the table of samples taken. The horizon is entered as a fraction describing what segment of the core the sample came from. For

example, the entry "1.2" would represent the first or top segment of two horizontal core segments, while "2.2" would represent the bottom segment.

Analysis Type

The "Analysis Type" describes dredging-related data. From the drop-down list, choose the "tier" that best describes the testing performed on each composite or sample.

- ☐ Tier I = chemical analysis only
- ☐ Tier II = chemical and bioassay analyses
- ☐ Tier III = chemical, bioassay, and bioaccumulation analyses

If you created special CompositeIDs just for bioassay test controls or bioaccumulation replicates, you should choose the lowest appropriate tier designation (II or III) and note in the comments column that the analysis for that CompositeID will be "bioassay only" or "bioaccumulation only."

Checking Your Progress

If you would like to double-check your work after entering all of your CompositeIDs, you can use the "generate a report" function to review the stations and composites you have entered.

1.2.5 Coring Event

The next step is to enter data on the individual core samples that make up the compositeIDs. Figure 1-x shows the supplementary data and locations for five cores entered into the Coring Event table. The supplementary data are normally found in the Methods or Results section, in a coring log, or in a field documentation appendix. Log sheets may note the physical characteristics of the sediment retrieved from each core.

CoreID

Each core needs a unique name, or CoreID. If the collection was actually a "grab" sample rather than a core, this section does not need to be filled out. (Reference and control samples are usually grab samples.)

Latitude and Longitude

Latitudes and longitudes must be recorded in decimal degrees (NAD83), so you may need to convert what you find before data entry.

Water Depth

Enter the water depth from where the core was taken, recorded here as seafloor elevation (MLLW) in meters.

Date and Time

Enter the date and time of the collection, with time recorded in military fashion.

Segments

Note the number of horizontal segments created (as in Figure 1-4 below).

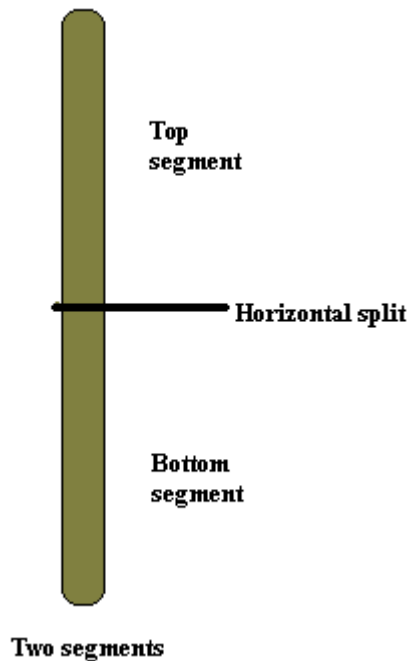


Figure 1-4. Vertical segments in a core.

Core Length

Note the length of the total core in cm below the sediment-water interface.

Penetration

How deep the coring instrument penetrated in cm below the sediment-water interface.

Refusal

Note whether the coring instrument met refusal, meaning if the core was retrieved prior to reaching full penetration because it was impeded by, for example, sand or rock. Options for this field are Yes, No, or Unknown.

Physical Characteristics

Note the physical characteristics of the core, such as color, composition, odor, presence of shell hash. Each of these fields is linked to a drop-down list that draws information from the Lookup Lists. You may enter a new value.

1.2.6 Core Samples

If multiple samples were taken from a core, for example, from both the upper and lower segments, you should fill out the Core Samples table.

Access the Core Samples table by clicking the button to the right of the Station Name box on the Core Event table.

CoreSampleID

Each core segment will need a unique CoreSampleID name, preferably based on the corresponding CoreID and horizon. Enter that name here.

Upper and Lower Sediment Depths

The upper and lower depths ('upper measure' and 'lower measure') of the core segments should be relative to the sediment water interface, in units of cm. For example, two samples are collected from one core, the first from 0-4 feet and the second from 4-8 feet. The Upper and Lower Measures for the first sample (in cm) will be 0 to 122 cm; the Upper and Lower Measures for the second sample (in cm) will be 122 to 244 cm.

◆Convention – Sediment Depths for Coring Data:

Lengths in coring reports are often reported in feet. The SOD stores most lengths in cm, except for total water depth, which is stored in meters. Be sure and convert depths and lengths to metric before entering data, or converting them after entry.

1.2.7 Station Occupation

The Station Occupation describes various parameters at the time of collection, usually shown in the methods section of the originating report. The fields to enter include:

Sample Method

Enter the method used to obtain a sediment sample, whether grab or core. Note that a different sampling method is often used to collect reference and control samples.

Agency

Enter the name of those responsible for collecting the sediment samples.

Vessel

Enter the name of the vessel(s) used to collect the sediment samples. Different vessels are often used to collect reference, control, and test sediment samples.

Navigation Type

Enter the instrumentation used to determine latitude and longitude of sample locations. In more recent reports, generally GPS (Global Positioning System) or differential GPS (DGPS) is used.

Habitat Type

If the sampling location is adjacent to piers, the habitat type would be "Port;" if it is the reference location, the habitat would be "Open Ocean." If you cannot find this information and are not comfortable inferring, this field can be entered as "Not Recorded."

Other environmental data, all linked to codes in associated Lookup Lists, include:

- ☐ Weather Code
- ☐ Wind Speed
- ☐ Wind Direction
- ☐ Swell Height
- ☐ Swell Period
- ☐ Swell Direction
- ☐ Sea State

Fill in as much information as is easily available. When finished, save your work and close out of this section using the "CLOSE" button on the lower right section of the screen.

1.3 Entering Chemical/Biological Data

Having entered all the station and substation information from the originating report, you may now enter the testing results. Begin by clicking on "Enter Data" from the "Welcome" screen. Then, at the "Study Information" screen, find and select the study you are entering on the "Study Name" drop-down list. Next, select the type of data you will be entering. We will start with instructions on how to enter Sediment/Tissue Chemistry data.



 **NOTE** : Bioaccumulation data is entered under Tissue Chemistry.

Figure 1-5. Enter Data options.

1.3.1 Sediment/Tissue Chemistry Data

Select the Data Type of Sediment/Tissue Chemistry from the drop down-list.

QA Batch

Your first step is to click on 'QA Batch' so you can enter information on the study's preparation and analysis methods (typically found in the Methods section of the report), the preparation and analysis dates, material tested, and the agency conducting the testing (typically found in the appendices.)

Choose the most appropriate QABatch type from the drop-down list. Each choice combines an analysis type with the matrix being analyzed – sediment, water (elutriate) or tissue.

- ❑ The elutriate analysis codes begin with "W_" (for water);
- ❑ Tissue analysis codes start with "T_";
- ❑ Tissue codes also end with initials for the species that was analyzed, such as "_MN" for *Macoma nasuta*.

NOTE: If you cannot find a QABatch code to match a particular method and matrix combination, you can add a new one to the QABatchID table (Lookup List 44). See the Technical Reference Manual for more information.

Other information to enter into the QA Batch information include:

- ❑ Analysis Date
- ❑ Material Code – tissue or sediment
- ❑ Species Code – for bioaccumulation data only

- ❑ Preparation Code
- ❑ Method Code
- ❑ Agency Code

Many of the fields are linked to drop-down lists for ease of data entry. This completes the batch information. You can close this form by clicking on the “Close” button.

AnalysisDate	QABatch	MaterialCode	Species	PreparationCode	Analysis
1/12/2001	%Solid-160.3M	Sediment			Percent solids by EPA
1/1/1900	GrSz-seive	Sediment			ASTM Grain Size 0422
1/9/2001	Metals-Hg-7471A	Sediment		Metals by total digest	Mercury by EPA Method
1/12/2001	Metals-ICPMS-6020	Sediment		Metals by total digest	Metals by EPA Method
1/12/2001	NH4-N-350.2	Sediment			Ammonia as Nitrogen b
1/22/2001	Organotin-RICE	Sediment			Organic Tins by Rice et
1/12/2001	PCB8082	Sediment			PCB arclors by EPA Mi
1/12/2001	Pest-PCB-8081A	Sediment			Pesticides/PCBs by EF
1/12/2001	Semivol-8270C	Sediment			PAHs by EPA Method i
3/5/2001	T_Metals-6020 - M.n.	Tissue	Macoma nasuta		Metals by EPA Method
3/5/2001	T_Metals-6020 - N.v.	Tissue	Nereis virens		Metals by EPA Method
2/26/2001	T_Metals-Hg-7471A_M.n.	Tissue	Macoma nasuta		Mercury by EPA Metho
2/26/2001	T_Metals-Hg-7471A_N.v.	Tissue	Nereis virens		Mercury by EPA Metho
2/18/2001	T_PCB8082-M.n.	Tissue	Macoma nasuta		PCB arclors by EPA Mi
2/26/2001	T_PCB8082-N.v.	Tissue	Nereis virens		PCB arclors by EPA Mi
2/26/2001	T_Pest-PCB-8081 - M.n.	Tissue	Macoma nasuta		Pesticides/PCBs by EF
2/18/2001	T_Pest-PCB-8081 - N.v.	Tissue	Nereis virens		Pesticides/PCBs by EF
3/6/2001	T_Semivol-8270 - M.n.	Tissue	Macoma nasuta		PAHs by EPA Method i
3/6/2001	T_Semivol-8270 - N.v.	Tissue	Nereis virens		PAHs by EPA Method i

CLOSE

Figure 1-6. Sediment QA batch information.

1.4 Entering Chemistry Data

After closing the “Chemistry Batch” QA screen, you should have been returned to the “Study Information” screen. Your next step is to click on “Organize Chems” to customize the data entry process and speed your work.

1.4.1 Organize Chems

At the “Organize Chemicals” screen, choose the first chemical group you wish to organize from the drop-down menu. Then determine the order in which the individual chemical names should appear during data entry. Ideally, you’ll want the names to appear in the same order as they do in the originating report, to speed your data entry. Order the chemicals by typing in the appropriate numeral in the “CHEMORDER” field across from the chemical name: Enter “1” for the first chemical you wish to see, and so on. A “zero” will put that chemical at the end of the list. Repeat this process for each

relevant Chemical Group. After organizing all of your chemicals, close this screen.

NOTE: The chemical order chosen for a particular data entry project will be retained indefinitely until it is changed. It will not revert to the alphabetical default even if the computer is shut down.

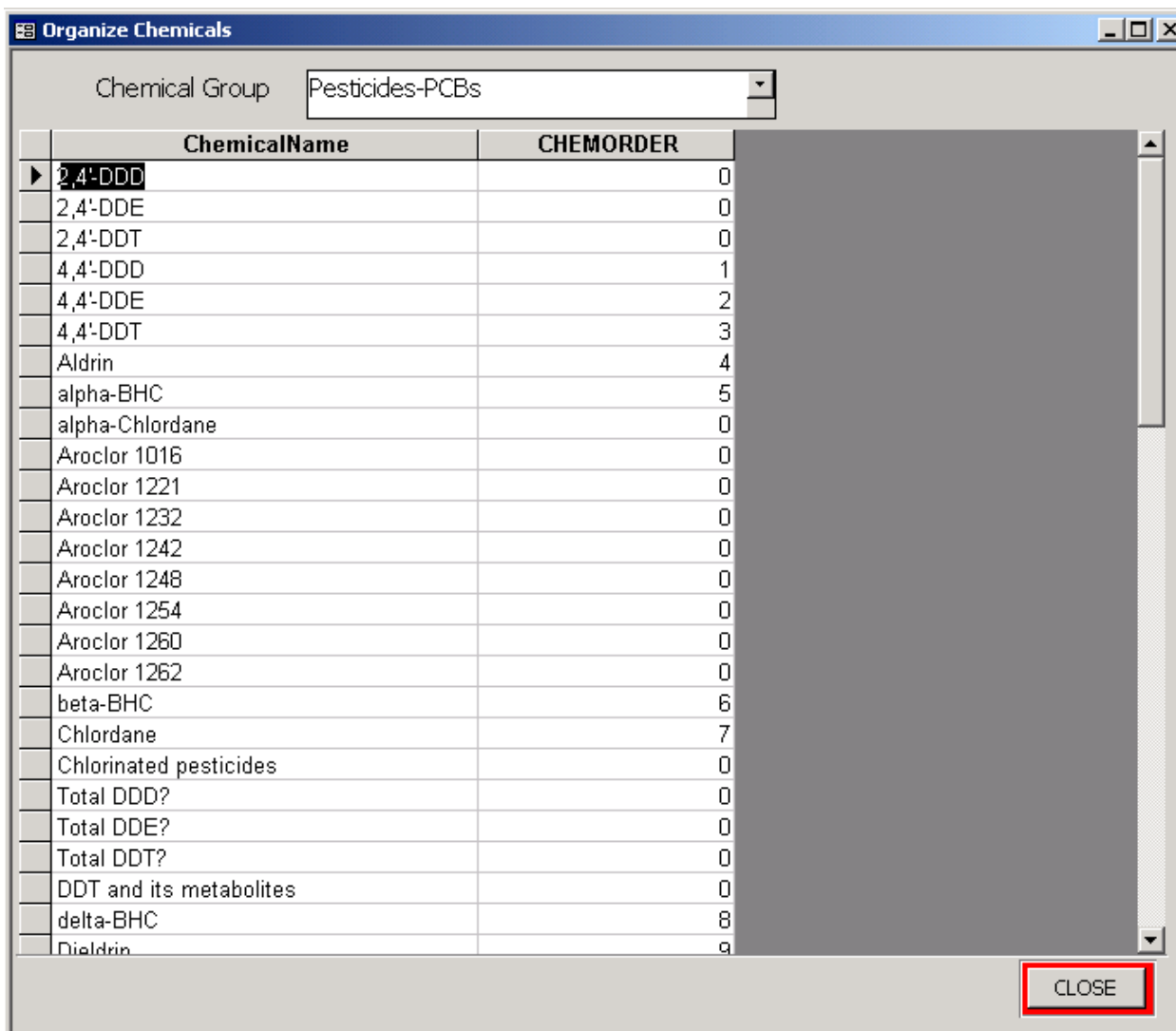


Figure 1-6. Ordering chemicals for data entry.

1.4.2 Chemical Data Entry

From the "Study Information" screen, make sure the appropriate Study Name and the Sediment/Tissue Chemistry data type are selected. Remember, you cannot enter chemical data unless the QABatch codes have been entered.

SCCWRP: Chemistry

Chemical Group: METALS

Refresh! Clears selected chemicals - use before entering new chem group

Spawn! Assigns chemicals selected below to each previously entered sample.

Enter Chemical Results Edit the results of the Spawn function and enter more information about each chemical result.

InBatch	ChemicalName	Units	Detection Limit	QABatch	SampleType
<input type="checkbox"/>	Aluminum	MG/KG			Numerical Result
<input type="checkbox"/>	Antimony	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Arsenic	MG/KG			Numerical Result
<input type="checkbox"/>	Barium	MG/KG			Numerical Result
<input type="checkbox"/>	Beryllium	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Cadmium	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Chromium	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Cobalt	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Copper	MG/KG			Numerical Result
<input type="checkbox"/>	Iron	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Lead	MG/KG			Numerical Result
<input type="checkbox"/>	Manganese	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Mercury	MG/KG			Numerical Result
<input type="checkbox"/>	Molybdenum	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Nickel	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Selenium	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Silver	MG/KG			Numerical Result
<input type="checkbox"/>	Thallium	MG/KG			Numerical Result
<input type="checkbox"/>	Tin	MG/KG			Numerical Result
<input type="checkbox"/>	Titanium	MG/KG			Numerical Result
<input type="checkbox"/>	Vanadium	MG/KG			Numerical Result
<input checked="" type="checkbox"/>	Zinc	MG/KG			Numerical Result

Figure 1-7. Set up chemistry batch information for spawning data entry forms.

NOTE: Before entering any information, click the "Refresh!" button to create a clean slate from which to work.

InBatch Boxes

Select the Chemical Group you would like to enter first from the drop-down menu in the upper left-hand corner. The chemicals for that group will appear, in the order you previously arranged. Mark the chemicals for which you have data by checking the appropriate "InBatch" boxes.

Chemical Units

The units for each chemical are set an appropriate default for the type of chemical, generally ppm (parts per million) for metals, and ppb (parts per billion) for organics. If the units being entered are differ from the default, you should either convert the values before entering them or remember to convert them after data entry.

Dry and Wet Weight Reporting Limits

For sediment chemistry, enter the dry weight reporting limit and units for each chemical. For tissue chemistry or elutriate data, enter the wet weight

limit. A timesaving utility built into the program will automatically place the detection level you selected in the results field, with a qualifier of below detection (U) in the data table. This is useful if you have a lot of data below the same detection level, which is particularly common in tissue data.

QABatch



The “QABatch” header will include a drop-down list of the codes you previously entered for this study. Each analyte must have a QABatch code assigned to it.

Sample Type



Your usual choice from the “Sample Type” header drop-down list will generally be “Numerical Result”, unless the sample is a duplicate. For negative control compositeIDs, select ‘negative control’ for the sample type. For reference samples, select ‘reference’ as the sample type.

Spawning Data

Once the appropriate analytes for the chemical group have been selected, click the “Spawn!!” button. Two message boxes will appear. Click “Yes” to run the append query and click “Yes” to append rows. The number of rows generated should equal the number of analytes selected, multiplied by the total number of CompositeIDs for that study.

 **TROUBLE SHOOTING** : If zero rows are to be appended, you may not have selected a study name before trying to enter data.

After spawning, press the “Open Form” button to ensure that the chemicals you just entered have been applied to all CompositeIDs. Delete the rows that do not apply to a specific CompositeID. For example, if a CompositeID was created specifically for a bioassay control and does not have associated chemistry, the chemicals must be deleted from that record.

 **NOTE** : To delete records from a form, select an entire row by clicking on the gray box on the far-left side of that row. Then press the keyboard “delete” button to remove.

Edit Detection Limits

For CompositeIDs with chemistry data, the reporting limits entered before spawning should be reflected in the results column. If not, you may need to update the results to the detected value for detected chemicals and delete the “U” (for undetected) under Qualifier.

Dilution of Samples

If the sample was diluted for analysis, update the Dilution factor from the default of one (1). This will also effect the reporting limit (reporting limit = method detection limit * dilution), and the result for data below detection

(should match the reporting limit).

◆Convention – Grain Size:

Grain size reporting limits should be entered as “-9” and all qualifiers deleted. Also, the most important data to enter is the percentage of silt, sand and clay. You do not need to enter the individual grain size data.

◆Convention – Summed Parameters:

If you are entering a value for Total PCBs, Total PAHs, Total Phthalate Esters, or Total DDTs, the reporting limit/detection limit should be –99 because these values are result from the sum of individual analytes.

Completing a Chemical Group

When all of the numerical results have been entered for that chemical group, close the data entry form. You should be returned to the “Chemistry” screen, where you can click on the “Refresh!” button and choose another chemical group to enter. Then repeat the process for the next chemical group.

1.4.3 Elutriate Chemistry Results

If your originating report includes elutriate chemistry results in addition to bulk sediment chemistry results, you may repeat the process described in section 1.4.2 of this User Guide.

Alternatively, you can spawn the data twice, making sure to select a different QABatch code before the second spawn. When you open the form after the second spawning, there should be two sets of analytes for each CompositeID. The two sets will be differentiated by their QABatch codes. However, this works well only if the chemical analytes in the sediment and elutriate chemistry were the same.

When editing the data in the Open Form, pay close attention to the fact that the QABatch, the reporting limits, and the units will be different between the bulk sediment and elutriate samples.

1.4.4 Sediment Toxicity Data

The data entry process for sediment toxicity data is similar to that for chemical data, except there is no ‘Organize Chems’ function. The first step is to establish batches for the toxicity data. In your originating report, the analyses performed can be found in the Methods section under Biological Testing.

QABatch

Choose from the drop-down list the QABatch. We used (and recommend) a

standardized approach to naming batches: SP for solid phase analyses, SPP for suspended particulate phase, and BIOACCUM for survival results for bioaccumulation data.

The screenshot shows a window titled "Toxicity Batch Information" with a table containing the following data:

AgencyCode	QABatch	MatrixCode	Species	TestDuration (days)	Protocol
AMEC Earth &	SPP_MB	Elutriate	Mysidopsis bahia	4	ACOE Green Book for d
▶ AMEC Earth &	SPP_MBE	Elutriate	Menidia beryllina	4	ACOE Green Book for d
AMEC Earth &	SPP_ME	Elutriate	Mytilus edulis	2	ACOE Green Book for d
AMEC Earth &	SP-static_renewal_A/	Bulk Sediment	Ampelisca abdita	10	ASTM 1990
AMEC Earth &	SP-static_renewal_ME	Bulk Sediment	Mysidopsis bahia	10	ASTM 1990
EnviroMatrix A	BIOACCUM_NV	Bulk Sediment	Macoma nasuta	28	ACOE Green Book for d
EnviroMatrix A	BIOACCUM_MN	Bulk Sediment	Nereis virens	28	ACOE Green Book for d
*					

A "CLOSE" button is visible in the bottom right corner of the window.

Figure 1-8. Set up toxicity batch information for spawning data entry forms.

The QABatch identifier should be unique to the group of samples related to a single negative control; i.e., the control and all associated samples should have the same QABatch.

NOTE: To avoid creating duplicate records, add an underscore followed by the initials of the species the bioassay was performed on, i.e. SPP_ME and SPP_MN, if more than one species was used with the same type of bioassay.

Other fields to be entered for sediment toxicity QABatch information include:

- ❑ Agency – the lab that performed the analysis
- ❑ Matrix
- ❑ Protocol
- ❑ Date
- ❑ Test Duration – in days (hours are entered as fraction of days)
- ❑ Temperature – the temperature that the analysis was performed at, in Celsius
- ❑ QA Code - acceptability of the data

NOTE: Suspended Particulate Phase analyses are considered elutriate matrices and Solid Phase analyses are considered bulk sediment.

At this point you should have entered all batch data and can click on the

“Close” button of the form.

1.4.5 Bioassay Data

Having closed out the Batch form, you should have returned to the Study Information screen. To begin entering bioassay data, click on the ‘Enter Data’ button.

You may find it helpful to begin by reviewing the originating report to locate and flag each type of bioassay performed. There may be more than one type of bioassay and more than one species for each type of bioassay. If you find handwritten and typed tables, take the data from the typed tables.

All Toxicity Results

CompositeID	SampleType	QABatch	AgencyCode	Species	Dilution	Concentration	EndPoint	QACod
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.5	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.5	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.5	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	0.5	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SPP_MBE	AMEC Earth	Menidia beryll	1	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Ampelisca ab	-99	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Ampelisca ab	-99	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Ampelisca ab	-99	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Ampelisca ab	-99	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Ampelisca ab	-99	-99	Survival (%)	Acceptable
Berth 240B	Numerical Resu	SP-static_re	AMEC Earth	Mysidopsis b	-99	-99	Survival (%)	Acceptable

Figure 1-8. Entering replicate toxicity results.



This form captures the individual laboratory replicates. Fields that are entered into this data entry form include:

- ❑ Agency - the lab that performed the analysis;
- ❑ Species;
- ❑ Endpoint - most commonly percent survival or percent normality;
- ❑ Units – units of the endpoint;
- ❑ LabRep – laboratory replicate number or letter;

- ❑ QA Code;
- ❑ Sample type - "numerical result" "negative control" or "reference;"
- ❑ QABatch – as previously entered;
- ❑ Dilution - as a fraction (0.5= 50%); reference and control samples should be given a dilution of "-99" because they are generally analyzed without any dilution;
- ❑ Concentration - applies specifically to reference toxicants should be given a concentration of "-99."

1.4.7 Summary Toxicity Results

Entering this information is very similar operation to the raw replicate data, except it requires the mean and standard deviation of each test. Look for mean, N (number of replicates), and standard deviation in a summary table in the Results section or Data Appendix of the originating report. This includes the mean and standard deviation data from the replicates, and including the toxicity significance.

 **NOTE** : To expedite entering the toxicity data, once you have filled in the first row of data: select the entire row by clicking on the gray box immediately to the left of the row, copy the row you just selected by pressing Ctrl-C or selecting "Edit", "Copy" from the file menu. Select the last row (the gray box will have an asterisk mark), and paste the row that you copied by pressing Ctrl-V or selecting "Edit", "Paste" from the file menu. As long as you change at least the LabRep before you leave the row (and preferably all other pertinent data), you should not encounter any resistance from the database.

SigEffect

The most critical and difficult field to fill out is the toxicity significance or SigEffect. After completion of the database, these codes were changed to represent not only the significance, but also the statistical test used and threshold value, if necessary. We recommend placing a 'T' or 'F' in this field (true or false for toxicity), and then adding a detailed comment on whether the sample was compared to control or reference, what statistical test was used, and what threshold was used.

For example: For Green Book analyses, generally solid phase tests are compared to reference data (e.g., samples collected outside of the offshore disposal site). The threshold used (the value below which no statistical tests are performed) is within 10%, or 20% for amphipod testing. Usually a paired Student's T-test or Dunnet's test is used. For more information on Green Book statistical methods, see <http://www.epa.gov/owow/oceans/gbook/index.html>.

Mean, N, and Standard Deviation

This is derived from the lab replicates.

PctControl

This is the mean result normalized to the control. The percent relative to control is the negative control-adjusted value, i.e., Abbott's correction. The Results Section of the report will sometimes provide summary tables with this information. If the results have not been normalized to the control, you will have to calculate that value yourself

1.4.8 Water Quality Data

The next phase is to enter water quality data. Most of this data will come from the appendices; they may be dispersed throughout the Toxicity data. If summary water quality data is not available (be sure to look at all of the data tables), skim through the data and enter only the minimum and maximum.

Water quality data is specific to each QABatch. Make sure to enter the Water Quality data for the appropriate CompositeID. The unique fields for water quality to be entered include:

STWQ Code

Sediment Toxicity Water Quality Parameters – type of analysis performed, i.e., dissolved oxygen, pH, and temperature.

Minimum/Maximum value

Enter the value found in the Water Quality data tables. Look for summary tables of the Water Quality data.

Minimum and Maximum Qualifiers

Enter "None" unless the minimum value was <, "less than", or <, "greater than", etc.

Mean/Standard Deviation

This is derived from all measurements for that parameter.