



SWAMP DATA MANAGEMENT PLAN

Chemistry Template

Surface Water Ambient Monitoring Program

January 26, 2015



http://www.waterboards.ca.gov/water_issues/programs/swamp

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E. Analytical Data

The typical method for submitting Laboratory Analytical Data to the SWAMP Database is electronically through the [online data checker](#). This section will focus on the tools and steps involved in submitting these data.

The following information and business rules should be used in conjunction with the [2013 SWAMP QAPrP](#) for complete compliance with the SWAMP program including [measurement quality objectives](#) and required Quality Control (QC) samples. In general, SWAMP requires the reporting of accuracy, precision and blank QC samples. This includes analyses based on a standardized method which use a calculation to determine the result, e.g. Hardness as CaCO3. For toxicity, the control samples are expected to be reported. SWAMP does not store internal calibration standards. More information on [submitting data](#) to the SWAMP Data Management Team is also available.

1. WATER QUALITY AND TISSUE ANALYSIS AUTHORIZATION FORMS

Prior to a sampling event, it is helpful to organize and identify what analyses are to be performed by the different laboratories. For those organizations contracting with the Department of Fish and Game (DFG) for sampling activity, the tool used for this expectation of work is called an Analysis Authorization Form.

The Analysis Authorization (AA) Form is provided to the labs in an electronic format prior to sampling. It is used as a detailed supplement to the Chain of Custody (COC) documentation that travels with the samples from the field to the lab. Should any discrepancy between the two types of documentation occur, contact the provider of the Analysis Authorization for further clarification.

An Analysis Authorization Form is an Excel workbook with various components. There is a worksheet for each laboratory that will be involved in analyzing the samples.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Analysis Authorization	Work Order	09-4-001	Contact Person:	Marco Sigala	Michael Lyons								
2	Contract	09-4-001	Group:	2011	Phone:	831-771-4173	MLYONS@waterboards.ca.gov							
3	Region:	4	Date:	May/June 2011	email:	msigala@miml.calstate.edu	(213) 576-6718							
4					Mailing Address:	7544 Sandholdt Rd.								
5						Moss Landing, CA 95039								
6														
7			Water	Water	Water	Water	Water	Water	Water	Water		Water	Water	Sediment
8			Inorganics ¹	Inorganics ²	Inorganics ³	Inorganics	TSS	SSC	DOC	Organics		Chl a	AFDM	Organics
9			1 L HDPE CL, CO4, ALK, TDS, SIO2	500ml HDPE Nutrients	125 ml HDPE OrthoPhosphate as P (dissolved, OPO4) Nitrite as N	125 ml HDPE Hardness as CaCO3	2L HDPE	1L HDPE	125ml Amber	Pyrethroids/Pyrethrins 8081B				Pyrethroids/Pyrethrins
10	Station	SampleType									SampleType			8081BM
11	FIELDQA	FieldBlank			x						FieldBlank			
12	FIELDQA	FieldBlank									FieldBlank			
13	FIELDQA	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
14	FIELDQA	Grab									Integrated	x	x	
15	403S01136	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
16	403S01536	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
17	403S01728	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
18	403S02363	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
19	403S02764	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
20	403S04868	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
21	404S11880	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
22	404S13416	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
23	404S13672	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
24	404S14952	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
25	404S16232	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
26	404S18666	Grab	x	x	x	x	x	x	x	x	Integrated	x	x	x
27	TOTAL		13	13	14	13	13	13	13	13		14	14	13
28	¹ Inorganics = Total Dissolved Solids (TDS), Sulfate (SO4), Alkalinity as CaCO3 (ALK), Chloride (CL), Silica as SIO2 (dissolved)													
29	² Inorganics = Ammonia as N (NH3), Nitrogen -Total (direct measurement), Nitrate as N (NO3), Phosphorous as P (total, TPPOS)													
30	³ Inorganics = Nitrite as N (NO2), OrthoPhosphate as P (dissolved, OPO4)													

- The lab-specific worksheet shows the Stations for which the samples are being collected along with a chart listing the variables that should be analyzed in each matrix for each Station.



- o This sheet also lists the general information for a sampling event, such as Region, Group, and Date. This information assists in maintaining consistency in reporting for all components of the sample in the database. Work Order and Contract Number are also listed.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	LabSampleID	StationCode	EventCode	ProtocolCode	LocationCode	SampleDate	CollectionTime	CollectionMethodCode	SampleTypeCode	Replicate	CollectionDepth	UnitCollectionDepth	ProjectCode	AgencyCode	CollectionComments	SampleID
2		FIELDQA	BA	Not Applicable	Not Applicable			None	FieldBlank	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
3		FIELDQA	BA	Not Applicable	Not Applicable			None	FieldBlank	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
4		FIELDQA	BA	SWAMP_2007_WS	X			Water_Grab	Grab	2	0.1 m		RWB4_SMC_2011	MPSL-DFG		
5		403S01136	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
6		403S01536	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
7		403S01728	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
8		403S02363	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
9		403S02764	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
10		403S04868	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
11		404S11880	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
12		404S13416	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
13		404S13672	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
14		404S14952	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
15		404S16232	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
16		404S18666	BA	SWAMP_2007_WS	X			Water_Grab	Grab	1	0.1 m		RWB4_SMC_2011	MPSL-DFG		
17		FIELDQA	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	2	-88 m		RWB4_SMC_2011	MPSL-DFG		
18		FIELDQA	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	2	-88 m		RWB4_SMC_2011	MPSL-DFG		
19		403S01136	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
20		403S01536	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
21		403S01728	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
22		403S02363	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
23		403S02764	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
24		403S04868	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
25		404S11880	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
26		404S13416	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
27		404S13672	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
28		404S14952	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
29		404S16232	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
30		404S18666	BA	SWAMP_2007_WS	X			Algae_SWAMP	Integrated	1	-88 m		RWB4_SMC_2011	MPSL-DFG		
31		FIELDQA	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	2	2 cm		RWB4_SMC_2011	MPSL-DFG		
32		403S01136	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	1	2 cm		RWB4_SMC_2011	MPSL-DFG		
33		403S01536	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	1	2 cm		RWB4_SMC_2011	MPSL-DFG		
34		403S01728	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	1	2 cm		RWB4_SMC_2011	MPSL-DFG		
35		403S02363	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	1	2 cm		RWB4_SMC_2011	MPSL-DFG		
36		403S02764	BA	SWAMP_2007_WS	X			Sed_Grab	Integrated	1	2 cm		RWB4_SMC_2011	MPSL-DFG		

- The **Data** worksheet provides the sample information in the correct format for the laboratory to paste into the template or transformer in order to enter the analysis results.
- The **LabBatch** worksheet lists the headers needed for the chemistry template.
- A **DataExample** worksheet is also listed which gives an example of the final formatting of the chemistry template.
- The remaining worksheets are named by analytical method and include SWAMP organic analytes and the SWAMP target reporting limits for each of those analytes.

Regardless of whether an organization chooses to use these Analysis Authorization Forms, or others like them that serve the same purpose, they are useful tools to help communicate and maintain consistency regarding samples collected and analyzed. If interested, contact the SWAMP DMT to receive an electronic version of an AA form template.



3. WATER QUALITY (CHEMISTRY AND BACTERIA) DATA

The data for sediment chemistry, water column chemistry, and bacteria analyses are treated in a similar way in the SWAMP Database and for this reason will be treated together in this portion of the document.

a. Chemistry Data Template

The Chemistry Data Template is available online at <http://swamp.mpsl.mlml.calstate.edu/resources-and-downloads/database-management-systems/swamp-25-database/templates-25/#Chem>.

b. Formatting the Data

A Microsoft Excel template exists for laboratories to use to format the chemistry laboratory data in a manner that can be easily loaded into the SWAMP database. As previously discussed, for many labs working under the SWAMP master contract, the station collection information can be obtained from the Analysis Authorization form. This section will discuss each of the fields in the template and how to populate them.

All valid LookUp list values are available at http://checker.swamp.mpsl.mlml.calstate.edu/SWAMP_Checker/LookUpLists.php. At any time, if the necessary field does not appear in the LookUp list, the SWAMP Data Management Team (DMT) must be contacted to have it added.



i. Chemistry Results Worksheet

There are two worksheets that must travel with the data for the data package to be considered complete. The first holds all chemistry or bacteria results, including quality control (QC) data, and should be named **Results** in a worksheet tab. Each record in this sheet represents a result from a specific analysis for a particular parameter at a single station or for a single QC sample. This worksheet will also contain all supporting QC sample results. If beginning with an Analysis Authorization form, the following fields will likely be pre-populated in the **Data** worksheet: *EventCode*, *ProtocolCode*, *StationCode*, *LocationCode*, *CollectionMethodCode*, *SampleTypeCode*, *Replicate*, *CollectionDepth*, *UnitCollectionDepth*, *ProjectCode*, and *AgencyCode*. Please note that all fields are required to have data except when otherwise noted below. Examples of special types of samples are listed in the [Special Circumstances](#) section.



Template Field Name	LookUp List	Description & Business Rules
LabSampleID		<p>The LabSampleID is a recommended field intended to provide lab specific identification for an analyzed sample.</p> <p>BR: The format and content is determined by the lab. It is preferable to add -Dup, -MS, -MSD to the end of the ID to help confirm the SampleType and the LabSampleID of the native sample.</p>
StationCode	<u>StationLookUp</u>	<p>StationCode represents a unique sampling site in a sampling design. A single waterbody may have multiple stations.</p> <p>BR: StationCode should represent a geographic location not a geographic location combined with a replicate reference. There cannot be multiple StationCodes and/or StationNames in the StationLookUp with the same target latitude/longitude coordinates.</p> <p>The format for the unique alphanumeric description of the station is ###ABC123, where ### is the first 3 digits preceding the decimal in the Calwater Watershed ID Number from CALWater221 data layer and ABC123 is a minimum of 3 and a maximum of 6 character length combination of an alphanumeric description of the Station. One example is 103SM6897 which is Regional Board/Hydrologic Unit Number 103 and an abbreviated code to indicate "Smith River above South Fork". Another example is 304SOK which is Regional Board/Hydrologic Unit Number 304 and an abbreviated code to indicate "Soquel Creek at Knob Hill Parking Lot".</p> <p>If the correct Hydrologic Unit is not known, populate the first number with the regional board number; i.e. the station is known to be in California Regional Water Board 3, the StationCode would be 300##### or 300###. If the station is not in California (Nevada, Arizona, Oregon, Mexico, etc.), the Regional Board/Hydrologic Unit Number is 000, for example 000MLP1xx.</p>



Template Field Name	LookUp List	Description & Business Rules
EventCode	<u>EventLookUp</u>	<p>EventCode represents the primary intent of the sampling event at a particular station.</p> <p>BR: The EventCode will be in a hierarchical order as follows:</p> <p>BA – If the initial intent of sampling is for Bioassessment (PHab, BMI [freshwater], and/or Algae) (Tissue and/or WaterQuality samples may or may not also be collected)</p> <p>TI – If the initial intent of sampling is for Tissue (WaterQuality samples may or may not also be collected; no associated Bioassessment samples collected)</p> <p>WQ – If the initial intent of sampling is for WaterQuality (Water, Sediment, Toxicity, and/or Marine Benthic Abundance) (no associated Bioassessment or Tissue samples collected)</p> <p>For example, if the initial intent of sampling on Day 1 was for Tissue and WaterQuality, the EventCode would be TI. If for some reason the WaterQuality had to be re-sampled the next day, on Day 2, the event for the re-sampling would still be TI because Tissue was the initial intent of sampling on Day 1 even though WaterQuality was sampled on Day 2.</p>
ProtocolCode	<u>ProtocolLookUp</u>	<p>ProtocolCode represents the sampling protocol used, which includes the set of methods, methodology, and/or specifications; e.g. MPSSL-DFG_Field_v1.0 or SWAMP_WS_2007. Established protocols may be used or regions may document their own sampling protocols.</p> <p>BR: It is preferable to combine protocols per StationCode and date so that all WaterQuality, Bioassessment, and Tissue data are combined under the same EventCode and Protocol. For example, if Tissue and WaterQuality are sampled at a station, the EventCode would be TI. If the protocols are different for Tissue and WaterQuality, the Tissue protocol would be used and the WaterQuality protocol would be listed in the SampleComments. If that is not preferable, separate EventCodes may be used with each individual protocol.</p> <p>Not Recorded is only used for historic data. All non-historic SWAMP projects require a true protocol reference. Not Applicable is used for LABQA and 000NONPJ samples only.</p>



Template Field Name	LookUp List	Description & Business Rules
LocationCode	<u>LocationLookUp</u>	<p>LocationCode describes the physical location in the waterbody where the sample was collected. One sampling event may have a single or multiple locations.</p> <p>BR: For a single point of sampling, the physical location in the waterbody can be used such as Bank, Thalweg, Midchannel, X (general location for bioassessments), OpenWater, or Transect 1.</p> <p>For field results, the LocationCode should be the same as the location for the WaterQuality collection method.</p> <p>For BA EventCode sampling, a location of X is used to associate the water quality, field measure, and taxonomy data to one bioassessment sampling location regardless of where they were sampled in the waterbody.</p> <p>For TI EventCode sampling, the physical location plus the CollectionMethod is used such as BankNet1, BankShock1, OpenWaterTrawl1, OpenWaterNet1. For resident mussel or clam collections, the LocationCode would be the physical location in the water body plus the generic CollectionMethod, e.g. BankTissue_Grab1.</p> <p>OpenWater sampling with multiple sub-locations within a single water body or station could have locations of OpenWaterTrawl1, OpenWaterTrawl2 describing one large location with two smaller areas of sampling within the OpenWater Location.</p> <p>Multiple physical locations within a single station could consist of a LocationCode such as BankShock1, BankNet1, OpenWaterHook1.</p> <p>If recording specific locations within a station are necessary for the project, a LocationCode such as Location1Net1, Location1Net2, Location2Shock1 may be used.</p>



Template Field Name	LookUp List	Description & Business Rules
SampleDate		<p>SampleDate refers to the date the sample was collected in the field.</p> <p>BR: The format for date in the templates is dd/mmm/yyyy, such as 10/Nov/2013. When entering data using the forms, the format is mm/dd/yy.</p> <p>For WQ samples with collection times that last longer than one day, like autosamplers, the sample date is the date sample was retrieved. For transplanted bivalves, the SampleDate is the date the transplanted organisms were collected, removed, or retrieved from the field. For overnight tissue collections, the SampleDate is the date the sample was retrieved.</p>
CollectionTime		<p>CollectionTime refers to the time when the first sample of a sampling event at a specific station was collected in the field.</p> <p>BR: If the sampling crew collects 18 bottles at a single station, the CollectionTime for each would be the time of the first bottle collected. By doing so, the samples can easily be linked and any holding time issues will be consistent and conservative for laboratory work.</p> <p>The CollectionTime format should be expressed as hh:mm in 24 hour time, such as 13:30 for 1:30 pm.</p> <p>For BA sampling events, the CollectionTime should reflect the shortest holding time for the chemistry samples that were collected. Other CollectionTimes (e.g., Field, Habitat, Benthic) may be different times than the LabCollectionTime.</p>
CollectionMethodCode	<u>CollectionMethodLookUp</u>	<p>CollectionMethodCode refers to the general method of collection such as Sed_Grab, Sed_Core, Water_Grab, Autosampler24h, Autosampler7d, Algae_SWAMP.</p> <p>BR: The SWAMP water default is Water_Grab and the sediment default is Sed_Grab.</p>
SampleTypeCode	<u>SampleTypeLookUp</u>	<p>SampleTypeCode refers to the type of sample collected or analyzed.</p> <p>BR: Some commonly used SampleTypeCode choices include Grab, Integrated, MS1, CRM, LCS, LabBlank, CNEG, Composite. If a bottle is broken, the submitting laboratory should not delete the sample and collection row from the MS Excel results file.</p>



Template Field Name	LookUp List	Description & Business Rules
Replicate		<p>The Replicate number is used to distinguish between replicates created for a single collection in the field.</p> <p>BR: The default is 1. Field Duplicates will be identified by a Replicate of 2. Field Blind Duplicates will be identified with a different SampleTypeCode of FieldBLDup, not a collection Replicate, because they are collected blind. Laboratory replicates will be identified by a replicate of 2 in the LabReplicate field, not a collection Replicate. The intent of any replicate greater than 1 is to compare the data to the native or first replicate.</p> <p>When field duplicates are collected, the samples are given a StationCode of FIELDQA and a SampleTypeCode of Grab or Integrated with a Replicate of 2. When the chemistry data are loaded into the database, the StationCode FIELDQA will be given the correct StationCode of the native sample and the Replicate will be used to distinguish the duplicate sample from the native sample. EventCode, ProtocolCode, LocationCode, SampleDate, CollectionTime, CollectionMethodCode, CollectionDepth, UnitCollectionDepth, ProjectCode and AgencyCode should be identical for both samples taken.</p>



Template Field Name	LookUp List	Description & Business Rules
CollectionDepth		<p>CollectionDepth records the level, from the surface in the water or sediment column, at which the sample was collected.</p> <p>BR: This information should be listed on the Chain of Custody (COC) document that accompanies the samples from the field or it is a default value if using the bioassessment field forms. CollectionDepth for water samples would be measured from the water surface and recorded in meters (m) while depth collected for sediment would be measured from the sediment surface and recorded in centimeters (cm).</p> <p>Since depths for ambient monitoring Grab samples are generally “subsurface”, defaults have been established to indicate this. For water samples, the default value is 0.1 m and for sediment samples, the default value is 2 cm. A single sediment core should receive a depth indicating the maximum depth of the core.</p> <p>For Integrated samples collected from the same depth at different points across a waterbody or for samples collected at multiple times, i.e. an autosampler, the actual sample depth should be recorded. This applies to both water and sediment samples. Integrated samples collected at multiple depths, i.e. samples integrated from the water column or multiple sediment cores, should receive a depth of -88 and the actual depths of collection should be recorded in the CollectionComments field.</p>
UnitCollectionDepth	<u>VariableCodesLookUp</u>	UnitCollectionDepth refers to the units used in the CollectionDepth including cm (centimeters) and m (meters). This information should be listed on the Chain of Custody (COC) document that accompanies samples from the field.
ProjectCode	<u>ProjectLookUp</u>	<p>ProjectCode is a unique code referencing a project which includes data from a single study design; e.g. RWB5_StS_FY0708, RWB2_Status_YR1, RWB7_Trend_2003, SWB_RCMP_2008.</p> <p>BR: ProjectCodes with FY in the name indicate samples were collected in a fiscal year calendar cycle, e.g. FY0708 would indicate fiscal year 2007-2008 which is July 1, 2007 through June 30, 2008. ProjectCodes without FY indicate samples were collected in a calendar year, e.g. 2003 would indicate calendar year 2003 which is January 1, 2003 through December 31, 2003. Each Project must have an associated QAPrP or Project QAPP listed. SWAMP moves data to the permanent side of the database by ProjectCode.</p>



Template Field Name	LookUp List	Description & Business Rules
AgencyCode	<u>AgencyLookUp</u>	<p>AgencyCode refers to the organization or agency that collected the sample. This should be listed on the Chain of Custody (COC) document that accompanies the samples from the field.</p> <p>BR: If an environmental sample is used to perform laboratory QC, i.e. a matrix spike or lab duplicate, the AgencyCode still refers to the agency that collected the native sample, not the agency that created the QC sample.</p> <p>See 'Special Circumstances' for LABQA business rules.</p>
LabCollectionComments (Not Required)		<p>LabCollectionComments records any comments relating to the collection of the field sample for laboratory analysis.</p> <p>BR: This field can also be used for laboratory QC samples, e.g. Matrix Spike was performed on a FieldBlank. If certain PurposeFailureCodes do not apply to all SampleTypeCodes, include this information in the LabCollectionComments field. If a sample collection is missing an expected bottle for an analyte or analyte group, or the bottle broke or was lost enroute to or at the laboratory, enter a comment here describing which analyte and why results are not reported. The submitting laboratory should not delete the sample row from the MS Excel file.</p>
SampleID (Not Required)		<p>SampleID is a unique identifier supplied by the organization directing the sampling or sampling agency and is used to track the sample throughout the sampling and analysis processes. This field can be used to tie a result to the sample.</p> <p>BR: This SampleID, which is different from the StationCode, will likely be on the sample container the laboratory receives from the field crew or on the COC. If there is no number, leave this field blank.</p>



Template Field Name	LookUp List	Description & Business Rules
PrepPreservationName	<u>PrepPreservationLookUp</u>	<p>PrepPreservation references the preparation or preservation method performed on the samples prior to analysis.</p> <p>BR: If no preparation or preservation method was performed the default value is None. A PrepPreservation begins with "Lab" when the sample is prepared or preserved in a clean laboratory environment. A PrepPreservation begins with "Field" when the sample is prepared or preserved onsite or outside a clean laboratory environment. When a laboratory adds a preservative to a bottle in the laboratory (or a bottle is prefilled with preservative from the manufacturer) and that bottle is transported to the field with the preservative and the sample is then added to the bottle, this would be considered "Field" not "Lab" because the sample was actually preserved in the field.</p> <p>The PrepPreservation and PrepPreservationDate should reflect any filtering that is performed as part of the method or to remove organic materials prior to loading onto an instrument.</p>
PrepPreservationDate		<p>PrepPreservationDate is the date and time the preparation or preservation was started.</p> <p>BR: The format is dd/mmm/yyyy hh:mm. If there is no preparation or preservation method performed (None) then the PreparationPreservationDate should be listed as 01/Jan/1950 00:00 (the SWAMP default date/time value for none).</p>
DigestExtractMethod	<u>DigestExtractLookUp</u>	<p>DigestExtractMethod references the digestion or extraction method performed on the sample prior to analysis.</p> <p>BR: If no digestion or extraction method was performed the default value is None.</p>
DigestExtractDate		<p>DigestExtractDate is the date and time the digestion or extraction was started.</p> <p>BR: The format is dd/mmm/yyyy hh:mm. If there is no digestion or extraction performed on the sample (None) then the DigestExtractDate should be listed as 01/Jan/1950 00:00 (the default value for none).</p>



Template Field Name	LookUp List	Description & Business Rules
LabBatch		<p>The LabBatch is a unique code, provided by the laboratory, which represents a group of samples processed together. It groups all environmental samples with their supporting QC samples and will be used to verify completeness based on the SWAMP QAPrP.</p> <p>BR: The LabBatch is assigned to and identifies all samples digested or extracted together in one batch. When a digestion or extraction is not performed as part of the method, the LabBatch represents all samples within a unique analysis run. Please see the File and Batch Naming Convention to correctly format the LabBatch name.</p> <p>All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.</p>
AnalysisDate		<p>AnalysisDate is the date and time the sample was processed on the analytical instrument.</p> <p>BR: This date/time should be expressed as dd/mmm/yyyy hh:mm. For bacteria results, this analysis date/time is the time samples were put into the incubator, not the time the samples were read. For other analyses, individual injection or run times should be provided for analytes with hourly analysis holding time criteria, e.g. NO2, OPO4.</p>
LabReplicate		<p>The LabReplicate number is used to distinguish between replicates created in the laboratory. It differentiates the original field sample that was analyzed from all subsequent laboratory duplicates.</p> <p>BR: The default is 1 for the first sample and increases by one for each successive replicate analyzed in the laboratory. The intent of any replicate greater than 1 is to compare the data to the native or first replicate.</p>



Template Field Name	LookUp List	Description & Business Rules
MatrixName	<u>MatrixLookUp</u>	<p>MatrixName refers to the sample matrix. In cases where water or sediment are filtered to obtain a certain portion or fraction of the sample for analysis (not the dissolved portion of the analyte) the filtration size would be included in the MatrixName; e.g. sediment, <63um; samplewater, <125um. See ConstituentLookUp for Matrix, Method, Analyte, Fraction, and Unit combinations.</p> <p>BR: Water - For field-generated water samples, the MatrixName is samplewater. For lab-generated QC samples, the matrix should be the type of water that was used for the analysis of the sample, either labwater or blankwater. Labwater is water coming either directly from the tap in the laboratory or purchased spring water. Blankwater is laboratory Type I or Type II water, purchased reagent water or water that is run through a filtration process in a laboratory, such as Deionized (DI) or Milli-Q (MQ) water.</p> <p>Sediment - For field-generated sediment samples, the MatrixName is sediment. For lab-generated QC samples, blankmatrix could be used as the MatrixName which is a matrix used to identify a commercial- or lab-produced medium in tissue or sediment QC samples. If this is not the case then the MatrixName for lab-generated QC samples would be sediment which would include samples where water, solvent or nothing was used as a matrix.</p> <p>Tissue - For field-generated tissue samples, the MatrixName is tissue. For lab-generated QC samples, blankmatrix could be used as the MatrixName which is a matrix used to identify a commercial- or lab-produced medium in tissue or sediment QC samples. If this is not the case then the MatrixName for lab-generated QC samples would be tissue which would include samples where water, solvent or nothing was used as a matrix.</p>



Template Field Name	LookUp List	Description & Business Rules
MethodName	<u>MethodLookUp</u>	<p>MethodName refers to the analysis method used by the laboratory to analyze the sample. See ConstituentLookUp for Matrix, Method, Analyte, Fraction, and Unit combinations.</p> <p>BR: Methods are expressed with a MethodName such as SM 4500-NH3 C or EPA 600/R-99-064 and must be fully described in the Method Lookup list and in the laboratory records. If a laboratory has modified an EPA or Standard Method, the laboratory agency needs to add "M" to end of the MethodName. In such situations, the modification should be documented and communicated to the SWAMP DMT for notation in the database. For instance, a lab would report a modified EPA 600/R-99-064 as EPA 600/R-99-064M accompanied by a description of the modification made. Any method for the SWAMP Project which is not in the current SWAMP database lookup list must be approved by the SWAMP QA Team prior to being added to the database.</p> <p>For BA sampling, reference the most recent version of the Bioassessment Analyte and Location Crosswalk document on the SWAMP DMT/QAT website to help populate the correct constituent parameters for corresponding analytes and locations. This document will help in distinguishing the differences between the habitat and field methods FieldObservation, Field Measure, and ObservedFieldMeasure.</p>
AnalyteName	<u>AnalyteLookUp</u>	<p>The AnalyteName is the name of the analyte or parameter for which the analysis is conducted and result is reported. The lookup list includes the acceptable abbreviation or name of the variable used by the database, enabling consistency across reporting. See ConstituentLookUp for Matrix, Method, Analyte, Fraction, Unit combination.</p>



Template Field Name	LookUp List	Description & Business Rules
FractionName	<u>FractionLookUp</u>	<p>FractionName is a specific descriptor of the Analyte. See ConstituentLookUp for Matrix, Method, Analyte, Fraction, and Unit combinations.</p> <p>BR: Analytes are often expressed as Total or Dissolved, each of which would be expressed as the Fraction, distinguishing the appropriate Analyte. This is usually when a preparation is performed in addition to the analysis method; e.g. Mercury, Dissolved; Aldrin, Total.</p> <p>Some analyses may have sample filtering as part of the method intended for particulate cleanup, this would not necessarily constitute a Dissolved fraction.</p> <p>Refer to the Analytes and Units per Matrix file on the SWAMP DMT-QAT website for appropriate Analyte, Fraction, Unit combinations per matrix.</p>
UnitName	<u>UnitLookUp</u>	<p>Unit refers to how the chemistry result is measured or expressed. See ConstituentLookUp for Matrix, Method, Analyte, Fraction, and Unit combinations.</p> <p>BR: Each combination of Analyte and Matrix requires that a specific Unit be used in the SWAMP database to ensure comparability across data. This listing can be found on the SWAMP Online Data Checker website under the LookUp List "Analyte with Unit per Matrix" at http://checker.swamp.mpsl.mlml.calstate.edu/SWAMP_Checker/LookUpLists.php.</p> <p>Water units are indicated by weight/volume, i.e. ng/L. Sediment and tissue units are indicated by weight/weight and includes whether the sample result is reported as wet weight (ww) or dry weight (dw). For example, ng/g ww for ng/g wet weight. Surrogates recovery results will use a unit of %.</p>



Template Field Name	LookUp List	Description & Business Rules
DilutionFactor		<p>DilutionFactor is the factor by which a sample was diluted and is reported as a whole number.</p> <p>BR: Default value is 1. A dilution other than 1 is recorded when a sample requires an additional dilution to fit into the standard curve of the instrument. It does not apply to dilutions that are standard in the method being used for analysis.</p> <p>Final reported results, along with the MDL and RL, must be corrected for dilution that was carried out during the process of analysis.</p> <p>1 part sample plus 9 parts blank is a DilutionFactor of 10. A 50% dilution is equivalent to a DilutionFactor of 2.</p> <p>A QACode of D is required when a dilution is performed on the sample.</p>
Result		<p>Result is the final numeric result of a given analyte, stored as text to retain trailing zeros.</p> <p>BR: The chemistry Result is expressed as a real number rather than a calculation. The result should be reported with appropriate number of significant figures.</p> <p>A result of 3.7266945 with 3 significant figures should be reported as 3.73.</p> <p>A result of 1.350 with 4 significant figures must display 1.350 in the Excel file. If you only see 1.35, that is the result that will be loaded to the database and the 4th significant figure will be dropped.</p>



Template Field Name	LookUp List	Description & Business Rules
ResQualCode (Not Required)	<u>ResQualLookUp</u>	<p>The ResQualCode is the result qualifier code that qualifies the analytical result of the sample.</p> <p>BR: This field may be left blank for results that are considered detected. The database will be populated with an equal sign (=) when the data are loaded. When a result is Not Detected (ND) or Detected Not Quantified (DNQ) a ResQualCode is required and the appropriate code would be applied.</p> <p>When the result is -88, a ResQualCode is required. If the ResQualCode value is NR for Not Recorded, then a reason for this code must be written into the LabResultComments field and/or an appropriate QACode would be applied.</p>
MDL		<p>Method Detection Limit (MDL) is the minimum concentration of an analyte that undergoes the entire measurement process and can be reported with a stated level of confidence that the analyte concentration is greater than zero. It is the detection limit associated with the method used to analyze the analyte, or parameter, in the sample.</p> <p>BR: If no MDL is used, enter -88. A value other than -88 must be used for either the MDL or the RL.</p>
RL		<p>Reporting Limit (RL) is the minimum value below which data are documented as nonquantifiable. It is the reporting limit for the sample analyzed, as determined by the laboratory.</p> <p>BR: If no RL is used, enter -88. A value other than -88 must be used for either the RL or the MDL.</p>
QACode	<u>QALookUp</u>	<p>QACode is applied to the result to describe any special conditions, situations or outliers that occurred during or prior to the analysis to achieve the result.</p> <p>BR: The default code, indicating no special conditions, is None. If more than one code should be applied to a record, the convention is to list them in alphabetical order separated by commas and no spaces; e.g. GB,SC.</p>



Template Field Name	LookUp List	Description & Business Rules
ExpectedValue (Not Required)		<p>The ExpectedValue is the concentration of the analyte in a reference standard, laboratory control sample or matrix spike sample or the value expected to obtain from analysis of the QC Sample. This consists of the native sample result concentration plus the spike amount.</p> <p>BR: This field is required for SampleTypeCodes of MS1, MS2, CRM and LCS.</p>
LabResultComments (Not Required)		<p>The LabResultComments field holds any comments related to the lab result or analysis of the sample.</p> <p>BR: These could be comments needed to clarify any portion of the analysis or a comment that is not accommodated by any other field, e.g. Percent Recovery or Relative Percent Difference. For reference standards, laboratory control samples and matrix spikes, it is recommended to include the Percent Recovery as PR xx and the Relative Percent Difference as RPD xx. When used in combination, as in Matrix Spike Duplicate samples, the convention would be PR xx, RPD xx.</p> <p>See 'Special Circumstances' for Matrix Spike and Lab Duplicate business rules.</p>



ii. Chemistry LabBatch Worksheet

The second worksheet to travel with the data holds information specific to the laboratory batch in which data is analyzed. This worksheet should be named **LabBatch** (with no spaces) in a worksheet tab. The fields in this sheet are and should be completed as follows:

Template Field Name	LookUp List	Description & Business Rules
LabBatch		<p>The LabBatch is a unique code, provided by the laboratory, which represents a group of samples processed together. It groups all environmental samples with their supporting QC samples and will be used to verify completeness based on the SWAMP QAPrP.</p> <p>BR: The LabBatch is assigned to and identifies all samples digested or extracted together in one batch. When a digestion or extraction is not performed as part of the method, the LabBatch represents all samples within a unique analysis run. Please see the File and Batch Naming Convention to correctly format the LabBatch name.</p> <p>All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.</p>
LabAgencyCode	<u>AgencyLookUp</u>	LabAgencyCode refers to the organization, agency or laboratory that performed the analysis on the sample.
LabSubmissionCode	<u>LabSubmissionLookUp</u>	<p>The LabSubmissionCode is a unique batch qualifier code assigned to the LabBatch as a whole by the analyzing laboratory which references the quality of the data in the LabBatch.</p> <p>BR: If the LabSubmissionCode of A is used, meaning Acceptable, the laboratory is ensuring that all SWAMP QAQC protocols were met for the lab batch. If anything other than A is used, a LabBatchComment is required.</p>
SubmittingAgencyCode	<u>AgencyLookUp</u>	SubmittingAgencyCode is the organization or agency that is responsible for submission of the data to the database. This agency may be different from LabAgencyCode if the analytical data were subcontracted to another agency.
LabBatchComm (Not Required)		<p>LabBatchComments records any comments relating to the LabBatch as a whole.</p> <p>BR: If the LabSubmissionCode is anything other than "A", a LabBatchComment is required.</p>



c. Quality Control Results

SWAMP requires that all associated Quality Control (QC) data (when applicable: blanks, reference material, matrix spikes, and lab duplicates) for a batch be reported in one file along with the corresponding SWAMP field samples. The exception to this is that SWAMP does not require initial or continuing calibrations, internal standards or bacteria controls or sterility checks to be reported however, they are still required to be performed and documented internally by the laboratory. The batch QC will be used to verify the Measurement Quality Objectives stated in the QAPrP.

d. Special Circumstances

There are several types of special circumstances discussed in this section. One type includes samples that are generated or created by the laboratory (LABQA). Another type includes environmental samples that are modified by the laboratory. A third type includes samples that are created by the sampling agency that are not environmental samples and may or may not have been created in the field (FIELDQA).

For a list of QA sample types required for each type of chemical analysis, please see the QAPrP.

i. Laboratory-generated QA samples (LABQA)

All samples generated from within the laboratory, such as LabBlank, LCS, CRM, etc. have specific business rules, which are as follows:

<i>LabSampleID</i>	Recommended - provide lab specific identification for an analyzed sample
<i>StationCode</i>	LABQA
<i>EventCode</i>	WQ for water and sediment chemistry
<i>ProtocolCode</i>	Not Applicable
<i>LocationCode</i>	Not Applicable
<i>SampleDate</i>	Date sample was digested/extracted, expressed as dd/mmm/yyyy. When no digestion/extraction was performed, <i>SampleDate</i> is equal to the analysis date.
<i>CollectionTime</i>	0:00 There are situations within a batch when two identical sample types are used for QA reasons and the only way to differentiate between them is to give them each a different <i>CollectionTime</i> . For example, when more than one LabBlank, CRM, or LCS is digested, extracted, or analyzed in the same batch on the same day but are not replicates of each other, one <i>CollectionTime</i> should be 0:00 and the other 0:15, increasing the time by 15 minutes for each additional sample.
<i>CollectionMethodCode</i>	Not Applicable
<i>SampleTypeCode</i>	Select from <u>SampleTypeLookUp</u> List
<i>Replicate</i>	1
<i>CollectionDepth</i>	-88
<i>UnitCollectionDepth</i>	m for water or cm for sediment



<i>ProjectCode</i>	Not Applicable
<i>AgencyCode</i>	Organization or agency that analyzed the sample
<i>Matrix</i>	Water samples - labwater or blankwater Sediment samples - blankmatrix (commercially generated product) or sediment (if laboratory is using solvent, water, or nothing)

The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

<i>ParentProjectCode</i>	Not Applicable
<i>ProgramCode</i>	QA
<i>CollectionDeviceCode</i>	None

ii. Laboratory-modified QA samples

There are several types of samples discussed in this section that are generated or modified within the laboratory. The first is a Matrix Spike, which is a modified or analyte-spiked field sample. The second is a laboratory-generated duplicate of a field sample. At times, laboratories use samples not generated through the SWAMP program to satisfy SWAMP batch QA requirements. This third type is a Non-Project sample.

(a) Matrix Spike and Laboratory Duplicate Samples

For these samples, all fields describing the sample (*StationCode*, *EventCode*, *ProtocolCode*, *LocationCode*, *SampleDate*, *CollectionTime*, *CollectionMethodCode*, *CollectionDepth*, *UnitCollectionDepth*, *ProjectCode*, *AgencyCode*) remain the same as the native sample. For Matrix Spike samples, the only fields that are different than the native field sample is the *SampleTypeCode*, which should be MS1, MS2, or MSBLDup, and potentially the *Replicate*. For laboratory-generated Duplicate samples, the only field that is different than the native field sample is the *LabReplicate*.

<i>LabSampleID</i>	Recommended - provide lab specific identification for an analyzed sample. It is preferable to add -Dup, -MS, -MSD to the end of the Lab ID to help confirm the <i>SampleTypeCode</i> and the <i>LabSampleID</i> of the native sample.
<i>StationCode</i>	Same as native field sample
<i>EventCode</i>	Same as native field sample
<i>ProtocolCode</i>	Same as native field sample
<i>LocationCode</i>	Same as native field sample
<i>SampleDate</i>	Same as native field sample
<i>CollectionTime</i>	Same as native field sample
<i>CollectionMethodCode</i>	Same as native field sample



<i>SampleTypeCode</i>	<p>Same as native field sample - laboratory-generated Duplicates MS1 - Matrix Spike performed on a Grab or Integrated sample MS2 - Matrix Spike performed on a FieldDup (Grab or Integrated with a <i>Replicate</i> of 2) MSBLDup - Matrix Spike performed on a FieldBLDup</p> <p>There are situations when a Matrix Spike was unintentionally performed on a blank sample such as a FieldBlank, TravelBlank, EquipBlank, DIBLank or FilterBlank. A batch may include two or more of these types of native samples where the only difference between them is the <i>SampleTypeCode</i>. The only way to differentiate them is to give each a different <i>CollectionTime</i>. For example, when a batch contains both a DIBLank and an EquipBlank (both with an original time of 0:00) and a Matrix Spike was performed on the EquipBlank, one <i>CollectionTime</i> should be 0:00 and the other 0:15. Then the MS1 <i>CollectionTime</i> should correspond to the correct native sample time.</p>
<i>Replicate</i>	1
<i>CollectionDepth</i>	Same as native field sample
<i>UnitCollectionDepth</i>	Same as native field sample
<i>ProjectCode</i>	Same as native field sample
<i>AgencyCode</i>	Same as native field sample
<i>LabReplicate</i>	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
<i>Matrix</i>	Same as native field sample
<i>LabResultComments</i>	<p>For Laboratory Duplicates, if either the native or duplicate (or both) are less than the Reporting Limit then the RPD is reported as RPD NA. If both results are ND, then the RPD is reported as RPD 0.</p> <p>For Matrix Spike samples, see Calculating Matrix Spike Percent Recovery and Calculating Matrix Spike Relative Percent Difference for more information</p>

The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

<i>CollectionDeviceCode</i>	Same as native field sample
<i>PositionWaterColumn</i>	Same as native field sample



(i) Matrix Spike Samples performed on Field Duplicates

Following is a table that describes the way to format matrix spike samples performed on field duplicates, field blind duplicates, and composite blind duplicates. The *SampleTypeCode* MS represents an MS/MSD pair.

Field Sampling Scenario			SWAMP Database Format	
<i>SampleTypeCode</i>	<i>Sample Replicate</i>		<i>SampleTypeCode</i>	<i>Replicate</i>
One sample - sampled or split in triplicate - blind				
Grab	1	=	Grab	1
FieldBLDup	1	=	FieldBLDup or CompBLDup	1
FieldBLTrip	1	=	FieldBLDup or CompBLDup	2
One sample - sampled or split in triplicate				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
FieldTrip	1	=	Grab	3
One pair of MS/MSD associated to one grab				
Grab	1	=	Grab	1
MS	1	=	MS1	1
One pair of MS/MSD associated to one grab - FieldDup present				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MS	1	=	MS1	1
One pair of MS/MSD associated to one FieldDup				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MSFDup	1	=	MS2	1
One pair of MS/MSD associated to one FieldBLDup				
Grab	1	=	Grab	1
FieldBLDup	1	=	FieldBLDup or CompBLDup	1
MSFBLDup	1	=	MSBLDup	1
Two pairs of MS/MSD, one associated to the Grab and one associated to the FieldDup				
Grab	1	=	Grab	1
FieldDup	1	=	Grab	2
MS	1	=	MS1	1
MSFDup	1	=	MS2	1



(ii) Calculating Matrix Spike Percent Recovery

The reported lab *Result* is the number gathered from the instrument and is the net amount recovered from the sample including the spike concentration. For spiked samples, the *ExpectedValue* is the total concentration of the analyte in the native sample plus the spiked concentration. Matrix Spike Percent Recovery is calculated by subtracting the native result from both the MS lab *Result* and the MS *ExpectedValue*, then dividing the two by each other and multiplying by 100. To illustrate:

$$\frac{\text{MS Lab Result} - \text{Native}}{\text{MS Expected} - \text{Native}} \times 100 \quad \text{or} \quad \frac{5 - 1}{10 - 1} = \frac{4}{9} \times 100 = 44\%$$

If the sample being used for the matrix spike requires a dilution, the reported values for the MS and the native sample are the dilution corrected values, not the actual values from the instrument.

Always calculate PR unless:

- both the native sample and MS or MSD are ND, then percent recovery is 0 and reported as **PR 0.0**
- if the native sample is significantly greater than the spike concentration, then percent recovery cannot be calculated and is reported as **PR Not Calculable**

(iii) Calculating Matrix Spike Relative Percent Difference

The Relative Percent Difference (RPD) between the MS and MSD is calculated to evaluate how matrix affects precision. There are two different ways to calculate RPD, depending on how the samples are spiked. These are detailed in Appendix A: Measurement Quality Objective Tables of the [QAPrP](#).

RPDs are calculated regardless of the result (detect or not), however if:

- one result is ND and one is detect, then the RPD is reported as **RPD 200**
- both results are ND, then the RPD is reported as **RPD 0**
- both results are DNQ, then the RPD is calculated based on the DNQ results
- if the native sample is significantly greater than the spike concentration then RPD cannot be calculated and is reported as **RPD Not Calculable**

If the RPD is out of compliance, the IL QACode is applied to both the native sample and the duplicate result for that analyte.

(b) Non-Project Matrix Spike and Duplicate Samples (000NONPJ)

At times, laboratories use samples not generated through the SWAMP program to satisfy SWAMP batch QA requirements. These samples have different formatting rules, as follows:

<i>LabSampleID</i>	Recommended - provide lab specific identification for an analyzed sample. It is preferable to add -Dup, -MS, -MSD to the end of the Lab ID to help confirm the <i>SampleTypeCode</i> and the <i>LabSampleID</i> of the native sample.
<i>StationCode</i>	000NONPJ
<i>EventCode</i>	WQ for water, sediment, or benthic chemistry
<i>ProtocolCode</i>	Not Applicable
<i>LocationCode</i>	Not Recorded



<i>SampleDate</i>	Date sample was digested/extracted, expressed as dd/mmm/yyyy. When no digestion/extraction was performed, <i>SampleDate</i> is equal to the analysis date.
<i>CollectionTime</i>	0:00 There are situations within a batch when two identical sample types are used for QA reasons and the only way to differentiate between them is to give them each a different <i>CollectionTime</i> . For example, when more than one 000NONPJ sample with the same <i>SampleTypeCode</i> is digested, extracted or analyzed in the same batch on the same day but are not replicates of each other, one <i>CollectionTime</i> should be 0:00 and the other 0:15, increasing the time by 15 minutes for each additional sample.
<i>CollectionMethodCode</i>	Not Recorded
<i>SampleTypeCode</i>	Grab - lab-generated Duplicates MS1 - Matrix Spikes
<i>Replicate</i>	1
<i>CollectionDepth</i>	-88
<i>UnitCollectionDepth</i>	m for water or cm for sediment
<i>ProjectCode</i>	Not Applicable
<i>AgencyCode</i>	Organization or agency that analyzed the sample
<i>SampleID</i>	The <i>LabSampleID</i> or <i>Source ID</i> can be used here as the <i>SampleID</i> as an indicator to identify the native sample
<i>PrepPreservation</i>	Actual preparation or preservation performed
<i>PrepPreservationDate</i>	Actual preparation or preservation date and time expressed as dd/mmm/yyyy xx:xx
<i>LabReplicate</i>	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
<i>Matrix</i>	samplewater or sediment or benthic
<i>QACode</i>	QAX, when the native sample is not included in the batch reported
<i>LabResultComments</i>	For Laboratory Duplicates, if either the native or duplicate (or both) are less than the Reporting Limit then the RPD is reported as RPD NA . If both results are ND, then the RPD is reported as RPD 0 . For Matrix Spike samples, see Calculating Matrix Spike Percent Recovery and Calculating Matrix Spike Relative Percent Difference for more information



iii. Field-generated QA samples (FIELDQA)

There are two types of samples discussed in this section that are generated in the field. The first is when a field-generated QA sample is created at a specific station and that station information is important to record. The second is when a field-generated QA sample is created for a sampling trip or if the station is not recorded.

(a) Station Specific

For analyses that require an EquipBlank, FieldBlank, or FilterBlank to accompany a sampling event and it is important to record the station information, the data is entered into the SWAMP database in the same manner as the samples in the same group. The specifics are as follows:

<i>LabSampleID</i>	Recommended - provide lab specific identification for an analyzed sample
<i>EventCode</i>	WQ for water and sediment chemistry
<i>ProtocolCode</i>	Protocol associated with the sample
<i>StationCode</i>	Station where sample was created
<i>LocationCode</i>	Location where sample was created
<i>SampleDate</i>	Date sample was created
<i>CollectionTime</i>	Time sample was created or 00:00 There are situations within a batch when two identical sample types are used for QA reasons and the only way to differentiate between them is to give them each a different <i>CollectionTime</i> . For example, when more than one EquipBlank, FieldBlank, or FilterBlank is created on the same day but are not replicates of each other, one <i>CollectionTime</i> should be 00:00 and the other 00:15, increasing the time by 15 minutes for each additional sample.
<i>CollectionMethodCode</i>	Not Applicable
<i>SampleTypeCode</i>	EquipBlank, FieldBlank, or FilterBlank
<i>Replicate</i>	1
<i>CollectionDepth</i>	-88
<i>UnitCollectionDepth</i>	m for water or cm for sediment
<i>ProjectCode</i>	Project associated with the sample
<i>AgencyCode</i>	Organization or agency that created the sample
<i>CollectionComment</i>	EquipBlank - comment includes type of equipment cleaned and location (lab or field)
<i>Matrix</i>	labwater or blankwater



The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

<i>FundingCode</i>	Funding associated with the sample and project
<i>GroupSamples</i>	GroupSample associated with the sample and project
<i>CollectionDeviceCode</i>	None EquipBlank - CollectionDevice used or None
<i>PositionWaterColumn</i>	Not Applicable

(b) Not Station-Specific (FIELDQA)

For analyses that require an EquipBlank, FieldBlank, FilterBlank, TravelBlank or DIBLank to accompany a sampling event and it is not important to record the station information, the data is entered into the SWAMP database in the same manner as the samples in the same group. The specifics are as follows:

<i>LabSampleID</i>	Recommended - provide lab specific identification for an analyzed sample
<i>EventCode</i>	WQ for water and sediment chemistry
<i>ProtocolCode</i>	Protocol associated with the sample
<i>StationCode</i>	FIELDQA
<i>LocationCode</i>	Not Applicable
<i>SampleDate</i>	Date sample was created TravelBlank should be entered as the date the TravelBlank becomes part of the sample group (i.e., leaves the lab for the sampling event).
<i>CollectionTime</i>	Time sample was created or 0:00 There are situations within a batch when two identical sample types are used for QA reasons and the only way to differentiate between them is to give them each a different <i>CollectionTime</i> . For example, when more than one EquipBlank, FieldBlank, FilterBlank, TravelBlank, or DIBLank is created on the same day but are not replicates of each other, one <i>CollectionTime</i> should be 00:00 and the other 00:15, increasing the time by 15 minutes for each additional sample.
<i>CollectionMethodCode</i>	Not Applicable
<i>SampleTypeCode</i>	EquipBlank, FieldBlank, FilterBlank, TravelBlank, or DIBLank
<i>Replicate</i>	1
<i>CollectionDepth</i>	-88
<i>UnitCollectionDepth</i>	m for water or cm for sediment
<i>ProjectCode</i>	Project associated with the sample
<i>AgencyCode</i>	Organization or agency that created the sample



<i>CollectionComment</i>	EquipBlank - comment includes type of equipment cleaned and location (lab or field)
<i>Matrix</i>	labwater or blankwater

The following information will be loaded into the database by the data management team. Laboratories are not required to submit this information.

<i>FundingCode</i>	Funding associated with the sample and project
<i>GroupSamples</i>	GroupSample associated with the sample and project
<i>CollectionDeviceCode</i>	None EquipBlank - CollectionDevice used or None
<i>PositionWaterColumn</i>	Not Applicable

iv. Other Types of Samples

There are three types of samples discussed in this section that have special circumstances. The first is a pore water matrix sample, second is a sample where bacteria is analyzed, and third is benthic Chlorophyll a, Pheophytin, and AFDM_Algae samples.

(a) Interstitial Water (Pore Water) Analysis

Certain sampling events create a special set of rules that apply for a few of the entry fields in the SWAMP database. One of these would be the collection of sediment from which interstitial water is extracted and then analyzed. Below are the fields that differentiate these samples from the norm and how they should be completed.

<i>CollectionMethodCode</i>	Sed_Grab
<i>SampleTypeCode</i>	Integrated
<i>UnitCollectionDepth</i>	cm
<i>PreparationPreservation</i>	Centrifuged plus any additional preparation done at the lab (Centrifuged, X)
<i>PreparationPreservationDate</i>	If no preparation was performed at the analyzing lab, enter the centrifuge date for <i>PreparationPreservationDate</i> . If a preparation or preservation was performed at the analyzing laboratory, enter the preparation date and time and include the date of centrifuge in the <i>CollectionComments</i> .
<i>Matrix</i>	sediment, interstitialwater
<i>Unit</i>	water units

(b) Bacteria Samples

Bacteria/Pathogen samples are generally recorded in the same way as chemistry samples, except as follows:

<i>AnalysisDate</i>	<i>AnalysisDate</i> is the start of incubation. Include the analysis time in the <i>AnalysisDate</i> field as dd/mmm/yyyy xx:xx.
<i>DilFactor</i>	Dilution factor should be recorded



<i>Result</i>	Qualitative: -88 (will be converted to a blank when loaded to the database) Quantitative: Final numeric result of a given analyte, stored as text to retain trailing zeros
<i>ResQualCode</i>	Qualitative: P (present) or A (absent) Quantitative: This field records <, <= and >, >= as related to the results. Please note that if the result is less than the reporting limit and the lab is confident in reporting “Non Detect”, this should be entered as ND in the <i>ResQualCode</i> with a value of -MDL in <i>Result</i> field.
<i>Unit</i>	SWAMP convention for the analyte; e.g. MPN/100mL. Unit should not be “None”.
<i>LabResultComments</i>	Rlog is reported for Laboratory Duplicates The time samples are pulled from the incubator may be recorded if desired

Sometimes there are situations where under dilution has occurred, there is confluent growth, or the bacteria colonies are too numerous to count on the plate. Follow the guidelines below in these situations or use best professional judgement.

Situation	Result	ResQualCode	QACode
Applies to situations where the plate can not be counted because the colonies are confluent	colonies able to be counted	CG	None
Applies to situations where under dilution has occurred and the plate can not be counted due to method limits or the plate can only be partially counted	colonies able to be counted	>	TNC
Applies to situations where under dilution has occurred and plate cannot be counted at all	-88 (will be blank in database)	NR	TNC
Applies to situations where under dilution has occurred and the total plate count can be derived by counting a subset of grids and using a statistical analysis to calculate the result	calculated colonies based on a subset counted and statistical analysis	blank or >=	CSG,TNC

* ResQualCode CG (Confluent Growth)

* QACode TNC (Too Numerous to Count)

* QACode CSG (Bacteria result calculated using a subset of grids when the filter is too concentrated)

(i) Calculating Rlog for Bacteria Data

In order to determine precision for bacterial analysis the Rlog must be calculated and reported in the LabResultComments column of the template. This calculation is described in the [Indicator Bacteria in Freshwater Quality Control and Sample Handling Guidelines Table](#).

The business rules for reporting Rlog are as follows:

- Rlog format is as follows:
 - **Rlog #.## > #.##**
 - **Rlog #.## < #.##**
- Rlog is reported with two decimal places
- If both the native and the duplicate are ND, then Rlog is reported as **Rlog 0.00 < 0.00**
- If only one result is ND, then the Rlog is still calculated
- When Rlog is #.## > #.## there should be an associated QACode of **ILN** (Rlog exceeds control limit)



(c) Benthic Chlorophyll a, Pheophytin, and AFDM_Algae Samples

Benthic Chlorophyll a, Pheophytin, and AFDM_Aglae samples are generally recorded in the same way as chemistry samples, except as follows:

<i>Fraction</i>	Particulate (including LABQA)
<i>MDL</i>	Different values within a batch are acceptable because it is based on the conversion from water column to benthics
<i>RL</i>	Different values within a batch are acceptable because it is based on the conversion from water column to benthics

(ii) *Conversion for Benthic Chlorophyll a, Pheophytin, and AFDM_Algae Samples*

Results for Benthic Chlorophyll a, Pheophytin, and AFDM_Algae samples must be converted from water column data (mass/volume) to benthic data (mass/area). These analytes are typically required when the [Collecting Stream Algae Samples and Associated Physical Habitat and Chemical Data for Ambient Bioassessments in California SOP](#) is being followed. The conversion and reporting business rules are as follows:

CONVERSION

- $\frac{\text{WaterColumn Value} \times \text{CompositeVolume}}{\text{GrabSize}}$ or $(\text{WaterColumn Value}) \times (\text{Composite Volume}) / \text{Grab Size}$
- MUST be done on all 4 values where WaterColumn Value equals:
 - Result
 - MDL
 - RL
 - Expected value
- For Samples:
 - Volume Filtered (ml), Composite Volume (ml) and Grab Size (cm²) will be provided on the COC
 - If these values are not provided on the COC, contact the field crew and/or project manager for this information
- For LABQA and Non-Project samples:
 - Default Composite Volume: 500 ml
 - Default GrabSize: 138.6 cm²

REPORTING

- Benthic batches will have _B_ in the LabBatch ID for benthic matrix
- Report results to 2 decimal places
- WaterColumn and benthic results need to be **analyzed in different batches** so they must be **reported as two separate batches** each having it's own set of QC
- Blanks must be reported with all batches including Pheophytin
- AFDM_Algae batches will have an AFDM at the end for the acronym – not AFDM_Algae

SAMPLE

- Matrix: benthic
- Analyte: AFDM_Algae, chlorophyll a, or pheophytin
- Fraction: Particulate
- Chl and Pheo Unit: mg/m²
- AFDM Unit: g/m²



LABQA

- Matrix: blankwater
- Analyte: AFDM_Algae, chlorophyll a, or pheophytin
- Fraction: Total
- Chl and Pheo Unit: mg/m2
- AFDM Unit: g/m2

EXAMPLE

Example of conversion for Chlorophyll a or Pheophytin:

$$[300 \text{ ug/L} \times (1 \text{ mg}/1000\text{ug})] \times [535\text{mL} \times (1 \text{ L}/1000\text{mL})] / [138.6\text{cm}^2 \times (1\text{m}^2/10,000\text{cm}^2)] = 11.58 \text{ mg/m}^2$$

Example of conversion for AFDM_Algae:

$$[412 \text{ mg/L} \times (1 \text{ g}/1000\text{mg})] \times [535\text{mL} \times (1 \text{ L}/1000\text{mL})] / [138.6\text{cm}^2 \times (1\text{m}^2/10,000\text{cm}^2)] = 15.90 \text{ g/m}^2$$

e. Converting the Data

Analysis results in many laboratories are produced in a format that does not easily fit into the format described above. Many labs' instruments provide reports in a vertical rather than horizontal format, for instance. The SWAMP DMT has developed a program to assist in the conversion of data from the analysis instrument-provided format to that required by the SWAMP Database. While this conversion program does not complete all of the work for the lab personnel, it greatly reduces the effort involved. Because each situation is unique, the SWAMP DMT should be contacted to make arrangements.

8. SUBMITTING DATA TO SWAMP DATA MANAGEMENT TEAM

The following sections describe the process used by the Moss Landing Marine Laboratory (MLML) Data Management Team (DMT) to receive and begin to process electronic data reports from laboratories and other agencies submitting data for inclusion in the SWAMP Database.

This process will be introduced when each laboratory or other agency working with SWAMP data is trained on SWAMP business rules and formats for data submission.

As an overview, data reports are submitted to SWAMP through the [Online Data Checker](#) website. After a manual review for completeness and accuracy, the data is loaded by the DMT into the temporary side of the SWAMP database. Data reports will be rejected and returned if any of the following is true:

- The [SWAMP File and Batch Naming Convention](#) is not followed
- The report is incomplete, such as missing or incomplete QC data or LabBatch tab
- Incorrect values appear in any fields, such as calculated results or invalid codes
- More than 3 'typos' appear, such as misspelled names or codes (which makes them impossible to load into the database). In the case where 3 or fewer such instances exist in the report, the DMT representative will correct the error(s) unless otherwise requested by the lab.

Data reports that have been returned for resolution should be resubmitted to the DMT through the Online Data Checker with "_Resub" at the end of the file name within 5 business days for entry into the SWAMP database.

Once the data has been loaded into the database, the SWAMP DMT will verify the data (see SWAMP Data Verification SOPs <http://swamp.mpsl.mlml.calstate.edu/resources-and-downloads/standard-operating-procedures#Database>) and prepare for validation and eventual transfer to the permanent and public side of the SWAMP Database.

The process for addressing issues raised during verification is as follows:

- Issues will be compiled as discovered and forwarded to the appropriate lab contact for resolution.
- Laboratory needs to provide answer and/or resolution within 5 business days so as not to impede reporting data to the appropriate Regional Board and public users.



a. Checking Data for Quality Assurance

As it is the responsibility of the submitting laboratory to insure the accuracy and completeness of the data, it is necessary to QA the data prior to submitting it to the DMT. This process should include verifying that all data fields are complete, that required QC data is included and properly notated with recoveries, estimated values and RPDs, when applicable, as well as checking that appropriate replicate values are assigned.

i. SWAMP Laboratory QC Requirements

Generally, laboratories must report each Quality Control (QC) sample type once per 20 samples or per batch, whichever is more frequent. For example, if an analytical batch contains 10 samples, there must be one of each applicable QC sample type included with the data report. If the batch contains 21 to 40 samples, two of each type of QC samples must be included. Internal and calibration standards should be performed but not reported to the SWAMP database.

To determine what QC samples are required to be included with each batch of data per analysis type review the [Quality Control and Sample Handling Guidelines](#). More details including percent recovery and RPD calibrations are listed in Appendix A of the [QAPrP](#).

b. File and Batch Naming Conventions

The file and batch naming convention that should be followed appears in the [SWAMP File and Batch Naming Conventions](#) document.

c. Data Submittal

Once the data has been properly formatted and QA'd by the laboratory for accuracy and completeness, it is ready to be submitted to the SWAMP DMT. The following sections will guide the user through this process.

i. Online Data Checker and Submittal Process

Before submitting the Excel file it needs to be checked for formatting and adherence to SWAMP business and database rules using the Online Data Checker program at http://checker.swamp.mpsl.mlml.calstate.edu/SWAMP_Checker/SWAMPUpload.php.



SWAMP Data Checker Main Menu - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://ftp.mpsl.mml.calstate.edu/swampupload.php

Most Visited Getting Started Latest Headlines

SWAMP Data Checker Main Menu

SWAMP Data Checker August 5, 2010

Water Boards SWAMP Marine Pollution Studies Lab

Surface Water Ambient Monitoring Program

Data Category:

Your Email Address:

Your Agency:

ABCL	ABC Laboratories
ALPHA	Alpha Analytical, Inc.
AMS	Applied Marine Sciences, Inc.
AMS-CA	Applied Marine Sciences, Inc. California
APPL	Agriculture & Priority Pollutants Laboratories, Inc
AquaSci	AquaScience
AXYS	Axys Analytical Services Ltd .
Babcock	E.S. Babcock & Sons, Inc.

File to Upload:

Browse... Check Excel File

Instructions For Data Category: [Chemistry](#) [Tissue](#) [Toxicity](#)

Please Note: The valid values contained in the lookup lists are specific to SWAMP-funded projects. Lookup list errors generated for non-SWAMP project data should be addressed through the appropriate Regional Data Center.

Done

- Select the correct *Data Category* from the pull-down menu. In this example, select 'Chemistry'.
- Enter *Your Email Address*. The results of the data check and a confirmation of submittal will be sent to this email address.
- Select the submitting agency of the data from the *Your Agency* pull-down menu. **Not Recorded** is also an option if the correct agency is not found.
- Select the file to check under *File to Upload* by clicking on BROWSE to open the File Selection Dialog box. It is recommended to save and close the Excel data file before checking it.
- After selecting the file, click CHECK EXCEL FILE to check the file.
- The file will now be checked for basic formatting errors such as missing the 'Results' or 'LabBatch' worksheets. Any errors will be listed. These errors must be corrected before checking can continue.
- If the file had no basic formatting errors, the data will then be checked for compliance with SWAMP business and database rules. When the testing is complete you will automatically be redirected to the online results page.



Chemistry Data Checker Results - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://ftp.mpsl.mml.calstate.edu/Results/results051509133717.html

Back to Main Page

Errors found in Results Worksheet:

Error	Excel Row	Error Field	Erroneous Value	LabSampleID	StationCode	SampleDate	SampleTypeCode	Replicate	AnalyteName	CollectionMethod
Constituent not found in ConstituentLookUp	2	MethodName, MatrixName, AnalyteName, FractionName, Unit	"EPA 1638M, samplewater, Boron, Dissolved, mg/L"	"2008-3419"	"603LPC001"	"Jul 18 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
ProtocolCode not found in ProtocolLookUp table.	2	ProtocolCode	"RVQCB6_Field_2005"	"2008-3419"	"603LPC001"	"Jul 18 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
Sample not found in database	2	Columns B-N	"	"2008-3419"	"603LPC001"	"Jul 18 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
Constituent not found in ConstituentLookUp	3	MethodName, MatrixName, AnalyteName, FractionName, Unit	"EPA 1638M, samplewater, Boron, Dissolved, mg/L"	"2008-3418"	"603MAM006"	"Jul 17 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
ProtocolCode not found in ProtocolLookUp table.	3	ProtocolCode	"RVQCB6_Field_2005"	"2008-3418"	"603MAM006"	"Jul 17 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
Sample not found in database	3	Columns B-N	"	"2008-3418"	"603MAM006"	"Jul 17 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"
Constituent not found in ConstituentLookUp	4	MethodName, MatrixName, AnalyteName, FractionName, Unit	"EPA 1638M, samplewater, Boron, Dissolved, mg/L"	"2008-3403"	"628CRB001"	"Jun 2 2008 12:00AM"	"Grab"	"1"	"Boron"	"Water_Grab"

Done

- On the results page a congratulatory message will appear if there aren't any errors with the data file. If not, any suspected errors with the file will be listed.



Microsoft Excel - Loading Test File_SLM051509131701_ResultsErrors

File Edit View Insert Format Tools Data Window Help

Type a question for help

100%

Arial Unicode MS 10

Go to Office Live | Open | Save

A5 Error

Errors in Results Worksheet

Error	ExcelRd	Field	Value	LabSampleI	Statio
Constituent not found in ConstituentLookUp	2	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3419	603LP
Constituent not found in ConstituentLookUp	3	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3418	603MA
Constituent not found in ConstituentLookUp	4	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3403	628CR
Constituent not found in ConstituentLookUp	5	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3402	628DE
Constituent not found in ConstituentLookUp	6	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3404	628HC
Constituent not found in ConstituentLookUp	7	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3407	628MC
Constituent not found in ConstituentLookUp	8	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3406	628MC
Constituent not found in ConstituentLookUp	9	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3405	628SH
Constituent not found in ConstituentLookUp	10	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3421	630EW
Constituent not found in ConstituentLookUp	11	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3421-ms	630EW
Constituent not found in ConstituentLookUp	12	MethodName, MatrixName, AnalyteName, FractionName, Unit	EPA 1638M, samplewater, Boron, Dissolved, mg/L	2008-3421-msd	630EW

Loading Test File_SLM0515091317/

36 of 130 records found

- An email is also sent to the address entered on the previous page. It contains an Excel file attachment listing any errors for both the 'Results' and 'LabBatch' worksheets individually. The Excel format listing these errors is often easier to view rather than the online format as the filter column function can be used in Excel.
- A troubleshooting and list of error message descriptions is also available for reference at http://checker.swamp.mpsl.mlml.calstate.edu/SWAMP_Checker/Troubleshooting.php.
- Correct the errors in the Excel data file, save and close the file, and check the file again by clicking BACK TO MAIN PAGE on the online results page and re-running the checker.

SWAMP Data Checker Results - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back

Address: <http://ftp.mpsl.mlml.calstate.edu/Results/results071408112949.html>

Google

403 blocked

Settings

Congratulations! Your file has passed our data checks and is ready to be submitted to the SWAMP Data Management Team.

[Submit Data To SWAMP](#)

[Back to Main Page](#)



- Once all the errors are either corrected, or after discussing it with the DMT are okay to ignore, submit the SWAMP-funded file to the SWAMP DMT to be loaded into the SWAMP database by clicking **SUBMIT DATA TO SWAMP**. If it is not a SWAMP-funded file the data should not be submitted to SWAMP.

Please limit submittals to SWAMP funded data only.

Add comma delimited email addresses to be cc'd here:
 CC:

Type in an optional message to the SWAMP DMT here:
 Comments:

Click the big green button to send your file to Marco

Submit Data To SWAMP

- A new webpage will open and additional email addresses, separated by commas, can be added in the *cc:* field. Additional comments to the SWAMP administrator and cc email addresses can also be added in the *Comments* field if necessary. If these comments are important to the data loading and verification process, the comments should also be in the notes tab of the excel file. If a file is being resubmitted with corrections indicate that in the *Comments* field. To finalize the submittal process, click **SUBMIT DATA TO SWAMP**.
- Congratulations, the Excel file has been submitted! An email should also be received confirming the file submittal. Click **BACK TO MAIN PAGE** to return to the main page to check another file or close the window if you are done using the checker.

d. Data Resubmittal

If a file has been submitted to the DMT through the online data checker and for some reason needs to be resubmitted with changed or additional data, only the original data should be resubmitted. i.e. same batches and number of results unless missing results from the original batch. General changes made to the file should be indicated in the notes tab in the template and the name of the file should be the same as the original with the addition of **_Resub** at the end. In addition, a comment indicating that the file is a resubmittal should be provided in the comments section on the last page of the data checker submittal process.

