2006 303(d) ASSESSMENT METHODS FOR CHESAPEAKE BAY BENTHOS

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FOREWORD

This report, *2006 303(d) Assessment Methods for Chesapeake Bay Benthos*, was prepared by Versar at the request of the Virginia Department of Environmental Quality, under Purchase Order # 11646 between Versar, Inc. and the Commonwealth of Virginia. Old Dominion University contributed to the diagnostic (discriminant tool) assessment and to project conceptualization and evaluation. The statistical analyses for the 2006 impairment assessment were conducted by Dr. Ed Weber and Ms. Jody Dew, of Versar. Dr. Weber also contributed to the development of the Degraded Area method presented in this report.

TABLE OF CONTENTS

1.0 INTRODUCTION

To meet the requirements of the Clean Water Act, the States of Maryland and Virginia are using benthic biological criteria for reporting overall condition and identification of impaired waters in Chesapeake Bay. The Chesapeake Bay benthic index of biotic integrity (B-IBI) is the basis for these biological criteria. Previous work conducted by Versar and Old Dominion University had two objectives: to develop a methodology for the assessment of benthic community status for 303(d) impairment decisions and to produce an assessment for each of the Chesapeake Bay segments and sub-segments containing benthic community data. A statistical procedure was developed that tests whether the distribution of B-IBI scores from probability-based samples collected from a Bay segment is significantly different from the distribution of scores from reference sites (Llansó et al. 2003). This procedure, a stratified Wilcoxon rank sum test, was evaluated and applied to the 2004 assessment data. The assessment resulted in 26 segments considered impaired based upon benthic community condition. The Wilcoxon approach, however, was sensitive to small shifts in B-IBI scores relative to the reference condition, even in some cases where a majority of the B-IBI scores in a segment met the restoration goals. For stratified data (i.e., the habitat types of the B-IBI, see below) it was not possible to estimate the magnitude of the shift, for example by using a Hodges-Lehman confidence interval. Thus, with the Wilcoxon approach we were unable to estimate the magnitude of degradation: the difference between the segment and the reference condition. A small difference could be statistically significant but of little ecological relevance. It was recommended that alternative methods be evaluated, especially those that take into account magnitude of departure from reference conditions and whether this magnitude is above specific thresholds of protection that the States may wish to implement. For the 2006 303(d) report, we developed a new method that quantifies magnitude of degradation. We call this method "Degraded Area". In the present report, we describe the Degraded Area method, apply this method and the Wilcoxon approach to the 2006 assessment data, and compare the results.

In addition, a benthic diagnostic tool has been developed that can be used to identify potential sources of stress affecting benthic community condition in the Chesapeake Bay (Dauer et al. 2002). The tool can distinguish stress due to contaminants versus stress due to other factors (e.g., low dissolved oxygen, or unknown). This screening tool was used to identify which impaired segments have a high probability of sediment contamination. These segments could then be targeted for additional sampling or evaluation. The B-IBI metric scores for abundance and biomass were also used to identify (1) insufficient abundance patterns consistent with a low dissolved oxygen effect and (2) excessive abundance patterns consistent with eutrophication effects.

2.0 OBJECTIVES

1. Develop a new method for the assessment of Chesapeake Bay benthic community status for 303(d) impairment decisions.
2. Produce an assessment for the 2006 303(d) report using both the new method and the Wilcoxon approach.
3. Apply the benthic diagnostic tool and the insufficient/excessive abundance criteria to the 2006 assessment data.

3.0 METHODS

3.1. DATA

Like the Wilcoxon (described in Llansó et al. 2003), the Degraded Area method compares reference data sets to assessment data sets. The reference data set consisted of the calibration and validation data used to develop the Chesapeake Bay benthic index of biotic integrity (B-IBI). The Chesapeake Bay B-IBI is described in Weisberg et al. (1997) and Alden et al. (2002). The B-IBI consists of benthic community metrics and scoring thresholds (metric values) that were developed separately for seven habitat types (Table 1). The numbers of reference samples in each habitat used to develop the B-IBI, the Wilcoxon approach, and the method described in this report are listed in Table 2. The reference samples were either "good" (=undegraded, collected at sites known to have good sediment and water quality) or "degraded" (collected at sites with low dissolved oxygen, organic enrichment, or high sediment contaminant concentrations and toxicity). To develop the B-IBI, Weisberg et al. (1997) used averages of three replicate samples per site for mesohaline and polyhaline habitats, while Alden et al. (2002) used single replicate samples for tidal fresh and oligohaline habitats. We used the same metrics values produced by these two studies, but re-calculated B-IBI scores from these metrics to be consistent with the latest B-IBI methodology. The methods for the calculation of the Chesapeake B-IBI are described in the World Wide Web at: http://www.baybenthos.versar.com/ referenc.htm.

The assessment data for the 2006 303(d) report consisted of random samples collected from 2000 to 2004 throughout the Chesapeake Bay. A total of 1,430 samples (single replicates) were used, including 750 samples collected by the Maryland Chesapeake Bay benthic monitoring program, 500 samples collected by the Virginia Chesapeake Bay benthic monitoring program, 150 samples collected by the Elizabeth River benthic biological monitoring program, and 10 samples collected for a gear comparison study in each of Mobjack Bay, the tidal fresh Mattaponi River, and the Nansemond River. All assessment samples were collected with a Young grab (440 cm^2 surface area, 0.5-mm screen). For sample collection methods, see the benthic monitoring program comprehensive reports posted at the World Wide Web address given above.

Assessments were produced for each of 85 Chesapeake Bay Program segments and sub-segments containing benthic data. Segments (TMWA 1999) are Chesapeake Bay regions having similar salinity and hydrographic characteristics. In Virginia, segments were sub-divided into smaller units by the Virginia Department of Environmental Quality. Sub-segments were produced for each of the mainstems of rivers and bays (e.g., James River mesohaline) and for some of the smaller systems opening into the mainstem (e.g., Pagan River). Assessment samples were assigned to segments and sub-segments using GIS software. Hydrographic data collected synoptically with the benthic data were used to assign each sample to one of seven habitat classes used in the calculation of the B-IBI. These are the same habitat classes used in the reference data set.

3.2. DEGRADED AREA

The new method developed for the 2006 assessment was based on the confidence limit and bootstrap simulation concepts described in Alden et al. (2002). Specifically, bootstrap simulation (Efron and

Tibshirani 1998) was applied to incorporate uncertainty in reference conditions. Bootstrap simulation is used to assess the accuracy of an estimate by randomly sampling n times, with replacement, from an original data set. In our case, we wished to estimate the score corresponding to the 5th percentile of the B-IBI reference distributions for the good sites (by habitat). Because the reference distributions were based on small sample sizes, the percentiles were not well defined and would likely vary if different sets of reference sites were sampled. Thus the need to estimate this parameter more accurately with bootstrap simulations. Bootstrap simulations make no assumptions, except that the reference data are a representative sample from a "super population" of reference sites.

For each habitat, a threshold based on the 5th percentile B-IBI score of the reference data set for the good sites (or the maximum B-IBI score observed for the degraded sites, see below), was determined. This threshold was not intended to serve as a criterion for classifying individual B-IBI scores, rather it was used to categorize the segment as impaired or not based on the proportion of sites below the threshold (i.e., degraded area) and the variance associated with this estimate. The variance in the estimates of proportions for each segment was estimated by the simulations.

The B-IBI scores for the reference good and degraded sites had degrees of overlap that ranged from quite high in the tidal freshwater and oligohaline habitats to moderately low in the mesohaline and polyhaline habitats. An assessment sample is more likely to come from an impaired benthic community if the B-IBI score for this sample is within the range of scores observed for sites known to be degraded. Therefore, two criteria were established for determining the threshold: its score had to be within the lower bound of the good reference distribution (i.e., 5th percentile), and it had to be within the upper range of observed scores for known degraded sites (i.e., the reference degraded sites). If the 5th percentile score for a simulation run was not within the range of scores for the reference degraded sites, then the maximum B-IBI score for the reference degraded sites was selected as the threshold. Thus, in this study, sites with low B-IBI scores below thresholds were likely to be impaired and unlikely to come from good reference areas.

In each simulation run, a subset of the reference good sites for each habitat was selected at random, and the B-IBI threshold for this subset was determined (i.e., the IBI score at the 5th percentile, or the maximum score for the reference degraded samples). The scores of the assessment data for each habitat were then compared to the threshold to estimate the proportion of sites below the threshold. By repeating this process over and over again (5,000 runs) we were able to estimate the variance in the proportion of sites below the threshold from the bootstrap estimates. This variance reflects variability in the thresholds as well as sampling variability in the assessment data.

In the final step of the method, segments were declared impaired if the proportion of sites below the threshold (i.e., degraded area) was significantly higher than expected under the null hypothesis. Under the null hypothesis, a small number of sites (defined as 5% of the sites) would be expected to have low IBI scores even if all sites in a segment were in good condition (i.e., no low dissolved oxygen, contaminant, or nutrient enrichment problems). This is because of natural variability in the benthic communities, the effects of natural stressors, and sampling and methodological error. For a segment to be declared as impaired, the lower bound of the 95% confidence interval of the estimate

had to be higher than 5% (the expected proportion under the null hypothesis), with a minimum sample size of 10. A 5% level was used in agreement with standard statistical practice.

The steps described above are summarized below and in Appendix A:

1. Thresholds are set for each of seven benthic habitats in Chesapeake Bay.
2. The threshold is set as the smaller of two values: 5th percentile IBI score for the good reference sites or maximum observed IBI score for the degraded reference sites.
3. The 5th percentile score and its variance is estimated by bootstrap simulations.
4. For each iteration of the bootstrap simulation, a subset (of same sample size) of the good reference sites for each habitat is selected at random (with replacement), and the 5th percentile score determined.
5. At each iteration, the threshold is set according to #2.
6. At each iteration, the assessment data are compared to the reference data to estimate the proportion of sites (P) with scores below the threshold. This is done for each of one or more habitats within a segment.
7. P is averaged over all the iterations.
8. Under the null hypothesis, 5% of the sites (P_o) would be expected to have low IBI scores, even if all sites in a segment were in good condition.
9. Segments are declared impaired if $P - P_o > 0$ (greater than expected under the null hypothesis, with 95% confidence) (See Schenker and Gentleman 2001).

3.3. WILCOXON

A stratified Wilcoxon rank sum test was applied as described in Llansó et al. (2003) using Proc-StatXact 5 software (Cytel Software Corporation 2002). B-IBI scores were grouped into three ordered condition categories (1.0-2.0, 2.1-2.9, 3.0-5.0) and the distribution of scores in each category within a segment was compared for each habitat to the distribution of scores for the good reference condition. Under the null hypothesis (H_o) of no impairment, the two populations (segment and reference) were considered to have the same underlying multinomial distributions of samples among the ordered categories. The assessment of impairment was based on a one-sided exact test of H_o against the alternative hypothesis that the segment had a distribution shifted towards lower B-IBI scores than for the reference condition. The ranking was done separately by habitat, and then combined across habitats. Segments with a minimum of 10 samples for which the test was significant at the 1% alpha level and 90% power, were considered impaired under this method.

3.4. BENTHIC DIAGNOSTIC TOOL

The benthic diagnostic tool allows environmental managers to identify potential sources of anthropogenic stress to benthic communities within Chesapeake Bay. The development and application of the tool was described in detail in Dauer et al. (2002, 2005). The benthic diagnostic tool is based on a linear discriminant function that classifies sites in Chesapeake Bay identified as having degraded benthic communities into categories distinguished by the type of stress experienced by those communities. Presently, the function is capable of discriminating contaminated sites from sites affected by all other potential sources of stress in any of the seven benthic habitat types of

Chesapeake Bay. Sites are classified into two groups: 1) a contaminant group and 2) the other group representing all other potential sources of stress (eutrophication, low dissolved oxygen, etc.). This function is a linear combination of variables that includes over 60 measures of diversity, dominance, and function of benthic communities. The score for the function is used to calculate the probabilities that a sample is drawn from both groups and the sample is assigned to the group to which it has the highest probability of belonging. These probabilities are typically referred to as posterior probabilities of group membership.

For this assessment, sites with B-IBI scores < 2.7 were defined as "degraded" for benthic diagnostic tool application purposes. A score of 2.7 is used in the Chesapeake Bay benthic monitoring programs to define benthic community degradation. This cutoff value may differ from the threshold used by the Degraded Area method to determine proportion of sites with degraded benthic communities, but it should be very close to that threshold. Because cutoff values differ, diagnostic tool percentages should only be used as a general guide for identifying potential causes of degradation. For each "degraded" site, benthic metric values were submitted to the function and posterior probabilities of group membership calculated. Posterior probabilities for impaired segments were then used to identify the most likely source of stress affecting benthic communities in these segments. Sites with posterior probabilities of membership in the contaminant group that were greater than 0.50 were classified as putatively contaminated.

3.5. INSUFFICIENT AND EXCESSIVE ABUNDANCE OR BIOMASS

Insufficient and excessive abundance or biomass was determined from the abundance and biomass metric scores for all sites not classified as putatively contaminated. In the B-IBI, a score of 1 is assigned to total species abundance and total biomass if the value of these metrics for the site being evaluated is below the 5th percentile or above the 95th percentile of corresponding reference values. A score of 1 is assigned for both insufficient and excessive abundance or biomass because abundance and biomass of organisms respond bimodally to pollution. An increase in abundance or biomass is expected at polluted sites when stress from pollution is moderate, such as at sites where there is organic enrichment of the sediment. Excessive abundance and excessive biomass are phenomena usually associated with eutrophic conditions. A decrease in abundance and biomass is expected at sites with high degrees of stress from pollution; for example, sites affected by low dissolved oxygen. The insufficient and excessive abundance or biomass criteria can then be used to determine the likelihood of low dissolved oxygen problems versus eutrophic conditions for each of the Chesapeake Bay segments evaluated.

4.0 RESULTS

4.1. DEGRADED AREA

Based on the bootstrap-degraded area procedure, 22 segments with sample size of at least 10 were considered impaired (Table 3). Impaired segments were sorted according to the lower 95% bound of the confidence interval of the difference between the proportion of sites in the segment below threshold (P) and the proportion of sites below threshold under the null hypothesis (P_o), from high to low. The estimated P for the impaired segments ranged from 28 to 76%, and the average B-IBI score

was below 3.0 for most segments (Table 3). The estimates for CB4MH and CB5MH exclude the deep trough (>12 m) of the mainstem which is not monitored because this area is subjected to summer anoxia and has consistently be found to be azoic.

Nineteen of the segments declared impaired in this assessment were also declared impaired by the Wilcoxon test in the 2004 assessment. Three segments (JMSMHb, PMKOHa, MOBPHa) were declared impaired in this assessment but not in the 2004 assessment, and seven segments (LAFMHa, POCMH, POTOH, GUNOH, TANMH, NANMH, CB7PHa) were declared impaired in the 2004 assessment but not in the current assessment. Of the new impaired segments, the Nansemond River (JMSMHb) and Mobjack Bay (MOBPHa) were sampled with additional effort in 2004. Previously, these two segments and the Pamunkey River (PMKOHa) had sample size <10. Of the segments that are no longer classified as impaired, only the Pocomoke River mesohaline (POCMH) had sample size <10 in the current assessment.

4.2. WILCOXON

The stratified Wilcoxon rank sum test identified 27 segments with sample size of at least 10 as impaired (Table 3). Segments impaired by the Wilcoxon test but not impaired by the Degraded Area method were the lower Bay meainstem (CB7PHa), Tangier Sound (TANMH), the Lafayette River (LAFMHa), Severn River (SEVMH), and Gunpowder River (GUNOH). Except for the Severn River, these segments were also identified as impaired in the 2004 assessment.

4.3. DIAGNOSTIC TOOL AND INSUFFICIENT AND EXCESSIVE ABUNDANCE OR BIOMASS

The diagnostic tool and the insufficient and excessive abundance/biomass criteria can be used as ancillary information to determine most likely source of stress affecting benthic communities in segments classified as impaired. The results of this part of the assessment should be used only as a screening tool to identify probable causes of degradation and to prioritize segments for further study. There is always a risk of misclassifying sites as affected by toxic contamination, low dissolved oxygen, or nutrient enrichment, so independent measurements of sediment and water quality should be made whenever possible. Table 4 presents the results of the diagnostic tool and the insufficient and excessive abundance/biomass characterization for sites with contaminant group posterior probabilities >=0.50, and Table 5 presents the results for sites with contaminant group posterior probabilities >=0.90. A general decision tree for segment assessment and characterization is provided in Figure 1. Results are summarized below.

James River – The percentages of degraded samples with a contaminant effect ranged from 67% in the upper James River (JMSTFa) to 78% in the middle James River (JMSOHa) for P >=0.5, with average contaminant group posterior probabilities ranging from 0.64 to 0.79. At P >=0.9 contaminant percentages ranged from 33-50% (Table 4). At the James River mouth (JMSPHa) no samples were classified as contaminated. In addition, an examination of all samples collected indicated that only one sample had excessive abundance/biomass and only one had insufficient abundance/biomass. In the Nansemond River (JMSMHb), 90% of the degraded samples were classified as contaminated with an average contaminant group posterior probability of 0.87. Eighty

percent of degraded samples had contaminant group posterior probabilities of at least 0.90. Only three samples were collected in the Chuckatuck River/Pagan River segment (JMSMHc), and three in the Warwick River (JMSMHd). Although the low number of samples makes reliable assessments difficult, degraded samples were collected in both segments and each was classified as contaminated with high posterior probabilities of contaminant group membership. Although only three samples were collected in Willoughby Bay (JMSPHd), each sample was classified as contaminated. Contaminated samples in this segment had an average contaminant group posterior probability of 0.84. Additional samples are required in these segments to determine the extent of benthic degradation and potential sources of stress.

In summary, results indicate that contaminants may account for a large portion of the degradation in the James River, except for the James River mouth. The primary source of degradation in the Nansemond River appears to be anthropogenic contamination. Sampling was not sufficient for a reliable assessment in the Chucktuck/Pagan River and Warwick River segments.

Elizabeth River – Percentages of degraded samples with a contaminant effect ranged from 50% in the lower Elizabeth River mainstem (ELIPHa) to nearly 91% in the Eastern Branch (EBEMHa). At least 80% of degraded samples were classified as contaminated in both the Southern Branch (SBEMHa) and the Lafayette River (LAFMHa) and 68% were classified as contaminated in the upper Elizabeth River mainstem (ELIMHa). Of the remaining degraded samples without a contaminant effect, excessive abundance/biomass was found in 9.1%, 12.5%, and 5.3% in the Western Branch (WBEMHa), Southern Branch (SBEMHa) and upper Elizabeth River mainstem (ELIMHa), respectively, indicating the potential of stress due to eutrophication. Only one sample had excessive abundance in the lower Elizabeth River mainstem (ELIPHa). Insufficient abundance/biomass was found in 12.5%, 5.9%, and 15.8% of the degraded samples without a contaminant effect in the Southern Branch (SBEMHa), the Lafayette River (LAFMHa) and the upper Elizabeth River (ELIMHa), respectively, indicating low dissolved oxygen as an additional source of stress to benthic communities in these segments.

In summary, the predominant source of stress to benthic communities within the Elizabeth River is anthropogenic contamination. Both eutrophication and low dissolved oxygen appear to be additional sources of stress within the Southern Branch (SBEMHa) and upper Elizabeth River mainstem (ELIMHa).

York River – None of the upper Pamunkey River (PMKTF) samples had B-IBI scores <2.7, so none were assessed by the diagnostic tool. Over 57% of the lower Pamunkey River (PMKOH) degraded samples were classified as contaminated by the tool, but the average contaminant group posterior probability was low at 0.62. One additional sample in this last segment was not classified as contaminated and had insufficient abundance/biomass. Few samples were degraded in the upper Mattaponi River (MPNTFa), and 67% of these were classified as contaminated. However, the average contaminant group posterior probability was low at 0.65 and no samples collected had a probability of contaminant group membership >=0.90. No samples were classified as having excessive or insufficient abundance/biomass within this segment. In the lower Mattaponi River (MPNOHa) 80% of the degraded samples were classified as contaminated. The average contaminant group posterior probability in this segment was high at 0.87 and group membership probabilities for

7

all samples classified as contaminated were >=0.90. No uncontaminated degraded samples had excessive or insufficient abundance/biomass. In the middle York River (YRKMHa) 64% of the degraded samples were classified as contaminated. An additional 9.1% of degraded samples had excessive abundance/biomass and were not classified as contaminated by the tool, while 12.1% of the uncontaminated degraded samples had insufficient abundance/biomass. In the lower York River (YRKPHa) only 46% of the degraded samples were classified as contaminated. An additional 9.1% and 27.3% of uncontaminated degraded samples were found with excessive abundance/biomass and insufficient abundance/biomass, respectively, in this segment. In Mobjack Bay (MOBPHa), 50% of the degraded samples were classified as contaminated, all with contaminant group posterior probabilities >=0.90. An additional 12.5% and 25% of uncontaminated degraded samples were found with excessive abundance/biomass and insufficient abundance/biomass, respectively. Insufficient sample size in Severn Creek (MOBPHe), Ware River (MOBPHf), and East River (MOBPHh), precluded reliable assessments of degradation within these segments.

In summary, contaminants are likely to be substantial contributors to benthic community degradation in the York River, particularly in the lower Mattaponi River (MPNOHa) and the middle York River (YRKMHa). Contamination sources of stress are unlikely in both the lower York River (YRKPHa) and Mobjack Bay (MOBPHa), but both eutrophication and low dissolved oxygen may affect benthic communities in these segments, as well as in the lower York River (YRKMHa).

Rappahannock River – All of the degraded samples in the upper Rappahannock River (RPPTFa) were classified as contaminated. Only five samples were collected in the middle Rappahannock River (RPPOH), making assessments of benthic community degradation unreliable. In the lower Rappahannock River (RPPMHa), 67% of the degraded samples were classified as contaminated, with an average contaminant group posterior probability of 0.67. The remaining degraded samples that were not classified into the contaminant group had insufficient abundance/biomass. Only eight samples were collected in the Corrotoman River. One of these samples was classified as contaminated and another as uncontaminated with insufficient abundance/biomass.

In summary, degradation in the upper Rappahannock River (RPPTFa) appears to be the result of anthropogenic contamination while degradation in the lower Rappahannock River may be the result of a combination of contamination and low dissolved oxygen effects. The small number of samples collected makes assessments of overall benthic community condition in the middle Rappahannock River (RPPOHa) and Corrotoman River (CRRMHa) difficult but, the degradation observed appears to be from a variety of sources in both segments.

Potomac River – Fifty percent of the degraded samples in the upper Potomac River (POTTF) were classified as contaminated by the diagnostic tool. None of the uncontaminated degraded samples had excessive or insufficient abundance/biomass. In the middle Potomac River (POTOH), 80% of the degraded samples were classified as contaminated. Of the uncontaminated degraded samples, 20% had excessive abundance/biomass and none had insufficient abundance/biomass. In the lower Potomac River (POTMH), 31% of the degraded samples were classified as contaminated. Of the remaining degraded samples classified as uncontaminated, 65% had insufficient abundance/biomass while only 2.6% had excessive abundance/biomass.

In summary, benthic community degradation in much of the upper Potomac River (POTTF) appears to be the result of anthroprogenic contamination. In the middle Potomac River (POTOH), the primary source of stress appears to be contamination; however, eutrophication is likely to also affect benthic communities in this segment, as indicated by the samples with excessive abundance/biomass. The predominant source of stress in the lower Potomac River (POTMH) appears to be from low dissolved oxygen, as indicated by the high percentage of samples classified as uncontaminated and having insufficient abundance/ biomass.

Patuxent River – An inadequate number of samples were collected in the upper Patuxent River (PAXTF) and middle Patuxent River (PAXOH) for assessing benthic community degradation using the benthic diagnostic tool. In the upper Patuxent River (PAXTF), two samples were classified as contaminated and one had excessive abundance/biomass without likelihood of contamination. In the middle Patuxent River (PAXOH), three samples were classified as contaminated and none had excessive or insufficient abundance/biomass. In the lower Patuxent River (PAXMH), 46% of the degraded samples were classified as contaminated, with an average posterior probability of contaminant group membership of 0.51. Of the remaining uncontaminated samples, 50% had insufficient abundance/biomass while only 1.5% had excessive abundance/biomass.

In summary, accurate assessment of benthic community degradation in the upper Patuxent River (PAXTF) and middle Patuxent River (PAXOH) requires additional sampling; however, available data suggest contaminants may be a source of stress in these segments. Degradation in the lower Patuxent River (PAXMH) is likely to be the result of a combination of contamination and low dissolved oxygen stress.

Chester River – Over 38% of the degraded samples in the lower Chester River (CHSMH) were classified as contaminated. Of the remaining uncontaminated samples, 11% had excessive abundance/biomass and 33% had insufficient abundance/biomass. Benthic community degradation in this segment would appear to be the result of contamination, eutrophication, and low dissolved oxygen effects. All other segments in the Chester River had low sample size.

Choptank River – Accurate assessment of benthic degradation the upper Choptank River (CHOTF), middle Choptank River (CHOOH) and Choptank River mouth (CHOMH1) will require additional sampling. In the lower Choptank River (CHOMH2), 67% of the degraded samples were classified as contaminated, with group membership probabilities >0.90. Of the remaining uncontaminated degraded samples, 22% had excessive abundance/biomass while 11% had insufficient abundance/biomass. Contamination appears to account for most of the benthic community degradation in the lower Choptank River (CHOMH2), but eutrophication and low dissolved oxygen are also likely to play a role.

Pocomoke River –Pocomoke River segments had low sample size; however, most of the degraded samples in the lower Pocomoke were classified as contaminated.

Pocomoke Sound – Again, Pocomoke Sound had low sample size; however, 75% of the degraded samples were classified as contaminated by the benthic diagnostic tool. Twenty-five percent of the uncontaminated samples had insufficient abundance/biomass. Results suggest that benthic

community degradation in this segment stems from a combination of contaminants and low dissolved oxygen.

Manokin River – Of the Maryland small Eastern Tributaries, only the Manokin River (MANMH) had adequate sample size. Seventy-five percent of the degraded samples were classified as contaminated. Of the remaining uncontaminated and degraded samples, 25% had insufficient abundance/biomass.

Maryland Upper Western Tributaries – In the Gunpowder River (GUNOH), only 17% of the samples were classified as contaminated. Of the uncontaminated samples, 50% had insufficient abundance/biomass and another 17% had excessive abundance/biomass. The predominant source of stress to benthic communities in this segment appears to be low dissolved oxygen. In the Magothy River (MAGMH), 38% of the degraded samples were classified as contaminated. Excessive abundance/biomass was observed in 13% and insufficient abundance/biomass in 50% of the uncontaminated degraded samples. Results suggest a mixed source of stress. In the Patapsco River (PATMH), 58% of the degraded samples were classified as contaminated. The remaining degraded samples had insufficient abundance/biomass, suggesting contaminants and low dissolved oxygen as sources of stress. In the Severn River (SEVMH), 60% of the degraded samples were classified as contaminated. An additional 20% and 40% of the uncontaminated degraded samples had excessive and insufficient abundance/biomass, respectively. Results suggest a variety of sources of stress for this segment.

Chesapeake Bay Mainstem – Sixty-seven percent of the upper Chesapeake Bay (CB1TF) degraded samples had possible contaminant effects, and 17% of the remaining degraded samples had excessive abundance/biomass. Segment CB2OH, on the other hand, had no degraded samples. In Segment CB3MH, 55% of the degraded samples were classified as contaminated while 32% of the remaining degraded samples had insufficient abundance/biomass. In Segment CB4MH, 35% of the degraded samples were classified as contaminated, 25% of the uncontaminated degraded samples had excessive abundance/biomass, and 35% had insufficient abundance/biomass. Few samples in Tangier Sound were degraded. In Segment CB5MH, 18% of degraded samples were classified as contaminated and 82% of the uncontaminated degraded had insufficient abundance/biomass, indicating a low dissolved oxygen effect. In the lower mainstem, Segment CB6PH had 67% of the degraded samples classified as contaminated and 33% of the uncontaminated degraded samples classified with insufficient abundance/biomass. Segment CB7PHa had 63% of the degraded samples classified as contaminated, but none had contaminant group posterior probabilities above 0.90 and the average probability for the segment was 0.58. Of the degraded samples not classified as contaminated in this last segment, 13% had excessive abundance/biomass and 25% had insufficient abundance/biomass. Finally, none of the samples near the Bay mouth in Segment CB8PHa were classified as contaminated.

In summary, contaminants were likely sources of stress to benthic communities in CB1TF and CB3MH, while a variety of stresses were likely in CB4MH. Low dissolved oxygen was the predominant source of stress in CB5MH, contaminants and low dissolved oxygen in CB6PHa and CB7PHa, and low dissolved oxygen alone in CB8PHa.

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Table 1. Habitat classification for the Chesapeake Bay B-IBI.

Habitat Class	Bottom Salinity (psu)	Silt-clay (<62 µ) content by Weight (%)
1. Tidal freshwater	0-0.5	N/A
2. Oligohaline	≥0.5-5	N/A
3. Low mesohaline	≥5-12	N/A
4-1. High mesohaline sand	≥12-18	0-40
4-2. High mesohaline mud	≥12-18	>40
5-1. Polyhaline sand	≥18	0-40
5-2. Polyhaline mud	≥18	>40

Table 2. Number of samples by habitat in the original index development data files used by Weisberg et al. (1997) and Alden et al. (2002). Calibration (Cal) and validation (Val) samples combined. Habitat Class designations as in Table 1.

	Habitat Class						
	1	2	3	4-1	4-2	5-1	5-2
Cal + Val							
Reference Degraded	136	92	49	5	81	7	136
Reference Good	75	32	20	14	39	39	24

Table 3. Degraded Area and Wilcoxon rank sum test results for 85 Chesapeake Bay segments and sub-segments for the period 2000-2004. Shown is sample size, proportion of sites in segment below threshold (P), proportion of sites below threshold under the null hypothesis (P_o), difference between P and P_o, lower 95% confidence limit bound for the difference (CL-L), upper 95% confidence limit bound for the difference (CL-U), power and p-values for the Wilcoxon test, impaired segments by the Degraded Area method (lower 95% confidence bound for the difference > 0), impaired segments for the Wilcoxon test (reference and segment B-IBI score distributions differ, with lower scores in segment than in reference), mean B-IBI value, number of sites in segment with B-IBI scores equal to or greater than 2.7, number of sites in segment with B-IBI scores equal to or greater than 3.0, percent of sites in segment with B-IBI scores equal to or grater than 2.7, and percent of sites in segment with B-IBI scores equal to or greater than 3.0. P-P_o confidence limits for segments with small sample size (<10) were not calculated.

Segment	Sample Size	P	P_o	P-Po	CL-L(P-Po)	CL-U(P-Po)	Power	p-value	Degraded Area	Wilcoxon	mean B-IBI	N >=2.7	N >=3.0	% >=2.7	% >=3.0
POTMH	91	0.76	0.05	0.71	0.60	0.82	1.00	0.0000	Yes	Yes	1.7	14	12	15	13
SBEMHa	47	0.70	0.05	0.65	0.49	0.80	1.00	0.0000	Yes	Yes	2.0	7	2	15	4
CB4MH	28	0.67	0.05	0.62	0.42	0.82	1.00	0.0000	Yes	Yes	2.3	8	7	29	25
PAXMH	112	0.49	0.05	0.44	0.31	0.58	1.00	0.0000	Yes	Yes	2.4	44	34	39	30
PATMH	49	0.52	0.05	0.47	0.31	0.63	1.00	0.0000	Yes	Yes	2.4	18	17	37	35
CHSMH	33	0.53	0.05	0.48	0.28	0.68	1.00	0.0000	Yes	Yes	2.6	15	13	45	39
CB3MH	61	0.44	0.05	0.39	0.24	0.54	1.00	0.0000	Yes	Yes	2.7	30	28	49	46
ELIMHa	37	0.48	0.05	0.43	0.23	0.64	1.00	0.0000	Yes	Yes	2.5	18	12	49	32
EBEMHa	15	0.57	0.05	0.52	0.22	0.82	1.00	0.0000	Yes	Yes	2.2	4	1	27	7
RPPMHa	98	0.37	0.05	0.32	0.18	0.45	1.00	0.0000	Yes	Yes	2.6	49	43	50	44
YRKMHa	64	0.43	0.05	0.38	0.15	0.61	1.00	0.0000	Yes	Yes	2.5	31	20	48	31
JMSMHa	46	0.37	0.05	0.32	0.14	0.51	1.00	0.0000	Yes	Yes	2.7	21	19	46	41
CHOMH2	22	0.41	0.05	0.36	0.13	0.60	1.00	0.0012	Yes	Yes	2.9	13	12	59	55
CB5MH	44	0.32	0.05	0.27	0.11	0.43	1.00	0.0000	Yes	Yes	2.7	27	21	61	48
YRKPHa	29	0.38	0.05	0.33	0.11	0.56	1.00	0.0000	Yes	Yes	3.0	18	14	62	48
JMSMHb	16	0.45	0.05	0.40	0.11	0.70	1.00	0.0000	Yes	Yes	2.4	6	6	38	38
MAGMH	17	0.41	0.05	0.36	0.08	0.63	1.00	0.0000	Yes	Yes	2.3	9	6	53	35
PMKOHa	11	0.46	0.05	0.41	0.07	0.75	1.00	0.0009	Yes	Yes	2.6	4	4	36	36
MOBPHa	20	0.36	0.05	0.31	0.06	0.56	1.00	0.0000	Yes	Yes	3.0	12	11	60	55

13

Table 3. Continued

Segment	Sample Size	Degraded Area Results					Wilcoxon Results		Impaired		mean B-IBI	N >=2.7	N >=3.0	% >=2.7	% >=3.0
		P	Po	P-Po	CL-L(P-Po)	CL-U(P-Po)	Power	p-value	Degraded Area	Wilcoxon					
ELIPHa	17	0.39	0.05	0.34	0.05	0.63	1.00	0.0017	Yes	Yes	2.8	11	10	65	59
WBEMHa	19	0.36	0.05	0.31	0.04	0.59	1.00	0.0000	Yes	Yes	2.4	8	4	42	21
JMSOHa	22	0.28	0.05	0.23	0.01	0.45	1.00	0.0030	Yes	Yes	2.9	13	11	59	50
CB7PHa	43	0.15	0.05	0.10	-0.04	0.24	1.00	0.0000	No	Yes	3.3	35	28	81	65
TANMH	48	0.13	0.05	0.08	-0.05	0.20	1.00	0.0000	No	Yes	3.2	40	30	83	63
LAFMHa	27	0.31	0.05	0.26	-0.06	0.57	1.00	0.0000	No	Yes	2.4	10	5	37	19
SEVMH	13	0.26	0.05	0.21	-0.09	0.50	1.00	0.0009	No	Yes	2.7	8	6	62	46
POTOH	21	0.16	0.05	0.11	-0.09	0.31	1.00	0.1524	No	No	3.4	16	14	76	67
GUNOH	15	0.22	0.05	0.17	-0.09	0.44	1.00	0.0062	No	Yes	2.9	9	8	60	53
MPNOHa	11	0.25	0.05	0.20	-0.11	0.52	1.00	0.0212	No	No	2.6	6	6	55	55
CB2OH	40	0.00	0.05	-0.05	-0.12	0.02	1.00	0.0251	No	No	3.8	40	40	100	100
CB6PHa	18	0.15	0.05	0.10	-0.12	0.32	1.00	0.0232	No	No	3.3	15	14	83	78
CB8PHa	15	0.00	0.05	-0.05	-0.17	0.07	0.93	0.1670	No	No	3.4	13	13	87	87
CB1TF	19	0.10	0.05	0.05	-0.17	0.26	1.00	0.3010	No	No	3.1	13	13	68	68
MPNTFa	13	0.00	0.05	-0.05	-0.17	0.07	1.00	0.2139	No	No	3.5	10	10	77	77
MANMH	13	0.10	0.05	0.05	-0.20	0.29	1.00	0.0195	No	No	3.1	9	9	69	69
RPPTFa	11	0.07	0.05	0.02	-0.20	0.24	1.00	0.2356	No	No	3.5	9	9	82	82
POTTF	12	0.08	0.05	0.03	-0.20	0.26	1.00	0.4703	No	No	3.1	8	8	67	67
JMSTFa	14	0.02	0.05	-0.03	-0.20	0.15	1.00	0.1250	No	No	3.2	8	7	57	50
JMSPHa	10	0.12	0.05	0.07	-0.36	0.49	0.97	0.4675	No	No	3.4	10	9	100	90
WICMH	9	0.42	0.05	0.37	-	-	0.98	0.0053	-	-	2.8	5	5	56	56
POCMH	9	0.29	0.05	0.24	-	-	1.00	0.0001	-	-	2.6	5	3	56	33
BSHOH	9	0.24	0.05	0.19	-	-	0.98	0.0272	-	-	2.6	6	5	67	56
NANMH	9	0.13	0.05	0.08	-	-	1.00	0.0097	-	-	3.0	6	5	67	56
SOUMH	8	0.88	0.05	0.83	-	-	1.00	0.0000	-	-	2.1	1	1	13	13
CHOMH1	8	0.38	0.05	0.33	-	-	1.00	0.0006	-	-	2.6	5	3	63	38

Table 3. Continued

| | | Degraded Area Results | | | | | Wilcoxon Results | | Impaired | | | | | | |
Segment	Sample Size	P	Po	P-Po	CL-L(P-Po)	CL-U(P-Po)	Power	p-value	Degraded Area	Wilcoxon	mean B-IBI	N >=2.7	N >=3.0	% >=2.7	% >=3.0
CRRMHa	8	0.23	0.05	0.18	-	-	1.00	0.0074	-	-	2.4	5	4	63	50
ELKOH	8	0.15	0.05	0.10	-	-	0.91	0.3037	-	-	3.2	6	6	75	75
POCOH	7	0.49	0.05	0.44	-	-	0.95	0.0001	-	-	2.5	1	1	14	14
RHDMH	7	0.43	0.05	0.38	-	-	0.34	0.0419	-	-	2.9	4	4	57	57
PAXOH	7	0.40	0.05	0.35	-	-	0.87	0.0075	-	-	2.8	3	3	43	43
LCHMH	6	0.31	0.05	0.26	-	-	0.92	0.0032	-	-	2.5	3	2	50	33
CHSOH	6	0.17	0.05	0.12	-	-	0.84	0.5341	-	-	3.2	5	5	83	83
PAXTF	6	0.17	0.05	0.12	-	-	1.00	0.0709	-	-	2.6	2	2	33	33
HNGMH	5	0.21	0.05	0.16	-	-	1.00	0.0001	-	-	2.8	4	2	80	40
CHOOH	5	0.21	0.05	0.16	-	-	1.00	0.0228	-	-	2.7	3	2	60	40
RPPOHa	5	0.06	0.05	0.01	-	-	1.00	0.3063	-	-	3.5	3	3	60	60
BIGMH	5	0.03	0.05	-0.02	-	-	0.82	0.0141	-	-	2.9	4	2	80	40
CHKOHa	5	0.00	0.05	-0.05	-	-	1.00	0.2488	-	-	3.7	5	5	100	100
EASMH	4	0.75	0.05	0.70	-	-	0.83	0.0056	-	-	2.1	1	1	25	25
BACOH	4	0.44	0.05	0.39	-	-	0.76	0.0006	-	-	2.1	2	0	50	0
NANOH	4	0.25	0.05	0.20	-	-	0.78	0.0828	-	-	3.5	3	2	75	50
FSBMH	4	0.25	0.05	0.20	-	-	0.36	0.1383	-	-	3.6	3	3	75	75
NORTF	4	0.08	0.05	0.03	-	-	1.00	0.2526	-	-	3.2	2	2	50	50
PMKTFa	4	0.00	0.05	-0.05	-	-	0.94	0.2105	-	-	3.9	4	4	100	100
JMSPHd	3	0.91	0.05	0.86	-	-	0.86	0.0004	-	-	1.7	0	0	0	0
JMSMHd	3	0.34	0.05	0.29	-	-	0.91	0.0287	-	-	2.8	2	1	67	33
JMSMHc	3	0.33	0.05	0.28	-	-	0.80	0.3049	-	-	3.1	2	2	67	67
MIDOH	3	0.00	0.05	-0.05	-	-	0.42	0.6203	-	-	3.4	3	3	100	100
SASOH	3	0.00	0.05	-0.05	-	-	0.99	0.5239	-	-	3.2	2	2	67	67
RPPMHm	2	0.50	0.05	0.45	-	-	0.85	0.3929	-	-	3.1	1	1	50	50

Table 3. Continued

Segment	Sample Size	Degraded Area Results					Wilcoxon Results		Impaired		mean B-IBI	N >=2.7	N >=3.0	% >=2.7	% >=3.0
		P	Po	P-Po	CL-L(P-Po)	CL-U(P-Po)	Power	p-value	Degraded Area	Wilcoxon					
MOBPHh	2	0.00	0.05	-0.05	-	-	0.40	0.0067	-	-	2.7	2	0	100	0
MOBPHf	1	1.00	0.05	0.95	-	-	0.00	0.1250	-	-	1.3	0	0	0	0
MOBPHg	1	1.00	0.05	0.95	-	-	0.12	0.0400	-	-	1.7	0	0	0	0
RPPMHd	1	1.00	0.05	0.95	-	-	0.12	0.0400	-	-	1.7	0	0	0	0
WSTMH	1	1.00	0.05	0.95	-	-	0.00	0.0952	-	-	2.2	0	0	0	0
YRKPHd	1	1.00	0.05	0.95	-	-	0.12	0.0400	-	-	1.3	0	0	0	0
MATTF	1	0.73	0.05	0.68	-	-	0.00	0.1212	-	-	1.7	0	0	0	0
YRKMHb	1	0.73	0.05	0.68	-	-	0.00	0.1250	-	-	1.7	0	0	0	0
YRKPHe	1	0.37	0.05	0.32	-	-	0.00	0.0800	-	-	2.7	1	0	100	0
CHSTF	1	0.19	0.05	0.14	-	-	0.00	0.1212	-	-	2.0	0	0	0	0
CHOTF	1	0.00	0.05	-0.05	-	-	0.00	0.8485	-	-	3.0	1	1	100	100
APPTFa	1	0.00	0.05	-0.05	-	-	0.00	0.6711	-	-	3.0	1	1	100	100
BOHOH	1	0.00	0.05	-0.05	-	-	0.00	0.6711	-	-	4.0	1	1	100	100
MOBPHe	1	0.00	0.05	-0.05	-	-	0.00	0.1333	-	-	2.7	1	0	100	0
POCTF	1	0.00	0.05	-0.05	-	-	0.00	0.3421	-	-	2.5	0	0	0	0

Table 4. Diagnostic assessment of benthic community degradation for random sites sampled within Chesapeake Bay segments and sub-segments for the period 2000-2004. Presented is the mean B-IBI score in each segment, the total number of samples collected, the mean posterior probability of membership in the Contaminant group (Cont. Post. Prob.), and the total number, percentage of degraded, and percentage of the total samples for the following: (1) samples with posterior probability of contaminant group membership >=0.50, (2) degraded samples with excessive abundance or biomass, and (3) degraded samples with insufficient abundance or biomass. w/o Cont. = Percentage of samples (of degraded or total) not classified in the contaminant group. Segments in bold were classified as impaired by the Degraded Area analysis.

A. James River and Elizabeth River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
APPTFa	3.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CHKOHa	3.7	5	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
JMSTFa	3.2	14	0.7190	4	66.67	28.57	1	16.67	0.00	0.00	0	0.00	0.00	0.00
JMSOHa	2.9	22	0.7892	7	77.78	31.82	1	11.11	0.00	0.00	6	66.67	11.11	4.55
JMSMHa	2.7	46	0.6422	18	72.00	39.13	6	24.00	4.00	2.17	10	40.00	4.00	2.17
JMSMHb	2.4	16	0.8690	9	90.00	56.25	7	70.00	0.00	0.00	4	40.00	0.00	0.00
JMSMHc	3.1	3	0.9855	1	100.00	33.33	1	100.00	0.00	0.00	1	100.00	0.00	0.00
JMSMHd	2.8	3	0.9547	1	100.00	33.33	1	100.00	0.00	0.00	0	0.00	0.00	0.00
JMSPHa	3.4	10	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
JMSPHd	1.7	3	0.8388	3	100.00	100.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
WBEMHa	2.4	19	0.7383	8	72.73	42.11	7	63.64	9.09	5.26	3	27.27	0.00	0.00
LAFMHa	2.4	27	0.8793	15	88.24	55.56	11	64.71	0.00	0.00	3	17.65	5.88	3.70
SBEMHa	2.0	47	0.7986	32	80.00	68.09	26	65.00	12.50	10.64	10	25.00	12.50	10.64
EBEMHa	2.2	15	0.8904	10	90.91	66.67	7	63.64	0.00	0.00	1	9.09	0.00	0.00
ELIMHa	2.5	37	0.6758	13	68.42	35.14	5	26.32	5.26	2.70	7	36.84	15.79	8.11
ELIPHa	2.8	17	0.4849	3	50.00	17.65	1	16.67	16.67	5.88	2	33.33	16.67	5.88

B. York River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
PMKTFa	3.9	4	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
PMKOHa	2.6	11	0.6200	4	57.14	36.36	3	42.86	0.00	0.00	1	14.29	14.29	9.09
MPNTFa	3.5	13	0.6501	2	66.67	15.38	0	0.00	0.00	0.00	0	0.00	0.00	0.00
MPNOHa	2.6	11	0.8684	4	80.00	36.36	2	40.00	0.00	0.00	2	40.00	0.00	0.00
YRKMHa	2.5	64	0.6433	21	63.64	32.81	17	51.52	9.09	4.69	10	30.30	12.12	6.25
YRKMHb	1.7	1	0.0937	0	0.00	0.00	1	100.00	100.00	100.00	0	0.00	0.00	0.00
YRKPHa	3.0	29	0.4256	5	45.45	17.24	1	9.09	9.09	3.45	4	36.36	27.27	10.34
YRKPHd	1.3	1	0.8476	1	100.00	100.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00
YRKPHe	2.7	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
MOBPHa	3.0	20	0.5545	4	50.00	20.00	1	12.50	12.50	5.00	6	75.00	25.00	10.00
MOBPHe	2.7	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
MOBPHf	1.3	1	0.5064	1	100.00	100.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00
MOBPHg	1.7	1	0.5968	1	100.00	100.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00
MOBPHh	2.7	2	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00

C. Rappahannock River, Potomac River and Patuxent River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
RPPTFa	3.5	11	0.9873	2	100.00	18.18	0	0.00	0.00	0.00	0	0.00	0.00	0.00
RPPOHa	3.5	5	0.5421	1	50.00	20.00	1	50.00	50.00	20.00	0	0.00	0.00	0.00
RPPMHa	2.6	98	0.6720	33	67.35	33.67	8	16.33	0.00	0.00	35	71.43	32.65	16.33
RPPMHd	1.7	1	0.5447	1	100.00	100.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00
RPPMHm	3.1	2	0.9911	1	100.00	50.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
CRRMHa	2.4	8	0.2693	1	33.33	12.50	0	0.00	0.00	0.00	2	66.67	33.33	12.50
MATTF	1.7	1	0.9511	1	100.00	100.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
POTTF	3.1	12	0.6016	2	50.00	16.67	2	50.00	0.00	0.00	0	0.00	0.00	0.00
POTOH	3.4	21	0.6851	4	80.00	19.05	2	40.00	20.00	4.76	2	40.00	0.00	0.00
POTMH	1.7	91	0.3637	24	31.17	26.37	5	6.49	2.60	2.20	68	88.31	64.94	54.95
PAXTF	2.6	6	0.3861	2	50.00	33.33	1	25.00	25.00	16.67	0	0.00	0.00	0.00
PAXOH	2.8	7	0.6677	3	75.00	42.86	1	25.00	0.00	0.00	1	25.00	0.00	0.00
PAXMH	2.4	112	0.5080	31	45.59	27.68	5	7.35	1.47	0.89	55	80.88	50.00	30.36

D. Maryland Eastern Tributaries: Chester River, Choptank River and Pocomoke River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
CHSTF	2.0	1	0.0008	0	0.00	0.00	1	100.00	100.00	100.00	0	0.00	0.00	0.00
CHSOH	3.2	6	0.9996	1	100.00	16.67	1	100.00	0.00	0.00	0	0.00	0.00	0.00
CHSMH	2.6	33	0.3800	7	38.89	21.21	5	27.78	11.11	6.06	10	55.56	33.33	18.18
CHOTF	3.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CHOOH	2.7	5	0.9252	2	100.00	40.00	1	50.00	0.00	0.00	0	0.00	0.00	0.00
CHOMH1	2.6	8	0.3992	1	33.33	12.50	0	0.00	0.00	0.00	2	66.67	66.67	25.00
CHOMH2	2.9	22	0.7173	6	66.67	27.27	6	66.67	22.22	9.09	4	44.44	11.11	4.55
POCTF	2.5	1	0.9637	1	100.00	100.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
POCOH	2.5	7	0.8117	5	83.33	71.43	4	66.67	0.00	0.00	1	16.67	0.00	0.00
POCMH	2.6	9	0.5791	3	75.00	33.33	0	0.00	0.00	0.00	3	75.00	25.00	11.11

E. Maryland Eastern Tributaries: Smaller tributaries

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
BIGMH	2.9	5	0.8676	1	100.00	20.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00
BOHOH	4.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
ELKOH	3.2	8	0.4419	1	50.00	12.50	2	100.00	50.00	12.50	0	0.00	0.00	0.00
MANMH	3.1	13	0.6549	3	75.00	23.08	0	0.00	0.00	0.00	3	75.00	25.00	7.69
NANOH	3.4	4	0.9984	1	100.00	25.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
NANMH	3.0	9	0.5083	1	33.33	11.11	1	33.33	0.00	0.00	1	33.33	33.33	11.11
SASOH	3.2	3	0.4439	0	0.00	0.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
WICMH	2.8	9	0.8935	4	100.00	44.44	2	50.00	0.00	0.00	1	25.00	0.00	0.00

F. Maryland Upper Western Tributaries

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
BACOH	2.1	4	0.7865	2	100.00	50.00	1	50.00	0.00	0.00	0	0.00	0.00	0.00
BSHOH	2.6	9	0.6381	2	66.67	22.22	1	33.33	0.00	0.00	1	33.33	33.33	11.11
GUNOH	2.9	15	0.2969	1	16.67	6.67	1	16.67	16.67	6.67	3	50.00	50.00	20.00
MAGMH	2.3	17	0.4106	3	37.50	17.65	2	25.00	12.50	5.88	6	75.00	50.00	23.53
PATMH	2.4	49	0.5638	18	58.06	36.73	6	19.35	0.00	0.00	22	70.97	38.71	24.49
RHDMH	2.9	7	0.6777	2	66.67	28.57	1	33.33	0.00	0.00	2	66.67	33.33	14.29
SEVMH	2.7	13	0.5965	3	60.00	23.08	3	60.00	20.00	7.69	2	40.00	40.00	15.38
SOUMH	2.1	8	0.7354	5	71.43	62.50	4	57.14	0.00	0.00	2	28.57	14.29	12.50
WSTMH	2.2	1	0.6504	1	100.00	100.00	0	0.00	0.00	0.00	1	100.00	0.00	0.00

22

G. Chesapeake Bay Mainstem and Associated Segments

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.50			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
EASMH	2.1	4	0.3610	1	33.33	25.00	1	33.33	0.00	0.00	2	66.67	66.67	50.00
FSBMH	3.6	4	0.1219	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	25.00
HNGMH	2.8	5	0.2766	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	20.00
LCHMH	2.5	6	0.1671	0	0.00	0.00	1	33.33	33.33	16.67	2	66.67	66.67	33.33
MIDOH	3.4	3	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
NORTF	3.2	4	0.5267	1	50.00	25.00	1	50.00	50.00	25.00	1	50.00	0.00	0.00
TANMH	3.2	48	0.2974	2	25.00	4.17	0	0.00	0.00	0.00	6	75.00	50.00	8.33
CB1TF	3.1	19	0.5671	4	66.67	21.05	4	66.67	16.67	5.26	0	0.00	0.00	0.00
CB2OH	3.8	40	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CB3MH	2.7	61	0.5487	17	54.84	27.87	3	9.68	3.23	1.64	23	74.19	32.26	16.39
CB4MH	2.3	28	0.3903	7	35.00	25.00	7	35.00	25.00	17.86	12	60.00	35.00	25.00
CB5MH	2.7	44	0.2125	3	17.65	6.82	1	5.88	5.88	2.27	17	100.00	82.35	31.82
CB6PHa	3.3	18	0.6078	2	66.67	11.11	1	33.33	0.00	0.00	2	66.67	33.33	5.56
CB7PHa	3.3	43	0.5762	5	62.50	11.63	1	12.50	12.50	2.33	6	75.00	25.00	4.65
CB8PHa	3.4	15	0.0199	0	0.00	0.00	0	0.00	0.00	0.00	2	100.00	100.00	13.33

Table 5. Diagnostic assessment of benthic community degradation for random sites sampled within Chesapeake Bay segments and sub-segments for the period 2000-2004. Presented is the mean B-IBI score in each segment, the total number of samples in each segment, the mean posterior probability of membership in the contaminant group (Cont. Post. Prob.), and the total number, percentage of degraded, and percentage of the total samples for the following: (1) samples with posterior probability of contaminant group membership >=0.90, (2) degraded samples with excessive abundance or biomass, and (3) degraded samples with insufficient abundance or biomass. w/o Cont. = Percentage of samples (of degraded or total) not classified in the contaminant group. Segments in bold were classified as impaired by the Degraded Area analysis.

A. James River and Elizabeth River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
APPTFa	3.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CHKOHa	3.7	5	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
JMSTFa	3.2	14	0.7190	3	50.00	21.43	1	16.67	0.00	0.00	0	0.00	0.00	0.00
JMSOHa	2.9	22	0.7892	3	33.33	13.64	1	11.11	0.00	0.00	6	66.67	44.44	18.18
JMSMHa	2.7	46	0.6422	8	32.00	17.39	6	24.00	12.00	6.52	10	40.00	28.00	15.22
JMSMHb	2.4	16	0.8690	8	80.00	50.00	7	70.00	0.00	0.00	4	40.00	0.00	0.00
JMSMHc	3.1	3	0.9855	1	100.00	33.33	1	100.00	0.00	0.00	1	100.00	0.00	0.00
JMSMHd	2.8	3	0.9547	1	100.00	33.33	1	100.00	0.00	0.00	0	0.00	0.00	0.00
JMSPHa	3.4	10	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
JMSPHd	1.7	3	0.8388	1	33.33	33.33	0	0.00	0.00	0.00	0	0.00	0.00	0.00
WBEMHa	2.4	19	0.7383	7	63.64	36.84	7	63.64	9.09	5.26	3	27.27	9.09	5.26
LAFMHa	2.4	27	0.8793	13	76.47	48.15	11	64.71	5.88	3.70	3	17.65	5.88	3.70
SBEMHa	2.0	47	0.7986	27	67.50	57.45	26	65.00	17.50	14.89	10	25.00	15.00	12.77
EBEMHa	2.2	15	0.8904	9	81.82	60.00	7	63.64	0.00	0.00	1	9.09	0.00	0.00
ELIMHa	2.5	37	0.6758	7	36.84	18.92	5	26.32	15.79	8.11	7	36.84	26.32	13.51
ELIPHa	2.8	17	0.4849	3	50.00	17.65	1	16.67	16.67	5.88	2	33.33	16.67	5.88

24

B. York River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
MPNOHa	2.6	11	0.8684	4	80.00	36.36	2	40.00	0.00	0.00	2	40.00	0.00	0.00
MPNTFa	3.5	13	0.6501	0	0.00	0.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
PMKOHa	2.6	11	0.6200	3	42.86	27.27	3	42.86	0.00	0.00	1	14.29	14.29	9.09
PMKTFa	3.9	4	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
YRKMHa	2.5	64	0.6433	16	48.48	25.00	17	51.52	18.18	9.38	10	30.30	18.18	9.38
YRKMHb	1.7	1	0.0937	0	0.00	0.00	1	100.00	100.00	100.00	0	0.00	0.00	0.00
YRKPHa	3.0	29	0.4256	3	27.27	10.34	1	9.09	9.09	3.45	4	36.36	27.27	10.34
YRKPHd	1.3	1	0.8476	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	100.00
YRKPHe	2.7	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
MOBPHa	3.0	20	0.5545	4	50.00	20.00	1	12.50	12.50	5.00	6	75.00	25.00	10.00
MOBPHe	2.7	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
MOBPHf	1.3	1	0.5064	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	100.00
MOBPHg	1.7	1	0.5968	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	100.00
MOBPHh	2.7	2	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00

C. Rappahannock River, Potomac River and Patuxent River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
RPPTFa	3.5	11	0.9873	2	100.00	18.18	0	0.00	0.00	0.00	0	0.00	0.00	0.00
RPPOHa	3.5	5	0.5421	1	50.00	20.00	1	50.00	50.00	20.00	0	0.00	0.00	0.00
RPPMHa	2.6	98	0.6720	21	42.86	21.43	8	16.33	4.08	2.04	35	71.43	53.06	26.53
RPPMHd	1.7	1	0.5447	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	100.00
RPPMHm	3.1	2	0.9911	1	100.00	50.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
CRRMHa	2.4	8	0.2693	0	0.00	0.00	0	0.00	0.00	0.00	2	66.67	66.67	25.00
MATTF	1.7	1	0.9511	1	100.00	100.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
POTTF	3.1	12	0.6016	2	50.00	16.67	2	50.00	0.00	0.00	0	0.00	0.00	0.00
POTOH	3.4	21	0.6851	2	40.00	9.52	2	40.00	20.00	4.76	2	40.00	40.00	9.52
POTMH	1.7	91	0.3637	15	19.48	16.48	5	6.49	2.60	2.20	68	88.31	76.62	64.84
PAXTF	2.6	6	0.3861	1	25.00	16.67	1	25.00	25.00	16.67	0	0.00	0.00	0.00
PAXOH	2.8	7	0.6677	1	25.00	14.29	1	25.00	25.00	14.29	1	25.00	25.00	14.29
PAXMH	2.4	112	0.5080	16	23.53	14.29	5	7.35	2.94	1.79	55	80.88	67.65	41.07

D. Maryland Eastern Tributaries: Chester River, Choptank River and Pocomoke River

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
CHSTF	2.0	1	0.0008	0	0.00	0.00	1	100.00	100.00	100.00	0	0.00	0.00	0.00
CHSOH	3.2	6	0.9996	1	100.00	16.67	1	100.00	0.00	0.00	0	0.00	0.00	0.00
CHSMH	2.6	33	0.3800	2	11.11	6.06	5	27.78	27.78	15.15	10	55.56	50.00	27.27
CHOTF	3.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CHOOH	2.7	5	0.9252	1	50.00	20.00	1	50.00	50.00	20.00	0	0.00	0.00	0.00
CHOMH1	2.6	8	0.3992	1	33.33	12.50	0	0.00	0.00	0.00	2	66.67	66.67	25.00
CHOMH2	2.9	22	0.7173	6	66.67	27.27	6	66.67	22.22	9.09	4	44.44	11.11	4.55
POCTF	2.5	1	0.9637	1	100.00	100.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
POCOH	2.5	7	0.8117	4	66.67	57.14	4	66.67	16.67	14.29	1	16.67	0.00	0.00
POCMH	2.6	9	0.5791	1	25.00	11.11	0	0.00	0.00	0.00	3	75.00	50.00	22.22

E. Maryland Eastern Tributaries: Smaller tributaries

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded w/o Cont.	% of Total w/o Cont.		Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
BIGMH	2.9	5	0.8676	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	20.00
BOHOH	4.0	1	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
ELKOH	3.2	8	0.4419	0	0.00	0.00	2	100.00	100.00	25.00	0	0.00	0.00	0.00
MANMH	3.1	13	0.6549	1	25.00	7.69	0	0.00	0.00	0.00	3	75.00	50.00	15.38
NANOH	3.4	4	0.9984	1	100.00	25.00	1	100.00	0.00	0.00	0	0.00	0.00	0.00
NANMH	3.0	9	0.5083	1	33.33	11.11	1	33.33	0.00	0.00	1	33.33	33.33	11.11
SASOH	3.2	3	0.4439	0	0.00	0.00	0	0.00	0.00	0.00	0	0.00	0.00	0.00
WICMH	2.8	9	0.8935	3	75.00	33.33	2	50.00	0.00	0.00	1	25.00	0.00	0.00

28

F. Maryland Upper Western Tributaries

Segment	B-IBI	Total Count	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
BACOH	2.1	4	0.7865	1	50.00	25.00	1	50.00	0.00	0.00	0	0.00	0.00	0.00
BSHOH	2.6	9	0.6381	1	33.33	11.11	1	33.33	0.00	0.00	1	33.33	33.33	11.11
GUNOH	2.9	15	0.2969	1	16.67	6.67	1	16.67	16.67	6.67	3	50.00	50.00	20.00
MAGMH	2.3	17	0.4106	2	25.00	11.76	2	25.00	12.50	5.88	6	75.00	62.50	29.41
PATMH	2.4	49	0.5638	10	32.26	20.41	6	19.35	3.23	2.04	22	70.97	58.06	36.73
RHDMH	2.9	7	0.6777	2	66.67	28.57	1	33.33	0.00	0.00	2	66.67	33.33	14.29
SEVMH	2.7	13	0.5965	1	20.00	7.69	3	60.00	60.00	23.08	2	40.00	40.00	15.38
SOUMH	2.1	8	0.7354	4	57.14	50.00	4	57.14	14.29	12.50	2	28.57	14.29	12.50
WSTMH	2.2	1	0.6504	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	100.00

G. Chesapeake Bay Mainstem and Associated Segments

Segment	B-IBI	Number of Samples	Cont. Post. Prob.	Samples with Contaminant Posterior Prob. >=0.90			Degraded Samples with Excessive Abundance/Biomass				Degraded Samples with Insufficient Abundance/Biomass			
				Total #	% of Degraded	% of Total	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.	Total #	% of Degraded	% of Degraded w/o Cont.	% of Total w/o Cont.
EASMH	2.1	4	0.3610	1	33.33	25.00	1	33.33	0.00	0.00	2	66.67	66.67	50.00
FSBMH	3.6	4	0.1219	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	25.00
HNGMH	2.8	5	0.2766	0	0.00	0.00	0	0.00	0.00	0.00	1	100.00	100.00	20.00
LCHMH	2.5	6	0.1671	0	0.00	0.00	1	33.33	33.33	16.67	2	66.67	66.67	33.33
MIDOH	3.4	3	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
NORTF	3.2	4	0.5267	0	0.00	0.00	1	50.00	50.00	25.00	1	50.00	50.00	25.00
TANMH	3.2	48	0.2974	1	12.50	2.08	0	0.00	0.00	0.00	6	75.00	62.50	10.42
CB1TF	3.1	19	0.5671	2	33.33	10.53	4	66.67	33.33	10.53	0	0.00	0.00	0.00
CB2OH	3.8	40	-	0	-	0.00	0	-	-	0.00	0	-	-	0.00
CB3MH	2.7	61	0.5487	9	29.03	14.75	3	9.68	3.23	1.64	23	74.19	54.84	27.87
CB4MH	2.3	28	0.3903	2	10.00	7.14	7	35.00	30.00	21.43	12	60.00	60.00	42.86
CB5MH	2.7	44	0.2125	2	11.76	4.55	1	5.88	5.88	2.27	17	100.00	88.24	34.09
CB6PHa	3.3	18	0.6078	1	33.33	5.56	1	33.33	33.33	5.56	2	66.67	66.67	11.11
CB7PHa	3.3	43	0.5762	0	0.00	0.00	1	12.50	12.50	2.33	6	75.00	75.00	13.95
CB8PHa	3.4	15	0.0199	0	0.00	0.00	0	0.00	0.00	0.00	2	100.00	100.00	13.33

30

Figure 1. General decision tree for segment assessment and characterization of B-IBI results.
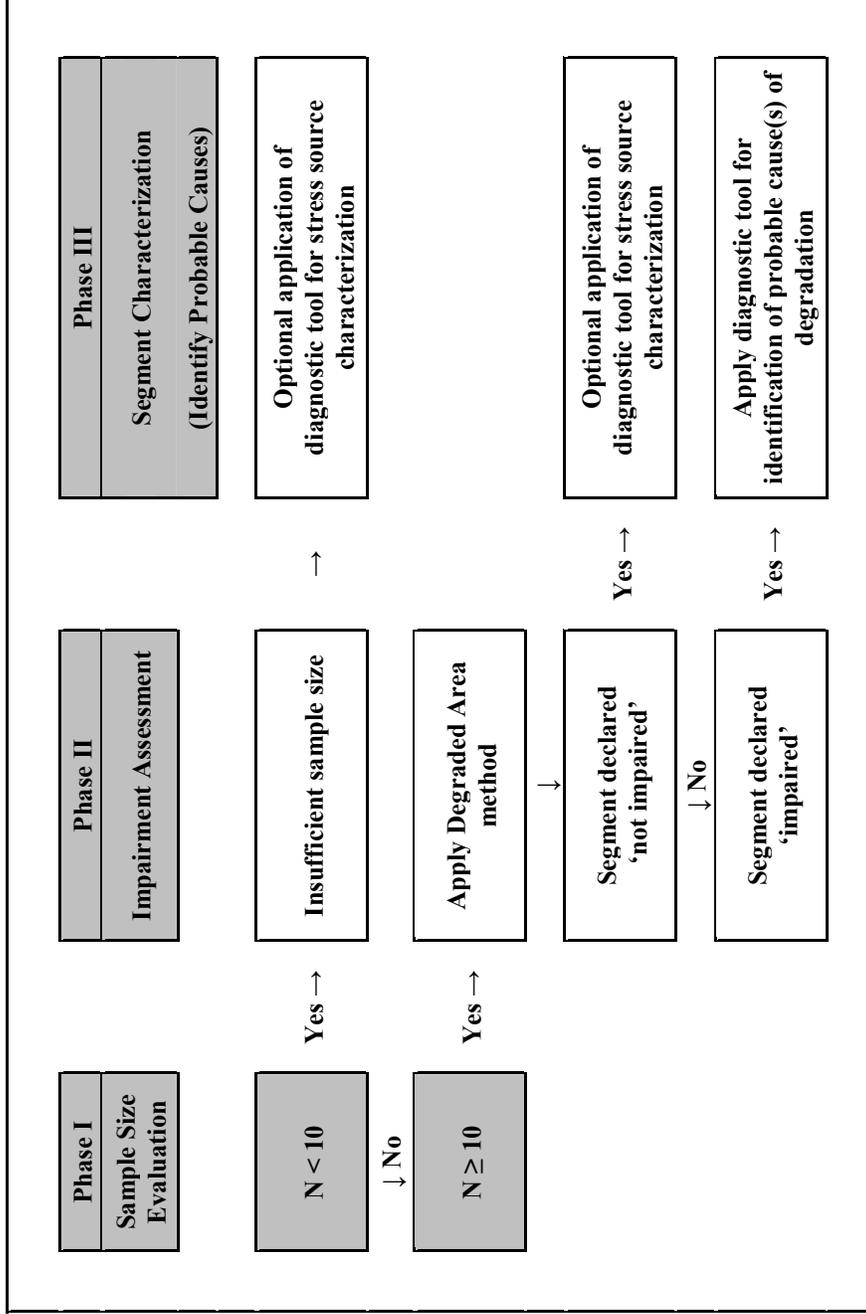
Appendix A
(Power Point Presentation)

Benthic Index of Biotic Integrity (B-IBI) for 2006 303(d) List

Alternative Assessment Methodology

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August 23, 2005

Summary

- The impairment assessment for each segment is based on the proportion of samples with "low" B-IBI scores (i.e., below a threshold)

- Two steps, estimate:

  1. Proportion of sites in a segment with scores below a threshold (P)

  2. Difference between P and the expected proportion under the null hypothesis (P_o), i.e., if the segment were in good condition (no low DO, contaminant, or nutrient enrichment problems), we would still expect a small proportion of sites to have "low" scores (e.g., because of natural variability); this proportion under the null hypothesis is defined as 5%.

Summary (cont.)

- Thresholds are set for each of seven benthic habitats in Chesapeake Bay: tidal fresh, oligohaline, low mesohaline, high mesohaline sand, high mesohaline mud, polyhaline sand, polyhaline mud.

- The threshold is set as the smaller of two values:

  1. 5^{Th} percentile IBI score for the good reference distribution (i.e., sites with low scores are unlikely to come from good reference conditions)

  2. Maximum observed IBI score for the degraded reference distribution (i.e, sites with low scores are likely to come from degraded conditions)

- See example next slide for two hypothetical habitats: 1) Habitat A, the distributions of scores for the good and the degraded reference sites do not overlap, 2) Habitat B, the distributions overlap.

Habitat A

Threshold

Frequency

5%

IBI scores

2.0   2.7

Habitat B

Threshold

Frequency

5%

IBI scores

2.2   3.0
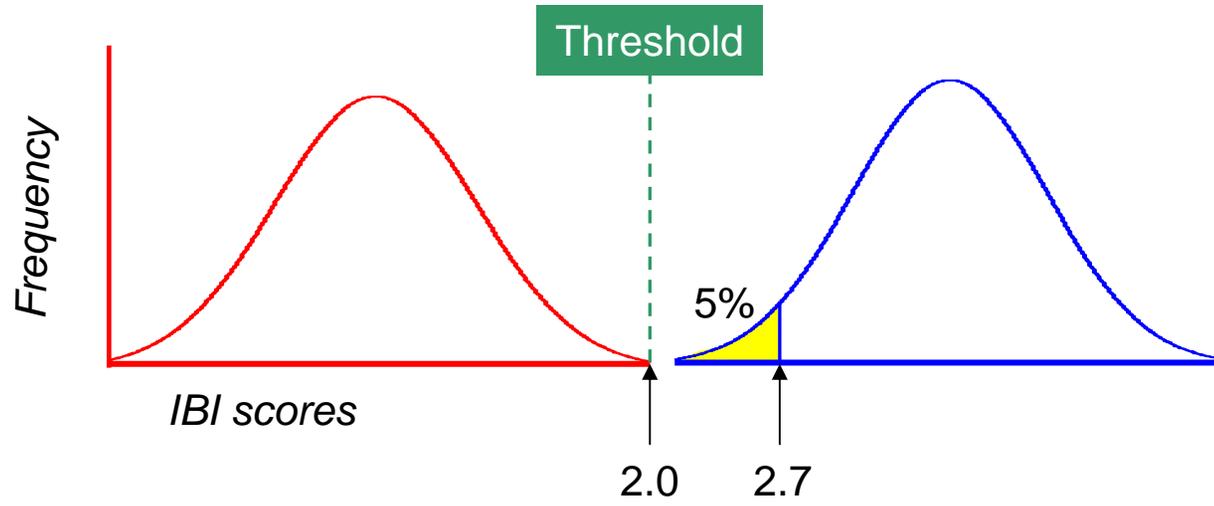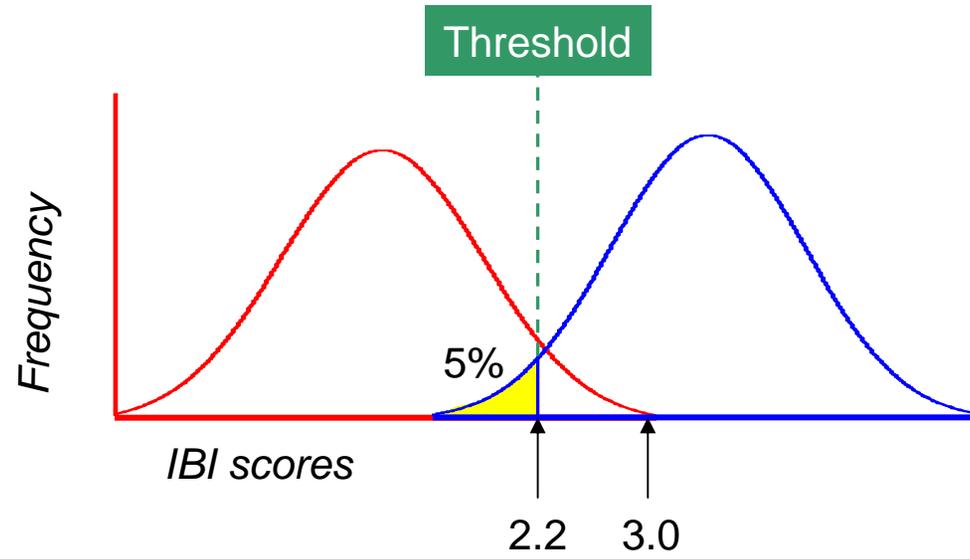
Summary (cont.)

- Reference distributions are sometimes based on a small number of samples; therefore the 5th percentile score is not well defined

- The 5th percentile score and its variance was estimated by bootstrap simulations

- For each iteration of the bootstrap simulation, a subset of the good reference data for each habitat was selected at random, and the 5th percentile score determined

- Over all the iterations, the 5th percentile score varied, and at each iteration the threshold was established according to the rule described earlier

- See next slide for the two habitat examples

Habitat A

Frequency

Threshold

IBI scores

2.0 2.7 3.3
     5%

By simulation

Habitat B

Frequency

Threshold range

IBI scores

1.7 2.2 3.5
     5%
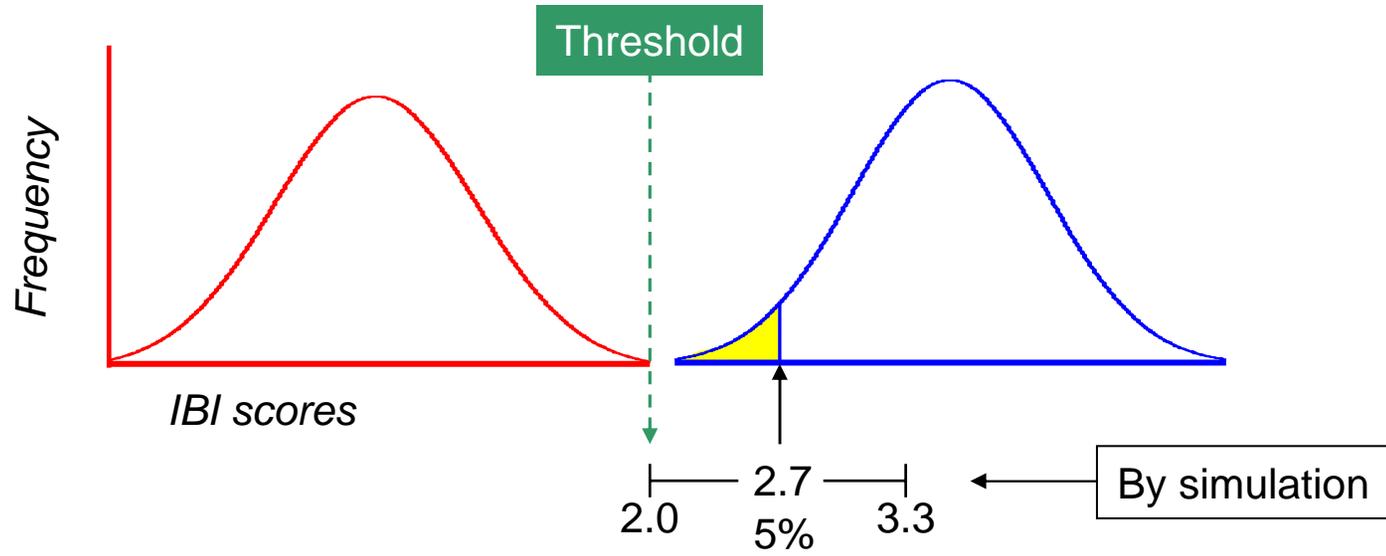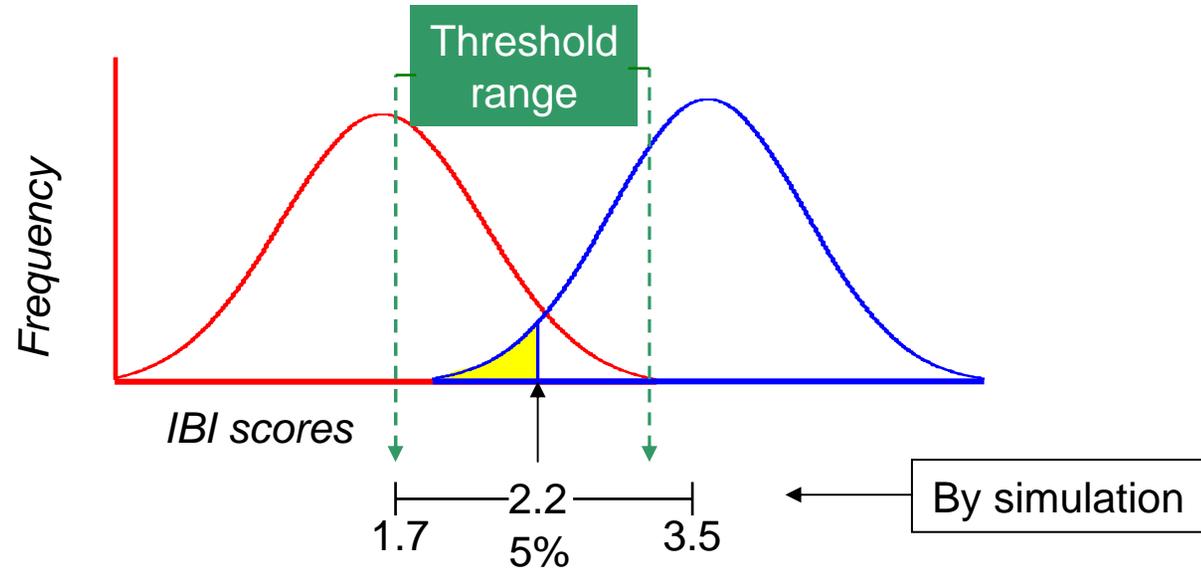
By simulation

Summary (cont.)

- For each iteration of the bootstrap simulation, the assessment data are compared to the reference data to estimate proportion of sites with scores below the threshold

- This is done for each of one or more habitats within a segment (i.e., some segments have sites in more than one habitat)

- See next slides for the two examples
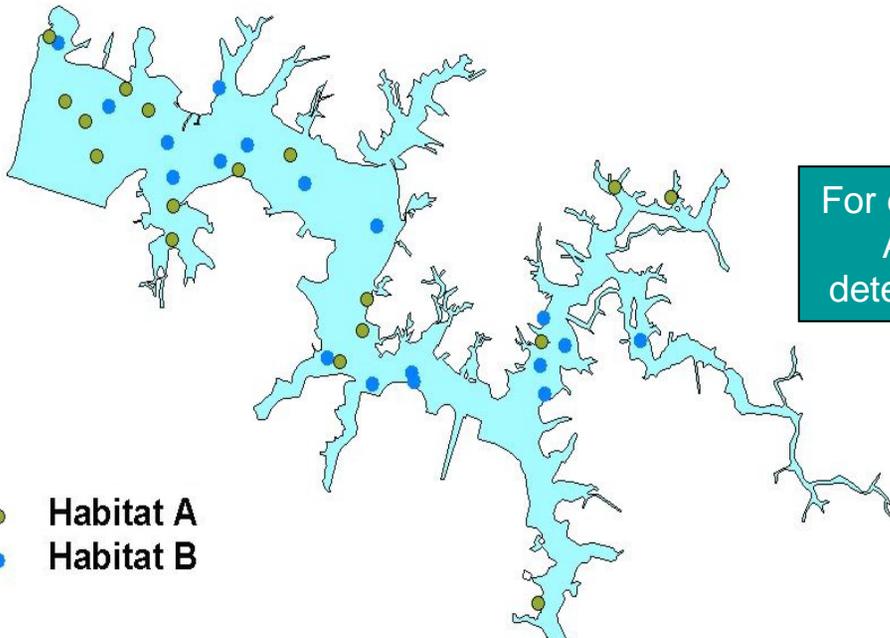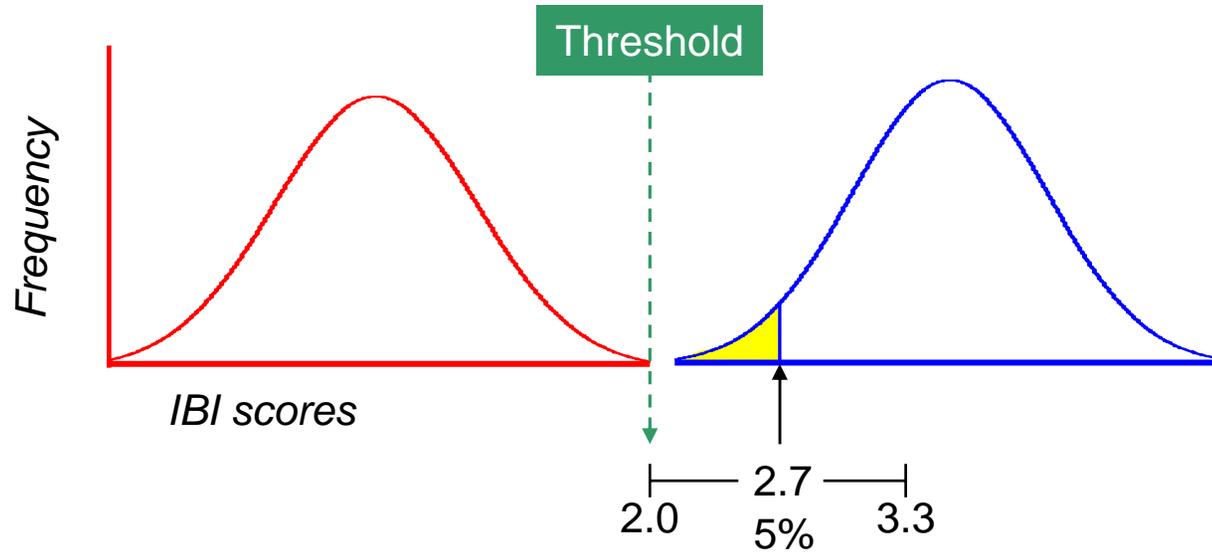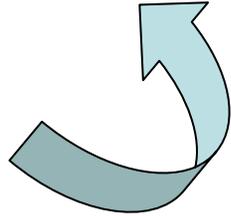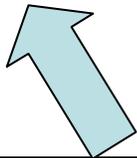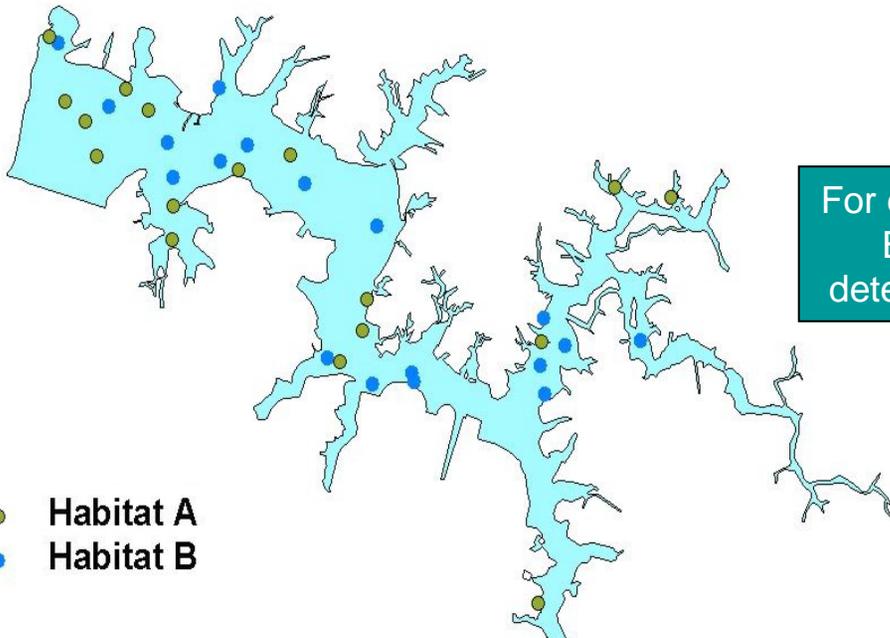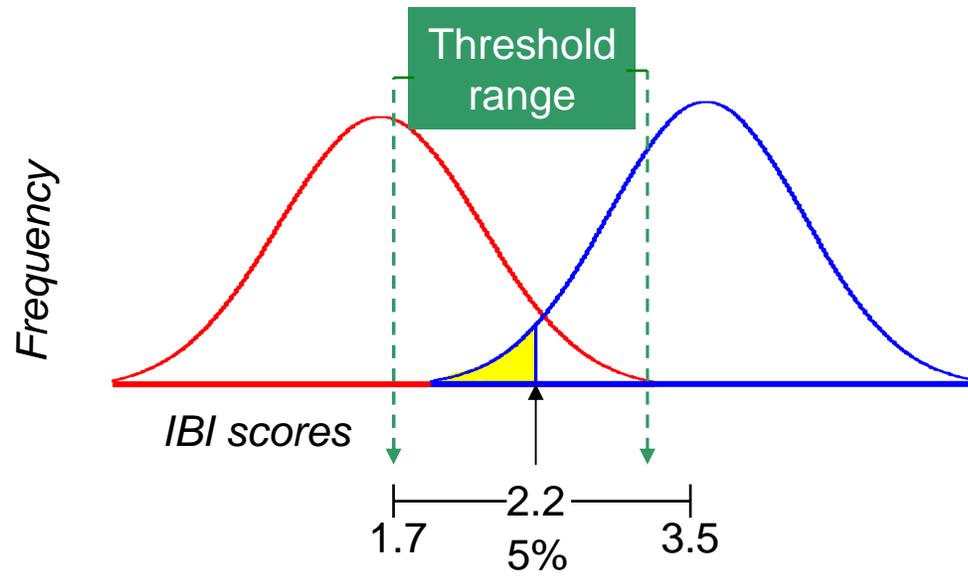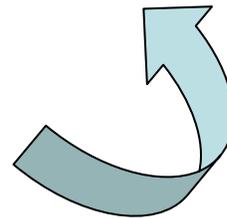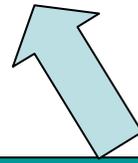
Summary (cont.)

- Example of calculations for a hypothetical segment with two habitats:

Iteration	n	Habitat A threshold	Habitat A P <threshold	n	Habitat B threshold	Habitat B P <threshold	P < threshold for A + B*
1	10	2.0	0.40	40	2.2	0.30	32.0
2	10	2.0	0.40	40	2.6	0.40	40.0
3	10	2.0	0.40	40	1.7	0.28	30.4
.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.
n	10	2.0	0.40	40	3.0	0.48	46.4
						P total < threshold =	Average + SE

*$(nP_a + nP_b)/(n_a + n_b)$, expressed as percent

Summary (cont.)

- Under the null hypothesis, 5% of the sites (P_o) would be expected to have low IBI scores, even if all sites in a segment were in good condition (i.e, no low DO, contaminant, nutrient enrichment problems)

5% of sites
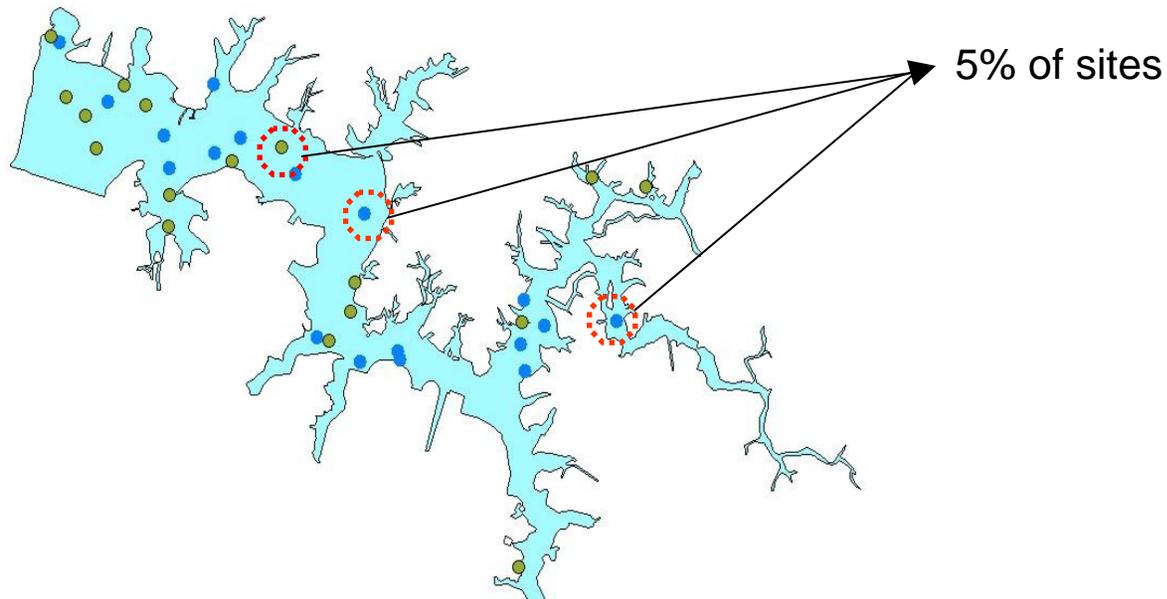
- Segments declared impaired if *P* greater than expected under the null hypothesis

$$P - P_0 > 0 \text{ (with 95\% confidence)}$$

Summary (cont.)

- Variance components in *P* added
  - Variance in P due to estimating thresholds – from bootstrap
  - Sampling variation within segment – binomial
- Confidence interval of $P - P_o =$

$$P - P_o \pm 1.96(SE_P + SE_{P_o}) = P - P_o \pm 1.96*SQRT(Var_P + Var_{P_o})$$

Var_P = Variance from bootstrap = $\displaystyle\sum_{i=1}^{i=5000} \frac{(P_i - \overline{P})^2}{5000 - 1}$ plus variance from segment = (pq/N-1)

Advantages of new method over Wilcoxon's

Wilcoxon

- evaluates differences in distributions based on ranks, cannot quantify magnitude of shift

- sensitive to small shifts in distribution of B-IBI scores

New method

- estimates proportion of area below thresholds and magnitude of departure from reference conditions

- tests if this magnitude is above specific thresholds of protection

- incorporates uncertainty in reference conditions as well as sampling variability in the assessment data

- does not require purchase of special statistical analysis package (Wilcoxon does)

- Both methods are suitable for data segregated into multiple habitats for which reference distributions are not homogeneous