SWAMP
Surface Water Ambient Monitoring Program

SWAMP DATA MANAGEMENT PLAN

Chemistry Template

Surface Water Ambient Monitoring Program

April 13, 2009

CALIFORNIA Water Boards

www.waterboards.ca.gov/swamp

TABLE OF CONTENTS

A. 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 should be used in conjunction with the SWAMP QAPrP for complete compliance with the SWAMP program including measurement quality objectives and required quality assurance (QA) samples.

1. Analysis Authorization Forms

2. 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 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.

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 QA 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 QA sample. This worksheet will also contain all supporting QA 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.

All valid LookUp list values are available at http://ftp.mpsl.mlml.calstate.edu/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.

Template Field Name	LookUp List	Description & Business Rules
LabSampleID		The LabSampleID is a recommended field intended to provide lab specific identification for an analyzed sample. **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.
StationCode	StationLookUp	StationCode represents a unique sampling site in a sampling design. A single waterbody may have multiple stations. **BR:** The format for the unique alphanumeric description of the station is ###ABC123, where ### is the Hydrologic Unit number and ABC123 is an alphanumeric description of the Station. An example is 111EELBRN which is Hydrologic Unit 111 and an abbreviated code to indicate “Eel River - South Fork near Branscomb”.

Template Field Name	LookUp List	Description & Business Rules
EventCode	EventLookUp	EventCode represents the initial intent of the sampling event at a particular station. **BR:** The EventCode will be in a hierarchical order as follows: BA – If the initial intent of sampling is for Bioassessment (Tissue and/or WaterQuality samples may or may not also be collected) TI – If the initial intent of sampling is for Tissue (WaterQuality samples may or may not also be collected; no associated Bioassessment samples collected) WQ – If the initial intent of sampling is for WaterQuality (no associated Bioassessment or Tissue samples collected) 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 the WaterQuality was sampled on Day 2.
ProtocolCode	ProtocolLookUp	ProtocolCode represents the sampling protocol used, which includes the set of methods, methodology and/or specifications, such as MPSL-DFG_Field_v1.0. Established protocols may be used or Regions may document their own sampling protocols. **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. 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. Default value is Not Recorded.

Template Field Name	LookUp List	Description & Business Rules
LocationCode (previously SampleLocation)	LocationLookUp	LocationCode describes the physical location in the waterbody where the sample was collected. One sampling event may have a single or multiple locations. **BR:** For a single point of sampling, the physical location in the waterbody can be used such as Bank, Thalweg, Midchannel, OpenWater. The LocationCode for field results should be the same as the location for the WaterQuality collection method. For TI EventType 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_Grab. 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. Multiple physical locations within a single station could consist of a LocationCode such as BankShock1, BankNet1, OpenWaterHook1. If recording specific locations within a station are necessary for the project, a LocationCode such as Location1Net1, Location1Net2, Location2Shock1 may be used.
SampleDate		SampleDate refers to the date the sample was collected in the field. **BR:** The format for date in the templates is dd/mmm/yyyy, such as 10/Nov/2007. For samples with collection times that last longer than one day, like autosamplers, the sample date is the date sampling began. When entering data using the forms, the format is mm/dd/yy. For transplanted bivalves, the SampleDate is the date when the bivalves were deployed in the field.

Template Field Name	LookUp List	Description & Business Rules
CollectionTime (previously SampleTime)		CollectionTime refers to the time when the first sample of a sampling event at a specific station was collected in the field. **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 the laboratory work. The CollectionTime format should be expressed as xx:xx in 24 hour time, such as 13:30 for 1:30 pm.
CollectionMethodCode	CollectionMethodLookUp	CollectionMethodCode refers to the general method of collection such as Sed_Grab, Sed_Core, Water_Grab, Autosampler24h, Autosampler7d. **BR:** The SWAMP water default is Water_Grab and the sediment default is Sed_Grab.
SampleTypeCode	SampleTypeLookUp	SampleTypeCode refers to the type of sample collected or analyzed. **BR:** Some commonly used SampleTypeCode choices include Grab, Integrated, MS1, CRM, LCS, LabBlank, CNEG, Composite.
Replicate (previously SampleReplicate)		The Replicate number is used to distinguish between replicates created at a single collection in the field. **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. 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.

Template Field Name	LookUp List	Description & Business Rules
CollectionDepth (previously DepthSampleCollection)		CollectionDepth records the level, from the surface in the water or sediment column, at which the sample was collected. **BR:** This information should be listed on the Chain of Custody (COC) document that accompanies the samples from the field. 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). 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. 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 sediment cores, should receive a depth of -88 and the actual depths of collection should be recorded in the CollectionComments field.
UnitCollectionDepth (previously DepthUnit)	VariableCodesLookUp	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 the samples from the field.
ProjectCode (previously ParentProjectID)	ProjectLookUp	ProjectCode references the project that is associated with the sample. **BR:** The formatting for a ProjectCode is as follows Program_Project. For example, the format for a SWAMP Regional Board project is SWAMP_RBX where SWAMP is the program, RB indicates it is a Regional Board sample and X is the Regional Board number. The format for a SWAMP State Board project is SWAMP_SB_XXX where SWAMP is the program, SB indicates it is a State Board sample and XXX represents the State Board project. For example, the ProjectCode for the Bioaccumulation Oversight Group would be SWAMP_SB_BOG. For a project other than SWAMP such as the Friends of the Los Angeles River, the project is FLAR_XXX where FLAR indicates it is a Friends of the Los Angeles River program and XXX represents the Friends of the Los Angeles River project. In some cases, there may not be a specific project but only a program. In this case the ProjectCode would be just the program; e.g. UMD.

Template Field Name	LookUp List	Description & Business Rules
AgencyCode	AgencyLookUp	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. **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. See 'Special Circumstances' for LABQA business rules.
CollectionComments (Not Required)		CollectionComments records any comments relating to the collection of the field sample for laboratory analysis. **BR:** This field can also be used for laboratory QC samples, e.g. Matrix Spike was performed on a FieldBlank.
SampleID (Not Required)		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. **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.
PreparationPreservation (previously Preparation)	PrepPreservationLookUp	PreparationPreservation references the preparation or preservation method performed on the samples prior to analysis. **BR:** If no preparation or preservation method was performed the default value is None.
PreparationPreservationDate		PreparationPreservationDate is the date and time the preparation or preservation was started. **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).

Template Field Name	LookUp List	Description & Business Rules
DigestExtractMethod	DigestExtractLookUp	DigestExtractMethod references the digestion or extraction method performed on the sample prior to analysis. **BR:** If no digestion or extraction method was performed the default value is None.
DigestExtractDate		DigestExtractDate is the date and time the digestion or extraction was started. **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).
LabBatch		The LabBatch is a unique code, provided by the laboratory, that 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. **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. All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.
AnalysisDate		AnalysisDate is the date and time the sample was processed on the analytical instrument. **BR:** This date/time should be expressed as dd/mmm/yyyy hh:mm.
LabReplicate		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. **BR:** The default is 1 for the first sample and increases by one for each successive replicate analyzed in the laboratory.

Template Field Name	LookUp List	Description & Business Rules
MatrixName	MatrixLookUp	MatrixName refers to the sample matrix. **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. 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. 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.
MethodName	MethodLookUp	MethodName refers to the analysis method used by the laboratory to analyze the sample. **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.

Template Field Name	LookUp List	Description & Business Rules
AnalyteName	AnalyteLookUp	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.
FractionName	FractionLookUp	FractionName is a specific descriptor of the Analyte. **BR:** For instance, metals are often expressed as Total or Dissolved, each of which would be expressed as the Fraction, distinguishing the appropriate Analyte. If there is no need for further description of the analyte, type 'None' in this field.
Unit	UnitLookUp	Unit refers to how the chemistry result is measured or expressed. **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 in the SWAMP QAPrP, online at http://www.swrcb.ca.gov/swamp/qapp.html. ??? 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 %.

Template Field Name	LookUp List	Description & Business Rules
DilFactor		DilutionFactor is the factor by which a sample was diluted and is reported as a whole number. It is equal to the final volume divided by the initial volume of solution, or DF = Vf ÷ Vi. ??? **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. Final reported results must be corrected for dilution that was carried out during the process of analysis. 1 part sample plus 9 parts blank is a DilutionFactor of 10. A 50% dilution is equivalent to a DilutionFactor of 2. When a sample requires a dilution, the MDL and RL must also be raised by that DilutionFactor. A QACode of D is required when a dilution is performed on the sample.
Result		Final numeric result of a given analyte, stored as text to retain trailing zeros **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. A result of 3.7266945 with 3 significant figures should be reported as 3.73. 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.

Template Field Name	LookUp List	Description & Business Rules
ResultQualCode (previously ResQualCode) (Not Required)	ResQualLookUp	The Result Qualifier Code or ResultQualCode qualifies the analytical result of the sample. **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 ResultQualCode is required and the appropriate code would be applied. When the result is -88, a ResultQualCode is required. If the ResultQualCode 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.
MDL		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. **BR:** If no MDL is used, enter -88. A value other than -88 must be used for either the MDL or the RL.
RL		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. **BR:** If no RL is used, enter -88. A value other than -88 must be used for either the RL or the MDL.
QACode	QALookUp	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. **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; i.e. GB,SC

Template Field Name	LookUp List	Description & Business Rules
ExpectedValue (Not Required)		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. **BR:** For surrogate samples, the expected value should be 100, representing 100%. This field is required for SampleTypeCodes of MS1, MS2, CRM and LCS.
LabResultComments (Not Required)		The LabResultComments field holds any comments related to the lab result or analysis of the sample. **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.

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		The LabBatch is a unique code, provided by the laboratory, that 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. **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. All lab batches listed in the Results worksheet need to be listed one time only in the LabBatch worksheet.
LabAgencyCode	AgencyLookUp	LabAgencyCode refers to the organization, agency or laboratory that performed the analysis on the sample.
LabSubmissionCode (previously BatchQualifierCode)	LabSubmissionLookUp	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. **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.
SubmittingAgencyCode	AgencyLookUp	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)		LabBatchComments records any comments relating to the LabBatch as a whole. **BR:** If the LabSubmissionCode is anything other than "A", a LabBatchComment is required.

c. 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 SWAMP 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:

LabSampleID	Recommended - provide lab specific identification for an analyzed sample
StationCode	LABQA
EventCode	WQ for water and sediment chemistry
ProtocolCode	Not Applicable
LocationCode	Not Applicable
SampleDate	Date sample was digested/extracted, expressed as dd/mmm/yyyy. When no digestion/extraction was performed, *SampleDate* is equal to the analysis date.
CollectionTime	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 *CollectionTime*. 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 *CollectionTime* should be 0:00 and the other 0:15, increasing the time by 15 minutes for each additional sample.
CollectionMethodCode	Not Applicable
SampleTypeCode	Select from SampleTypeLookUp List
Replicate	1
CollectionDepth	-88
UnitCollectionDepth	m for water or cm for sediment
ProjectCode	Not Applicable
AgencyCode	Organization or agency that analyzed the sample
Matrix	Water samples - labwater or blankwater Sediment samples - blankmatrix (commercially generated product) or sediment (if laboratory is using solvent, water, or nothing)

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*.

LabSampleID	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 *SampleTypeCode* and the *LabSampleID* of the native sample.
StationCode	Same as native field sample
EventCode	Same as native field sample
ProtocolCode	Same as native field sample
LocationCode	Same as native field sample
SampleDate	Same as native field sample
CollectionTime	Same as native field sample
CollectionMethodCode	Same as native field sample
SampleTypeCode	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 *Replicate* of 2) MSBLDup - Matrix Spike performed on a FieldBLDup 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 *SampleTypeCode*. The only way to differentiate them is to give each a different *CollectionTime*. 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 *CollectionTime* should be 0:00 and the other 0:15. Then the MS1 *CollectionTime* should correspond to the correct native sample time.
Replicate	1
CollectionDepth	Same as native field sample
UnitCollectionDepth	Same as native field sample

ProjectCode	Same as native field sample
AgencyCode	Same as native field sample
LabReplicate	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
Matrix	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 in both the v2.2 and v2.5 SWAMP databases. The *SampleTypeCode* MS represents an MS/MSD pair.

v2.2 SWAMP Database			**v2.5 SWAMP Database**	
SampleTypeCode	*Sample Replicate*		*SampleTypeCode*	*Replicate*
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.

(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:

LabSampleID	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 *SampleTypeCode* and the *LabSampleID* of the native sample.
StationCode	000NONPJ
EventCode	WQ for water and sediment chemistry
ProtocolCode	Not Applicable
LocationCode	Not Recorded
SampleDate	Date sample was digested/extracted, expressed as dd/mmm/yyyy. When no digestion/extraction was performed, *SampleDate* is equal to the analysis date.
CollectionTime	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 *CollectionTime*. For example, when more than one 000NONPJ sample with the same *SampleTypeCode* is digested, extracted or analyzed in the same batch on the same day but are not replicates of each other, one *CollectionTime* should be 0:00 and the other 0:15, increasing the time by 15 minutes for each additional sample.
CollectionMethodCode	Not Recorded
SampleTypeCode	Grab - lab-generated Duplicates MS1 - Matrix Spikes
Replicate	1
CollectionDepth	-88
UnitCollectionDepth	m for water or cm for sediment

ProjectCode	Not Applicable
AgencyCode	Organization or agency that analyzed the sample
SampleID	The *LabSampleID* or *Source ID* can be used here as the *SampleID* as an indicator to identify the native sample
PreparationPreservation	Actual preparation or preservation performed
PreparationPreservationDate	Actual preparation or preservation date and time expressed as dd/mmm/yyyy xx:xx
LabReplicate	2 - lab-generated Duplicates 1 - Matrix Spike 2 - Matrix Spike Duplicate
Matrix	samplewater or sediment
QACode	QAX, when the native sample is not included in the batch reported

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.

(c) 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:

LabSampleID	Recommended - provide lab specific identification for an analyzed sample
EventCode	WQ for water and sediment chemistry
ProtocolCode	Protocol associated with the sample or Not Recorded
StationCode	Station where sample was created
LocationCode	Location where sample was created
SampleDate	Date sample was created
CollectionTime	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 *CollectionTime*. For example, when more than one EquipBlank, FieldBlank, or FilterBlank is created on the same day but are not replicates of each other, one *CollectionTime* should be 00:00 and the other 00:15, increasing the time by 15 minutes for each additional sample.
CollectionMethodCode	Not Applicable
SampleTypeCode	EquipBlank, FieldBlank, or FilterBlank

Replicate	1
CollectionDepth	-88
UnitCollectionDepth	m for water or cm for sediment
ProjectCode	Project associated with the sample
AgencyCode	Organization or agency that created the sample
CollectionComment	EquipBlank - comment includes type of equipment cleaned and location (lab or field)
Matrix	labwater or blankwater

(d) 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:

LabSampleID	Recommended - provide lab specific identification for an analyzed sample
EventCode	WQ for water and sediment chemistry
ProtocolCode	Protocol used or Not Recorded
StationCode	FIELDQA
LocationCode	Not Applicable
SampleDate	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).
CollectionTime	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 *CollectionTime*. 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 *CollectionTime* should be 00:00 and the other 00:15, increasing the time by 15 minutes for each additional sample.
CollectionMethodCode	Not Applicable
SampleTypeCode	EquipBlank, FieldBlank, FilterBlank, TravelBlank, or DIBlank
Replicate	1
CollectionDepth	-88
UnitCollectionDepth	m for water or cm for sediment

ProjectCode	Project associated with the sample
AgencyCode	Organization or agency that created the sample
CollectionComment	EquipBlank - comment includes type of equipment cleaned and location (lab or field)
Matrix	labwater or blankwater

iv. Other Types of Samples

There are two types of samples discussed in this section that have special circumstances. The first is a pore water matrix sample and the second is a sample where bacteria is analyzed.

(e) 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.

CollectionMethodCode	Sed_Grab
SampleTypeCode	Integrated
UnitCollectionDepth	cm
PreparationPreservation	Centrifuged plus any additional preparation done at the lab (Centrifuged, X)
PreparationPreservationDate	If no preparation was performed at the analyzing lab, enter the centrifuge date for *PreparationPreservationDate*. 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 *CollectionComments*.
Matrix	sediment, interstitialwater
Unit	water units

(f) Bacteria Samples

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

AnalysisDate	Include the analysis time in the *AnalysisDate* field as dd/mmm/yyyy xx:xx
DilFactor	Dilution factor should be recorded
ResultQualCode	This field records the <, <= 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 *ResultQualCode* with a value of -MDL in *Result* field.