



Bioassessment Data Call

The Colorado Department of Public Health and Environment, Water Quality Control Division (division) is requesting benthic macroinvertebrate, sediment, and benthic chlorophyll a (bioassessment) data for the 2022 Water Quality Control Commission's (commission) Regulation #93, 303(d) List of Impaired Waters. The bioassessment data received will be used for assessment purposes to make a preliminary determination of attainment or impairment of the aquatic life use for streams and rivers to present to the commission for approval.

Benthic Macroinvertebrate Data

When determining the biological condition of a stream or river, the division calculates a Multi-Metric Index (MMI) score using the benthic macroinvertebrates data collected at a station. For the division to calculate the MMI score, data needs to be collected using approved collection methodologies. The MMI bioassessment tool was developed using a semi-quantitative method, referred to as the Kick-net Method. This involves collecting the benthic macroinvertebrates with a modified kick-net device (see details in Policy Statement 10-1).

In 2014, and again in 2018, a study was conducted to compare the Hess Method to the Kick-net Method for the purpose of determining if data collected using the Hess Method could produce a similar MMI score as the Kick-net Method. The study indicated that data collected using the Hess Method could produce similar MMI scores, if certain rules/modifications were followed. The division included the set of rules that were developed for data collection using the Hess Method in the 2020 Listing Methodology under Appendix D. If the rules/modifications are followed, the division will use the data to determine the attainment status of the aquatic life use.

Kick-Net Method

Interested parties can submit benthic macroinvertebrate data in two ways.

First, parties can submit the raw data, with the Ecological Data Application System (EDAS) input sheets to the division. The division will calculate the MMI scores on behalf of the party and return the results directly to the party. The division prefers this process.

What to submit to the division:

- 2020 Master Bug Import File
- 2020 Stations Predictors Import File
- 2020 New Taxa File

To populate the import and new taxa files, follow the instructions located on the *Instructions* tab.



The second way is for parties to request a copy of EDAS and calculate the MMI scores themselves. The division will provide EDAS and supporting files via Google Share. If parties decide to calculate their own MMI scores, those parties will be required to submit all the associated input sheets as well as the resultant sub-sample counts so the division can recalculate and verify the MMI scores.

What to submit to the division:

- An Excel spreadsheet with MMI scores and auxiliary metrics (HBI and SDI) by site and date
- 2020 Master Bug Import File
- 2020 Stations Predictors Import File
- An Excel spreadsheet with results of the sub-sampling to a fixed 300-count
 - If working with a consultant, have the consultant open the query in EDAS called "*Chris's Special Query to Find Benthic Data*". Copy the contents of the query table into an Excel spreadsheet.

All the above information is required if the division will use the benthic macroinvertebrate data for listing purposes.

Hess Method

Parties with data collected using the Hess Method can submit data, but parties that submit data in this fashion need to calculate the MMI scores and submit them to the division. If a party were to submit Hess Method data, it is important for the parties to submit the sub-sample used for the MMI calculation, along with the raw data. If the rules/modifications were followed, this is the only way the division can confirm the MMI scores. It is important to note, that the qualifications for the data (see Rule/Modification #1 below) are met. To submit data using this option, parties need to request a version of EDAS and associated import sheets; and, most importantly, follow the rules/modifications.

What to submit to the division:

- An Excel spreadsheet with MMI scores and auxiliary metrics (HBI and SDI) by site and date
- 2020 Master Bug Import File
- 2020 Stations Predictors Import File
- An Excel spreadsheet with results of the sub-sampling to a fixed 300-count
 - If working with a consultant, have the consultant open the query in EDAS called "*Chris's Special Query to Find Benthic Data*". Copy the contents of the query table into an Excel spreadsheet.
- A description of the rules/modifications used to calculate the MMI (Under #4, Rules and allowable modifications, below)

Sediment and Benthic Chlorophyll a

If a party is planning on submitting sediment only data, sediment plus benthic macroinvertebrate data (per Narrative Sediment Standard Policy 98-1), or benthic chlorophyll



a data to the division, please contact Scott Garncarz or Chris Theel (see contact information below) for further instructions.

Data Submittal

All biological data submitted to the division will be used for Regulation #93, list of impaired waters; Standards Triennial Review Basin hearings; and Regulation #85, Nutrients Management Control.

All the forms that are required for submitting benthic macroinvertebrate data are located on the division's website: <https://www.colorado.gov/pacific/cdphe/rivers-lakes-and-streams-data>.

The division receives data submissions directly from the Colorado Data Sharing Network (CDSN), for willing data providers. If you utilize CDSN and would like your data used by the division in this process, please begin working with CDSN no later than February 5, 2020. This will help to ensure that the division has received all of the data. To learn more about how CDSN supports the division's data call, go to <http://www.coloradowaterdata.org>.

When submitting bioassessment data to the division, please email the following addresses: cdphe_wqcd_surfacewaterdata@state.co.us, scott.garncarz@state.co.us and christopher.theel@state.co.us. For more information or if you have any questions, please email or call Scott Garncarz at (303) 692-2374 or Chris Theel at (303) 692-3558. Information submitted to the division through this process will be available for public review after July 1.



Hess Method Rules/Modifications for MMI Calculations:

1. Qualifications

- a. The rules and modifications shall only apply to data from at least three (3) Hess samples. These samples need to be processed separately (without subsampling), then data from all samples must be composited.
- b. The rules and modifications shall only apply to samples collected in Biotypes 1 and 2.
- c. The rules and modifications shall only apply to original samples greater than 360 individuals.
- d. The rules and modifications shall only apply to samples where benthic macroinvertebrate identification is conducted to the Operational Taxonomic Unit (OTU) level recommended by the division.
- e. The sum of individuals reached through the process of adding large and rare (L+R) taxa shall not exceed 360. Doing so will activate another subsample, which would negate the rarification process.
- f. The rules and modifications listed below shall be followed to exact specifications in order to correctly duplicate (or mimic) the process of adding L+R taxa to the laboratory picked sub-sample. Deviations from these rules will invalidate the resultant MMIs.

2. Initial Data Preparation

- a. Upload a list of taxa and counts, as reported by the taxonomist, into COEDAS using the division's Bug Import Sheet, which is a specifically formatted spreadsheet.
- b. Run sub-sample program to generate a 300-fixed count. The data is now considered rarified.

3. Rarified Data Preparation

- a. Locate the sub-sample data results in EDAS "*Benthics*" table. These original results are identified as "*Individuals*" while the sub-sampled results are identified as "*Ind_300*".
- b. Re-enter the 300-fixed count data, as selected by the sub-sample program, into a new bug import sheet ("*Final Import Sheet*").
- c. Follow the rules, allowable modifications, and guidelines in Section 4.



4. Rules and Allowable Modifications

- a. If an L+R taxon is replaced in the Final Import Sheet it shall be represented by 1 individual.
- b. If a taxon constitutes more than 0.33% of the original sample, and has been excluded, it shall be included and represented by 1 individual.

Example: An original sample has 400 organisms, including 4 individuals from Species A (1% of original sample). However, all Species A were excluded during the sub-sampling process. One (1) individual representing Species A shall be included in the Final Import Sheet.

- c. Additional taxa may be added as L+R in the Final Import Sheet but they must have occurred in the original sample and had been omitted by the sub-sample program. These taxa must be larger than 1 cm during late stages of development and must be distinguishable from other similar taxa without the assistance of magnification.

Other more specific guidelines are as follows:

- i. Representatives from most aquatic macroinvertebrate Orders and Families can be considered L+R if they exceed 1 cm in length and there are no other representatives from that Order or Family already included in the sample.

Example: One (1) individual from the Genus *Cheumatopsyche* shall be included as L+R only if the Family Hydropsychidae is not already represented in the sample.

- ii. Members of the Family Chironomidae are not generally considered L+R. Only when there are no members of this Family in the Final Import Sheet and the sum of excluded members meets the requirements of step 4.b. should they be included.

- iii. Aquatic mites shall be treated with the same guidelines that apply to Family Chironomidae.

- iv. Aquatic worms and snails shall be included as L+R taxa, providing they meet the above requirements.

- v. Taxa that are large enough to be considered L+R, despite the presence of other members within the same family, include

Genus: *Drunella*, *Epeorus*, *Rhithrogena*, *Acroneuria*, *Claassenia*, *Hesperoperla*, *Diura*, *Skwala*, *Pteronarcys*, and *Arctopsyche*.

- vi. Any taxon added as L+R must be recognizable as a unique taxon without the assistance of magnification.



5. Post-Processing Steps

- a. Upload the Final Import Sheet back into CO-EDAS.
- b. Verify the 300 organism sub-sample. This is required because the "*Ind_300*" is the final individual count that operates the MMI. Please see qualification 1.e. above.
- c. Calculate MMI(s).

