Guidance for Understanding a Biomonitoring Wetland Macroinvertebrate Sampling Report

The ME DEP generates a Wetland Macroinvertebrate Sampling Report for each macroinvertebrate sampling event. The Wetland Macroinvertebrate Sampling Report contains many attributes about the biological sample. Any physical and chemical data collected in conjunction with the biological sampling can be found in the station's Wetland Station Report. This guidance document takes a representative Wetland Macroinvertebrate Sampling report and attempts to explain items from each section that may not be self-explanatory. See the Sampling and Analysis page of the Biomonitoring website for more details on our sampling methods (http://www.maine.gov/dep/blwq/docmonitoring/biomonitoring/sampling/index.htm). These reports can be found in the Biomonitoring Google Earth project by clicking on a station and then selecting the desired report from the 'Report' column. Access our Google Earth project through the Data and Maps page of our website (http://www.maine.gov/dep/blwq/docmonitoring/biomonitoring/data.htm).

Maine DEP Wetlands Sampling Report
Macroinvertebrate Attributes

Station:	W-001	Name:	MEADOW BROOK - W-001
Trip ID:	2005-001	Town:	NEW GLOUCESTER
Sample ID:	DN-2005-001		

Total Abundance:	63.333	Hilsenhoff Biotic Index:	7.434
Generic Richness:	16	Shannon-Weiner Diversity:	2.377

Dominant Taxa Abundance:	Rank	Taxon Name	Percent
	1	Caecidotea	42.63
	2	Amnicola	31.05
	3	Sphaeriidae	6.84
	4	Crangonyx	5.26
	5	Centroptilum	4.74

- **Trip ID** – Unique identifier assigned to each site visit (year sampled - station number).
- **Sample ID** – Unique identifier assigned to each biological sample. "DN" indicates that this macroinvertebrate sample was collected using the Dipnet measured sweep method.
- **Total Abundance** – This is actually the total mean abundance, which is the mean number of individuals in a sample, usually based on 3 replicates.
- **Generic Richness** – Richness is the total number of unique genera in a sample. In the example above, the total Generic Richness for the sample is 16.
- **Hilsenhoff Biotic Index** (Hilsenhoff 1987.) – The biotic index provides a measure of the general tolerance level of the sample community toward organic (nutrient) enrichment. The index ranges from 0 (no apparent organic pollution) to 10 (severe organic pollution).
- **Shannon-Wiener Diversity** (Shannon and Weaver 1963.) – Diversity is composed of a richness factor and an eveness factor. As both diversity and richness decline, the stability of most natural communities usually declines. Generally, the lower the number, the less stable the community is. Values can range from 0 to 4.6 but are usually between 1.5 and 3.5.

- **Dominant Taxa Abundance** – List of the top 5 most abundant taxa found in the sample and their percentage of the sample's total abundance.

	Abundance	Relative Abundance	Richness	Relative Richness
EOT Taxa:	3.667	0.058	3	0.188
EPT Taxa:	3.667	0.058	3	0.188
Insects:	5.667	0.089	7	0.438
Non-Insects:	57.667	0.911	9	0.563
Leeches:				
Oligochaetes:	0.667	0.011	2	
Snails:	21.667	0.342	3	
Bivalves:	4.333	0.068	1	
Isopods:	27.000	0.426	1	
Amphipods:	4.000	0.063	2	
Mites:				
Stoneflies:				
Mayflies:	3.667	0.058	3	0.188
Odonates:				
Caddisflies:				
Diptera:	1.000	0.016	3	0.188
Hemiptera:				
Beetles:	1.000	0.016	1	0.063
Chironomids:	0.667	0.011	2	0.125
Collector-Filterers:	4.667	0.074		
Collector-Gatherers:	4.000	0.063		
Predators:	0.333	0.005		
Piercers:				
Shredders:	27.000	0.426		
Scrapers:	20.000	0.316		

See the Benthic Macroinvertebrate page of the Biomonitoring website for a discussion of specific macroinvertebrates and their ecology (http://www.maine.gov/dep/blwq/docmonitoring/biomonitoring/sampling/bugs/index.htm). Please note that all calculations follow the counting rules as described in the Biomonitoring methods manual, "Methods for Biological Sampling and Analysis of Maine's Rivers and Streams" (DEP LW0387-B2002), which can be found here: http://www.maine.gov/dep/blwq/docmonitoring/biomonitoring/materials/finlmeth1.pdf.

- **Abundance** (mean abundance) - This is calculated independently for each unique taxon or group of taxa by adding the number of individuals from each replicate and dividing by the number of replicates. In the example above, three replicate samples were taken, two replicates held one mayfly each and the third replicate had 9 mayflies, so the mean abundance of mayflies in the whole sample would be listed as 3.667 [(1 + 1 + 9) / 3 = 3.667].
- **Relative Abundance** – This is calculated by dividing a group's (mean) abundance by the sample's total (mean) abundance. For example, a mayfly abundance of 3.667 divided by the total abundance of 63.333 makes the mayfly relative abundance 0.058
- **Richness** (generic richness) - This is calculated by totaling the number of unique taxa or group of taxa in a sample. In the example above, there were 11 mayflies collected comprised of 3 unique kinds of mayflies, therefore, the mayfly richness is 3.

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- **Relative Richness** - This is calculated by dividing a group's richness by the sample's generic richness. For example, a mayfly richness of 3 divided by the sample's total generic richness of 16 makes the mayfly relative richness 0.188.

Maine DEP Wetlands Sampling Report
Macroinvertebrate Taxa

Station:	W-001	Name:	MEADOW BROOK - W-001		Date Sampled:	6/15/2005
Sample ID:	DN-2005-001	Town:	NEW GLOUCESTER		Basin:	Presumpscot
Replicates:	3	Subsample Factor:	1			

Maine Taxonomic Code	Taxon	Average (Count)	Functional Feeding Group	Tribe	Taxa Group
08020202013	*Specaria*	0.33	--		Worm
08020203001	*Aulodrilus*	0.33	--		Tubificid Worm
09010101001	*Caecidotea*	27.00	SH		Isopod
09010202004	*Crangonyx*	3.33	--		Amphipod
09010203006011	*Hyalella azteca*	0.67	--		Amphipod
09020401003	*Centroptilum*	3.00	CG		Mayfly
09020401006	*Pseudocloeon*	0.33	SC		Mayfly
09020402007028	*Arthroplea bipunctata*	0.33	--		Mayfly
09021011015	*Procladius*	0.33	PR	T	Fly: Midge
09021011056	*Psectrocladius*	0.33	CG		Fly: Midge
09021014	Tabanidae	0.33	--		Fly: Horse And Deer
090211	Coleoptera	1.00	--		Beetle
10010104013	*Amnicola*	19.67	SC		Snail
10010201025	*Stagnicola*	1.00	--		Snail
10010203	Planorbidae	1.00	--		Snail
10020201	Sphaeriidae	4.33	CF		Mussel/clam

- **Subsample Factor** - The inverse of the fraction of the sample identified by the taxonomist. Only a portion of the sample is identified when the number of organisms exceeds established criteria. For example, a subsampling factor of 4 means that the taxonomist selected ¼ of the sample, using protocols established in the Biomonitoring Methods Manual, identified and counted the organisms in that subsample, and then multiplied the counts by 4. The example above has a subsampling factor of 1, indicating that the sample was not subsampled. The Methods Manual can be found here: http://www.maine.gov/dep/blwq/docmonitoring/biomonitoring/materials/finlmeth1.pdf.
- **Maine Taxonomic Code** – The Biomonitoring Unit use a hierarchical coding system to assign unique numeric identifiers to each taxa in our database.
- **Average (Count)**- This is calculated independently for each taxon by adding the number of individuals from each replicate and dividing by the number of replicates. In this example, there was one individual of *Specaria* in the three replicate samples, which makes the average count 0.33 [(1 + 0 + 0) / 3 = 0.33]. Note that for taxa that are only observed in the pupal stage, no average count is shown as pupae are excluded from model calculations.
- **Functional Feeding Group -** Aquatic invertebrates can be grouped into functional feeding groups according to how and what they eat:
  - Collector-filterers (CF) strain particles out of flowing water with brushes or nets.
  - Collector-gatherers (CG) are opportunistic omnivores that feed on whatever is easiest to find, using a variety of feeding methods.

- o Piercers (P) are organisms that obtain nourishment by piercing plant or animal tissue and sucking fluids.
  - o Predators (PR) are carnivores that hunt and eat other organisms.
  - o Scrapers (SC) remove algae, bacteria and fungus growing on the surface of rocks, twigs and leaf debris.
  - o Shredders (SH) chew on coarse leaves and twigs that have started to decay to obtain nourishment from associated fungi, bacteria and other organic material.
- **Tribe** – One or more genera that share certain characteristics are placed into tribes. In the MDEP taxa list, usually only members of the Chironomidae family have their tribes noted. In this example, the 'T' for *Procladius* indicates that it is in the Tanypodinae tribe. Other tribes are indicated by: 'O' for the Orthocladiinae Tribe, 'C' for the Chironominae-Chironomini Tribe, 'D' for the Diamesinae Tribe, 'P' for the Podonominae Tribe, 'R' for the Prodiamesinae Tribe, 'Y' for the Chironominae-Tanytarsini Tribe, 'S' for the Chironominae-Pseudochironomini Tribe, and 'H' for the Chironominae Tribe.