Society for Freshwater Science
Taxonomic Certification Program

Quality Control Procedure for Sample-Based Taxonomic Data

Benthic Macroinvertebrates

The Society for Freshwater Science's Taxonomic Certification Committee (SFS-TCC) considers successful completion of certification tests to be an objective reflection of the capability of an individual to perform accurate and precise taxonomic identifications consistently within the taxa groups for which they are certified. The committee also understands that valid certification does not guarantee that a holder will consistently produce high quality taxonomic data, and as such, that routine and rigorous quality control (QC) oversight is very important and necessary (Stribling et al. 2012). Key to this sample-based QC process is determining error types and sources, specifying and implementing corrective actions (CA), and, if necessary, confirming implementation. A critical aspect of any QC activity is that it should not be viewed as a special study, but rather, *as a fully-integrated, routine component of the monitoring program*. This vision should be shared by staff, coordinators, and all levels of management associated with the programmatic area. The procedure below is based on that used by the US Environmental Protection Agency's National Aquatic Resources Surveys (NARS), specifically, the Wadeable Streams Assessment (WSA [USEPA 2004, Stribling et al. 2008]), the National Rivers and Streams Assessment (NRSA [USEPA 2008]), and the National Lakes Assessment (NLA [USEPA 2012]).

This procedure addresses one data quality issue critical to biological assessments, and thus, should be recognized and used as part of a more comprehensive QC program. Coverage of those factors is beyond the immediate scope of this technique.

Staff resource requirements: A) QC officer or coordinator, B) primary taxonomist (T1), and C) QC taxonomist (T2). If individual laboratories divide samples by different taxonomic groups among specialists for identifications (e.g., for mollusks, oligochaetes, leeches, chironomids, EPT [mayflies, stoneflies, caddisflies], and general arthropods), multiple individual taxonomist**s** can represent either or both T1 and T2. It is advisable to have both T1 and T2 possess confirmation of their taxonomic ability such as that provided by the SFS Taxonomic Certification Program (SFS/TCP) or an acceptable alternative.

Assumptions:

A) Standard operating procedures (SOPs) for taxonomic identifications are provided to all individuals involved in the program, including the nomenclatural standard to be used, such as the Integrated Taxonomic Information System (ITIS; http://www.itis.gov/), or other

sources focused on relevant taxa;

B) Target hierarchical levels are specified by project or programmatic documentation, such as SOPs, the laboratory operations manuals of the NARS (USEPA 2004, 2008, 2012), the standard taxonomic effort (STE) of SAFIT (2015), or other;

C) All macroinvertebrates in samples are identified as near to targeted levels as is possible by both T1 and T2. Note that it is acceptable to identify macroinvertebrates to finer levels (e.g., species) than the target for a particular group, but the QC evaluation and analysis will be focused on the documented target level, most commonly, genus; and,

D) As this procedure represents a blind comparison, samples transferred to T2 for re-identification will not have any labels containing identification results; they must be removed by T1 prior to transferring, and (if desired) replaced with a neutral code label.

SUGGESTED PROCEDURE

1. Following completion of primary identifications for all samples by T1, the QC coordinator will randomly select 10% of the samples for use in QC evaluation. The primary lab will ensure that all samples are complete, including individual vials and slide-mounted fractions, remove labels showing the primary results (names and counts), and ship or otherwise deliver the samples to the QC laboratory or taxonomist (T2). A chain-of-custody form will be completed and sent with the samples.

2. T1 delivers identification and count results for the selected samples to the QC coordinator, in an agreed-upon format, and as soon as possible following receipt of the QC sample list.

3. The QC taxonomist (T2) will perform whole-sample re-identifications and record identification and count results on a standard bench sheet or electronic data entry form. Care should be taken to ensure inclusion of all slide-mounted specimens or those that may have been segregated into separate vials. Each bench sheet or file should be labeled with the term "QC Re-ID."

4. T2 delivers identification and count results to the QC coordinator in an agreed-upon format and schedule.

5. The QC coordinator directly compares results generated by T1 and T2 for each sample, noting three values by taxon, as follows:

- Number of matches, that is, the number of specimens counted for where T1 and T2 are in agreement.

- Number and types of errors, where the coordinator performs 'error typing', recording whether differences in counts are i) straight disagreements, ii) hierarchical differences, or iii) missing specimens. Error typing is the most imprecise portion of the comparison, but is extremely useful in helping clarify necessary corrective actions (CA).

- Number of identifications meeting target level, where the number of specimens identified to target level for each of T1 and T2 is recorded.

6. Direct entry of these numbers into a spreadsheet substantially facilitates subsequent calculation, thus, use of a spreadsheet.

7. The QC coordinator calculates the following three precision estimates as data quality indicators:

A. *Percent difference in enumeration* (PDE) quantifies the consistency of specimen counts in samples, and is determined by calculating a comparison of results from two independent laboratories or taxonomists using the formula:

$$PDE = \frac{|n_1 - n_2|}{n_1 + n_2} x100$$

where n_1 is the number of organisms in a sample counted by T1, and n_2, by T2. Note that these numbers are from the counts of the taxonomists from their identification results, not from the sorting and subsampling procedures.

B. *Percent taxonomic disagreement* (PTD) quantifies the sample-based precision of taxonomic identifications by comparing target level taxonomic results from two independent taxonomists, using the formula:

$$PTD = \left(1 - \left[\frac{a}{N}\right]\right) \times 100$$

where a is the number of matches (agreements), and N is the total number of organisms in the larger of the two counts.

C. *Percent taxonomic completeness* (PTC) is the percentage of individuals in a sample that are identified to the specified target level, calculated using the formula:

$$PTC = {}^{x}\!/_{N}\, x100$$

where x is the number of specimens identified to target level, and N is the total number of specimens identified in the sample.

It is also useful to calculate the absolute difference in PTC between T1 and T2 (PTC_{abs}).

8. Unless specified otherwise by project goals and objectives, the measurement quality objectives (MQO) are:

- PDE ≤ 5
- PTD ≤ 15

- PTC $\geq$ 95
- $PTC_{abs} \leq 5$

Individual sample results exceeding these values are not automatically taken as an indication of invalid or unacceptable data points, rather, they are targeted for closer scrutiny to determine possible reasons for the exceedance and might indicate a need for corrective actions. The QC coordinator will send comparison results to both T1 and T2.

9. Hold a taxonomic reconciliation conference call. At a minimum, call participants are the QC coordinator and both taxonomists (T1 and T2). Review taxa lists, counts, and performance measures. Determine most likely reasons for differences in both counts and nomenclature. Make changes in reported data *only if suggested by or with agreement from the taxonomist(s) (T1 and/or T2).*

10. Corrective actions (CA) will include determining problem areas and consistent disagreements, and addressing problems through taxonomist interactions. The QC coordinator will review all notes and results from the call and develop a list of CA for T1 to do on the entire sample lot, not just the QC samples. By request of the project owner or manager, the QC coordinator will forward the notes and CA list for review. Examples of potential CA include: 1) re-identification of certain taxa; 2) identify and count mollusk shells only when soft tissue is present (CA would be re-examination of specimens); 3) ensure samples sent to QC laboratory are complete, specifically including all slide-mounted material; and 4) proofread all data entries carefully.

11. The QC coordinator will update the comparison spreadsheet so that it reflects post-call performance measures. Those differences for which direct discussion between T1 and T2 do not result in resolution will be carried forward as part of the error rate summaries.

12. A report or technical memorandum will be prepared by the Project Leader or QC Coordinator (or designee). This document will quantify these aspects of taxonomic precision, present them as error rates, assess data acceptability (and thus, suitability for analysis), highlight taxonomic problem areas, and provide recommendations for improving precision (consistency, repeatability). This report is submitted to the project owner or manager, with copies sent to the primary and QC taxonomists and another copy maintained in the project file. Suggested report sections are:

1) Project summary/overview (*very brief*)
2) Test conditions and narrative summary
3) Hierarchical target levels
4) Summary statistics (by sample lot)
5) Summary statistics (by individual samples)
6) Taxon by taxon comparisons (within samples)
7) Corrective actions
8) Notes/comments

Literature cited

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