



**DRAFT SEMI-WADEABLE LARGE RIVER MACROINVERTEBRATE ASSESSMENT
METHOD**

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INTRODUCTION

Assessment of Aquatic Life Use (ALU) in large semi-wadeable rivers can be a complex process. To appropriately assess biological communities in large rivers and to increase the efficiency of ALU assessments, PADEP separates large rivers into two categories: semi-wadeable and non-wadeable. This assessment method is designed for semi-wadeable rivers within the Commonwealth. Semi-wadeable rivers are defined as predominantly free-flowing systems with drainage areas $>1,000$ mi², and have physical characteristics that allow for riffle and run sections to occur with relative frequency. These river systems tend to lack a well-defined and navigable U-shaped channel for any significant distance and frequently present difficulties for both wadeable and non-wadeable macroinvertebrate data collection methodologies. Well over half of the large rivers within the Commonwealth are considered semi-wadeable (Figure 1). Several studies have shown that semi-wadeable rivers can express substantial and reliable differences in water quality across their width for great distances. These chemical and physical differences drive variations observed in the macroinvertebrate communities that inhabit these regions (Guild et al. 2014, PADEP 2014, Shull 2017). The water quality differences across the width of large semi-wadeable rivers are usually the result of major tributary inputs that do not mix. Additionally, each major tributary input is driven by both the natural and anthropogenic influences within the respective basin.

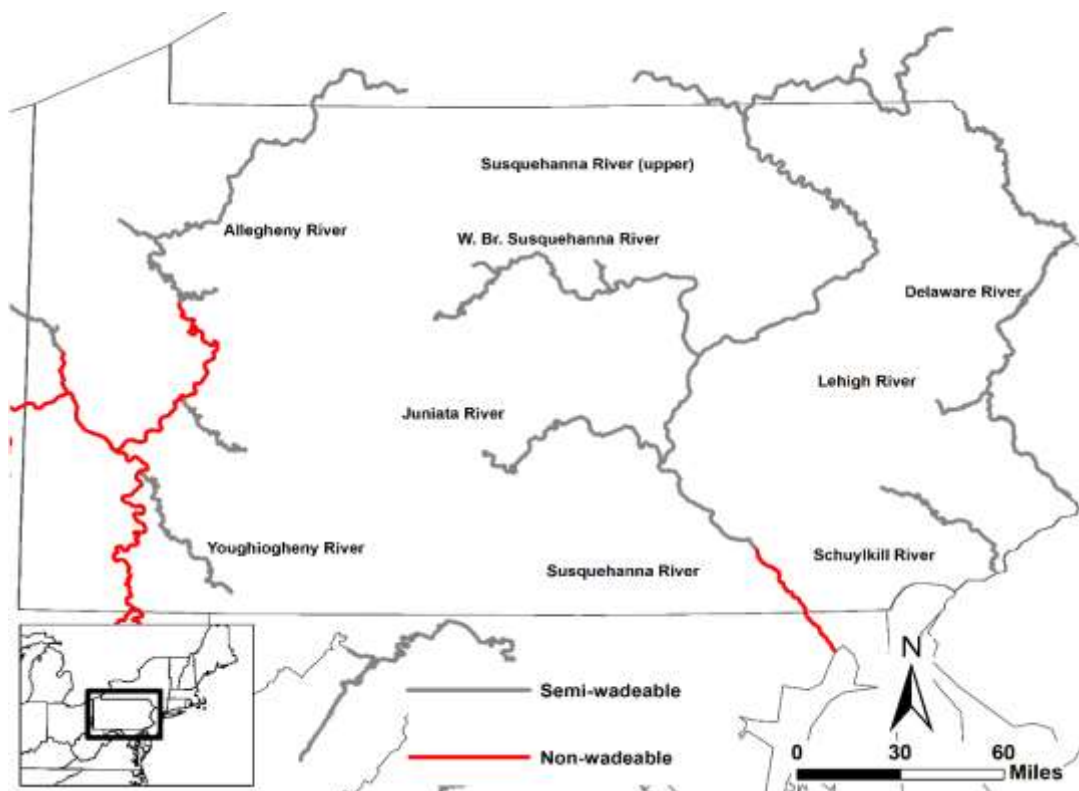


Figure 1. Large Rivers that are semi-wadeable and non-wadeable rivers throughout the Commonwealth. Assessment determinations will be made for semi-wadeable rivers using this assessment method. PADEP continues to develop assessment methods for non-wadeable large rivers.

No other large river biological assessment tool has sought to understand and deal with these chemical, physical, and biological differences at one location on a river separately. Yet, many large river collection methods have been created to capture and composite these variables into one measure; thereby, accounting for, but not giving heed to these important differential aspects (Applegate et al. 2007, Wessell et al. 2008, Blocksom and Johnson 2009, Weigel and Dimick 2011). Final assessments using these tools average or generalize biological condition to provide valuable assessment information, but they do not consider potentially important details in the environment. This effectively obscures the ability to account for biological community degradation within large and important zones on each river. It also reduces the ability to track major sources of impacts driving degradation. Even more problematic are the large river biological collection methods that only collect data along the shoreline of a large semi-wadeable river (Merritt et al. 2005, Angradi 2006, USEPA 2013). These methods are particularly questionable when making large scale inferences about water quality conditions, because shoreline habitats are likely affected by minor tributary influences and point source discharges that follow the shoreline in semi-wadeable rivers (PADEP 2014, Shull and Pulket 2015). Consequently, this assessment method does not use shoreline collection methods in large semi-wadeable rivers when making large scale assessment determinations. PADEP spent several years developing and refining the transect collection method, and because of this method, each semi-wadeable multimetric index (SWMMI) can not only be used to make assessment determinations that are reflective of overall water quality, but also produce results that retain the unique aspects of water quality variations. This should greatly improve the validity of each assessment on large semi-wadeable rivers, as well as provide important source tracking information for future restoration efforts, if needed.

The goal of this document is to lay the framework for how PADEP intends on making ALU assessment determinations in large semi-wadeable rivers. The semi-wadeable large river technical report (Shull 2017) goes into much detail about evaluating the complexity of large semi-wadeable rivers and how these assessment tools were developed to compensate. Making accurate and defensible assessment decisions requires both a sufficient number of data types (e.g., physical, chemical and biological) and a specificity of those data within a particular water influence (zone) – if needed – and season. Ultimately, ALU assessment determinations will be rather straightforward and similar to wadeable stream assessments if data can only be collected in one season and water influences are well mixed. However, ALU assessment determinations when water influences are not well mixed and when data are collected during both the summer and fall will require additional evaluation and discussion. To use this method for assessment purposes data collection must follow the protocols established in the Monitoring Book (Shull and Lookenbill 2017).

Each reach of river is assessed by the macroinvertebrate collection site immediately downstream. The length of each assessed reach is then determined by where the next potential impact to water quality exists upstream (i.e., major tributary or developed area). Therefore, the location of each upstream macroinvertebrate collection site should reflect this pattern. More explicitly, each macroinvertebrate collection site along the longitudinal gradient is determined by several factors including, where sufficient riffle-

run habitat exists, where changes in physiographic and demographic characteristics occur, and where additional major tributaries enter the system. Ideally, macroinvertebrate collections sites will occur at every viable riffle-run habitat, but at the very least, it is necessary to bracket major potential impacts to each system such as a major tributary or change in land use. In the example provided below (Figure 2), two semi-wadeable rivers converge to form another semi-wadeable river. Below this confluence, multiple water quality transects show that water influences do not mix so the non-mixing water influences were mapped. Hence, site 1 requires two unique 6D-200 samples composited completely within the delineated zone of each water influence. Additional macroinvertebrate collections sites (sites 2 – 5) are added upstream of the confluence to characterize each major water influence and to bracket the demographic characteristics across the drainage (e.g., communities, other land use transitions). It is important to note that water quality transect sites – used to delineate the area of specific water influences – can be collected at a higher frequency of locations than macroinvertebrate collections.

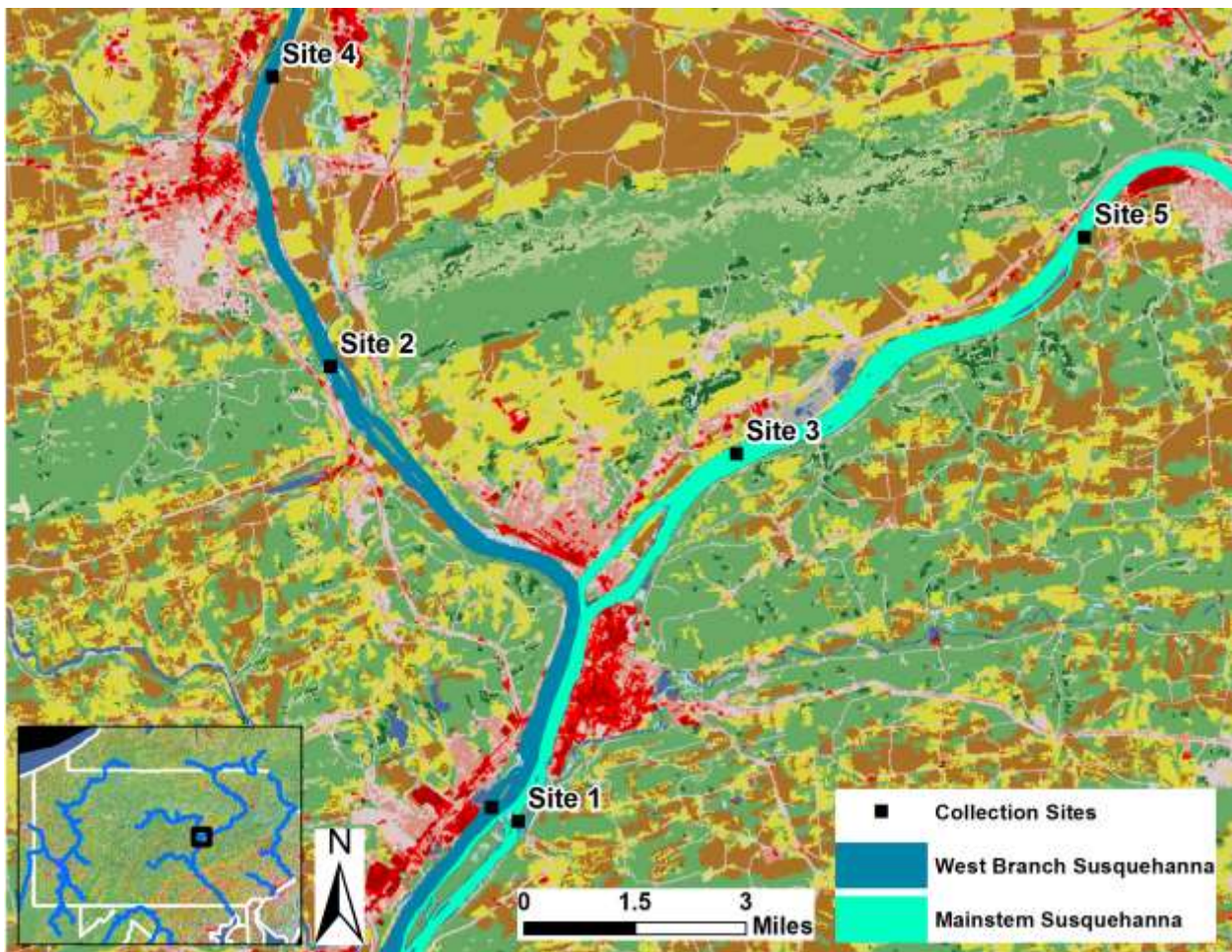


Figure 2. Macroinvertebrate collection sites on a large semi-wadeable river. Site locations were selected to bracket major land use changes and tributary inputs.

Habitat assessments are required with each semi-wadable macroinvertebrate sample. The PADEP habitat data sheet for high gradient streams is used, which has undergone several iterations from Plafkin et al. (1989). This habitat evaluation uses a 12 parameter – 20-point scoring method. Currently, it is recommended that all 12 parameters are recorded when conducting habitat assessments in a semi-wadeable river. Although, instream parameters such as instream cover, epifaunal substrate, and embeddedness are the most reliable habitat indicators for large semi-wadeable rivers. Instream cover evaluates the percent makeup of the substrate (boulders, cobble, other rock material) and submerged objects (logs, undercut banks) that provide refuge for fish. Epifaunal substrate evaluates riffle quality, i.e. areal extent relative to stream width and dominant substrate materials that are present. Embeddedness estimates the percent (vertical depth) of the substrate interstitial spaces filled with fine sediments. These three instream habitat measurements can be summed to provide a possible range of 0 (indicating worst possible instream conditions) to 60 (indicating best possible instream conditions) points at each sampling site. Instream habitat totals that fall below 30 points may be an indication of poor physical habitat conditions. The other parameters in the habitat assessment are also useful for informational purposes, but tend to become difficult to measure as river size increases.

SWMMI CALCULATION AND PRECISION

The assessment method development process (Shull 2017) identified two different macroinvertebrate communities existing in large semi-wadeable rivers between the summer and fall seasons. The macroinvertebrate communities were shown to be different enough to justify creating two independent assessment tools for semi-wadeable rivers. In addition, October sampling is not recommended if the intent is to make ALU assessment determinations as this is a critical transition period for the macroinvertebrate communities. Examples for each SWMMI (Summer and Fall) are provided to show the metric and index calculation process step-by-step. The summer and fall SWMMI calculations are separated into their respective sections for clarity.

Many different metric combinations were evaluated during method development. Each SWMMI had six metrics selected for inclusion into the final index. All metrics, which are further defined and described in Shull (2017) exhibited a strong ability to distinguish between relatively unimpacted and heavily impacted conditions. In addition, these metrics measure different aspects of the benthic macroinvertebrate communities, but when used together in an index, they provide a solid foundation for assessing the biological condition of benthic macroinvertebrate communities in large semi-wadeable rivers. A complete list of taxa and their attributes is provided in Appendix B of Shull (2017).

Summer SWMMI

The following summer sample was collected in the Delaware River on September 9th, 2016 and is used in the metric calculation and index standardization example below:

Taxa Name	Number of Individuals
Acroneuria	1
Agnetina	2
Baetisca	1
Brachycentrus	1
Cheumatopsyche	14
Chimarra	7
Chironomidae	10
Corbiculidae	8
Helicopsyche	14
Hydrobiidae	13
Hydropsyche	7
Isonychia	11
Lepidostoma	2
Leucrocuta	8
Maccaffertium	16
Micrasema	1
Oecetis	2
Oligochaeta	7
Optioservus	25
Physidae	1
Plauditus	7
Stenelmis	14
Teloganopsis	22
Tricorythodes	3

Percent Tolerant Individuals using Biological Condition Gradient (BCG) attribute 5 (BCGpct5)

$$= \left(\sum n_{\text{indvBCG5}} / N \right) * 100$$

Where n_{indvBCG5} is the number of individuals in the subsample with a BCG value of 5, and N is the total number of individuals in the subsample.

Taxa Name	Number of Individuals	BCG
Acroneuria	1	3
Agnetina	2	3
Baetisca	1	2
Brachycentrus	1	3
Cheumatopsyche	14	5
Chimarra	7	4
Chironomidae	10	5
Corbiculidae	8	5
Helicopsyche	14	3
Hydrobiidae	13	4
Hydropsyche	7	5
Isonychia	11	3
Lepidostoma	2	2
Leucrocuta	8	3
Maccaffertium	16	3
Micrasema	1	3
Oecetis	2	3
Oligochaeta	7	5
Optioservus	25	4
Physidae	1	5
Plauditus	7	
Stenelmis	14	5
Teloganopsis	22	3
Tricorythodes	3	5

There are 64 individuals with a BCG of 5, and a total of 197 individuals in the subsample.

$$(64/197)*100 = 32.5\%$$

Percent Intolerant Individuals using Pollution Tolerance Value (PTV) attributes 0-3 (PTVpct03)

$$= \left(\sum_{i=0}^3 n_{\text{indvPTVi}} / N \right) * 100$$

Where n_{indvPTVi} is the number of individuals in a sub-sample with PTV of i , and N = the total number of individuals in the subsample.

Taxa Name	Number of Individuals	PTV
Acroneuria	1	0
Agneta	2	2
Baetisca	1	4
Brachycentrus	1	1
Cheumatopsyche	14	6
Chimarra	7	4
Chironomidae	10	6
Corbiculidae	8	4
Helicopsyche	14	3
Hydrobiidae	13	8
Hydropsyche	7	5
Isonychia	11	3
Lepidostoma	2	1
Leucrocuta	8	1
Maccaffertium	16	3
Micrasema	1	2
Oecetis	2	8
Oligochaeta	7	10
Optioservus	25	4
Physidae	1	8
Plauditus	7	4
Stenelmis	14	5
Teloganopsis	22	2
Tricorythodes	3	4

There are 78 individuals with a PTV value of 0-3, and a total of 197 individuals in the subsample.

$$(78/197)*100 = 39.6\%$$

Hilsenhoff Index using BCG attributes (BCGindex2)

$$= \sum_{i=1}^6 [(i * n_{\text{indvBCGi}})] / N_{\text{BCG}}$$

Where n_{indvBCGi} is the number of individuals in a sub-sample with a BCG of i , and N_{BCG} is the total number of individuals with BCG values in the subsample.

Taxa Name	Number of Individuals	BCG
Acroneuria	1	3
Agnetina	2	3
Baetisca	1	2
Brachycentrus	1	3
Cheumatopsyche	14	5
Chimarra	7	4
Chironomidae	10	5
Corbiculidae	8	5
Helicopsyche	14	3
Hydrobiidae	13	4
Hydropsyche	7	5
Isonychia	11	3
Lepidostoma	2	2
Leucrocuta	8	3
Maccaffertium	16	3
Micrasema	1	3
Oecetis	2	3
Oligochaeta	7	5
Optioservus	25	4
Physidae	1	5
Plauditus	7	
Stenelmis	14	5
Teloganopsis	22	3
Tricorythodes	3	5

There are 0 individuals with a BCG of 1, 3 with a BCG of 2, 78 with a BCG of 3, 45 with a BCG of 4, 64 with a BCG of 5, 0 with a BCG of 6, and a total of 190 BCG individuals in the subsample.

$$[(1 * 0) + (2 * 3) + (3 * 78) + (4 * 45) + (5 * 64) + (6 * 0)] / 190 = 3.89$$

Percent Dominant Taxon (pctDOM)

$$= \left(\sum n_{\text{indvDOM}} / N \right) * 100$$

Where n_{indvDOM} is the number of individuals of the dominant taxon in the subsample, and N is the total number of individuals in the subsample.

Taxa Name	Number of Individuals
Acroneuria	1
Agetina	2
Baetisca	1
Brachycentrus	1
Cheumatopsyche	14
Chimarra	7
Chironomidae	10
Corbiculidae	8
Helicopsyche	14
Hydrobiidae	13
Hydropsyche	7
Isonychia	11
Lepidostoma	2
Leucrocuta	8
Maccaffertium	16
Micrasema	1
Oecetis	2
Oligochaeta	7
Optioservus	25
Physidae	1
Plauditus	7
Stenelmis	14
Teloganopsis	22
Tricorythodes	3

There are 25 individuals of the dominant taxon, *Optioservus* spp., and a total of 197 individuals in the subsample.

$$(25/197)*100 = 12.7\%$$

Percent Ephemeroptera using BCG attributes 1-3 (pctEbcg13)

$$= \left(\sum_{i=1}^3 n_{\text{EphemBCGi}} / N \right) * 100$$

Where $n_{\text{EphemBCGi}}$ is the number of Ephemeroptera individuals in a sub-sample with BCG of i , and N = the total number of individuals in the subsample.

Taxa Name	Number of Individuals	BCG
Acroneuria	1	3
Agnetina	2	3
Baetisca	1	2
Brachycentrus	1	3
Cheumatopsyche	14	5
Chimarra	7	4
Chironomidae	10	5
Corbiculidae	8	5
Helicopsyche	14	3
Hydrobiidae	13	4
Hydropsyche	7	5
Isonychia	11	3
Lepidostoma	2	2
Leucrocuta	8	3
Maccaffertium	16	3
Micrasema	1	3
Oecetis	2	3
Oligochaeta	7	5
Optioservus	25	4
Physidae	1	5
Plauditus	7	
Stenelmis	14	5
Teloganopsis	22	3
Tricorythodes	3	5

There are 58 Ephemeroptera individuals with BCG values of 1-3, and a total of 197 individuals in the subsample.

$$(58/197)*100 = 29.4\%$$

Richness of Sensitive Ephemeroptera, Plecoptera, and Trichoptera taxa using BCG attributes 1-3 (richEPTbcg)

$$= n_{\text{taxaEPTbcg}}$$

Where $n_{\text{taxaEPTbcg}}$ is the number of taxa belonging to the orders Ephemeroptera, Plecoptera, and Trichoptera that have BCG attributes of 1-3.

Taxa Name	BCG
Acroneuria	3
Agnetina	3
Baetisca	2
Brachycentrus	3
Cheumatopsyche	5
Chimarra	4
Chironomidae	5
Corbiculidae	5
Helicopsyche	3
Hydrobiidae	4
Hydropsyche	5
Isonychia	3
Lepidostoma	2
Leucrocuta	3
Maccaffertium	3
Micrasema	3
Oecetis	3
Oligochaeta	5
Optioservus	4
Physidae	5
Plauditus	
Stenelmis	5
Teloganopsis	3
Tricorythodes	5

There are 5 Ephemeroptera taxa with BCG attributes of 1-3, 2 Plecoptera taxa with BCG attributes of 1-3, and 5 Trichoptera taxa with BCG attributes of 1-3.

$$5 + 2 + 5 = 12$$

Metric Standardization and Index Calculation

Final ceiling and floor standardization values are needed to standardize each metric. All standardized metrics are then multiplied by 100 to get the metric standardized score, and the score must range between 0 and 100. Final adjusted metrics scores are then averaged to get a final Summer SWMMI score on a 0 to 100 scale.

Summer Metric Standardization Values

Metric	Floor Standardization (5 th percentile)	Ceiling Standardization (95 th percentile)
BCGpct5	28.5	80.6
PTVpct03	2.3	50.6
BCGindex2	3.76	4.76
pctDOM	14.4	46.8
pctEbcg13	0.4	49.7
richEPTbcg	1	10

For metrics like PTVpct03, pctEbcg13, and richEPTbcg (negative-response metrics), standardizations are calculated using the following equation:

$$(\text{observed value} - \text{floor}) / (\text{ceiling} - \text{floor}) * 100.$$

For metrics like BCGpct5, BCGindex2, and pctDOM (positive-response metrics) standardizations are calculated using the following equation:

$$(\text{ceiling} - \text{observed value}) / (\text{ceiling} - \text{floor}) * 100.$$

It is important to note that if a metric standardization score is < 0 then the score is set to 0, and if the metric standardization score is > 100 then the score is set to 100. This process creates the adjusted standardized metric score.

Metric / SWMMI	Observed Value	Standardized Metric Score	Adjusted Standardized Metric Score
BCGpct5	32.5	92.3	92.3
PTVpct03	39.6	77.7	77.7
BCGindex2	3.89	86.7	86.7
pctDOM	12.7	105.2	100
pctEbcg13	29.4	59.1	59.1
richEPTbcg	12	122.2	100
Summer SWMMI	--	--	86.0

Summer Precision Estimates

Summer SWMMI methodological precision is calculated using the coefficient of variation intrasite replicate samples (samples collected at the same site on the same day). The

summer SWMMI intrasite precision estimate was 8.8%, which was well below recommended limits (10 -15%, Stribling et al. 2008), indicated the summer SWMMI is a precise assessment tool. The summer SWMMI temporal precision is calculated using the 90% confidence interval and is typically used to show confidence around a change in biological condition at a site. The temporal precision estimate for the summer SWMMI using all available samples was 14.7, indicating that measured changes in index score of 15 or greater are not likely due to natural variation.

Fall SWMMI

The following fall sample was collected in the Delaware River on December 16th, 2015 and is used in the metric calculation and index standardization example below:

Taxa Name	Number of Individuals
Acroneuria	5
Cheumatopsyche	3
Chimarra	2
Chironomidae	65
Cultus	1
Epeorus	9
Ephemerella	53
Helopicus	2
Hydropsyche	15
Isonychia	3
Lepidostoma	5
Leucrocuta	5
Maccaffertium	28
Nematoda	1
Neophylax	1
Oligochaeta	4
Ophiogomphus	2
Optioservus	15
Oulimnius	1
Paraleptophlebia	2
Psephenus	1
Rhyacophila	2
Stenacron	1
Stenelmis	4
Taeniopteryx	1
Teloganopsis	6

Beck's Index using PTV attributes 0-2 (PTVBeck3)

$$= 3 * (n_{\text{taxaPTV0}}) + 2 * (n_{\text{taxaPTV1}}) + 1 * (n_{\text{taxaPTV2}})$$

Where n_{taxaPTV0} is the number of taxa with a PTV attribute of 0, n_{taxaPTV1} is the number of taxa with a PTV attribute of 1, and n_{taxaPTV2} is the number of taxa with a PTV attribute of 2.

Taxa Name	PTV
Acroneuria	0
Cheumatopsyche	6
Chimarra	4
Chironomidae	6
Cultus	2
Epeorus	0
Ephemerella	1
Helopicus	2
Hydropsyche	5
Isonychia	3
Lepidostoma	1
Leucrocuta	1
Maccaffertium	3
Nematoda	9
Neophylax	3
Oligochaeta	10
Ophiogomphus	1
Optioservus	4
Oulimnius	5
Paraleptophlebia	1
Psephenus	4
Rhyacophila	1
Stenacron	4
Stenelmis	5
Taeniopteryx	2
Teloganopsis	2

There are 2 taxa with PTV attributes of 0, 6 taxa with PTV attributes of 1, and 4 taxa with PTV attributes of 2.

$$3 * (2) + 2 * (6) + 1 * (4) = 22$$

Richness of Sensitive Ephemeroptera, Plecoptera, and Trichoptera taxa using PTV attributes 0-4 (richEPTptv)

$$= n_{\text{taxaEPTptv}}$$

Where $n_{\text{taxaEPTptv}}$ is the number of taxa belonging to the orders Ephemeroptera, Plecoptera, and Trichoptera that have PTV attributes of 0-4.

Taxa Name	PTV
Acroneuria	0
Cheumatopsyche	6
Chimarra	4
Chironomidae	6
Cultus	2
Epeorus	0
Ephemerella	1
Helopicus	2
Hydropsyche	5
Isonychia	3
Lepidostoma	1
Leucrocuta	1
Maccaffertium	3
Nematoda	9
Neophylax	3
Oligochaeta	10
Ophiogomphus	1
Optioservus	4
Oulimnius	5
Paraleptophlebia	1
Psephenus	4
Rhyacophila	1
Stenacron	4
Stenelmis	5
Taeniopteryx	2
Teloganopsis	2

There are 8 Ephemeroptera taxa with PTV attributes of 0-4, 4 Plecoptera taxa with PTV attributes of 0-4, and 4 Trichoptera taxa with PTV attributes of 0-4.

$$8 + 4 + 4 = 16$$

Percent Intolerant Individuals using PTV attributes 0-3 (PTVpct03)

$$= \left(\sum_{i=0}^3 n_{\text{indvPTVi}} / N \right) * 100$$

Where n_{indvPTVi} is the number of individuals in a sub-sample with PTV of i , and N = the total number of individuals in the subsample.

Taxa Name	Number of Individuals	PTV
Acroneuria	5	0
Cheumatopsyche	3	6
Chimarra	2	4
Chironomidae	65	6
Cultus	1	2
Epeorus	9	0
Ephemerella	53	1
Helopicus	2	2
Hydropsyche	15	5
Isonychia	3	3
Lepidostoma	5	1
Leucrocuta	5	1
Maccaffertium	28	3
Nematoda	1	9
Neophylax	1	3
Oligochaeta	4	10
Ophiogomphus	2	1
Optioservus	15	4
Oulimnius	1	5
Paraleptophlebia	2	1
Psephenus	1	4
Rhyacophila	2	1
Stenacron	1	4
Stenelmis	4	5
Taeniopteryx	1	2
Teloganopsis	6	2

There are 125 individuals with a PTV value of 0-3, and a total of 237 individuals in the subsample.

$$(125/237)*100 = 52.7\%$$

Percent Ephemeroptera using BCG attributes 1-3 (pctEbcg13)

$$= \left(\sum_{i=1}^3 n_{\text{EphemBCGi}} / N \right) * 100$$

Where $n_{\text{EphemBCGi}}$ is the number of Ephemeroptera individuals in a sub-sample with BCG of i , and N = the total number of individuals in the subsample.

Taxa Name	Number of Individuals	BCG
Acroneuria	5	3
Cheumatopsyche	3	5
Chimarra	2	4
Chironomidae	65	5
Cultus	1	1
Epeorus	9	2
Ephemerella	53	2
Helopicus	2	3
Hydropsyche	15	5
Isonychia	3	3
Lepidostoma	5	2
Leucrocuta	5	3
Maccaffertium	28	3
Nematoda	1	
Neophylax	1	3
Oligochaeta	4	5
Ophiogomphus	2	3
Optioservus	15	4
Oulimnius	1	2
Paraleptophlebia	2	2
Psephenus	1	4
Rhyacophila	2	2
Stenacron	1	4
Stenelmis	4	5
Taeniopteryx	1	3
Teloganopsis	6	3

There are 106 Ephemeroptera individuals with BCG values of 1-3, and a total of 237 individuals in the subsample.

$$(106/237)*100 = 44.7\%$$

Total Taxa Richness (Richness)

$$= n_{\text{taxa}}$$

Where n_{taxa} is the total number of taxa in the subsample.

Taxa Name

Acroneuria
Cheumatopsyche
Chimarra
Chironomidae
Cultus
Epeorus
Ephemerella
Helopicus
Hydropsyche
Isonychia
Lepidostoma
Leucrocuta
Maccaffertium
Nematoda
Neophylax
Oligochaeta
Ophiogomphus
Optioservus
Oulimnius
Paraleptophlebia
Psephenus
Rhyacophila
Stenacron
Stenelmis
Taeniopteryx
Teloganopsis

There are 26 taxa in the subsample.

Richness of taxa in the Functional Feeding Group (FFG) Scrapers (FFGrichSC)

$$= n_{\text{sctaxa}}$$

Where n_{sctaxa} is the number of scraper taxa.

Taxa Name	Number of Individuals	FFG
Acroneuria	5	PR
Cheumatopsyche	3	FC
Chimarra	2	FC
Chironomidae	65	CG
Cultus	1	PR
Epeorus	9	SC
Ephemerella	53	CG
Helopicus	2	PR
Hydropsyche	15	FC
Isonychia	3	CG
Lepidostoma	5	SH
Leucrocuta	5	SC
Maccaffertium	28	SC
Nematoda	1	CG
Neophylax	1	SC
Oligochaeta	4	CG
Ophiogomphus	2	PR
Optioservus	15	SC
Oulimnius	1	SC
Paraleptophlebia	2	CG
Psephenus	1	SC
Rhyacophila	2	PR
Stenacron	1	SC
Stenelmis	4	SC
Taeniopteryx	1	SH
Teloganopsis	6	CG

There are 9 scraper taxa in the subsample.

Metric Standardization and Index Calculation

Final ceiling and floor standardization values are needed to standardize each metric. All standardized metrics are then multiplied by 100 to get the metric standardized score, and the score must range between 0 and 100. Final adjusted metrics scores are then averaged to get a final fall SWMMI score on a 0 to 100 scale.

Fall Metric Standardization Values

Metric	Floor Standardization (5 th percentile)	Ceiling Standardization (95 th percentile)
PTVBeck3	2	15
richEPTptv	2	15
PTVpct03	3.3	65.3
pctEbcg13	0	62.3
Richness	11	27
FFGrichSC	2	10

For all fall metrics (negative-response metrics), standardizations are calculated using the following equation:

$$(\text{observed value} - \text{floor}) / (\text{ceiling} - \text{floor}) * 100.$$

It is important to note that if a metric standardization score is < 0 then the score is set to 0, and if the metric standardization score is > 100 then the score is set to 100. This process creates the adjusted standardized metric score.

Metric / SWMMI	Observed Value	Standardized Metric Score	Adjusted Standardized Metric Score
PTVBeck3	22	153.8	100
richEPTptv	16	107.7	100
PTVpct03	52.7	79.7	79.7
pctEbcg13	44.7	71.7	71.7
Richness	26	93.7	93.7
FFGrichSC	9	87.5	87.5
Fall SWMMI	--	--	88.8

Fall Precision Estimates

Fall SWMMI methodological precision is calculated using the coefficient of variation intrasite replicate samples (samples collected at the same site on the same day). The fall SWMMI intrasite precision estimate was 14.1%, which was within recommended limits (10 -15%, Stribling et al. 2008), indicating the fall SWMMI is a precise and repeatable assessment tool. The fall SWMMI temporal precision is calculated using the 90% confidence interval and is typically used to show confidence around a change in biological condition at a site. The temporal precision estimate for the fall SWMMI using

all available samples was 12.8, indicating that measured changes in index score of 13 or greater are not likely due to natural variation.

AQUATIC LIFE USE ASSESSMENTS

Both SWMMIs (summer and fall) are accurate and precise tools for making ALU assessment determinations in semi-wadeable rivers. Ideally, assessment in large rivers will understand and compensate for the complexity of the biological communities that exist in these rivers. This assessment tool is a substantial step toward that ideal situation. It is important to note that the transect method can produce multiple SWMMI results at any given location based on the number of major water influences discovered during transect data collection. To address this issue, PADEP will use transect data to create zones within each river to be assessed independently, if needed. For example, if transect data shows that 3 unique water quality zones exist, then PADEP will use the SWMMI to assess each zone independently. This determination will result in more accurate assessments on large semi-wadeable rivers without ignoring major impacts, or averaging major impacts with better conditions. This method also creates the ability to source track major impacts. Linking large river impacts to sources will inform more appropriate Total Maximum Daily Load (TMDL) and TMDL alternative solutions. In addition, the transect method specifically targets observed variations in water quality and measures biological conditions within those regions; therefore, SWMMI scores between defined zones across the width of a river should not be averaged.

The summer SWMMI impairment threshold is 49 and the fall SWMMI impairment threshold is 57. More information on the development of these impairment thresholds is found in the development report (Shull 2017). SWMMI scores below these thresholds will indicate impaired ALU. Each SWMMI (summer and fall) is independently applicable when making ALU determinations. This is based on USEPA guidance, which mandates that all biological communities PADEP has assessment methods for must be evaluated on a stand-alone basis (USEPA 2002). Consequently, each SWMMI is functionally equivalent to having two completely different biological assessment tools (e.g., fish MMI and a macroinvertebrate MMI). Therefore, it is not appropriate to average both SWMMI scores to obtain an overall result. It is also not appropriate to favor the results of one SWMMI over the other. PADEP will always strive to collect as much information as possible to make the most accurate assessment decisions. However, based on independent applicability, it is also understood that only one SWMMI (summer or fall) is required to make an ALU determination for a semi-wadeable river.

The following situation provides an example of this biological assessment rule. Multiple summer and fall samples were collected at the same site (Figure 3). Based on transect analysis the site had one homogeneous influence, so each macroinvertebrate sample was collected evenly across the entire width of the river during each visit. A total of five samples were collected; two samples during the summer and three samples during the fall. The summer samples consistently showed reduced, but attaining SWMMI scores, yet the fall samples resulted in impaired scores. The fall biological community was not

supporting the Aquatic Life Use; therefore, PADEP would determine that this section of the river is impaired. It may be concluded from this example that one SWMMI is more sensitive than the other; however, that is not the case. Examination of the entire development dataset showed no preference for one SWMMI consistently selecting for one assessment decision when biological communities were close to thresholds.

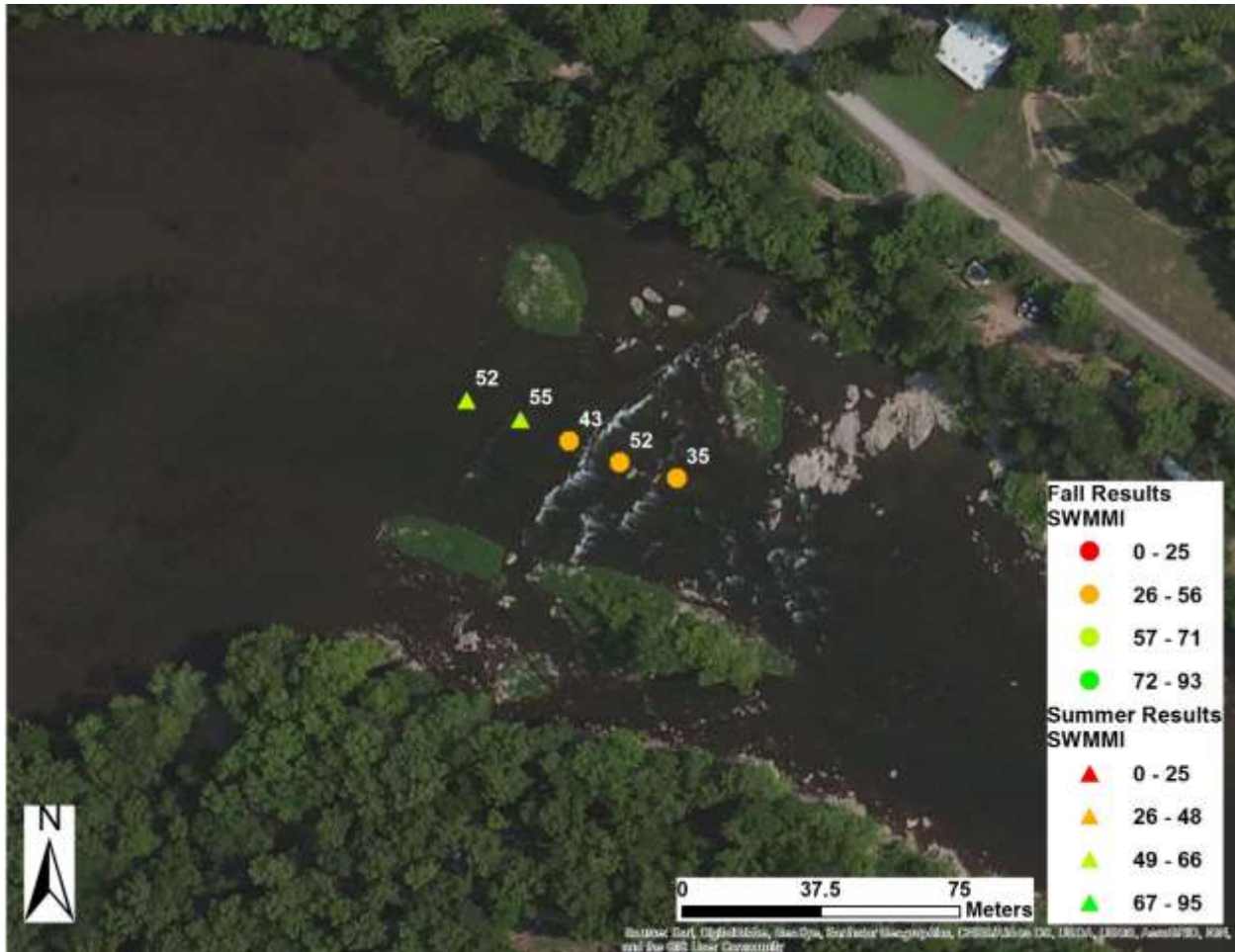


Figure 3. Multiple summer and fall SWMMI results over time at the same location on a semi-wadeable river. Location of points on the map do not indicate exact sample location; points were moved slightly to illustrate the results of sampling. Points are labeled with the respective SWMMI score.

ADDITIONAL APPLICATION CONSIDERATIONS

Data resulting from SWMMI scores may not be used in making ALU determinations in some situations. In fact, PADEP uses the wadeable freestone riffle-run method developed by Chalfant (2012) for several other purposes, including, but not limited to cause and effect surveys and incremental improvement reports. These surveys can collect biological information in areas that are not appropriate for making ALU determinations. For example, two macroinvertebrate samples were collected on a semi-

wadeable river near a city in Pennsylvania, just downstream of a sewage treatment plant. In this example, the SWMMI results showed that a major portion of this semi-wadeable river (laterally) was being impacted by a facility, perhaps, not operating within permitted limits. Sampling locations specifically targeted one city's sewage treatment facility, but were not necessarily representative of river conditions in this area. Therefore, it would not be appropriate to use these results in making assessment decisions on this river. However, this example does illustrate the usefulness of the semi-wadeable biological collection method for other purposes. This example also illustrates the necessity to differentiate between ALU assessments and reports on local scale impacts. All ALU assessments on semi-wadeable rivers should examine the longitudinal scale that each macroinvertebrate sample represents. If a macroinvertebrate sample is determined to be more representative of a local scale impact, then consideration of appropriate compliance actions may be appropriate.

The SWMMIs may also be used to evaluate whether conditions are degrading or improving at a given site (e.g., trend analysis). It is important to note that this is a different type of analysis than making assessment determinations using an impairment threshold. Methodological error is already incorporated during the development of the impairment threshold, so using variability measurements as "gray areas" while making assessment determinations is not appropriate (Stribling et al. 2008). However, for analyses such as trend analysis, the temporal precision estimate can be used to decide whether a macroinvertebrate community changes over time. When SWMMI scores at the same site change over time beyond the temporal precision estimate, there is a high level of confidence that the biological community change was driven by human influences. The summer SWMMI temporal precision estimate for all sites (where repeat data were available) was 14.7 points, which suggests that observed score changes at a site over time of 15 points or more can be considered a change in condition. The fall SWMMI temporal precision estimate for all sites (where repeat data were available) was 12.8 points, which suggests that observed score changes at a site over time of 13 points or more can be considered a change in condition.

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