Washington State Department of Ecology

Environmental Assessment Program

Standard Operating Procedure for Taxonomic Standardization of Benthic Invertebrate Data

Version 1.0

Author – Dany Burgess
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Reviewer – Carol Maloy
Date -

QA Approval - William R. Kammin, Ecology Quality Assurance Officer
Date –

EAP128

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Although Ecology follows the SOP in most instances, there may be instances in which the Ecology uses an alternative methodology, procedure, or process.

SOP Revision History

Revision Date	Revision History	Summary of changes	Sections	Reviser(s)
1/17/2018	1.0	Final edits	All	W.Kammin

1.0 Purpose and Scope

1.1 This document is the Environmental Assessment Program (EAP) Standard Operating Procedure (SOP) for Taxonomic Standardization of Benthic Invertebrate Data generated by Ecology's Marine Sediment Monitoring Program.

1.2 Taxonomic identifications of benthic invertebrates have changed over the course of Marine Sediment Monitoring's long-term programs, due to the use of different taxonomists in the early years than later, increase in skill over time among the consistently-used taxonomists, and ever-changing taxonomy. Name-changes have been kept up with and applied to all relevant identifications in the database. While combinations of two species into a single species are easily accomplished, division of one species into two cannot be applied to past data. In addition, immature life-stage or physical damage of a specimen can make identification to species difficult, if not impossible, and so animals of a single species are, in some cases, identified at multiple taxonomic levels. This can cause an over-inflation of species richness values when data analysis is performed.

In order to analyze the data, it is necessary first to standardize the taxonomy, with the goal of eliminating any redundancies in the dataset while preserving as much detailed information as possible. To this end, Ecology's Marine Sediment Monitoring Team developed and adopted the following standardization protocol.

2.0 Applicability

2.1 Taxonomic standardization will be performed whenever benthic invertebrate data will be compared across multiple stations, years, or projects.

3.0 Definitions

3.1 Taxonomy - the science of naming, describing and classifying organisms

3.2 Benthic invertebrate – organisms that lack a backbone and live in or on the bottom of freshwater or marine water bodies

3.3 Taxon (plural: taxa) – level of identification for an organism. Traditional Linnean taxonomic hierarchy for animals includes (from highest to lowest level) kingdom, phylum, class, order, family, genus, and species. Some taxonomic identifications use intermediate levels, such as subfamily

3.4 Redundant taxa - multiple levels of identification for the same organism

3.5 Taxonomic standardization – the process of ensuring consistency of taxon names in taxonomic datasets, so that they may be compared across multiple locations or years.

3.6 Species Richness – number of species, or taxa, within a biological community

3.7 Abundance – number of individuals

3.8 Univariate Analysis – the simplest form of statistical analysis, where only one variable is examined at a time

3.9 Multivariate Analysis - involves observation and analysis of more than one statistical outcome variable at a time

4.0 Personnel Qualifications/Responsibilities

4.1 Training and experience with taxonomy.

4.2 Training and experience with software programs e.g., Microsoft Excel.

4.3 Typical Job Class performing SOP: Natural Resource Scientist 1/2/3, Environmental Specialist 3/4.

5.0 Equipment, Reagents, and Supplies

5.1 Not applicable

6.0 Summary of Procedure

6.1 Decisions about whether to "roll up" identifications and sum abundances of taxa to higher taxonomic levels should be made using the following sets of rules.

6.2 In phyla (highest taxonomic groups) in which organisms are ordinarily identified to species or genus, organisms which are identified only to high taxonomic levels (e.g., order or class) should be excluded, except for phylum-level analyses. Because many organisms in less-well-known phyla (e.g., Nemertea) were not identified beyond phylum in the early years of the Program, it may be necessary to "roll up" all identifications to phylum for data analyses.

6.3 Colonial organisms and hard-substrate organisms such as barnacles are excluded from the dataset for analysis.

6.4 Rules for Univariate Measures

Calculate all univariate measures with and without redundant taxa.

1. Regardless of whether there are redundant taxa:

a. Count everything.
b. Calculate all univariate measures: total abundance, taxa richness, Pielou's evenness (which depends on Shannon-Wiener diversity), Swartz dominance.

2. When there are redundant taxa:
   a. Drop the higher level(s) and include only the lowest level.
   b. Calculate all univariate measures: total abundance, taxa richness, Pielou's evenness (which depends on Shannon-Wiener diversity), Swartz dominance.

6.5 **Rules for Redundant Taxa for Multivariate Analyses**

For each taxon, start at Rule 0 and follow the steps to resolution.

0. A. Taxon is to be excluded (reasons include: incidental, not picked in early years, etc.).....Delete the taxon
   B. Taxon is at lowest identified level and there are no redundant higher taxa.....Keep the taxon
   C. Taxon is redundant (one or more lower levels present)….....……1

1. A. Taxon level contains only one lower-level identification.....……..Roll up to higher level
   B. Taxon level contains >1 lower-level identification*…….....…….....2

2. A. Identifications have been taken to the same level consistently over multiple years.....3
   B. Identifications have NOT been taken to the same level consistently over multiple years (data look confused).....Roll all to higher level

3. A. Abundance at higher level is ≤20% (within a single year) of the total abundance within that taxon and lower (family/genus/species, etc.).....Delete higher level
   B. Abundance at higher level is >20% (within a single year) of the total abundance within that taxon and lower (family/genus/species, etc.).....4

4. A. Lower-level taxa that are easy to identify.....…….....……...5
   B. Mixed levels of difficulty……Leave easy-to-identify levels separate and roll up levels that are difficult to identify into the higher taxon level (Ex: species within the genera *Macoma*, *Chaetozone*)
   C. Lower-level taxa are difficult to identify..……..Roll to higher level

5. A. Higher-level taxon contains ≥2 lower-level identifications and <50% (within a single year) of the total abundance within that taxon and lower….....Delete the higher level

B. Higher-level taxon contains only 2 lower-level identifications and ≥50% (within a single year) of the total abundance within that taxon and lower.....……....Roll to higher level

C. Higher-level taxon contains >2 lower-level identifications and ≥50% (within a single year) of the total abundance within that taxon and lower (Ex: Euclymeninae, *Praxillella* sp, *Praxillella gracilis*)…….Leave the higher level AND lower levels

*Rules should be applied from highest to lowest taxonomic levels (Ex: delete family level before genus level).

7.0 Records Management

7.1 Results of taxonomic standardization will be maintained in documents (e.g., Excel files) as metadata specific to the analyses for which the standardization was performed.

8.0 Quality Control and Quality Assurance Section

8.1 Taxonomic standardization is, in itself, a QA/QC measure. However, it is recommended that the application of the rules, or at least, a subset thereof, be reviewed by a second party (other than the person performing the initial standardization) before the data is deemed ready for analysis.

9.0 Safety

9.1 Not applicable

10.0 References

10.1 Clarke K.R., R.N. Gorley, P.J. Somerfield, and R.M. Warwick. 2014. Change in marine communities: an approach to statistical analysis and interpretation, 3rd edition. PRIMER-E, Plymouth, UK.

10.2 Phillips, G.R., A. Anwar, L. Brooks, L.J. Martina, A.C. Miles, and A. Prior. 2014. Infaunal quality index: Water Framework Directive classification scheme for marine benthic invertebrates. Report SC080016. Environment Agency, Bristol, UK.