Vermont DEC Biomonitoring
Calculation of Macroinvertebrate Metrics

1. Density- Density refers to the relative abundance of macroinvertebrates in a sample.

Calculation: Number of macroinvertebrates in subsample / proportion of sample processed.

Example : 300 animals picked / 0.25 (or one quarter of sample picked) = 1200 animals/sample

2. Total Richness- Total richness is the number of unique taxa in a processed sample.

Calculation: A tally of the total number of unique taxa identified. Note that immature larva identified to family or genus are not considered a unique taxa if a genus or species identification has also been identified within that taxonomic group.

Example:

Taxon	# **organisms Rep 1**	# **organisms Rep 2**
Ephemerellidae Ephemerella sp	2	0
Ephemerellidae Ephemerella dorothea	3	4
Ephemerellidae Ephemerella invaria	0	2
Richness =	**1**	**2**
Mean Richness =	**1.5**	

3. EPT Richness - EPT richness is a subset of Total Richness. It is the number of unique taxa in a processed sample in the generally more environmentally sensitive orders Ephemeroptera, Plecoptera, and Trichoptera.

Calculation: A tally of the number of unique taxa identified from the insect orders Ephemeroptera, Plecoptera, Trichoptera. Note that same rules apply as above for Total Richness in determining the number of unique taxa.

4. EPT/EPT & Chironomidae - This is a measure of the ratio of the relative abundance of the generally intolerant organisms in EPT orders to the relative abundance of EPT organisms plus the generally more tolerant Diptera family Chironomidae.

Calculation: The number (relative abundance) of organisms from the orders Ephemeroptera, Trichoptera and Plecoptera, divided by the above plus the number of Chironomidae.

5. % Oligochaeta - Is a measure of the percent of the macroinvertebrate community made up of the Order Oligochaeta.

Calculation: The number (relative abundance) of Oligochaeta divided by the total number of animals in sample.

6. Percent Model Affinity of Orders (PMA-O) – PMA-O is a measure of taxonomic order level similarity to a model of expected order distribution based on reference streams.

Calculation: Determine the percent composition for each major taxonomic order in the sample (Coleoptera, Diptera, Ephemeroptera, Plecoptera, Trichoptera, Oligochaeta, Other). Compare to the "Model" for the appropriate stream type (see below), then add up the lower of the two values for each of the groups (assessment site vs Model), this is the PMA-O for the assessment site.

PMA-O = $\sum$ minimum (X_a or X_r)

Where: X_a = the percent composition of order X in the sample;

X_r = the expected percent composition of order X from the appropriate reference condition;

Example:

Major Taxonomic Orders	**Sample % Composition**	**Model for MHG (Medium High Gradient)**
Coleoptera	20	**6**
Diptera	55	**18**
Ephemeroptera	**10**	34
Plecoptera	**2**	8
Trichoptera	**3**	33
Oligochaeta	10	**0.5**
Other	**0**	0.5
PMA-O =	**39.5**	

7. Hilsenhoff Biotic Index (BI) - BI is a measure of the macroinvertebrate assemblage tolerance toward organic and/or nutrient enrichment. Most common taxa are assigned a BI number between zero (highly sensitive to enrichment) and ten (highly tolerant of enrichment.. In many ways this index is both an indicator taxa metric and functional group metric, since those taxa which become more dominant in moderately enriched streams are those which are taking advantage of shifts in the available food base in the stream.

Calculation : Use only taxa that have been assigned a BI value (o-10) by VTDEC based on published literature. Multiply the number of individuals of a taxon by its assigned tolerance. Total all of these products and divide by the total number of organisms.

$$HBI = \sum \frac{n_i a_i}{N}$$

Where: "n" is the number of individuals of the "i"th taxon;

"a" is the index value of that taxon;

N is the total number of individuals in the sample assigned a Biotic Index value

Example:

Taxon	**Count**	**BI Tolerance Value**	**Subtotal (Count × BI)**
Ephemerellidae imm	10	*NA*	*NA*
Ephemerella sp	10	4	40
Ephemerella needhami	10	1	10
Plecoptera Leuctridae imm	20	0	0
Diptera Cricotopus bicinctus	5	6	30
Trichoptera Hydropsyche alhedra	10	3	30
Trichoptera Hydropsyche sp	5	5	25
Totals	**60**		**145**
Sample Biotic Index value	**145 ÷ 60 = 2.42**		

8. Pinkham-Pearson Coefficient of Similarity of Functional Groups (PPCS-F) - PPCS-F is a measure of functional feeding group similarity to a model of expected feeding group distribution based on reference streams. It is similar in concept to the **PMA-O** in that a site is compared to a model of the composition of the functional feeding groups as opposed to order level taxonomic changes.

Calculation: Determine the percent composition of six major functional groups in a sample (collector-gatherer, collector-filterer, predator, shredder-detritivore, shredder-herbivore, scraper) as assigned by VTDEC based on published literature. For each functional group determine the ratio (min/max) between the sample and the reference model for that stream type. Sum these calculations and divide by six (i.e., the number of functional groups).

PPCS-F = $1/k \sum$ minimum (X_a or X_r)/maximum (X_a or X_r)

Where: k = the number of feeding group comparisons between stations (six)

X_a = the percent composition of feeding group "X" in the sample

X_r = the expected percent composition of feeding group "X" from the appropriate reference condition

Example:

Functional Group	**Sample % Composition**	**Model for MHG (Medium High Gradient)**	**Ratio (min/max)**
Collector-Gatherer	68	32	0.47
Collector-Filterer	10	30	0.33
Predator	2	13	0.15
Shredder-Detritivore	0	4	0.00
Shredder Herbivore	16	1	0.06
Scraper	2	13	0.15
Subtotal			**1.16**
PPCS-F =			**1.16 ÷ 6 = 0.19**