

The Mississippi-Benthic Index of Stream Quality (M-BISQ): Recalibration and Testing

Prepared for:

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Abstract

The Mississippi Department of Environmental Quality (MDEQ) uses a benthic macroinvertebrate multimetric index to assess stream degradation relative to least-disturbed streams throughout the state. The initial calibration of the M-BISQ in 2003 was based on data from 455 non-tidal streams throughout the state, excluding the Alluvial Plain. For this project, the index was recalibrated to improve index sensitivity to current disturbance conditions, and used additional data collected from 786 streams through 2012. All analyses were performed using only data of known quality, enhancing defensibility of index calibration and testing, and final site assessments. Performance characteristics of all data were acceptable, meeting programmatic measurement quality objectives (MQO) used by the agency for field sampling precision, sample sorting/subsampling bias, and sample-based taxonomic precision. We evaluated candidate metrics and index compilations using criteria previously defined by the agency for the stressor gradient (least-disturbed and most-disturbed streams [LD and MD, respectively]), defined bioregional site classes, and generated performance statistics in R code for over 1.8M index options. Index options were filtered by their sensitivity to stressors (discrimination efficiency [DE]), the variety of metric categories, redundancy, and ease of calculation. Final site classification included four bioregions: South Bluff, West, East, and Southeast, with index DE ranging from 82 to 91%. Site class-specific index formulations included 17 different metrics, seven of which are common to at least two bioregions. Guidelines are provided for calculation and application of the index, suggestions provided on use in stressor identification and causal analysis, and discussion of index relationship to potential efforts in calibration of a biological condition gradient.

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1. INTRODUCTION

The Federal Water Pollution Control Amendments of 1972, aka, the Clean Water Act (CWA), has as its primary objective the restoration and maintenance of the “chemical, physical, and biological integrity of the Nation’s waters” (§101[a]) (USGPO 1989). To strengthen the scientific foundation of the CWA, “biological integrity” has been defined as “the ability (of a water body) to support and maintain a balanced, integrated, biological community having a species composition, diversity, and functional organization comparable to that of natural habitats in the region” (Karr and Dudley 1981, Schneider 1992). The capacity for aquatic organisms to survive and reproduce in nature is controlled by both basic biological and physiological processes of the organisms and characteristics of their immediate environment. A water body with chemical and physical characteristics that are close to those found in a naturally occurring habitat can be considered to represent chemical and physical integrity, and therefore potentially supportive of a healthy biological condition. Karr et al. (1986) operationalized the concept by constructing an index of biological integrity (IBI) for stream fishes in Illinois. The index was calculated using data from whole samples (i.e., multiple species) that were field collected from a defined area, in the case of these Illinois fish, a stream reach.

The structure of the IBI is a combination of several quantitative descriptors of different sample characteristics; individually, the descriptors are called “metrics”, and the resulting composite index is a multimetric index (MMI [Barbour et al. 1995]). There have been IBI calibrated across the US, all designed to provide a framework for organizing and presenting field biological data as a composite of community or assemblage characteristics, such as taxonomic structure and function, feeding types, and relative tolerance to stressors. They have been adapted for use with several assemblages, based on the most common organism groups used by routine biological monitoring and assessment programs, including benthic macroinvertebrates (aquatic insects, snails, mollusks, crustaceans, worms, and mites), fish, and/or algae (Karr et al. 1986, Hughes et al. 1998, Barbour et al. 1999, Hill et al. 2000, 2003). Indexes of biological integrity have also been developed for other water body types including estuaries, lakes and reservoirs, large rivers, and wetlands; and, in many other geographic areas throughout North, Central, and South America, Europe, and increasingly, Asia. Regardless of the types of biological data used, reliability of these indexes depends on a number of factors, including consistency of sampling methods and their application (Stribling 2011), and calibration that sufficiently deals with variability resulting from seasonal, regional, and small-scale spatial influences.

The Mississippi Department of Environmental Quality (MDEQ) undertook development of a biological indicator of stream conditions in 2001 to address the extensive evaluated listings included on the State 1998 list of impaired waterbodies. These evaluated listings were placed on the list of impaired waters with no monitoring data, and the Mississippi-Benthic Index of Stream Quality (M-BISQ) was used to determine attainment status based on instream monitoring and

bioassessment, allowing the state to delist streams attaining the aquatic life use and focus state resources for pollution controls on streams where data indicated an actual impairment of the use. After addressing the evaluated listings, MDEQ continues to use the MBISQ to determine stream quality for attainment decisions for Wadeable streams throughout Mississippi (exclusive of the Alluvial Plain [“the Delta”]).

The initial version of the M-BISQ (MDEQ 2003) was based on data from 529 samples from 459 streams distributed throughout the state, data collections including benthic macroinvertebrates, physical habitat quality, and selected field chemistry. The first recalibration of the M-BISQ was undertaken with five additional years’ worth of data, and a broadened understanding of the watersheds, streams, and stressor sources of the state (Jessup and Stribling 2008). The M-BISQ is re-calibrated periodically to incorporate new data that may provide stronger evidence of distinct site classes (bioregions) or metric responses to stress, using analytical methods similar to those used in the past calibration and recalibration (MDEQ 2003, Jessup and Stribling 2008). One of the primary questions explored in this analysis is the potential need for a new site class for blackwater streams (primarily) in southeastern Mississippi. Similar blackwater streams are recognized as a unique bio-assessment site class in the New Jersey Pinelands (Jessup et al. 2005).

Overall, the recalibration process includes defining the stressor gradient, establishing site classification, testing sensitivity of metric response to stressors, and formulating the structure of the multimetric index. This report presents results of additional testing of metric and index response sensitivity, suitability of existing site classification, and an acceptable structure of the M-BISQ, and incorporates data from the initial year of sampling (2001) through Phase 14 (2014).

2. OVERVIEW OF FIELD AND LABORATORY METHODS

2.1 Field sampling

All fieldwork related to the M-BISQ occurs during an approximately 14 week index period spanning the first week of December through the first week of March (roughly December 01 – March 07), with occasional exceptions. Wadeable streams are sampled over 100m reaches, samples and measurements are taken for benthic macroinvertebrates (BMI), physical habitat quality, substrate particle size distribution, and selected field water chemistry. Field sampling for BMI employs a long-handled D-frame net, with 595 micron mesh netting; multiple habitats are sampled throughout the reach, composited in a single, labelled sample container, and preserved with approximately 95% ethanol. Physical habitat quality is visually assessed for the reach, rating each of 10 parameters along a 20-point continuum of optimal, suboptimal, marginal, and poor, with 20 being best. In general, those physical characteristics that are more complex are considered

in better condition and receive higher scores. Substrate particle size distribution is quantified using a modified Wolman 100 particle pebble count. *In situ* water chemistry (specific conductance, dissolved oxygen, pH, and water temperature) is measured using field meters and probes. For purposes of quality control (QC) comparisons and for calculating performance measures, duplicate 100m reaches are sampled for a randomly-selected 10% of the reaches, including the BMI samples, physical habitat assessments, and pebble counts. The duplicate reaches are immediately adjacent to the primary, and can be either upstream or downstream. Those sampled on the same day, the same field team are called *bioduplicates*; when sampled on different days by different teams, they are *biorepeats*. Samples and data from the repeated reaches are labelled with a “BD” or “BR”, respectively, trailing the primary site identification number (Site ID), such as XXXXX-BD.

2.2 Laboratory processing

Laboratory processing of the BMI samples includes sorting/subsampling and taxonomic identification. The sorting/subsampling process entails spreading sample material over a Caton gridded screen, and randomly selecting grid squares of material for specimen removal (Caton, 1991, Barbour et al. 1999, Stribling 2011). Sorting and subsampling results in three separate, labelled containers for each sample: 1) sort residue, which is the fraction of the sample material selected by grid and removed, and from which all organisms are picked; 2) unsorted sample remains, which is the portion of the sample still containing organisms; and 3) the clean subsample, which is ultimately given to the taxonomist for identification. Taxonomic identification is done primarily under a binocular dissecting microscope, except for those taxa requiring slide-mounting, midges and worms (respectively, Chironomidae and Oligochaeta), where a compound microscope is used. Hierarchical target levels for identifications are primarily genus, with a few exceptions (Table 1). Counting rules (Table 2) are used to enhance consistency in sample treatment focus on taxa that are bottom-dwellers, and meet the definition of benthic macroinvertebrates, that is, are visible to the naked eye and are retained by a U.S. standard no. 30 sieve (595 micron mesh). Following primary sorting/subsampling and taxonomic identifications, two techniques are used for QC analyses. Ten percent (10%) of the sample sort residues are randomly selected, and sent to a separate laboratory for sort re-checking to recover any missed specimens; likewise, 10% of the subsamples (already identified) are sent to an independent taxonomist in a separate laboratory for re-identification.

2.3 Quality control

Data quality is characterized with a series of method performance measures that are used as data quality indicators. The measures are organized by an ‘error partitioning framework’ (Stribling 2011, Flotemersch et al. 2006), and include either or both quantitative and qualitative terms for one or more of precision, accuracy, bias, representativeness, and completeness. For the biological sampling and analysis, performance measures are defined for the seven steps of the

Table 1. Hierarchical target levels used by Mississippi DEQ for taxonomic data.

ALL TAXA identified to genus level, unless noted otherwise below:	
Ceratopogonidae	(Ceratopogonidae)
Decapoda	family
Hirudinea	family
Hydracarina	(Hydracarina)
Mollusca	family
Nematoda	(Nematoda)
Nematomorpha	(Nematomorpha)
Nemertea	(Nemertea)
Simuliidae	(Simuliidae)
Turbellaria	(Turbellaria)
The following are combined under Cricotopus/Orthocladius:	
<i>Cricotopus</i>	
<i>Orthocladius</i>	
<i>Cricotopus/Orthocladius</i>	
<i>Orthocladius/Cricotopus</i>	
The following are combined under <i>Thienemannimyia</i> genus group:	
<i>Conchapelopia</i>	
<i>Helopelopia</i>	
<i>Telopelopia</i>	
<i>Meropelopia</i>	
<i>Hayesomia</i>	
<i>Thienemannimyia</i>	
The following are combined under <i>Hydropsyche</i>:	
<i>Hydropsyche</i>	
<i>Ceratopsyche</i>	
<i>Hydropsyche/Ceratopsyche</i>	
<i>Ceratopsyche/Hydropsyche</i>	

Table 2. Counting rules used by taxonomists for benthic macroinvertebrate sample content.

COUNT
<ul style="list-style-type: none"> • Damaged insects and crustaceans, <i>only if</i> they have at least a head and a thorax • Oligochaeta fragments, <i>only if</i> they are headed AND have enough segments for identification • Mollusk shells, <i>only if</i> there is soft tissue present
DO NOT COUNT
<ul style="list-style-type: none"> • Surface-dwellers (HETEROPTERA/HEMIPTERA: Veliidae, Gerridae; COLLEMBOLA) • Non-benthic water column taxa (HETEROPTERA/HEMIPTERA: Corixidae, Notonectidae, Naucoridae; DIPTERA: Culicidae, Chaoboridae; COLEOPTERA: Gyrinidae [adults only], Hydrophilidae [adults only], Dytiscidae (adults only), Noteridae [adults only]) • Terrestrial incidentals • Larval or pupal exuviae • Larvae or pupae where internal tissue has broken down to the point of floppiness • Chironomid pupae (means that sorters do not count as part of total) • Trichoptera pupae (means that sorters do not count as part of total) • Microinvertebrates such as copepods, cladocera, ostracods

process: field sampling; laboratory sorting/subsampling; taxonomic identification; data reduction/metric and index calculation; and site assessment and interpretation. Routine application of the M-BISQ by MDEQ uses five performance characteristics and nine measurement quality objectives (MQO) (Table 3). Field sampling precision is calculated using metric and index values from the set of sample pairs (primary and duplicate) from all sites. Sorting and subsampling bias is calculated using results from the sort residue re-checks, and taxonomic precision from a direct and independent comparison of identification and count results from the two taxonomists. Quantitative values from these performance measures are initially used to identify potential problems, i.e., unacceptable data quality, and to formulate and institute corrective actions. Then, they are used to provide an objective descriptor of data quality associated with the dataset. These procedures have been consistently applied and corrective actions implemented throughout all 15 phases of the M-BISQ development and re-calibration (MDEQ 2003, Jessup and Stribling 2008, and the current study).

Table 3. Key performance characteristics and measurement quality objectives (MQO) used for characterizing and documenting data quality associated with the Mississippi Benthic Index of Stream (M-BISQ).

Performance characteristic	Term	MQO
Field sampling precision (multimetric index)	<ul style="list-style-type: none"> • Coefficient of variability (%) (CV) • 90% detectable difference (DD90) • Relative percent difference (RPD) 	<ul style="list-style-type: none"> • CV < 10%, for a sampling event (field season, watershed, or other strata) • DD90 ≤ 15 index points, on a 100-point scale • RPD < 15
Field sampling completeness		<ul style="list-style-type: none"> • Completeness > 98%
Sorting/subsampling bias	<ul style="list-style-type: none"> • Percent sorting efficiency (PSE) 	<ul style="list-style-type: none"> • PSE ≥ 90, for ≥ 90% of externally QC'd sort residues
Taxonomic precision	<ul style="list-style-type: none"> • Percent taxonomic disagreement (PTD) • Percent difference in enumeration (PDE) 	<ul style="list-style-type: none"> • Median PTD ≤ 15% for overall sample lot; samples with PTD ≥ 15% examined for patterns of error • Median PDE ≤ 5%; samples with PDE ≥ 5% should be further examined for patterns of error
Taxonomic completeness	<ul style="list-style-type: none"> • Percent taxonomic completeness (PTC) 	<ul style="list-style-type: none"> • Median PTC ≥ 90% • Median PTC (absolute difference) < 5%

3. DATA DESCRIPTION

Data include sample results from stream sampling over a 14-year period (2001-2014) using standardized field and laboratory protocols discussed above. Analyses of data quality and use of corrective actions have been instituted for each phase of the M-BISQ; results of QC analyses for key performance measures are presented for Phase 12 (Table 4). Because comprehensive presentation of QC results for all 14 years is beyond the scope of this report, for purposes of this report, these performance measures can be taken as representative of all phases.

Site characteristics were derived from the latitude/longitude coordinates and GIS coverages for the sites and their catchments. Multiple samples were collected at some sites, in which case, the most recent sample with the most complete environmental data (physical, chemical) was used.

Samples that were not analyzed include replicates collected at the same site on the same day (bioduplicates), on a different day within the same sampling event (biorepeats), or in a different year. A total of 941 samples used in this recalibration (Table 5). The sites were further categorized for M-BISQ development or validation. Validation sites were generally those with samples collected in 2013 and 2014, though earlier samples were randomly selected for the validation set when insufficient samples for validation were available from 2013-2014.

4. RECALIBRATION

For this project, we replicated the process used in both the original development of the M-BISQ and the 2008 recalibration (MDEQ 2003, Jessup and Stribling 2008). Those steps include:

- Determining preliminary regional site classes,
- Establishing numeric criteria for site reference status, as either least disturbed (LD) or most disturbed (MD), or Other,
- Determining naturally occurring bioregional delineations,
- Testing metric sensitivity, and
- Combining metrics into an index.

We analyzed performance of the current version of the index (Jessup and Stribling 2008), and investigated potential new site classes, metrics, and index formulations. The geographical scope of this project is statewide, exclusive of the Alluvial Plain (“the Delta”).

Table 4. Summary table of QC results for M-BISQ Phase 12. The complete taxonomic data quality report is presented as Appendix A.

Method	Characteristic	Term	MQO	Result (mean)	No. samples in exceedance
Field sampling (M-BISQ)	Precision	DD90	<15 points	8.6	na
		CV	<10%	7.3	na
		RPD	<15	7.8	2
Sorting/sub-sampling	Bias	PSE	>/=90	97.2	0
Taxonomic identification	Precision	PDE	<5	0.3	0
		PTD	<15	4.6	0
		PTC	>/=90	95.6	0
		(abs)PTC	</=5	1.9	1

ABBREVIATIONS: DD90, 90% detectable difference; CV, coefficient of variability; RPD, relative percent difference; PSE, percent sorting efficiency; PDE, percent difference in enumeration; PTD, percent taxonomic disagreement; PTC, percent taxonomic completeness; (abs)PTC, absolute difference in PTC; na, not applicable.

Table 5. Numbers of samples used for recalibration and testing, by year and bioregion. These numbers represent primary samples only, not repeat or QC samples.

Sample Year	East	South Bluff	Southeast	West	Total
2000	1	0	0	0	1
2001	90	9	30	42	171
2002	12	0	5	5	22
2003	30	4	7	23	64
2004	22	1	4	10	37
2005	26	2	5	5	38
2006	12	0	2	5	19
2007	38	5	13	13	69
2008	40	8	13	33	94
2009	46	2	35	15	98
2010	41	5	10	19	75
2011	54	0	27	13	94
2012	23	3	16	25	67
2013	33	0	6	11	50
2014	23	4	6	9	42
TOTAL	491	43	179	228	941

5. METHODS

Site classification for purposes of biological indicator development is a highly iterative process, and entails the following activities:

1. Developing stressor gradient,
2. Defining least- and most-disturbed sites,
3. Specifying a preliminary framework to be tested,
4. Evaluating taxonomic groupings,
5. Metric and index testing and selection,
6. Defining final site classification

5.1 Developing stressor gradient

We defined the stressor gradient as the range of values for different stressor variables that were used to define the least- and most-disturbed sites (LD and MD, respectively). Practical thresholds were identified for those variables where the LD values looked better than those in other sites. For a site to be considered LD, it had to meet all of the criteria for its site class grouping. A site was considered most disturbed if it met one or more of the MD criteria. The simplified stressor gradient was categorically represented by LD, Other, and MD sites, where Other sites did not meet the criteria for either LD or MD.

5.2 Defining least- and most-disturbed sites

We used the same criteria established during the last recalibration (Jessup and Stribling 2008) to define least- and most-disturbed sites (LD and MD, respectively) among the existing bioregions (Table 6, Figure 1). The LD and MD sites were designated for index development or validation so that each potential site class could be tested and validated with sufficient sample sizes for meaningful evaluation of metric and index performance. Development data sets had at least seven samples in each data set when grouped by disturbance category and potential site class. This is adequate for deriving distribution quantiles and DE, though 10 or more are preferred. For validation, at least eight sites per data set is preferred. The West LD validation data set and both LD and MD South Bluff validation data sets were insufficient for robust index validation. Validation in the Southeast and West bioregions are sufficient when the sub-regions are combined.

5.3 Defining preliminary site classification

The four category bioregional framework developed in the previous M-BISQ recalibration (Table 7) (Jessup and Stribling 2008) served as the basis for evaluating the site classification, thus serving as the preliminary framework for spatial distribution of LD and MD sites. The primary

Table 6. Stressor and stressor source criteria for definition of least disturbed (LD) and most disturbed (MD) sites.

PrelimGroup	Natural % Catchment	Natural % Buffer	Habitat Score	Chloride mg/L	NPDES km upstream	DO mg/L	NO ₃ NO ₂ mg/L
LD criteria							
1 or 2	>50	>60	>100	<10	>5	>7	<0.5
3	>70	>80	>110	<10	>5	>7	<0.5
4	>70	>80	>110	<10	>5	>7	<0.3
5	>70	>80	>110	<30	>5	>7	<0.3
6	>70	>80	>100	<30	>5	>7	<0.3
MD criteria							
1 or 2	<20	<20	<60	>30		<5	>1
3, 4, 5, or 6	<40	<40	<60	>30		<5	>1

question investigated is the potential need for isolating a class for blackwater streams in the southeast.

5.4 Evaluating taxonomic groupings

We used multivariate/ordination analysis (non-metric multidimensional scaling [NMS]) of operational taxonomic units (OTU) and graphical analysis of biological and physical habitat measures to evaluate degrees of biological fidelity (Boesch 1977, Tichý et al. 2010) of potential classes relative to taxonomic groupings. All 132 LD sites were used in ordinations to find and test groupings based on taxonomic composition and in box plots of metric distributions to test whether classes have different metric values. The blackwater sites were identified in the Southeast class and the southern third of the East class. Specific blackwater streams were identified by MDEQ staff familiar with the specific sampling sites. Stream color, pH, conductivity, substrate, and surrounding vegetation were considered in the designations. For purposes of this analysis, once the specific blackwater streams were identified, the region they occupied was also considered as a blackwater region, regardless of the known blackwater characteristics.

5.5 Metric and index testing and selection

We calculated more than 100 candidate metrics in MSAccess, and R to generate all possible eight metric combinations (models) for each of the bioregions. Using 16 – 25 candidate metrics per bioregion, approximately 0.2 to 1.8 million models were generated for each. Those models including two or more correlated metrics ($-0.7 \leq r^2 \leq 0.7$) were excluded from consideration. Models were also screened and preference given to those:

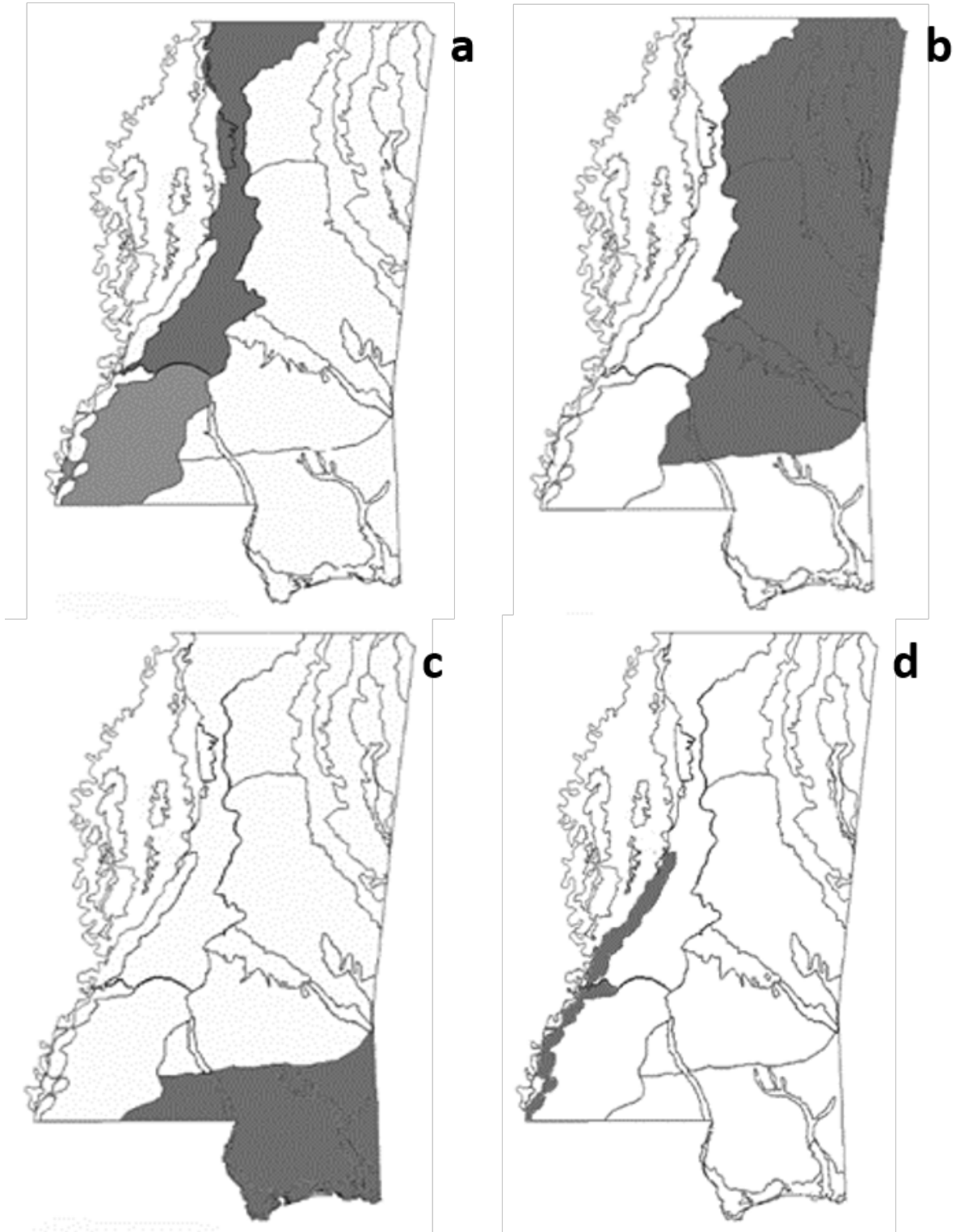


Figure 1. Bioregions of Mississippi for application of the M-BISQ; a, West; b, East; c, Southeast; and d, South Bluff.

Table 7. Bioregional classification (Jessup and Stribling 2008) and associated Level 4 subcoregions of Mississippi.

Bioregion	Subcoregions (EPA Level 4)	Description/Remarks
West	74b, 74c, and northern 74a	Loess Plains, northern Bluff Hills (West), and Southwest
East	65a, 65b, 65e, 65i, 65j, 65r, 65q, and parts of 65p	Includes the eastern subcoregions (Northeast, parts of the East-Central)
Southeast	65f, 75a, and parts of 65p	Southeast
South Bluff	southern sections of 74a	Southern Bluff Hills

- With improved DE relative to that for the M-BISQ2008
- With set of metrics representing a higher number of categories:
 - taxonomic richness
 - stressor tolerance
 - functional feeding group
 - composition
- Minimizing the number of metrics
- With individual metrics having the following characteristics:
 - Lower coefficient of variability (CV)
 - Higher overall DE for dataset
 - Were included in M-BISQ 2008
 - More straightforward calculations

Following these filters, we selected three models for each bioregion for detailed review.

With MSAcess and for each site class, we tested each metric and index to evaluate strength of response to stressor conditions (sensitivity) using discrimination efficiency (DE), which is calculated as:

$$DE = \frac{a}{b} * 100$$

where *a* is the number of *a priori* stressor sites identified as being below the degradation threshold (25th percentile of the LD site distribution), and *b* is the total number of stressor sites (Bressler et al. 2006, Stribling 2011, Flotemersch et al. 2006). Metrics exhibiting the highest DE per site class (generally, >65%) were combined into a series of different composite index formulations (multimetric indexes [MMI]), and trials run to quantify strength of response of the individual candidate indexes.

A second measure of metric discrimination was the Z-score, which was calculated as the difference between LD and MD metric or index values divided by the standard deviation of LD. The Z-score is similar to Cohen's D (Cohen 1992) and gives a combined measure of index sensitivity and precision. There is no single Z-score value that is used to indicate adequate metric performance, but generally higher scores suggest better separation of LD and MD values. Cohen proposed that Z values ≥ 0.80 indicated a "large" effect.

We used DE and Z-scores instead of a *t*-test or signal:noise ratio because they reflect the differences in distributions at critical potential threshold levels and incorporate precision of the reference (LD) distribution. The DE is an estimate of the percentage of correct impaired assessments and can be interpreted for management applications. While the *t*-test has been used elsewhere (Stoddard et al. 2008), we did not use it because we are not testing a hypothesis about the difference between reference and stressed sites.

5.6 Defining final site classification

Distinctness of metric and index response ranges between and among candidate site classes is used to determine whether the grouping should be maintained in the final site classification. For this recalibration effort, we tested the existing four category bioregional classification of west, east, southeast, and south bluff, and investigated the potential of a separate class for blackwater streams.

5.7 Recalibration and validation

Sampling and assessment results from 2001 – 2012 were used for index development (DEV) and those from 2013 – 2014 for validation (VAL). The DEV dataset was used to go through the above process to arrive at final models (multimetric indexes) for each bioregion. The VAL dataset was used to compare metric and index sensitivity (discrimination efficiency) to those from DEV.

6. RESULTS

6.1 Least- and most-disturbed sites

There were 132 LD and 227 MD sites identified, with 581 sites not meeting criteria for either categorized as other (Table 8). Bioregion East is the largest class and is represented by 490 samples, with 62 LD sites and 105 MD sites that were used for DEV and 16 and 22, respectively, used for VAL. The other bioregions have much smaller numbers of sites categorized as LD and MD, ranging from 21 and 56 in Bioregion West to 10 and 11 in Bioregion South Bluff. There are no LD or MD sites that can be used for VAL in Bioregion South Bluff.

6.2 Site classification based on taxonomic groupings and metric comparisons

Blackwater sites (n=108) were identified as a potential subcategory of Bioregion Southeast and the southern portion of Bioregion East (Figure 2). These were acidic, low gradient streams with tannic coloring due to needle fall from surrounding evergreen vegetation, suspected to be unique from other streams in the two bioregions. Similar blackwater streams are recognized as a unique bio-assessment site class in the New Jersey Pinelands (Jessup et al. 2005). NMS ordination of LD sites showed that there is little overlap between sites labelled as blackwater in the two bioregions (Figure 3), and thus, little support for their being considered a separate site class. The Southeast class encompasses the region where most of the blackwater is located, and LD sites in the Southeast are distinct from the other classes. The LD blackwater sites have slightly higher taxa richness (total, EPT, clinger, and intolerant) compared to those designated as unknown. They also have slightly higher metric values for percent individuals as EPT (*pi_EPT*) and percent individuals as scrapers FFG (*pi_ffg_scrap*) (Figures 4, 5). In the NMS ordination with taxa presence/absence, the site classes were more distinct than the blackwater designations (Figure 3). The majority of LD sites in Bioregion East are designated as non-blackwater; some known blackwater sites are located in the southern approximate 1/3 of the bioregion (Figure 2). There are only minimal distinctions between blackwater and unknown sites, including similar metric distributions (Figures 3, 4). LD sites in Bioregion South Bluff are largely distinct from most other sites (Figure 3), though overlapping somewhat with LD sites from Bioregion West. Metrics in Bioregion South Bluff exhibit low number of stressor intolerant taxa (*nt_intol*) and have high values for the Hilsenhoff Biotic Index (*x_HBI*) (Figure 5). There are similarities of the Bioregion West LD sites with those in both Bioregions East and South Bluff (Figure 3). The former has overall lower values for LD sites than Bioregion East LD, specifically for number of taxa as EPT taxa (*nt_EPT*), number of taxa as intolerant (*nt_intol*), and number of taxa as clingers (*nt_hab_clngr*) (Figures 4, 5). Bioregion West LD sites have lower values for HBI (*x_HBI*) as compared to Bioregion South Bluff (Figure 5). LD sites located in the northern and southern portions of Bioregion West have similar metric distributions, suggesting that it is appropriate as a single class.

Table 8. Sample sizes (number of sites) for data sets grouped by potential site class and disturbance category for development and validation analyses.

Reference status	Bioregions						TOTAL
	Southeast		East	West	South Bluff		
	Blackwater	Unknown	South	North			
	Development						
Least disturbed	8	7	62	7	8	10	102
Other	56	56	251	61	78	18	520
Most disturbed	8	12	104	15	28	11	178
<i>Sub-Total</i>	72	75	417	83	114	39	800
Validation							
Least disturbed	3	5	16	3	3	0	30
Other	2	8	35	8	4	4	61
Most disturbed	6	8	22	5	8	0	49
<i>Sub-Total</i>	8	16	73	13	12	4	110
TOTAL	83	96	490	99	129	43	940

The site classes established for the 2008 M-BISQ recalibration (Figure 1) were retained as possible site classes going forward. Though the East and West classes were overlapping in the ordination, they separated in the metric distributions. The north and south sub-classes of the West bioregion were not distinct in the metric distributions, but they were retained for testing in the index composition part of recalibration. The South Bluff and Southeast classes were clearly distinct in the ordinations and in some metric distributions. The blackwater and non-blackwater sites in the Southeast were retained as possible new sub-classes.

Metric and index performance in a potential site class encompassing blackwater streams was not substantially different from that in the overall classes for Bioregion Southeast or Bioregion East, and thus, it does not require a separate index. Also, the northern and southern subregions of Bioregion West had sufficient overlap with each other; similarly, Bioregion West will remain intact with a single index for assessments.

6.3 Metric and index testing and selection

With 16 – 25 candidate metrics, we used R-code to generate approximately 0.2 to 1.8 million index models for each bioregion (Table 9). The initial screen of the models was a redundancy analysis, which excluded those index models with highly correlated metrics ($|r| \geq 0.7$).

The 25th and 75th quantiles of metrics in the LD sites in each site class were identified and the percentage of MD metric values below the 25th quantile and above the 75th quantile were calculated as discrimination efficiencies (DE) for decreasing and increasing metric trends,

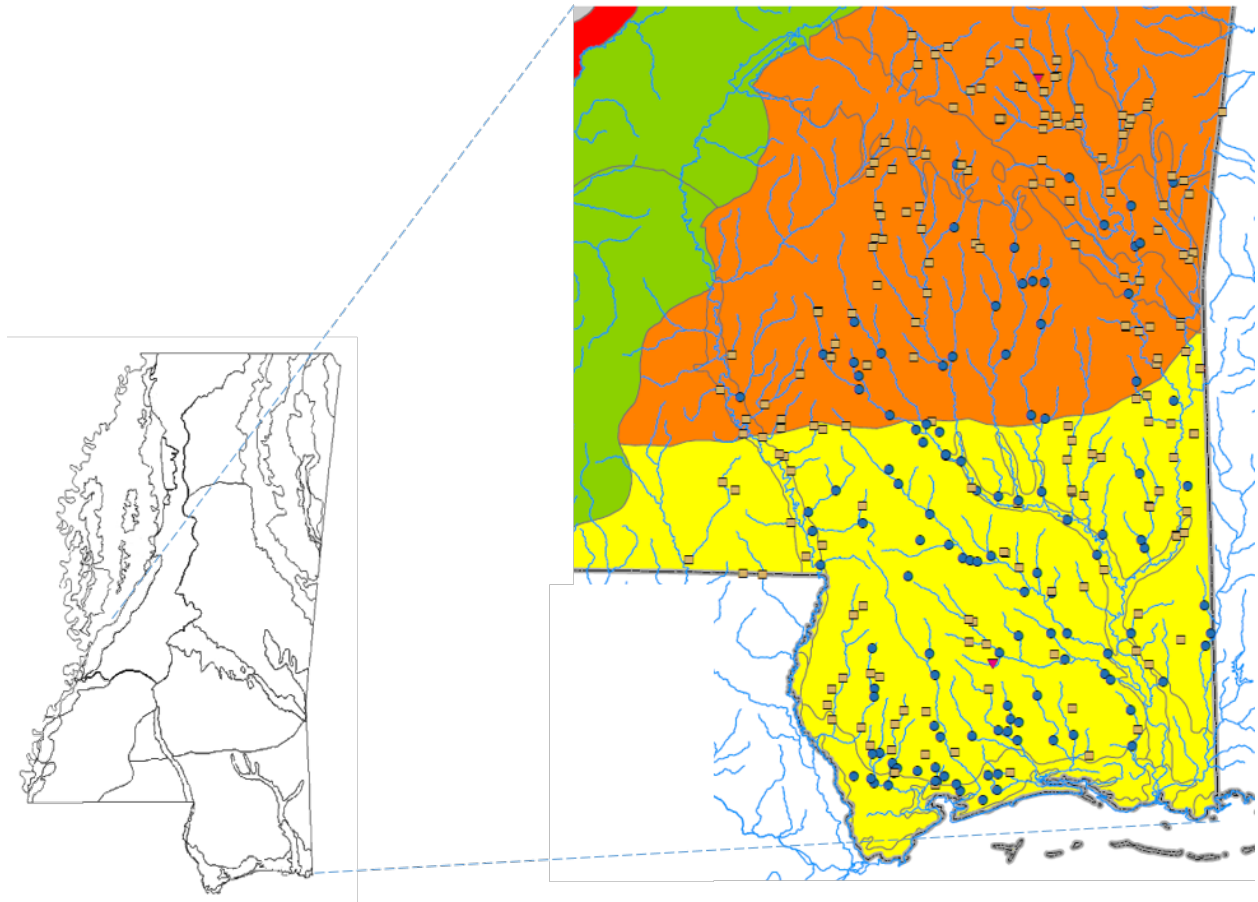


Figure 2. Distribution of actual or potential blackwater stream sites in southeastern Mississippi (Bioregion East, orange; Bioregion Southeast, yellow). Key: blue dots, known blackwater sites; unknown status, but in blackwater region; red triangles, known non-blackwater sites.

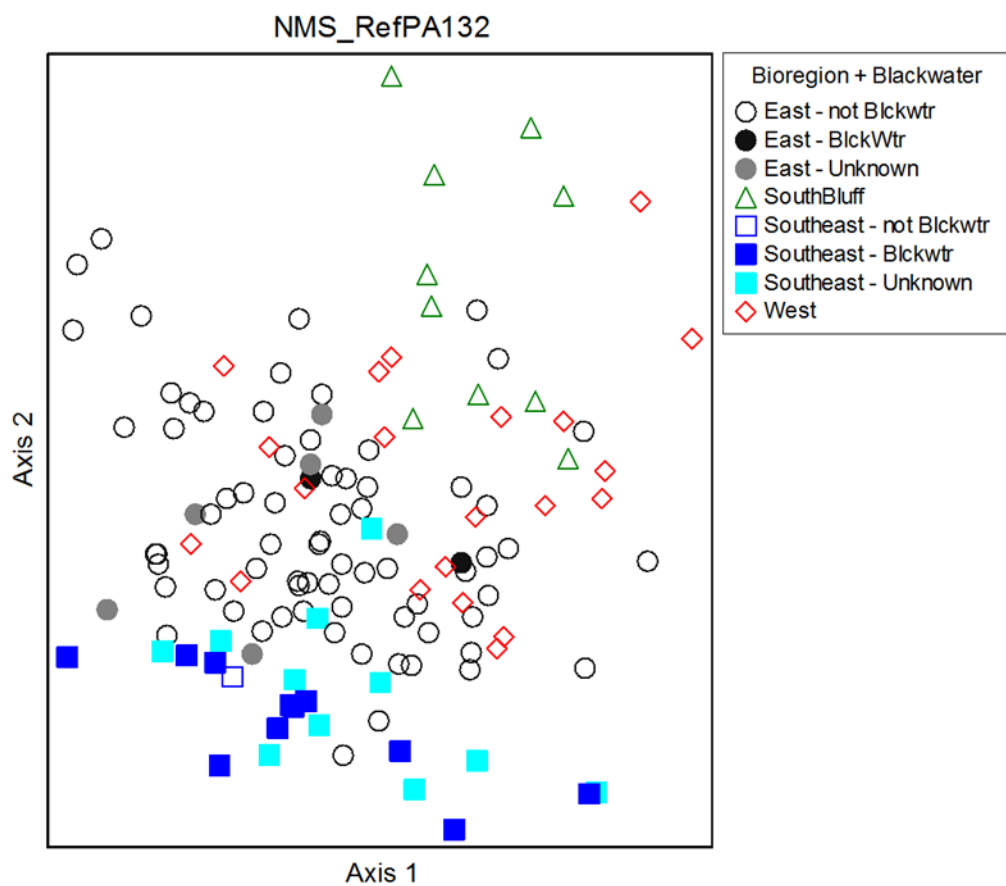


Figure 3. Non-metric multidimensional scaling (NMS) of sites in all bioregions relative to known designations as blackwater.

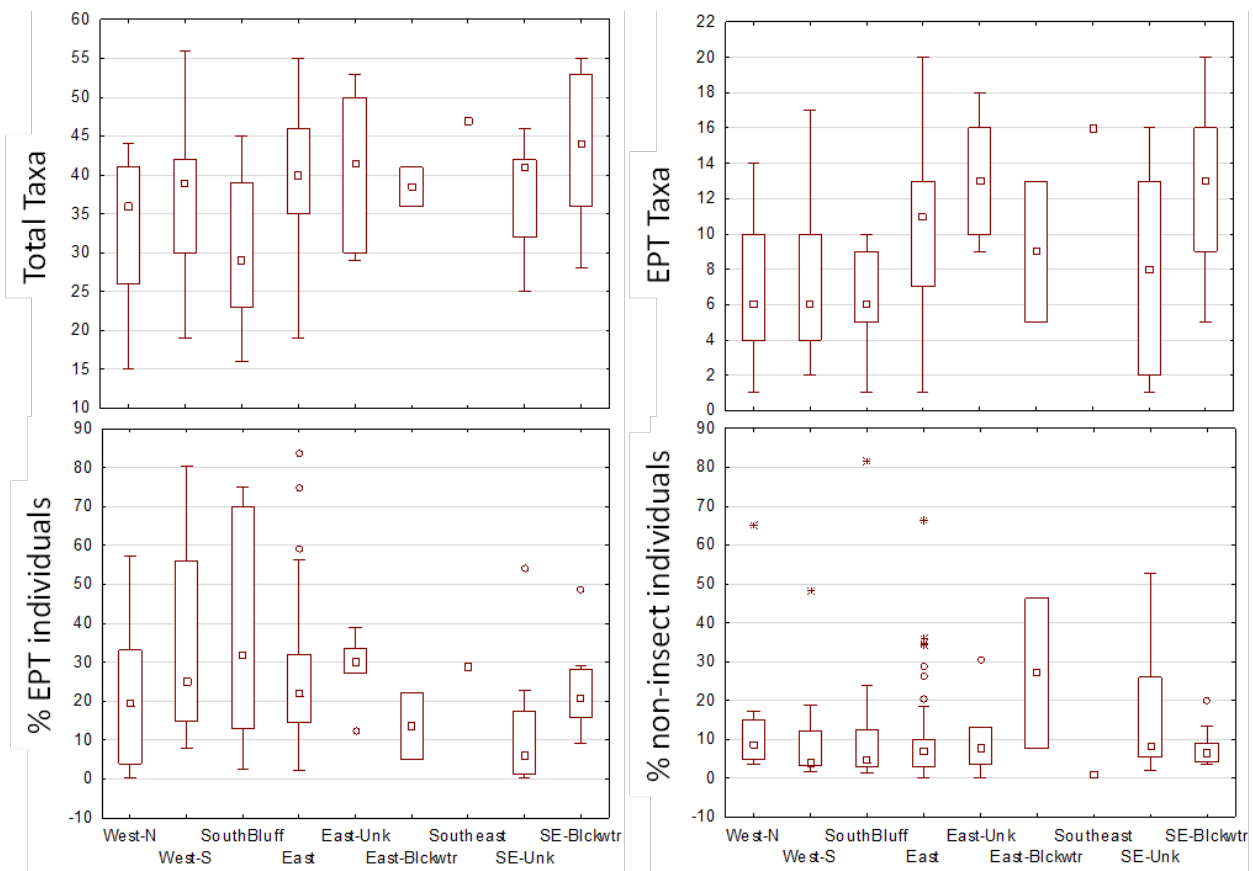


Figure 4. Metric value distributions within preliminary sites classes. Metrics shown are total taxa, EPT taxa, percent individuals as EPT, and percent individuals as non-Insects.

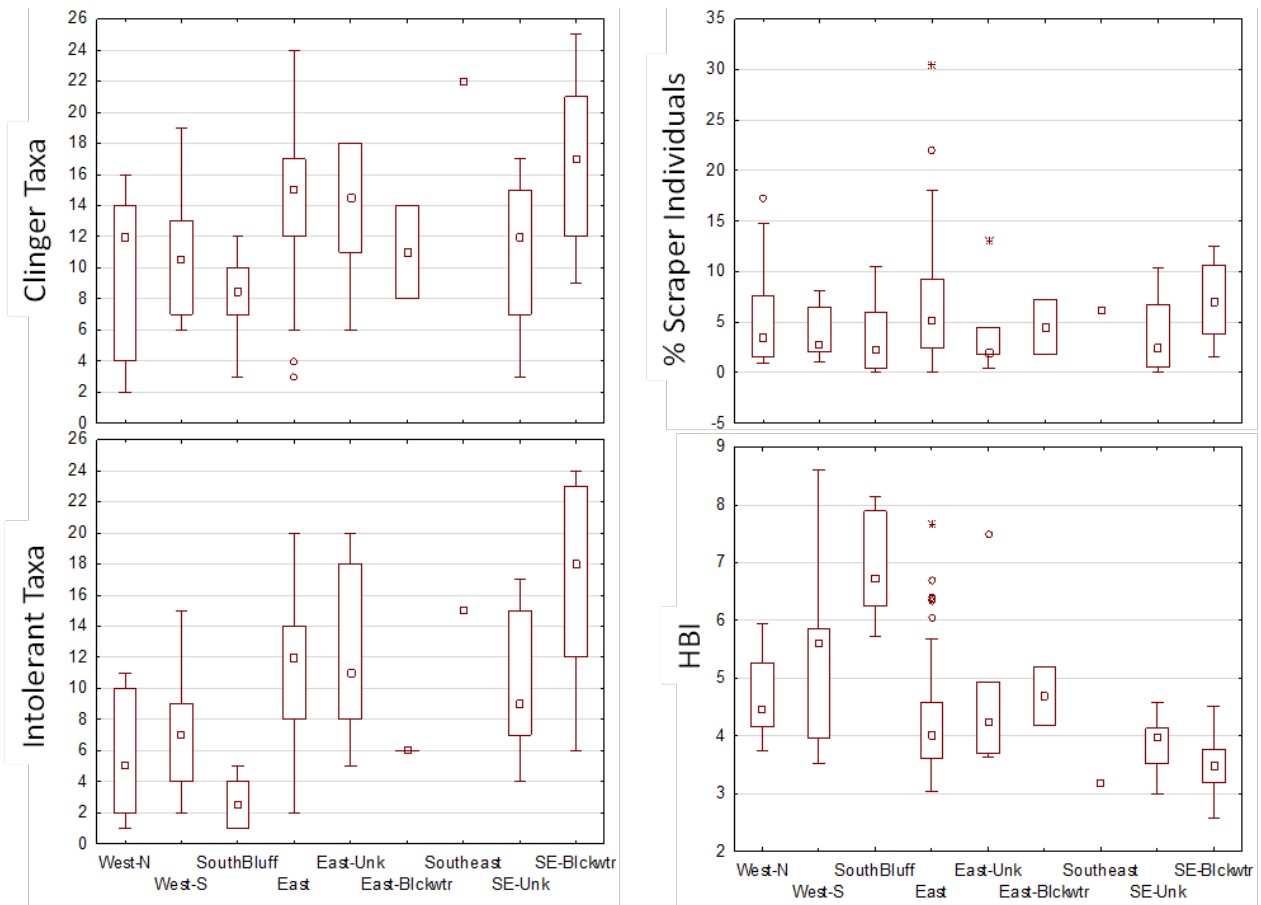


Figure 5. Metric value distributions within preliminary sites classes. Metrics shown are number of clinger taxa, percent individuals as scrapers, number of intolerant taxa, and Hilsenhoff biotic index (HBI).

Table 9. Numbers of candidate metrics, R code-generated models, and results of redundancy (correlation) analysis for each bioregion.

	Bioregion			
	West	Southeast	East	South bluff
Candidate metrics	16	21	22	25
Maximum metrics per model	8	8	8	8
Total no. models	39,202	401,929	600,369	1,807,780
Models without correlated* metrics	3,455	24,767	250,142	35,065

*Trial indexes excluded if metric correlations $|r| \geq 0.7$

respectively. The z-score was calculated as the difference in mean LD and MD metric values divided by the standard deviation of LD values. DE and z-scores were calculated for 121 metrics (Appendix Table B-1) within each of the four bioregions (Appendix Table B-2) and separately in each of the sub-classes of the West and Southeast bioregions (Appendix Table B-3).

Metric precision was also quantified using replicate samples collected from adjacent reaches of the same site on the same day. Using ANOVA in Statistica software, we calculated the mean squared error (MSE) for the sample pairs (replicates and duplicates), took the square root to establish the root mean squared error (RMSE), and calculated the coefficient of variability (CV) and 90% detectable difference (DD90) from the RMSE. This is the same procedure detailed in the 2008 M-BISQ report (Jessup and Stribling 2008). Precision results are shown in Appendix C.

For each bioregion, 15-24 candidate metrics were selected for inclusion in index trials based on DE, Z-score, and use in the 2008 M-BISQ. An “all subsets” routine in R was used to score metrics, combining up to eight for multiple index trials, and evaluating the performance of each using DE, Z-score, number of metric categories, and redundancy of component metrics.

In each bioregion, median index DE increased when more metrics were used (Figures 6-9). However, the highest DE were not follow the same pattern and were sometimes associated with indices with few metrics (e.g., in Bioregion West [Figure 1a, 6], the median DE increased with model orders 1-8, but the highest DEs were found in model orders 3, 4, and 6). Several index models had DE that were higher than those reported in the M-BISQ 2008 and even more were higher than the 50% (below that point, model performance is considered poor).

6.4 Final index recalibration and validation

The final indexes for each bioregion were selected subjectively from among the best performing options. Of the index alternatives tested, three of the best performers in each bioregion were scrutinized for application as the recalibrated index, M-BISQ2015. Performance was determined by the index DE and Z-score, minimal redundancy among component metrics, and the number of metric categories represented. Because the performance statistics were similar

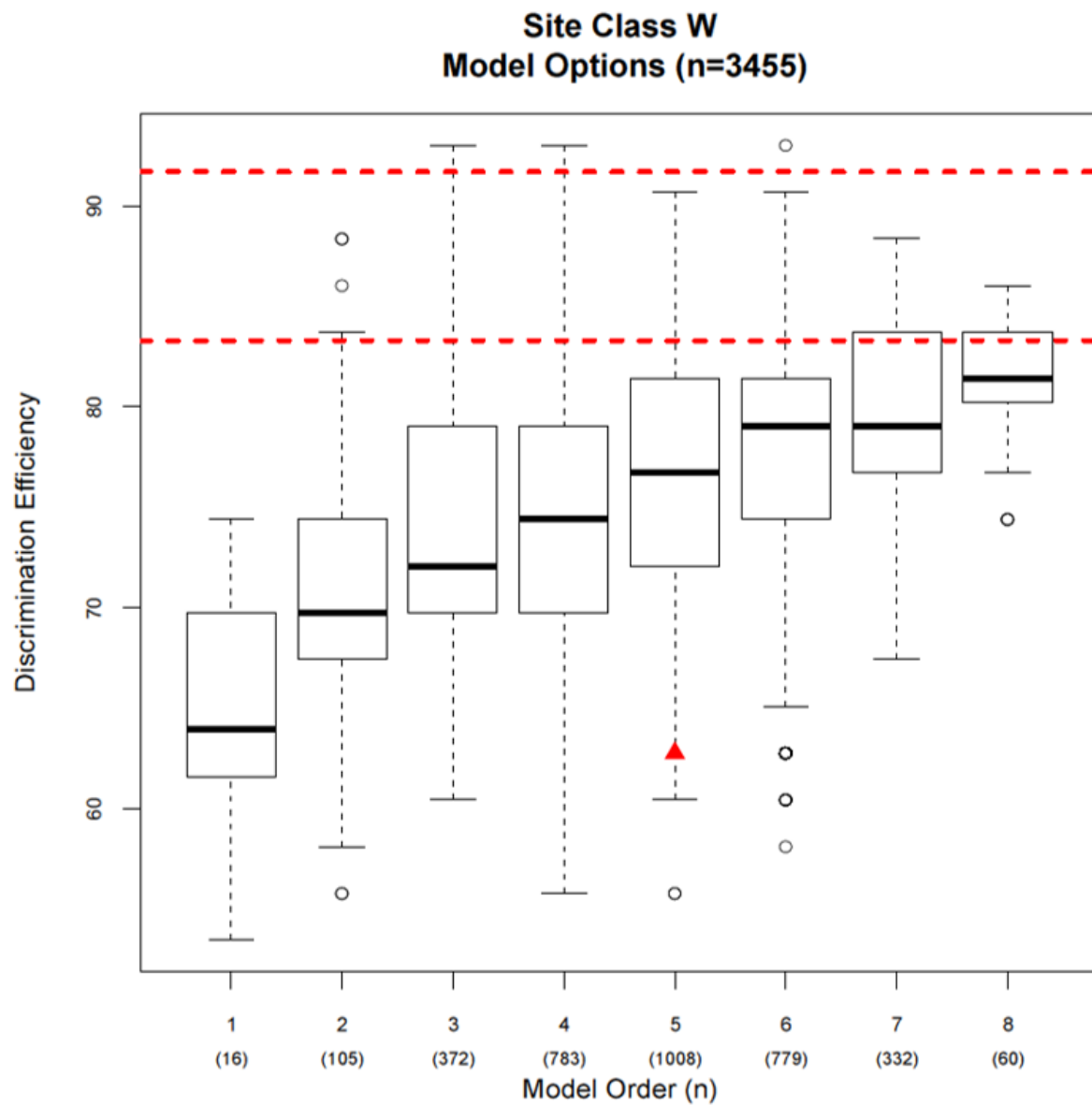


Figure 6. Boxplots of DE for all non-correlated models in Bioregion West. Red dashed lines illustrate the reported DE for the north and south subregions (M-BISQ2008). The red triangle is the M-BISQ 2008 index calculated with the dataset from this study.

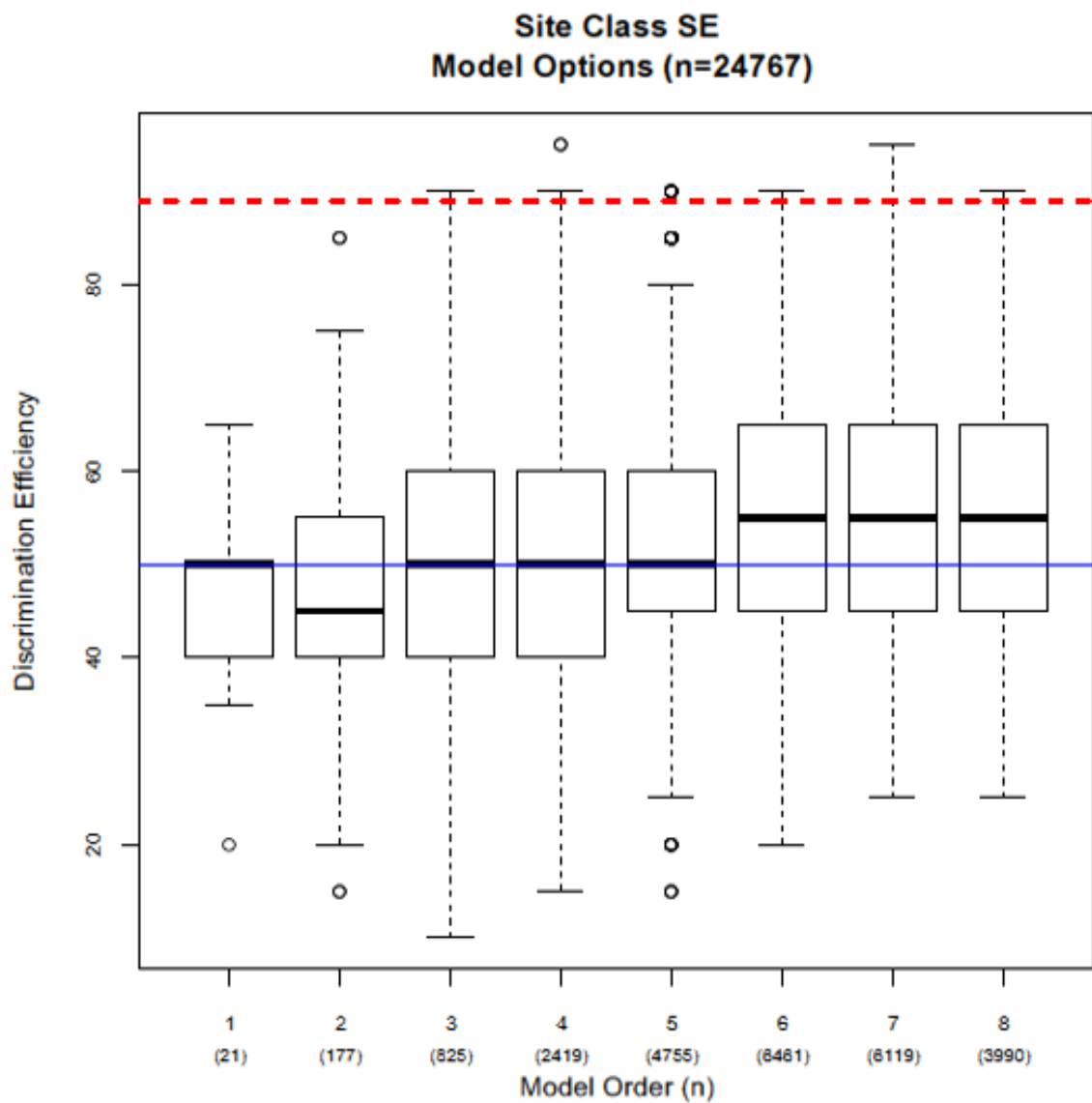


Figure 7. Boxplots of DE for all non-correlated models in Bioregion Southeast. Red dashed line illustrates DE of M-BISQ2008. Blue line is DE=50%.

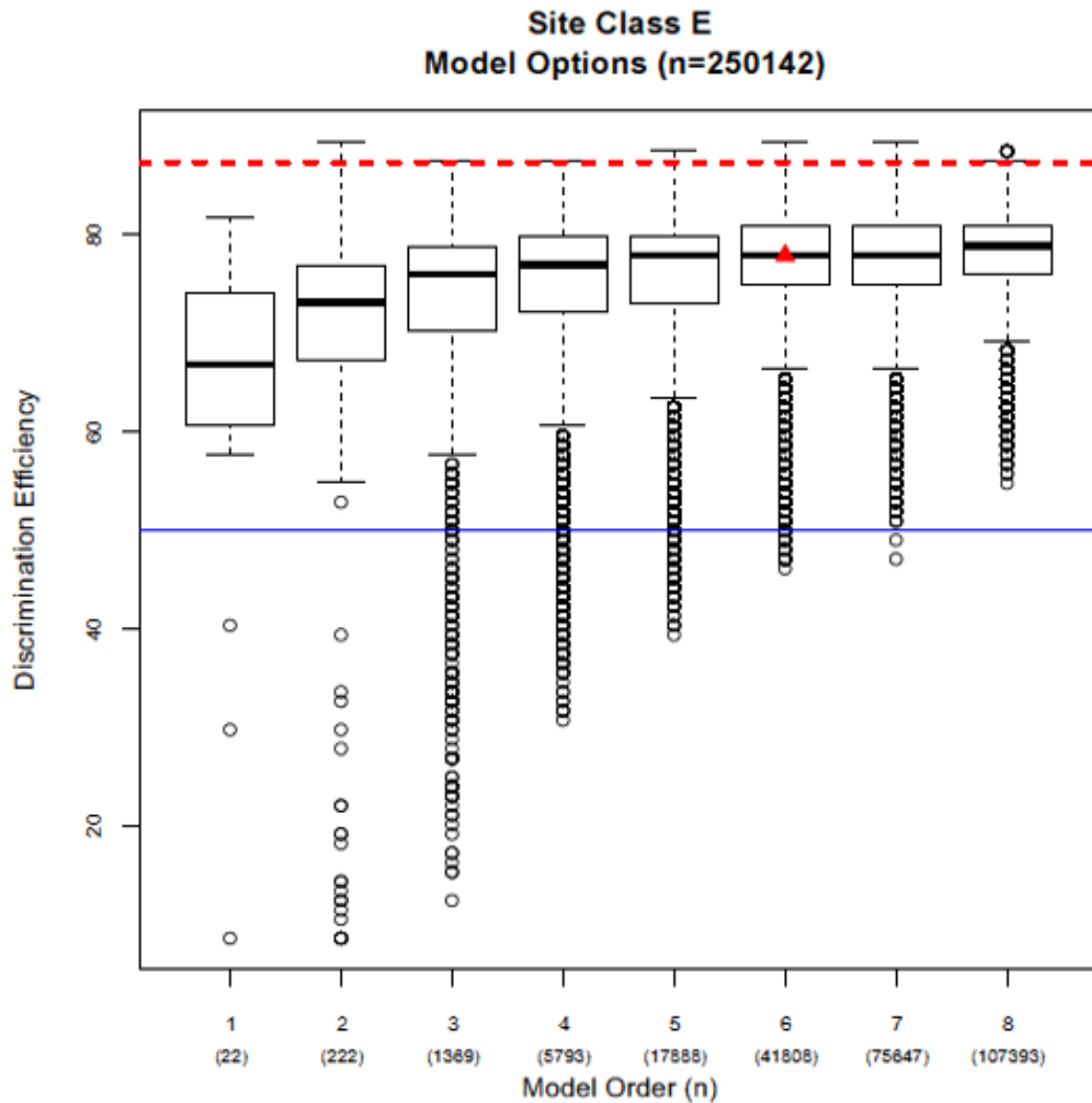


Figure 8. Boxplots of DE for all non-correlated models in Bioregion East. Red dashed line illustrates DE of M-BISQ2008. Blue line is DE=50%. The red triangle is the M-BISQ 2008 index calculated with the dataset from this study.

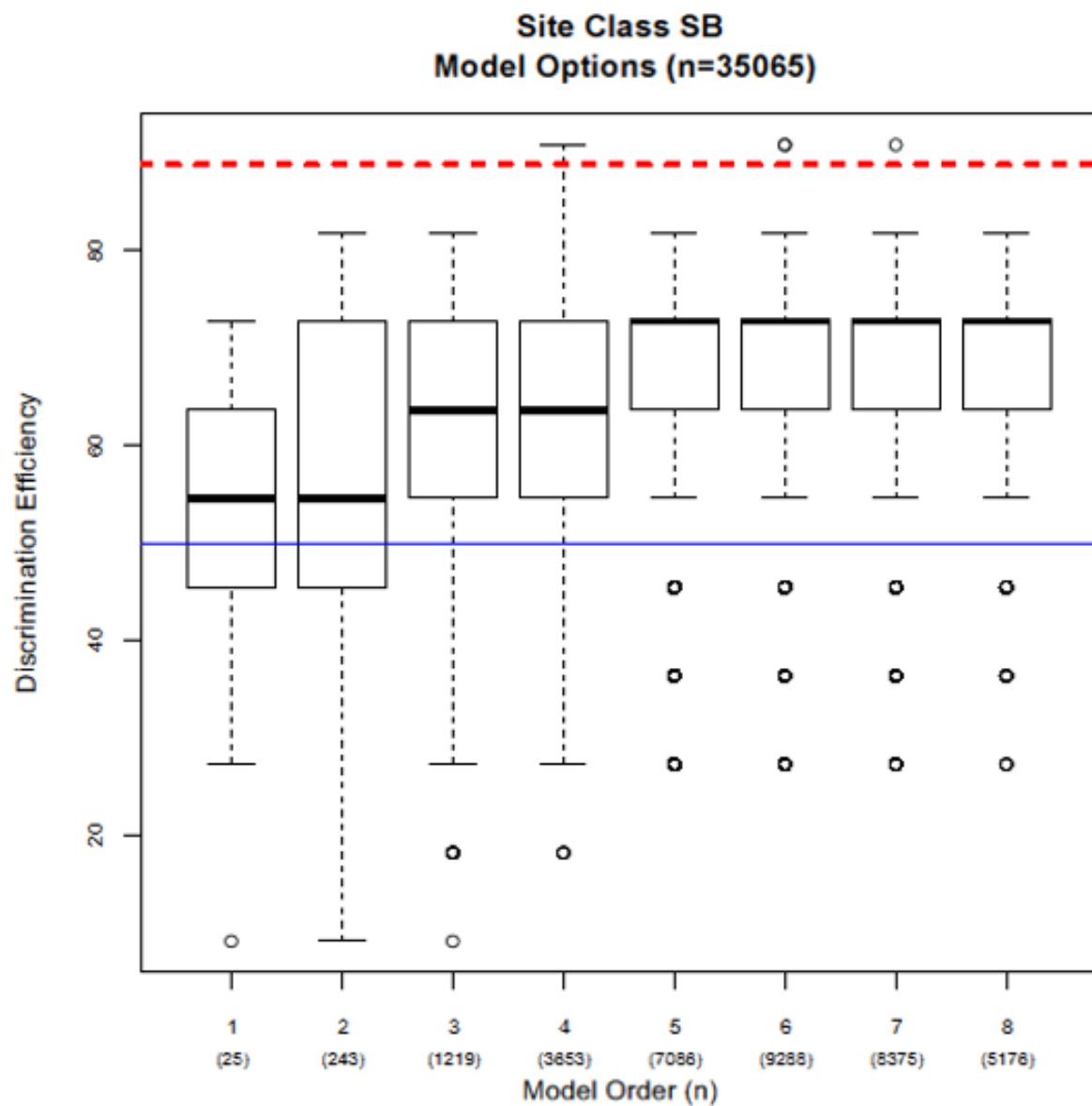


Figure 9. Boxplots of DE for all non-correlated models in Bioregion South Bluff. Red dashed line illustrates DE of M-BISQ2008. Blue line is DE=50%.

among the final candidate indices or tradeoffs in performance were evident (e.g., higher DE was associated with fewer metric categories), the final index selection was based not only on performance, but also on subjective preference for an index and the component metrics. MDEQ used subjective judgement and preferences for higher DE, maximum number of metric categories, lower variation (lower index CV), usage in the MBISQ 2008, and ability to calculate and communicate the metrics.

6.4.1 West Bioregion – Index Description

In the West bioregion (Figure 1a), 14 metrics were candidate for inclusion in the index (Table 10). Of the 3,455 combinations evaluated, three index options with similar performance statistics were finalists and one was selected as the final index for the West bioregion. The final index had seven metrics from four metric categories, a DE of 88.4, and a Z-score of 1.5 (Table 10). North and South divisions were not maintained because of similar performance and metric distributions in each area. The selected index did not include metrics from the habitat category because including them resulted in exclusion of other categories. The selected index was validated with 92% of MD validation sites having values less than the 25th percentile of development LD sites (Figure 10).

6.4.2 East Bioregion – Index Description

In the East bioregion (Figure 1b), 21 metrics were candidate for inclusion in the index (Table 11). Of the 250,142 combinations evaluated, three index options with similar performance statistics were finalists and one was selected as the final index for the East bioregion. The final index had seven metrics from four metric categories, a DE of 88.5, and a Z-score of 2.2 (Table 11). The selected index did not include metrics from the richness category. The options with a richness metric had fewer metrics overall and slightly lower Z-scores. The selected index was validated with 82% of MD validation sites having values less than the 25th percentile of development LD sites (Figure 11).

6.4.3 Southeast Bioregion – Index Description

In the Southeast bioregion (Figure 1c), 21 metrics were candidate for inclusion in the index (Table 12). Of the 24,767 combinations evaluated, four index options with similar performance statistics were finalists and one was selected as the final index for the East bioregion. The final index had six metrics from four metric categories, a DE of 70.0, and a Z-score of 1.2 (Table 12). The selected index did not include metrics from the richness category. The option with a richness metric had a slightly lower Z-score and was lacking a metric in the feeding group category. The selected index was validated with 92.9% of MD validation sites having values less than the 25th percentile of development LD sites (Figure 12).

6.4.4 South Bluff Bioregion – Index Description

In the South Bluff bioregion (Figure 1d), 21 metrics were candidate for inclusion in the index (Table 13). Of the 24,767 combinations evaluated, four index options with similar performance statistics were finalists and one was selected as the final index for the East bioregion. The final index had six metrics from five metric categories, a DE of 81.8 and a Z-score of 1.4 (Table 13). The selected index was not validated LD or MD sites because of low sample sizes from which all samples were used in calibration. The Other category had a distribution of validation index scores that resembled the development Other category (Figure 13).

Table 10. The best three index options for the West bioregion, also showing candidate metrics that were tested but not included. Asterisk (*) indicates the final index selected.

Category	Metric	Index Options			Metric Statistics		
		1*	2	3	RMSE	CV	DD90
FFG	nt_ffg_pred	x		x	2.2	25.3	3.7
Habit	nt_hab_sprwl		x		2.5	21.7	4.1
Composition	pi_Tanyp	x	x	x	1.6	60.7	2.6
Composition	pi_Colesens	x		x	2.1	64.5	3.4
Composition	pi_Pleco	x	x		2.1	54.5	3.5
Composition	pi_EPTsens				5.2	40.0	8.6
Richness	nt_Pleco	x	x	x	0.9	47.7	1.4
Richness	nt_total				5.4	15.1	8.9
Richness	nt_Insect				4.4	14.9	7.3
Tolerance	x_HBI	x		x	0.4	7.1	0.6
Tolerance	nt_intol				2.2	30.0	3.6
Tolerance	pt_toler				3.4	28.5	5.6
Tolerance	pt_tv_intol	x			4.4	23.3	7.2
Tolerance	x_BeckBI				3.4	22.6	5.7
DE		88.4	90.7	88.4			
Z-score		1.5	1.4	1.6			

Table 11. The best three index options for the East bioregion, also showing candidate metrics that were tested but not included. Asterisk (*) indicates the final index selected.

Category	Metric	Index Options			Metric Statistics		
		1	2*	3	RMSE	CV	DD90
FFG	pi_ffg_cllct	x	x	x	7.7	22.1	12.7
FFG	nt_ffg_pred		x		2.2	25.3	3.7
FFG	nt_ffg_shred				1.0	25.7	1.6
Habit	pi_hab_sprwl				6.4	19.1	10.5
Habit	pi_hab_clngr	x	x	x	8.2	21.2	13.4

Category	Metric	Index Options			Metric Statistics		
		1	2*	3	RMSE	CV	DD90
Habit	nt_hab_clngr				2.4	20.6	4.0
Composition	pt_nonIns	x	x	x	5.0	28.6	8.2
Composition	pi_COC2Chi	x	x		6.4	55.0	10.5
Composition	pi_Pleco				2.1	54.5	3.5
Composition	pi_Chir.COC				8.0	22.9	13.2
Composition	pi_Trich				2.6	49.3	4.3
Composition	pi_EPTsens				5.2	40.0	8.6
Composition	pi_EphemNoCaen				4.3	51.8	7.1
Composition	pi_dom01				8.4	29.3	13.8
Richness	nt_EPT	x		x	1.9	23.1	3.1
Richness	nt_total				5.4	15.1	8.9
Richness	nt_Insect				4.4	14.9	7.3
Tolerance	pt_tv_intol	x		x	4.4	23.3	7.2
Tolerance	pt_toler		x	x	3.4	28.5	5.6
Tolerance	x_HBI				0.4	7.1	0.6
Tolerance	x_BeckBI		x		3.4	22.6	5.7
DE		88.5	88.5	87.5			
Z-score		2.1	2.2	2.0			

Table 12. The best four index options for the Southeast bioregion, also showing candidate metrics that were tested but not included. Asterisk (*) indicates the final index selected.

Category	Metric	Index Options				Metric Statistics		
		1	2*	3	4	RMSE	CV	DD90
FFG	nt_ffg_cllct					3.1	22.9	5.2
FFG	nt_ffg_shred	x				1.0	25.7	1.6
FFG	pi_ffg_pred		x	x		4.2	31.6	6.9
Habit	nt_hab_clmbr	x	x	x	x	1.3	38.1	2.1
Habit	pi_hab_clngr	x	x	x	x	8.2	21.2	13.4
Habit	nt_hab_sprwl					2.5	21.7	4.1
Composition	pi_COC2Chi	x	x		x	6.4	55.0	10.5
Composition	pi_Coleo	x				2.3	55.1	3.7
Composition	pt_nonIns					5.0	28.6	8.2
Composition	pi_Pleco	x	x	x	x	2.1	54.5	3.5
Composition	pi_dom01					8.4	29.3	13.8
Richness	nt_Trich					1.1	39.4	1.9
Richness	nt_Pleco					0.9	47.7	1.4

Category	Metric	Index Options				Metric Statistics		
		1	2*	3	4	RMSE	CV	DD90
Richness	nt_total				x	5.4	15.1	8.9
Tolerance	x_HBI	x	x	x	x	0.4	7.1	0.6
	DE	70	70	70	70			
	Z-score	1.0	1.2	1.0	1.1			

Table 13. The best four index options for the South Bluff bioregion, also showing candidate metrics that were tested but not included. Asterisk (*) indicates the final index selected.

Category	Metric	Index Options				Metric Statistics		
		1	2	3	4*	RMSE	CV	DD90
FFG	nt_ffg_pred					2.2	25.3	3.7
FFG	nt_ffg_shred	x	x	x	x	1.0	25.7	1.6
FFG	nt_ffg_cllct	x				3.1	22.9	5.2
Habit	pi_hab_swmmr					1.6	62.6	2.6
Habit	pi_hab_brrwr	x		x	x	5.4	62.2	8.9
Habit	pi_hab_sprwl		x			6.4	19.1	10.5
Composition	pi_Colesens	x		x	x	2.1	64.5	3.4
Composition	pi_Crus					3.6	62.2	5.9
Composition	pi_Odon					2.3	65.2	3.8
Composition	pi_CruMol		x			5.2	58.0	8.6
Composition	pt_nonIns			x		5.0	28.6	8.2
Composition	pi_EPTsens					5.2	40.0	8.6
Composition	pi_Pleco					2.1	54.5	3.5
Richness	nt_Trich	x	x	x		1.1	39.4	1.9
Richness	nt_Oligo					1.3	58.3	2.2
Richness	nt_EPT	x			x	1.9	23.1	3.1
Richness	nt_POET					2.5	23.3	4.2
Richness	nt_Pleco					0.9	47.7	1.4
Richness	nt_nonInsect					2.1	34.6	3.4
Tolerance	x_BeckBI	x	x	x	x	3.4	22.6	5.7
Tolerance	pt_toler					3.4	28.5	5.6
	DE	81.8	81.8	81.8	81.8			
	Z-score	1.2	1.8	1.5	1.4			

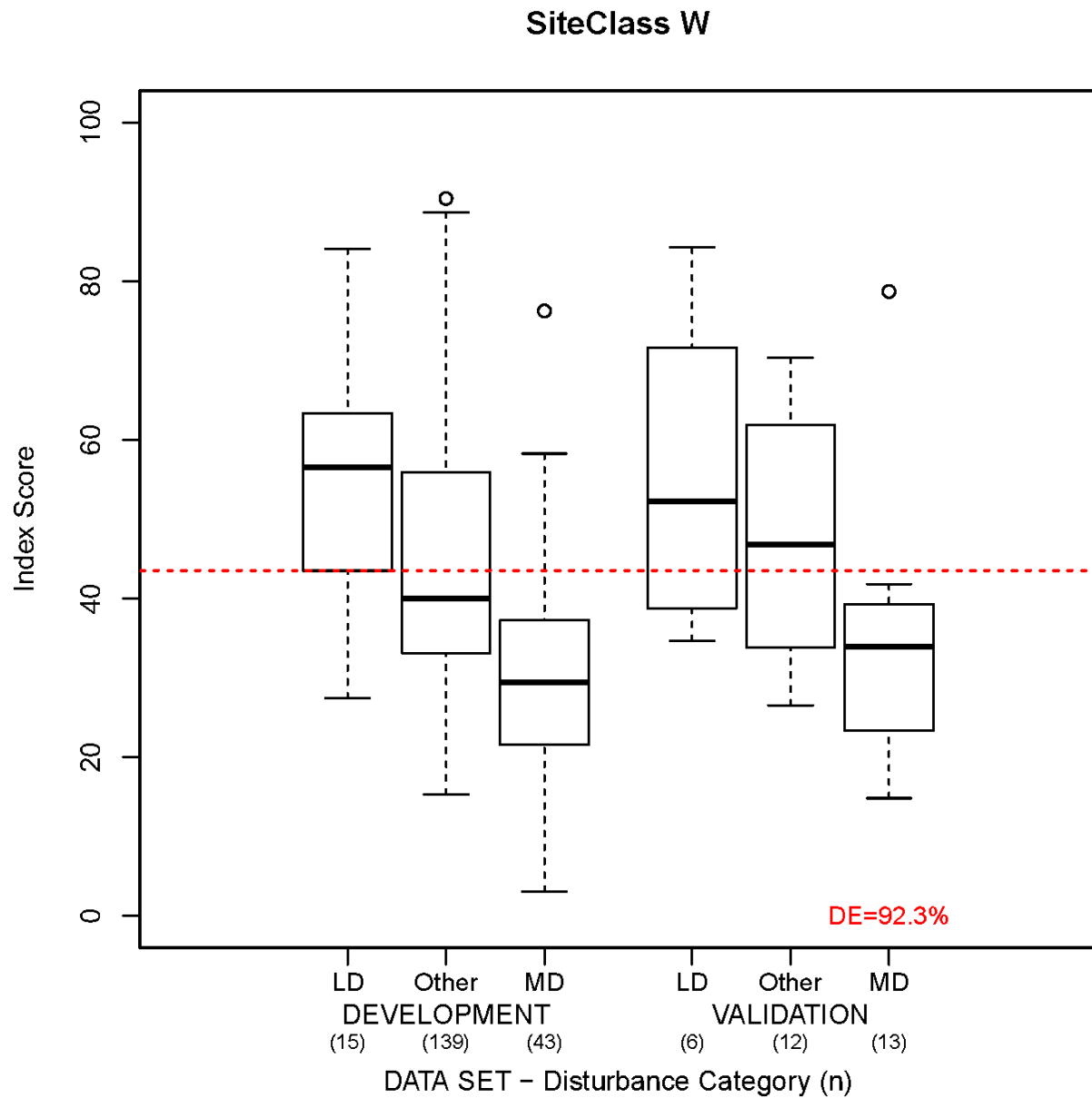


Figure 10. Boxplots index values in LD, MD, and other sites in Bioregion West, showing development (D) and validation (V) datasets. Red dashed line illustrates the 25th percentile of development reference index values, to which the validation distributions were compared.

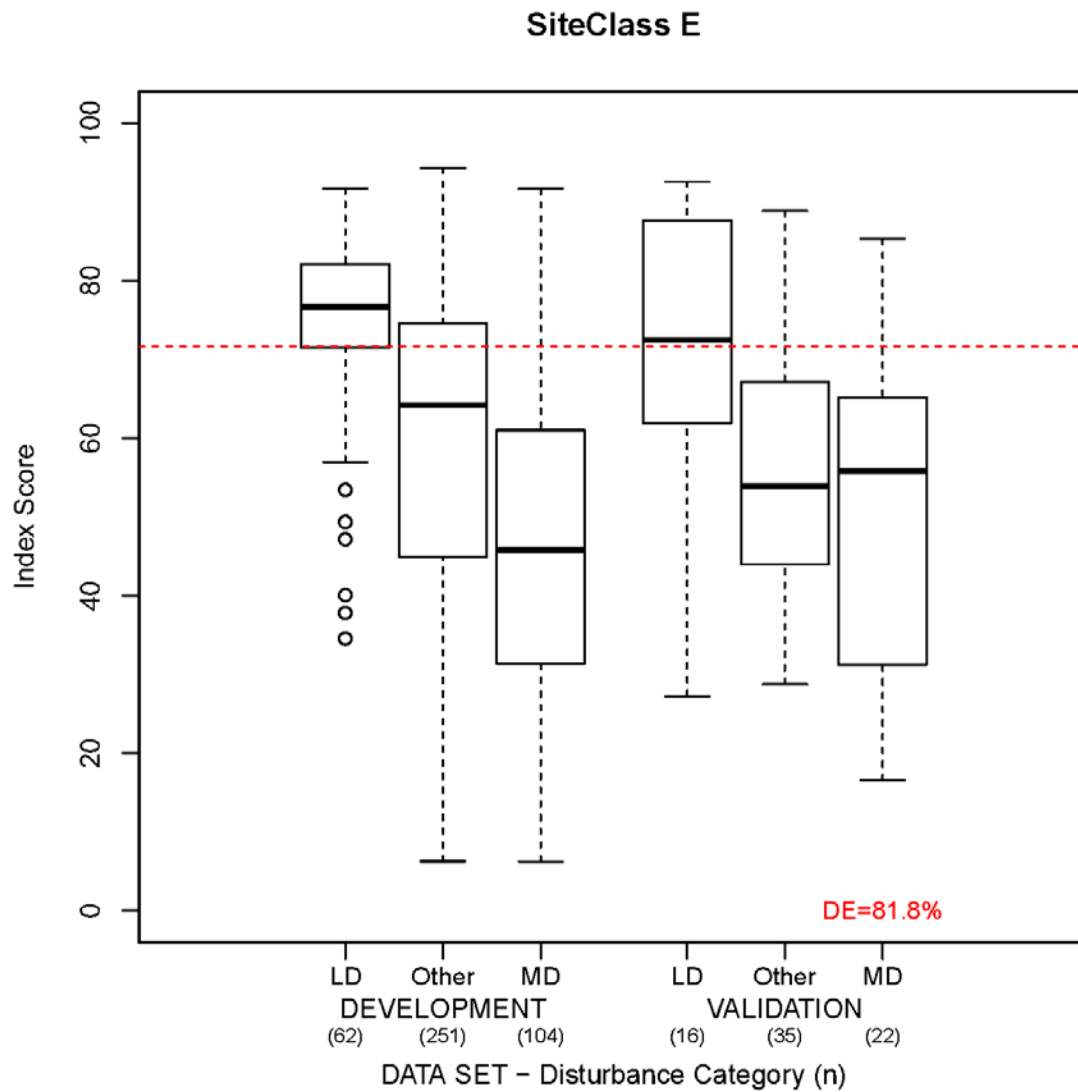


Figure 11. Boxplots index values in LD, MD, and other sites in Bioregion East, showing development (D) and validation (V) datasets. Red dashed line illustrates the 25th percentile of development reference index values, to which the validation distributions were compared.

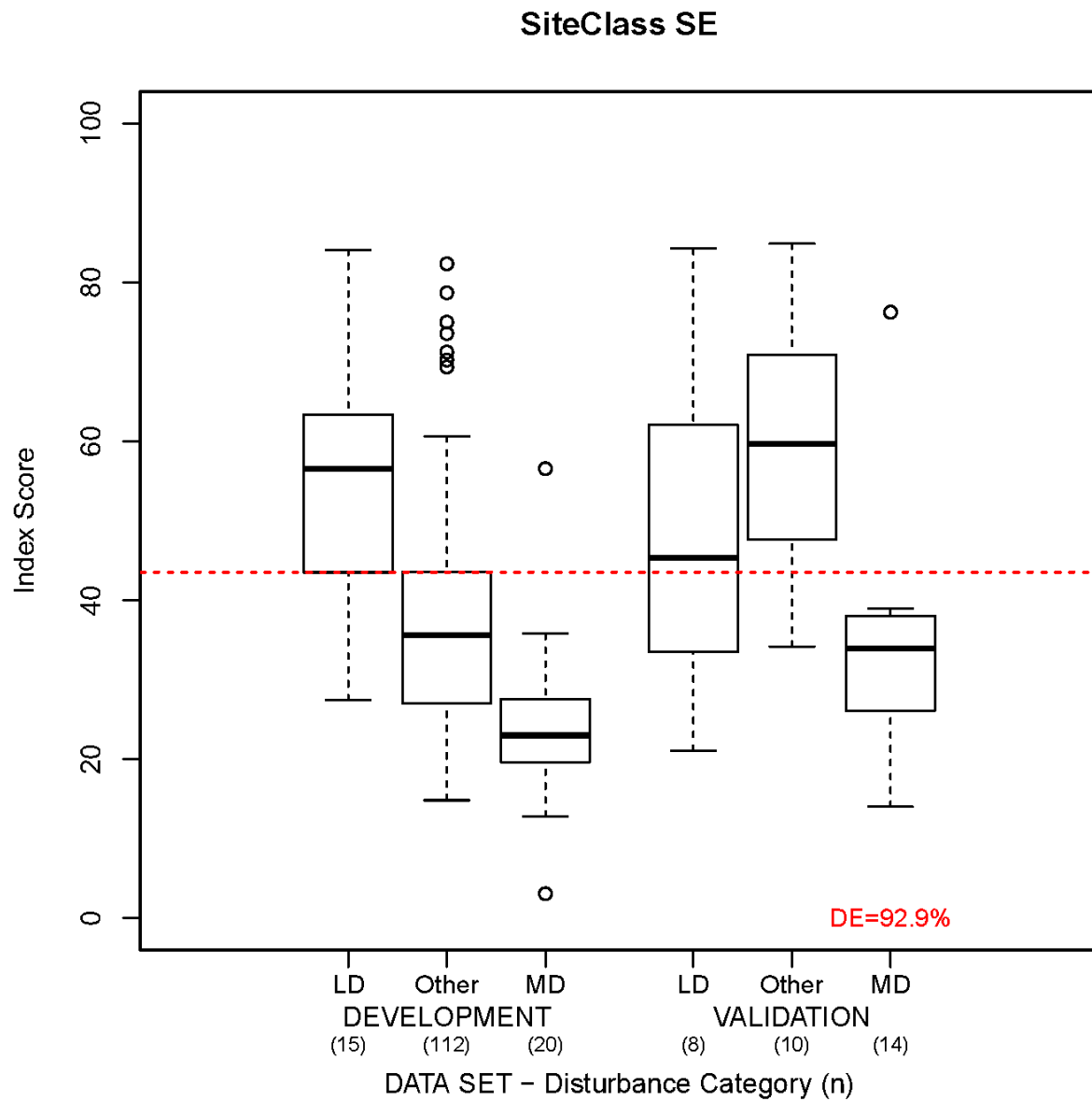


Figure 12. Boxplots of index values in LD, MD, and other sites in Bioregion Southeast, showing development (D) and validation (V) datasets. Red dashed line illustrates the 25th percentile of development reference index values, to which the validation distributions were compared.

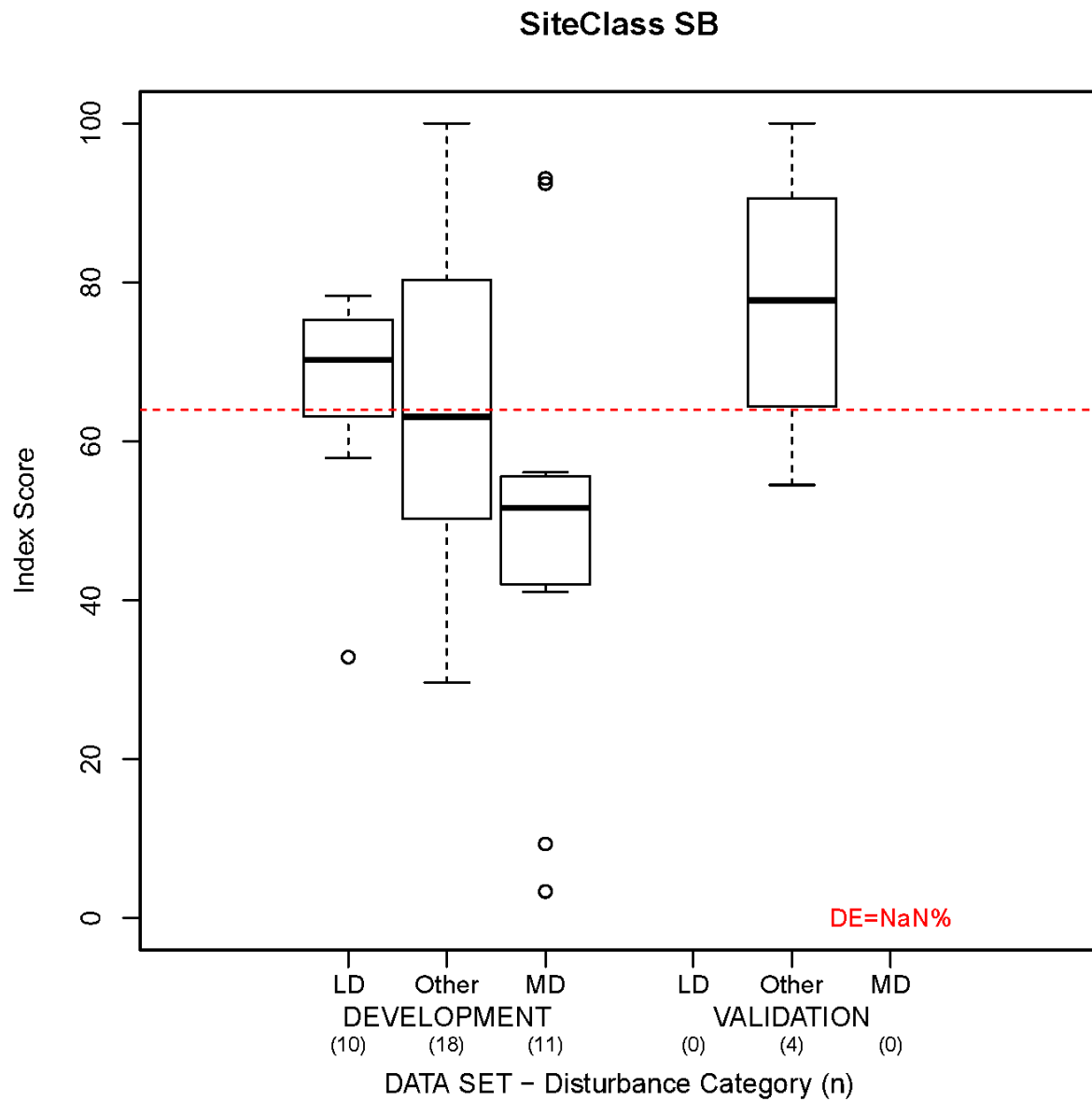


Figure 13. Boxplots index values in LD, MD, and other sites in Bioregion South Bluff, showing development (D) and validation (V) datasets. Red dashed line illustrates the 25th percentile of development reference index values, to which the validation distributions were compared.

5. DISCUSSION AND INDEX APPLICATION

Application of the M-BISQ requires use of data of known quality, produced from benthic macroinvertebrate samples collected and processed in adherence to field and laboratory standard procedures (Appendix D). Once metrics for each bioregion-specific index are calculated, the metric values can be converted to scores using formulas (Table 14) that will place each on a 100-point scale. The final index is an average of the scores. If the formula for an individual metric results in a score outside of the 0-100 range, the score is re-set to the closest extreme (0 or 100) before being averaged.

The 25th percentile of LD index scores is used as the threshold for indicating acceptable biological conditions similar to conditions observed in LD sites of the same class (Table 15). Index values above the threshold are assessed as supporting aquatic life uses, while those below indicate biological degradation. Any reported M-BISQ values should be supported with the data quality information associated with each bioregional index, including DE to communicate index accuracy and the DD90 to communicate index precision. By following these guidelines, it is valid to compare index results to the bioregional degradation thresholds (Table 15) for rating stream conditions. Additionally, using sample data from appropriately executed repeat sampling, detectable difference (DD) can be calculated and used to determine the significance of differences in an index score over time (Time A to Time B), or for different locations in the same stream (Point A to Point B) (Stribling et al. 2008, Stark 1993). For example, for Bioregion East, the 90 percent detectable difference (DD90) is 5.7, indicating that two M-BISQ scores differing more than that are significantly different with 90% confidence. This information is important for evaluating effectiveness of stressor control activities in terms of biological response.

Other uses of M-BISQ assessment results include investigations into causes of biological degradation, and application to understanding biological potential or restoration goals. Stressor identification (SI) and causal analysis help determine causes of stream degradation so that the most appropriate environmental management actions can be designed and implemented (Norton et al. 2014). Differences in index scores and site degradation ratings are the impetus for initiating the process. Part of the SI process is determining the relationship of site environmental characteristics (physical, chemical, and hydrologic) to that of biological conditions. That investigation is enhanced by the nature of the M-BISQ, that is, by maintaining the capacity for disaggregating the index into individual benthic metrics and having direct access to raw sample data (list of taxa and number of individuals of each taxon), and their associated autecological attributes (stressor tolerance values, functional feeding groups, and habit). It is often useful to be able to quickly see which metric(s) is or are most influencing index score, and then, which taxa are most influencing those metrics. A biologist evaluating sample and site data at this level will often be able to determine, with some confidence, the type of stressors most likely causing biological degradation as well as the most probable sources of those stressors.

Table 14. Final metrics and scoring formulas for M-BISQ2015, by bioregion (E, East; SB, South Bluff; SE, Southeast; and W, West).

Bioregion	Metrics	Metric code	Scoring formulas
E	Number of taxa, predators	nt_ffg_pred	$100 * (\text{metric value}) / 14$
E	Percent individuals, <i>Cricotopus</i> , <i>Orthocladius</i> , and <i>Chironomus</i> of Chironomidae	pi_COC2Chi	$100 * (50 - (\text{metric value})) / 50$
E	Percent individuals, collectors	pi_ffg_cllct	$100 * (76.9 - (\text{metric value})) / 66.49$
E	Percent individuals, clingers	pi_hab_clngr	$100 * (\text{metric value}) / 73.99$
E	Percent taxa, non-Insecta	pt_nonIns	$100 * (37.64 - (\text{metric value})) / 32.9$
E	Percent taxa, tolerant	pt_toler	$100 * (30.4 - (\text{metric value})) / 28.6$
E	Beck's Biotic Index	x_BeckBI	$100 * (\text{metric value}) / 30$
SB	Number of taxa, Ephemeroptera, Plecoptera, and Trichoptera	nt_EPT	$100 * (\text{metric value}) / 10.9$
SB	Number of taxa, shredders	nt_ffg_shred	$100 * (\text{metric value}) / 6$
SB	Percent individuals, sensitive Coleoptera	pi_Colesens	$100 * (\text{metric value}) / 4.2$
SB	Percent individuals, burrowers	pi_hab_brrwr	$100 * (43.5 - (\text{metric value})) / 42.1$
SB	Beck's Biotic Index	x_BeckBI	$100 * (\text{metric value}) / 15$
SE	Percent individuals, predators	pi_ffg_pred	$100 * (\text{metric value}) / 24.7$
SE	Number of taxa, climbers	nt_hab_clmbr	$100 * (1 - (\text{metric value})) / -5$
SE	Percent individuals, clingers	pi_hab_clngr	$100 * (\text{metric value}) / 79.8$
SE	Percent individuals, <i>Cricotopus</i> , <i>Orthocladius</i> , and <i>Chironomus</i> of Chironomidae	pi_COC2Chi	$100 * (26.5 - (\text{metric value})) / 26.5$
SE	Percent individuals, Plecoptera	pi_Pleco	$100 * (\text{metric value}) / 10.9$
SE	Hilsenhoff Biotic Index	x_HBI	$100 * (5.1 - (\text{metric value})) / 2$
W	Number of taxa, predators	nt_ffg_pred	$100 * (\text{metric value}) / 14$
W	Number of taxa, Plecoptera	nt_Pleco	$100 * (\text{metric value}) / 4$
W	Percent individuals, sensitive Coleoptera	pi_Colesens	$100 * (\text{metric value}) / 7.5$
W	Percent individuals, Plecoptera	pi_Pleco	$100 * (\text{metric value}) / 11.9$
W	Percent individuals, Tanypodinae	pi_Tanyp	$100 * (8.3 - (\text{metric value})) / 8.3$
W	Percent taxa, intolerant	pt_tv_intol	$100 * (\text{metric value}) / 30.7$
W	Hilsenhoff Biotic Index	x_HBI	$100 * (7.5 - (\text{metric value})) / 3.8$

Table 15. Discrimination efficiency (DE), degradation threshold, and 90 percent detectable difference (DD90) of the M-BISQ bioregions and statewide.

Bioregion	DE	Degradation threshold	DD90
East	88.5	71.6	5.7
South Bluff	82	55.7	NA
Southeast	70	56.8	14.9
West	88.4	43.7	7.8
Statewide	NA	NA	8.6

Calibration of biological indexes for waterbody assessment requires some understanding of the range of conditions that exist in the region of concern, so that measured values can be objectively evaluated. MDEQ uses the terms “least disturbed” (LD) and “most disturbed” (MD) to represent opposites end of that range, roughly equivalent to the concept of reference and stress conditions (MDEQ 2003, Jessup and Stribling 2008). It is understood that pristine, completely undegraded and stressor free conditions do not exist, and that LD represents our understanding of the best conditions that are known to exist, at least in terms of stressors. Because of that recognition, reference sites within a region, watershed, or jurisdiction, will have some level of degradation, even in the context of the reference condition concept (Stoddard et al. 2006). Development of a biological condition gradient (BCG) (Davies and Jackson 2006, Jessup and Gerritsen 2014) is a consensus process involving a group of expert biologists who rate the samples/sites along a standardized scale of conditions from Level 1 (absolute best, pristine) to Level 6 (severely altered from natural conditions, little chance of recovery). Use of the BCG in concert with the MMI approach used for the M-BISQ would provide more realism in understanding overall ecological potential. Calibrating a BCG for Mississippi would further enhance defensibility of stream and watershed assessments using the M-BISQ.

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Appendix A

Taxonomic Data Quality Report

Taxonomic Data Quality Control Report

Analysis completed (date)	November 6, 2013
Report completed (date)	November 6, 2013
Tetra Tech project number	100-BLT-T28423-12
Project name	M-BISQ Phase 12
Client	Mississippi Department of Environmental Quality, Field Services Division
Client contact	Ms. Alice Dossett ([601] 961-5664)
Primary taxonomist(s)	Mike Winnell (T1, Freshwater Benthic Services)
QC taxonomist(s)	Todd Askegaard (T2, Aquatic Resources Center)
QC analyst	C. Gallardo/J. Stribling

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Taxonomic Data Quality Control Report

Analysis completed (date)	November 6, 2013
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Test conditions and narrative summary – There were 9 benthic macroinvertebrate samples (most are approximately 200 organisms each) randomly selected as approximately 10% of the sample lot, Mississippi-Benthic Index of Stream Quality (M-BISQ) Phase 12 (n=90 samples). These taxonomic comparison (taxcomp) results represent a direct comparison of identification results by independent taxonomists in separate laboratories. The mean percent taxonomic disagreement (PTD) is 4.6%, substantially better than MDEQ's programmatic 15% measurement quality objective (MQO). Overall, the comparisons were very good, with no (zero) samples exceeding the MQO. Sample PTD ranged from 2.8-6.9%; the sample with the highest PTD of 6.9% was primarily due to hierarchical differences in identifications of mayflies (Baetidae, Heptageniidae), likely due to early instars or specimen damage. The mean percent difference in enumeration (PDE) is 0.3%, well below the programmatic MQO of 5%. Consistency of effort in meeting hierarchical target levels by the primary taxonomist is characterized by percent taxonomic completeness (PTC) with values ranging from 92.9-99.0% (mean 95.6%) for this set of QC samples. The mean absolute difference of PTC between T1 and T2 for this sample dataset is 1.9, illustrating good consistency. There are no corrective actions necessary. The rate of error in this dataset is trivial, and thus, the overall data quality acceptable for additional analyses.

Standard operating procedures (SOP) for identifications documented and provided to all primary and QC taxonomists? Yes.

Additional comments: None.

Hierarchical target levels

ALL TAXA identified to genus level, unless noted otherwise below:

Ceratopogonidae	(Ceratopogonidae)
Decapoda	family
Hirudinea	family
Hydracarina	(Hydracarina)
Mollusca	family
Nematoda	(Nematoda)
Nematomorpha	(Nematomorpha)
Nemertea	(Nemertea)
Simuliidae	(Simuliidae)
Turbellaria	(Turbellaria)

the following are combined under *Cricotopus/Orthocladus*:

Cricotopus
Orthocladus
Cricotopus/Orthocladus
Orthocladus/Cricotopus

the following are combined under *Thienemannimyia* genus group:

Conchapelopia
Helopelopia
Telopelopia
Meropelopia
Hayesomia
Thienemannimyia

the following are combined under *Hydropsyche*:

Hydropsyche
Ceratopsyche
Hydropsyche/Ceratopsyche
Ceratopsyche/Hydropsyche

Other than whole specimens, below are guidelines for biological material which should or should not be included as part of sample data:

Count

- Damaged insects and crustaceans only if they have at least a head and a thorax
- Oligochaeta fragments only if they are headed AND have enough segments for identification
- Mollusk shells only if there is soft tissue present



TETRA TECH

Do not count

- Surface-dwellers (HETEROPTERA/HEMIPTERA: Veliidae, Gerridae)
- Non-benthic water column taxa (HETEROPTERA/HEMIPTERA: Corixidae, Notonectidae, Naucoridae; DIPTERA: Culicidae, Chaoboridae; COLEOPTERA: Gyrinidae [adults only], Hydrophilidae [adults only], Dytiscidae (adults only), Noteridae [adults only])
- Terrestrial incidentals
- Larval or pupal exuviae
- Larvae or pupae where internal tissue has broken down to the point of floppiness
- Chironomid pupae (means that sorters do not count as part of total)
- Trichoptera pupae (means that sorters do not count as part of total)
- Microinvertebrates such as copepods, cladocera, ostracods

SUMMARY STATISTICS (by sample lot)

Number of samples in lot	90
Number of samples for taxonomic comparison	9
Percent of sample lot	10%
Percent taxonomic disagreement (PTD)	
Average	4.6
Standard deviation	1.5
Measurement quality objective	15
<i>No. samples exceeding</i>	0
Percent difference in enumeration (PDE)	
Average	0.3
Standard deviation	0.3
Measurement quality objective	5
<i>No. samples exceeding</i>	0
Percent taxonomic completeness (PTC [absolute difference T1xT2])	
Average	1.9
Standard deviation	2.6
Measurement quality objective	none designated

The following provides definitions for abbreviations and columns headers in tables found in subsequent pages:

Abbreviations/column headers

A - no_ind_T1	number of individuals counted by primary taxonomist
B - no_ind_T2	number of individuals counted by QC taxonomist
C - Matches	number of agreements between the two taxonomists



TETRA TECH

D - PDE	percent difference in enumeration
E - PTD	percent taxonomic disagreement
F - Target_T1	number of individuals identified to target level, primary taxonomist
G - Target_T2	number of individuals identified to target level, QC taxonomist
H - PTC_T1	percent taxonomic completeness, primary taxonomist
I - PTC_T2	percent taxonomic completeness, QC taxonomist
J - PTC (abs diff)	percent taxonomic completeness (absolute difference)
K - Diff_strt	number of straight disagreements
L - Diff_hier	number of hierarchical differences
M - Diff_miss	number of apparently missing specimens

SUMMARY STATISTICS (by individual samples)

Sample ID	A	B	C	D	E	F	G	H	I	J
PA029	200	200	189	0	5.5	196	194	98	97	1
PA238	196	196	187	0	4.6	182	199	92.9	101.5	8.6
PA347	220	219	207	0.2	5.9	205	202	93.2	92.2	1
PL1006	208	209	198	0.2	5.3	196	198	94.2	94.7	0.5
PL329-BD	202	202	196	0	3	194	194	96	96	0
SI149-BD	203	199	189	1	6.9	193	185	95.1	93	2.1
TB553	215	214	205	0.2	4.7	205	209	95.3	97.7	2.4
YZ074	209	211	205	0.5	2.8	203	206	97.1	97.6	0.5
YZ087	207	206	201	0.2	2.9	205	206	99	100	1

TAXON BY TAXON COMPARISONS (within samples)

Note: Identifications having zeros in both columns A and B were initially recognized by either T1 or T2 as being in the sample, but after discussion were determined not to be, or changed to a different nomenclature

Sample ID	Taxon	A	B	C	K	L	M
PA029	Hydracarina	1	0	0			1
PA029	Enchytraeidae	1	1	1			
PA029	Aulodrilus	1	1	1			
PA029	Physidae	2	2	2			
PA029	Hydrobiidae	3	3	3			
PA029	Neoporus	3	3	3			
PA029	Dubiraphia	3	3	3			
PA029	Macronychus	4	4	4			
PA029	Stenelmis	1	1	1			
PA029	Dineutus	1	1	1			
PA029	Cecidomyiidae	0	1	0			1



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PA029	Ablabesmyia	2	2	2			
PA029	Brillia	2	2	2			
PA029	Corynoneura	1	1	1			
PA029	Corynoneura/Thienemanniella	0	0	0			1
PA029	Cricotopus/Orthocladius	1	1	1			
PA029	Cryptochironomus	1	1	1			
PA029	Labrundinia	1	1	1			
PA029	Microtendipes	1	1	1			
PA029	Polypedilum	96	96	96			1
PA029	Rheotanytarsus	7	6	6	1		
PA029	Tanytarsus	3	4	3			
PA029	Thienemannimyia Gr.	1	1	1			
PA029	Tribelos	1	1	1			
PA029	Simuliidae	15	15	15			
PA029	Baetis	5	5	5			
PA029	Caenis	1	2	1			
PA029	Hexagenia	1	1	1			
PA029	Heptageniidae	0	5	0		5	
PA029	Maccaffertium	13	8	8			
PA029	Neoephemera	1	0	0	1		
PA029	Isonychia	2	2	2			
PA029	Isoperla	8	8	8			
PA029	Cheumatopsyche	4	5	4	1		
PA029	Hydropsyche	3	2	2			
PA029	Nectopsyche	1	1	1			
PA029	Oecetis	3	3	3			
PA029	Triaenodes	4	4	4			
PA029	Crangonyctidae	2	0	0		2	
PA029	Crangonyx	0	2	0			
PA238	Corbiculidae	1	1	1			
PA238	Enchytraeidae	1	1	1			
PA238	Pristina	1	1	1			
PA238	Limnodrilus	3	0	0	3		
PA238	Naididae (Tubificinae)	2	2	2			
PA238	Spirosperma	1	1	1			
PA238	Varichaetadrilus	0	3	0			
PA238	Coptotomus	1	1	1			
PA238	Dubiraphia	2	2	2			
PA238	Macronychus	3	3	3			
PA238	Berosus	1	1	1			
PA238	Ablabesmyia	3	3	3			
PA238	Corynoneura	8	8	8			3
PA238	Labrundinia	1	1	1			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PA238	Orthoclaadiinae	0	0	0		1	
PA238	Parametriocnemus	2	0	0			
PA238	Paraphaenocladus	0	2	0			2
PA238	Polypedilum	67	67	67			4
PA238	Pseudorthocladus	1	1	1			
PA238	Rheocricotopus	5	5	5			1
PA238	Rheotanytarsus	6	6	6			1
PA238	Tanytarsus	5	5	5			
PA238	Thienemanniella	2	2	2			1
PA238	Simuliidae	35	35	35			
PA238	Baetis	3	3	3			
PA238	Eurylophella	1	1	1			
PA238	Heptageniidae	0	1	0			
PA238	Maccaffertium	2	1	1		1	
PA238	Tricorythodes	1	1	1			
PA238	Enallagma	1	1	1			
PA238	Progomphus	1	1	1			
PA238	Macromia	2	2	2			
PA238	Perlesta	3	0	0			
PA238	Perlidae	0	3	0		3	
PA238	Isoperla	14	14	14			
PA238	Cheumatopsyche	11	11	11			
PA238	Hydropsyche	2	2	2			
PA238	Hydropsychidae	1	1	1			
PA238	Chimarra	2	2	2			
PA238	Hyaella	1	1	1			
PA347	Nematoda	1	1	1			
PA347	Hydracarina	5	5	5			
PA347	Enchytraeidae	1	1	1			
PA347	Dero	1	0	0	1		
PA347	Nais	1	2	1			
PA347	Aulodrilus	1	0	0			1
PA347	Naididae (Tubificinae)	2	2	2			
PA347	Ancylidae	2	2	2			
PA347	Physidae	1	1	1			
PA347	Planorbidae	1	1	1			
PA347	Coleoptera	0	1	0			1
PA347	Helichus	1	1	1			
PA347	Neoporus	2	2	2			
PA347	Ancyronyx	1	1	1			
PA347	Dubiraphia	1	1	1			
PA347	Prionocyphon	0	3	0	3		
PA347	Scirtes	3	0	0			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PA347	Ceratopogonidae	1	1	1			
PA347	Ablabesmyia	2	2	2			
PA347	Cladotanytarsus	1	1	1			
PA347	Corynoneura	16	16	16			
PA347	Cricotopus/Orthocladius	2	2	2			
PA347	Dicrotendipes	1	1	1			
PA347	Hydrobaenus	1	0	0	1		
PA347	Parakiefferiella	0	1	0			
PA347	Paratanytarsus	7	7	7			
PA347	Polypedilum	57	57	57			
PA347	Rheotanytarsus	6	6	6			
PA347	Tanytarsus	30	30	30			
PA347	Thienemannimyia Gr.	8	8	8			
PA347	Zavrelimyia	1	1	1			
PA347	Dixella	5	5	5			
PA347	Simuliidae	10	10	10			
PA347	Pseudolimnophila	2	2	2			
PA347	Acerpenna	4	4	4			
PA347	Caenis	0	3	0			3
PA347	Heptageniidae	0	1	0			
PA347	Maccaffertium	6	6	6			
PA347	Stenacron	3	2	2		1	
PA347	Leptophlebiidae	1	1	1			
PA347	Microvelia	0	0	0			
PA347	Cordulegaster	1	1	1			
PA347	Corduliinae/Libellulinae	1	0	1		1	
PA347	Libellulidae	0	1	0			
PA347	Plecoptera	0	1	0			1
PA347	Perlesta	1	0	0		1	
PA347	Perlidae	0	1	0			
PA347	Isoperla	5	5	5			
PA347	Perlodidae	2	0	0	1	1	
PA347	Cheumatopsyche	5	5	5			
PA347	Triaenodes	2	2	2			
PA347	Pycnopsyche	1	1	1			
PA347	Turbellaria	2	2	2			
PA347	Hyalella	5	5	5			
PA347	Cambaridae	1	1	1			
PA347	Caecidotea	6	3	3			3
PL1006	Hydracarina	1	1	1			
PL1006	Enchytraeidae	4	4	4			
PL1006	Allonais	0	2	0	2		
PL1006	Dero	4	5	4			1



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PL1006	Haemonais	1	1	1			
PL1006	Naidinae	0	1	0		1	
PL1006	Pristina	3	0	0			
PL1006	Naididae (Tubificinae)	1	1	1			
PL1006	Physidae	1	1	1			
PL1006	Hydroporinae	0	3	0		3	
PL1006	Neoporus	5	2	2			
PL1006	Dubiraphia	2	2	2			
PL1006	Gyrinus	1	1	1			
PL1006	Scirtes	6	6	6			
PL1006	Ceratopogonidae	3	3	3			
PL1006	Ablabesmyia	3	3	3			
PL1006	Chironomus	1	1	1			
PL1006	Cladotanytarsus	2	2	2			
PL1006	Clinotanytus	1	1	1			
PL1006	Corynoneura	2	2	2			5
PL1006	Cricotopus/Orthocladius	1	1	1			
PL1006	Cryptochironomus	1	1	1			
PL1006	Dicrotendipes	1	1	1			
PL1006	Djalmabatista	2	2	2			
PL1006	Glyptotendipes	7	7	7			
PL1006	Kiefferulus	2	2	2			
PL1006	Labrundinia	1	1	1			
PL1006	Microtendipes	2	2	2			
PL1006	Nanocladius	1	1	1			
PL1006	Orthoclaadiinae	0	0	0			
PL1006	Paracladopelma	1	1	1			
PL1006	Paraphaenocladius	1	0	0	1		
PL1006	Paratanytarsus	7	6	6			
PL1006	Phaenopsectra	1	1	1			
PL1006	Polypedilum	17	17	17			
PL1006	Pseudorthocladius	1	1	1			
PL1006	Rheotanytarsus	8	8	8			
PL1006	Smittia	0	1	0	1		
PL1006	Stempellinella	1	0	0			
PL1006	Tanytarsus	49	51	49			2
PL1006	Thienemannimyia Gr.	3	3	3			
PL1006	Dixella	1	1	1			
PL1006	Chrysops	1	1	1			
PL1006	Limnophila	1	0	0	1		
PL1006	Limonia	0	1	0			
PL1006	Caenis	1	1	1			
PL1006	Eurylophella	1	1	1			
PL1006	Leptophlebiidae	2	2	2			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PL1006	Ranatra	1	1	1			
PL1006	Lepidoptera	1	1	1			
PL1006	Gomphus	1	1	1			
PL1006	Allocapnia	2	2	2			
PL1006	Triaenodes	2	2	2			
PL1006	Limnephilidae	1	1	1			
PL1006	Pycnopsyche	1	1	1			
PL1006	Turbellaria	1	1	1			
PL1006	Hyaella	29	29	29			
PL1006	Caecidotea	14	14	14			
PL329-BD	Hydracarina	1	1	1			
PL329-BD	Enchytraeidae	1	1	1			
PL329-BD	Ancyronyx	2	2	2			
PL329-BD	Dubiraphia	8	8	8			
PL329-BD	Macronychus	3	3	3			
PL329-BD	Microcylloepus	1	1	1			
PL329-BD	Stenelmis	2	2	2			
PL329-BD	Berosus	2	2	2			
PL329-BD	Ceratopogonidae	2	2	2			
PL329-BD	Ablabesmyia	1	1	1			
PL329-BD	Brillia	1	1	1			
PL329-BD	Cladotanytarsus	1	1	1			
PL329-BD	Clinotanytus	1	1	1			
PL329-BD	Corynoneura	2	2	2			
PL329-BD	Cricotopus/Orthocladius	1	1	1			
PL329-BD	Eukiefferiella	1	1	1			
PL329-BD	Orthocladiinae	0	0	0		1	
PL329-BD	Parametriocnemus	5	5	5			
PL329-BD	Paratanytarsus	1	1	1			
PL329-BD	Pentaneurini	1	0	0		1	
PL329-BD	Polypedilum	20	20	20			
PL329-BD	Pseudorthocladius	2	2	2			
PL329-BD	Rheotanytarsus	1	1	1			
PL329-BD	Robackia	1	1	1			
PL329-BD	Stempellinella	2	1	1	3		
PL329-BD	Tanytarsini	1	0	0			
PL329-BD	Tanytarsus	57	59	57			
PL329-BD	Thienemannimyia genus grp.	5	5	5			
PL329-BD	Zavrelimyia	0	1	0			1
PL329-BD	Hemerodromia	9	9	9			
PL329-BD	Pericoma	0	1	1			
PL329-BD	Pericoma/Telmatoscopus	1	0	0			
PL329-BD	Simuliidae	4	4	4			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
PL329-BD	Pseudolimnophila	1	1	1			
PL329-BD	Acerpenna	1	0	0	1		
PL329-BD	Dipheter	0	1	0			
PL329-BD	Labiobaetis	1	0	0			1
PL329-BD	Maccaffertium	16	16	16			
PL329-BD	Microvelia	0	0	0			
PL329-BD	Argia	1	1	1			
PL329-BD	Enallagma	4	4	4			
PL329-BD	Hagenius	1	1	1			
PL329-BD	Progomphus	1	1	1			
PL329-BD	Perlesta	2	1	1			
PL329-BD	Neoperla	16	16	16			
PL329-BD	Perlidae	0	1	0	1		
PL329-BD	Cheumatopsyche	8	8	8			
PL329-BD	Hydropsychidae	0	1	0			1
PL329-BD	Oecetis	3	3	3			
PL329-BD	Triaenodes	2	2	2			
PL329-BD	Chimarra	3	3	3			
PL329-BD	Turbellaria	1	1	1			
PL329-BD	Caecidotea	1	1	1			
SI149-BD	Enchytraeidae	3	1	1			2
SI149-BD	Lumbricidae	1	1	1			
SI149-BD	Limnodrilus	1	0	0	1		
SI149-BD	Varichaetadrilus	0	1	0			
SI149-BD	Helichus	1	1	1			
SI149-BD	Dubiraphia	1	1	1			
SI149-BD	Microcylloepus	1	1	1			
SI149-BD	Stenelmis	1	1	1			
SI149-BD	Hydrobius	1	0	0			
SI149-BD	Hydrophiloidea	0	1	0		1	
SI149-BD	Ceratopogonidae	11	11	11			
SI149-BD	Ablabesmyia	1	1	1			
SI149-BD	Corynoneura	1	1	1			
SI149-BD	Cricotopus/Orthocladus	2	2	2			
SI149-BD	Diplocladius	2	2	2			
SI149-BD	Labrundinia	1	1	1			
SI149-BD	Parakiefferiella	3	3	3			
SI149-BD	Parametriocnemus	1	1	1			
SI149-BD	Paraphaenocladus	1	1	1			
SI149-BD	Polypedilum	4	4	4			
SI149-BD	Pseudosmittia	1	1	1			
SI149-BD	Rheocricotopus	1	1	1			
SI149-BD	Rheotanytarsus	2	2	2			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
SI149-BD	Stempellinella	1	1	1			
SI149-BD	Tanytarsini	2	1	1		1	
SI149-BD	Tanytarsus	15	16	15			
SI149-BD	Thienemannimyia Gr.	3	3	3			
SI149-BD	Tvetenia	1	1	1			
SI149-BD	Hemerodromia	1	1	1			
SI149-BD	Simuliidae	6	6	6			
SI149-BD	Hexatoma	1	1	1			
SI149-BD	Pseudolimnophila	1	1	1			
SI149-BD	Baetidae	0	3	0		3	
SI149-BD	Plauditus	3	0	0			
SI149-BD	Caenis	28	27	27	1		
SI149-BD	Eurylophella	1	1	1			
SI149-BD	Heptageniidae	0	3	0		3	
SI149-BD	Maccaffertium	9	6	6			
SI149-BD	Isonychia	2	2	2			
SI149-BD	Tricorythodes	35	36	35	1		
SI149-BD	Aeshnidae	1	1	1			
SI149-BD	Boyeria	1	1	1			
SI149-BD	Calopteryx	2	2	2			
SI149-BD	Argia	1	1	1			
SI149-BD	Perlesta	3	3	3			
SI149-BD	Neoperla	24	24	24			
SI149-BD	Isoperla	4	4	4			
SI149-BD	Cheumatopsyche	8	8	8			
SI149-BD	Lepidostoma	1	1	1			
SI149-BD	Trienodes	1	1	1			
SI149-BD	Pycnopsyche	1	1	1			
SI149-BD	Chimarra	1	1	1			
SI149-BD	Cambaridae	2	2	2			
SI149-BD	Synurella	1	1	1			
SI149-BD	Caenis/Tricorythodes	2	0	0			2
TB553	Enchytraeidae	1	1	1			
TB553	Naididae (Tubificinae)	1	1	1			
TB553	Lymnaeidae	1	1	1			
TB553	Planorbidae	2	2	2			
TB553	Carabidae	0	1	0	1		
TB553	Helichus	1	1	1			
TB553	Stenelmis	2	2	2			
TB553	Peltodytes	1	1	1			
TB553	Staphylinidae	2	0	0			1
TB553	Chaetocladius	0	1	0	1		
TB553	Cladotanytarsus	1	0	0	1		



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
TB553	Corynoneura	2	2	2			3
TB553	Cricotopus/Orthocladius	9	9	9			
TB553	Dicrotendipes	12	12	12			
TB553	Diplocladius	1	1	1			
TB553	Hydrobaenus	2	1	1			
TB553	Micropsectra	1	0	0	1		
TB553	Orthoclaudiinae	0	0	0		1	
TB553	Paratanytarsus	0	1	0			1
TB553	Paratendipes	1	1	1			
TB553	Paratrachocladius	0	1	0			
TB553	Polypedilum	8	8	8			
TB553	Rheotanytarsus	1	1	1			
TB553	Saetheria	1	1	1			
TB553	Tanytarsus	8	9	8			
TB553	Thienemanniella	1	1	1			
TB553	Thienemannimyia Gr.	3	3	3			
TB553	Simuliidae	11	11	11			
TB553	Caloparyphus	1	0	0	1		
TB553	Nemotelus	0	1	0			
TB553	Acerpenna	1	0	0	1		
TB553	Dipheter	0	1	0			
TB553	Caenis	117	116	116			1
TB553	Maccaffertium	1	1	1			
TB553	Stenonema	5	5	5			
TB553	Leptophlebia	1	2	1		1	
TB553	Leptophlebiidae	2	1	1			
TB553	Dromogomphus	1	0	0	1		
TB553	Ophiogomphus	0	1	0			
TB553	Perlidae	1	1	1			
TB553	Cliperla	1	1	1			
TB553	Oecetis	2	2	2			
TB553	Synurella	9	9	9			
YZ074	Corbiculidae	23	23	23			
YZ074	Megascolecidae	1	1	1			
YZ074	Aulodrilus	4	4	4			
YZ074	Naididae (Tubificinae)	2	2	2			
YZ074	Ancylidae	1	1	1			
YZ074	Berosus	1	1	1			
YZ074	Ceratopogonidae	1	1	1			
YZ074	Cladotanytarsus	6	6	6			
YZ074	Corynoneura	1	1	1			
YZ074	Cricotopus/Orthocladius	44	44	44			
YZ074	Micropsectra	1	0	0			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
YZ074	Paratanytarsus	1	1	1			
YZ074	Paratrachocladus	0	3	0	2		
YZ074	Polypedilum	2	2	2			
YZ074	Rheocricotopus	13	13	13			
YZ074	Rheotanytarsus	12	11	11			1
YZ074	Saetheria	1	1	1			
YZ074	Tanytarsus	30	31	30			1
YZ074	Thienemanniella	2	2	2			
YZ074	Thienemannimyia Gr.	2	2	2			
YZ074	Simuliidae	31	31	31			
YZ074	Baetis	1	1	1			
YZ074	Maccaffertium	1	0	0	1		
YZ074	Stenonema	0	1	0			
YZ074	Progomphus	2	2	2			
YZ074	Cheumatopsyche	13	14	13			
YZ074	Hydropsychidae	1	0	0		1	
YZ074	Hydroptila	12	12	12			
YZ087	Nemertea	1	1	1			
YZ087	Hydracarina	3	3	3			
YZ087	Aulodrilus	1	1	1			
YZ087	Ancyronyx	1	1	1			
YZ087	Macronychus	2	2	2			
YZ087	Berosus	3	3	3			
YZ087	Ceratopogonidae	4	4	4			
YZ087	Corynoneura	1	0	0			
YZ087	Cricotopus/Orthocladus	23	23	23			
YZ087	Dicrotendipes	1	1	1			
YZ087	Labrundinia	1	1	1			
YZ087	Paralauterborniella	1	1	1			
YZ087	Paratanytarsus	4	6	4	2		
YZ087	Polypedilum	9	9	9			
YZ087	Rheocricotopus	3	3	3			
YZ087	Rheotanytarsus	16	14	14			
YZ087	Tanytarsus	70	70	70			
YZ087	Thienemannimyia Gr.	2	2	2			
YZ087	Hemerodromia	1	1	1			
YZ087	Sciaridae	0	0	0			
YZ087	Simuliidae	5	5	5			
YZ087	Gonomyia	1	1	1			
YZ087	Baetis	2	1	1			
YZ087	Diphetor	0	1	0	1		
YZ087	Caenis	2	2	2			
YZ087	Maccaffertium	12	14	12			



TETRA TECH

Sample ID	Taxon	A	B	C	K	L	M
YZ087	Stenacron	2	0	0	2		
YZ087	Corydalis	1	1	1			
YZ087	Gomphus	1	1	1			
YZ087	Macromia	2	2	2			
YZ087	Cheumatopsyche	10	10	10			
YZ087	Hydropsychidae	0	0	0			
YZ087	Hydroptila	17	17	17			
YZ087	Oxyethira	1	1	1			
YZ087	Hyaella	3	3	3			
YZ087	Cambaridae	1	1	1			

Notes/comments (*these are not corrective actions*)

1. Ensure sufficient attention is given to counting rules (count/noncount, and non-target)
2. Chironomidae pupae are not identified or counted other than family level
3. Ensure distinction of Hydrobaenus and Parakiefferiella
4. Ensure distinction of Allonais and Pristina
5. Ensure distinction of Limonia and Limnophila
6. Ensure distinction of Limnodrilus and Varichaetadrilus
7. Ensure distinction of Chaetocladius and Hydrobaenus
8. Ensure distinction of Micropsectra and Tanytarsus
9. Ensure distinction of Paratanytarsus and Rheotanytarsus

Appendix B

Metric Results

Table B-1. Metrics calculated from sample taxonomic identification results, including code or abbreviation, category, and description.

Table B-2. Metric analysis results. Results include trends with increasing disturbance, discrimination efficiency (DE), and Z-score for sub-classes of two bioregions (development data only).

Table B-3. Metric analysis results. Results include trends with increasing disturbance, discrimination efficiency (DE), and Z-score for sub-classes of two bioregions (development data only).

Appendix B. Metric Results

Table B-1. Metrics calculated from sample taxonomic identification results, including code or abbreviation, category, and description.

MetricCode	Category	Description
ni_total	Abundance	Total number of individuals in the sample
nt_total	Richness	Total number of taxa in the sample
nt_Insect	Richness	Total number of Insect Taxa
nt_EPT	Richness	Total number of EPT taxa in the sample
nt_Ephem	Richness	Total number of Ephemeroptera (E) taxa in the sample
nt_Pleco	Richness	Total number of Plecoptera (P) taxa in the sample
nt_Trich	Richness	Total number of Trichoptera (T)taxa in the sample
nt_Ptero	Richness	Total number of Pteronarcyidae
nt_POET	Richness	Total number of POET Taxa (EPT + Odonata)
nt_Coleo	Richness	Total number of Coleoptera taxa in the sample
nt_Dip	Richness	Total number of Diptera Taxa
nt_Chiro	Richness	Total number of chironomid taxa in the sample
nt_Ortho	Richness	Total number of Orthoclaadiinae (Chironomidae) taxa
nt_Tanyt	Richness	Total number of Tanytarsini (Chironomidae) taxa in the sample
nt_nonInsect	Richness	Total number of non-insect taxa in the sample
nt_Amph	Richness	Total number of amphipod taxa in the sample
nt_Bival	Richness	Total number of bivalve taxa in the sample
nt_CruMol	Richness	Total number of Crustacea or Mollusca taxa in the sample
nt_Deca	Richness	Total number of Decapoda taxa in the sample
nt_Gast	Richness	Total number of Gastropoda taxa in the sample
nt_Isop	Richness	Total number of isopod taxa in the sample
nt_Oligo	Richness	Total number of Oligochaeta Taxa
nt_Tubif	Richness	Total number of Tubificidae Taxa
pt_nonIns	RichComp	Non-insect % of Taxa
pt_POET	RichComp	POET % of Taxa
pt_Dip	RichComp	Diptera % of Taxa
pt_Chiro	RichComp	Chironomidae % of Taxa
pt_Amph	RichComp	Amphipod % of Taxa
pt_Bival	RichComp	Bivalve % of Taxa
pt_Deca	RichComp	Decapoda % of Taxa
pt_Gast	RichComp	Gastropoda % of Taxa
pt_Isop	RichComp	Isopod % of Taxa
pi_EPT	Composition	% EPT individuals
pi_EPTnoCaen	Composition	% EPT excluding Caenidae
pi_EPTsens	Composition	% EPT excl. Caenidae, Baetidae, Hydropsychidae, Hydroptilidae
pi_Ephem	Composition	% Ephemeroptera individuals
pi_EphemNoCaen	Composition	% Ephemeroptera excl. Caenidae

MetricCode	Category	Description
pi_Baet	Composition	% Baetidae individuals
pi_Caen	Composition	% Caenidae individuals
pi_Pleco	Composition	% Plecoptera individuals
pi_Trich	Composition	% Trichoptera individuals
pi_Hydro	Composition	% Hydropsychidae individuals
pi_Cole2Odon	Composition	Ratio of Coleoptera to Odonata
pi_Coleo	Composition	% Coleoptera individuals
pi_Colesens	Composition	% Coleoptera excluding Hydrophilidae
pi_Corb	Composition	% Corbicula individuals
pi_Dip	Composition	% Diptera individuals
pi_Chir-COC	Composition	% Chiron. excl. Cricotopus/ Orthocladius/Chironomus
pi_Chiro	Composition	% Chironomidae individuals
pi_CrCh2Chi	Composition	% Cricotopus + Chironomus of Chironomidae individuals
pi_Orth2Chi	Composition	% Orthocladinae of Chironomidae individuals
pi_COC2Chi	Composition	% Cricotopus/Orthocladius/Chironomus of Chironomidae
pi_Tanyp2Chiro	Composition	% Tanypodinae of Chironomidae individuals
pi_Tanyp	Composition	% Tanypodinae of Chironomidae individuals
pi_Tanyt	Composition	% Tanytarsini individuals
pi_Tnyt2Chi	Composition	% Tanytarsini of Chironomidae individuals
pi_NonIns	Composition	% Non-Insect individuals
pi_CruMol	Composition	% Crustacea & Mollusca
pi_Crus	Composition	% Crustacea individuals
pi_Deca	Composition	Decapoda individuals
pi_Gastr	Composition	% Gastropoda individuals
pi_Iso	Composition	% Isopoda individuals
pi_Moll	Composition	% Mollusca individuals
pi_Amph	Composition	% Amphipoda individuals
pi_Bival	Composition	% Bivalvia individuals
pi_Odon	Composition	% Odonata individuals
pi_Oligo	Composition	% Oligochaeta individuals
pi_Tubif	Composition	% Tubificidae individuals
pi_dom01	Evenness	% Dominant Taxon individuals
x_D	Evenness	Simpson's Index
x_D_Mg	Evenness	Margaleff's Index
x_Pielou	Evenness	Pielou's Index
x_Shan_e	Evenness	Shannon-Weiner Index (base 2)
nt_ffg_cllct	FFG	% Collector individuals
nt_ffg_filtr	FFG	% Filterer individuals
nt_ffg_pred	FFG	% Predator individuals
nt_ffg_scrap	FFG	% Scraper individuals
nt_ffg_shred	FFG	% Shredder individuals
pi_ffg_cllct	FFG	Collector Taxa

MetricCode	Category	Description
pi_ffg_filt	FFG	Filterer Taxa
pi_ffg_pred	FFG	Predator Taxa
pi_ffg_scrap	FFG	Scraper Taxa
pi_ffg_shred	FFG	Shredder Taxa
nt_hab_brrwr	Habit	Burrower Taxa
nt_hab_clmbr	Habit	Climber Taxa
nt_hab_clngr	Habit	Clinger Taxa
nt_hab_sprwl	Habit	Sprawler Taxa
nt_hab_swmmr	Habit	Swimmer Taxa
pi_hab_brrwr	Habit	% Burrower individuals
pi_hab_clmbr	Habit	% Climber individuals
pi_hab_clngr	Habit	% Clinger individuals
pi_hab_sprwl	Habit	% Sprawler individuals
pi_hab_swmmr	Habit	% Swimmer individuals
pt_hab_swmmr	Habit	Swimmer % of Taxa
nt_intol	Tolerance	Intolerant Taxa
nt_tol	Tolerance	Tolerant Taxa
pi_intol	Tolerance	% Intolerant
pi_tol	Tolerance	% Tolerant
pt_tol	Tolerance	Tolerant % of Taxa
pt_tv_intol	Tolerance	Intolerant % of Taxa
x_BeckBI	Tolerance	Beck's Index
x_HBI	Tolerance	Hilsenhoff's Index (average tolerance value of individuals)
x_NCBI	Tolerance	North Carolina Index
nt_intolMol	Tolerance	Intolerant Mollusca Taxa
nt_att2	BCG	Total number of BCG attribute 2 taxa in the sample
nt_att23	BCG	Total number of BCG attribute 2 and 3 taxa in the sample
nt_att234	BCG	Total number of BCG attribute 2, 3, and 4 taxa in the sample
nt_att5	BCG	Total number of BCG attribute 5 taxa in the sample
nt_att23EPT	BCG	Total number of BCG attribute 2 and 3 EPT taxa in the sample
pi_att2	BCG	% BCG attribute 2 individuals
pi_att23	BCG	% BCG attribute 2 and 3 individuals
pi_att234	BCG	% BCG attribute 2, 3, and 4 individuals
pi_att5	BCG	% BCG attribute 5 individuals
pi_att23EPT	BCG	% BCG attribute 2 and 3 EPT individuals
pi_dom01_att4	BCG	% individuals of the most abundant BCG attribute 4 taxon
pi_dom01_att5	BCG	% individuals of the most abundant BCG attribute 5 taxon
pt_att2	BCG	BCG attribute 2 % of Taxa
pt_att23	BCG	BCG attribute 2 and 3 % of Taxa
pt_att234	BCG	BCG attribute 2, 3, and 4 % of Taxa
pt_att5	BCG	BCG attribute 5 % of Taxa
pt_att23EPT	BCG	BCG attribute 2 and 3 EPT % of Taxa

Table B-2. Metric analysis results. Results include trends with increasing disturbance, discrimination efficiency (DE), and Z-score for sub-classes of two bioregions (development data only). *Trend codes*: D, decreasing with increasing disturbance; I, increasing with increasing disturbance; X, poor discrimination performance; c, candidate index metric; 1, used in the M-BISQ 2008 version.

Metric Code	Trend	East		South Bluff			West			Southeast		
		DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score
nt_total	D-c-1	62.5	0.95	X	<40	0.47	D-c-1	62.8	0.66	X-c-1	<40	0.47
nt_Insect	D-c	73.1	1.22	X	<40	0.70	D-c	55.8	0.64	X	<40	0.36
nt_EPT	D-c-1	72.1	1.23	D-c	63.6	0.71	D	44.2	0.46	D-c	40.0	0.30
nt_Ephem	D	57.7	0.75	X	<40	0.64	X	<40	0.20	X	<40	0.05
nt_Pleco	D	47.1	0.85	D-c	54.5	0.46	D-c	65.1	0.92	X	<40	0.23
nt_Trich	D	54.8	0.92	D-c	54.5	0.52	X	<40	0.24	D-c	50.0	0.45
nt_Ptero	X	<40	0.22	X	<40	NA	X	<40	NA	X	<40	NA
nt_POET	D	61.5	0.92	D-c	63.6	0.71	X	<40	0.45	X	<40	0.27
nt_Coleo	X	<40	0.05	X	<40	0.16	X	<40	0.68	X	<40	-0.29
nt_Dip	D	63.5	0.92	X	<40	0.54	X	<40	0.37	X	<40	0.24
nt_Chiro	D	55.8	0.76	X	<40	0.37	X	<40	0.24	X	<40	0.08
nt_Ortho	D	40.4	0.60	X	<40	0.56	X	<40	0.44	X	<40	0.15
nt_Tanyt	D	34.6	0.88	X	<40	0.09	X	<40	0.22	X	<40	-0.03
nt_nonInsect	I	42.3	-0.52	D-c	45.5	-0.56	X	<40	0.25	X	<40	0.15
nt_Amph	X	<40	-0.34	D	45.5	0.11	D	41.9	0.49	X	<40	-0.13
nt_Bival	X	<40	-0.23	X	<40	0.24	X	<40	0.03	X	<40	-0.03
nt_CruMol	I	40.4	-0.47	X	<40	0.27	D	46.5	0.27	X	<40	0.13
nt_Deca	X	<40	0.19	X	<40	0.07	D	51.2	0.60	X	<40	0.48
nt_Gast	X	<40	-0.60	X	<40	-0.36	X	<40	-0.23	I	40.0	-0.40
nt_Isop	X	<40	-0.28	X	<40	0.36	X	<40	0.05	D	45.0	0.32
nt_Oligo	X	<40	-0.35	I-c-1	45.5	-0.70	X	<40	0.07	X	<40	0.38
nt_Tubif	X	<40	-0.02	X	<40	-0.27	X	<40	0.10	X	<40	-0.03
pt_nonIns	I-c	71.2	-1.16	D-c	72.7	-2.73	X	<40	-0.20	I-c-1	50.0	-0.15
pt_POET	D	52.9	0.65	D	45.5	0.79	X	<40	0.16	X	<40	0.29
pt_Dip	X	<40	0.46	D	54.5	0.68	X	<40	-0.21	X	<40	-0.24

Metric Code	East			South Bluff			West			Southeast		
	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score
pt_Chiro	X	<40	0.27	X	<40	0.45	X	<40	-0.37	X	<40	-0.44
pt_Amph	I	58.7	-0.76	D	45.5	0.09	D	41.9	0.35	X	<40	-0.40
pt_Bival	I	46.2	-0.58	X	<40	0.23	X	<40	-0.09	X	<40	0.01
pt_Deca	I	43.3	-0.05	X	<40	0.06	D	51.2	0.27	X	<40	0.41
pt_Gast	I	53.8	-0.83	X	<40	-0.93	I	60.5	-0.22	I	40.0	-0.37
pt_Isop	X	<40	-0.50	X	<40	0.45	X	<40	0.01	D	45.0	-0.20
pi_EPT	I	42.3	-0.39	X	<40	0.04	X	<40	0.15	X	<40	0.17
pi_EPTnoCaen	D	72.1	0.74	D	45.5	-0.28	D	44.2	0.55	X	<40	0.15
pi_EPTsens	D-c-1	76.9	0.90	D-c-1	63.6	-0.54	D-c-1	72.1	0.61	X	<40	0.25
pi_Ephem	I	47.1	-1.06	X	<40	0.08	X	<40	-0.36	X	<40	0.10
pi_EphemNoCaen	D-c	66.3	0.55	D	45.5	-0.14	X	<40	0.24	X	<40	0.06
pi_Baet	X	<40	-0.25	D	63.6	0.24	X	<40	-0.33	X	<40	-0.09
pi_Caen	I	61.5	-2.02	X	<40	0.11	I	60.5	-0.45	X	<40	0.16
pi_Pleco	D-c	67.3	0.54	D-c	63.6	-0.66	D-c	67.4	0.53	X	<40	0.21
pi_Trich	D-c	62.5	0.37	D	45.5	-0.06	X	<40	0.02	X	<40	-0.02
pi_Hydro	D	50.0	0.26	X	<40	-0.03	X	<40	-0.23	I-c	55.0	-1.75
pi_Cole2Odon	I	47.1	-0.39	D	54.5	-0.28	X	<40	-0.50	D	45.0	0.24
pi_Coleo	X	<40	-0.21	X	<40	0.19	X	<40	0.00	D-c	50.0	0.56
pi_Colesens	X	<40	-0.17	D-c	54.5	0.41	D-c-1	60.5	0.43	X	<40	0.33
pi_Corb	X	<40	0.11	X	<40	NA	X	<40	NA	X	<40	NA
pi_Dip	D	52.9	0.93	X	<40	0.40	X	<40	-0.04	D	60.0	0.58
pi_Chir-COC	D-c	62.5	0.93	X	<40	-0.1	X	<40	-0.3	X	<40	-0.16
pi_Chiro	D	56.7	0.74	D	45.5	0.41	I	41.9	-0.37	X	<40	-0.22
pi_CrCh2Chi	I	44.2	-0.64	X	<40	-0.52	X	<40	-0.85	I	45.0	-1.82
pi_Orth2Chi	I	51.0	-0.73	D	63.6	0.71	D	44.2	0.28	X	<40	0.08
pi_COC2Chi	I-c-1	77.9	-2.14	D	54.5	0.55	X	<40	-0.14	I-c-1	60.0	-3.09
pi_Tanyp2Chiro	X	<40	-0.01	X	<40	-0.19	X	<40	-0.38	D	40.0	-0.25
pi_Tanyp	D	45.2	0.33	X	<40	-0.01	I	62.8	-1.21	X	<40	-0.08
pi_Tanyt	D	62.5	0.68	X	<40	-0.17	I	41.9	-0.42	X	<40	-0.18

Metric Code	East			South Bluff			West			Southeast		
	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score
pi_Tnyt2Chi	D	51.9	0.66	X	<40	0.23	X	<40	-0.19	X	<40	-0.05
pi_NonIns	I	46.2	-0.94	X	<40	-0.36	X	<40	-0.07	I-c	50.0	-0.89
pi_CruMol	I	47.1	-0.91	X-c-1	<40	0.29	X	<40	-0.02	D	55.0	-1.98
pi_Crus	I	41.3	-0.98	D-c	45.5	0.32	D	51.2	0.11	D	50.0	-2.22
pi_Deca	X	<40	-0.16	X	<40	0.26	D	55.8	-0.01	X	<40	0.52
pi_Gastr	I	51.0	-1.20	X	<40	-0.92	I	55.8	-0.39	I	40.0	-1.15
pi_Iso	X	<40	-0.11	X	<40	0.26	X	<40	0.22	D	45.0	-2.90
pi_Moll	I	41.3	-0.47	X	<40	-0.16	X	<40	-0.41	X	<40	-2.03
pi_Amph	I	45.2	-1.25	D	45.5	0.32	D	48.8	-0.50	X	<40	-0.22
pi_Bival	X	<40	-0.19	X	<40	0.27	X	<40	-0.39	X	<40	-2.16
pi_Odon	I	40.4	-0.26	D-c-1	54.5	-0.94	X	<40	-0.63	D	40.0	0.05
pi_Oligo	X	<40	-0.58	I	45.5	-4.99	X	<40	-0.06	D	55.0	0.21
pi_Tubif	X	<40	-0.57	I	54.5	-0.61	X	<40	-0.19	X	<40	0.09
pi_dom01	I-c	59.6	-0.93	X	<40	0.54	X	<40	0.28	I-c	40.0	-0.10
x_D	D	60.6	1.22	X	<40	-0.50	X	<40	-0.25	X	<40	0.08
x_D_Mg	D	62.5	1.02	X	<40	0.38	D	58.1	0.63	X	<40	0.34
x_Pielou	D	56.7	1.09	I	45.5	-0.76	X	<40	-0.29	X	<40	0.02
x_Shan_e	D	60.6	1.17	X	<40	-0.26	X	<40	0.00	X	<40	0.15
nt_ffg_cllct	D	58.7	0.74	X-c-1	<40	0.14	D	65.1	0.59	D	40.0	0.35
nt_ffg_filtr	D	66.3	0.93	D	54.5	0.54	X	<40	0.38	I-c	45.0	-0.12
nt_ffg_pred	D-c	40.4	0.58	D-c	45.5	0.62	D-c	55.8	0.55	X	<40	0.50
nt_ffg_scrap	I	50.0	-0.57	X	<40	0.05	X	<40	-0.11	I	50.0	-0.17
nt_ffg_shred	X-c-1	<40	0.64	D-c	54.5	0.40	D	41.9	0.61	X	<40	0.10
pi_ffg_cllct	I-c	57.7	-1.16	X	<40	-0.27	I	41.9	-0.47	X	<40	0.21
pi_ffg_filtr	D	57.7	0.72	X	<40	-0.08	X	<40	0.08	D-c-1	60.0	0.50
pi_ffg_pred	D	49.0	0.47	I	45.5	-0.18	X	<40	0.07	D	40.0	0.53
pi_ffg_scrap	X	<40	-0.32	X	<40	0.09	D	41.9	0.09	X	<40	0.32
pi_ffg_shred	D	42.3	0.13	X	<40	0.33	X	<40	0.29	X	<40	-0.59
nt_hab_brwr	X	<40	0.27	X	<40	-0.19	X	<40	0.30	D	45.0	0.49

Metric Code	East			South Bluff			West			Southeast		
	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score
nt_hab_clmbr	X	<40	-0.44	X	<40	0.26	X	<40	-0.07	I	40.0	-0.34
nt_hab_clngr	D-c	72.1	1.17	X	<40	0.37	X	<40	0.52	X	<40	0.11
nt_hab_sprwl	D	51.0	0.67	X	<40	0.92	D-c	53.5	0.80	D-c-1	40.0	0.36
nt_hab_swmmr	X	<40	0.32	X	<40	0.37	X	<40	0.07	X	<40	0.02
pi_hab_brrwr	X	<40	0.10	D-c	72.7	-2.78	X	<40	-0.11	X	<40	0.32
pi_hab_clmbr	X	<40	0.08	X	<40	-0.55	X	<40	0.08	X	<40	-0.70
pi_hab_clngr	D-c	66.3	1.11	X	<40	-0.42	X	<40	0.32	D-c	65.0	0.82
pi_hab_sprwl	I-c	60.6	-1.64	D-c	63.6	1.26	X	<40	-0.24	I	45.0	-1.17
pi_hab_swmmr	D	37.5	-0.12	X-c-1	<40	0.09	X	<40	-0.86	I-c	50.0	-0.37
pt_hab_swmmr	X	<40	0.15	D	45.5	0.27	X	<40	-0.19	X	<40	-0.15
nt_intol	D	75.0	1.62	X	<40	0.09	D-c	69.8	0.85	D	45.0	0.52
nt_toler	I	61.5	-1.57	X	<40	0.12	I	48.8	-0.58	X	<40	0.15
pi_intol	D	75.0	1.08	X	<40	-1.28	D	62.8	0.29	X	<40	0.44
pi_toler	I	74.0	-2.68	X	<40	0.23	I	62.8	-0.79	D	55.0	-0.54
pt_toler	I-c	80.8	-2.32	D-c	45.5	-0.71	I-c-1	62.8	-1.61	X	<40	-0.11
pt_tv_intol	D-c	81.7	2.04	X	<40	0.06	D-c	69.8	0.91	D-c	45.0	0.69
x_BeckBI	D-c	77.9	1.60	D-c	45.5	0.69	D-c-1	62.8	1.08	D-c	45.0	0.53
x_HBI	I-c-1	74.0	-2.28	X	<40	0.31	I-c	67.4	-0.77	I-c-1	50.0	-1.05
x_NCBI	I	76.9	-1.27	D	45.5	-0.45	I	62.8	-0.89	X	<40	-0.20
nt_intolMol	X	<40	NA	X	<40	NA	X	<40	NA	X	<40	NA
nt_att2	D	47.1	0.7	X	<40	0.3	D	65.1	1.0	D	45.0	0.5
nt_att123	D	79.8	1.4	D	54.5	0.7	D	55.8	1.1	D	45.0	0.6
nt_att23	D	79.8	1.4	D	54.5	0.7	D	55.8	1.1	D	45.0	0.6
nt_att234	D	73.1	1.3	D	45.5	0.8	D	67.4	0.9	X	<40	0.3
nt_att5	I	46.2	-1.0	D-c	63.6	-0.4	I	60.5	-0.7	X	<40	-0.4
nt_att123EPT	D	75.0	1.2	X	<40	0.4	X	<40	0.8	D	45.0	0.6
pi_att12	D	62.5	0.3	X	<40	-0.7	D	62.8	0.3	D	45.0	0.3
pi_att23	D	79.8	0.8	D-c	72.7	0.5	D-c	74.4	0.6	D	45.0	0.4
pi_att123	D	79.8	0.8	D	72.7	0.5	D	74.4	0.6	D	45.0	0.4

Metric Code	East			South Bluff			West			Southeast		
	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score	Trend	DE	Z-score
pi_att5	I	71.2	-2.4	X	<40	-0.5	I	60.5	-0.8	X	<40	0.0
pi_att123EPT	D	69.2	0.6	D	63.6	-0.1	D	55.8	0.6	D	45.0	0.3
pi_dom01_att4	D	38.5	0.2	D	45.5	0.6	X	<40	0.2	I	40.0	-0.1
pi_dom01_att5	I	65.4	-2.2	X	<40	-0.2	I	46.5	-0.5	X	<40	0.2
pt_att12	D	51.9	0.6	X	<40	0.3	D	65.1	0.8	D	40.0	0.5
pt_att123	D	79.8	1.5	D	72.7	0.7	D	60.5	1.2	D	45.0	0.8
pt_att23	D-c	79.8	1.5	D	72.7	0.7	D	60.5	1.2	D	45.0	0.8
pt_att234	D	74.0	1.6	D	63.6	1.9	D	58.1	1.1	X	<40	0.2
pt_att5	I	75.0	-1.9	D-c	72.7	-2.1	I-c	69.8	-1.9	I	40.0	-0.9
pt_att123EPT	D	70.2	1.2	X	<40	0.3	D	60.5	0.9	D-c	50.0	0.8

Table B-3. Metric analysis results. Results include trends with increasing disturbance, discrimination efficiency (DE), and Z-score for sub-classes of two bioregions (development data only). *Trend codes*: D, decreasing with increasing disturbance; I, increasing with increasing disturbance; X, poor discrimination performance; c, candidate index metric; 1, used in the M-BISQ 2008 version.

MetricCode	West-North			West-South			Southeast-Blackwater			Southeast-Non-Blackwater		
	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score
nt_total	D	71.4	0.72	D	53.3	0.48	D	62.5	0.89	I	50.0	-0.56
nt_Insect	D	75.0	0.69	X	<40	0.33	D	62.5	1.02	X	16.7	-0.45
nt_EPT	D	64.3	0.93	I	60.0	-0.31	D	62.5	1.06	X	0.0	-0.43
nt_Ephem	D	71.4	0.60	I	53.3	-0.39	D	62.5	0.62	I	41.7	-0.73
nt_Pleco	D	75.0	1.02	D	60.0	0.60	X	0.0	0.26	X	16.7	0.09
nt_Trich	D	57.1	0.84	I	60.0	-0.83	D	75.0	1.49	X	0.0	-0.42
nt_Ptero	X	<40	NA	X	<40	NA	X	0.0	NA	X	0.0	NA
nt_POET	D	67.9	0.77	I	53.3	-0.17	D	62.5	1.11	X	0.0	-0.48
nt_Coleo	X	<40	0.88	X	<40	0.21	D	50.0	-0.12	I	41.7	-1.10
nt_Dip	D	42.9	0.20	X	<40	0.48	X	37.5	0.54	I	50.0	-0.08
nt_Chiro	X	<40	0.09	X	<40	0.35	X	25.0	0.54	I	41.7	-0.27
nt_Ortho	X	<40	0.36	X	<40	0.52	I	62.5	0.00	D	41.7	0.36
nt_Tanyt	X	<40	0.27	X	<40	-0.05	X	37.5	0.33	X	16.7	-0.37
nt_nonInsect	X	<40	-0.14	D	53.3	0.61	X	12.5	-0.09	X	16.7	0.16
nt_Amph	X	<40	-0.15	D	66.7	1.40	X	0.0	-0.30	X	33.3	0.10
nt_Bival	X	<40	0.20	X	<40	-0.10	X	0.0	-0.65	X	0.0	-0.18
nt_CruMol	I	50.0	0.00	D	60.0	0.73	X	25.0	0.16	X	8.3	0.02
nt_Deca	D	46.4	0.42	D	60.0	1.03	D	50.0	1.07	X	0.0	0.13
nt_Gast	I	71.4	-0.19	X	<40	-0.20	I	50.0	-0.76	X	0.0	-0.27
nt_Isop	X	<40	-0.03	X	<40	0.07	X	37.5	NA	X	0.0	0.17
nt_Oligo	X	<40	-0.16	D	46.7	0.28	X	25.0	-0.11	X	33.3	0.33
nt_Tubif	X	<40	-0.03	D	40.0	0.26	X	0.0	0.19	X	0.0	-0.50
pt_nonIns	X	<40	-0.36	D	46.7	0.47	I	62.5	-1.95	X	33.3	0.28
pt_POET	D	42.9	0.57	I	60.0	-0.57	D	62.5	1.30	I	50.0	-0.44
pt_Dip	I	42.9	-0.55	X	<40	0.12	I	75.0	-0.59	D	75.0	1.03

MetricCode	West-North			West-South			Southeast-Blackwater			Southeast-Non-Blackwater		
	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score
pt_Chiro	I	57.1	-0.59	X	<40	-0.04	I	50.0	-0.31	X	16.7	0.03
pt_Amph	I	53.6	-0.39	D	80.0	1.45	I	62.5	-1.02	X	33.3	0.22
pt_Bival	X	<40	0.13	X	<40	-0.46	X	0.0	-1.06	X	0.0	0.09
pt-Deca	D	46.4	0.25	D	60.0	0.81	D	50.0	0.84	X	0.0	0.14
pt_Gast	I	57.1	-0.15	I	40.0	-0.36	I	50.0	-1.77	X	0.0	0.00
pt_Isop	X	<40	0.03	X	<40	-0.04	X	37.5	0.24	X	0.0	0.18
pi_EPT	X	<40	-0.30	X	<40	0.57	D	62.5	1.02	I	41.7	-0.12
pi_EPTnoCaen	D	53.6	0.73	X	<40	0.30	D	62.5	0.89	I	41.7	-0.10
pi_EPTsens	D	78.6	0.73	D	46.7	0.47	D	75.0	1.18	X	0.0	-0.01
pi_Ephem	I	71.4	-1.76	X	<40	0.26	D	62.5	0.54	I	41.7	-0.55
pi_EphemNoCaen	D	50.0	0.56	I	46.7	-0.90	D	62.5	0.41	I	41.7	-0.50
pi_Baet	D	78.6	0.71	I	40.0	-2.62	X	0.0	-0.44	X	0.0	-0.18
pi_Caen	I	71.4	-9.59	X	<40	0.37	X	0.0	0.34	X	0.0	NA
pi_Pleco	D	75.0	0.62	D	86.7	0.52	X	0.0	0.49	X	16.7	0.32
pi_Trich	D	46.4	0.55	I	53.3	-2.04	D	75.0	0.69	I	58.3	-0.62
pi_Hydro	X	<40	0.34	I	66.7	-2.21	X	0.0	-4.57	I	66.7	-1.83
pi_Cole2Odon	X	<40	-0.80	D	40.0	-0.07	D	87.5	0.52	I	41.7	-0.60
pi_Coleo	X	<40	-0.38	D	66.7	0.49	D	75.0	0.39	X	33.3	0.24
pi_Colesens	D	60.7	0.45	D	53.3	0.36	D	75.0	0.33	X	0.0	-0.28
pi_Corb	X	<40	NA	X	<40	NA	X	0.0	NA	X	0.0	NA
pi_Dip	X	<40	0.52	I	66.7	-0.80	D	62.5	0.18	X	33.3	0.35
pi_Chiro	X	<40	0.03	I	73.3	-1.04	D	62.5	-0.20	I	66.7	-0.50
pi_CrCh2Chi	X	<40	-1.26	X	<40	-0.29	I	62.5	-4.54	X	0.0	-5.39
pi_Orth2Chi	D	46.4	0.40	D	46.7	0.44	I	62.5	-1.23	D	58.3	0.54
pi_COC2Chi	D	50.0	0.12	I	53.3	-1.19	I	87.5	-11.49	X	0.0	-2.02
pi_Tanyp2Chiro	I	75.0	-1.05	D	60.0	0.31	X	25.0	0.09	D	50.0	-0.17
pi_Tanyp	I	60.7	-1.11	I	73.3	-1.42	X	37.5	0.23	I	41.7	-0.47
pi_Tanyt	X	<40	0.34	I	80.0	-3.34	D	50.0	-0.12	I	83.3	-0.46
pi_Tnyt2Chi	D	53.6	0.34	I	66.7	-2.02	D	50.0	0.02	X	16.7	-0.36

MetricCode	West-North			West-South			Southeast-Blackwater			Southeast-Non-Blackwater		
	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score
pi_NonIns	I	53.6	-0.16	D	53.3	0.21	I	50.0	-2.58	I	50.0	-0.30
pi_CruMol	X	<40	0.07	D	60.0	-0.38	D	62.5	-3.28	I	41.7	-1.14
pi_Crus	D	42.9	0.21	D	66.7	-0.40	D	50.0	-1.47	D	50.0	-0.74
pi_Deca	D	46.4	-0.15	D	60.0	0.11	D	50.0	0.63	X	0.0	0.45
pi_Gastr	I	42.9	-0.32	I	40.0	-0.69	I	50.0	-6.69	X	0.0	-0.65
pi_Iso	X	<40	0.32	X	<40	-0.38	I	50.0	-7.07	X	0.0	-1.07
pi_Moll	X	<40	-0.39	X	<40	-0.10	X	0.0	-4.05	X	0.0	-2.41
pi_Amph	X	<40	-0.53	D	66.7	-0.41	X	0.0	-0.24	X	33.3	0.25
pi_Bival	X	<40	-0.45	X	<40	0.05	X	0.0	-3.13	X	0.0	-3.54
pi_Odon	X	<40	-1.86	X	<40	-0.10	D	75.0	0.74	I	50.0	-0.96
pi_Oligo	I	53.6	-1.34	D	40.0	0.29	D	87.5	-0.48	D	41.7	0.31
pi_Tubif	I	50.0	-1.28	D	40.0	0.27	X	0.0	0.15	X	0.0	-2.76
pi_dom01	X	<40	0.15	X	<40	0.42	I	62.5	-0.36	D	58.3	0.44
x_D	X	<40	-0.09	X	<40	-0.43	D	75.0	0.32	I	50.0	-0.44
x_D_Mg	D	67.9	0.66	D	60.0	0.46	D	62.5	0.89	I	50.0	-0.55
x_Pielou	X	<40	-0.20	X	<40	-0.37	D	75.0	0.47	I	50.0	-0.45
x_Shan_e	D	53.6	0.09	X	<40	-0.14	D	75.0	0.75	I	58.3	-0.49
nt_ffg_cllct	D	57.1	0.60	D	53.3	0.50	D	75.0	0.40	I	58.3	-0.54
nt_ffg_filtr	X	<40	0.79	X	<40	-0.16	D	50.0	0.19	I	58.3	-0.85
nt_ffg_pred	D	53.6	0.39	D	53.3	0.71	D	62.5	0.71	X	16.7	-0.16
nt_ffg_scrap	I	42.9	-0.07	X	<40	-0.03	D	62.5	0.50	I	66.7	-0.75
nt_ffg_shred	D	46.4	0.55	X	<40	0.53	D	62.5	0.95	X	16.7	-0.25
pi_ffg_cllct	I	89.3	-2.29	D	60.0	0.46	D	62.5	-0.04	X	16.7	-0.06
pi_ffg_filtr	D	71.4	0.82	I	80.0	-2.97	D	62.5	0.08	D	50.0	0.37
pi_ffg_pred	X	<40	0.00	D	46.7	0.27	D	62.5	0.86	X	33.3	-0.03
pi_ffg_scrap	D	50.0	0.22	X	<40	0.17	D	62.5	0.43	X	0.0	-0.39
pi_ffg_shred	D	46.4	0.20	X	<40	0.36	X	25.0	-0.95	X	8.3	-0.21
nt_hab_brwr	X	<40	0.05	X	<40	0.48	D	75.0	0.26	D	50.0	-0.06
nt_hab_clmbr	I	50.0	-0.56	D	40.0	0.23	X	25.0	-0.49	X	8.3	-0.58

MetricCode	West-North			West-South			Southeast-Blackwater			Southeast-Non-Blackwater		
	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score
nt_hab_clngr	D	53.6	0.80	X	<40	-0.09	D	62.5	0.77	I	58.3	-0.62
nt_hab_sprwl	D	50.0	0.55	D	66.7	1.09	D	62.5	0.92	X	25.0	-0.04
nt_hab_swmmr	X	<40	0.80	I	66.7	-1.04	X	12.5	0.34	I	41.7	-0.30
pi_hab_brwr	I	60.7	-0.90	X	<40	0.39	D	50.0	0.23	D	41.7	0.14
pi_hab_clmbr	X	<40	-0.30	X	<40	0.25	X	37.5	-0.51	I	58.3	-0.60
pi_hab_clngr	D	89.3	1.27	I	86.7	-2.35	D	62.5	0.67	D	66.7	0.55
pi_hab_sprwl	I	89.3	-1.09	D	60.0	0.64	I	62.5	-0.99	I	41.7	-0.60
pi_hab_swmmr	D	57.1	-0.38	I	86.7	-2.84	I	50.0	0.10	I	50.0	-1.12
pt_hab_swmmr	D	42.9	0.60	I	80.0	-1.46	X	12.5	0.28	I	41.7	-0.38
nt_intol	D	89.3	1.03	X	<40	0.38	D	75.0	1.12	X	16.7	-0.35
nt_toler	I	46.4	-1.35	X	<40	0.06	X	12.5	-0.31	X	8.3	0.18
pi_intol	D	78.6	0.86	X	<40	-0.54	D	75.0	1.18	X	16.7	0.10
pi_toler	I	92.9	-7.02	D	40.0	0.38	D	75.0	-0.75	D	50.0	-1.49
pt_toler	I	78.6	-2.55	I	46.7	-0.37	X	12.5	-1.19	X	33.3	0.18
pt_tv_intol	D	89.3	1.21	X	<40	0.20	D	75.0	1.52	X	16.7	-0.09
x_BeckBI	D	82.1	1.31	D	40.0	0.55	D	75.0	1.17	X	16.7	-0.19
x_HBI	I	96.4	-3.85	D	73.3	0.64	I	62.5	-1.61	I	50.0	-0.94
x_NCBI	I	96.4	-1.56	X	<40	-0.34	I	62.5	-1.26	D	41.7	0.39
nt_intolMol	X	<40	NA	X	<40	NA	X	0.0	NA	X	0.0	NA
nt_att2	X	<40	0.5	D	93.3	2.8	D	75.0	1.0	X	16.7	-0.2
nt_att23	D	71.4	1.0	D	66.7	1.0	D	75.0	1.3	X	25.0	-0.3
nt_att23	D	71.4	1.0	D	66.7	1.0	D	75.0	1.3	X	25.0	-0.3
nt_att234	D	75.0	1.0	D	53.3	0.6	D	62.5	0.9	I	50.0	-0.5
nt_att5	I	67.9	-1.1	I	46.7	-0.4	X	12.5	-0.2	I	50.0	-1.0
nt_att23EPT	D	50.0	0.8	X	<40	0.6	D	75.0	1.2	X	8.3	-0.2
pi_att2	X	<40	0.3	D	86.7	0.5	D	75.0	0.9	I	58.3	-0.4
pi_att23	D	71.4	0.7	D	60.0	0.6	D	75.0	0.9	X	25.0	0.1
pi_att23	D	71.4	0.7	D	60.0	0.6	D	75.0	0.9	X	25.0	0.1
pi_att5	I	85.7	-5.0	X	<40	0.2	X	37.5	-0.6	X	16.7	-0.1

MetricCode	West-North			West-South			Southeast-Blackwater			Southeast-Non-Blackwater		
	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score	Trend	DE25	Z-score
pi_att23EPT	D	64.3	0.6	D	73.3	0.6	D	75.0	1.0	I	50.0	0.2
pi_dom01_att4	D	67.9	0.7	I	80.0	-0.6	I	50.0	-0.3	X	8.3	0.2
pi_dom01_att5	I	85.7	-6.1	X	<40	0.4	D	62.5	-0.5	X	25.0	0.3
pt_att2	X	<40	0.4	D	93.3	1.5	D	62.5	1.0	X	25.0	0.0
pt_att23	D	71.4	1.2	D	73.3	1.1	D	75.0	1.8	X	25.0	-0.1
pt_att23	D	71.4	1.2	D	73.3	1.1	D	75.0	1.8	X	25.0	-0.1
pt_att234	D	78.6	1.2	X	<40	0.5	X	37.5	0.8	I	58.3	-0.4
pt_att5	I	75.0	-2.2	I	66.7	-1.1	X	12.5	-1.4	I	50.0	-0.9
pt_att23EPT	D	57.1	1.0	D	40.0	0.5	D	75.0	1.4	X	25.0	0.0

Trend codes: D: decreasing with increasing disturbance, I: increasing with increasing disturbance, X: poor discrimination performance

Appendix C

Metric Precision Statistics

Appendix C. Precision statistics, by metric. Includes metric code or abbreviation, category, mean square error (MSE), mean, root-mean square error (RMSE), and 90% detectable difference (DD90).

Appendix C. Precision statistics, by metric. Includes metric code or abbreviation, category, mean square error (MSE), mean, root-mean square error (RMSE), and 90% detectable difference (DD90).

MetricCode	Category	MSE	Mean	RMSE	CV	DD90
ni_total	Abundance	412.0	203.0	20.30	10.0	33.4
nt_total	Richness	29.3	35.8	5.41	15.1	8.9
nt_Insect	Richness	19.8	29.8	4.45	14.9	7.3
nt_EPT	Richness	3.6	8.2	1.90	23.1	3.1
nt_Ephem	Richness	1.1	3.5	1.04	29.5	1.7
nt_Pleco	Richness	0.7	1.8	0.85	47.7	1.4
nt_Trich	Richness	1.3	2.9	1.14	39.4	1.9
nt_Ptero	Richness	0.0	0.0	0.00	na	0.0
nt_POET	Richness	6.5	10.9	2.54	23.3	4.2
nt_Coleo	Richness	1.1	2.8	1.05	38.2	1.7
nt_Dip	Richness	9.4	15.9	3.07	19.3	5.0
nt_Chiro	Richness	6.2	12.5	2.50	20.0	4.1
nt_Ortho	Richness	2.6	4.4	1.62	36.5	2.7
nt_Tanyt	Richness	0.6	2.8	0.78	28.1	1.3
nt_nonInsect	Richness	4.3	6.0	2.06	34.6	3.4
nt_Amph	Richness	0.3	0.9	0.55	61.1	0.9
nt_Bival	Richness	0.3	0.6	0.50	81.4	0.8
nt_CruMol	Richness	1.5	3.3	1.22	36.6	2.0
nt_Deca	Richness	0.2	0.7	0.45	67.3	0.7
nt_Gast	Richness	0.3	0.6	0.56	97.0	0.9
nt_Isop	Richness	0.2	0.6	0.47	82.3	0.8
nt_Oligo	Richness	1.7	2.3	1.31	58.3	2.2
nt_Tubif	Richness	0.4	0.7	0.67	96.2	1.1
pt_nonIns	RelRich	24.7	17.4	4.97	28.6	8.2
pt_POET	RelRich	31.3	29.8	5.60	18.8	9.2
pt_Dip	RelRich	38.8	44.4	6.23	14.0	10.2
pt_Chiro	RelRich	31.7	35.0	5.63	16.1	9.3
pt_Amph	RelRich	2.5	2.7	1.58	58.5	2.6
pt_Bival	RelRich	2.7	1.8	1.64	89.2	2.7
pt_Deca	RelRich	1.7	1.9	1.32	68.8	2.2
pt_Gast	RelRich	3.0	1.8	1.72	96.6	2.8
pt_Isop	RelRich	1.9	1.7	1.39	83.3	2.3
pi_EPT	Composition	52.1	29.4	7.22	24.6	11.9
pi_EPTnoCaen	Composition	36.4	17.6	6.03	34.3	9.9
pi_EPTsens	Composition	27.1	13.0	5.20	40.0	8.6
pi_Ephem	Composition	38.5	20.1	6.20	30.8	10.2
pi_EphemNoCaen	Composition	18.7	8.4	4.32	51.8	7.1
pi_Baet	Composition	1.3	1.2	1.16	93.3	1.9
pi_Caen	Composition	25.1	11.8	5.01	42.6	8.2

MetricCode	Category	MSE	Mean	RMSE	CV	DD90
pi_Pleco	Composition	4.6	3.9	2.14	54.5	3.5
pi_Trich	Composition	6.9	5.3	2.62	49.3	4.3
pi_Hydro	Composition	2.5	2.3	1.58	69.3	2.6
pi_Cole2Odon	Composition	11.9	7.1	3.45	48.3	5.7
pi_Coleo	Composition	5.1	4.1	2.25	55.1	3.7
pi_Colesens	Composition	4.3	3.2	2.08	64.5	3.4
pi_Corb	Composition	1.4	0.2	1.20	532.1	2.0
pi_Dip	Composition	92.8	49.2	9.64	19.6	15.9
pi_Chir-COC	Composition	64.8	35.1	8.05	22.9	13.2
pi_Chiro	Composition	73.6	37.5	8.58	22.9	14.1
pi_CrCh2Chi	Composition	10.8	3.3	3.28	100.2	5.4
pi_Orth2Chi	Composition	110.1	27.2	10.49	38.6	17.3
pi_COC2Chi	Composition	40.7	11.6	6.38	55.0	10.5
pi_Tanyp2Chiro	Composition	30.4	8.7	5.51	63.3	9.1
pi_Tanyp	Composition	2.5	2.6	1.57	60.7	2.6
pi_Tanyt	Composition	31.4	13.0	5.60	43.1	9.2
pi_Tnyt2Chi	Composition	112.6	30.9	10.61	34.3	17.5
pi_NonIns	Composition	54.5	13.6	7.38	54.2	12.1
pi_CruMol	Composition	27.2	9.0	5.21	58.0	8.6
pi_Crus	Composition	12.8	5.7	3.57	62.2	5.9
pi_Deca	Composition	2.5	1.0	1.58	154.9	2.6
pi_Gastr	Composition	1.7	0.8	1.31	164.2	2.1
pi_Iso	Composition	2.4	1.7	1.54	89.1	2.5
pi_Moll	Composition	10.2	3.2	3.20	98.8	5.3
pi_Amph	Composition	7.7	3.0	2.78	92.7	4.6
pi_Bival	Composition	7.4	2.4	2.71	111.1	4.5
pi_Odon	Composition	5.3	3.5	2.31	65.2	3.8
pi_Oligo	Composition	28.5	4.3	5.34	122.9	8.8
pi_Tubif	Composition	11.7	1.8	3.42	193.3	5.6
pi_dom01	Evenness	70.7	28.7	8.41	29.3	13.8
x_D	Evenness	0.0	0.9	0.06	7.0	0.1
x_D_Mg	Evenness	0.9	6.6	0.97	14.8	1.6
x_Pielou	Evenness	0.0	0.7	0.06	8.5	0.1
x_Shan_e	Evenness	0.1	2.7	0.28	10.6	0.5
nt_ffg_cllct	FFG	9.9	13.7	3.15	22.9	5.2
nt_ffg_filtr	FFG	1.1	4.7	1.06	22.3	1.7
nt_ffg_pred	FFG	5.0	8.9	2.24	25.3	3.7
nt_ffg_scrap	FFG	0.9	2.3	0.94	41.4	1.6
nt_ffg_shred	FFG	1.0	3.8	0.98	25.7	1.6
pi_ffg_cllct	FFG	59.5	34.9	7.71	22.1	12.7
pi_ffg_filtr	FFG	74.0	24.7	8.60	34.8	14.1
pi_ffg_pred	FFG	17.8	13.3	4.21	31.6	6.9

MetricCode	Category	MSE	Mean	RMSE	CV	DD90
pi_ffg_scrap	FFG	9.3	6.4	3.04	47.9	5.0
pi_ffg_shred	FFG	26.4	14.7	5.14	34.9	8.5
nt_hab_brrwr	Habit	3.2	5.7	1.78	31.0	2.9
nt_hab_clmbr	Habit	1.7	3.4	1.29	38.1	2.1
nt_hab_clngr	Habit	5.9	11.8	2.43	20.6	4.0
nt_hab_sprwl	Habit	6.1	11.4	2.47	21.7	4.1
nt_hab_swmmr	Habit	0.7	1.6	0.81	50.6	1.3
pi_hab_brrwr	Habit	29.2	8.7	5.40	62.2	8.9
pi_hab_clmbr	Habit	23.0	11.6	4.80	41.4	7.9
pi_hab_clngr	Habit	66.7	38.5	8.16	21.2	13.4
pi_hab_sprwl	Habit	41.0	33.5	6.40	19.1	10.5
pi_hab_swmmr	Habit	2.6	2.6	1.60	62.6	2.6
pt_hab_swmmr	Habit	4.8	4.4	2.20	49.8	3.6
nt_intol	Tolerance	4.9	7.3	2.20	30.0	3.6
nt_toler	Tolerance	1.8	3.9	1.34	34.2	2.2
pi_intol	Tolerance	18.5	11.9	4.30	36.1	7.1
pi_toler	Tolerance	38.2	18.6	6.18	33.2	10.2
pt_toler	Tolerance	11.7	12.0	3.43	28.5	5.6
pt_tv_intol	Tolerance	19.2	18.8	4.39	23.3	7.2
x_BeckBI	Tolerance	11.8	15.2	3.44	22.6	5.7
x_HBI	Tolerance	0.1	5.1	0.36	7.1	0.6
x_NCBI	Tolerance	0.1	6.7	0.38	5.7	0.6
nt_intolMol	Tolerance	0.0	0.0	0.06	321.2	0.1
nt_att2	BCG	0.7	1.4	0.84	58.9	1.4
nt_att23	BCG	3.5	6.8	1.88	27.7	3.1
nt_att234	BCG	16.4	27.3	4.06	14.9	6.7
nt_att5	BCG	2.6	5.2	1.62	31.2	2.7
nt_att23EPT	BCG	1.8	3.7	1.34	36.0	2.2
pi_att2	BCG	2.9	2.2	1.70	76.2	2.8
pi_att23	BCG	18.8	11.5	4.34	37.8	7.1
pi_att5	BCG	41.7	21.3	6.45	30.3	10.6
pi_att23EPT	BCG	13.7	7.3	3.70	50.5	6.1
pi_dom01_att4	BCG	61.7	21.4	7.86	36.8	12.9
pi_dom01_att5	BCG	33.3	14.5	5.77	39.7	9.5
pt_att2	BCG	5.0	3.7	2.24	61.2	3.7
pt_att23	BCG	17.3	17.7	4.16	23.5	6.8
pt_att234	BCG	29.8	75.3	5.46	7.3	9.0
pt_att5	BCG	15.8	15.2	3.97	26.1	6.5
pt_att23EPT	BCG	11.3	9.7	3.36	34.7	5.5

Appendix D

Calculation Procedures for M-BISQ2015

Includes appendix: Benthic macroinvertebrate taxa used in M-BISQ metric calculations, including attributes of tolerance value (TV), functional feeding group (FFG), and habit.

Calculation Procedures

for use of the

Mississippi–Benthic Index of Stream Quality (M-BISQ)

Updated for M-BISQ 2015

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This document presents guidelines for calculating the Mississippi Benthic Index of Stream Quality (M-BISQ), and is current through the 2015 recalibration. The M-BISQ is the benthic macroinvertebrate-based biological indicator developed by Mississippi Department of Environmental Quality (MDEQ) for use in biological assessment of wadeable streams in the state.

M-BISQ calculation procedures

Use of the M-BISQ requires that field sampling, laboratory sample processing and taxonomic identification, and metric and index calculation and scoring be done following MDEQ procedures. Data preparation includes all of those activities necessary for producing sample results suitable for the calculations.

Data preparation

Field sampling should be completed in accordance with MDEQ-SOP-FLD-007, “Macroinvertebrate Collection in Low Gradient Glide/Pool Streams: Aquatic Dip Net - 20-Jab Method” (Appendix H [MDEQ 2001]). Collect samples from multiple stream habitats using a D-frame net with 800 × 900 micron mesh net. Of the 20 total jabs used for the entire benthic collection process, 15 were proportionally-allocated to productive habitats (gravel/cobble, undercut banks and root material, snags/woody debris, and submerged aquatic vegetation). The other five jabs should be allocated to sandy bottom substrate. All benthic macroinvertebrate sampling should occur within a restricted time frame (**index period**) of early December through early March, at the discretion of MDEQ.

Sorting/subsampling. The subsample target count is 200 individuals ($\pm 20\%$), and bias in the sorting process is evaluated by independent checks of sort residue for missed specimens. The number of samples failing the measurement quality objective (MQO) for percent sorting efficiency (PSE) of 90% ($PSE_{MQO} \leq 90$) should be minimized (Flotemersch et al. 2006, Stribling 2011). No subsample being identified or analyzed should be <160 individuals if the entire sample has not been sorted (all 30 Caton grid cells, or otherwise 100%). Samples fully-sorted and still with <160 individuals should be evaluated for having come from stream sites with naturally low productivity, that is, having extremely low nutrients (oligotrophic) or with unusual habitat, such as continuous bedrock. Samples with >220 individuals should be virtually resampled to at least 220 individuals before calculating metrics. For descriptions of subsampling techniques and QC analyses, see Flotemersch et al. (2006) and Stribling (2011).

Taxonomic identification. Hierarchical target levels are primarily genus (Table 1), with consistency of effort (taxonomic precision) evaluated by direct comparison of results on a subset of samples re-identified by independent taxonomist in separate laboratories. The number of samples failing the MQO for percent taxonomic disagreement (PTD) of 15% ($PTD_{MQO} \geq 15\%$)

should be minimized (Stribling et al. 2003, Stribling 2011, Flotemersch et al. 2006). Attention should also be given to non-count organisms or other biological material (Table 1).

Corrective actions. Data quality and performance measures should be documented, and problems reconciled, prior to calculating metrics. Corrective actions specified and implemented will be tailored to the nature of the problem/failure.

Metric calculations. All are performed in a relational database, the MDEQ version of EDAS (the Ecological Data Analysis System [Tetra Tech 2007]). The calculations are based on target taxonomic levels (Table 1) with attributes (Appendix A) (MDEQ 2001). Most taxonomic groups are analyzed at the genus level, though some are collapsed to family or other levels if identification levels are inconsistent. No species level identifications are used. Other than taxonomic hierarchies, attributes used in metric calculations relate to feeding mechanisms, habit (methods of attachment or locomotion), and degrees of pollution or stressor tolerance (MDEQ 2001, 2003, Bressler et al. 2006). Tolerance metrics are calculated using values from Bressler et al. (2006), Lenat (1993), and Hilsenhoff (1987), which range from 0 (most sensitive) to 10 (most tolerant).

All richness metrics (e.g., total taxa or EPT taxa) are calculated such that only unique taxa are counted within each sample. Those taxa identified at higher taxonomic levels because of damage or under-developed features are not counted as unique taxa if other individuals in the sample are identified to a lower taxonomic level within the same sample, and are coded as "excluded taxa" in EDAS. This exclusion happens in individual samples, not across samples, as it is dependent on relative levels of identification within samples. Also, the exclusion is not applied to percentage metrics, where counts of individuals are included for all taxa in the sample.

Table 1. Target identification levels, inclusions (count), and exclusions (no count) used for the M-BISQ.	
ALL TAXA Genus level, unless noted below	
<u>Taxon</u>	<u>Identify to</u>
Ceratopogonidae	(Ceratopogonidae)
Decapoda	Family
Hirudinea	Family
Hydracarina	(Hydracarina)
Mollusca	Family
Nematoda	(Nematoda)
Nematomorpha	(Nematomorpha)
Nemertea	(Nemertea)
Simuliidae	(Simuliidae)
Turbellaria	(Turbellaria)
The following are combined under <i>Cricotopus/Orthocladius</i>:	
<i>Cricotopus</i>	<i>Cricotopus/Orthocladius</i>
<i>Orthocladius</i>	<i>Cricotopus/Orthocladius</i>

Table 1. Target identification levels, inclusions (count), and exclusions (no count) used for the M-BISQ.

<i>Cricotopus/Orthocladius</i>	<i>Cricotopus/Orthocladius</i>
<i>Orthocladius/Cricotopus</i>	<i>Cricotopus/Orthocladius</i>

The following are combined under *Thienemannimyia* genus group:

<i>Conchapelopia</i>	<i>Thienemannimyia</i> genus group
<i>Rheopelopia</i>	<i>Thienemannimyia</i> genus group
<i>Helopelopia</i>	<i>Thienemannimyia</i> genus group
<i>Telopelopia</i>	<i>Thienemannimyia</i> genus group
<i>Meropelopia</i>	<i>Thienemannimyia</i> genus group
<i>Hayesomia</i>	<i>Thienemannimyia</i> genus group
<i>Thienemannimyia</i>	<i>Thienemannimyia</i> genus group

The following are combined under *Hydropsyche*:

<i>Hydropsyche</i>	<i>Hydropsyche</i>
<i>Ceratopsyche</i>	<i>Hydropsyche</i>
<i>Hydropsyche/Ceratopsyche</i>	<i>Hydropsyche</i>
<i>Ceratopsyche/Hydropsyche</i>	<i>Hydropsyche</i>

INCLUDE (in identifications and sample counts)

- Damaged insects and crustaceans only if they have at least a head and a thorax
- Oligochaeta fragments only if they are headed AND have enough segments for identification
- Mollusk shells only if there is soft tissue present

EXCLUDE (from identifications and sample counts)

- Surface-dwellers
- Non-benthic water column taxa
- Terrestrial incidentals
- Larval or pupal exuviae
- Larvae or pupae where internal tissue has broken down to the point of floppiness
- Chironomid pupae (means that sorters do not count as part of total)
- Trichoptera pupae (means that sorters do not count as part of total)
- Microinvertebrates such as copepods, cladocera, ostracods

Metric calculation

The taxa lists produced by the laboratory may need revision to meet the specifications listed above. The taxa lists used for metric calculation includes the appropriate target level identification, taxonomic hierarchies (class, order, family), number of individual per taxon, excluded taxa status, and attribute designations for stressor tolerance, functional feeding groups, and habit. All tolerance and attribute designations are available in Appendix A. The following glossary of metrics gives details for calculation and interpretation of the metrics used in the M-BISQ. 'Site class' is the bioregion of the state for which the individual metric is included as part of the composite index. 'Metric categories' include richness, composition, functional feeding group, habit, and tolerance. 'Trend' is the direction of change in the presence of stressors which was documented during the calibration process. 'Reference' indicates literature in which the ecological rationale for using the metric is explained or its value as an indicator is demonstrated.

Metric name: Number of taxa, as predators

Metric abbreviation: nt_ffg_pred

Description: Number of distinct taxa identified in the subsample and categorized as predators

Bioregion/Site Class: East, West

Metric Category: Functional feeding group, richness

Trend with increasing stressor load: Decreases

Reference: Barbour et al. (1999)

Metric name: Number of taxa, as EPT (EPT index)

Metric abbreviation: nt_EPT

Description: Number of distinct taxa identified in the subsample from the insect orders Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies)

Bioregion/Site Class: South Bluff

Metric Category: Tolerance, richness

Trend with increasing stressor load: Decreases

References: Barbour et al. (1999)

Metric name: Number of taxa, as shredders

Metric abbreviation: nt_ffg_shred

Description: Number of distinct taxa that shred coarse organic material for food (primarily, leaf litter)

Bioregion/Site Class: South Bluff

Metric Category: Functional feeding group, richness

Trend with increasing stressor load: Increases

References: U.S. EPA (2006)

Metric name: Number of taxa, as Plecoptera

Metric abbreviation: nt_Pleco

Description: Number of distinct taxa identified in the subsample as a taxon of stonefly (Plecoptera)

Bioregion/Site Class: West

Metric Category: Richness, tolerance

Trend with increasing stressor load: Decreases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: Number of taxa, as climbers

Metric abbreviation: nt_hab_clmbr

Description: Number of distinct taxa in the subsample categorized as climbers, adapted for living on the surfaces of aquatic macrophytes or detrital debris

Bioregion/Site Class: Southeast

Metric Category: Habit, richness

Trend with increasing stressor load: Decreases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi data set.

Metric name: % individuals, as sensitive Coleoptera

Metric abbreviation: pi_Colesens

Description: The percentage of individuals in the subsample that are identified as Coleoptera (beetles), exclusive of Hydrophilidae (predaceous diving beetles)

Bioregion/Site Class: West, South Bluff

Metric Category: Composition, tolerance

Trend with increasing stressor load: Decreases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % individuals, as burrowers

Metric abbreviation: pi_hab_brrwr

Description: Percent of the individuals in the sample that burrow in substrate in pools within streams.

Bioregion/Site Class: South Bluff

Metric Category: Habit, composition

Trend with increasing stressor load: Decreases

References: Kerans and Karr (1994)

Metric name: % individuals, as predators

Metric abbreviation: pi_ffg_pred

Description: Percent of the individuals in the sample that are categorized as a predator functional feeding group

Bioregion/Site Class: Southeast

Metric Category: Functional Feeding Group, composition

Trend with increasing stressor load: Increases

References: Kerans and Karr (1994)

Metric name: % individuals, as Plecoptera

Metric abbreviation: pi_Pleco

Description: Percent of the individuals in the sample that are identified as Plecoptera (stoneflies)

Bioregion/Site Class: Southeast

Metric Category: Composition, tolerance

Trend with increasing stressor load: Decreases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % individuals, as *Cricotopus/Orthocladius/Chironomus* of total Chironomidae

Metric abbreviation: pi_COC2Chi

Description: Percent of the midge individuals in these relatively tolerant genera of overall Chironomidae

Bioregion/Site Class: East

Metric Category: Tolerance, composition

Trend with increasing stressor load: Increases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % individuals, as collectors

Metric abbreviation: pi_ffg_cllct

Description: Percentage of individuals identified in the sample with the functional feeding group categorized as collectors

Bioregion/Site Class: East

Metric Category: Functional feeding group, composition

Trend with increasing stressor load: Increases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % individuals, as clingers

Metric abbreviation: pi_hab_clngr

Description: Percent of the individuals in the sample that are categorized as swimmers, with the capacity for controlling the direction and velocity of their movements

Bioregion/Site Class: East, Southeast

Metric Category: Habit, composition

Trend with increasing stressor load: Increases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % of taxa, as non-insect

Metric abbreviation: pt_nonIns

Description: Of all taxa in the sample, the percentage of taxa that are not insects

Bioregion/Site Class: East

Metric Category: Richness

Trend with increasing stressor load: Increases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric name: % of taxa, as tolerant

Metric abbreviation: pt_toler

Description: Percent of taxa in sample with tolerance values ranging from 7 to 10 ($7 \leq TV \leq 10$).

Bioregion/Site Class: West

Metric Category: Tolerance

Trend with increasing stressor load: Increases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi data set.

Metric name: Beck's Biotic Index

Metric abbreviation: x_BeckBI

Description: Calculated as $(2x)$ the number of unique taxa with tolerance values of 0 or 1 plus $(1x)$ the number of taxa with tolerance values 2 – 4.

Bioregion/Site Class: East, South Bluff

Metric Category: Tolerance

Trend with increasing stressor load: Decreases

References: Beck (1955)

Metric name: Hilsenhoff Biotic Index (HBI)

Metric abbreviation: x_HBI

Description: This metric represents the relative sensitivity of the sample to nutrient perturbation. It is calculated as the average tolerance value of all individuals in the sample (excluding those without tolerance values). The range of the tolerance values is 0-10, 0 being stressor sensitive and 10 being stressor tolerant (see Appendix A).

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

Where n is the number of individuals in a taxon i ; a is the tolerance value assigned to that taxon; and N is the total number of individuals in the sample.

Bioregion/Site Class: Southeast, west

Metric Category: Tolerance

Trend with increasing stressor load: Increases

References: Hilsenhoff (1987), Barbour et al. (1999), Hayslip (1993), Kerans and Karr (1994)

Metric name: % individuals as Tanypodinae

Metric abbreviation: pi_Tanyp

Description: The percentage of individuals in the subsample that are identified as midges of the subfamily Tanypodinae.

Bioregion/Site Class: West

Metric Category: Composition

Trend with increasing stressor load: Increases

References: Barbour et al. (1999)

Metric name: % of taxa as intolerant

Metric abbreviation: pt_tv_intol

Description: Percent of taxa in sample with tolerance values ranging from 0 to 3 ($0 \leq TV \leq 3$).

Bioregion/Site Class: West

Metric Category: Tolerance

Trend with increasing stressor load: Decreases

References: No literature citation was identified for this metric. It was selected based on the strength of evidence within the Mississippi calibration data set.

Metric scoring

Metrics are scored on a common scale prior to combination (as an average of scores) in an index (Table 2). The scale ranges from 0-100 (Blocksom 2003, Barbour et al. 1999) with the optimal score is determined by the distribution of data. For metrics that decrease with increasing stress

(increasers), the 95th percentile of all data within the site class is considered optimal (to lessen the influence of outliers [Barbour et al. 1999]), and scored as 100 points using the equation:

$$\text{MetricScore} = \frac{\text{MetricValue}}{95^{\text{th}} \text{ Percentile}}$$

Metrics that increase with increasing stress (reverse metrics) were scored using the 5th percentile of data as the optimal, receiving a score of 100. Decreasing scores were calculated as metric values increased to the 95th percentile using the equation:

$$\text{MetricScore} = \frac{95^{\text{th}} \text{ Percentile} - \text{MetricValue}}{95^{\text{th}} \text{ Percentile} - 5^{\text{th}} \text{ Percentile}}$$

Table 2. Scoring formulas for metrics in the bioregional indices. Note, if the score formula results in a value of 0 or >100, the score was reset to the appropriate extremes of the scoring scale (0-100) before being averaged in the M-BISQ.

Bioregion	Metric names	Abbrev	Scoring formulas
East	Number of taxa, predators	nt_ffg_pred	100*(metric value)/14
East	Percent individuals, <i>Cricotopus</i> , <i>Orthocladius</i> , and <i>Chironomus</i> of Chironomidae	pi_COC2Chi	100*(50-(metric value))/50
East	Percent individuals, collectors	pi_ffg_cllct	100*(76.9-(metric value))/66.49
East	Percent individuals, clingers	pi_hab_clngr	100*(metric value)/73.99
East	Percent taxa, non-Insecta	pt_nonIns	100*(37.64-(metric value))/32.9
East	Percent taxa, tolerant	pt_toler	100*(30.4-(metric value))/28.6
East	Beck's Biotic Index	x_BeckBI	100*(metric value)/30
South Bluff	Number of taxa, Ephemeroptera, Plecoptera, and Trichoptera	nt_EPT	100*(metric value)/10.9
South Bluff	Number of taxa, shredders	nt_ffg_shred	100*(metric value)/6
South Bluff	Percent individuals, sensitive Coleoptera	pi_Colesens	100*(metric value)/4.2
South Bluff	Percent individuals, burrowers	pi_hab_brrwr	100*(43.5-(metric value))/42.1
South Bluff	Beck's Biotic Index	x_BeckBI	100*(metric value)/15
Southeast	Percent individuals, predators	pi_ffg_pred	100*(metric value)/24.7
Southeast	Number of taxa, climbers	nt_hab_clmbr	100*(1-(metric value))/5
Southeast	Percent individuals, clingers	pi_hab_clngr	100*(metric value)/79.8
Southeast	Percent individuals, <i>Cricotopus</i> , <i>Orthocladius</i> , and <i>Chironomus</i> of Chironomidae	pi_COC2Chi	100*(26.5-(metric value))/26.5
Southeast	Percent individuals, Plecoptera	pi_Pleco	100*(metric value)/10.9
Southeast	Hilsenhoff Biotic Index	x_HBI	100*(5.1-(metric value))/2
West	Number of taxa, predators	nt_ffg_pred	100*(metric value)/14
West	Number of taxa, Plecoptera	nt_Pleco	100*(metric value)/4
West	Percent individuals, sensitive Coleoptera	pi_Colesens	100*(metric value)/7.5
West	Percent individuals, Plecoptera	pi_Pleco	100*(metric value)/11.9
West	Percent individuals, Tanypodinae	pi_Tanyp	100*(8.3-(metric value))/8.3

Bioregion	Metric names	Abbrev	Scoring formulas
West	Percent taxa, intolerant	pt_tv_intol	$100 * (\text{metric value}) / 30.7$
West	Hilsenhoff Biotic Index	x_HBI	$100 * (7.5 - (\text{metric value})) / 3.8$

Index application

Following all QC analyses and full implementation of necessary corrective actions, the M-BISQ should be applied as follows.

1. Determine appropriate Bioregion/site class for the site (Table 3).
2. Calculate appropriate M-BISQ metrics (Table 2).
3. Score metrics based on formulas in Table 2.
Reset scores above 100 or below 0 to 100 or 0, respectively.
4. Calculate the M-BISQ as the average of the metric scores.
5. Report the results.
Include the M-BISQ scores, impairment thresholds, and performance statistics (DE and DD90) (Table 4)

Table 3. Bioregions and their associated subcoregions.

Bioregion	Subcoregions	Description/remarks
West	North: 74b and northern 74a South: 74c	North: Loess Plains, northern Bluff Hills (Vicksburg and north) South: Southern Rolling Plains
East	65a, 65b, 65e, 65i, 65j, 65r, 65q, and parts of 65p	Includes the eastern subcoregions (Northeast, parts of the East-Central)
Southeast	65f, 75a, and parts of 65p.	Southeast
South Bluff	southern sections of 74a	Southern Bluff Hills (adjacent to the Southern Rolling Plains)

Table 4. Performance statistics to be reported with the M-BISQ.

Bioregion	DE	Degradation threshold	DD90
West	88.4	43.7	7.76
East	88.5	71.6	5.66
Southeast	70	56.8	14.92
South Bluff	82	55.7	NA
Overall	NA	NA	8.56

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Appendix A. Benthic macroinvertebrate taxa used in M-BISQ metric calculations, including attributes of tolerance value (TV), functional feeding group (FFG), and habit. Abbreviations: *for FFG* - PR, predator; PA, parasite; OM, omnivore; CG, collector-gatherer; CF, collector-filterer; SC, scraper; SV, scavenger; SH, shredder; PI, piercer; CO, collector; *for habit* – BU, burrower; SP, sprawler; CB, climber; CN, clinger; SW, swimmer).

Order	Family	Tribe	FinalID	TV	FFG	Habit
<u>Enopla</u>						
Hoplonemertea	Tetrastemmatidae		Nemertea	5.9	PR	
Acanthocephala (Phylum)			Acanthocephala			
Entoprocta (Phylum)	Barentsiidae		Urnatella			
Nematomorpha (Phylum)			Nematomorpha		PA	BU
<u>Hydrozoa</u>						
Hydroida	Hydridae		Hydra	5.0	PR	
<u>Turbellaria</u>						
Tricladida	Dugesiidae		Cura	8.5		SP
Tricladida	Dugesiidae		Dugesiidae			
Tricladida	Dugesiidae		Girardia			
Tricladida	Planariidae		Dugesia	5.5	OM	SP
Tricladida	Planariidae		Phagocata			
Tricladida	Planariidae		Planariidae	5.7	PR	SP
			Turbellaria	6.8	PR	SP
<u>Hirudinea</u>						
			Hirudinea	7.8	PR	SP
Branchiobdellida	Branchiobdellidae		Branchiobdellidae	6.0	CG	CB
Rhynchobdellida	Glossiphoniidae		Glossiphoniidae	9.0	PR	SP
Rhynchobdellida	Piscicolidae		Piscicolidae			
<u>Oligochaeta</u>						
Aeolosomatida	Aeolosomatidae		Oligochaeta	6.2	CG	BU
			Aeolosomatidae		CF	
Arhynchobdellida	Erpobdellidae		Erpobdellidae	8.0	PR	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Haplotaxida			Haplotaxida		CG	
Haplotaxida	Enchytraeidae		Enchytraeidae	4.9	CG	BU
Haplotaxida	Enchytraeidae		Enchytraeus			
Haplotaxida	Enchytraeidae		Fridericia			
Haplotaxida	Enchytraeidae		Mesenchytraeus			
Haplotaxida	Haplotaxidae		Haplotaxidae		CG	
Haplotaxida	Haplotaxidae		Haplotaxis			
Haplotaxida	Haplotaxidae		Haplotaxis gordioides			
Haplotaxida	Lumbricidae		Eiseniella			
Haplotaxida	Lumbricidae		Lumbricidae	8.3	CG	BU
Haplotaxida	Lumbricidae		Lumbricus			
Haplotaxida	Megascolecidae		Megascolecidae			
Haplotaxida	Naididae		Arcteonais lomondi	6.0	CG	
Haplotaxida	Naididae		Bratislavia		CG	
Haplotaxida	Naididae		Chaetogaster	6.0	PR	
Haplotaxida	Naididae		Dero	6.6	CG	BU
Haplotaxida	Naididae		Haemonais	5.7	CG	
Haplotaxida	Naididae		Naididae		CG	BU
Haplotaxida	Naididae		Nais	7.8	CG	BU
Haplotaxida	Naididae		Ophidonais			
Haplotaxida	Naididae		Paranais			
Haplotaxida	Naididae		Piguetiella			
Haplotaxida	Naididae		Pristina	9.0	CG	
Haplotaxida	Naididae		Pristinella	7.0	CG	

Appendix A. Benthic macroinvertebrate taxa used in M-BISQ metric calculations, including attributes of tolerance value (TV), functional feeding group (FFG), and habit. Abbreviations: *for FFG* - PR, predator; PA, parasite; OM, omnivore; CG, collector-gatherer; CF, collector-filterer; SC, scraper; SV, scavenger; SH, shredder; PI, piercer; CO, collector; *for habit* – BU, burrower; SP, sprawler; CB, climber; CN, clinger; SW, swimmer).

Order	Family	Tribe	FinalID	TV	FFG	Habit
Haplotaxida	Naididae		Ripistes			
Haplotaxida	Naididae		Slavina	6.0	CG	
Haplotaxida	Naididae		Specaria		CG	
Haplotaxida	Naididae		Stephensoniana			
Haplotaxida	Naididae		Stylaria	9.0	CG	
Haplotaxida	Sparganophilidae		Sparganophilidae	6.1		
Haplotaxida	Sparganophilidae		Sparganophilus	6.1		
Haplotaxida	Tubificidae		Aulodrilus	5.0	CG	SP
Haplotaxida	Tubificidae		Bothrioneurum vej dovskyanum		SC	BU
Haplotaxida	Tubificidae		Branchiura	10.0	CG	CB
Haplotaxida	Tubificidae		Ilyodrilus	10.0		
Haplotaxida	Tubificidae		Isochaetides			
Haplotaxida	Tubificidae		Limnodrilus	8.6	CG	CN
Haplotaxida	Tubificidae		Potamothrrix			
Haplotaxida	Tubificidae		Quistradrilus	10.0	CG	
Haplotaxida	Tubificidae		Rhyacodrilus			
Haplotaxida	Tubificidae		Spirosperma	1.5	CG	CN
Haplotaxida	Tubificidae		Tubificidae	7.3	CG	bu
Haplotaxida	Tubificidae		Tubificidae - immature (with capillary setae)			
Haplotaxida	Tubificidae		Tubificidae - immature (without capillary setae)			
Haplotaxida	Tubificidae		Tubificinae	7.3	CG	bu
Haplotaxida	Tubificidae		Varichaetodrilus			
Haplotaxida	Tubificidae	Tubificinae	Varichaetadrilus			

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Lumbriculida	Lumbriculidae		Eclipidrilus	4.4	CG	
Lumbriculida	Lumbriculidae		Lumbriculidae	5.1	CG	BU
Lumbriculida	Lumbriculidae		Lumbriculus	4.6	CG	
<u>Bivalvia</u>						
Eulamellibranchia			Eulamellibranchia			
Basommatophora	Physidae		Bivalvia	6.0	CF	
Unionoida	Unionidae		Unionidae	5.0	CF	BU
Veneroida	Corbiculidae		Corbiculidae	6.1	CF	
Veneroida	Pisidiidae		Pisidiidae	5.3	CF	
<u>Gastropoda</u>						
Architaenioglossa	Ampullariidae		Ampullariidae			
Architaenioglossa	Viviparidae		Viviparidae	6.0	SC	
Basommatophora			Basommatophora			
Basommatophora	Ancylidae		Ancylidae	4.0	SC	CB
Basommatophora	Lymnaeidae		Lymnaeidae	9.6	CG	CB
Basommatophora	Physidae		Physidae	6.5	SC	CB
Basommatophora	Planorbidae		Planorbidae	6.1	SC	CB
Heterostropha	Valvatidae		Valvatidae		SC	
Mesogastropoda	Pomatiopsidae		Pomatiopsidae			
Neotaenioglossa	Bithyniidae		Bithyniidae			
Neotaenioglossa	Hydrobiidae		Hydrobiidae	3.9	SC	CB
Neotaenioglossa	Pleuroceridae		Pleuroceridae	3.0	SC	
			Gastropoda	5.8	SC	
<u>Crustacea</u>						

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Amphipoda			Amphipoda	7.4	CG	SP
Amphipoda	Crangonyctidae		Crangonyctidae	7.3	CG	SP
Amphipoda	Crangonyctidae		Crangonyx	6.9	CG	SP
Amphipoda	Gammaridae		Gammaridae		CG	
Amphipoda	Gammaridae		Gammarus	9.0	CG	SP
Amphipoda	Gammaridae		Stygobromus		PR	
Amphipoda	Gammaridae		Synurella	8.5	CG	SP
Amphipoda	Hyalellidae		Hyalella	6.8	CG	SP
Amphipoda	Melitidae		Melita			
Decapoda	Decapoda		Decapoda		SV	
Decapoda	Palaemonidae		Palaemonidae	2.0	SV	
Isopoda			Isopoda	5.4	SV	
Isopoda	Asellidae		Asellidae	5.4	SV	SP
Isopoda	Asellidae		Caecidotea	4.9	SV	SP
Isopoda	Asellidae		Lirceus	7.3	SV	SP
<u>Arachnida</u>						
Acari	Hydracarina		Hydracarina	4.4	PR	CB
<u>Insecta</u>						
Coleoptera	Carabidae		Carabidae		PR	CN
Coleoptera	Chrysomelidae		Chrysomelidae		SH	CN
Coleoptera	Coleoptera		Coleoptera		PR	
Coleoptera	Curculionidae		Curculionidae		SH	CN
Coleoptera	Dryopidae		Dryopidae		SC	CN
Coleoptera	Dryopidae		Helichus	5.0	CG	CN

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Coleoptera	Dryopidae		Pelonomus			CB
Coleoptera	Dytiscidae		Acilius		PR	SW
Coleoptera	Dytiscidae		Agabus	8.0	PR	SW
Coleoptera	Dytiscidae		Bidessonotus		PR	SW
Coleoptera	Dytiscidae		Celina		PR	SW
Coleoptera	Dytiscidae		Copelatus	9.0	PR	SW
Coleoptera	Dytiscidae		Coptotomus	9.0	PR	SW
Coleoptera	Dytiscidae		Cybister		PR	SW
Coleoptera	Dytiscidae		Desmopachria	4.0	PR	SW
Coleoptera	Dytiscidae		Dytiscidae	3.4	PR	CB
Coleoptera	Dytiscidae		Heterosternuta			
Coleoptera	Dytiscidae		Hydaticus	9.0	PR	SW
Coleoptera	Dytiscidae		Hydroporus	8.0	PR	SW
Coleoptera	Dytiscidae		Hydrovatus	4.0	PR	SW
Coleoptera	Dytiscidae		Hygrotus	4.0	PR	SW
Coleoptera	Dytiscidae		Ilybius		PR	SW
Coleoptera	Dytiscidae		Laccophilus	10.0	PR	SW
Coleoptera	Dytiscidae		Laccornis		PR	SW
Coleoptera	Dytiscidae		Liodessus		PR	SW
Coleoptera	Dytiscidae		Lioporeus		PR	SW
Coleoptera	Dytiscidae		Matus		PR	SW
Coleoptera	Dytiscidae		Neoporus	3.1	PR	SW
Coleoptera	Dytiscidae		Thermonectus		PR	SW
Coleoptera	Dytiscidae		Uvarus		SH	SW

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Coleoptera	Dytiscidae		Hydroporini		PR	SW
Coleoptera	Elmidae		Ancyronyx	2.0	OM	CN
Coleoptera	Elmidae		Dubiraphia	4.5	CG	CN
Coleoptera	Elmidae		Elmidae	4.3	CG	CN
Coleoptera	Elmidae		Gonielmis		CG	CN
Coleoptera	Elmidae		Macronychus	2.4	OM	CN
Coleoptera	Elmidae		Microcylloepus	1.9	CG	BU
Coleoptera	Elmidae		Optioservus	2.0	SC	CN
Coleoptera	Elmidae		Promoresia		SC	CN
Coleoptera	Elmidae		Stenelmis	4.8	SC	CN
Coleoptera	Gyrinidae		Dineutus	4.5	PR	SW
Coleoptera	Gyrinidae		Gyretes		PR	
Coleoptera	Gyrinidae		Gyrinidae		PR	SW
Coleoptera	Gyrinidae		Gyrinus	5.5	PR	SW
Coleoptera	Haliplidae		Haliplus	8.0	PI	CN
Coleoptera	Haliplidae		Peltodytes	8.2	PI	CN
Coleoptera	Heteroceridae		Heteroceridae			
Coleoptera	Hydraenidae		Hydraena		PR	CN
Coleoptera	Hydrophilidae		Berosus	8.6	PI	SW
Coleoptera	Hydrophilidae		Cymbiodyta		CG	SW
Coleoptera	Hydrophilidae		Enochrus	8.0	CG	BU
Coleoptera	Hydrophilidae		Helochares	4.0	OM	
Coleoptera	Hydrophilidae		Helocombus			
Coleoptera	Hydrophilidae		Helophorus		SH	SW

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Coleoptera	Hydrophilidae		Hydrobius		PR	CN
Coleoptera	Hydrophilidae		Hydrochus	6.0	SH	SW
Coleoptera	Hydrophilidae		Hydrophilidae	7.9	CG	SW
Coleoptera	Hydrophilidae		Paracymus		PR	CN
Coleoptera	Hydrophilidae		Phaenonotum			
Coleoptera	Hydrophilidae		Sperchopsis	5.0	PR	CN
Coleoptera	Hydrophilidae		Tropisternus	6.4	PR	CN
Coleoptera	Hydrophilidae	Berosini	Derallus		OM	
Coleoptera	Hydrophiloidea		Hydrophiloidea			
Coleoptera	Lampyridae		Lampyridae			
Coleoptera	Noteridae		Hydrocanthus	7.0	PR	CB
Coleoptera	Noteridae		Noteridae		PR	CB
Coleoptera	Noteridae		Suphisellus		PR	CB
Coleoptera	Psephenidae		Dicranopselaphus		SC	CN
Coleoptera	Psephenidae		Ectopria	4.0	SC	CN
Coleoptera	Psephenidae		Psephenidae		SC	CN
Coleoptera	Psephenidae		Psephenus		SC	CN
Coleoptera	Ptilodactylidae		Anchytarsus	4.0	SH	CN
Coleoptera	Ptilodactylidae		Ptilodactylidae		SH	CN
Coleoptera	Salpingidae		Salpingidae			
Coleoptera	Scirtidae		Cyphon	6.6	SC	CB
Coleoptera	Scirtidae		Ora			
Coleoptera	Scirtidae		Prionocyphon		SC	cb
Coleoptera	Scirtidae		Scirtes		SH	CB

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Coleoptera	Staphylinidae		Staphylinidae		PR	CN
Coleoptera	Staphylinidae		Stenus			SK
Collembola	Collembola		Collembola	8.0	CG	
Collembola	Isotomidae		Isotomidae		OM	
Diptera			Diptera		CG	CB
Diptera			Muscamorpha			
Diptera	Athericidae		Atherix	2.0	PR	SP
Diptera	Brachycera		Brachycera		PR	SP
Diptera	Brachyceridae		Brachyceridae			
Diptera	Cecidomyiidae		Cecidomyiidae			
Diptera	Ceratopogonidae		Ceratopogonidae	4.6	PR	SP
Diptera	Ceratopogonidae	Sphaeromiini	Sphaeromias			
Diptera	Chaoboridae		Chaoboridae	9.0	PR	SP
Diptera	Chaoboridae		Chaoborus	8.0	PR	SP
Diptera	Chaoboridae/Culicidae		Chaoboridae/Culicidae			
Diptera	Chironomidae		Camptocladius			
Diptera	Chironomidae		Chironomidae	4.8	CO	BU
Diptera	Chironomidae		Chironominae		CO	BU
Diptera	Chironomidae		Comptosmittia		CG	SP
Diptera	Chironomidae		Cryptochironomus			
Diptera	Chironomidae		Doithrix			
Diptera	Chironomidae		Kloosia			
Diptera	Chironomidae		Parasmittia			
Diptera	Chironomidae		Platysmittia			

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae		Sympotthastia		CO	SP
Diptera	Chironomidae		Unniella		CG	BU
Diptera	Chironomidae		Xenochironomus		PR	
Diptera	Chironomidae		Zalutschia		SH	
Diptera	Chironomidae	Chironomini	Apedilum			
Diptera	Chironomidae	Chironomini	Asheum beckae	6.0	CG	
Diptera	Chironomidae	Chironomini	Axarus	2.0	CG	SP
Diptera	Chironomidae	Chironomini	Chernovskiiia			
Diptera	Chironomidae	Chironomini	Chironomini	4.5	CG	BU
Diptera	Chironomidae	Chironomini	Chironomus	7.8	PR	CB
Diptera	Chironomidae	Chironomini	Cladopelma	3.0	CG	BU
Diptera	Chironomidae	Chironomini	Cryptochironomus	5.4	PR	SP
Diptera	Chironomidae	Chironomini	Cryptotendipes	6.0	CG	BU
Diptera	Chironomidae	Chironomini	Demicryptochironomus	2.0	CG	BU
Diptera	Chironomidae	Chironomini	Demicryptotendipes		CO	BU
Diptera	Chironomidae	Chironomini	Dicrotendipes	6.9	CG	BU
Diptera	Chironomidae	Chironomini	Einfeldia	4.3	CG	BU
Diptera	Chironomidae	Chironomini	Endochironomus	10.0	SH	CN
Diptera	Chironomidae	Chironomini	Gillotia		CG	
Diptera	Chironomidae	Chironomini	Glyptotendipes	9.9	SH	BU
Diptera	Chironomidae	Chironomini	Goeldichironomus	10.0	CG	BU
Diptera	Chironomidae	Chironomini	Harnischia	8.0	CG	CB
Diptera	Chironomidae	Chironomini	Hyporhygma			BU
Diptera	Chironomidae	Chironomini	Kiefferulus	4.7	CG	BU

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae	Chironomini	Lauterborniella		CG	CN
Diptera	Chironomidae	Chironomini	Lipiniella			
Diptera	Chironomidae	Chironomini	Microchironomus		CG	BU
Diptera	Chironomidae	Chironomini	Microtendipes	1.4	CF	CN
Diptera	Chironomidae	Chironomini	Nilothauma	5.0		
Diptera	Chironomidae	Chironomini	Omisus	4.0		
Diptera	Chironomidae	Chironomini	Pagastiella		CG	SP
Diptera	Chironomidae	Chironomini	Parachironomus	9.0	PR	SP
Diptera	Chironomidae	Chironomini	Paracladopelma	5.0	CG	SP
Diptera	Chironomidae	Chironomini	Paralauterborniella	4.2	CG	BU
Diptera	Chironomidae	Chironomini	Paratendipes	1.9	CG	BU
Diptera	Chironomidae	Chironomini	Phaenopsectra	6.3	SC	CN
Diptera	Chironomidae	Chironomini	Polypedilum	4.1	SH	Cb
Diptera	Chironomidae	Chironomini	Robackia		CG	BU
Diptera	Chironomidae	Chironomini	Saetheria	7.0	CG	BU
Diptera	Chironomidae	Chironomini	Stelechomyia		CG	BU
Diptera	Chironomidae	Chironomini	Stenochironomus	1.5	CG	BU
Diptera	Chironomidae	Chironomini	Stictochironomus	5.1	CG	BU
Diptera	Chironomidae	Chironomini	Tribelos	2.9	CG	BU
Diptera	Chironomidae	Chironomini	Xestochironomus		PR	BU
Diptera	Chironomidae	Coelotanypodini	Alotanypus			BU
Diptera	Chironomidae	Coelotanypodini	Clinotanypus	4.5	PR	BU
Diptera	Chironomidae	Coelotanypodini	Coelotanypus	8.0	PR	BU
Diptera	Chironomidae	Coelotanypodini	Fittkauimyia			SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae	Diamesinae	Diamesinae		CG	SP
Diptera	Chironomidae	Diamesini	Potthastia	6.0	CG	SP
Diptera	Chironomidae	Macropelopiini	Apsectrotanypus	0.0	PR	BU
Diptera	Chironomidae	Natarsiini	Natarsia	6.2	PR	SP
Diptera	Chironomidae	Orthocladiinae	Brillia	2.9	SH	BU
Diptera	Chironomidae	Orthocladiinae	Bryophaenocladus			SP
Diptera	Chironomidae	Orthocladiinae	Chaetocladus		CG	SP
Diptera	Chironomidae	Orthocladiinae	Corynoneura	3.2	CG	SP
Diptera	Chironomidae	Orthocladiinae	Cricotopus/Orthocladus	5.8	SH	SP
Diptera	Chironomidae	Orthocladiinae	Diplocladus	10.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Endotribeles		CG	BU
Diptera	Chironomidae	Orthocladiinae	Epoicocladus	0.0	CG	
Diptera	Chironomidae	Orthocladiinae	Eukiefferiella	6.1	CG	SP
Diptera	Chironomidae	Orthocladiinae	Eukiefferiella/Tvetenia		CG	SP
Diptera	Chironomidae	Orthocladiinae	Georthocladus			SP
Diptera	Chironomidae	Orthocladiinae	Gymnometriocnemus	7.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Heterotrissocladus	4.2	CG	SP
Diptera	Chironomidae	Orthocladiinae	Hydrobaenus	10.0	SC	SP
Diptera	Chironomidae	Orthocladiinae	Krenosmittia		CG	SP
Diptera	Chironomidae	Orthocladiinae	Limnophyes	8.5	CG	SP
Diptera	Chironomidae	Orthocladiinae	Lopescladius	1.0	CG	BU
Diptera	Chironomidae	Orthocladiinae	Mesocricotopus		CO	SP
Diptera	Chironomidae	Orthocladiinae	Mesosmittia			SP
Diptera	Chironomidae	Orthocladiinae	Nanocladus	4.7	CG	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae	Orthocladiinae	Orthocladiinae	5.7	CG	BU
Diptera	Chironomidae	Orthocladiinae	Parachaetocladius	0.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Paracricotopus		CG	SP
Diptera	Chironomidae	Orthocladiinae	Parakiefferiella	2.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Parametriocnemus	3.1	CG	SP
Diptera	Chironomidae	Orthocladiinae	Paraphaenocladius	1.2	CG	SP
Diptera	Chironomidae	Orthocladiinae	Paratrichocladius		CG	SP
Diptera	Chironomidae	Orthocladiinae	Psectrocladius		CG	SP
Diptera	Chironomidae	Orthocladiinae	Pseudorthocladius	1.1	CG	SP
Diptera	Chironomidae	Orthocladiinae	Pseudosmittia	5.5	CG	SP
Diptera	Chironomidae	Orthocladiinae	Psilometriocnemus		CG	
Diptera	Chironomidae	Orthocladiinae	Rheocricotopus	2.7	CG	SP
Diptera	Chironomidae	Orthocladiinae	Rheosmittia	7.0	CG	BU
Diptera	Chironomidae	Orthocladiinae	Smittia	8.4	CG	BU
Diptera	Chironomidae	Orthocladiinae	Stilocladius	1.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Synorthocladius	4.0	CG	unk
Diptera	Chironomidae	Orthocladiinae	Thienemanniella	4.0	CG	SP
Diptera	Chironomidae	Orthocladiinae	Tvetenia	2.2	CG	SP
Diptera	Chironomidae	Orthocladiinae	Xylotopus		unk	BU
Diptera	Chironomidae	Pentaneurini	Ablabesmyia	5.0	PR	SP
Diptera	Chironomidae	Pentaneurini	Denopelopia			
Diptera	Chironomidae	Pentaneurini	Krenopelopia		PR	SP
Diptera	Chironomidae	Pentaneurini	Labrundinia	2.4	PR	SP
Diptera	Chironomidae	Pentaneurini	Labrundinia/Nilotempus		PR	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae	Pentaneurini	Larsia	9.0	PR	SP
Diptera	Chironomidae	Pentaneurini	Monopelopia		PR	SP
Diptera	Chironomidae	Pentaneurini	Nilotanypus	3.0	PR	SP
Diptera	Chironomidae	Pentaneurini	Paramerina	4.0	PR	SP
Diptera	Chironomidae	Pentaneurini	Pentaneura		PR	SP
Diptera	Chironomidae	Pentaneurini	Trissopelopia		PR	SP
Diptera	Chironomidae	Pentaneurini	Zavreliomyia	5.6	PR	SP
Diptera	Chironomidae	Pentaneurini	Pentaneurini			
Diptera	Chironomidae	Procladiini	Djalmabatista	3.4	PR	SP
Diptera	Chironomidae	Procladiini	Djalmabatista/Procladius		PR	SP
Diptera	Chironomidae	Procladiini	Procladius	5.2	PR	SP
Diptera	Chironomidae	Prodiamesinae	Monodiamesa	7.0	CG	BU
Diptera	Chironomidae	Prodiamesinae	Odontomesa	5.0	CG	SP
Diptera	Chironomidae	Pseudochironomini	Pseudochironomus	4.4	CG	BU
Diptera	Chironomidae	Tanypodinae	Bethbilbeckia			
Diptera	Chironomidae	Tanypodinae	Cantopelopia gesta			
Diptera	Chironomidae	Tanypodinae	Tanypodinae	5.8	PR	BU
Diptera	Chironomidae	Tanypodinae	Telopelopia		PR	
Diptera	Chironomidae	Tanypodinae	Thienemannimyia genus Gr.	6.0	PR	SP
Diptera	Chironomidae	Tanypodini	Tanypodini			
Diptera	Chironomidae	Tanypodini	Tanypus	9.0	PR	SP
Diptera	Chironomidae	Tanytarsini	Cladotanytarsus	3.8	CG	CB
Diptera	Chironomidae	Tanytarsini	Clinotanytarsus			
Diptera	Chironomidae	Tanytarsini	Constempellina		CG	CB

Appendix A. Benthic macroinvertebrate taxa used in M-BISQ metric calculations, including attributes of tolerance value (TV), functional feeding group (FFG), and habit. Abbreviations: *for FFG* - PR, predator; PA, parasite; OM, omnivore; CG, collector-gatherer; CF, collector-filterer; SC, scraper; SV, scavenger; SH, shredder; PI, piercer; CO, collector; *for habit* – BU, burrower; SP, sprawler; CB, climber; CN, clinger; SW, swimmer).

Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Chironomidae	Tanytarsini	Micropsectra	1.5	CG	CN
Diptera	Chironomidae	Tanytarsini	Paratanytarsus	5.9	CG	CN
Diptera	Chironomidae	Tanytarsini	Rheotanytarsus	3.3	CF	CN
Diptera	Chironomidae	Tanytarsini	Stempellina	2.0	CG	CB
Diptera	Chironomidae	Tanytarsini	Stempellinella	1.5	CG	CN
Diptera	Chironomidae	Tanytarsini	Sublettea	1.0	CF	
Diptera	Chironomidae	Tanytarsini	Tanytarsini	3.6	CF	BU
Diptera	Chironomidae	Tanytarsini	Tanytarsus	3.5	CF	CN
Diptera	Chironomidae	Tanytarsini	Zavrelia		CG	SW
Diptera	Chironomidae	Tanytarsini	Zavreliella	6.0	CG	BU
Diptera	Culicidae		Anopheles		CF	SW
Diptera	Culicidae		Culicidae	8.0	CF	SW
Diptera	Culicidae	Culicini	Aedes		CG	SW
Diptera	Culicidae	Culicini	Culex		CF	SW
Diptera	Dixidae		Dixa	3.0	CG	CB
Diptera	Dixidae		Dixella	2.0	CG	SW
Diptera	Dixidae		Dixidae		CO	SW
Diptera	Dolichopodidae		Dolichopodidae	5.3	PR	BU
Diptera	Empididae		Empididae	7.0	PR	SP
Diptera	Empididae		Roederiodes			
Diptera	Empididae		Wiedemannia		PR	CN
Diptera	Empididae	Hemerodromiini	Chelifera	7.0	CG	BU
Diptera	Empididae	Hemerodromiini	Hemerodromia	4.2	PR	SP
Diptera	Empididae	Hemerodromiini	Neoplasta			SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Ephydriidae		Ephydriidae	6.0	CG	BU
Diptera	Ephydriidae	Ephydrini	Ephydra		SH	BU
Diptera	Muscidae		Muscidae		PR	SP
Diptera	Muscidae	Limnophorini	Limnophora		PR	BU
Diptera	Phoridae		Phoridae		CG	BU
Diptera	Psychodidae		Pericoma	4.0	CG	BU
Diptera	Psychodidae		Psychoda	9.0	CG	BU
Diptera	Psychodidae		Psychodidae		CG	BU
Diptera	Ptychopteridae		Bittacomorpha		CO	BU
Diptera	Sciaridae		Sciaridae	4.2		
Diptera	Sciomyzidae		Sciomyzidae		PR	BU
Diptera	Simuliidae		Simuliidae	3.5	CF	CN
Diptera	Stratiomyidae		Allognosta		CG	
Diptera	Stratiomyidae		Caloparyphus		CG	SP
Diptera	Stratiomyidae		Myxosargus			
Diptera	Stratiomyidae		Nemotelus		CG	SP
Diptera	Stratiomyidae		Odontomyia		CG	SP
Diptera	Stratiomyidae		Stratiomyidae	6.0	CG	SP
Diptera	Stratiomyidae	Stratiomyini	Stratiomys		CG	SP
Diptera	Tabanidae		Chlorotabanus		PI;P	SP
Diptera	Tabanidae		Hybomitra		PI	SP
Diptera	Tabanidae		Hybomitra/Tabanus		PR	SP
Diptera	Tabanidae		Tabanidae	5.2	PR	SP
Diptera	Tabanidae	Chrysopsini	Chrysops	5.0	PR	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Diptera	Tabanidae	Chrysopsini	Silvius		PR	SP
Diptera	Tabanidae	Tabanini	Tabanus	7.4	PR	SP
Diptera	Tanyderidae		Protoplasa		CG	SP
Diptera	Tanyderidae		Tanyderidae		CG	SP
Diptera	Tipulidae		Epiphragma			
Diptera	Tipulidae		Helius		CG	BU
Diptera	Tipulidae		Limoniinae		CG	
Diptera	Tipulidae		Pedicia	4.0	PR	bu
Diptera	Tipulidae		Tipula	4.9	SH	BU
Diptera	Tipulidae		Tipulidae	4.2	SH	BU
Diptera	Tipulidae	Eriopterini	Cryptolabis		SH	BU
Diptera	Tipulidae	Eriopterini	Erioptera	4.6	CG	BU
Diptera	Tipulidae	Eriopterini	Gonomyia	4.3	CG	BU
Diptera	Tipulidae	Eriopterini	Molophilus	5.0	SH	BU
Diptera	Tipulidae	Eriopterini	Ormosia		CG	BU
Diptera	Tipulidae	Hexatomini	Hexatoma		PR	BU
Diptera	Tipulidae	Hexatomini	Limnophila	0.2	PR	BU
Diptera	Tipulidae	Hexatomini	Pilaria	3.0	PR	BU
Diptera	Tipulidae	Hexatomini	Pseudolimnophila	2.0	PR	BU
Diptera	Tipulidae	Limoniini	Antocha		CG	CN
Diptera	Tipulidae	Limoniini	Limonia	9.0	SH	BU
Diptera	Tipulidae	Pediciini	Dicranota		PR	SP
Ephemeroptera			Ephemeroptera		CG	
Ephemeroptera	Baetidae		Acentrella	3.0	CG	SW

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Ephemeroptera	Baetidae		Acerpenna	5.9	CG	SW
Ephemeroptera	Baetidae		Baetidae	5.5	CG	SW
Ephemeroptera	Baetidae		Baetis	3.6	CG	SW
Ephemeroptera	Baetidae		Callibaetis		CG	SW
Ephemeroptera	Baetidae		Callibaetis/Cloeon		CO	SW
Ephemeroptera	Baetidae		Centroptilum		CG	SW
Ephemeroptera	Baetidae		Centroptilum/Procloeon	7.7	OM	SW
Ephemeroptera	Baetidae		Heterocloeon		SC	SW
Ephemeroptera	Baetidae		Labiobaetis		CG	SW
Ephemeroptera	Baetidae		Paracloeodes		SC	SW
Ephemeroptera	Baetidae		Plauditus			SW
Ephemeroptera	Baetidae		Procloeon		OM	SW
Ephemeroptera	Baetidae		Pseudocentroptiloides			
Ephemeroptera	Baetidae		Pseudocloeon	3.4	SC	SW
Ephemeroptera	Baetiscidae		Baetisca	0.9	CG	SP
Ephemeroptera	Caenidae		Brachycercus		CG	SP
Ephemeroptera	Caenidae		Caenidae	9.7	CG	sp
Ephemeroptera	Caenidae		Caenis	9.7	CG	SP
Ephemeroptera	Ephemerellidae		Attenella		CG	CN
Ephemeroptera	Ephemerellidae		Clinocera		PR	CN
Ephemeroptera	Ephemerellidae		Ephemerella	3.3	CG	CN
Ephemeroptera	Ephemerellidae		Ephemerella/Serratella		CO	CN
Ephemeroptera	Ephemerellidae		Ephemerellidae	1.3	CG	CN
Ephemeroptera	Ephemerellidae		Eurylophella	0.6	CG	CN

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Ephemeroptera	Ephemerellidae		Serratella	2.2	CG	CN
Ephemeroptera	Ephemerellidae		Teloganopsis			
Ephemeroptera	Ephemerellidae		Timpanoga (Danella)		CG	CN
Ephemeroptera	Ephemeridae		Ephemera		CG	BU
Ephemeroptera	Ephemeridae		Ephemeridae	2.4	CG	BU
Ephemeroptera	Ephemeridae		Hexagenia	2.4	CG	BU
Ephemeroptera	Heptageniidae		Heptagenia	2.0	SC	CN
Ephemeroptera	Heptageniidae		Heptageniidae	4.6	SC	CN
Ephemeroptera	Heptageniidae		Leucrocuta	1.0	SC	CN
Ephemeroptera	Heptageniidae		Maccaffertium			
Ephemeroptera	Heptageniidae		Pseudiron centralis			
Ephemeroptera	Heptageniidae		Rhithrogena	0.0	SC	CN
Ephemeroptera	Heptageniidae		Stenacron	6.0	CG	CN
Ephemeroptera	Heptageniidae		Stenonema	4.2	SC	CN
Ephemeroptera	Isonychiidae		Isonychia	1.9	CF	SW
Ephemeroptera	Leptohyphidae		Leptohyphes		PR	CN
Ephemeroptera	Leptohyphidae		Leptohyphidae		CG	
Ephemeroptera	Leptohyphidae		Tricorythodes	2.2	CG	SP
Ephemeroptera	Leptophlebiidae		Leptophlebia	5.0	CG	SW
Ephemeroptera	Leptophlebiidae		Leptophlebiidae	2.7	CG	CN
Ephemeroptera	Leptophlebiidae		Paraleptophlebia	0.0	CG	SW
Ephemeroptera	Metretopodidae		Siphloplecton		CG	SW
Ephemeroptera	Neoephemeridae		Neoephemera		CG	SP
Ephemeroptera	Siphonuridae		Siphonuridae		CG	

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Ephemeroptera	Siphonuridae		Siphonurus		CG	SW
Ephemeroptera	Tricorythidae		Tricorythidae		CG	CN
Hemiptera	Belostomatidae		Belostoma		PR	CB
Hemiptera	Corixidae		Corixidae			
Hemiptera	Corixidae		Trichocorixa			
Hemiptera	Gerridae		Gerridae		PR	SK
Hemiptera	Hydrometridae		Hydrometra		PR	SK
Heteroptera	Gerridae		Limnopus		PR	SK
Heteroptera	Gerridae		Metrobates		PR	SK
Heteroptera	Gerridae		Rheumatobates		PR	SK
Heteroptera	Gerridae		Trepobates		PR	CB
Heteroptera	Mesoveliidae		Mesovelia		PR	SK
Heteroptera	Naucoridae		Pelocoris		PR	CB
Heteroptera	Nepidae		Ranatra	7.0	PR	CN
Heteroptera	Notonectidae	Notonectini	Notonecta			
Heteroptera	Pleidae		Neoplea		PR	SW
Heteroptera	Veliidae		Microvelia	6.0	PR	SK
Heteroptera	Veliidae		Platyvelia		PR	SK
Heteroptera	Veliidae		Rhagovelia		PR	SK
Homoptera	Aphididae		Coloradoa			
Lepidoptera			Lepidoptera	6.0	SH	
Lepidoptera	Cosmopterygidae		Cosmopterygidae		SH	
Lepidoptera	Crambidae		Crambidae			
Lepidoptera	Crambidae	Nymphulini	Synclita		CF	

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Lepidoptera	Nepticulidae		Nepticulidae		SH	BU
Lepidoptera	Pyralidae		Acentria		SH	CB
Lepidoptera	Pyralidae		Paraponyx	5.0	SH	CN
Lepidoptera	Pyralidae		Pyralidae		SH	CB
Megaloptera	Corydalidae		Chauliodes	9.0	PR	CN
Megaloptera	Corydalidae		Corydalidae	3.6	PR	CN
Megaloptera	Corydalidae		Corydalus	3.7	PR	CN
Megaloptera	Corydalidae		Nigronia	5.0	PR	CN
Megaloptera	Sialidae		Sialis	4.1	PR	BU
Megaloptera	Sisyridae		Climacia	8.0	PR	CB
Megaloptera	Sisyridae		Sisyra		PI	
Odonata	Aeshnidae		Aeshna		PR	CB
Odonata	Aeshnidae		Aeshnidae	5.4	PR	CN
Odonata	Aeshnidae		Anax	4.0	PR	CN
Odonata	Aeshnidae		Basiaeschna	7.0	PR	CB
Odonata	Aeshnidae		Boyeria	4.3	PR	CB
Odonata	Aeshnidae		Epiaeschna		CF,CG	CB
Odonata	Aeshnidae		Nasiaeschna	8.0	PR	CB
Odonata	Anisoptera		Anisoptera		PR	
Odonata	Calopterygidae		Calopterygidae	5.2	PR	CB
Odonata	Calopterygidae		Calopteryx	5.6	PR	CB
Odonata	Calopterygidae		Hetaerina	4.2	PR	CN
Odonata	Coenagrionidae		Argia	6.5	PR	CN
Odonata	Coenagrionidae		Chromagrion		PR	CB

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Odonata	Coenagrionidae		Coenagrion		PR	CN
Odonata	Coenagrionidae		Coenagrion/Enallagma		PR	CB
Odonata	Coenagrionidae		Coenagrionidae	7.0	PR	CB
Odonata	Coenagrionidae		Enallagma	7.9	PR	CB
Odonata	Coenagrionidae		Ischnura	9.7	PR	CB
Odonata	Coenagrionidae		Zoniagrion		PR	
Odonata	Cordulegastridae		Cordulegaster	5.0	PR	BU
Odonata	Cordulegastridae		Cordulegastridae		PR	BU
Odonata	Corduliidae		Corduliidae		PR	CB
Odonata	Corduliidae		Epithea (Epicordulia)		PR	CB
Odonata	Corduliidae		Neurocordulia	5.0	PR	CB
Odonata	Corduliidae		Tetragoneuria		PR	
Odonata	Corduliidae	Corduliinae	Corduliinae	3.6	PR	SP
Odonata	Corduliidae	Corduliinae/Libellulinae	Corduliinae/Libellulinae	3.6	PR	
Odonata	Corduliidae	Macromiinae	Macromiinae	3.0	PR	SP
Odonata	Corduliidae/Libellulidae		Corduliidae/Libellulidae		PR	CB
Odonata	Corduliidae/Libellulidae		Odonata		PR	CB
Odonata	Corduliidae/Macromiidae		Corduliidae/Macromiidae			
Odonata	Gomphidae		Arigomphus		CF	BU
Odonata	Gomphidae		Dromogomphus	2.7	PR	BU
Odonata	Gomphidae		Erpetogomphus	4.0	PR	BU
Odonata	Gomphidae		Gomphidae	5.3	PR	BU
Odonata	Gomphidae		Gomphus	5.2	PR	BU
Odonata	Gomphidae		Hagenius	4.0	PR	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Odonata	Gomphidae		Lanthus		PR	BU
Odonata	Gomphidae		Ophiogomphus	5.0	PR	BU
Odonata	Gomphidae		Progomphus	6.5	PR	BU
Odonata	Gomphidae		Stylogomphus		PR	BU
Odonata	Gomphidae		Stylurus	5.0	PR	SP
Odonata	Lestidae		Lestes		PR	CB
Odonata	Libellulidae		Celithemis		PR	CB
Odonata	Libellulidae		Didymops	2.0	PR	SP
Odonata	Libellulidae		Erythemis	9.0	PR	CB
Odonata	Libellulidae		Helocordulia	4.0	PR	SP
Odonata	Libellulidae		Libellula	10.0	PR	SP
Odonata	Libellulidae		Libellulidae	7.2	PR	SP
Odonata	Libellulidae		Macromia	4.9	PR	SP
Odonata	Libellulidae		Miathyria		PR	CB
Odonata	Libellulidae		Pachydiplax	8.0	PR	SP
Odonata	Libellulidae		Perithemis		PR	SP
Odonata	Libellulidae		Plathemis	3.0	PR	
Odonata	Libellulidae		Somatochlora	8.4	PR	CB
Odonata	Libellulidae		Sympetrum		PR	SP
Odonata	Macromiidae		Macromiidae	3.0	PR	
Pepidoptera	Pyralidae		Crambus		SH	
Plecoptera			Plecoptera		PR	CN
Plecoptera	Capniidae		Allocapnia	5.9	SH	SP
Plecoptera	Capniidae		Capniidae	5.9	SH	SP

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Plecoptera	Capniidae		Nemocapnia			
Plecoptera	Chloroperlidae		Alloperla	1.0	PR	CN
Plecoptera	Chloroperlidae		Chloroperlidae	1.8	PR	CN
Plecoptera	Chloroperlidae		Haploperla		SC	CN
Plecoptera	Chloroperlidae		Perlinella	2.0	PR	CN
Plecoptera	Leuctridae		Leuctra	0.0	SH	SP
Plecoptera	Leuctridae		Leuctridae		SH	CN
Plecoptera	Leuctridae		Zealeuctra		SH	
Plecoptera	Nemouridae		Amphinemura	4.4	SH	CN
Plecoptera	Nemouridae		Nemouridae	5.8	SH	CN
Plecoptera	Nemouridae		Ostrocerca		SH	SP
Plecoptera	Nemouridae		Prostoia		SH	SP
Plecoptera	Nemouridae		Shipsa		SH	SP
Plecoptera	Perlidae		Acroneuria	0.0	PR	CN
Plecoptera	Perlidae		Agnetina	0.0	PR	CN
Plecoptera	Perlidae		Agnetina/Paragnetina		PR	CN
Plecoptera	Perlidae		Attaneuria ruralis		PR	CN
Plecoptera	Perlidae		Beloneuria	0.0	PR	CN
Plecoptera	Perlidae		Eccoptura	3.0	PR	CN
Plecoptera	Perlidae		Neoperla	0.0	PR	CN
Plecoptera	Perlidae		Paragnetina		PR	CN
Plecoptera	Perlidae		Perlesta	1.8	PR	CN
Plecoptera	Perlidae		Perlidae	0.8	PR	CN
Plecoptera	Perlodidae		Clioperla clio	3.7	PR	CN

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Plecoptera	Perlodidae		Helopicus	0.0	PR	CN
Plecoptera	Perlodidae		Hydroperla		PR	CN
Plecoptera	Perlodidae		Isoperla	3.7	PR	CN
Plecoptera	Perlodidae		Perlodidae	3.5	PR	CN
Plecoptera	Pteronarcyidae		Pteronarcys	1.0	SH	CN
Plecoptera	Taeniopterygidae		Paracapnia		SH	SP
Plecoptera	Taeniopterygidae		Strophopteryx		SH	
Plecoptera	Taeniopterygidae		Taeniopterygidae	2.1	SH	SP
Plecoptera	Taeniopterygidae		Taeniopteryx	2.1	SH	CN
Trichoptera			Trichoptera	3.8	CG	SP
Trichoptera	Brachycentridae		Brachycentridae		CF	CN
Trichoptera	Brachycentridae		Brachycentrus	2.0	CF	CN
Trichoptera	Brachycentridae		Micrasema	0.0	SH	CN
Trichoptera	Calamoceratidae		Anisocentropus	2.0	SH	SP
Trichoptera	Calamoceratidae		Heteroplectron		SH	SP
Trichoptera	Dipseudopsidae		Phylocentropus	6.0	CF	CN
Trichoptera	Glossosomatidae		Glossosomatidae	0.0	SC	CN
Trichoptera	Glossosomatidae		Protoptila	1.0	SC	CN
Trichoptera	Hydropsychidae		Ceratopsyche	1.6	CF	CN
Trichoptera	Hydropsychidae		Cheumatopsyche	5.8	CF	CN
Trichoptera	Hydropsychidae		Diplectrona	2.0	CF	CN
Trichoptera	Hydropsychidae		Hydropsyche	3.0	CF	CN
Trichoptera	Hydropsychidae		Hydropsychidae	5.2	CF	CN
Trichoptera	Hydropsychidae		Macrostemum	3.0	CF	CN

Appendix A. Benthic macroinvertebrate taxa used in M-BISQ metric calculations, including attributes of tolerance value (TV), functional feeding group (FFG), and habit. Abbreviations: *for FFG* - PR, predator; PA, parasite; OM, omnivore; CG, collector-gatherer; CF, collector-filterer; SC, scraper; SV, scavenger; SH, shredder; PI, piercer; CO, collector; *for habit* – BU, burrower; SP, sprawler; CB, climber; CN, clinger; SW, swimmer).

Order	Family	Tribe	FinalID	TV	FFG	Habit
Trichoptera	Hydropsychidae		Potamyia		CF	CN
Trichoptera	Hydroptilidae		Agraylea		CF,CG	CB
Trichoptera	Hydroptilidae		Dibusa		SC	CN
Trichoptera	Hydroptilidae		Hydroptila	3.8	PI	CN
Trichoptera	Hydroptilidae		Hydroptilidae	3.5	PI	CN
Trichoptera	Hydroptilidae		Neotrichia		SC	CN
Trichoptera	Hydroptilidae		Ochrotrichia		CG	CB
Trichoptera	Hydroptilidae		Orthotrichia		PI	CN
Trichoptera	Hydroptilidae		Oxyethira	1.3	PI	CN
Trichoptera	Hydroptilidae		Stactobiella		SH	CB
Trichoptera	Hydroptilidae	Neotrichiini	Mayatrichia		SC	CN
Trichoptera	Lepidostomatidae		Lepidostoma		SH	CB
Trichoptera	Leptoceridae		Ceraclea	3.0	CG	CN
Trichoptera	Leptoceridae		Leptoceridae	1.9	CG	CB
Trichoptera	Leptoceridae		Mystacides		CG	SP
Trichoptera	Leptoceridae		Nectopsyche	5.4	SH	SP
Trichoptera	Leptoceridae		Setodes		OM	SP
Trichoptera	Leptoceridae		Triaenodes	0.7	SH	SW
Trichoptera	Leptoceridae	Oecetini	Oecetis	2.4	PR	CN
Trichoptera	Leptoceridae	Triaenodini	Ylodes			
Trichoptera	Limnephilidae		Hesperophylax		SH	SP
Trichoptera	Limnephilidae		Ironoquia	7.0	SH	CN
Trichoptera	Limnephilidae		Limnephilidae	1.5	SH	CB
Trichoptera	Limnephilidae		Limnephilus		SH	CB

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Trichoptera	Limnephilidae		Neophylax	2.0	SC	CN
Trichoptera	Limnephilidae	Stenophylacini	Hydatophylax		SH	SP
Trichoptera	Limnephilidae	Stenophylacini	Pycnopsyche	1.4	SH	SP
Trichoptera	Molannidae		Molanna	4.0	SC	SP
Trichoptera	Molannidae		Molannidae			
Trichoptera	Odontoceridae		Psilotreta	0.0	SC	SP
Trichoptera	Philopotamidae		Chimarra	1.2	CF	CN
Trichoptera	Philopotamidae		Dolophilodes		CF	CN
Trichoptera	Philopotamidae		Philopotamidae	1.2	CF	CN
Trichoptera	Phryganeidae		Agrypnia		SH	CB
Trichoptera	Phryganeidae		Phryganeidae		SH	CB
Trichoptera	Phryganeidae		Ptilostomis	3.0	SH	CN
Trichoptera	Polycentropodidae		Cernotina	1.2	PR	CN
Trichoptera	Polycentropodidae		Cernotina/Polycentropus		PR	CN
Trichoptera	Polycentropodidae		Cyrnellus	5.0	CF	CN
Trichoptera	Polycentropodidae		Neureclipsis	2.7	CF	CN
Trichoptera	Polycentropodidae		Nyctiophylax	0.0	PR	CN
Trichoptera	Polycentropodidae		Paranyctiophylax			
Trichoptera	Polycentropodidae		Polycentropodidae	2.1	CF	CN
Trichoptera	Polycentropodidae		Polycentropus	1.9	PR	CN
Trichoptera	Psychomyiidae		Lype		SC	BU
Trichoptera	Psychomyiidae		Psychomyiidae		CG	CN
Trichoptera	Rhyacophilidae		Rhyacophila	0.0	PR	CN
Trichoptera	Rhyacophilidae		Rhyacophilidae		PR	CN

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Order	Family	Tribe	FinalID	TV	FFG	Habit
Trichoptera	Sericostomatidae		Agarodes	0.0	SH	SP