Atlantic Benthic Metrics Normal Ranges (2002-2021)

Metric reference values for use in Canadian Aquatic Biomonitoring Network (CABIN) assessments

Canada

Authors and contributors

Édith Lacroix, *Biomonitoring Specialist*, Freshwater Quality Monitoring and Surveillance, Environment and Climate Change Canada

Noelle Racine, *CABIN Student*, Freshwater Quality Monitoring and Surveillance, Environment and Climate Change Canada

Liang Zhu, *CABIN Atlantic Regional Contact*, Freshwater Quality Monitoring and Surveillance, Environment and Climate Change Canada.

Emma Garden, *CABIN Training Coordinator*, Freshwater Quality Monitoring and Surveillance, Environment and Climate Change Canada.
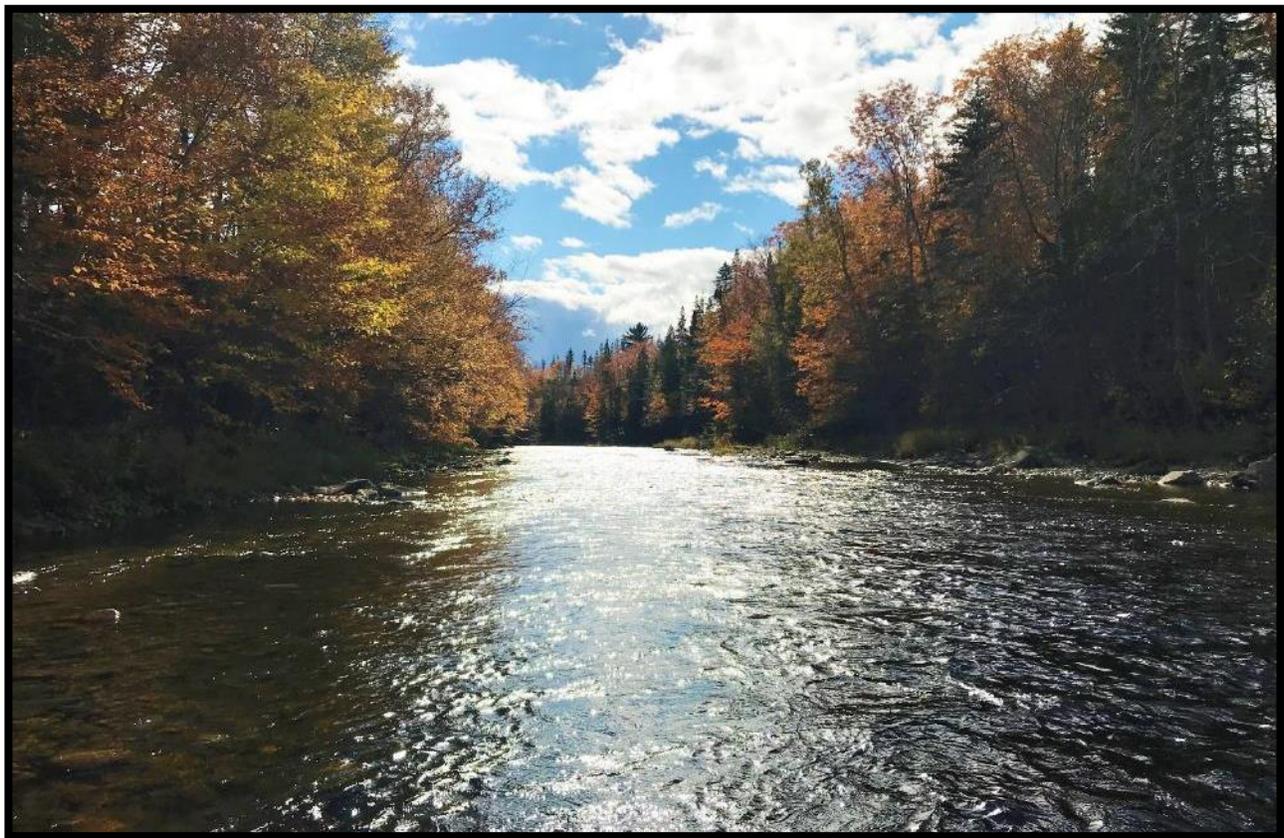
Middle River, Nova Scotia

Photo Credit: ECCC, 2021

Executive summary

Within the Atlantic Region, there is a need for more tools to help with the interpretation of benthic data collected by the Canadian Aquatic Biomonitoring Network (CABIN). This is why we, the ECCC CABIN team in Atlantic, calculated the Atlantic benthic normal ranges reference values. These normal ranges can be used 1) in combination with a Reference Condition Approach model to better explain the divergence observed in the benthic community, or 2) on their own to investigate the condition of the benthic macroinvertebrate community at a site and see how it compares to metrics from the broader Atlantic region.

The normal ranges were calculated using benthic data from all 26 CABIN studies within the Atlantic Provinces that have reference and potential reference sites, for the period 2002 to 2021. This document is shared with all the CABIN users in the Atlantic region.

Table of contents

Introduction

What is CABIN?

The [Canadian Aquatic Biomonitoring Network](#) (CABIN) is a national aquatic biological monitoring program led by [Environment and Climate Change Canada](#) (ECCC), which assesses the biological condition of freshwater habitats across Canada. Monitoring biological communities such as fish, invertebrates, and algae can provide an indicator of ecosystem health. Biological indicators of aquatic ecosystem health can complement indicators of water quality because aquatic life can be affected by factors not incorporated into the water quality indicator such as:

- the effects of chemicals interacting with each other,
- contaminant releases are not detected at the time of sample collection,
- unknown contaminants in the water,
- introduction of exotic species,
- habitat degradation in the water or surrounding land,
- climate change,
- and changes in water levels, flows, and timing (ice formation and spring thaw).

CABIN collects benthic macroinvertebrates in streams, rivers, lakes and wetlands using standardized data collection methods. Benthic macroinvertebrates are aquatic, bottom-dwelling animals without backbones that are generally visible to the naked eye. They include worms, crustaceans, molluscs and the larval stages of many insects. Macroinvertebrate communities have many advantages as biological indicators:

- They reflect conditions at specific locations and also show cumulative impacts.
- They are sensitive to a variety of disturbances.
- They are present in all fresh water ecosystems.
- They are a key part of aquatic food webs.
- Their assessment methods are well-developed.

How CABIN works?

GOALS
WHAT DO YOU WANT TO MONITOR?

CHOOSE REFERENCE SITES
LOOK AT BUGS IN UNIMPACTED / PRISTINE SITES

BUILD REFERENCE MODEL
RELATIONSHIP BETWEEN HABITATS ⟷ INVERTS

CHOOSE TEST SITES
IDENTIFY INVERTS AND HABITAT

COMPARE
HOW DIFFERENT ARE TEST SITES FROM REFERENCE SITES OF SIMILAR HABITAT?

CABIN provides standardized protocols, a national Web accessible database, online analysis and reporting tools, and a training and certification program. CABIN data collection is growing across the country with extensive data in some areas and data gaps in others. Data gathered by CABIN participants (government and non-government organizations, indigenous organisations, and academia) are entered into the national database. They are shared among the network to achieve consistent and comparable collection and reporting on freshwater aquatic ecosystem conditions in Canada. CABIN data are publicly available on the [Open Data Portal](#) from the Government of Canada.
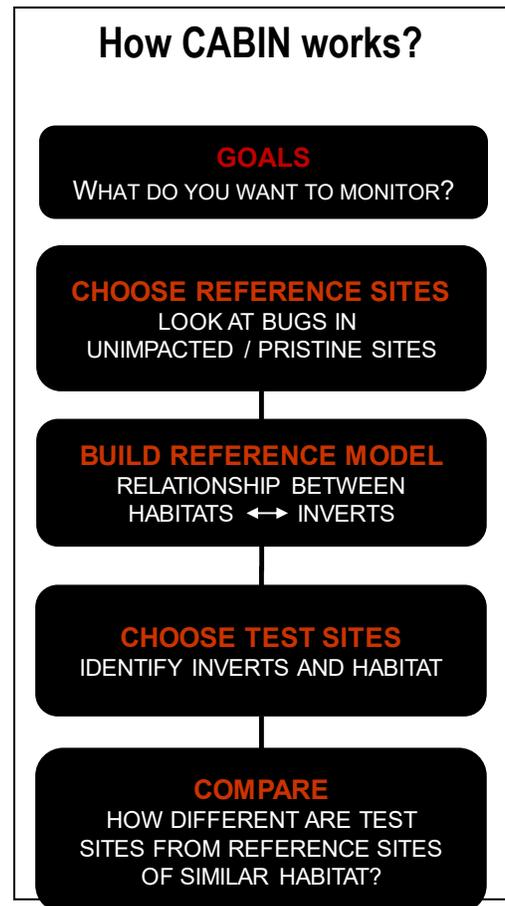
To analyse data and assess sites, the CABIN program uses the well-established Reference Condition Approach (RCA) for consistent interpretation and assessment of aquatic ecosystem condition (Reynoldson *et al*. 1999). Two types of sites are identified using RCA; reference sites and test sites. Reference sites represent best available conditions or minimally disturbed by human impact within a region, and are used to establish a baseline of expected variability within benthic macroinvertebrate communities. In CABIN, the data from these sites are used to develop predictive bioassessment models to determine if a test site (a site exposed to environmental stressors) is similar or divergent from reference. Metrics calculated at test sites can also be compared against metrics calculated at reference sites to assess ecosystem conditions in regions where no RCA model is available.

In Atlantic Canada, the preliminary RCA model included the rich taxonomic dataset from New Brunswick, as well as other reference sites collected throughout Atlantic Canada (New Brunswick, Nova Scotia and the island portion of Newfoundland and Labrador) up to 2010 using the standard CABIN protocol (Armanini *et al*. 2013).

Giant stonefly instars collected in Annapolis River, Nova Scotia
Photo Credit: ECCC, 2021

Objectives of the Atlantic benthic metrics normal ranges

The Atlantic benthic metrics normal ranges can be used as follows:

- Benthic metrics can help describe invertebrate communities based on the number of taxa (richness), the type of taxa (pollution tolerant or sensitive), and whether certain taxa are dominant.

- Once results are obtained from the RCA model, the normal range for the benthic metrics can help to better explain the divergence observed in the benthic community. As an example, the RCA model might indicate reduced diversity but the metrics would give you more information on the shift in the benthic community composition from reference sites.

- The normal range metrics provide a quicker and simpler tool for comparing test sites to reference sites. However, they may not be as sensitive as RCA models for detecting changes in community structure.

Note that these normal ranges are calculated using data for CABIN sites in Atlantic Canada, and therefore are not/may not be suitable for use at sites from other regions.

Methodology

Data collection

For the normal ranges calculations, we extracted data from all studies within the Atlantic Provinces that have **reference** and **potential reference** sites (i.e. unaffected by human activities), for the period **2002 to 2021**. We used data from **430 sampling sites**, distributed among **26 CABIN studies** (see Table 1 and Map 1 below).

TABLE 1: LIST OF THE 26 CABIN STUDIES INCLUDED IN THE ATLANTIC PROVINCES BENTHIC NORMAL RANGES CALCULATIONS

Atlantic CABIN	NL-Terra Nova National Park CABIN
CABIN Research - Atlantic	NL-Torngat National Park Reserve
GRDI - Atlantic	NS-ACAP Cape Breton
NB-Fundy NP - Stream condition Monitoring Sites	NS-Annapolis River
NB-Havelock Watershed Study	NS-Bluenose ACAP
NB-MAES Mainsteam	NS-Cape Breton Highlands National Park
NB-Petitcodiac Little River	NS-Kejimkujik National Park
NB-St. Croix River Benthic Invertebrate Sampling	NS-Kejimkujik NP - Upper Mersey
NB-TWA Tabusintac Watershed Association	NS-Kejimkujik RCA
NB - Kouchibouguac NP	NS-NB-PEI- SGSL - Coalition
NL-ACAP Humber Arm	NS-UINR Project
NL-Gros Morne NP	PEI CABIN - Province
NL-Newfoundland Labrador Province - Water Resources Management Division	QC-NB-Biomonitoring Appalaches
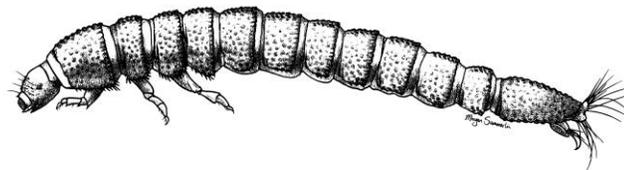
Coleoptera larvae
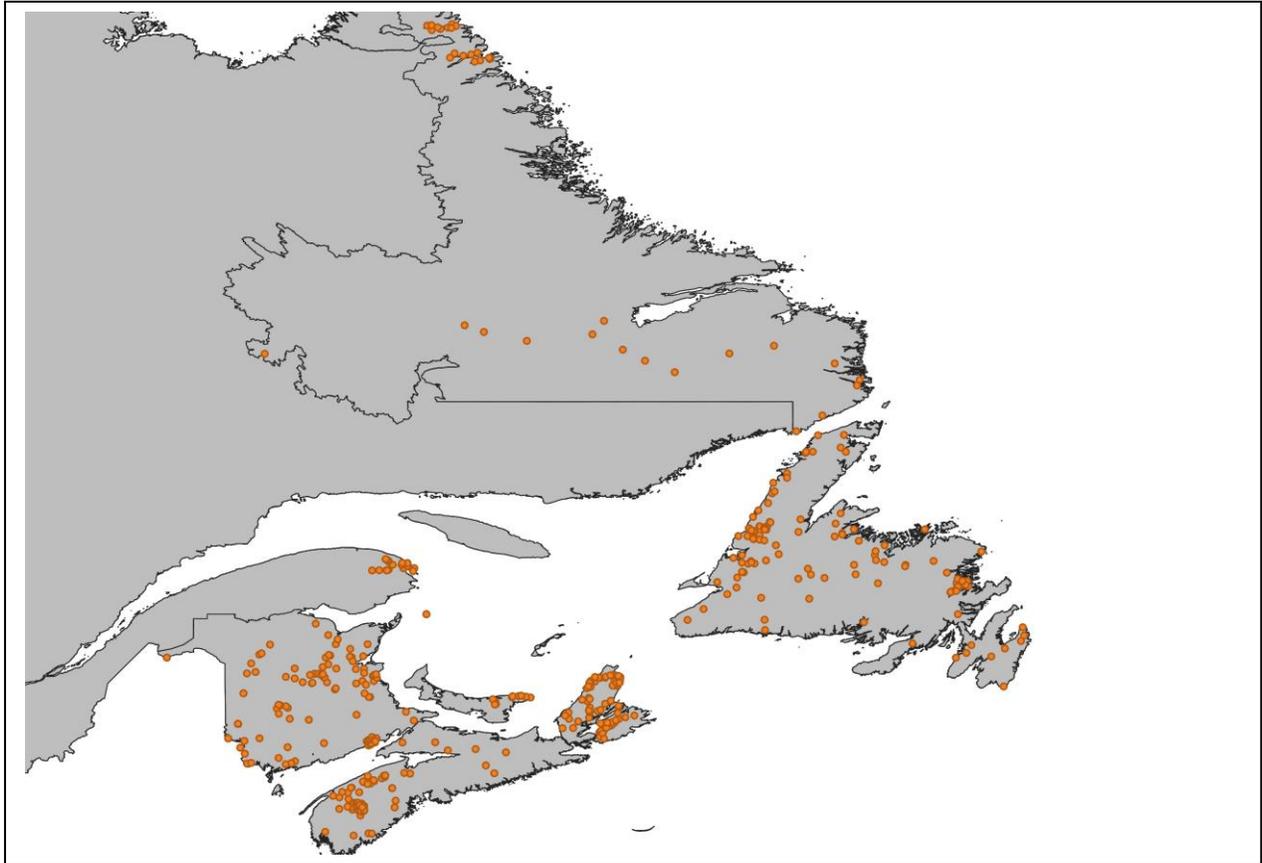Photo credit: Macroinvertebrates.org and NSF

FIGURE 1. MAP OF THE SITES USED FOR THE CALCULATIONS OF THE ATLANTIC NORMAL RANGES BENTHIC METRICS (2002-2021)

Summary of the CABIN protocol

At each of the CABIN sampling sites, the invertebrate samples were collected using the standardized Canadian Aquatic Biomonitoring Network wadeable streams protocol (ECCC, 2012). Invertebrates were collected with a kick net of **400 μm mesh size**, using a zigzag pattern, over a period of exactly three minutes.

The samples were transferred to a jar where a preservative agent was added. The samples were then sent to a certified taxonomist for identification. Identification of macroinvertebrates was made to the Standard Taxonomic Effort as recommended in the Appendix A of the CABIN laboratory methods : processing, taxonomy, and quality control of benthic macroinvertebrate samples (ECCC, 2021).

Some taxa were removed from the samples (such as Cladocera, Copepoda, Ostracoda, etc.) because of some difficulties in their numbering or because they are not considered benthic. See the CABIN Lab Manual for more details (ECCC, 2021).

Description of benthic metrics and calculations

Data extraction

For the Normal Ranges calculations presented here, we exported the taxonomic data from the CABIN database in a .csv file. This was needed, as we wanted to calculate benthic metrics on reference and potential reference sites.

Metric calculations using the CABIN Database

The CABIN database allows calculating several benthic. Those metrics can only be calculated on **test** sites. Note that you must have your Project Manager or Data Analyst training in order to use database tools.

You can find more details on how to calculate and interpret those metrics in the *Benthic Macroinvertebrate Metric Reference Guide*, available on the CABIN Website.

Data validation

Benthic data were cleaned using *OpenRefine* software. The following steps were taken:

1. All Unverified benthic data were added to the overall benthic list.
2. Tubificidae at sites FNT01 and KCC01 (study NB – Kouchibouguac NP) were changed to Naididae for 2019 due to updates to taxonomic classifications.
3. We removed Glaumnidae for sites BJ01 and BLA03 as these records were doubtful and have not been verified.
4. We removed all samples that were collected using a mesh size different from 400 micron mesh (250um, 300um, 363um, 500um).
5. We corrected the name "Site" Mar-01 to MAR01.
6. As recommended in the Lab manual, we excluded some taxa from the dataset:
   a. Removed Phylum Nemata
   b. Removed Class Ostracoda
   c. Removed Class Polycheata as they are a very rare taxa
   d. Removed Phylum Platyhelminthes
   e. Removed Class Maxillopoda
   f. Kept Enchytraeidae as they contribute to the %GOID metric
   g. Removed family Lumbricidae as they are not aquatic invertebrates
   h. Removed class Branchiopoda as they are not aquatic invertebrates
7. The clean data CSV file was then exported in *R* software to calculate the metrics.

Some sites have multiple years of data (more than one benthic sample). For this exercise, we created a unique identification code for each year, thus each visit at each site are included and are considered replicates.

Metric calculations

The 16 metrics (listed in the table below) were calculated using the *R* statistical software (version 4.1.0) within the R Studio interface (version 1.4.1103). The metric calculations used taxonomic data at the **Family level**, so we summed up data at the Genus and Species levels up to the Family level such that there was one abundance value for each Family per sample.

The metrics included in this analysis were chosen because they are the most commonly used in aquatic biomonitoring (Table 2). **Total abundance** measures the overall count of individual specimens within a sample. **Richness** measures the number of unique taxa represented in the sample at a given taxonomic level, in this case at the Family level. It is generally used as a measure for biodiversity. **Dominance** is calculated as the proportion of the top two most dominant taxa in the sample. **Diversity** and **evenness** measures such as **Simpson's Diversity, Shannon Wiener's Diversity, Simpson's Evenness** and **Pielou's evenness** were chosen because each calculation takes into consideration the number of taxa available in a sample and their relative abundances.

Community composition metrics take into consideration the proportion of specific taxa within the sample in order to make assumptions about water quality based on their abundances. Measurements of **EPT** families (Ephemeroptera, Plecoptera and Trichoptera) are frequently reported in literature. All of the calculated metrics are commonly used and can be searched in the literature except **%GOID**. This one is uncommon, but has been used in some Atlantic work as taxa in these taxa are known to be tolerant of pollution.

Normal ranges (percentiles) calculations

We calculated the value of each metric at several percentiles to use as comparison values (5, 10, 25, 50, 75, 90 and 95th).

What is a normal range?

Normal ranges are metric values that are within the 25th and 75th percentiles of the values obtained at reference sites.

As an example, at a site X, the observed taxa richness is 22, which corresponds to the 50th percentile. This is considered normal. For another site, the observed taxa richness is 15, which corresponds to the 10th percentile. This value is then viewed as divergent.

TABLE 2: LIST OF METRICS CALCULATED FOR THE NORMAL RANGES ANALYSIS

Metrics	Description
Total Abundance	The abundance of benthic macroinvertebrates in a stream changes according to many factors. Abundance will often decrease with toxic water conditions but may increase in nutrient enriched conditions. Abundance is calculated by summing the total number of individuals in a sample.
Total Richness (total number of taxa)	Stream biodiversity may decline as water quality deteriorates. When this occurs, there is usually an increase of tolerant taxa and a decrease in intolerant taxa. Total richness is calculated by summing the number of individual taxa (differentiated by family level) in a sample.
Dominance (% top 2 dominant taxa)	Dominance is calculated as the abundance of the two most dominant taxa. As diversity declines, a few taxa tend to dominate within the sample. As water quality declines, more tolerant taxa usually dominate.
Total EPT Taxa	Total number of Ephemeroptera, Plecoptera, Trichoptera taxa at the Family level. Calculated as the sum of all EPT taxa within a sample. These taxa are typically considered to be intolerant to unfavorable conditions. The EPT population typically declines as water quality decreases.
Percent (%) EPT	The percentage of the sample that are EPT taxa. It is calculated as the total number of EPT individuals divided by the total number of individuals in the sample. Percent EPT typically decreases along with water quality.
Total Chironomidae Taxa	Total number of Chironomidae taxa identified to the Family level. Calculated as the sum of all Chironomidae taxa within a sample. These taxa are typically considered to be tolerant to unfavorable conditions. The chironomid population typically increases as water quality decreases.
Percent (%) Chironomidae	The percentage of the sample that are Chironomidae. It is calculated as the total number of Chironomids divided by the total number of individuals in the sample. Percent Chironomidae typically increases as water quality decreases.
Total GOID Count (Gastropods, Oligochaeta, Isopods, Diptera)	Gastropods, Oligochaetes, Isopods and Diptera are all pollution tolerant species. As diversity declines, these may tend to dominate the community. Total GOID is calculated by summing the total number of individuals within these groups, at the family level.
Percent (%) GOID	Percent GOID is calculated as the proportion of GOID individuals within the entire sample.
EPT / Chironomidae + EPT	EPT tend to decline in the presence of most anthropogenic influences to stream conditions. In contrast, Chironomids tend to be pollution tolerant. The metrics calculates the proportion of EPT taxa within the overall population of EPT and Chironomids within a sample.
Simpson's Diversity (D)	Measures the relative abundance and distribution of taxa present in the sample. Simpson's Diversity gives results between 0 and 1, where 0 indicates no diversity and 1 indicates complete diversity in the sample
Shannon Wiener's Diversity (H)	Measures the relative abundance and distribution of taxa present in the sample. As these factors increase, so does Shannon Wiener's Diversity (H).
Simpson's Evenness (E)	Measures the relative distribution of species in a sample based on species richness and their relative abundance. Values range between 0 and 1, with 0 meaning there is no equitability in the distribution of individuals among taxa groups and 1 meaning complete equitability. The calculation utilizes Simpson's Diversity to calculate evenness

Metrics	Description
Pielou's Evenness (j)	Measures the relative distribution of species in a sample based on species richness and their relative abundance. Values range between 0 and 1, with 0 meaning there is no equitability in the distribution of individuals among taxa groups and 1 meaning complete equitability. The calculation utilizes Shannon Wiener's Diversity to determine evenness
Hilsenhoff Family Index (Mid-Atlantic) - HBI	This index takes into account tolerance values for each family, and the abundance of those families. Tolerance values are largely based on the response to organic pollution, with sensitive species having low scores and tolerant species having high scores. According to the HBI, a value of 0 indicates excellent water quality, while a value of 10 indicates very poor water quality.
Canadian Ecological Flow Index (CEFI)	This index is sensitive to change in hydrological conditions (e.g., timing, intensity of flows). The CEFI is calculated as follows: $$\text{CEFI} = \frac{\sum_{i=1}^{n} F_i * R_i * V_i * W_i}{\sum_{i=1}^{n} F_i * R_i * W_i}$$ where F_i is relative frequency class of ith taxon, R_i is relative abundance of ith taxon in the sample, V_i is optimum of the ith taxon (current velocity preference), W_i is indicator weight score of ith taxon (Armanini *et al.*, 2011).

Adapted from the CABIN Online Training Program.

Stoneflies (Plecoptera) larvae
Photo Credit: ECCC CABIN, 2019

Results and how to use them

We calculated metrics and percentiles using the benthic data for all reference and potential reference sites from 2002 to 2021, for all the 26 Atlantic studies mentioned above.

TABLE 3: BENTHIC NORMAL RANGES CALCULATED FOR THE ATLANTIC PROVINCES

Percentile	5th	10th	25th	50th	75th	90th	95th
			Normal Range				
Total Abundance	232.05	366.68	870.32	1962.50	4539.10	9316.50	14748.90
Richness	12.00	15.00	19.00	22.00	25.00	29.00	31.00
Dominance	33.54	36.17	41.98	51.24	62.71	75.00	82.34
Total EPT	140.00	230.29	528.89	1170.68	2607.48	4839.33	7497.00
Percent EPT	22.74	33.92	49.70	65.79	79.99	90.11	93.37
Total Chironomidae	10.00	20.00	88.38	327.75	1041.48	2737.75	4795.83
Percent Chironomidae	1.93	3.13	7.74	16.47	29.27	49.27	61.07
Total GOID	18.00	33.00	128.00	431.99	1283.35	3149.97	5357.50
Percent GOID	3.43	5.65	11.99	22.32	35.65	56.51	67.11
EPT/EPT+Chironomidae	0.29	0.42	0.65	0.80	0.91	0.97	0.98
Simpson's Diversity	0.53	0.62	0.75	0.83	0.87	0.89	0.90
Simpson's Evenness	0.13	0.15	0.19	0.26	0.32	0.38	0.43
Shannon Wiener's Diversity	1.21	1.48	1.88	2.17	2.38	2.55	2.63
Pielou's Evenness	0.46	0.54	0.63	0.70	0.76	0.79	0.81
CEFI	0.31	0.32	0.34	0.36	0.39	0.42	0.43
HBI	1.71	1.96	2.38	3.04	3.77	4.74	5.50

Benthic reference values, also called normal ranges, are used to compare the metrics values calculated for benthic communities. Usually, if a metric value is observed between the 25th and 75th percentiles, it is considered within the "normal range". Values below or above these percentiles is considered divergent to a certain extent (see Table 4 below for details on divergence categories).

The directionality of the divergence is also important, this depends on whether the metric is above or below the normal range. Interpretation of the directionality depends on the metric that is being considered. For example, a divergent Percent Chironomidae value that is above the normal range suggests possible impairment as they make up a larger part of the benthic community. However, a divergent Percent Chironomidae value that is below the normal range does not necessarily suggest an absence of impairment as the community could be dominated by another more tolerant taxa. It is important to note that for a sample there may be one or more divergent metrics. Each metric can tell you something different. Combined, they can help explain what is occurring in the benthic community.

TABLE 4: INTERPRETATION OF THE BENTHIC NORMAL RANGES

Site Assessment	Lower Range (percentile)	Upper Range (percentile)
Normal	> 25th	< 75th
Mildly divergent	> 10th and < 25th	> 75th and < 90th
Divergent	> 5th and < 10th	> 90th and < 95th
Highly divergent	< 5th	> 95th

Here is an example of how you can use normal ranges for the interpretation of your benthic data

A test site on the Miramichi River (New Brunswick) was determined to be divergent using a Reference Condition Approach (RCA) model. To further interpret the model results, metrics were calculated using the CABIN database.

Results revealed that several metrics were outside their normal ranges. Percent EPT fell within the 5-10th percentiles and was considered divergent while Percent GOID fell within the 90-95th percentiles and was also considered divergent. The directionality of these metrics indicate that the benthic community had lower contributions from EPT taxa and greater contributions from GOID taxa than reference sites did. Combined with an HBI score observed in the 90th-95th percentile, these metrics indicate possible poor water quality due to organic pollution. At the same time, the CEFI score fell within the normal range, indicating that the benthic community is not being affected by alterations in flow conditions. This analysis suggests that this test site is likely impaired to some degree, possibly due to impacts to water quality.

Sampling in the Miramichi River.
Photo Credit: ECCC CABIN

Conclusion

The Atlantic normal ranges presented in this report (2002-2021) provide an additional tool to interpret CABIN data in the region. Hopefully, along with the Atlantic Reference Model, you now have access to a series of tools to help you tell the story of benthic communities in your watershed.

Should you have any questions, please contact your CABIN Regional Contact or the National CABIN team.

References

Armanini D. G., N. Horrigan, W. A. Monk, D. L. Peters And D. J. Baird, 2011. Development of a benthic macroinvertebrate flow sensitivity index for Canadian rivers, River Res. Applic. 27: 723–737 (2011).

Armanini D.G., W. A. Monk, L. Carter, D. Cote and D. J. Baird, 2013. Towards generalised reference condition models for environmental assessment: a case study on rivers in Atlantic Canada. Environ Monit Assess (2013) 185: 6247–6259.

Environment and Climate Change Canada (ECCC), 2012. Canadian Aquatic Biomonitoring Network (CABIN) Field Manual, wadeable streams. 49 p. + appendices.

Environment and Climate Change Canada (ECCC), 2021. CABIN laboratory methods : processing, taxonomy, and quality control of benthic macroinvertebrate samples. 34 p.

Reynoldson, T.B., M. Bombardier, D.B. Donald, H. O'Neill, D.M. Rosenberg, H. Shear, T.M. Tuominen and H.H. Vaughan. 1999. Strategy for a Canadian aquatic biomonitoring network. Environment Canada, National Water Research Institute, Burlington/Saskatoon, NWRI Contribution No. 99-248.