SWAMP
Surface Water Ambient Monitoring Program

SWAMP Bioassessment Procedures 2015

Standard Operating Procedures (SOP) for External Quality Control of Benthic Macroinvertebrate Taxonomy Data Collected for Stream Bioassessment in California

July 2015

Andrew C. Rehn[1], Joseph Slusark[1] and Marco A. Sigala[2]

[1] Aquatic Bioassessment Lab-California Department of Fish and Wildlife
Center for Water and the Environment-California State University, Chico
400 West 1st Street
Chico, CA 95929-0555

[2] Marine Pollution Studies Lab-Moss Landing Marine Lab
7544 Sandholt Road
Moss Landing, CA 95039

SWAMP-SOP-2015-0002

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ACKNOWLEDGEMENTS

This standard operating procedure (SOP) represents the contributions of a wide range of researchers and laboratory personnel. The benthic macroinvertebrate (BMI) laboratory procedures are those of the California Department of Fish and Wildlife's (CDFW's) Aquatic Bioassessment Laboratory (ABL) - the designated BMI reference laboratory for the California State Water Resources Control Board's (State Board's) Surface Water Ambient Monitoring Program (SWAMP). Portions of the ABL procedures are modified from the United States Geological Survey (USGS) National Water Quality Assessment Program (NAWQA) protocols (Moulton, et al. 2000).

This SOP was written with contributions from the following people:
Kevin Lunde (San Francisco Regional Water Quality Control Board)
Raphael Mazor (Southern California Coastal Water Research Project)
Melissa Morris (State Water Resources Control Board, SWAMP QAO & DBA)
Peter Ode (Department of Fish and Wildlife Aquatic Bioassessment Laboratory)
Brady Richards (Department of Fish and Wildlife Aquatic Bioassessment Laboratory)
Melinda Woodard (SWAMP QA Team)

Citation for this Document:

Rehn, A.C., J. Slusark, M.A. Sigala. 2015. Standard Operating Procedures for External Quality Control of Benthic Macroinvertebrate Taxonomy Data Collected for Stream Bioassessment in California. California State Water Resources Control Board Surface Water Ambient Monitoring Program (SWAMP) Bioassessment SOP SWAMP-SOP-2015-0002.

LIST OF ACRONYMS AND ABBREVIATIONS

Term	Definition
ABL	CDFW Aquatic Bioassessment Laboratory
BMI	Benthic Macroinvertebrates
DMT	SWAMP Data Management Team
ID	Identification
KOH	Potassium hydroxide
MQO	Measurement Quality Objectives
PM	Project Manager
OR	Original Laboratory
QA	Quality Assurance
QAPP	Quality Assurance Project Plan
QC	Quality Control
SAFIT	Southwest Association of Freshwater Invertebrate Taxonomists
SOP	Standard Operating Procedure
STE	Standard Taxonomic Effort
SWAMP	Surface Water Ambient Monitoring Program

A. PURPOSE

This document outlines the procedure for external quality control (QC) of benthic macroinvertebrate (BMI) data generated and stored for SWAMP and participating SWAMP-comparable bioassessment projects. External QC occurs when BMI samples that have been processed and identified by an original lab (or taxonomist) are sent to a second, independent lab (or taxonomist) for confirmation of the identification and count of vouchered specimens. The procedures outlined here are intended to complement SWAMP's procedures for field collection (Ode et al. 2007) and laboratory processing (Woodard et al. 2012) of BMI samples[1]. In addition, BMI specimens should be identified to a standard level of taxonomic resolution, and identifications should be accurate according to available (published) taxonomic literature and keys[2].

The goal of external QC is twofold: i) it ensures that taxonomic identifications produced by multiple labs are consistent and in accordance with standard effort; and ii) it provides quantitative measures of the accuracy and precision of taxonomic data that can be compared against established standards, known as Measurement Quality Objectives (MQOs), that allow end users to evaluate data quality. Direct evaluation of raw taxonomic data quality is critical when monitoring data are shared among regional, state and federal programs for combined assessments. Most taxonomy labs conduct internal QC as part of their standard operating procedures. External QC is not a replacement for internal QC, but is an additional measure that provides independent validation of data quality.

SWAMP-comparable projects are encouraged to use SWAMP tools in the QC process to aid in data submission. The primary mode of data transfer among entities is currently through a Microsoft Excel QC Submittal data template. The current template can be found on the SWAMP website under the Database Management Resources Templates page (see Appendix 1). SWAMP also maintains current online data dictionaries and LookUp lists that should be used to ensure data comparability.

[1] For both documents see SWAMP Standard Operating Procedures in Appendix 1

[2] The Standard Taxonomic Effort (STE) for bioassessment projects in California has been defined by the Southwest Association of Freshwater Invertebrate Taxonomists (SAFIT) and can be found at http://safit.org/ste.html

B. PROCEDURE

The procedure for external QC of BMI taxonomy data comprises 4 primary steps, each with several associated substeps (Figure 1).

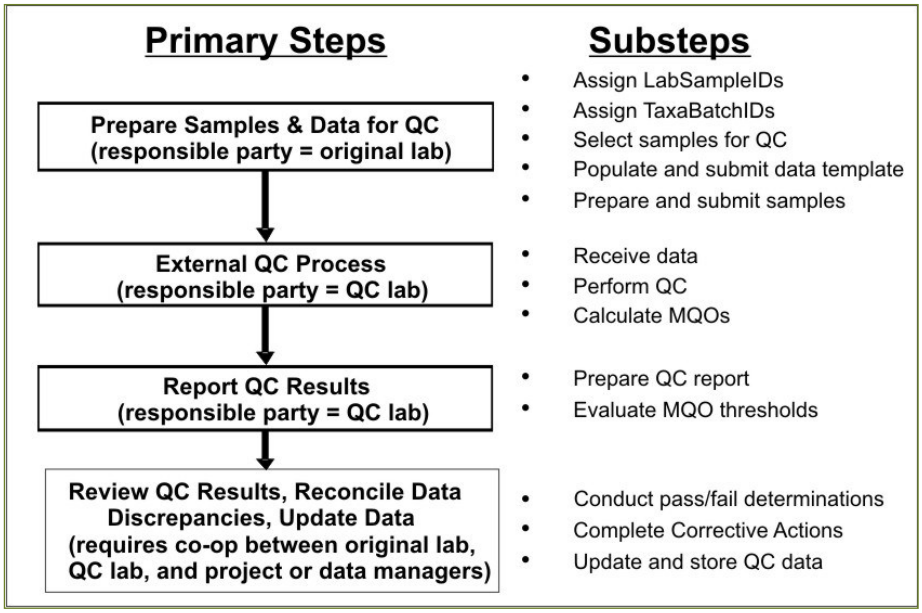


Figure 1. Flow chart showing primary steps and substeps in the external taxonomy QC process.

Prepare Samples and Data for QC

1. Assign LabSampleIDs

The Original Lab (OR) and/or Project Manager (PM) assigns each BMI sample a unique identifier (i.e., LabSampleID) that corresponds to a single replicate collected at a single site, on a single date, using a single collection method. Unique identifiers are required to link QC data to original sample data, but typically get assigned when samples are collected, not during the QC phase. Existing LabSampleIDs used by the OR lab or PM are acceptable and there are no naming restrictions.

2. Assign TaxaBatchIDs

The OR Lab and/or PM decide which BMI samples will undergo external QC as a batch, and a unique TaxaBatchID is created and assigned to all selected samples. Typically, all samples within a project are assigned the same TaxaBatchID, and a single TaxaBatchID will be associated with a single project. However, samples from multiple small projects may be combined under a single TaxaBatchID.

TaxaBatchIDs are assigned to track all samples associated with given QC results, including samples not ultimately selected for QC (see Step 3 below). TaxaBatchIDs are applied at the sample level (or at the "collection" level in SWAMP terminology), so are associated with each final BMI record, including records from samples not ultimately selected for QC, but which selected QC samples represent.

TaxaBatchIDs must be unique. SWAMP recommends, but does not require, the following naming convention:

ORAgencyCode_XXXX_CalendarYear_BMI###

where XXXX can be an identifier such as Project Name and ### is a unique number for the OR agency within a specific calendar year (e.g., DFG-ABL_2012_BMI032 or WestonSolu_SMC_2011_BMI001).

3. Select Samples for QC Batch

The PM randomly selects 10% of samples within a given TaxaBatchID (current SWAMP requirement) to serve as the QC batch[3]. **Random selection of samples for inclusion in the QC Batch is recommended in nearly all cases. It is critical that QC samples are not selected with bias and do not receive special care with respect to taxonomic identifications; otherwise QC results will not be representative of the larger batch.** However, samples with very low taxa richness (e.g., <10 taxa) and/or low counts (e.g., <100 individuals) may not be representative of a larger batch selected for QC. Also, if vials from a selected sample are in poor condition from improper storage or preservation, voucher specimens from that sample may no longer be identifiable and therefore inappropriate for QC. Discretion of the PM should be used in such cases to select alternate samples.

Note: The QC lab should not be responsible for choosing 10% of samples from a TaxaBatchID identified for external QC. This would require all samples in the batch to be shipped, creating additional and unnecessary expense, and QC labs may not have storage facilities for entire batches of samples from other labs.

[3] The PM should always round up when determining how many samples to submit in a QC batch, e.g., if the TaxaBatch contains 11 samples, submit 2 QC samples; if the TaxaBatch contains 21 samples, submit 3 QC samples, etc.

4. Populate and Submit Excel QC Submittal Data Template

The OR lab and/or PM populates the Excel QC Submittal data template with the OR data for the QC batch. The template has two tabs (worksheets): the BMI_QC_Template tab (Figure 2) contains the taxonomy data while the TaxaBatch tab (Figure 3) contains information regarding the TaxaBatchID. The current template can be found on the SWAMP website under the Database Management Resources Templates page (see Appendix 1).

BMI_QC_Template Tab

The BMI_QC_Template tab has three sections: OR, QC, and Project (Figure 2). Field (column) names within the template follow field names within the SWAMP database structure. There are more fields in the actual template than those shown in Figure 2. Documentation of all field names can be found on the SWAMP website with the current template. The following key fields are referenced throughout this document and are central to the external QC process, including calculation of MQOs:

- **FinalID:** Refers to the taxonomic name of a specimen (or specimens) as determined by the OR or QC taxonomist. FinalIDs should follow SAFIT STE whenever possible[4] and are the basis for MQO calculations described in this document.

- **Stage:** Represents the Life Stage (e.g., pupae, larvae, adult) for a given FinalID.

- **Distinct:** SWAMP taxonomists may label specimens not identified to STE as "Distinct" if there are good confirming characters indicating that the specimens in question do not belong to the same taxon (FinalID) as others in the sample, whether the others are identified to STE or not. See the section below on MQO calculations for an example of how the "Distinct" concept is applied.

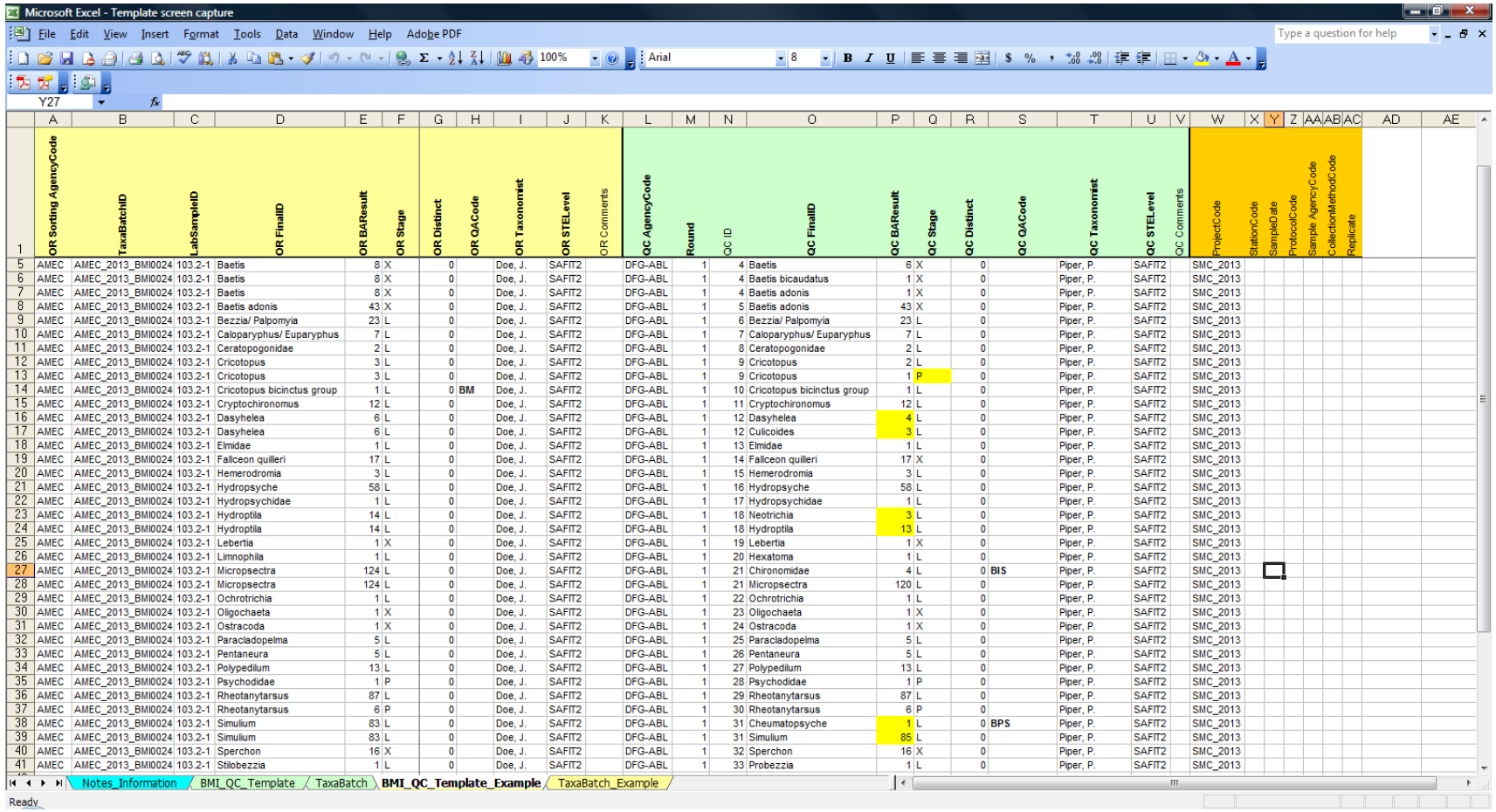
- **BAResult:** Refers to the number of specimens, or count, associated with each FinalID/LifeStage/ Distinct combination. Please read the documentation provided with the template for specific details regarding each field.

The OR section contains original FinalIDs and counts submitted by the OR lab. If only OR data are submitted, there should be one record per unique FinalID/LifeStage/Distinct combination.

[4] Early instar and/or damaged specimens often cannot be identified to the target STE level.

The QC section contains FinalIDs and counts determined through the external QC process by the QC lab. Once QC is completed, external QC data must always be submitted with OR data; there may be one or more records per unique FinalID/LifeStage/Distinct combination if a single taxon identified by the OR lab was determined to contain multiple taxa in the QC process. The OR and QC sections look similar because they contain many of the same fields for identifications and counts. The Project section is not required to be populated but provides additional information regarding the samples (e.g., ProjectCode, StationCode, SampleDate, CollectionMethod).

Both the OR and QC sections have required fields that must be populated for data to load into the SWAMP database. Specific combinations of required fields form the key, or unique constraint, to maintain unique records. The OR section key is based on OR Sorting AgencyCode, LabSampleID, OR FinalID, OR Stage, and OR Distinct, while the QC section key is based on QC AgencyCode, Round, QC FinalID, QC Stage, and QC Distinct. Non-required fields should be populated if possible. Please view the SWAMP online LookUp list for the most current valid values for given fields (see Appendix 1).



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE
1	OR Sorting AgencyCode	TaxaBatchID	LabSampleID	OR FinalID	OR BAResult	OR Stage	OR Distinct	OR QACode	OR Taxonomist	OR STELevel	OR Comments	QC AgencyCode	Round	QC ID	QC FinalID	QC BAResult	QC Stage	QC Distinct	QC QACode	QC Taxonomist	QC STELevel	QC Comments	ProjectCode	StationCode	SampleDate	ProtocolCode	Sample AgencyCode	CollectionMethodCode	Replicate		
5	AMEC	AMEC_2013_BMI0024	103.2-1	Baetis	8	X	0		Doe, J.	SAFIT2		DFG-ABL	1	4	Baetis	6	X	0		Piper, P.	SAFIT2		SMC_2013								
6	AMEC	AMEC_2013_BMI0024	103.2-1	Baetis	8	X	0		Doe, J.	SAFIT2		DFG-ABL	1	4	Baetis bicaudatus	1	X	0		Piper, P.	SAFIT2		SMC_2013								
7	AMEC	AMEC_2013_BMI0024	103.2-1	Baetis	8	X	0		Doe, J.	SAFIT2		DFG-ABL	1	4	Baetis adonis	1	X	0		Piper, P.	SAFIT2		SMC_2013								
8	AMEC	AMEC_2013_BMI0024	103.2-1	Baetis adonis	43	X	0		Doe, J.	SAFIT2		DFG-ABL	1	5	Baetis adonis	43	X	0		Piper, P.	SAFIT2		SMC_2013								
9	AMEC	AMEC_2013_BMI0024	103.2-1	Bezzia/ Palpomyia	23	L	0		Doe, J.	SAFIT2		DFG-ABL	1	6	Bezzia/ Palpomyia	23	L	0		Piper, P.	SAFIT2		SMC_2013								
10	AMEC	AMEC_2013_BMI0024	103.2-1	Caloparyphus/ Euparyphus	7	L	0		Doe, J.	SAFIT2		DFG-ABL	1	7	Caloparyphus/ Euparyphus	7	L	0		Piper, P.	SAFIT2		SMC_2013								
11	AMEC	AMEC_2013_BMI0024	103.2-1	Ceratopogonidae	2	L	0		Doe, J.	SAFIT2		DFG-ABL	1	8	Ceratopogonidae	2	L	0		Piper, P.	SAFIT2		SMC_2013								
12	AMEC	AMEC_2013_BMI0024	103.2-1	Cricotopus	3	L	0		Doe, J.	SAFIT2		DFG-ABL	1	9	Cricotopus	2	L	0		Piper, P.	SAFIT2		SMC_2013								
13	AMEC	AMEC_2013_BMI0024	103.2-1	Cricotopus	3	L	0		Doe, J.	SAFIT2		DFG-ABL	1	9	Cricotopus	1	P	0		Piper, P.	SAFIT2		SMC_2013								
14	AMEC	AMEC_2013_BMI0024	103.2-1	Cricotopus bicinctus group	1	L	0	BM	Doe, J.	SAFIT2		DFG-ABL	1	10	Cricotopus bicinctus group	1	L	0		Piper, P.	SAFIT2		SMC_2013								
15	AMEC	AMEC_2013_BMI0024	103.2-1	Cryptochironomus	12	L	0		Doe, J.	SAFIT2		DFG-ABL	1	11	Cryptochironomus	12	L	0		Piper, P.	SAFIT2		SMC_2013								
16	AMEC	AMEC_2013_BMI0024	103.2-1	Dasyhelea	6	L	0		Doe, J.	SAFIT2		DFG-ABL	1	12	Dasyhelea	4	L	0		Piper, P.	SAFIT2		SMC_2013								
17	AMEC	AMEC_2013_BMI0024	103.2-1	Dasyhelea	6	L	0		Doe, J.	SAFIT2		DFG-ABL	1	12	Culicoides	3	L	0		Piper, P.	SAFIT2		SMC_2013								
18	AMEC	AMEC_2013_BMI0024	103.2-1	Elmidae	1	L	0		Doe, J.	SAFIT2		DFG-ABL	1	13	Elmidae	1	L	0		Piper, P.	SAFIT2		SMC_2013								
19	AMEC	AMEC_2013_BMI0024	103.2-1	Fallceon quilleri	17	L	0		Doe, J.	SAFIT2		DFG-ABL	1	14	Fallceon quilleri	17	X	0		Piper, P.	SAFIT2		SMC_2013								
20	AMEC	AMEC_2013_BMI0024	103.2-1	Hemerodromia	3	L	0		Doe, J.	SAFIT2		DFG-ABL	1	15	Hemerodromia	3	L	0		Piper, P.	SAFIT2		SMC_2013								
21	AMEC	AMEC_2013_BMI0024	103.2-1	Hydropsyche	58	L	0		Doe, J.	SAFIT2		DFG-ABL	1	16	Hydropsyche	58	L	0		Piper, P.	SAFIT2		SMC_2013								
22	AMEC	AMEC_2013_BMI0024	103.2-1	Hydropsychidae	1	L	0		Doe, J.	SAFIT2		DFG-ABL	1	17	Hydropsychidae	1	L	0		Piper, P.	SAFIT2		SMC_2013								
23	AMEC	AMEC_2013_BMI0024	103.2-1	Hydroptila	14	L	0		Doe, J.	SAFIT2		DFG-ABL	1	18	Neotrichia	3	L	0		Piper, P.	SAFIT2		SMC_2013								
24	AMEC	AMEC_2013_BMI0024	103.2-1	Hydroptila	14	L	0		Doe, J.	SAFIT2		DFG-ABL	1	18	Hydroptila	13	L	0		Piper, P.	SAFIT2		SMC_2013								
25	AMEC	AMEC_2013_BMI0024	103.2-1	Lebertia	1	X	0		Doe, J.	SAFIT2		DFG-ABL	1	19	Lebertia	1	X	0		Piper, P.	SAFIT2		SMC_2013								
26	AMEC	AMEC_2013_BMI0024	103.2-1	Limnophila	1	L	0		Doe, J.	SAFIT2		DFG-ABL	1	20	Hexatoma	1	L	0		Piper, P.	SAFIT2		SMC_2013								
27	AMEC	AMEC_2013_BMI0024	103.2-1	Micropsectra	124	L	0		Doe, J.	SAFIT2		DFG-ABL	1	21	Chironomidae	4	L	0	BIS	Piper, P.	SAFIT2		SMC_2013								
28	AMEC	AMEC_2013_BMI0024	103.2-1	Micropsectra	124	L	0		Doe, J.	SAFIT2		DFG-ABL	1	21	Micropsectra	120	L	0		Piper, P.	SAFIT2		SMC_2013								
29	AMEC	AMEC_2013_BMI0024	103.2-1	Ochrotrichia	1	L	0		Doe, J.	SAFIT2		DFG-ABL	1	22	Ochrotrichia	1	L	0		Piper, P.	SAFIT2		SMC_2013								
30	AMEC	AMEC_2013_BMI0024	103.2-1	Oligochaeta	1	X	0		Doe, J.	SAFIT2		DFG-ABL	1	23	Oligochaeta	1	X	0		Piper, P.	SAFIT2		SMC_2013								
31	AMEC	AMEC_2013_BMI0024	103.2-1	Ostracoda	1	X	0		Doe, J.	SAFIT2		DFG-ABL	1	24	Ostracoda	1	X	0		Piper, P.	SAFIT2		SMC_2013								
32	AMEC	AMEC_2013_BMI0024	103.2-1	Paracladopelma	5	L	0		Doe, J.	SAFIT2		DFG-ABL	1	25	Paracladopelma	5	L	0		Piper, P.	SAFIT2		SMC_2013								
33	AMEC	AMEC_2013_BMI0024	103.2-1	Pentaneura	5	L	0		Doe, J.	SAFIT2		DFG-ABL	1	26	Pentaneura	5	L	0		Piper, P.	SAFIT2		SMC_2013								
34	AMEC	AMEC_2013_BMI0024	103.2-1	Polypedilum	13	L	0		Doe, J.	SAFIT2		DFG-ABL	1	27	Polypedilum	13	L	0		Piper, P.	SAFIT2		SMC_2013								
35	AMEC	AMEC_2013_BMI0024	103.2-1	Psychodidae	1	P	0		Doe, J.	SAFIT2		DFG-ABL	1	28	Psychodidae	1	P	0		Piper, P.	SAFIT2		SMC_2013								
36	AMEC	AMEC_2013_BMI0024	103.2-1	Rheotanytarsus	87	L	0		Doe, J.	SAFIT2		DFG-ABL	1	29	Rheotanytarsus	87	L	0		Piper, P.	SAFIT2		SMC_2013								
37	AMEC	AMEC_2013_BMI0024	103.2-1	Rheotanytarsus	6	P	0		Doe, J.	SAFIT2		DFG-ABL	1	30	Rheotanytarsus	6	P	0		Piper, P.	SAFIT2		SMC_2013								
38	AMEC	AMEC_2013_BMI0024	103.2-1	Simulium	83	L	0		Doe, J.	SAFIT2		DFG-ABL	1	31	Cheumatopsyche	1	L	0	BPS	Piper, P.	SAFIT2		SMC_2013								
39	AMEC	AMEC_2013_BMI0024	103.2-1	Simulium	83	L	0		Doe, J.	SAFIT2		DFG-ABL	1	31	Simulium	85	L	0		Piper, P.	SAFIT2		SMC_2013								
40	AMEC	AMEC_2013_BMI0024	103.2-1	Sperchon	16	X	0		Doe, J.	SAFIT2		DFG-ABL	1	32	Sperchon	16	X	0		Piper, P.	SAFIT2		SMC_2013								
41	AMEC	AMEC_2013_BMI0024	103.2-1	Stilobezzia	1	L	0		Doe, J.	SAFIT2		DFG-ABL	1	33	Probezzia	1	L	0		Piper, P.	SAFIT2		SMC_2013								

Figure 2. Partial list of fields in the BMI_QC_Template Tab populated by the OR and QC labs during the external QC process. The full template and documentation of all field names can be found on the SWAMP website under the Database Management Resources Templates page (see Appendix 1).

TaxaBatch Tab

The TaxaBatch tab (Figure 3) stores information regarding the TaxaBatchID(s) for data sets submitted for external QC. The LabSubmissionCode field is used by the OR lab to state the quality of the original data prior to external QC (Table 1). AgencyCode represents the agency or data management personnel responsible for assigning a BatchVerificationCode once data verification and, if applicable, validation is performed. Please view the SWAMP online LookUp list for the most current valid values for given fields (see Appendix 1).

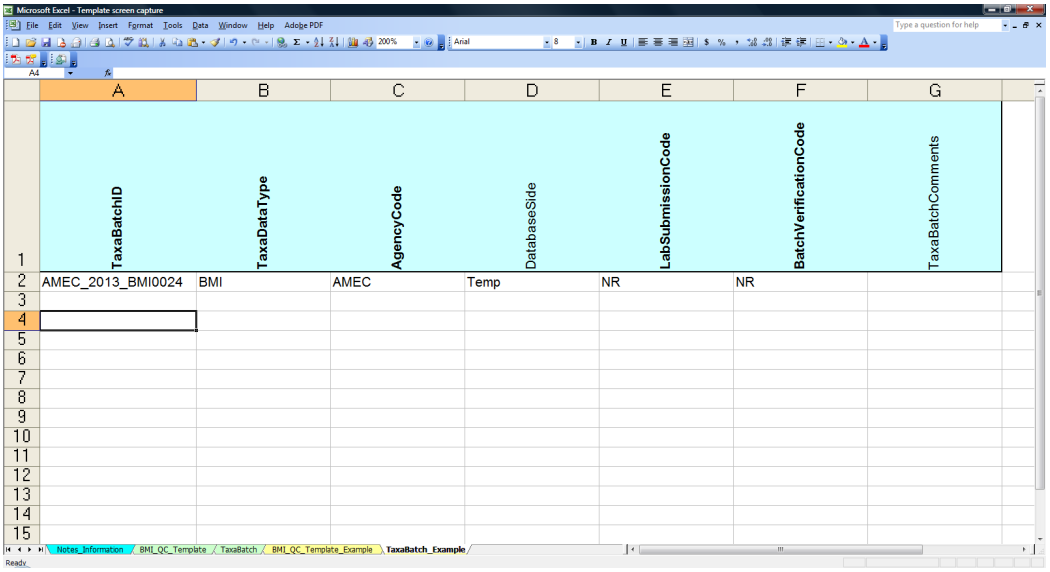


Figure 3. The TaxaBatch tab from the Excel QC Submittal data template.

Table 1. Partial list of LabSubmissionCodes used by the Original (OR) lab prior to external QC.

Lab Submission	Lab Submission	Lab Submission Description
A	Acceptable	Batch met Project QA/QC protocols
A,MD	Acceptable, Minor Deviations	Batch met Project QA/QC protocols; minor deviations in test conditions; Batch Comment required
MD	Minor Deviations	Minor deviations in test conditions; Batch Comment required
NR	Not Recorded	Not Recorded or result has not been verified
QI	Incomplete QC	Batch has incomplete QC; Batch Comment required
QN	No QC	No QA/QC performed or performed but not reported, used with historical data, Batch Comment required
R	Rejected	Data rejected

Once the QC Submittal data template is populated by the OR lab, check it for errors. Check for formatting issues such as missing required fields, invalid entries (e.g., FinalID not in the LookUp list), and incorrect data types (e.g., text in a number field). Errors should be corrected in the template and re-checked before submittal to the External QC lab. If a LookUp value or FinalID does not exist and you would like it considered for addition to the SWAMP database, please contact the Project Manager.

5. Prepare and Submit Samples

The OR lab submits the samples and data to the external QC lab. Samples can be transported to the QC lab in person or shipped in accordance with federal regulations.

Note: Voucher specimens from each sample MUST be sorted into separate vials corresponding to unique taxonomic FinalIDs and life stages. For example, larval specimens of the caddisfly *Rhyacophila betteni* should be placed in one vial, pupal specimens of *R. betteni* should be placed in a second vial, larval specimens of *R. arnaudi* should be placed in a third vial, etc. This is to ensure any discrepancies between original and QC identifications and/or enumerations can be tracked on a one-to-one basis, at the specimen level, for each FinalID and life stage combination. Education and training have been a primary goal of the taxonomic QC program in California since its inception in 2001, with the ABL serving as SWAMP's referee lab. By having the original determination labels present, the QC taxonomist can immediately respond to any discrepancies by providing narrative comments about key characters, taxonomic literature, etc., thereby improving consistency of taxonomic identifications produced for bioassessment.

Each vial should contain a determination label with the following information:

- FinalID (taxon)
- Life stage abbreviation (A =adult, P =pupa, L =larva, X =non-insect)
- Specimen count
- Determining taxonomist name
- Year determination was made

Example:

Hesperoperla sp. L 23

det.: J. Slusark, 2007

Each vial should also contain a locality label with the following (recommended) information:

- State

- County
- Water body (stream name) and sampling location
- StationCode
- Laboratory sample ID
- Replicate number (if applicable)
- Date of collection

Example:

CA; San Diego Co.

Santa Ysabel Creek at Highway 79

905DGSY1x

Lab# 19440; 07/20/10

External QC Procedure

1. Receiving Data

The external QC lab should use the Excel QC Submittal template for direct entry of QC data. Remember, it is important for the OR section of the template to be duplicated for each corresponding QC record if multiple QC records are required, i.e., if a single taxon identified by the OR lab was determined to contain multiple taxa in the QC process.

Before external QC begins, it is important to verify that the TaxaBatchID, LabSampleID, and BenthicResult Agency Code (i.e., OR lab) match information in the data entry form with the sample being processed. The OR data should be scanned for qualifier codes (QACode) and the specified BMIEffortList and SAFIT STE Level followed to aid in the QC process. If a different BMIEffortList and STE Level is used by the QC taxonomist, it should be noted in the QC section.

2. QC Process

The external QC process is similar to the one detailed in the Internal QC section of the BMI Lab SOP (Woodard et al. 2012); users should read that document for guidance on equipment, chemicals, health and safety warnings, etc.

Step 1. Retrieve all vials and slides from selected sample(s) from the sample storage area.

Step 2. Open the Excel data template or the Add/Edit QC Data form within the Lab Entry form. It is required to use standardized data dictionaries and valid LookUp values maintained by SWAMP when applying or choosing values for the various fields in the following steps.

Step 3. Select a vial from the first sample selected for QC. Again, each vial should contain all specimens associated with a single FinalID, life stage, and distinct combination. Transfer specimens to a Petri dish, adding 70% ethanol as necessary to cover the specimens.

Step 4. Move the Petri dish to the dissecting microscope stage.

Step 5. Identify all specimens to the designated SAFIT STE level, i.e., to the same level of effort as used by the OR lab, using appropriate taxonomic keys and/or literature as necessary. Specimens may be cleared with KOH or slide mounted as necessary to facilitate identification (see Section 4.2 of the BMI Lab SOP for clearing instructions).

Step 6. Count all specimens in the Petri dish.

Step 7. Record the determination (FinalID), life stage, count and, if applicable, any data qualifiers (QACode) for specimens from the first vial in the QC portion of the data entry form. Table 2 includes examples of QACodes and taxonomic qualifiers such as probable sorting error (BPS), non-target taxa identified in sample (BNT), immature specimen (BIS), and damaged beyond identification (BDI). The full list of QACodes can be found on the SWAMP LookUp list pages (see Appendix 1).

Table 2. QACodes associated with taxonomy data. For additional codes contact the OIMA helpdesk.

Process	QACode	Description
Lab Sorting/ Taxonomy		
	BZ	Sample preserved improperly
	LST	Sample was lost or destroyed
	BDI	Damaged beyond identification
	BIS	Immature specimen
	BTL	Taxonomist's literature not sufficient
	BBM	Bad Mount
	BOT	Other - see comments
Taxonomy QC		
	BNV	Sample or vial not submitted for analysis
	BLI	Additional sample or vial received than expected
	BLS	Sample or vial labels switched
	BLE	Sample or vial Label and Electronic Data do not match
	BNO	No specimens found in vial
	BPS	Probable sorting error
	BNT	Non-Target taxa identified in sample
	BET	Excluded Taxon
Data Updates		
	BQC	Record underwent QC
	BDC	Data corrected based on QC

Step 8. In vials where QC determination confirms initial determination and count of all specimens in that vial:

- Return all specimens to the original vial and fill with 70% ethanol.
- Return the original locality and determination labels to the vial.
- Place a colored QC label in the vial, indicating that all specimens have been examined and no additional action is needed. The QC label contains the following information:

  "QC Checked"

QC taxonomist name and year

Laboratory name

Example:

QC Checked

Det. Brady Richards 2011

ABL Chico

Step 9. In vials where QC determination conflicts with the initial determination of all specimens:

- Return the specimen(s) to the original vial and fill with 70% ethanol.
- Return the original locality and determination labels to each vial.
- Create a new determination label with the corrected determination on it and place it in the vial.
- Place a colored QC label in the vial, indicating that all specimens have been examined and no additional action is needed. The QC label contains the following information:

"QC Checked"

QC taxonomist name and year

Laboratory name

Example:

QC Checked

Det. Brady Richards 2011

ABL Chico

Step 10. In vials where QC determination conflicts with the initial determination of some, but not all, specimens in that vial[5]:

- Proceed as in Step 8 for correctly identified specimens.

[5] Cases where the QC determination conflicts with some, but not all, specimens in a vial will result in two or more entries for a given vial in the data entry form.

- Place specimens with corrected determination(s) into new vial(s) as appropriate, sorting by FinalID and life stage.
- Place a new determination label into the vial(s).
- Place a new locality label into the vial(s), duplicating the original locality label as closely as possible.
- Place a colored QC label into the vial(s), indicating that all specimens have been verified.

Step 11. Place any specimen parts that were cleared or dissected during identification in a ¼-dram shell vial or genitalia microvial containing 70% ethanol and plug with cotton. Place the shell vial or microvial inside the associated specimen vial. Each shell vial should contain pieces from only one specimen. Use as many shell vials as necessary.

Step 12. Repeat the process from Step 3 through Step 11, working through all vials in the sample one at a time until all vials have had determination, counts, and life stage verified.

Step 13. If a vial listed in the data submittal sheet from the OR lab cannot be located, or if a vial contains no specimens, the QC taxonomist records the following:

- Enter the missing FinalID and life stage in the QC section of the data entry form, record a zero in the QC count data field, and enter the appropriate QACode.
- Notify the OR lab and, if necessary, Project Manager.

Step 14. After checking all vials, if vials are found that were not listed in the original data submittal sheet, a new line of data is created in the OR section of the data entry form and the vial contents analyzed as above with the appropriate QACode applied to QC results indicating the vial was left out of the original inventory.

Step 15. Repeat steps 3-14 for all QC samples.

Step 16. If any specimens are determined to be suitable for addition to the QC lab reference collection, permission for the QC lab to keep the specimens must be obtained from the OR lab and/or PM. The removal of specimens/vials is then recorded, e.g., in the Comments field of the data entry form, and the specimens cataloged in the QC reference collection as appropriate.

3. Calculation of MQOs

The QC lab is responsible for calculating and reporting MQO results. MQOs may be calculated by hand using the formulas in this document or by using SWAMP tools available at Data Management Resources (See Appendix 1). A data calculation tool, the BMI QC Tool, is available to help with MQO calculations.

Once the QC lab has populated the BMI_QC_Template with final results, the template file is then loaded into the tool and MQOs are automatically generated. Outputs from the tool can be used to write narratives and reports. An SOP will accompany the tool for operating procedures.

Two types of MQOs are calculated: Assessment MQOs and Descriptive MQOs. Assessment MQOs establish a limit of disagreement or error between the OR lab and QC lab and contribute to pass/fail determinations for a batch of QC samples. Batches that fail the QC process will trigger corrective actions to resolve discrepancies and harmonize processes and knowledge between labs. Descriptive MQOs convey additional information about discrepancies between OR lab and QC lab results, but are not as influential for assessing the utility of data for bioassessment applications. Appendix 2 provides an example data set with calculations and results to illustrate the use of different types of MQOs. The MQO thresholds listed below are provisional and subject to change as more information becomes available regarding failure rates encountered through the external QC process.

Assessment MQOs

Absolute Recount Error Rate: Compares number of specimens in a sample per FinalID according to QC lab counts with number of specimens per FinalID according to OR lab counts.

$$\frac{\sum|\text{QC lab count} - \text{OR lab count}|}{\text{QC lab count}} \times 100$$

where absolute difference between QC lab count and OR lab count is per FinalID

Threshold: <10% of QC lab count

Taxa ID Error Rate: The percentage of misidentified[6] taxa (FinalIDs) in a sample. Higher and Lower Resolution discrepancies are not included as misidentifications.

$$\frac{\text{Number of FinalIDs misidentified by OR lab}}{\text{Number of FinalIDs per QC lab}} \times 100$$

Threshold: <10% error rate

Individual ID Error Rate: The percentage of misidentified specimens in a sample. Higher and Lower Resolution discrepancies are not included as misidentifications.

$$\frac{\text{Number of specimens misidentified per QC lab count}}{\text{Total number of specimens in sample per QC lab count}} \times 100$$

Threshold: <10% error rate

[6] ABL's goal as SWAMP's taxonomic referee lab has been to define, promote, and to some extent enforce, a consistent standard of analytical truth to which taxonomic identifications are compared. This standard is upheld through SAFIT and the trainings it provides, ABL's library of taxonomic literature and vouchered reference collection, and the experience of ABL taxonomists. Therefore, discrepancies between the OR lab and QC lab (ABL) are treated as misidentifications by the OR lab unless the reconciliation process shows otherwise. Other programs adopting these procedures for inter-lab comparisons may prefer more neutral terminology.

Lower Taxonomic Resolution Individual Error Rate: The percentage of specimens in a sample not identified to the desired STE.

$$\frac{\text{Number of specimens where QC lab FinalID is more resolved than OR lab FinalID}}{\text{Total number of specimens in sample per QC lab count}} \times 100$$

Threshold: <10% error rate. Note: The greater resolution attained by QC lab must be consistent with the target STEs defined by SAFIT Level 1 or SAFIT Level 2.

Lower Taxonomic Resolution Count Error Rate: The percentage of taxa (FinalIDs) in a sample not identified to the desired STE.

$$\frac{\text{Number of FinalIDs where QC lab is more resolved than OR lab}}{\text{Number of FinalIDs per QC lab}} \times 100$$

Threshold: <10% error rate. Note: The greater resolution attained by QC lab must be consistent with the target STEs defined by SAFIT 1 or SAFIT 2.

Descriptive MQOs

Recount Accuracy: Compares total number of specimens in a sample according to QC count with total number of specimens according to OR count.

$$\frac{\text{Number of specimens in smaller of the two counts}}{\text{Number of specimens in larger of the two counts}}$$

Threshold: none; MQO has poor sensitivity. Individual taxa could be grossly miscounted, or counts transposed, but as long as the sample totals are close the errors would not be detected.

Taxa Count Error Rate: Compares the number of taxa (FinalIDs) in a sample according to the OR lab with the number of taxa (FinalIDs) according to the QC lab.

$$\frac{|\text{Number of FinalIDs per QC lab} - \text{Number of FinalIDs per OR lab}|}{\text{Number of FinalIDs per QC lab}} \times 100$$

Threshold: none; MQO has poor sensitivity. OR lab could misidentify all taxa in a sample, but have the number of taxa correct, and would pass this MQO.

Higher Taxonomic Resolution Individual Error Rate: The percentage of specimens in a sample identified beyond STE, e.g., specimens identified to species when STE requires only genus-level identifications.

$$\frac{\text{Number of specimens where QC lab FinalID is less resolved than OR lab FinalID}}{\text{Total number of specimens in sample per QC lab count}} \times 100$$

Threshold: none; identification of specimens beyond STE does not affect data quality for bioassessment.

Taxonomic Resolution Individual Error Rate: The sum of Higher and Lower Taxonomic Resolution Individual Error Rates.

Higher Taxonomic Resolution Individual Error Rate + Lower Taxonomic Resolution Individual Error Rate

Threshold: none; combines an assessment MQO with a descriptive MQO for overall summary of discrepancies in taxonomic resolution.

Higher Taxonomic Resolution Count Error Rate: The percentage of taxa (FinalIDs) in a sample identified beyond STE, e.g., taxa identified to species when STE requires only genus-level identifications.

$$\frac{\text{Number of FinalIDs where QC lab is less resolved than OR lab}}{\text{Number of FinalIDs per QC lab}} \times 100$$

Threshold: none; identification of specimens beyond STE does not affect data quality for bioassessment.

Taxonomic Resolution Count Error Rate: The sum of Higher and Lower Taxonomic Resolution Count Error Rates

Higher Taxonomic Resolution Count Error Rate + Lower Taxonomic Resolution Count Error Rate

Threshold: none; combines an assessment MQO with a descriptive MQO for overall summary of discrepancies in taxonomic resolution.

Notes About MQO Calculations

MQOs are based only on unique FinalIDs: do not include LifeStage or Distinct in MQO calculations.

Life stage: The primary purpose of separating life stages is to track potential identification errors related to one life stage but not another, as different life stages normally have separate identification keys based on different morphological characters. If the OR lab places more than one life stage of a given taxon in a single vial, but all specimens are correctly identified, do not create a discrepancy that contributes to MQO failure. The only exceptions are certain genera in the beetle families Hydrophilidae and Hydraenidae where larvae and adults belong to different functional feeding groups and combining life stages could influence functional feeding group metrics.

Distinct taxa: SWAMP taxonomists have the option of labeling specimens not identified to STE as "distinct" if there are good confirming characters indicating that the specimens in question do not belong to the same taxon as others in the sample, whether the others are identified to STE or not. However, QC discrepancies are not to be based solely on "distinct" designations. For example, consider the following results from a sample where target STE for the mayfly genus *Baetis* is to species where possible (i.e., target STE = SAFIT Level 2):

OR lab		**QC lab**	
Final ID	Count	Final ID	Count
Baetis sp.	8	*Baetis* sp.	5
Baetis sp.	8	*Baetis adonis*	1
Baetis sp.	8	*Baetis tricaudatus*	1
Baetis sp.	8	*Baetis* sp. "distinct"	1

In this example, the OR taxonomist identified all 8 *Baetis* specimens to genus. The QC taxonomist agreed that 5 of the specimens could not be identified beyond genus, but also identified one specimen as *B. adonis*, one specimen as *B. tricaudatus*, and one specimen as *Baetis* sp. "distinct", meaning that the latter specimen was morphologically distinct from all other specimens in the sample but still unidentifiable to species. The first two discrepancies are errors in taxonomic resolution by the OR taxonomist. In the case of the Baetis sp. "distinct" record, neither taxonomist could successfully identify the specimen to the target STE, so there should be no discrepancy created that would contribute to MQO failure, and the record will not be considered a unique FinalID in the calculation of MQOs. Also note that no count discrepancies would derive from these results.

Reporting QC Results

1. Preparation of QC Report

Once external QC is completed, the QC lab submits the OR and QC data in the Excel QC Submittal template format and the MQO calculation results back to the OR lab and PM. The QC taxonomist also provides a narrative explanation that summarizes MQO results, describes discrepancies in more detail, and focuses on specific taxonomic issues that may have been encountered but that are not captured by MQOs. For example, important taxonomic characters and/or literature that may help the OR lab with identifications may be recommended.

2. MQO Thresholds

Five assessment MQOs are used to assess pass/fail of each sample submitted for QC (Table 3). Assessment MQOs emphasize accuracy of identification per taxon (Taxa ID Error Rate), accuracy of raw counts per taxon (Absolute Recount Error Rate), accuracy of relative abundance estimates (Individual ID Error Rate), and successful identification to specified SAFIT Levels (Lower Taxonomic Resolution Individual Error Rate and Lower Taxonomic Resolution Count Error Rate). The five assessment MQOs address errors in raw data parameters most likely to translate into errors in BMI metrics and/or taxa lists, and therefore into errors in biological assessment itself. Other errors that focus on total richness estimates (where the OR lab could misidentify all taxa but still have the correct number of taxa), or discrepancies where the OR lab identified specimens beyond SAFIT requirements, have much less influence on data quality for bioassessment. In addition, MQO thresholds were selected so that low-frequency, random errors typical of taxonomic QC should not trigger corrective action, e.g., occasional

misidentifications, "tagalongs" where tiny specimens are attached to much larger specimens, or "mis-sorts" where the OR taxonomist accidentally places a chironomid midge in a snail vial, etc. However, more frequent occurrences of these types of errors, alone or in combination, could lead to MQO failure.

Table 3. MQO thresholds.

MQO Type	MQO Name	SWAMP Threshold
	Assessment MQOs	
Count	Absolute Recount Error Rate	< 10%
Identification	Taxa ID Error Rate	< 10%
Identification	Individual ID Error Rate	< 10%
Identification	Lower Taxonomic Resolution Individual Error Rate	< 10%
Identification	Lower Taxonomic Resolution Count Error Rate	< 10%
	Descriptive MQOs	
Count	Recount Accuracy	N/A
Identification	Taxa Count Error Rate	N/A
Identification	Higher Taxonomic Resolution Individual Error Rate	N/A
Identification	Taxonomic Resolution Individual Error Rate	N/A
Identification	Higher Taxonomic Resolution Count Error Rate	N/A
Identification	Taxonomic Resolution Count Error Rate	N/A

Reviewing QC Results, Reconciling Data Discrepancies, and Data Updates

1. Pass/Fail Determinations

Count how many assessment MQOs were failed per sample, per batch. For typical QC batch sizes of <10 QC samples, failure of any one or more assessment MQOs in a single sample triggers corrective action. For larger QC batch sizes, 2 in 20 QC samples, 3 in 30 QC samples, etc., must fail one or more MQOs before corrective action is required. For example, in a QC Batch of 15 samples chosen to represent a TaxaBatch of 150 samples, if two or more of the 15 QC samples fail any one or more assessment MQOs in Round 1, corrective action is required.

2. Reconciliation

When an MQO has failed, there is a reconciliation phase during which the OR lab may dispute QC lab results. If the OR lab can demonstrate, based on sound evidence, that QC lab results are erroneous, the discrepancy may be overturned and a new QC report generated that incorporates any changes and reasons for them. In the case of unresolved disputes, it is the responsibility of the PM to serve as arbiter and make the final decision about which identification(s) to accept.

3. Corrective Action

If the number of MQO failures per batch indicates that corrective action is required, and if the OR lab accepts QC lab results that indicate failure of MQOs, it is the responsibility of the OR lab to go back through the entire TaxaBatch represented by the QC sample(s) (including those not selected for QC in Round 1), correct discrepancies based on feedback from the QC lab, and then select another random 10% of samples to submit for a second round of QC. Samples that underwent QC in Round 1 should not be selected for Round 2 and subsequent rounds. If an additional round of QC is needed, all steps in the process are performed again, including submittal of an Excel QC Submittal template with data from the second set of samples, except that round would equal 2. The process continues until the OR lab, QC lab, and PM agree the data meet QC requirements, discrepancies have been resolved, and data are finalized.

Enforcement of corrective actions is the responsibility of the PM, not the QC lab. In rare cases, the iterative QC process may reveal that published knowledge of a taxonomic group is incomplete, thereby causing repeated failures; for example, cryptic or undescribed species may cause difficulty or ambiguity in running specimens through published taxonomic keys. In these cases, the PM may choose to suspend additional rounds of QC and the specimens in question may be left at whatever level of identification is unambiguous.

When the OR lab, QC lab and PM agree the external QC process is complete, all QC material from the given batch (with the exception of any reference collection specimens retained by the external QC lab) will be returned to the PM or OR lab at their expense.

4. Update and Storage of QC Data and Metadata

Once the BMI_QC_Template is populated by the OR and QC labs and the QC process is complete (e.g., lab reconciliation and corrective actions), the BMI_QC_Template can be submitted to SWAMP by emailing the BMI_QC_Template Excel file to the OIMA helpdesk. The data template will be stored by the OIMA helpdesk until the database has been updated to accept and store external QC data.

Result-Level Updates

If samples pass QC, there is no requirement to update errors or discrepancies in the original data. In fact, updating just the QC samples that pass MQOs, but not all other samples within a given TaxaBatchID, would mean that the updated QC samples are no longer representative of the larger batch. If samples do not pass QC due to MQO failures, the original data in the BenthicResult table is updated for FinalID and count errors; updates will be based on reconciled discrepancies between the OR and QC labs once all corrective actions are completed, provided such communication occurs between labs, or based on

external QC results alone if it does not. The updated BenthicResult table stores the final taxonomic data set for use in data analysis, IBI scoring, etc. NOTE: Labs may choose to withhold submission of finalized data to the BenthicResult table until after the external QC process is complete. In such cases, all data updates would be performed in the OR lab's data management system as part of corrective actions as described above, and there would be no need to update taxonomic identifications or counts in the BenthicResult table once finalized data are submitted. Updates to the BenthicResult table would be required only of labs within the SWAMP program that submit "real-time" data to the BenthicResult table prior to external QC, or labs outside of the SWAMP program that submit data to the BenthicResult table prior to external QC.

The QACode field in the final BenthicResult table is updated by the PM or data manager to identify two situations on a record-by-record basis. First, all records that underwent QC but did not require corrective actions are assigned a code of BQC. Second, all records that were corrected for FinalID and/ or count errors are assigned a code of BDC. For example, all records from a QC Batch that passed all Assessment MQOs are assigned a QACode of BQC. By contrast, records from a QC Batch that failed one or more assessment MQOs are assigned a QACode of BQC if they did not contribute to MQO failure, but are assigned a QACode of BDC if they contributed to MQO failure and were changed as part of the corrective actions process. Additionally, data users may request copies of any narrative reports, prepared by the QC Lab and submitted to the PM and OR Lab (see above), that are associated with records of interest.

Batch-Level Updates

When external QC is completed for as many rounds as necessary, and all corrective actions are completed, either the PM or the data manager for a given project must make a final assessment of whether taxonomic QC requirements have been fulfilled and update BatchVerificationCodes (Table 4) within the TaxaBatch table. The BatchVerificationCode is the final assessment of data quality for a given TaxaBatchID and applies to the QC Batch and to samples not selected for QC. Data are verified to determine if the required frequency of QC was performed and whether final data in the BenthicResult table are within QC specifications according to MQO thresholds defined in this SOP. The PM or data manager must evaluate the completeness, correctness, and conformance/compliance of all samples belonging to a given TaxaBatchID against all procedural and contractual specifications for BMI taxonomy. If an additional round of QC is not performed on a batch of failed samples as required, the batch is flagged using the BatchVerificationCode as having incomplete QC ("VQI") or no QC ("VQN").

Table 4. BatchVerificationCodes. For additional codes contact the OIMA helpdesk.

Batch Verification Code	Batch Verification Name	Batch Verification Description
NA	Not Applicable	Verification not applicable
NR	Not Recorded	Not Recorded or result has not been verified
VAC	Cursory Verification	Full verification of electronic data against MQOs; includes evaluation of raw QC data and recalculation of MQO results
VAC,VQI	Cursory Verification, Incomplete QC	Full verification of electronic data against MQOs; includes evaluation of raw QC data and recalculation of MQO results. Batch has incomplete QC; Batch Comment required
VAP	Alternate Level Validation	Validation of electronic data against alternate MQOs; may or may not include an evaluation of raw QC data and recalculation of MQO results
VAP,VQI	Alternate Level Validation, Incomplete QC	Validation of electronic data against alternate MQOs; may or may not include an evaluation of raw QC data and recalculation of sample results. Batch has incomplete QC; Batch Comment required
VQI	Incomplete QC	Batch has incomplete QC; Batch Comment required
VQN	No QC	No QA/QC performed or performed but not reported; used with historical data; Batch comment required

After verification, the ComplianceCode must also be updated in the BenthicResult table by the PM or data manager for each TaxaBatchID to indicate the overall compliance level (Table 5) of taxonomic data relative to specifications within each project's Quality Assurance Project Plan (QAPP). "Compliant" indicates all data meets requirements while "Qualified" is assigned to data that fails to meet the SOP and QAPP requirements or are insufficiently documented to make an assessment. A detailed description of the Data Classification System can be found on the SWAMP Quality Assurance (QA) Documents webpage (see Appendix 1).

Table 5. ComplianceCodes. For additional codes contact the OIMA helpdesk.

Compliance Code	Compliance Name	Compliance Description
Com	Compliant	Compliant with associated QAPP
Est	Estimated	Data is considered to be non-quantifiable, estimated
Hist	Historical	Historical; no supporting QC data
NA	Not Applicable	Not Applicable, therefore result did not undergo verification
NR	Not Recorded	Not Recorded
Pend	Pending QA review	Pending QA review
Qual	Qualified	Non-compliant with associated QAPP, analytes not covered in associated QAPP, insufficiently documented need supplementary info for data to be used
Rej	Rejected	Rejected; unusable for all intended purposes
Scr	Screening	Data is for information purposes only and is considered to be non-quantifiable

Note: The LabSubmissionCode, stored in the TaxaBatch tab in the QC Submittal template and also within the TaxaBatch table, describes data quality prior to submitting samples for external QC and should not be updated during or after the external QC process.

Project managers may opt to take the additional step of assessing data usability through a validation process documented within that project's QAPP to determine the taxonomic quality and any limitations. For example, a PM may reject all data not taken to the SAFIT2 STE level if a given project requires it. A TaxaBatchID undergoing validation will receive a BatchVerificationCode of "VAP" for alternate level validation.

References

Moulton S. R., J. L. Carter, S. A. Grotheer, T. F. Cuffney, and T. M. Short. 2000. Methods of Analysis by the U. S. Geological Survey National Water Quality Laboratory – Processing, Taxonomy, and Quality Control of Benthic Macroinvertebrate Samples. U.S. Geological Survey Open File Report 00-212.

Ode, P.R. 2007. Standard Operating Procedures for Collecting Macroinvertebrate Samples and Associated Physical and Chemical Data for Ambient Bioassessments in California. California State Water Resources Control Board Surface Water Ambient Monitoring Program (SWAMP) Bioassessment SOP 001.

Woodard, M.E., J. Slusark, and P.R. Ode. 2012. Standard Operating Procedures for Laboratory Processing and Identification of Benthic Macroinvertebrates in California. California State Water Resources Control Board Surface Water Ambient Monitoring Program (SWAMP) Bioassessment SOP 003.

Glossary

Taxa Batch = All samples in the project(s) for which data quality will be inferred from external QC (e.g., all samples in three small projects processed by Lab X). These samples are all designated with the same TaxaBatchID.

QC Batch = 10% of samples in a Taxa Batch, generally selected randomly, that are sent to an external lab or taxonomist for QC (e.g., three QC samples from a Taxa Batch containing 30 samples).

Comparability = A measure of the confidence with which one data set, element, or method can be considered as similar to another.

Completeness = A measure of the amount of valid data obtained from a measurement system.

Corrective Action = Any measures taken to rectify conditions adverse to quality and/or to eliminate the causes of an existing nonconformity, defect, or other undesirable situation in order to prevent reoccurrence.

Validation = Assessing usability of data. An analyte- and sample-specific process that evaluates the information after the verification process (i.e., determination of method, procedural, or contractual compliance) to determine analytical quality and any limitations.

Verification = Checking to see if frequency of QC was performed and if within QC specs (i.e., against MQOs and thresholds). The process of evaluating the completeness, correctness, and conformance/ compliance of a specific information set against the method, procedural, or contractual specifications for that activity.

Appendix 1. List of Online Links

SWAMP

Data Management Resources
http://www.waterboards.ca.gov/water_issues/programs/swamp/data_management_resources/index.shtml

Standard Operating Procedures
http://www.waterboards.ca.gov/water_issues/programs/swamp/tools.shtml#methods

Data Checker
http://swamp.waterboards.ca.gov/swamp_checker/

LookUp lists
http://swamp.waterboards.ca.gov/SWAMP_Checker/LookUpLists.php

Quality Assurance Documents
http://www.waterboards.ca.gov/water_issues/programs/swamp/tools.shtml#qapgd

SAFIT

Home Page
http://safit.org/ste.html

Appendix 2. Example data set with enumeration and taxonomic discrepancies where required taxonomic level of effort is SAFIT 2. MQO calculations and assessments follow the data set.

VIAL #	OR Lab ID	OR Life Stage	OR Count	QC ID	QC Life Stage	QC Count	Count Error	Absolute Difference	ID Error Type	QC Lab Comments
1	Ambrysus	X	1	Ambrysus	A	1	Equal Count	0		
2	Apedilum	L	1	Apedilum	L	1	Equal Count	0		
3	Atractides	X	1	Atractides	X	1	Equal Count	0		
4	Baetis	X	8	Baetis	L	6	Equal Count	0		ABR: damaged but probably B. adonis
4	Baetis	X	8	Baetis bicaudatus	L	1	Equal Count	0	Lower Resolution Error	
4	Baetis	X	8	Baetis adonis	L	1	Equal Count	0	Lower Resolution Error	
5	Baetis adonis	X	43	Baetis adonis	L	43	Equal Count	0		
6	Bezzia/ Palpomyia	L	23	Bezzia/ Palpomyia	L	23	Equal Count	0		
7	Caloparyphus/ Euparyphus	L	7	Caloparyphus/ Euparyphus	L	7	Equal Count	0		
8	Ceratopogonidae	L	2	Ceratopogonidae	L	2	Equal Count	0		
9	Cricotopus	L	3	Cricotopus	L	2	Equal Count	0		
9	Cricotopus	L	3	Cricotopus	P	1	Equal Count	0	life stages mixed; don't count	
10	Cricotopus bicinctus group	L	1	Cricotopus bicinctus group	L	1	Equal Count	0		
11	Cryptochironomus	L	12	Cryptochironomus	L	12	Equal Count	0		
12	Dasyhelea	L	6	Dasyhelea	L	4	Under Count	1		
12	Dasyhelea	L	6	Culicoides	L	3	Under	1	Misidentification	

VIAL #	OR Lab ID	OR Life Stage	OR Count	QC ID	QC Life Stage	QC Count	Count Error	Absolute Difference	ID Error Type	QC Lab Comments
13	Elmidae	L	1	Elmidae	L	1	Equal Count	0		
14	Fallceon	L	17	Fallceon	X	17	Equal Count	0		
15	Hemerodromia	L	3	Hemerodromia	L	3	Equal Count	0		
16	Hydropsyche	L	58	Hydropsyche	L	58	Equal Count	0		
17	Hydropsychidae	L	1	Hydropsychidae	L	1	Equal Count	0		
18	Hydroptila	L	14	Neotrichia	L	3	Under Count	2	Misidentification	
18	Hydroptila	L	14	Hydroptila	L	13	Under Count	2		
19	Lebertia	X	1	Lebertia	X	1	Equal Count	0		
20	Limnophila	L	1	Hexatoma	L	1	Equal Count	0	Misidentification	
21	Micropsectra	L	120	Micropsectra	L	120	Equal Count	0		
22	Ochrotrichia	L	1	Ochrotrichia	L	1	Equal Count	0		
23	Enchytraeidae	X	4	Oligochaeta	X	4	Equal Count	0	Higher Resolution Error	
24	Ostracoda	X	1	Ostracoda	X	1	Equal Count	0		
25	Paracladopelma	L	5	Paracladopelma	L	5	Equal Count	0		
26	Pentaneura	L	5	Pentaneura	L	5	Equal Count	0		
27	Polypedilum	L	13	Polypedilum	L	13	Equal Count	0		
28	Psychodidae	P	1	Psychodidae	P	1	Equal Count	0		
29	Rheotanytarsus	L	87	Rheotanytarsus	L	87	Equal Count	0		
30	Rheotanytarsus	P	6	Rheotanytarsus	P	6	Equal	0		

VIAL #	OR Lab ID	OR Life Stage	OR Count	QC ID	QC Life Stage	QC Count	Count Error	Absolute Difference	ID Error Type	QC Lab Comments
31	Simulium	L	83	Cheumatopsyche	L	1	Under Count	3	Misidentification	tagalong specimen
31	Simulium	L	83	Simulium	L	85	Under Count	3		
32	Sperchon	X	16	Sperchon	X	16	Equal Count	0		
33	Stilobezzia	L	1	Probezzia	L	1	Equal Count	0	Misidentification	
34	Tanypodinae	L	1	Tanypodinae	L	1	Equal Count	0		immature
35	Tanytarsus	L	1	Tanytarsus	L	1	Equal Count	0		
36	Tanytarsus	P	2	Tanytarsus	P	2	Equal Count	0		
37	Thienemannimyia group	L	7	Thienemannimyia group	L	7	Equal Count	0		
38	Cheumatopsyche	P	2	Cheumatopsyche	P	2	Equal Count	0		
39	Cheumatopsyche	L	3	Cheumatopsyche	P	1	Equal Count	0	life stages mixed; don't count	
39	Cheumatopsyche	L	3	Cheumatopsyche	L	2	Equal Count	0		
40	Tricorythodes explicatus	X	127	Tricorythodes explicatus	X	127	Equal Count	0		
	# OR Taxa = 37		**OR Count = 691**	**# QC Taxa = 41**		**QC Count = 697**				

MQO Name	Formula	Result (%)	SWAMP Threshold (%)	Threshold Comparison[1]
Absolute Recount Error Rate	(6/697) x 100	0.9	10	NE
Taxa ID Error Rate	(5/41) x 100	12.2	10	EX
Individual ID Error Rate	(9/697) x 100	1.3	10	NE
Lower Taxonomic Resolution Individual Error Rate	(2/697) x 100	0.3	10	NE
Lower Taxonomic Resolution Count Error Rate	(2/41) x 100	4.9	10	NE
Recount Accuracy	(691/697) x 100	99.1		
Taxa Count Error Rate	((37-41)/41) x 100	9.8		
Higher Taxonomic Resolution Individual Error Rate	(4/697) x 100	0.6		
Taxonomic Resolution Individual Error Rate	0.6 + 0.3	0.9		
Higher Taxonomic Resolution Count Error Rate	(1/41) x 100	2.4		
Taxonomic Resolution Count Error Rate	2.4 + 4.9	7.3		

[1] **NE = Non-Exceedance, EX = Exceedance.**