United States
Environmental Protection
Agency

Ballast Water BAT Data Analysis: Analysis of Newly Acquired U.S. Coast Guard Ballast Water Management System Type-Approval Data to Assess System Performance

U.S. Environmental Protection Agency
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August 2023

ACKNOWLEDGEMENTS

This report was prepared by the U.S. EPA Office of Wetlands, Oceans, and Watersheds (OWOW), Oceans, Wetlands and Communities Division (OWCD), Ocean and Coastal Management Branch (OCMB) with contractor support provided by individuals from Eastern Research Group, Inc. under contract number 68HERC22D0006.

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Contents

List of Figures

List of Tables

List of Abbreviations

BAT	Best Available Technology Economically Achievable
BDL	Below detection limit
BWMS	Ballast Water Management System
CFR	Code of Federal Regulations
CWA	Clean Water Act
EPA	U.S. Environmental Protection Agency
ETV	Environmental Technology Verification
GAIC	Generalized Akaike Information Criterion
IG	Inverse Gaussian
IMO	International Maritime Organization
IQR	Interquartile range
MDL	Method detection limit
ND	Non-detect
PSU	Practical salinity unit
QA/QC	Quality assurance and quality control
SAB	Scientific Advisory Board
TSS	Total suspended solids
USCG	United States Coast Guard
VF	Variability factor
VGP	Vessel General Permit

1. Summary of 2020 Proposed Numeric Ballast Water Discharge Standard and Public Comments

In 2020, EPA proposed to continue, as part of the ballast water discharge standard (expressed as instantaneous maximums), the 2013 VGP numeric discharge standard for biological parameters as follows:

- For organisms greater than or equal to 50 micrometers (µm) in minimum dimension: discharge must include less than 10 living organisms per cubic meter (m^3) of ballast water.
- For organisms less than 50 µm and greater than or equal to 10 µm: discharge must include less than 10 living organisms per milliliter (mL) of ballast water.
- For indicator microorganisms:
  - Toxicogenic *Vibrio cholerae* (serotypes O1 and O139): a concentration of less than 1 colony forming unit (cfu) per 100 mL.
  - *Escherichia coli*: a concentration of less than 250 cfu per 100 mL.
  - Intestinal enterococci: a concentration of less than 100 cfu per 100 mL.

The proposed rule provided EPA's evaluation of BWMS USCG type-approval data available to the Agency at the time of proposal, with the conclusion that a more stringent numeric discharge standard was not achievable because test results were within the same order of magnitude as the current standard and fall within the margin of error expected due to the great variability associated with the characteristics of ballast water and challenges associated with monitoring, analyzing, and enumerating organisms in the different size classes.

EPA received numerous comments on the proposed rule about its Best Available Technology Economically Achievable (BAT) analysis for the numeric ballast water discharge standard. Commenters stated that EPA only reviewed less than one-quarter of the USCG BWMS data and that these data were supplied to EPA by an industry group with a conflict of interest in the standard setting process. Other comments expressed concerns that EPA:

- Used outdated information when it relied on the 2011 SAB report and 2011 National Academy of Sciences' National Research Council report;
- Rejected data from IMO type-approval testing based on an incomplete, undocumented, and questionable "independent review," and that the USCG type-approval data EPA did review could very well have the same QA/QC concerns as the IMO data;
- Established the standard first and then worked backwards toward the 2013 VGP standard rather than evaluating the data to determine what standard could be achieved independent of the existing standard;
- Relied inappropriately on international consistency;
- Failed to consider whether a more stringent standard could be met by reasonable and feasible modifications to existing BWMS designs; and,
- Asserted incorrectly that:
  - Available information does not justify a more stringent numeric discharge standard, be it 100 times, 10 times, or even 2 to 9 times more stringent than the proposed standard;
  - A more stringent numeric discharge standard would represent an insignificant improvement in treatment system effectiveness;

- Limitations in the monitoring of organisms in ballast water do not support establishing a more stringent standard; and,
- Comparing type-approval data for different systems would only be appropriate if all other variables were held constant or under complete control during the test.

2. Data Introduction

2.1 Ballast Water Type-Approval Data Acquired Since the Proposal

As a result of concerns raised during the comment period that EPA reviewed insufficient USCG BWMS data, EPA requested USCG BWMS type-approval data directly from the USCG. EPA requested that the data be provided in a form that would allow EPA to conduct a transparent and comprehensive assessment of the performance of BWMS and to share those data and EPA's analysis of those data with the public. Acknowledging that the USCG continues to receive new data packages, the Agency requested data for all systems type-approved by the date of the proposed rule (October 2020). EPA does not expect that more time or additional applications would meaningfully alter the results of the analysis. Additionally, recognizing the statutory deadline for finalizing this standard and the significant effort required to extract, transcribe, and validate test data, EPA focused on obtaining the most important and relevant data to perform its BAT analysis. For example, EPA determined that it was unnecessary to obtain data from the USCG regarding the number and size of subsamples, or system operating parameters such as flow rates, disinfectant dosages, or turbidity. The complete set of USCG BWMS type-approval data provided to EPA by the USCG to support this analysis are included in the docket for this rulemaking.

The USCG provided EPA with non-confidential/non-proprietary test data for 37 type-approved BWMSs, as well as 16 sets of amendment test data for those type-approved systems[1]. EPA considered the amendments as additional independent systems because the original BWMS remains type-approved even when an amendment is submitted and approved for that system. EPA excluded 2 sets of amendment data from the analysis due to incomplete data. EPA also identified and excluded two duplicate data sets from the analysis to prevent weighing the same results twice in the statistical methodology. This resulted in a total of 49 data sets for the statistical analysis.

The data provided by the USCG included both land-based and shipboard testing results (uptake, discharge, and control) for select parameters, including the two largest organism size classes, for all valid tests[2]. For land-based testing, the USCG provided test results for medium and large organisms, the three small organism size class parameters, and other water quality data, such as salinity and total suspended solids (TSS). For shipboard testing, the USCG provided test results for medium and large organisms and salinity.

The USCG masked the data to exclude information the USCG deems to be proprietary, such as the vendor, make, and model of the BWMSs and the treatment technology used by each BWMS. However, the USCG developed a labeling system to allow EPA to analyze the performance data for each individual

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[1] The USCG BWMS type-approval regulations at 46 CFR 162.060 require that testing be performed consistent with EPA's Environmental Technology Verification (ETV) Protocol (USEPA, 2010). As of January 1, 2023, the USCG has type-approved 50 BWMSs.

[2] A test is considered valid if it met all uptake and testing challenge requirements of the ETV Protocol (EPA/600/R-10/146, *Generic Protocol for the Verification of Ballast Water Treatment Technologies, version 5.1*, (dated September 2010)), as incorporated by reference in USCG BWMS type approval regulations at 46 CFR § 162.060.5. Invalid tests (test data not provided by USCG) are not counted as a test for purposes of counting required consecutive tests if it can be shown that the failure to meet the discharge standard was not a failure of the BWMS to demonstrate biological efficacy (USCG, 2018 – Ballast Water Frequently Asked Questions – Revised April 24, 2018 - Ballast_Water_FAQs.pdf (uscg.mil)).

BWMS and its treatment technology type classification without disclosing the details of the BWMS or identifying the technology.

The data provided to EPA is the result of an approximately yearlong effort by the USCG to transcribe information from BWMS type-approval application test reports, standardize terms to facilitate analysis, and perform a quality assurance review of the data provided by as many as six USCG-approved independent laboratories, located in five different countries, each supported by no fewer than six approved sub-laboratories. Importantly, this means that the values are not all reported with the same precision (i.e., the number of digits or significant figures). This is especially relevant to values based on calculations or averages, where the calculated value (e.g., 0.333 or 7,341 organisms per milliliter) is reported at a higher precision than could be supported based on the counting method. Values are reported without confidence intervals, so the values represent a mean of a range of likely estimates.

2.2 Focus on Organism Size Classes

The Agency used these newly acquired data to reassess the 2020 proposed numeric ballast water discharge standard, pursuant to the BAT framework under the CWA. Specifically, EPA performed an analysis to determine whether the newly acquired data justify a different standard for the two largest organism size classes: (a) organisms greater than or equal to 50 µm in minimum dimension, referred to here as "large organisms," and (b) organisms less than 50 µm and greater than or equal to 10 µm, referred to here as "medium organisms." EPA focused on these two parameters as these are the two key parameters EPA uses to assess invasion potential from ballast water discharges and for which the type-approval data provide a meaningful assessment of treatment system capabilities.

EPA did not reassess the smallest organism size class: toxicogenic *Vibrio cholerae* (serotypes O1 and O139), *Escherichia coli*, and intestinal enterococci. As described in the ETV Protocol, USCG type-approval testing establishes challenge conditions based on culturable heterotrophic bacteria rather than on the three smallest indicator microorganisms for which EPA, the USCG, and IMO have established a numeric discharge standard (toxicogenic *Vibrio cholerae* (serotypes O1 and O139), *Escherichia coli*, and intestinal enterococci). EPA does not consider the type-approval data to adequately represent the range of water quality conditions that may be experienced by vessels for these three smallest indicator microorganisms; therefore, the type-approval data does not provide an appropriate basis for calculating the numeric ballast water discharge standard for these parameters. The USCG land-based type-approval data available to EPA, however, show that even prior to treatment, untreated "challenge water" (i.e., the water supplied to a treatment system under test, which must meet specified ranges for living organism densities and water quality parameters) exceeded the enterococci discharge standard in only about 15 percent of the samples and the *Escherichia coli* discharge standard in less than seven percent of the samples, while *Vibrio cholerae* was never detected in any challenge water samples. These data also show that the treated discharge achieved the numeric discharge standard in every test trial (100 percent) assessed for these three biological parameters.

Thus, while the data demonstrate that discharges from BWMS during USCG type-approval testing can meet the proposed numeric ballast water discharge standard for the smallest biological parameters, these data also demonstrate the USCG type-approval process does not challenge BWMS performance in treating these parameters the way it does for medium and large organisms. Notably, these data fail to demonstrate that systems are technologically available to meet a different numeric discharge standard when faced with the full range of water quality conditions vessels may face while in operation. As such, the analysis presented here focuses solely on medium and large organisms. Additionally, EPA did not receive new data upon which to reassess the proposed numeric discharge standard for biocide parameters.

2.3 Data Validation

EPA assumes these USCG data are relevant, accurate, reliable, and representative, and the Agency performed a quality control review of the data provided. EPA validated USCG-provided type-approval data to ensure that these data are fit for use for calculating a numeric discharge standard for the two largest organism classes (using Stata software; StataCorp, 2017). Data validation consisted of checks for completeness, range, and logic. Completeness checks included assessing whether type-approval data were provided for all valid test cycles (pass and fail), that each test cycle had both influent (challenge water, treatment uptake, or control uptake) and effluent (treatment discharge) data, that each test cycle had data for both medium and large organism classes, and that there were no instances of multiple results for the same test cycle. Range and logic checks assessed the validity and magnitude of all treatment discharge results that exceed the discharge standard, that challenge water and control or treatment uptake organism concentrations were greater than discharge concentrations, and that uptake and control discharge organism concentrations met the criteria for a minimum concentration of living organisms per Tables 4 and 7 of the ETV Protocol (USEPA, 2010).

Instances of incomplete data were resolved by USCG by correcting post-processing assignments or other errors, or by reclassifying as invalid tests (e.g., instances of commissioning or IMO style tests). However, some incomplete data could not be resolved because the data were not reported in the test reports. As such, EPA excluded a test cycle or an amendment from the analysis (see Data Processing in Section 2.4). BWMSs with biological efficacy data available for only one organism size class were excluded from this analysis since the data omission precluded EPA from assessing those systems' performance.

2.4 Data Processing

EPA processed the provided USCG type-approval data compiled in two validated spreadsheet files (land-based and shipboard testing) for analysis by addressing amendment data, samples with no detected organisms, gaps in salinity classifications, and missing or duplicate results to ensure consistent analysis.

Type-approval amendments were submitted to the USCG for a variety of reasons, such as changes to filters, components, and hold times. Land-based re-testing of the BWMS with amendments is required to ensure the systems still meet ETV Protocol treatment requirements. EPA included amendments that tested the full BWMSs and excluded those that tested only individual components. Since the original BWMSs remain type-approved for use on vessels, EPA did not replace them with their amendment(s), but rather, considered the amendments as additional independent systems. USCG provided brief descriptions of the update(s) made in each amendment, which EPA numbered and used for identification. For example, system HH had two amendments, which EPA labeled HH1 and HH2; all three were included in this analysis as separate BWMSs (all amendments listed in Table A-1 in Appendix A). EPA excluded an amendment to system C since it had no accompanying description provided, and very low uptake concentrations of medium organisms, including <10 organisms/mL. An amendment to system XXX was also omitted because it included only two trials[3]. In total, 14 amendments from 12 different BWMSs were added to this analysis.

EPA also identified and excluded from the analysis duplicate results from two BWMSs to prevent weighing the same results twice in the statistical methodology. All organism results of system R were also within system SS results, so EPA deleted all R results and renamed SS as SS/R. Similarly, all results of system LLLL were also within system LLL results, so EPA deleted all LLLL results and renamed LLL as LLL/LLLL. With the removal of these two duplicate systems, the total number of original type-approved systems decreased from 37 to 35, plus 14 amendments for a final total of 49 systems.

Following treatment, many trials' discharge samples contained no detectable organisms. EPA represented these non-detects (NDs) as their method detection limits (MDLs), which were determined and provided by the USCG where available. The volume of water used in the analytical methodology determines the MDL, since units are in organisms per volume of water. Note that test facilities did not report sample-specific MDLs, and USCG did not enter the intricacies of sample volumes, sample concentration, and

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[3] The USCG data did not identify USCG-approved deviations from test procedures pursuant to 46 CFR 162.060-10(b)(1) nor USCG-granted reconsiderations or appeals.

volume analyzed into the spreadsheet provided to EPA that would be required to calculate sample-specific MDLs. Instead, USCG reviewed test facility methods and techniques to determine a best-case-scenario estimated MDL, or range of MDLs, typically by BWMS and sample type (e.g., treatment discharge). Because USCG transcribed type-approval data "as written," NDs were expressed using a variety of formats. If the original values were reported as "0" or non-numeric (such as "BDL"), EPA substituted, or imputed, given organism concentrations using the following methodology (using Stata software; StataCorp, 2017):

- For MDLs expressed as a single number, EPA used the MDL.
- For MDLs expressed as a range, EPA used the midpoint of the provided range. One exception is that EPA identified MDLs ranges of 0.01 – 0.02 organisms/mL and 0.01 – 0.30 organisms/mL as unrealistically low for medium organisms and unsupported by an assessment of the detected values. Specifically, the lowest detected values for medium organisms were 0.08 organisms/mL, not 0.01 organisms/mL. In these cases, EPA imputed an MDL of 0.15 and 0.20 organisms/mL, respectively, rather than the midpoints of 0.015 and 0.155 organisms/mL, respectively.
- In cases where MDLs were not provided by USCG:
  - For land-based testing, EPA imputed NDs using the lowest detected value for those systems. Specifically, these values were 0.30 organisms/m^3 for large organisms, 0.40 org/m^3 for medium organisms from systems C or E, and 0.15 org/m^3 for medium organisms from system VVV.
  - For shipboard testing, EPA imputed an MDL of 0.30 org/m^3 for large organisms and an MDL of 0.20 organisms/mL for medium organisms.

All values that EPA imputed with MDLs were identified as ND. Additionally, as advised by the USCG, if units were expressed as "<org/m3" or "<org/mL," or if descriptions were "<Average," EPA identified the result as ND. Any detected values greater than zero but below their given MDL were used as-is in this analysis and were not identified as ND. Organism concentrations that were missing or marked as "NR" were removed because their values were unknown.

The type-approval process tested BWMS effectiveness in different salinities. The USCG provided land-based data to EPA categorized by salinities as marine, brackish, or fresh; however, the same categorization was not provided for the shipboard data. Salinities in shipboard data were provided as quantitative measurements that EPA used to classify into types defined by <1 Practical Salinity Unit (PSU) for fresh, ≥28 PSU for marine, and measurements in between for brackish. For shipboard trials in which a salinity was provided for only the treatment discharge sample, EPA applied that salinity to the uptake sample for that trial, since salinity values were consistent across samples for all other trials that reported salinities for both uptake and discharge. Shipboard trials without any reported salinity (in any of the sampling locations) were omitted from this analysis, since the statistical methodology requires classification of trials by salinity category (12 trials removed).

3. Statistical Analysis Methods

This section describes EPA's statistical analysis for calculating a numeric ballast water discharge standard for the two largest organism size classes: organisms greater than or equal to 50 µm in minimum dimension, referred to here as "large organisms," and organisms less than 50 µm and greater than or equal to 10 µm, referred to here as "medium organisms." These two size classes are the two key parameters EPA uses to assess invasion potential from ballast water discharges and for which EPA determined type-approval test data are adequate for purposes of evaluating performance capabilities of these systems. The Agency used the newly acquired data to analyze whether a different standard from the proposed rule should be established for medium and large organisms. The section describes how EPA defined sets of trials, tested for correlations, identified a distribution shape and calculated distribution parameters, combined land-based and shipboard trials, identified best available technology, and calculated the numeric discharge standard. Analyses were performed using R software (R Core Team, 2023). Results are also summarized alongside a discussion of the analysis limitations.

3.1 Data Structure

The BWMS type-approval data were stratified across several variables. Applicants carried out trials in two test platforms (land-based or shipboard; shipboard testing not required for amendments) and in up to three salinities (marine, brackish, or fresh). The focus of this analysis is the two largest organism size classes regulated under the VGP, both of which have results for all trials. Each unique combination of these characteristics – BWMS, test platform, salinity, and organism size – define one "set" in this analysis. Land-based sets each typically comprised at least five trials, as required by the ETV Protocol. Shipboard sets did not have a minimum number of trials required per salinity category, but rather, required variability in testing location (46 CFR § 162.060-28(e)).

These available sets comprise the input data to this analysis, which was performed using R software (R Core Team, 2023). The means and variabilities of organism concentrations within these sets form the basis of the numeric discharge standard calculations, as described in the following sections.

3.2 Evaluation of Uptake Versus Discharge Concentrations

The focus of numeric discharge standard development is on organism concentrations output from BWMSs, based on treatment discharge water samples. However, EPA acknowledges that uptake water characteristics also varied across the type-approval data, which might have affected the resulting treatment discharge concentrations. As such, this analysis also checked for this possibility.

During type-approval testing, uptake water samples were taken at sampling points called treatment uptake, control uptake, and/or challenge water (Figure 1). Often, only one of these is reported per trial. When more than one was available, EPA defined the untreated organism concentration using the order of preference of treatment uptake, control uptake, then challenge water, and used the sampling point that contained both organism size classes. Although TSS concentrations were also included in the given data, EPA could not use them for this step of the analysis because they were not available for all trials (37 percent missing TSS).

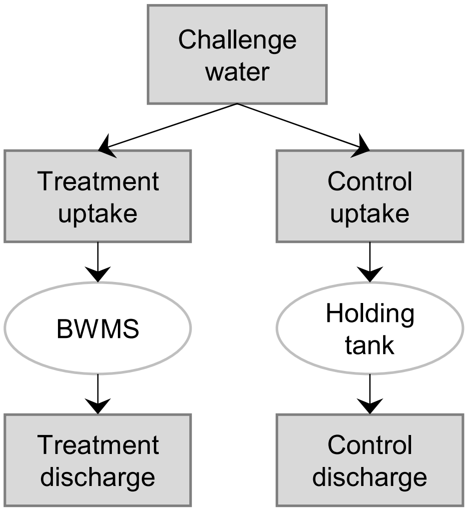

Figure 1. Diagram of the five locations (rectangles) at which water samples were taken in the BWMS type-approval process.

EPA used regression methods to test whether uptake organism concentrations were statistically significantly associated with treatment discharge organism concentrations. In other words, EPA determined whether uptake concentrations were likely to have affected discharge concentrations. The regression method used was linear mixed-effects modeling, which accounts for known grouping of points in the data, called dependence (Kuznetsova et al. 2017). In these data, concentrations are grouped within different systems, test platforms, and salinity categories (treated as random effects in the models). EPA ran one regression on large organisms only and another on medium organisms only. Discharge concentration was the predicted variable, and uptake concentration was the predictor variable, each transformed by natural logarithm to adhere to statistical assumptions. For this regression, all ND discharge concentrations, explained in Section 2.4, were substituted with half their upper bound. As a check, EPA also re-ran the regressions by substituting the values' upper bounds, then substituting 0.01 as a lower bound, to check whether the substitution impacted statistical results. An R^2_β metric for linear mixed-effects models was calculated to quantify level of explanation (Jaeger, 2017, standardized generalized variance approach), and regressions were evaluated for adherence to assumptions of normality and homoscedasticity.

Results showed that for both organism size classes, the variability in uptake concentrations explained only one percent of the variability in discharge concentrations overall (see further details in Section 4.2 and Appendix B), indicating that the variability in discharge concentrations among trials is due to other reasons not defined in the type-approval database. With these negligible effects, there was no need to adjust the treatment discharge concentrations or perform additional analyses to account for the variability of uptake concentrations. Rather, EPA used treatment discharge concentrations as given for the remainder of the methodology.

3.3 Distribution Shape

The numeric discharge standard is based on means and variabilities of the treatment discharge concentrations, to accommodate the fact that normal operation of any filtration system occurs within a range of expected performance. Calculating this variability requires fitting statistical distributions to the data. For each set (defined by unique combinations of BWMS, salinity, test platform, and organism size), EPA fit a variety of candidate distributions to the discharge organism concentrations. The distribution that best described the most sets was applied for the remainder of the analysis. This section describes that procedure.

Although the type-approval data were originally based on counts of organisms and were therefore discrete (i.e., results are integers), test facilities generally reported results as averages of subsamples, and standardized them to common water volumes of medium organisms/mL and large organisms/m^3. Thus, the values are continuous (that is, values include fractions of organisms per volume). Therefore, Poisson and negative binomial discrete distributions, identified as being descriptive of organism counts in ballast water literature sources (such as Lemieux et al., 2008 and Lee II et al., 2010), could not describe these data. Instead, sets were evaluated for fit to the following distributions that were continuous, positive, and adaptable to skewness: lognormal, gamma, inverse Gaussian, Weibull, and exponential.

EPA only fit these candidate distributions to sets with at least five detected treatment discharge measurements, 97 in total. A goodness-of-fit metric called the Generalized Akaike Information Criterion (GAIC) was calculated for each candidate distribution and each set (using R software package gamlss.dist, Stasinopoulos and Rigby, 2022) to quantify the amount of error associated with each distribution shape. EPA ranked GAICs from lowest (best) to highest within each set, and then calculated an average rank for each of the five distribution shapes. The inverse Gaussian (IG) distribution, also called the Wald distribution, achieved the top average rank across all evaluated sets (see Section 4.3 for results) and therefore was the distribution applied for the final analysis.

Organism concentrations in treated discharges were often low, with many sample analyses resulting in zero organisms found or otherwise identified as non-detects (NDs) (see Section 2.4 for details). Once analyzed water volumes are factored in, each ND is more accurately represented as a range of values between zero and their MDL in organisms per unit of volume (to the left of the MDL), making these values left-censored. This recognizes that although an observation's exact value is unknown, it is known to be small with a given upper bound. Therefore, EPA used a left-censored IG distribution (using R package gamlss.cens; Stasinopoulos et al., 2018) in this analysis.

In this step, EPA input all ND values as left-censored under their upper bound (using R package survival; Therneau, 2023 and Therneau and Grambsch, 2000). For most ND values, the upper bound was their imputed MDL, as described in Section 2.4; for values with units or descriptions accompanied by "<" symbols, the upper bound was the reported concentration.

3.4 Distribution Parameters

The characteristics of an IG distribution can be summarized with two parameters: the mean, a measure of centrality, and sigma, a measure of scale (Figure 2). These parameters were the basis of calculations to determine the distribution-based numeric discharge standard for both large and medium organisms.

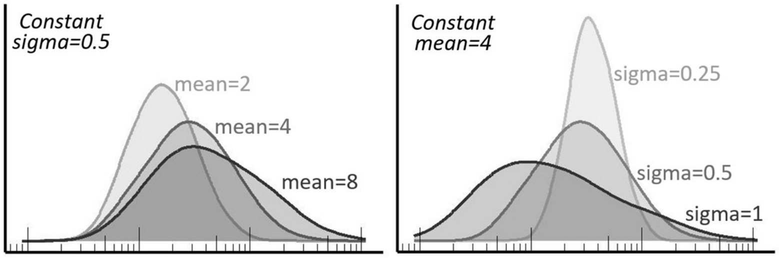

Figure 2. Inverse Gaussian distributions, shown with varying mean parameters (left) and sigma parameters (right).

The mean of a left-censored IG distribution is equal to the arithmetic mean of the data when all values are detected. However, when a set includes NDs, the left-censored IG mean is slightly less than the actual arithmetic mean, which uses the MDLs in place of the ND values. The sigma parameter scales the IG distribution and quantifies its spread. For all sets with at least two distinct detected values, EPA fit both parameters using R packages gamlss.dist and gamlss.cens (Stasinopoulos and Rigby, 2022; Stasinopoulos et al., 2018), which are based on a maximum likelihood estimation technique (Rigby et al., 2020; Rigby and Stasinopoulos, 2005). In turn, these mean and sigma parameters were the basis of 99th percentile calculations for each set.

Sets with zero or one distinct detected value had insufficient data to estimate the variance, sigmas, or 99th percentiles. These sets were instead represented later in this analysis by their arithmetic means, calculated using upper limits for NDs and the given measurement for any detected values (as done when calculating BAT discharge limitations for Effluent Limitations Guidelines such as US EPA, 2015).

For development of Effluent Limitations Guidelines, the Agency defines the maximum daily limitation as an estimate of the 99th percentile of the distribution of the daily measurements and the average monthly limitation as an estimate of the 95th percentile of the distribution of the monthly averages of the daily measurements. EPA used the 99th percentile as a conservative estimate of the distribution for calculation of an instantaneous maximum never-to-be-exceeded discharge standard.

3.5 Combination of Land-based and Shipboard Trials

For each combination of BWMS, salinity, and organism size, EPA combined the land-based and shipboard results proportionally based on their respective sample sizes (the number of trials from each). A weighted mean was calculated for each aggregated set using:

$$M_W = M_L P_L + M_S (1-P_L)$$

Where:

M_W = weighted mean organism concentration (in organisms/mL or m^3)
M_L = land-based mean organism concentration (in organisms/mL or m^3)
M_S = shipboard mean organism concentration (in organisms/mL or m^3)
P_L = proportion of trials in the set that were land-based (unitless)

Therefore, a BWMS with more land-based than shipboard trials (for a given salinity and organism size) had a mean more strongly influenced by its land-based test results. Weighted 99th percentiles were calculated for each aggregated set using the same method. This step did not affect amendments, which were only land-based.

3.6 Variability Factors

Next, for each aggregated set of BWMS, salinity, and organism size, EPA calculated the variability factor (VF) as the weighted 99th percentile divided by the weighted mean. VFs, therefore, are only available for sets in which at least one test platform had at least two distinct detected values. While sets with zero or one detected value have insufficient data to estimate variability and therefore do not have VFs, their arithmetic means were still used to calculate the numeric discharge standard calculations. VFs have been used by EPA to establish the numeric discharge standard that is to be met at all times, accounting for the statistical relationship between average treatment system performance and higher concentrations that would be expected to occur less frequently in well-designed, well-operated systems. This definition of VFs has been used in various Effluent Limitations Guidelines (e.g., US EPA, 2015 and US EPA, 2002).

3.7 Best Available Technology

An important decision in evaluating the USCG type-approval data was whether any BWMSs should be excluded from the calculation of the standard based on a determination that they do not represent BAT. Typically, this assessment would be based on an engineering analysis of treatment system design and operation; however, that information was not provided to EPA by the USCG. Another important aspect of the analysis was whether the selected technologies are appropriate for the range of vessels subject to the numeric discharge standard; however, USCG deemed the treatment technology used by each BWMS to be proprietary.

EPA considered whether BAT should be based on any specific BWMS(s), or on any specific treatment technology type(s) into which the USCG categorized these BWMS. Five of the ten technology types contained only one BWMS. Two types each contained amendments of the same original system, and the remaining three contained 4, 14, and 21 different BWMSs each. EPA tested whether enough similarity existed among the treatment discharge concentrations of BWMSs, for the five technology types with more than one BWMS, to evaluate them as a homogeneous group. To do so, EPA ran 30 Kruskal-Wallis tests (all combinations of five technology types, two organism sizes classes, and three salinity categories) since some combinations had nonnormal and/or unequal variances of trial distributions (as indicated by a Shapiro-Wilk test and/or Levene's test with a p value <0.01; Fox and Weisberg, 2019). Of the 30 tests that compared systems within technology-size-salinity groups, 14 had significant Kruskal-Wallis results (p <0.05), indicating that at least one system's discharge concentrations were statistically significantly different than the others in their group (further detail in Section 4.6). This precluded an analysis of discharge concentrations aggregated at the level of technology type, since statistically significant heterogeneities exist within technology types. Therefore, EPA used systems, rather than technology types, as the basis of the next step.

EPA compared treatment discharge concentrations of BWMSs within six groups defined by the two common organism size classes and three salinity categories using two methods. The goal of the first method was to evaluate whether statistically significant differences in treatment effectiveness among the (up to) 49 systems per group could inform how BWMSs might be narrowed to represent BAT. EPA ran six Kruskal-Wallis tests, one per group. EPA identified which system(s) statistically differed from other system(s) using pairwise Dunn's tests with Bonferroni-Holm p value adjustments, which systematically compared all systems' mean discharge concentrations to each other in pairs (Kassambara, 2023). For each group, the pairwise comparisons showed that at least some systems were statistically significantly different, but frequent overlap in significance among systems prevented any clear stratifications of "best" or "worst" systems. Furthermore, the effectiveness of systems varied by organism size and/or salinity, such that systems had different relative comparisons depending on the group within which they were evaluated. For example, one system may have had lower concentrations in one organism size class than the other, making an overall determination of that system's treatment effectiveness unclear (further detail in Section 4.6). Therefore, this first method did not point to any clear identifications of systems that should or should not be considered BAT.

The second method comparing among systems was instead based on relative comparisons of percentiles of means, rather than statistically significant differences among all trials. Within each group of organism size and salinity, EPA calculated percentiles of the weighted means of all systems. If a BWMS produced a result beyond the 90th percentile (the greatest treatment discharge concentrations) of any of the six groups, it was not considered "best." Among the 49 BWMSs, 25 never produced such a high result, and were therefore identified as "best" (further detail in Section 4.6). EPA calculated the numeric discharge standard using all BWMSs, and again using only this subset of best BWMSs to quantify the impact of such a reduction in number of systems.

3.8 Numeric Discharge Standard

EPA calculated separate values of the numeric discharge standard for medium and large organism size classes. Additionally, EPA considered separating the three salinity categories by statistically comparing their weighted means and VFs. Since not all distributions were normal (evaluated using Shapiro-Wilk normality tests, R Core Team 2023), EPA compared the three salinity categories using four Kruskal-Wallis tests: one each for large-organism means, medium-organism means, large-organism VFs, and medium-organism VFs. Since none of the salinity categories were statistically significantly different (see corresponding results in Section 4.7), EPA did not carry out separate standard calculations by salinity.

EPA evaluated the skewness of the distributions of means and VFs using graphs and normality tests (Shapiro-Wilk tests) to determine the most appropriate aggregation metric: grand mean or median. Since the distributions were skewed (see corresponding results in Section 4.7), EPA calculated the grand median of all individual BWMSs' weighted means, and the grand median of all BWMSs' VFs, within each organism size class.

A standard is defined as the organism-size-class mean multiplied by the organism-size-class VF, with one value per organism size class. This standard comprises the results of the analysis in units of medium organisms/mL and large organisms/m^3, not to be exceeded.

3.9 Sensitivity Analyses

EPA performed sensitivity analyses to quantify the impacts of three factors in this analysis. These factors were affected by uncertainty due to incomplete information and had the potential to have a nonnegligible impact on the resulting numeric discharge standard.

First, amendments to BWMSs had less information than original BWMS submissions because they were not accompanied by shipboard tests and tended to have fewer trials per set. Amendments also had lower mean treatment discharge concentrations on average, making it plausible for them to decrease the final standard calculations. Although EPA included them in the main analysis because they represent type-approved systems currently on the market, EPA also reran the full analysis without amendments to quantify their impact.

Second, although EPA suggested a quantitative method to narrow the selection of BWMSs to represent BAT, this process was based on considerably less information than other past BAT analyses, such as those for EPA's Effluent Limitations Guidelines. EPA could not perform an engineering analysis of treatment system design and operation to explain highly variable results among trials, investigate instances where treatment discharge concentrations exceed the current VGP standard, nor conduct other assessments that would have been possible if the technology was known and if the Test Reports were available to EPA for review. Therefore, EPA included all BWMSs in the main standard calculations, but also reran the analysis for the subset of BWMSs determined as BAT using the relative comparison method in Section 3.7.

Third, the type-approval data included a variety of MDLs. Since the MDLs varied by test facility and therefore also by BWMS, they introduced a source of variability unrelated to BWMS treatment effectiveness, the target of this analysis. A BWMS with lower treatment discharge concentrations may have been due to more effective ballast water treatment, or simply due to a lower MDL. For example, a set of all-ND trials with MDLs of 0.1 – 0.2 organisms/m^3 would have an arithmetic mean of 0.15 organisms/m^3 in this analysis, as compared to a mean of 1.0 organisms/m^3 from a different set of all-ND trials with an MDL of 1.0 organisms/m^3. It is possible that the true mean from the larger-MDL set may have been less than the true mean of the smaller-MDL set, but the varying precisions of the different test facilities' methodologies precluded EPA from discerning such a possibility. In recognition of this additional variability, as well as the uncertainty associated with the given MDLs, EPA substituted "baseline" values for organism concentrations less than those baselines. EPA has performed baseline substitutions in other Effluent Limitations Guidelines (e.g., USEPA, 2000 and USEPA, 2015). EPA used baseline values of 1.0 large organisms/m^3, and 0.40 medium organisms/mL. These values were the second-highest MDLs in each size class, making all smaller concentrations consistent (the highest MDLs applied to fewer trials and were considerable jumps above the second-highest MDLs). EPA repeated all steps in the calculation of the numeric discharge standard using the baseline substitutions to quantify their effects.

4. Results

4.1 Data Structure

In all, EPA used 1,820 treatment discharge results from 49 BWMSs (including amendments). Each unique combination of BWMS, test platform, salinity category, and organism size class defined one of 384 sets in this analysis. Of these sets, 73 percent were from land-based testing. Most land-based sets of original BWMSs comprised 5 trials each, as required by the ETV Protocol (actual sample sizes ranged from 2 to 14 trials). Shipboard sets and amendment sets were smaller, averaging 3 trials each (shipboard sets ranged from 1 to 8 trials; amendments' sets ranged from 1 to 13 trials). Thirty-nine percent of the sets were in marine salinity, followed by 35 percent brackish and 26 percent fresh. Not all combinations of these characteristics occurred in the data. Results for both large- and medium-organism-size classes were available for all these trials. All trials are visualized in Figure 3.

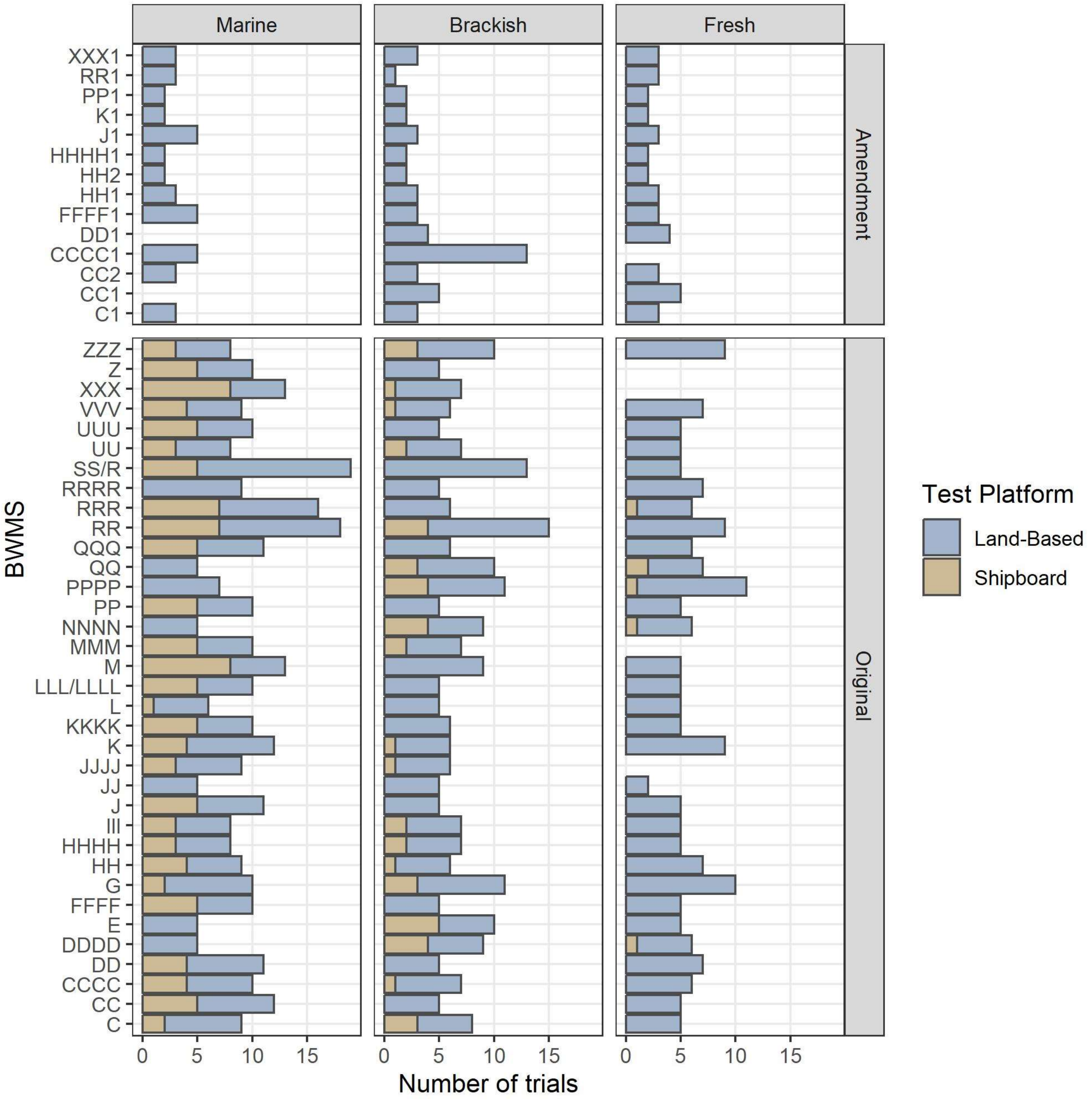

Figure 3. Count of trials in the input data used in this analysis.

Trials are divided among salinities (top labels), BWMSs that were original or amendment submissions (right labels), and test platforms (colors). Each trial has discharge concentrations for both large and medium organism size classes.

4.2 Evaluation of Uptake vs. Discharge Concentrations

To determine whether organism concentrations in uptake samples may have impacted treatment discharge concentrations from the BWMSs, EPA fit separate regression models to large- and medium-organism concentrations.

Although the large-organism regression found that uptake and discharge concentrations were significantly and positively associated (p value = 0.03, from the model using ½ MDLs for ND values), the strength of this association was extremely weak, and the effect was negligible. The relationship explained only one percent of the variability of discharge concentrations (R^2_β value). This extremely low percentage makes the result highly sensitive and suggests that 99 percent of the variability in discharge concentrations was for other reasons. Re-fitting the large-organism regression using MDLs for ND values (upper bound) produced a similar result (p value = 0.16 with 1 percent R^2_β), as did the regression setting the NDs to 0.01 organisms/m^3 (lower bound; p value = 0.15 with 1 percent R^2_β).

The medium-organism regressions were singular and therefore could not be evaluated when all three random-effects variables were included. Singularity in linear mixed-effect models is not uncommon and occurs for a variety of reasons, resulting in an inability to compute reliable statistical probabilities (Bates et al., 2015). The test platform random-effects variable was the source of the singularity. Without it, substituting ½ MDLs for NDs resulted in uptake concentrations significantly and positively correlated to treatment discharge concentrations (p value = 0.003); however, as with all of the large-organism regressions, more relevant is the fact that the model explained only one percent of the variability in discharge concentrations (R^2_β value). The alternate regressions substituting upper and lower bounds for NDs gave the same results (singular with the test platform variable, and significant but one percent R^2_β without). Scatter plots confirmed a wide range of values between uptake and discharge concentrations. Further details are included in Appendix B.

Since uptake concentrations negligibly explained the variability in treatment discharge concentrations, there was no need to account for the variation in mean uptake concentrations in this analysis. Rather, EPA used treatment discharge concentrations as given for the remainder of the methodology.

4.3 Distribution Shape

Organism concentrations within sets were best described by the inverse Gaussian (IG) distribution, also called the Wald distribution. It achieved the highest average rank, as evaluated among all 97 sets that contained at least five detected treatment discharge concentrations (Figure 4). The IG is effective at modeling positively skewed distributions, meaning that sets had more trials with low than high treatment discharge concentrations, and could have wide variance.

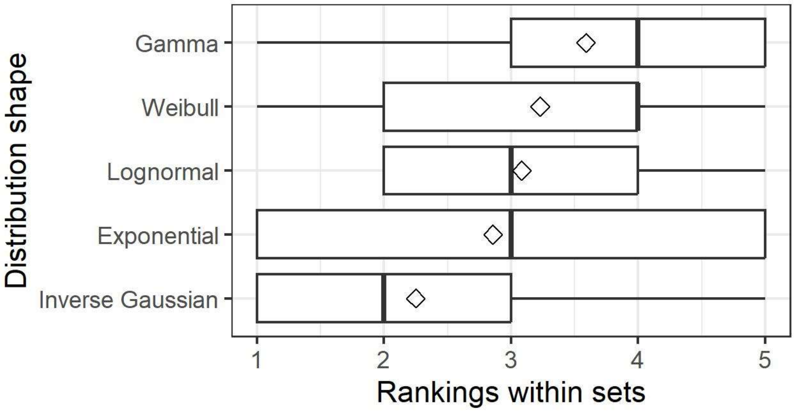

Figure 4. Comparison of distribution shapes ranked across sets.

Lower rankings mean the distributions fit the data better relative to the other shapes. Each box extends from the 25th to the 75th percentile (interquartile range, or IQR), with a thick line at the median, a diamond at the mean, and whiskers extending up to 1.5 times the IQR.

NDs comprised 35 percent of the treatment discharge concentrations in the dataset, and most were in the large organism size class (Figure 5). The upper bounds of the ND results (which were analyzed as a range less than a concentration) varied among the BWMSs and among their trials (Figure 6). NDs' upper bounds were often the MDLs for that trial but were the given concentrations in cases where the measurement was accompanied by a "<" symbol in the given type-approval data. The most common MDL was 1 organism/m^3 among the large organism results, and 0.15 organisms/mL among medium organism results, including the imputations described in Section 2.4. Since EPA statistically analyzed each trial with an ND treatment discharge result as a range between zero and its upper bound (a left-censored analysis), the upper bounds informed the calculation of the distributions' parameters in the next step, which in turn were used to calculate the standard.

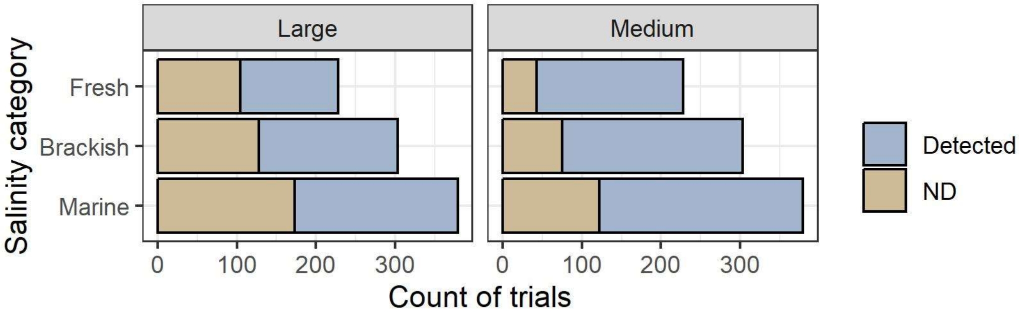

Figure 5. Number of trials with detected and ND treatment discharge concentrations, split by organism size class and salinity category.

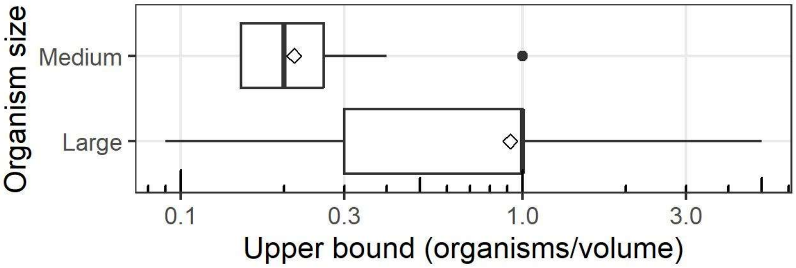

Figure 6. Upper bounds for ND treatment discharge results, by organism size class.

Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median, a diamond at the mean, and whiskers extending up to 1.5 times the IQR, with points beyond. Units are medium organisms/mL, or large organisms/m3.

4.4 Distribution Parameters

Among all 384 sets, 64 percent had at least two distinct detected values, allowing for the use of the left-censored IG distribution to calculate mean, sigma, and 99th percentile values. For the remaining 36 percent of sets with fewer than two distinct detected values, EPA calculated their arithmetic means. All sets' fitted IG parameters (or arithmetic means, if data were insufficient) are listed in Table C-1 in Appendix C.

4.5 Combination of Land-based and Shipboard Trials

EPA averaged the mean discharge concentration from the land-based trials and the shipboard trials, using weights equal to each platform's number of trials in the given BWMS, salinity, and organism size. Weighted 99th percentiles were computed in the same manner but excluding sets with fewer than 2 distinct detected concentrations. These metrics were often more strongly weighted by land-based results because they comprised 80 percent of all trials, and thus provided more reliable estimates. After combining discharge concentrations from the two test platforms, the total number of aggregated sets with the same BWMS, organism size, and salinity category was 280. The weighted means and 99th percentiles, as well as the resulting variability factors, are listed in Table C-2 in Appendix C.

4.6 Best Available Technology

The quantitative analysis of BAT involved three parts: statistical comparison of BWMSs within technology types, statistical comparison of BWMSs within size-salinity groups, and relative comparison of BWMSs' percentiles within size-salinity groups.

First, an evaluation of BAT can be based on comparison of individual BWMSs, or on technology types if the BWMSs within them are not statistically significantly different than one another. With five technology types that contained more than one BWMS, three salinity categories, and two organism size classes, EPA compared treatment discharge concentrations of BWMSs within 30 different groups. Detailed results of each group's statistical tests and accompanying plots are in Table A-2 and Figure A-1 in Appendix A. These graphs and statistical tests show that systems within technology types had significantly different discharge concentrations. Therefore, technology types did not represent the variability of the systems within them. Instead, in the next step, EPA compared among systems rather than technology types.

Second, EPA compared treatment discharge concentrations among systems within size-salinity groups. This analysis found statistically significant differences among BWMSs within each organism size-salinity group (six Kruskal-Wallis tests' p values < 0.05; see Table A-3 in Appendix A). The pairwise Dunn's tests that were run to identify specific differences revealed much overlap in combinations of systems, making it very difficult to identify any systems as BAT or not BAT. For example, system A and B may be similar (i.e., not statistically significantly different), and system B and C may be similar, but systems A and C may be statistically significantly different. Figure A-2 in Appendix A displays these Dunn's test results for each of the six groups. With up to 49 systems in each group, clear delineations of "best" performers did not emerge. Additionally, system results varied relative to one another in different groups. For example, one system may have produced low treatment discharge concentrations for medium organisms, but high concentrations of large organisms (as can be seen visually when comparing the means in Figure 7 for individual systems). The complexity of these results prevented EPA from using statistical hypothesis tests to distinguish some BWMSs as "best." Instead, the next step used a relative comparison method.

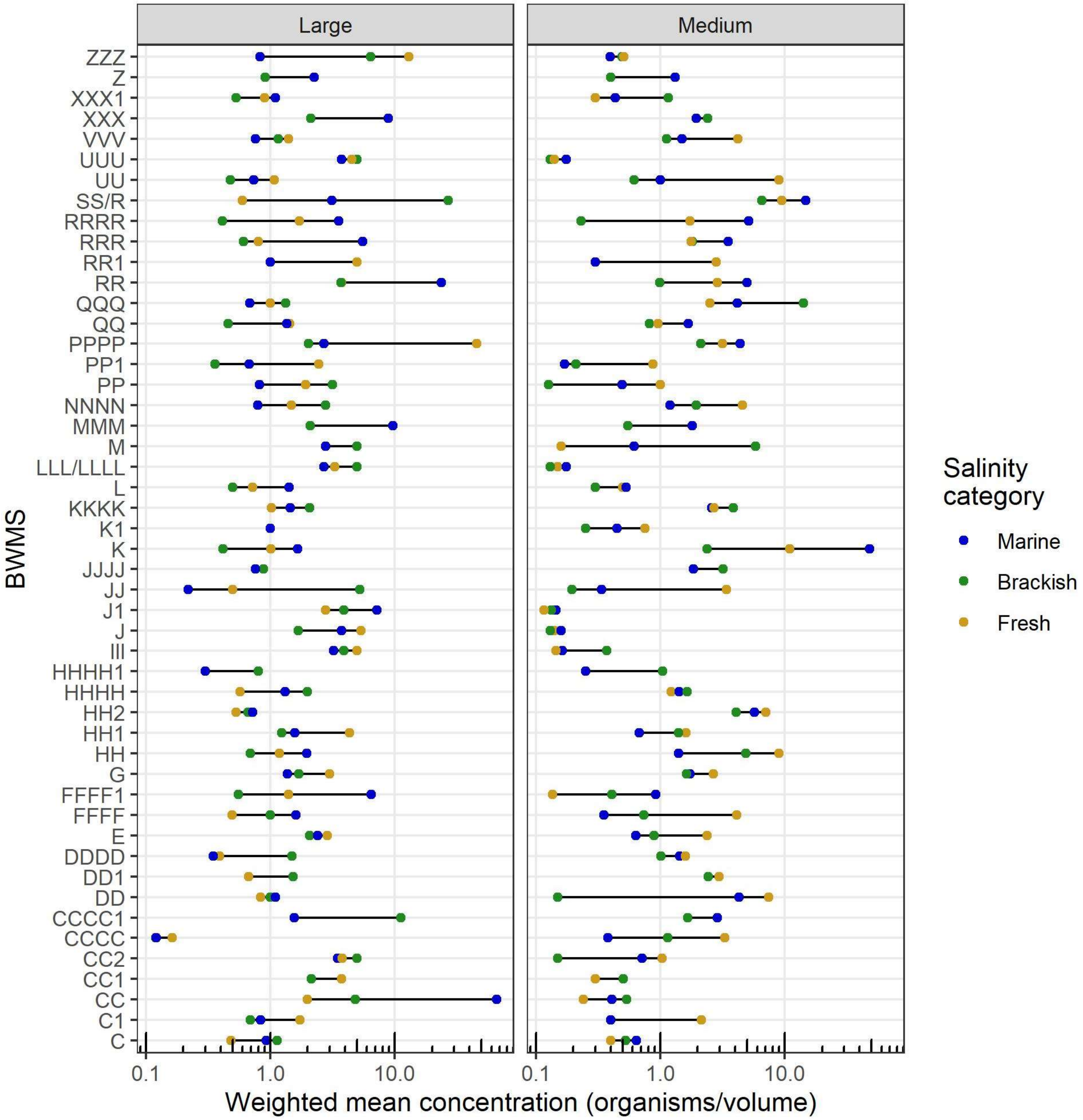

Figure 7. Comparison of weighted mean organism concentrations among all systems.

Means vary by salinity category (color) and organism size class (left/right plots), showing a lack of consistency in treatment discharge concentrations within and among systems.

Third, EPA instead used percentiles to relatively compare among BWMS' mean discharge concentrations. EPA defined "best" systems as those without treatment discharge means in the upper (i.e., worst) 90th percentile of any of the size-salinity groups (shown in Figure A-3 and quantified in Table A-4 in Appendix A). Based on this definition, 25 systems were distinguished from the 49 as BAT. A system did not need to have data for all salinities to be considered "best," but all systems had data for both organism size classes. The calculations of the standard were repeated using all BWMSs, as well as only using these 25 BAT systems, to quantify the impact of such a reduction. However, EPA had insufficient information to advise whether this reduction in systems would provide sufficient variety to vessel owners.

4.7 Numeric Discharge Standard

EPA calculated a different ballast water discharge standard for the two organism size classes. EPA also considered the three salinity categories for separate standard calculations. Statistical results of Kruskal-Wallis tests showed that the salinity categories did not have statistically significantly different means and VFs (details in Table A-5 and shown in Figure A-4 in Appendix A). Therefore, EPA did not separately evaluate the standard by salinity category.

All available means and VFs are shown in Figure 8. Each point represents the mean or VF of one BWMS in one salinity category. All boxes are skewed rather than symmetrical, indicated by the consistently higher mean points (diamonds) than the medians (thick center lines) and confirmed with normality tests (all Shapiro-Wilk p values <0.001, therefore nonnormal). To account for this skewness, EPA calculated the grand medians as a more representative measure of centrality for these groups than means.

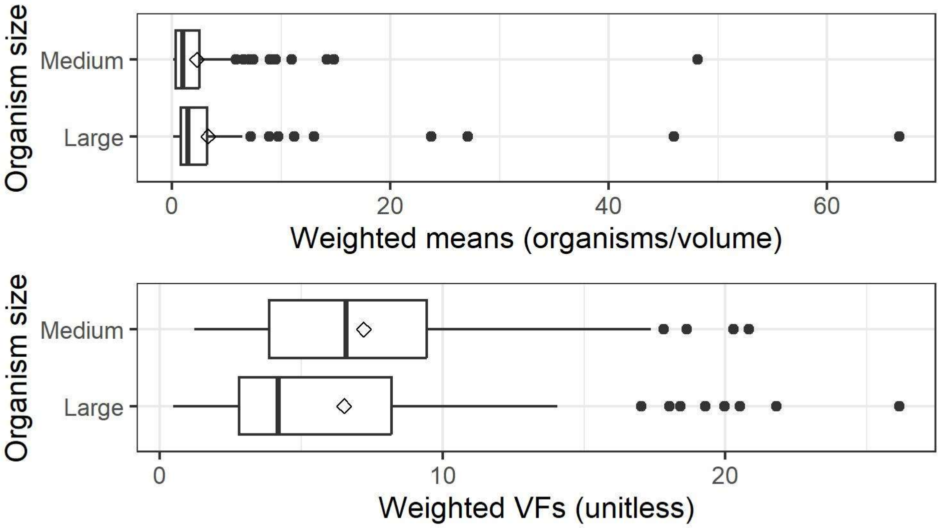

Figure 8. Box plots of weighted means and weighted VFs for each organism size class.

Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median, a diamond at the mean, and whiskers extending up to 1.5 times the IQR, with points beyond. The means' units are in medium organisms/mL, and large organisms/m^3.

The grand median of the weighted means, and the grand median of the weighted VFs, are listed in Table 1. Their products define the numeric discharge standard of each group. These calculations include all BWMSs and amendments, and use MDLs as given. The number of means exceeded the number of VFs because not all BWMSs had at least two distinct detected values to calculate a VF. The group VFs were approximately three to seven times larger than their respective group means, indicating that the variability in concentrations among trials was an important driver of this resulting discharge standard.

Table 1. Numeric discharge standard for large and medium organism size classes.

Includes all BWMSs and amendments, with MDLs used as given. Values have been rounded to two digits after the decimal.

Organism Size Class	Number of BWMS Weighted Means	Number of BWMS VFs	Grand Median of Weighted Means	Grand Median of VFs (unitless)	Numeric Discharge Standard
Large	140	91	1.44 organisms/m^3	4.17	6.01 organisms/m^3
Medium	140	110	1.01 organisms/mL	6.59	6.66 organisms/mL

4.8 Sensitivity Analyses

EPA recalculated the numeric discharge standard to quantify the potential sensitivity of the results to three factors: with or without amendments, including all systems or only the "best" using the percentile method (Section 3.7), and using MDLs as given or substituted with baseline values (Section 3.9). The resulting numeric discharge standard for all combinations are shown in Table 2.

Table 2. Sensitivity analysis of numeric ballast water discharge standard.

Means and standards are in units of medium organisms/mL and large organisms/m^3. Values have been rounded to two digits after the decimal. The first row of each organism size class, in bold, is the national standard from Table 1 for comparison.

Organism Size Class	Amend-ments Included	BWMSs Narrowed	MDLs Used	Number of BWMS Weighted Means	Number of BWMS VFs	Grand Median of Weighted Means (org./volume)	Grand Median of VFs (unitless)	Numeric Discharge Standard (org./volume)
Large	Yes	All systems	As given	**140**	**91**	**1.44**	**4.17**	**6.01**
Large	Yes	All systems	Baseline	140	62	1.59	4.77	7.59
Large	Yes	Best only	As given	71	50	1.03	4.10	4.21
Large	Yes	Best only	Baseline	71	32	1.29	3.60	4.63
Large	No	All systems	As given	101	75	1.50	4.17	6.28
Large	No	All systems	Baseline	101	52	1.73	4.95	8.56
Large	No	Best only	As given	49	40	1.11	4.30	4.76
Large	No	Best only	Baseline	49	25	1.36	4.17	5.68
Medium	Yes	All systems	As given	**140**	**110**	**1.01**	**6.59**	**6.66**
Medium	Yes	All systems	Baseline	140	93	1.10	6.33	6.94
Medium	Yes	Best only	As given	71	59	1.02	5.84	5.93
Medium	Yes	Best only	Baseline	71	48	1.11	6.09	6.76
Medium	No	All systems	As given	101	83	1.31	7.07	9.28
Medium	No	All systems	Baseline	101	77	1.41	6.82	9.65
Medium	No	Best only	As given	49	43	1.43	6.93	9.87
Medium	No	Best only	Baseline	49	41	1.43	6.84	9.78

The three factors in this sensitivity analysis had different effects on the two organism size classes. When systems were narrowed to BAT only, large organisms' results in Table 2 decreased more than those of medium organisms. This difference was because the BWMSs removed in the BAT step had the greatest treatment discharge concentrations in the data set – concentrations of large rather than medium organisms. Without them, BWMSs with lower large-organism means remained. Also, although baseline MDL substitutions most often increased the resulting standard, the increase was greater for large organisms because they had a higher proportion of NDs, as well as a wider range of given MDLs than did medium organisms. Results for the medium organisms' standard were greater without amendments, reflecting that amendments' medium-organism treatment discharge concentrations were generally lower than those of original submissions, to a greater extent than for large organisms.

The sensitivity analysis implementing baseline MDLs for medium and large organisms showed that standard was less impacted by differences in analytical limitations, though at the cost of measurement precision at lower concentrations. From the comparisons of baseline MDLs to as-given MDLs in Table 2, the baseline-MDL substitutions increased mean concentrations but increased or decreased VFs, depending on the set. The group VFs were also impacted by fewer BWMSs, since fewer sets had at least two distinct detected concentrations from which to calculate variability. Most of the baseline comparisons resulted in a higher numeric discharge standard, which suggests that the standards in Table 1 would be greater, were it not for the MDLs that USCG estimated from reports.

4.9 Limitations of the Analysis

The main limitations of the analysis are associated with the inherent uncertainty of MDLs and the lack of information about treatment technologies in the type-approval database. Although organism concentration results were provided for each sample by the facilities that conducted the type-approval testing, the volume of water they sampled, and volume of water analyzed to determine those results were not reported for each sample. Therefore, a finding of zero organisms could not directly be translated into a concentration of less-than units of organisms per volume. As a result, the USCG interpreted information in facilities' reports to suggest MDLs or ranges of MDLs as information was available, with blanks otherwise. In the database, results columns were therefore reported by test facilities, whereas MDL columns were estimated by USCG.

In recognition of this incomplete information, EPA erred on the side of using the results as-is rather than the MDLs, in circumstances where results were less than the listed MDL. In contrast, the other option of replacing results less than the given MDL with their MDL would have prioritized values discerned from incomplete information. Doing so would have also increased the number of values that would have been interpreted as NDs based solely on inference. In turn, more NDs would have meant that fewer variability factors would have been calculated, and more means would have been arithmetic using MDL imputations, rather than calculated using the left-censored IG distribution. Given this potential loss of information, and the preference of reported concentrations over estimated MDLs, EPA used values less than their MDLs as reported.

Where MDLs were provided as a range, EPA used the midpoint so that imputations would most fairly estimate the possible true MDL per sample. An alternate option would have been to use the upper bound of the range to conservatively assume a greater concentration for NDs. Among all MDLs associated with treatment discharge concentrations, 44 percent were ranges, with most associated with medium organisms. All ranges for treatment discharge samples spanned only 0.1 or 0.2 organisms/volume, so using the upper bound for imputed concentrations would have increased imputations by half of these values: 0.05 to 0.10 organisms/volume. Relative to the resulting standard, this magnitude of increase would have been relatively small.

In relation to MDLs, an important consideration is that the ETV Protocol specifies that to determine the number of organisms in the large organism size class, a minimum sample size of three cubic meters is to be collected and concentrated to one liter, with enumeration of organisms in 20, one-milliliter subsamples of that one-liter concentrate. Strict adherence to those procedures for a single three-cubic-meter sample results in an MDL of <17 organisms/m^3 (First et al, 2022), a value well above even the current VGP numeric discharge standard. By comparison, the MDLs assigned to type-approval tests with non-detects were generally much lower. Although EPA did not have information on the number of samples collected or analyzed, it is likely that the actual MDLs were lower than the MDL described above for a single concentrated three-liter sample with 20 subsamples. To highlight the importance of sample size, Lee II, et al. (2010) describe that not detecting organisms in a one-liter sample could represent concentrations of organisms as high as almost 3,000 organisms/m^3 in the original volume of water (within the 95 percent confidence interval), while for a 10-cubic-meter sample, detecting no organisms has an upper 95 percent confidence level of 0.3 organisms/m^3.

Lastly, the lack of identifying information about the individual BWMSs and their technologies preclude a BAT analysis based on an engineering analysis of treatment system design and operation. Despite this lack of information, this type-approval database contains considerable amounts of standardized information associated with the ETV Protocol, making it the most reliable data source for this analysis of the numeric discharge standard.

4.10 Need for Multiple BWMS Compliance Options

The variety of operational and environmental conditions under which BWMS must operate supports EPA's position that it is critical that a range of BWMS be available to the global shipping industry to reduce ANS discharges. Vessels have different treatment needs due to the size of the vessel, type of operations, and environmental challenges in different waterbodies. Establishing a uniform national numeric discharge standard and applying a type-approval process allows for the installation and use of various BWMS disinfection technologies (including UV, electro-chlorination, chemical addition, ozonation, deoxygenation, pasteurization, and others) to meet various vessel needs and comply with the BAT-based standard. Further, when selecting a BWMS, shipowners also need to consider costs related to both capital and operational expenditures, to include, among other things, financing, spare parts and other supplies, energy demands, crew responsibilities and training, and operation and maintenance activities. The combination of factors described above has guided both the U.S. and IMO BWMS type-approval process that establishes a procedure to ensure that a range of BWMS are available to meet specific vessel characteristics. Ease of operation and maintenance requirements are also a consideration, with the understanding that more complicated systems may lead to more problems. As an example, shipowners may opt to select a single vendor across the company's entire fleet to simplify fleetwide operation and maintenance.

In addition to meeting the discharge standard, the USCG type-approval process separately requires that the BWMS be practicable onboard a vessel (e.g., able to operate despite roll, pitch, and vibration considerations), compatible with other onboard systems, durable, and be supported by credible and sustainable system manufacturers, suppliers, and servicers. For example, to be installed on any U.S.-flagged vessel, the USCG must verify the system meets certain installation and engineering requirements specified in 46 CFR Subchapters F and J. The majority of USCG type-approved BWMSs have not been verified to comply with these requirements, so these systems are not approved for use onboard U.S.-flagged vessels. EPA did not have the information necessary to correlate BWMS test data with onboard acceptance; therefore, some of the systems analyzed may not be approved for use on U.S.-flagged vessels.

Multiple BWMS compliance options are also beneficial to shipowners with vessels subject to other requirements, most notably the IMO International Convention for the Control and Management of Ships' Ballast Water and Sediments (hereafter abbreviated as "BWM Convention") and any member state requirements promulgated pursuant to that state being a party to the BWM Convention. A vessel that voyages internationally may be subject to similar, but not necessarily identical, requirements that may shape the selection of an appropriate BWMS. As described in the proposed rule, over 75 percent of vessels discharging ballast water in waters of the United States spent 25 percent or less of their time in those waters, with more than 80 percent of these vessels also subject to the BWM Convention.

4.11 Data Fail to Demonstrate a More Stringent Numeric Discharge Standard is BAT

Public comments did not include an alternative technology-based solution to EPA's BAT analysis in the proposed rule that addresses the breadth of issues associated with establishing a numeric ballast water discharge standard. Some commenters appeared to suggest that EPA should collect the universe of performance data, identify the perceived single, or top few, best performing system(s), and impose that perceived level of performance on the entirety of the universe of potentially affected entities, without considering whether such a system is workable for most vessels. EPA disagrees that such an approach would be scientifically sound or grounded in the statutory considerations of the Clean Water Act (CWA). Among other shortcomings of that approach, test results that appear to indicate greater removal of organisms are not an indication that any particular BWMS can achieve a more stringent standard in all conditions. Rather, the test results are the product of a variety of situations where BWMS manufacturers are testing their systems in different environmental conditions and locations around the world, all with the goal of obtaining type-approval by demonstrating that the BWMS can consistently meet the 2013 VGP and 2012 USCG discharge standard. As such, EPA's analysis of the newly obtained USCG BWMS type-approval data retains the proposed rule rationale that the numeric ballast water discharge standard needs to preserve a level of flexibility for the shipowner to select a technology that is appropriate for the vessel.

Based on the data analysis of the USCG type-approval data and the need for multiple compliance options to suit different vessels and circumstances, EPA is not proposing a different discharge standard for consideration.

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Appendix A. Additional Figures and Tables

Table A-1. List of amendments in this analysis.

BWMS	Amendment description text
C1	update approves an alternative filter.
CC1	update approves new hold time limitation.
CC2	updates manufacturer and approves alternate filter and components.
CCCC1	update approves additional BWMS models.
DD1	update approves alternate filter and components.
FFFF1	an additional filter has been approved for use.
HH1	update approves additional UV-units and alternate filters.
HH2	update approves change to performance claim and hazardous area installation.
HHHH1	update approves new performance claim.
J1	update approves change to performance claim and strainer in the freshwater cooling line.
K1	update approves 24-hour hold time mode.
PP1	update approves new performance claim.
RR1	update approves alternate filter.
XXX1	update approves alternative filter, new control cabinet, and new UV models.

Table A-2. Results of statistical comparisons of BWMSs within each technology type and size-salinity group.

Shapiro-Wilk tests for normality and Levene's tests for homoscedasticity were run on ln(concentration) to test for the option of natural-log transformation, but some still violated these assumptions. Therefore, nonparametric Kruskal-Wallis tests informed the main question of difference among systems. Each row corresponds to one plot in Figure A-1 below. An asterisk indicates statistical significance of p<0.01 for assumption tests and p<0.05 for the main test.

Technology Type	Organism Size Class	Salinity Category	Number of BWMSs	Normality Test p Value	Homoscedasticity Test p Value	Kruskal-Wallis Test p Value
1	Large	Marine	2	0.091	0.130	0.230
1	Large	Brackish	2	0.033	0.493	0.424
1	Large	Fresh	2	0.070	0.320	0.058
1	Medium	Marine	2	0.003 *	0.856	0.951
1	Medium	Brackish	2	0.002 *	0.875	0.860
1	Medium	Fresh	2	0.295	0.725	0.217
4	Large	Marine	4	0.004 *	0.120	<0.001 *
4	Large	Brackish	4	0.219	0.071	<0.001 *
4	Large	Fresh	3	<0.001 *	0.379	<0.001 *
4	Medium	Marine	4	0.047	0.252	0.006 *
4	Medium	Brackish	4	0.038	0.854	0.241
4	Medium	Fresh	3	0.132	0.052	0.784
5	Large	Marine	13	<0.001 *	0.529	0.764
5	Large	Brackish	14	0.003 *	0.249	0.087
5	Large	Fresh	14	<0.001 *	0.186	0.006 *
5	Medium	Marine	13	<0.001 *	0.095	<0.001 *
5	Medium	Brackish	14	0.013	0.056	<0.001 *
5	Medium	Fresh	14	0.062	0.329	<0.001 *
6	Large	Marine	21	0.111	0.001 *	0.017 *
6	Large	Brackish	21	<0.001 *	0.047	<0.001 *
6	Large	Fresh	17	0.061	0.153	<0.001 *
6	Medium	Marine	21	0.002 *	0.041	<0.001 *
6	Medium	Brackish	21	0.736	0.685	<0.001 *
6	Medium	Fresh	17	0.364	0.174	<0.001 *
13	Large	Marine	2	0.024	0.477	0.883
13	Large	Brackish	3	0.214	0.429	0.258
13	Large	Fresh	3	0.064	0.931	0.709
13	Medium	Marine	2	0.100	0.748	0.648
13	Medium	Brackish	3	0.702	0.170	0.268
13	Medium	Fresh	3	0.117	0.183	0.360

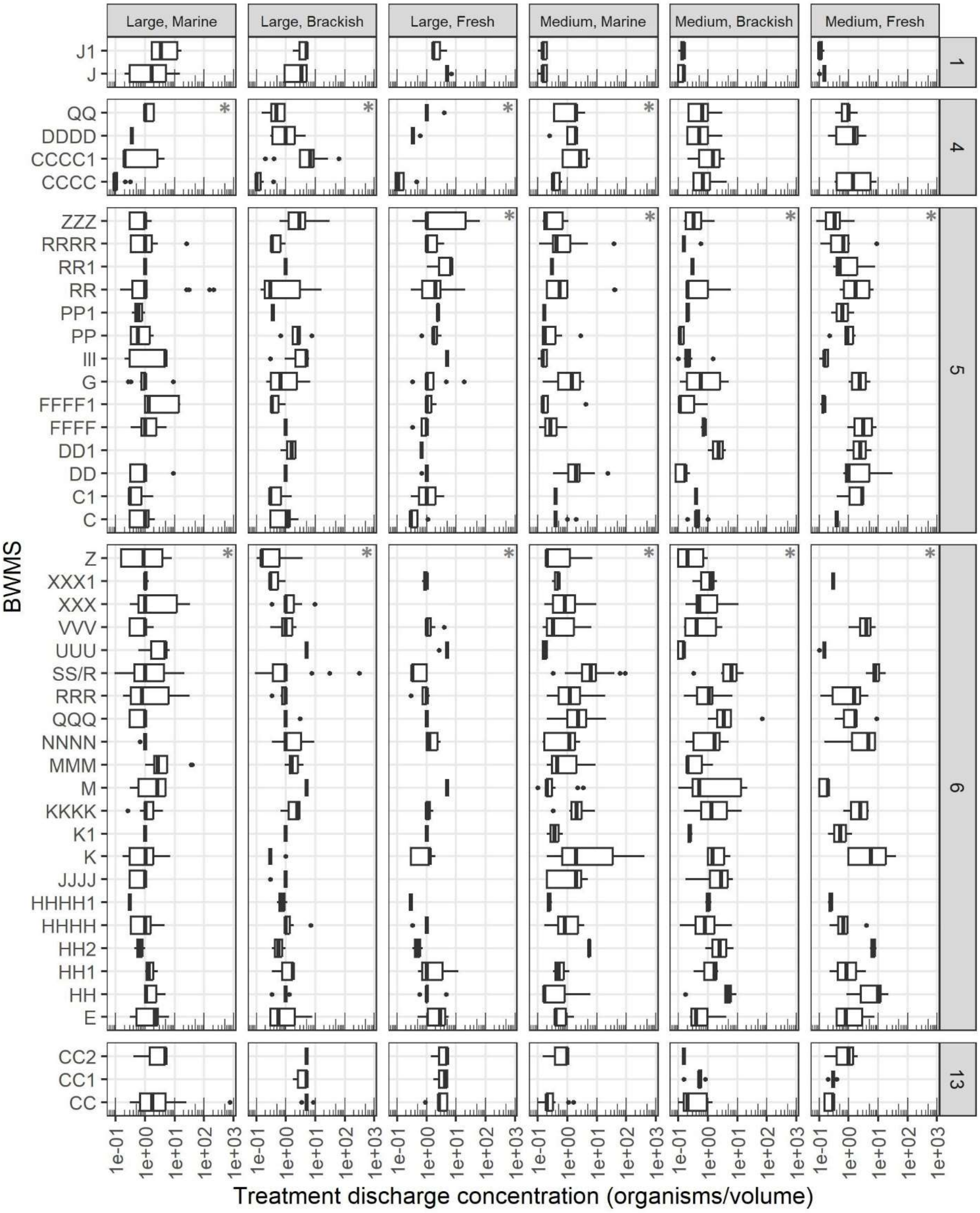


Figure A-1. Box plots of concentrations among BWMSs within technology types (right labels) and size-salinity groups (top labels).

Each plot is associated with one Kruskal-Wallis test, of 30. A gray asterisk in the top right corner indicates that at least one BWMS was statistically significantly different from another, corresponding to Table A-2. Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median and whiskers extending up to 1.5 times the IQR.

Table A-3. Results of statistical comparisons among BWMSs within size-salinity groups.

Shapiro-Wilk tests for normality and Levene's tests for homoscedasticity were run on ln(concentration) to test for the option of natural-log transformation, but some still violated these assumptions. Therefore, nonparametric Kruskal-Wallis tests informed the main question of difference among systems. An asterisk indicates statistical significance of p<0.01 for assumption tests and p<0.05 for the main test. Each row corresponds to one plot in Figure A-2 below.

Organism Size Class	Salinity Category	Number of BWMSs	Normality Test p Value	Homoscedasticity Test p Value	Kruskal-Wallis Test p Value
Large	Marine	47	<0.001 *	<0.001 *	<0.001 *
Large	Brackish	49	<0.001 *	0.011 *	<0.001 *
Large	Fresh	44	<0.001 *	0.006 *	<0.001 *
Medium	Marine	47	<0.001 *	<0.001 *	<0.001 *
Medium	Brackish	49	0.135	0.017	<0.001 *
Medium	Fresh	44	0.053	0.013	<0.001 *

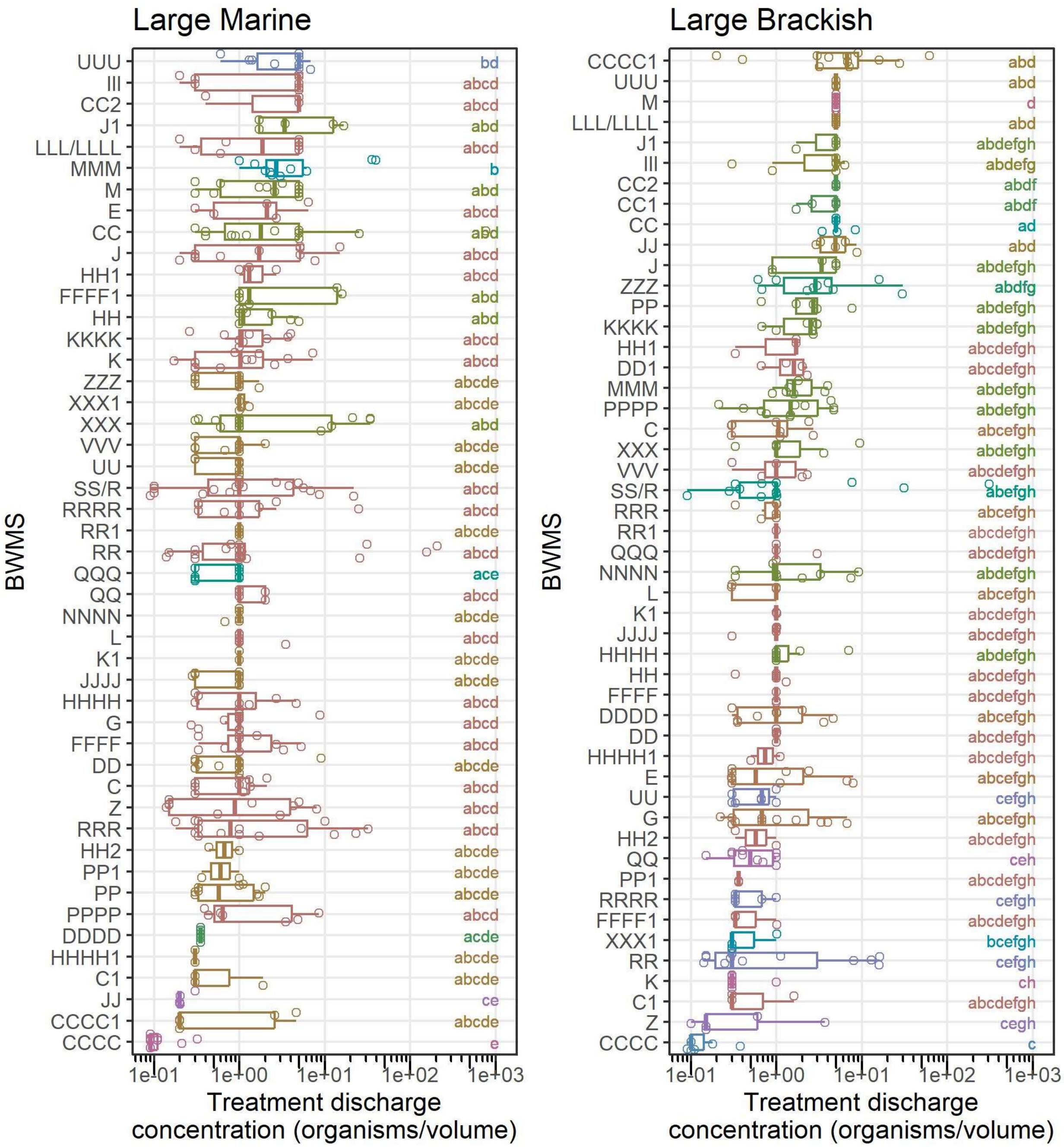
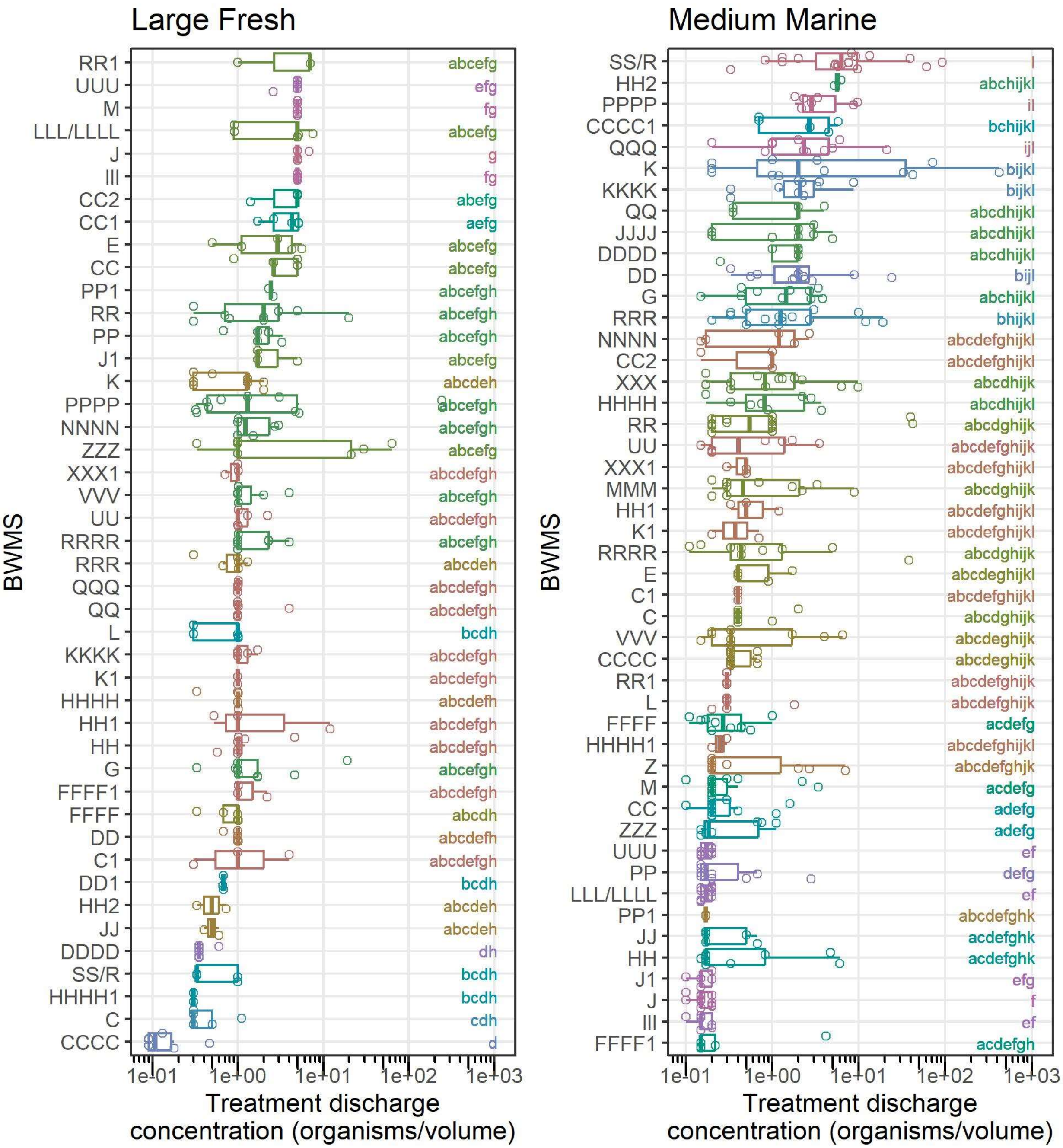


Figure A-2. Box plots of results of statistical tests among BWMSs within size-salinity groups (top labels).

BWMSs are ordered by median treatment discharge concentration; order therefore varies by plot. Circles mark individual trials' concentrations. Letters along the right summarize results of Dunn's pairwise tests: BWMSs that are statistically similar to one another share a letter; e.g., all with an "a" are statistically different from those without an "a." Long strings of letters demonstrate the complex overlap of significances. Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median and whiskers extending up to 1.5 times the IQR.


Large Fresh

Medium Marine

Figure A-2. Box plots showing results of statistical tests among BWMSs within size-salinity groups (top labels).

BWMSs are ordered by median treatment discharge concentration; order therefore varies by plot. Circles mark individual trials' concentrations. Letters along the right summarize results of Dunn's pairwise tests: BWMSs that are statistically similar to one another share a letter; e.g., all with an "a" are statistically different from those without an "a." Long strings of letters demonstrate the complex overlap of significances. Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median and whiskers extending up to 1.5 times the IQR.

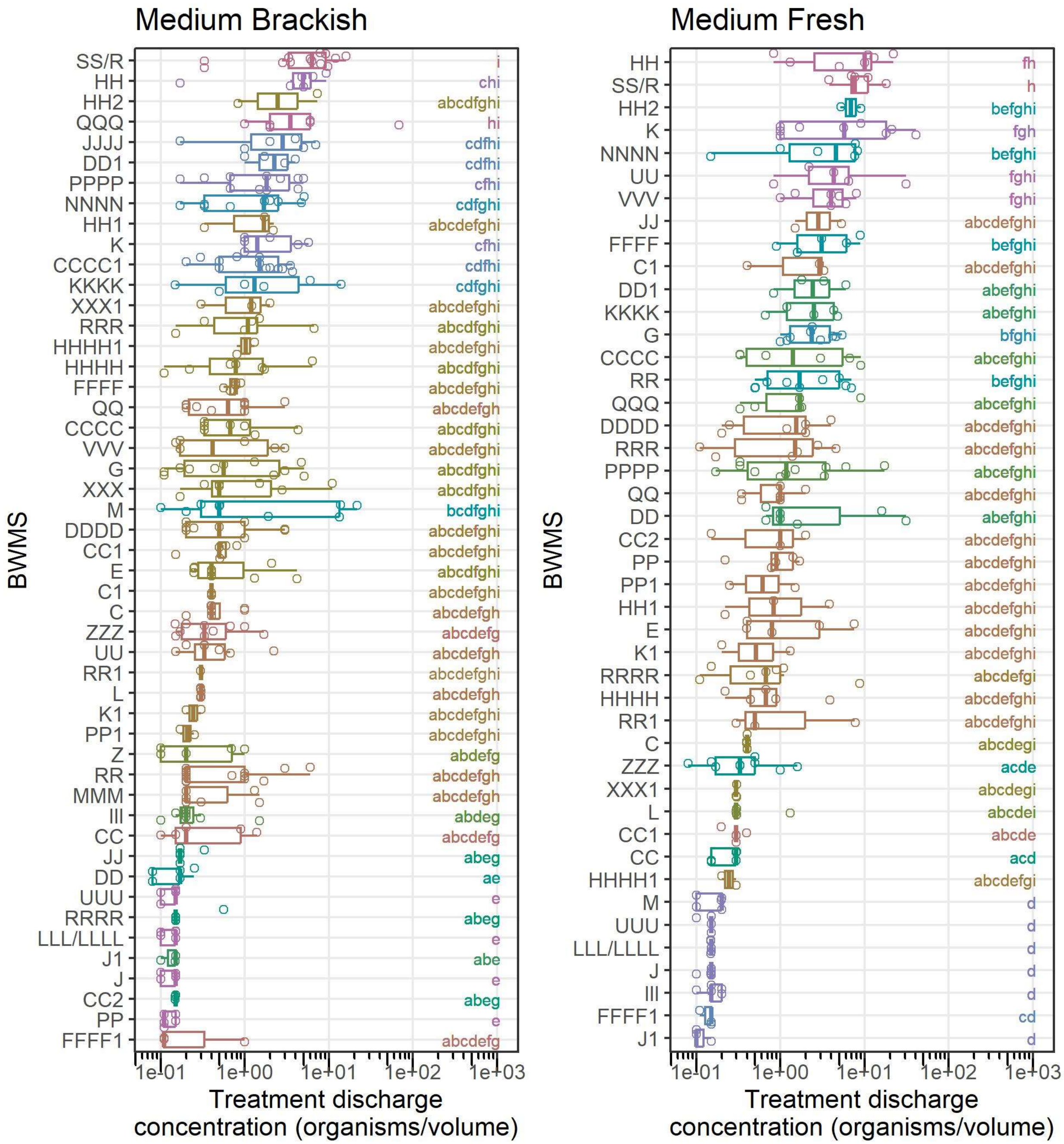


Figure A-2. Box plots showing results of statistical tests among BWMSs within size-salinity groups (top labels).

BWMSs are ordered by median treatment discharge concentration; order therefore varies by plot. Circles mark individual trials' concentrations. Letters along the right summarize results of Dunn's pairwise tests: BWMSs that are statistically similar to one another share a letter; e.g., all with an "a" are statistically different from those without an "a." Long strings of letters demonstrate the complex overlap of significances. Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median and whiskers extending up to 1.5 times the IQR.

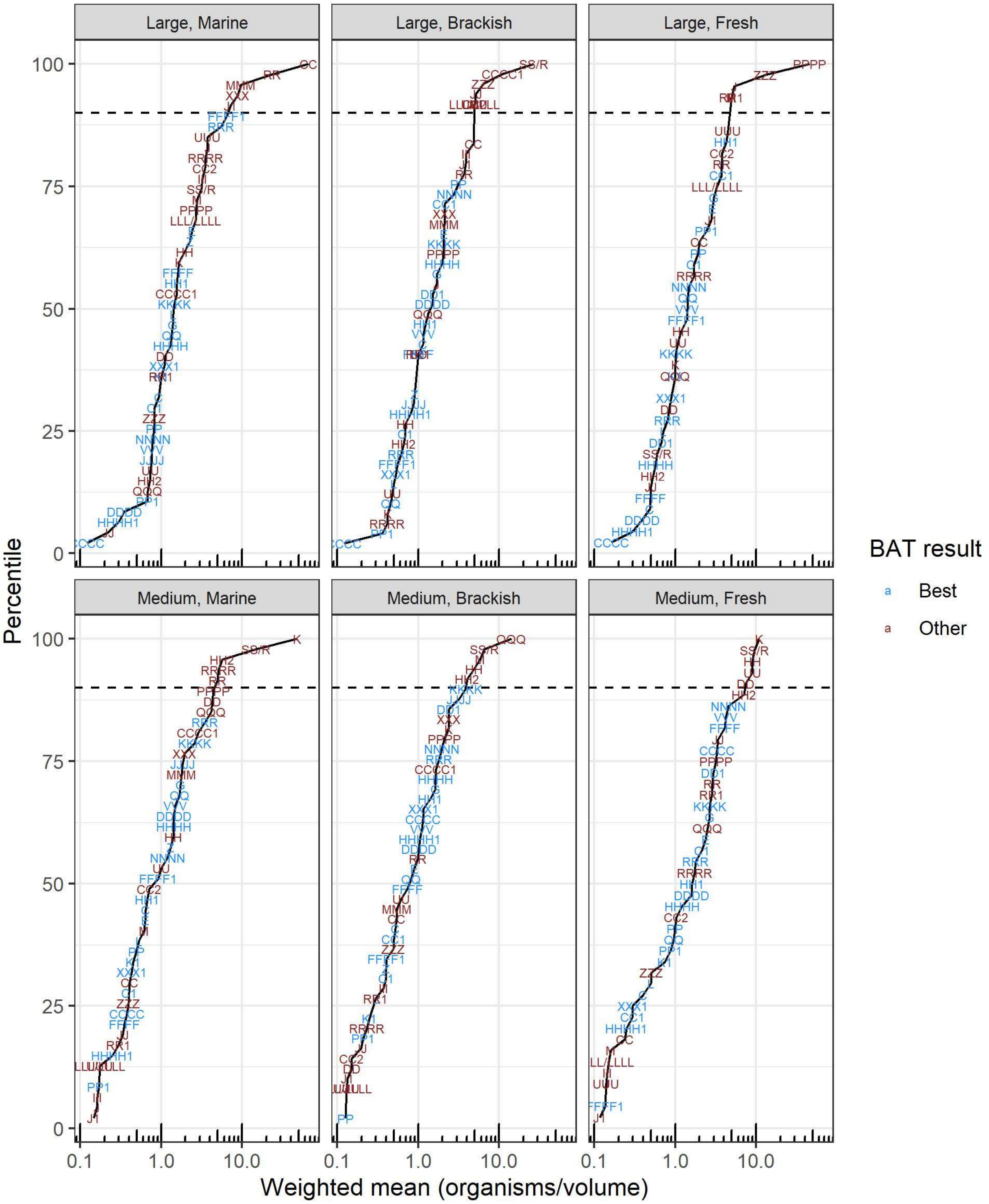


Figure A-3. Weighted means of BWMSs (letter labels within graphs) ordered by percentile within each size-salinity group (top labels).

BWMSs are colored by their result: those that appeared above the dotted 90th percentile line in at least one of the six groups were not considered as “best” or BAT. For clarification on labels that may not be fully visible, including those that overlap at ties, see Table A-4.

Table A-4. Percentiles accompanying Figure A-3.

Sorted by BWMS. Asterisks mark percentiles > 90. Blank cells occur where a salinity was not included in test results.

BWMS	Large, Marine	Large, Brackish	Large, Fresh	Medium, Marine	Medium, Brackish	Medium, Fresh	BAT Result
C	31.9	42.9	9.1	44.7	40.8	27.3	Best
C1	29.8	24.5	59.1	27.7	30.6	56.8	Best
CC	100.0 **	83.7	63.6	29.8	42.9	18.2	Other
CC1		71.4	77.3		38.8	22.7	Best
CC2	78.7	91.8 **	81.8	48.9	14.3	43.2	Other
CCCC	2.1	2.0	2.3	23.4	63.3	77.3	Best
CCCC1	53.2	98.0 **		80.9	73.5		Other
DD	40.4	40.8	29.5	87.2	12.2	90.9 **	Other
DD1		53.1	22.7		85.7	72.7	Best
DDDD	8.5	51.0	6.8	63.8	57.1	47.7	Best
E	66.0	65.3	70.5	42.6	53.1	59.1	Best
FFFF	57.4	40.8	11.4	21.3	49.0	81.8	Best
FFFF1	89.4	18.4	47.7	51.1	34.7	4.5	Best
G	46.8	57.1	72.7	70.2	69.4	63.6	Best
HH	61.7	26.5	45.5	59.6	93.9 **	95.5 **	Other
HH1	55.3	46.9	84.1	46.8	67.3	50.0	Best
HH2	14.9	22.4	15.9	95.7 **	91.8 **	88.6	Other
HHHH	42.6	59.2	18.2	61.7	71.4	45.5	Best
HHHH1	6.4	28.6	4.5	14.9	59.2	20.5	Best
III	76.6	81.6	93.2 **	6.4	28.6	11.4	Other
J	83.0	55.1	95.5 **	4.3	8.2	9.1	Other
J1	91.5 **	79.6	68.2	2.1	10.2	2.3	Other
JJ	4.3	93.9 **	13.6	19.1	16.3	79.5	Other
JJJJ	19.1	30.6		74.5	87.8		Best
K	59.6	8.2	38.6	100.0 **	81.6	100.0 **	Other
K1	36.2	40.8	36.4	34.0	22.4	34.1	Best
KKKK	51.1	63.3	40.9	78.7	89.8	65.9	Best
L	48.9	14.3	25.0	38.3	26.5	29.5	Best
LLL/LLLL	68.1	91.8 **	75.0	12.8	8.2	13.6	Other
M	72.3	91.8 **	93.2 **	40.4	95.9 **	15.9	Other
MMM	95.7 **	67.3		72.3	44.9		Other
NNNN	23.4	73.5	54.5	55.3	77.6	86.4	Best
PP	25.5	75.5	61.4	36.2	2.0	40.9	Best
PP1	10.6	4.1	65.9	8.5	18.4	36.4	Best
PPPP	70.2	61.2	100.0 **	89.4	79.6	75.0	Other
QQ	44.7	10.2	52.3	68.1	51.0	38.6	Best
QQQ	12.8	49.0	36.4	85.1	100.0 **	61.4	Other
RR	97.9 **	77.6	79.5	91.5 **	55.1	70.5	Other
RR1	36.2	40.8	93.2 **	17.0	26.5	68.2	Other
RRR	87.2	20.4	27.3	83.0	75.5	54.5	Best
RRRR	80.9	6.1	56.8	93.6 **	20.4	52.3	Other
SS/R	74.5	100.0 **	20.5	97.9 **	98.0 **	97.7 **	Other
UU	17.0	12.2	43.2	53.2	46.9	93.2 **	Other
UUU	85.1	91.8 **	86.4	12.8	8.2	9.1	Other
VVV	21.3	44.9	50.0	66.0	61.2	84.1	Best
XXX	93.6 **	69.4		76.6	83.7		Other
XXX1	38.3	16.3	31.8	31.9	65.3	25.0	Best

Table A-5. Results of statistical tests comparing among salinity categories' metrics.

Shapiro-Wilk tests for normality and Levene's tests for homoscedasticity were run on ln(metric) to test for the option of natural-log transformation, but one still violated these assumptions. Therefore, nonparametric Kruskal-Wallis tests informed the main question of difference among salinities. An asterisk indicates statistical significance of $p<0.01$ for assumption tests and $p<0.05$ for the main test. Each row corresponds to one plot in Figure A-4 below.

Organism Size Class	Metric	Number of BWMSs	Normality Test p Value	Homoscedasticity Test p Value	Kruskal-Wallis Test p Value
Large	Weighted mean	49	0.015	0.980	0.931
Large	Weighted VF	49	0.121	0.507	0.141
Medium	Weighted mean	49	0.045	0.606	0.209
Medium	Weighted VF	49	0.006 *	0.597	0.555

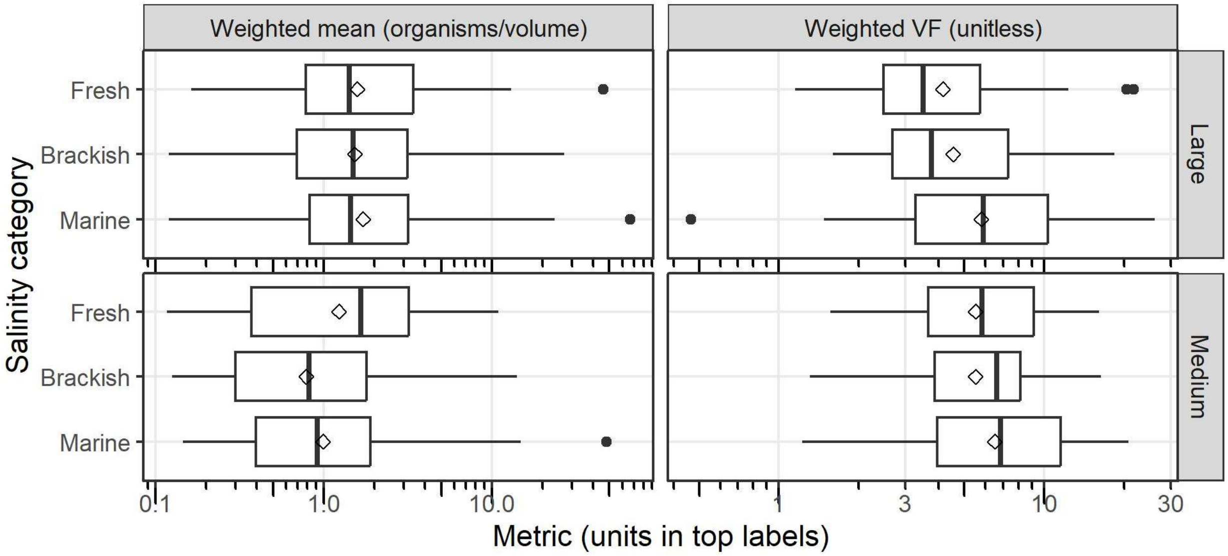


Figure A-4. Box plots comparing among the salinity categories of BWMSs' weighted means (left) and weighted VFs (right), between the two organism size classes (right labels).

The boxes show considerable overlap along the X axis, explaining the insignificant Kruskal-Wallis results in Table A-5. Each box extends from the 25th to the 75th percentile (IQR), with a thick line at the median, a diamond at the mean, and whiskers extending up to 1.5 times the IQR.

Appendix B. Regression Results Details

This appendix supplements details about the regressions comparing uptake organism concentrations to treatment discharge organism concentrations.

Figure B-1 displays the tested relationship between the two variables for each organism size class. The range of points is wide and highly noisy, with NDs plotted at half the left-censored observation (e.g., an ND of <1.0 is plotted at 0.5). One BWMS (PP1) is excluded because uptake concentrations were not available. Thin lines show linear trendlines within each set of trials; their slopes vary widely among positive, flat, and negative. Uptake concentrations were often limited within sets, demonstrated by the relatively narrow ranges of the lines across the X axis. This considerably limits potential for generalization or extrapolation of trends across sets. Rather, the relationship of points from all BWMSs is evaluated as a whole in the linear mixed-effects models.

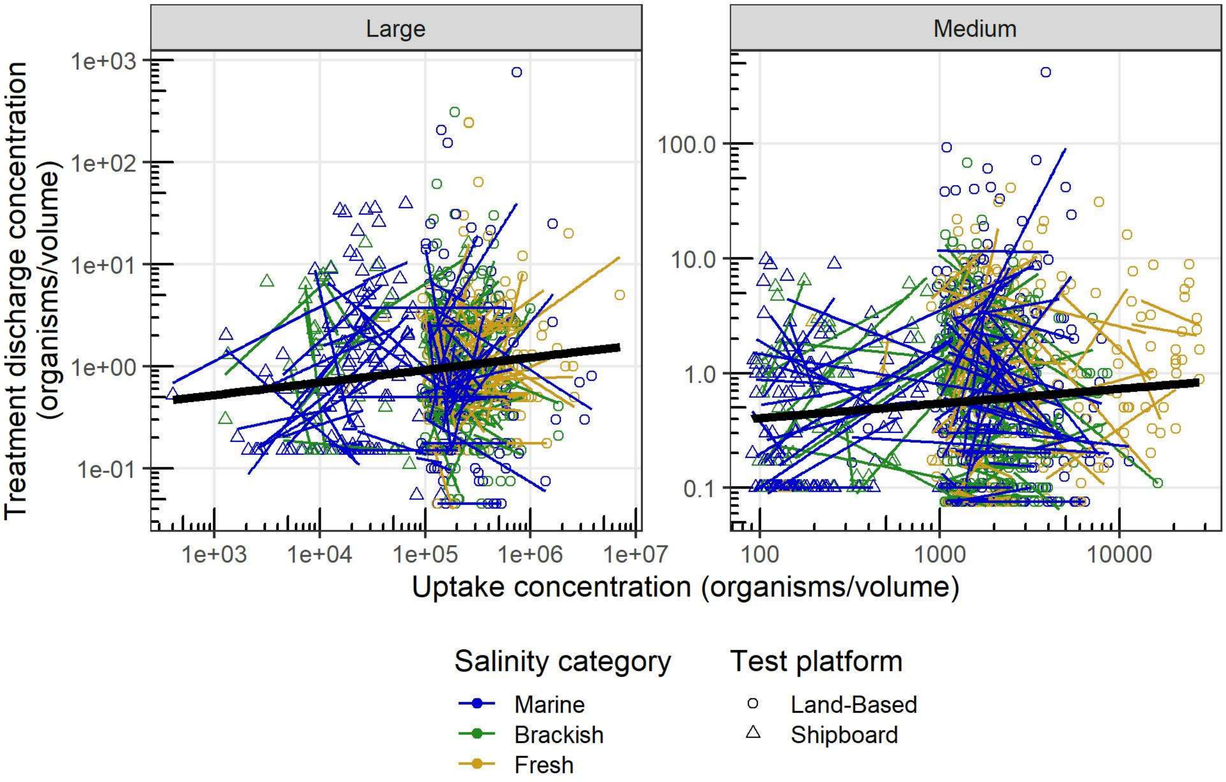


Figure B-1. Scatter plots of treatment discharge organism concentrations vs. uptake concentrations. Plots are split by organism size classes. Lines are explained in the text above. Units are large organisms/m^3 and medium organisms/mL.

The thick black line in the large organisms panel of Figure B-1 is the linear mixed-effects regression model in Table B-1. Based on the coefficient, a 10 percent increase in uptake concentration would correspond to a 1.2 percent increase in treatment discharge concentration on average $((1.10^{0.1227} – 1)*100 = 1.2\%)$.This further verifies the fact that uptake concentration has a negligible effect on discharge concentration, which is also evident from the extremely low R^2_β of one percent.

Table B-1. Results of the linear mixed-effects regression model on large organisms, using ½ MDLs for NDs.

Its form was $\ln(discharge) = Intercept + Coefficient \times \ln\,(uptake)$, with random-effects variables of BWMS, salinity category, and test platform. Units are large organisms/m^3. Its R^2_β value was 1.3 percent. This model included all BWMSs and MDLs as given. An asterisk indicates a significant p value <0.05.

Random effects				
Group	Variance	# observations		
BWMS	0.422	48		
Salinity category	0.005	3		
Test platform	0.045	2		
(Residual)	1.577			
Fixed effects				
Variable	Coefficient	Standard error	Degrees of freedom	p value
Intercept	-1.4927	0.6337	19.9738	0.0288*
ln(Uptake concentration)	0.1227	0.0535	30.6168	0.0289*

The thick line in the medium organisms panel of Figure B-1 is summarized in Table B-2, using ½ MDLs for NDs. Although its one-percent R^2_β means the relationship is negligibly explanatory of treatment concentrations, on average, a 10 percent increase in uptake concentration would correspond to a 1.2 percent increase in treatment discharge concentration ($(1.10^{0.1278} – 1)*100 = 1.2\%$). The remainder of the models, which substituted NDs with 0.01 for a lower bound or the MDL (or upper limit) for the upper bound, are similarly summarized in Table B-2 and showed similar results of positive and often significant coefficients, paired with very low R^2_β values. Residual graphs did not suggest deviations from assumptions of normality and non-uniform variance in these models.

Table B-2. Summary of the results of the six linear mixed-effects regression models.

The form of each equation was $\ln(discharge) = Intercept + Coefficient \times \ln\,(uptake)$, with random-effects variables of BWMS, salinity category, and test platform. Medium organisms' models shown do not include the test platform random-effects variable due to singularity. All BWMSs are included, and MDLs were used as given. An asterisk indicates a significant p value <0.05.

Regression model (organism size, ND substitution)	R^2_β of model (%)	Intercept	Coefficient of ln(uptake concentration)	p value of ln(uptake concentration)
Large organisms, ½ MDL	1.3	-1.493	0.1227	0.0289*
Large organisms, 0.01 (lower)	0.6	-3.304	0.1575	0.1499
Large organisms, MDL (upper)	1.1	-1.032	0.1049	0.1550
Medium organisms, ½ MDL	1.1	-1.492	0.1278	0.0026*
Medium organisms, 0.01 (lower)	0.6	-2.204	0.1428	0.0234*
Medium organisms, MDL (upper)	1.2	-1.254	0.1195	0.0019*

Since uptake concentrations negligibly explained the variability in treatment discharge concentrations, EPA used treatment discharge concentrations as given for the remainder of the analysis, without need for adjustment based on uptake.

Appendix C. Concentration Summary Tables by Set

Table C-1. All sets, their numbers of trials, and calculated parameters.

For sets containing at least two distinct detected trials, the mean, sigma, and 99th percentiles were calculated based on a left-censored IG distribution; for the other sets, the arithmetic mean was calculated. These parameters' units are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
C	Large	Marine	Land-Based	7	4	Yes	0.91	1.54	6.63
C	Large	Marine	Shipboard	2	0	No	1.00		
C	Large	Brackish	Land-Based	5	4	Yes	1.50	0.90	8.29
C	Large	Brackish	Shipboard	3	1	No	0.53		
C	Large	Fresh	Land-Based	5	4	Yes	0.48	0.92	1.58
C	Medium	Marine	Land-Based	7	2	No	0.40		
C	Medium	Marine	Shipboard	2	2	Yes	1.50	0.29	3.13
C	Medium	Brackish	Land-Based	5	0	No	0.40		
C	Medium	Brackish	Shipboard	3	2	No	0.73		
C	Medium	Fresh	Land-Based	5	0	No	0.40		
C1	Large	Marine	Land-Based	3	1	No	0.83		
C1	Large	Brackish	Land-Based	3	2	Yes	0.69	1.47	4.23
C1	Large	Fresh	Land-Based	3	2	Yes	1.73	1.43	16.11
C1	Medium	Marine	Land-Based	3	0	No	0.40		
C1	Medium	Brackish	Land-Based	3	1	No	0.40		
C1	Medium	Fresh	Land-Based	3	2	Yes	2.15	1.14	17.95
CC	Large	Marine	Land-Based	7	4	Yes	113.74	0.84	2279.66
CC	Large	Marine	Shipboard	5	4	Yes	0.61	0.84	2.02
CC	Large	Brackish	Land-Based	5	3	Yes	4.84	0.18	10.78
CC	Large	Fresh	Land-Based	5	3	Yes	1.99	0.36	5.39
CC	Medium	Marine	Land-Based	7	7	Yes	0.56	1.45	3.01
CC	Medium	Marine	Shipboard	5	0	No	0.20		
CC	Medium	Brackish	Land-Based	5	4	Yes	0.54	2.05	4.04
CC	Medium	Fresh	Land-Based	5	3	No	0.24		
CC1	Large	Brackish	Land-Based	5	2	Yes	2.15	0.15	3.45
CC1	Large	Fresh	Land-Based	5	5	Yes	3.76	0.23	9.24
CC1	Medium	Brackish	Land-Based	5	4	Yes	0.50	1.08	1.94
CC1	Medium	Fresh	Land-Based	5	5	Yes	0.30	0.41	0.49
CC2	Large	Marine	Land-Based	3	1	No	3.47		
CC2	Large	Brackish	Land-Based	3	0	No	5.00		
CC2	Large	Fresh	Land-Based	3	1	No	3.80		
CC2	Medium	Marine	Land-Based	3	2	No	0.72		
CC2	Medium	Brackish	Land-Based	3	0	No	0.15		
CC2	Medium	Fresh	Land-Based	3	2	Yes	1.03	1.96	10.16

Table C-1. All sets, their numbers of trials, and calculated parameters.

For sets containing at least two distinct detected trials, the mean, sigma, and 99th percentiles were calculated based on a left-censored IG distribution; for the other sets, the arithmetic mean was calculated. These parameters' units are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
CCCC	Large	Marine	Land-Based	6	0	No	0.09		
CCCC	Large	Marine	Shipboard	4	2	Yes	0.17	2.13	0.72
CCCC	Large	Brackish	Land-Based	6	2	Yes	0.12	4.06	0.86
CCCC	Large	Brackish	Shipboard	1	1	No	0.11		
CCCC	Large	Fresh	Land-Based	6	4	Yes	0.16	2.20	0.72
CCCC	Medium	Marine	Land-Based	6	2	Yes	0.30	1.12	0.95
CCCC	Medium	Marine	Shipboard	4	4	Yes	0.50	0.51	1.06
CCCC	Medium	Brackish	Land-Based	6	4	Yes	1.12	1.51	8.88
CCCC	Medium	Brackish	Shipboard	1	1	No	1.33		
CCCC	Medium	Fresh	Land-Based	6	4	Yes	3.29	1.50	42.68
CCCC1	Large	Marine	Land-Based	5	5	Yes	1.56	1.57	15.21
CCCC1	Large	Brackish	Land-Based	13	13	Yes	11.22	0.89	157.85
CCCC1	Medium	Marine	Land-Based	5	5	Yes	2.88	0.61	14.96
CCCC1	Medium	Brackish	Land-Based	13	13	Yes	1.66	0.85	9.10
DD	Large	Marine	Land-Based	7	2	Yes	1.53	2.40	21.35
DD	Large	Marine	Shipboard	4	1	No	0.37		
DD	Large	Brackish	Land-Based	5	1	No	1.00		
DD	Large	Fresh	Land-Based	7	3	Yes	0.84	0.18	1.22
DD	Medium	Marine	Land-Based	7	7	Yes	4.90	0.86	46.30
DD	Medium	Marine	Shipboard	4	4	Yes	3.29	0.61	18.10
DD	Medium	Brackish	Land-Based	5	5	Yes	0.15	1.22	0.38
DD	Medium	Fresh	Land-Based	7	7	Yes	7.42	0.82	81.83
DD1	Large	Brackish	Land-Based	4	3	Yes	1.53	0.53	5.11
DD1	Large	Fresh	Land-Based	4	2	No	0.67		
DD1	Medium	Brackish	Land-Based	4	4	Yes	2.42	0.36	7.12
DD1	Medium	Fresh	Land-Based	4	4	Yes	2.98	0.47	12.18
DDDD	Large	Marine	Land-Based	5	0	No	0.35		
DDDD	Large	Brackish	Land-Based	5	3	Yes	0.89	1.24	5.18
DDDD	Large	Brackish	Shipboard	4	4	Yes	2.27	0.97	16.54
DDDD	Large	Fresh	Land-Based	5	0	No	0.35		
DDDD	Large	Fresh	Shipboard	1	1	No	0.60		
DDDD	Medium	Marine	Land-Based	5	4	Yes	1.44	0.97	8.32
DDDD	Medium	Brackish	Land-Based	5	4	Yes	1.64	1.05	11.00
DDDD	Medium	Brackish	Shipboard	4	2	Yes	0.24	1.43	0.85
DDDD	Medium	Fresh	Land-Based	5	4	Yes	1.88	1.03	13.16
DDDD	Medium	Fresh	Shipboard	1	0	No	0.20		

Table C-1. All sets, their numbers of trials, and calculated parameters.

For sets containing at least two distinct detected trials, the mean, sigma, and 99th percentiles were calculated based on a left-censored IG distribution; for the other sets, the arithmetic mean was calculated. These parameters' units are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
E	Large	Marine	Land-Based	5	5	Yes	2.40	0.92	17.10
E	Large	Brackish	Land-Based	5	3	Yes	0.41	1.26	1.69
E	Large	Brackish	Shipboard	5	5	Yes	3.72	0.83	29.72
E	Large	Fresh	Land-Based	5	5	Yes	2.88	0.62	15.12
E	Medium	Marine	Land-Based	5	2	Yes	0.63	1.78	4.49
E	Medium	Brackish	Land-Based	5	2	Yes	0.46	1.50	2.37
E	Medium	Brackish	Shipboard	5	2	Yes	1.32	3.18	21.35
E	Medium	Fresh	Land-Based	5	4	Yes	2.37	1.17	21.26
FFFF	Large	Marine	Land-Based	5	3	Yes	0.44	0.51	0.89
FFFF	Large	Marine	Shipboard	5	5	Yes	2.78	0.37	8.84
FFFF	Large	Brackish	Land-Based	5	1	No	1.00		
FFFF	Large	Fresh	Land-Based	5	2	Yes	0.49	0.49	1.01
FFFF	Medium	Marine	Land-Based	5	4	Yes	0.24	1.28	0.78
FFFF	Medium	Marine	Shipboard	5	4	Yes	0.46	1.26	1.99
FFFF	Medium	Brackish	Land-Based	5	5	Yes	0.74	0.19	1.05
FFFF	Medium	Fresh	Land-Based	5	5	Yes	4.12	0.48	19.84
FFFF1	Large	Marine	Land-Based	5	3	Yes	6.46	1.05	82.55
FFFF1	Large	Brackish	Land-Based	3	2	No	0.55		
FFFF1	Large	Fresh	Land-Based	3	1	No	1.40		
FFFF1	Medium	Marine	Land-Based	5	2	Yes	0.92	4.48	16.34
FFFF1	Medium	Brackish	Land-Based	3	3	Yes	0.41	1.98	2.56
FFFF1	Medium	Fresh	Land-Based	3	1	No	0.14		
G	Large	Marine	Land-Based	8	3	Yes	0.59	0.54	1.38
G	Large	Marine	Shipboard	2	2	Yes	4.54	1.30	59.87
G	Large	Brackish	Land-Based	8	7	Yes	2.24	0.86	14.42
G	Large	Brackish	Shipboard	3	1	No	0.27		
G	Large	Fresh	Land-Based	10	6	Yes	3.01	1.23	31.57
G	Medium	Marine	Land-Based	8	7	Yes	1.72	1.20	13.50
G	Medium	Marine	Shipboard	2	2	Yes	1.74	0.59	6.78
G	Medium	Brackish	Land-Based	8	8	Yes	1.20	1.64	10.81
G	Medium	Brackish	Shipboard	3	3	Yes	2.76	1.33	29.97
G	Medium	Fresh	Land-Based	10	10	Yes	2.67	0.38	8.54
HH	Large	Marine	Land-Based	5	1	No	1.60		
HH	Large	Marine	Shipboard	4	4	Yes	2.42	0.42	8.12
HH	Large	Brackish	Land-Based	5	2	Yes	0.57	0.67	1.55
HH	Large	Brackish	Shipboard	1	1	No	1.30		

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./volume)	Sigma (org./volume)	99th Percentile (org./volume)
HH	Large	Fresh	Land-Based	7	3	Yes	1.18	1.12	7.13
HH	Medium	Marine	Land-Based	5	4	Yes	2.36	1.89	32.35
HH	Medium	Marine	Shipboard	4	4	Yes	0.21	0.64	0.39
HH	Medium	Brackish	Land-Based	5	5	Yes	5.82	0.14	11.74
HH	Medium	Brackish	Shipboard	1	1	No	0.17		
HH	Medium	Fresh	Land-Based	7	7	Yes	9.02	0.49	66.78
HH1	Large	Marine	Land-Based	3	2	Yes	1.58	0.49	4.96
HH1	Large	Brackish	Land-Based	3	3	Yes	1.24	0.77	5.36
HH1	Large	Fresh	Land-Based	3	2	Yes	4.33	1.23	53.50
HH1	Medium	Marine	Land-Based	3	3	Yes	0.68	0.69	2.00
HH1	Medium	Brackish	Land-Based	3	3	Yes	1.41	0.81	6.72
HH1	Medium	Fresh	Land-Based	3	3	Yes	1.62	1.18	12.07
HH2	Large	Marine	Land-Based	2	1	No	0.72		
HH2	Large	Brackish	Land-Based	2	1	No	0.66		
HH2	Large	Fresh	Land-Based	2	2	Yes	0.53	0.56	1.22
HH2	Medium	Marine	Land-Based	2	2	Yes	5.70	0.04	6.97
HH2	Medium	Brackish	Land-Based	2	2	Yes	4.06	0.65	26.63
HH2	Medium	Fresh	Land-Based	2	2	Yes	7.10	0.10	12.87
HHHH	Large	Marine	Land-Based	5	3	Yes	1.07	0.96	5.31
HHHH	Large	Marine	Shipboard	3	1	No	1.73		
HHHH	Large	Brackish	Land-Based	5	2	No	1.00		
HHHH	Large	Brackish	Shipboard	2	2	Yes	4.45	0.33	15.77
HHHH	Large	Fresh	Land-Based	5	2	Yes	0.57	0.67	1.55
HHHH	Medium	Marine	Land-Based	5	5	Yes	1.54	0.83	7.83
HHHH	Medium	Marine	Shipboard	3	3	Yes	1.24	1.31	9.03
HHHH	Medium	Brackish	Land-Based	5	5	Yes	0.88	1.45	5.97
HHHH	Medium	Brackish	Shipboard	2	2	Yes	3.53	0.74	24.39
HHHH	Medium	Fresh	Land-Based	5	5	Yes	1.22	1.06	7.14
HHHH1	Large	Marine	Land-Based	2	0	No	0.30		
HHHH1	Large	Brackish	Land-Based	2	2	Yes	0.80	0.45	1.83
HHHH1	Large	Fresh	Land-Based	2	0	No	0.30		
HHHH1	Medium	Marine	Land-Based	2	2	Yes	0.25	0.41	0.39
HHHH1	Medium	Brackish	Land-Based	2	2	Yes	1.05	0.24	1.79
HHHH1	Medium	Fresh	Land-Based	2	2	Yes	0.25	0.41	0.39
III	Large	Marine	Land-Based	5	0	No	5.00		
III	Large	Marine	Shipboard	3	1	No	0.27		

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
III	Large	Brackish	Land-Based	5	1	No	4.18		
III	Large	Brackish	Shipboard	2	1	No	3.30		
III	Large	Fresh	Land-Based	5	0	No	5.00		
III	Medium	Marine	Land-Based	5	1	No	0.14		
III	Medium	Marine	Shipboard	3	0	No	0.20		
III	Medium	Brackish	Land-Based	5	4	Yes	0.44	2.05	2.97
III	Medium	Brackish	Shipboard	2	0	No	0.20		
III	Medium	Fresh	Land-Based	5	3	Yes	0.15	0.90	0.30
J	Large	Marine	Land-Based	6	6	Yes	6.62	0.28	24.03
J	Large	Marine	Shipboard	5	4	Yes	0.32	0.73	0.76
J	Large	Brackish	Land-Based	5	3	Yes	1.68	0.50	5.60
J	Large	Fresh	Land-Based	5	1	No	5.36		
J	Medium	Marine	Land-Based	6	1	No	0.14		
J	Medium	Marine	Shipboard	5	1	No	0.18		
J	Medium	Brackish	Land-Based	5	2	No	0.13		
J	Medium	Fresh	Land-Based	5	1	No	0.14		
J1	Large	Marine	Land-Based	5	5	Yes	7.22	0.43	41.40
J1	Large	Brackish	Land-Based	3	1	No	3.90		
J1	Large	Fresh	Land-Based	3	2	No	2.80		
J1	Medium	Marine	Land-Based	5	3	Yes	0.15	0.90	0.30
J1	Medium	Brackish	Land-Based	3	1	No	0.13		
J1	Medium	Fresh	Land-Based	3	2	No	0.12		
JJ	Large	Marine	Land-Based	5	0	No	0.22		
JJ	Large	Brackish	Land-Based	5	5	Yes	5.24	0.18	12.29
JJ	Large	Fresh	Land-Based	2	2	Yes	0.50	0.29	0.78
JJ	Medium	Marine	Land-Based	5	5	Yes	0.34	1.12	1.11
JJ	Medium	Brackish	Land-Based	5	4	Yes	0.20	0.71	0.38
JJ	Medium	Fresh	Land-Based	2	2	Yes	3.42	0.37	11.76
JJJJ	Large	Marine	Land-Based	6	0	No	1.00		
JJJJ	Large	Marine	Shipboard	3	1	No	0.29		
JJJJ	Large	Brackish	Land-Based	5	0	No	1.00		
JJJJ	Large	Brackish	Shipboard	1	0	No	0.30		
JJJJ	Medium	Marine	Land-Based	6	6	Yes	2.67	0.32	7.38
JJJJ	Medium	Marine	Shipboard	3	0	No	0.20		
JJJJ	Medium	Brackish	Land-Based	5	5	Yes	3.80	0.39	14.69
JJJJ	Medium	Brackish	Shipboard	1	1	No	0.17		

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
K	Large	Marine	Land-Based	8	5	Yes	1.14	1.49	9.05
K	Large	Marine	Shipboard	4	4	Yes	2.71	1.23	27.22
K	Large	Brackish	Land-Based	5	1	No	0.30		
K	Large	Brackish	Shipboard	1	0	No	1.00		
K	Large	Fresh	Land-Based	9	7	Yes	1.01	1.08	5.48
K	Medium	Marine	Land-Based	8	6	Yes	71.95	0.73	1463.37
K	Medium	Marine	Shipboard	4	4	Yes	0.45	1.32	1.99
K	Medium	Brackish	Land-Based	5	3	Yes	1.71	0.72	8.05
K	Medium	Brackish	Shipboard	1	1	No	5.70		
K	Medium	Fresh	Land-Based	9	7	Yes	10.96	0.74	131.23
K1	Large	Marine	Land-Based	2	0	No	1.00		
K1	Large	Brackish	Land-Based	2	0	No	1.00		
K1	Large	Fresh	Land-Based	2	0	No	1.00		
K1	Medium	Marine	Land-Based	2	2	Yes	0.45	1.00	1.53
K1	Medium	Brackish	Land-Based	2	2	Yes	0.25	0.41	0.39
K1	Medium	Fresh	Land-Based	2	2	Yes	0.75	1.25	4.03
KKKK	Large	Marine	Land-Based	5	2	Yes	1.21	1.20	7.93
KKKK	Large	Marine	Shipboard	5	5	Yes	1.69	0.81	8.93
KKKK	Large	Brackish	Land-Based	6	5	Yes	2.07	0.51	7.61
KKKK	Large	Fresh	Land-Based	5	2	Yes	1.03	0.46	2.57
KKKK	Medium	Marine	Land-Based	5	5	Yes	2.03	0.68	9.72
KKKK	Medium	Marine	Shipboard	5	5	Yes	3.15	0.79	22.08
KKKK	Medium	Brackish	Land-Based	6	5	Yes	3.88	1.45	52.52
KKKK	Medium	Fresh	Land-Based	5	5	Yes	2.69	0.51	11.34
L	Large	Marine	Land-Based	5	0	No	1.00		
L	Large	Marine	Shipboard	1	1	No	3.50		
L	Large	Brackish	Land-Based	5	3	Yes	0.50	0.80	1.47
L	Large	Fresh	Land-Based	5	2	No	0.72		
L	Medium	Marine	Land-Based	5	1	No	0.28		
L	Medium	Marine	Shipboard	1	1	No	1.80		
L	Medium	Brackish	Land-Based	5	0	No	0.30		
L	Medium	Fresh	Land-Based	5	1	No	0.50		
LLL/LLLL	Large	Marine	Land-Based	5	0	No	5.00		
LLL/LLLL	Large	Marine	Shipboard	5	4	Yes	0.38	1.05	1.26
LLL/LLLL	Large	Brackish	Land-Based	5	0	No	5.00		
LLL/LLLL	Large	Fresh	Land-Based	5	4	Yes	3.29	0.60	17.97

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
LLL/LLLL	Medium	Marine	Land-Based	5	0	No	0.15		
LLL/LLLL	Medium	Marine	Shipboard	5	0	No	0.20		
LLL/LLLL	Medium	Brackish	Land-Based	5	2	No	0.13		
LLL/LLLL	Medium	Fresh	Land-Based	5	0	No	0.15		
M	Large	Marine	Land-Based	5	0	No	5.00		
M	Large	Marine	Shipboard	8	6	Yes	1.39	1.17	9.55
M	Large	Brackish	Land-Based	9	0	No	5.00		
M	Large	Fresh	Land-Based	5	0	No	5.00		
M	Medium	Marine	Land-Based	5	5	Yes	1.28	1.59	11.47
M	Medium	Marine	Shipboard	8	0	No	0.20		
M	Medium	Brackish	Land-Based	9	9	Yes	5.83	1.55	95.89
M	Medium	Fresh	Land-Based	5	5	Yes	0.16	0.87	0.33
MMM	Large	Marine	Land-Based	5	5	Yes	2.38	0.34	6.54
MMM	Large	Marine	Shipboard	5	5	Yes	17.10	0.41	146.03
MMM	Large	Brackish	Land-Based	5	5	Yes	2.26	0.42	7.39
MMM	Large	Brackish	Shipboard	2	2	Yes	1.70	0.05	1.95
MMM	Medium	Marine	Land-Based	5	4	Yes	0.61	1.47	3.45
MMM	Medium	Marine	Shipboard	5	5	Yes	3.00	1.08	27.96
MMM	Medium	Brackish	Land-Based	5	3	Yes	0.21	0.51	0.34
MMM	Medium	Brackish	Shipboard	2	2	Yes	1.40	0.06	1.65
NNNN	Large	Marine	Land-Based	5	2	Yes	0.80	0.20	1.18
NNNN	Large	Brackish	Land-Based	5	4	Yes	1.09	1.06	5.99
NNNN	Large	Brackish	Shipboard	4	4	Yes	4.90	0.51	27.37
NNNN	Large	Fresh	Land-Based	5	2	Yes	1.18	0.81	5.19
NNNN	Large	Fresh	Shipboard	1	1	No	3.00		
NNNN	Medium	Marine	Land-Based	5	4	Yes	1.19	1.74	11.28
NNNN	Medium	Brackish	Land-Based	5	5	Yes	1.59	1.27	12.73
NNNN	Medium	Brackish	Shipboard	4	4	Yes	2.38	0.78	14.38
NNNN	Medium	Fresh	Land-Based	5	4	Yes	4.94	1.46	73.95
NNNN	Medium	Fresh	Shipboard	1	1	No	2.80		
PP	Large	Marine	Land-Based	5	4	Yes	0.69	1.03	2.95
PP	Large	Marine	Shipboard	5	3	Yes	0.95	1.43	6.61
PP	Large	Brackish	Land-Based	5	5	Yes	3.15	0.52	14.42
PP	Large	Fresh	Land-Based	5	5	Yes	1.93	0.41	5.68
PP	Medium	Marine	Land-Based	5	0	No	0.15		
PP	Medium	Marine	Shipboard	5	3	Yes	0.84	2.05	7.80

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
PP	Medium	Brackish	Land-Based	5	3	No	0.13		
PP	Medium	Fresh	Land-Based	5	5	Yes	1.00	0.81	4.03
PP1	Large	Marine	Land-Based	2	2	Yes	0.68	0.65	1.91
PP1	Large	Brackish	Land-Based	2	0	No	0.36		
PP1	Large	Fresh	Land-Based	2	2	Yes	2.45	0.04	2.82
PP1	Medium	Marine	Land-Based	2	1	No	0.17		
PP1	Medium	Brackish	Land-Based	2	1	No	0.21		
PP1	Medium	Fresh	Land-Based	2	2	Yes	0.87	1.09	4.45
PPPP	Large	Marine	Land-Based	7	7	Yes	2.70	0.94	20.68
PPPP	Large	Brackish	Land-Based	7	7	Yes	1.38	0.96	7.75
PPPP	Large	Brackish	Shipboard	4	4	Yes	3.20	0.26	8.04
PPPP	Large	Fresh	Land-Based	10	9	Yes	50.01	1.27	1001.20
PPPP	Large	Fresh	Shipboard	1	1	No	5.21		
PPPP	Medium	Marine	Land-Based	7	7	Yes	4.40	0.32	15.08
PPPP	Medium	Brackish	Land-Based	7	7	Yes	2.05	0.78	11.36
PPPP	Medium	Brackish	Shipboard	4	4	Yes	2.25	1.15	19.27
PPPP	Medium	Fresh	Land-Based	10	10	Yes	3.48	0.92	29.88
PPPP	Medium	Fresh	Shipboard	1	1	No	0.17		
QQ	Large	Marine	Land-Based	5	4	Yes	1.36	0.35	3.14
QQ	Large	Brackish	Land-Based	7	4	Yes	0.43	1.03	1.46
QQ	Large	Brackish	Shipboard	3	0	No	0.53		
QQ	Large	Fresh	Land-Based	5	3	No	1.00		
QQ	Large	Fresh	Shipboard	2	1	No	2.50		
QQ	Medium	Marine	Land-Based	5	3	Yes	1.68	1.47	15.91
QQ	Medium	Brackish	Land-Based	7	6	Yes	0.97	1.18	5.66
QQ	Medium	Brackish	Shipboard	3	1	No	0.47		
QQ	Medium	Fresh	Land-Based	5	3	No	0.74		
QQ	Medium	Fresh	Shipboard	2	2	Yes	1.50	0.29	3.13
QQQ	Large	Marine	Land-Based	6	0	No	1.00		
QQQ	Large	Marine	Shipboard	5	0	No	0.30		
QQQ	Large	Brackish	Land-Based	6	1	No	1.33		
QQQ	Large	Fresh	Land-Based	6	0	No	1.00		
QQQ	Medium	Marine	Land-Based	6	6	Yes	6.50	0.45	37.55
QQQ	Medium	Marine	Shipboard	5	4	Yes	1.36	1.16	9.11
QQQ	Medium	Brackish	Land-Based	6	6	Yes	14.17	0.57	148.90
QQQ	Medium	Fresh	Land-Based	6	6	Yes	2.50	0.86	17.08

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BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
RR	Large	Marine	Land-Based	11	9	Yes	36.14	1.86	657.92
RR	Large	Marine	Shipboard	7	3	Yes	4.21	1.65	64.99
RR	Large	Brackish	Land-Based	11	5	Yes	0.94	3.51	14.44
RR	Large	Brackish	Shipboard	4	4	Yes	11.40	0.77	142.36
RR	Large	Fresh	Land-Based	9	7	Yes	3.77	1.23	43.69
RR	Medium	Marine	Land-Based	11	4	Yes	7.55	4.51	128.84
RR	Medium	Marine	Shipboard	7	7	Yes	0.90	0.47	2.21
RR	Medium	Brackish	Land-Based	11	3	Yes	0.47	5.14	7.41
RR	Medium	Brackish	Shipboard	4	4	Yes	2.43	0.53	9.95
RR	Medium	Fresh	Land-Based	9	9	Yes	2.87	0.71	17.16
RR1	Large	Marine	Land-Based	3	0	No	1.00		
RR1	Large	Brackish	Land-Based	1	0	No	1.00		
RR1	Large	Fresh	Land-Based	3	2	No	5.00		
RR1	Medium	Marine	Land-Based	3	3	No	0.30		
RR1	Medium	Brackish	Land-Based	1	1	No	0.30		
RR1	Medium	Fresh	Land-Based	3	3	Yes	2.83	1.21	28.58
RRR	Large	Marine	Land-Based	9	7	Yes	3.57	1.42	45.99
RRR	Large	Marine	Shipboard	7	5	Yes	8.01	1.83	155.42
RRR	Large	Brackish	Land-Based	6	3	Yes	0.61	0.55	1.46
RRR	Large	Fresh	Land-Based	5	3	Yes	0.91	0.28	1.61
RRR	Large	Fresh	Shipboard	1	0	No	0.30		
RRR	Medium	Marine	Land-Based	9	9	Yes	5.51	0.84	53.88
RRR	Medium	Marine	Shipboard	7	6	Yes	0.93	1.02	4.55
RRR	Medium	Brackish	Land-Based	6	5	Yes	1.81	1.45	17.47
RRR	Medium	Fresh	Land-Based	5	5	Yes	2.10	1.31	19.87
RRR	Medium	Fresh	Shipboard	1	1	No	0.17		
RRRR	Large	Marine	Land-Based	9	7	Yes	3.55	1.34	43.41
RRRR	Large	Brackish	Land-Based	5	4	Yes	0.41	0.49	0.80
RRRR	Large	Fresh	Land-Based	7	5	Yes	1.71	0.56	6.37
RRRR	Medium	Marine	Land-Based	9	8	Yes	5.17	1.80	89.77
RRRR	Medium	Brackish	Land-Based	5	1	No	0.23		
RRRR	Medium	Fresh	Land-Based	7	6	Yes	1.73	1.81	20.13
SS/R	Large	Marine	Land-Based	14	12	Yes	3.00	1.98	46.56
SS/R	Large	Marine	Shipboard	5	5	Yes	3.55	0.78	26.16
SS/R	Large	Brackish	Land-Based	13	8	Yes	27.10	2.11	498.57
SS/R	Large	Fresh	Land-Based	5	3	No	0.60		

Table C-1. All sets, their numbers of trials, and calculated parameters.

For sets containing at least two distinct detected trials, the mean, sigma, and 99th percentiles were calculated based on a left-censored IG distribution; for the other sets, the arithmetic mean was calculated. These parameters' units are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
SS/R	Medium	Marine	Land-Based	14	14	Yes	19.75	0.25	110.83
SS/R	Medium	Marine	Shipboard	5	5	Yes	1.15	0.62	3.92
SS/R	Medium	Brackish	Land-Based	13	13	Yes	6.56	0.68	56.62
SS/R	Medium	Fresh	Land-Based	5	5	Yes	9.50	0.18	27.14
UU	Large	Marine	Land-Based	5	0	No	1.00		
UU	Large	Marine	Shipboard	3	0	No	0.30		
UU	Large	Brackish	Land-Based	5	3	Yes	0.55	0.44	1.10
UU	Large	Brackish	Shipboard	2	0	No	0.30		
UU	Large	Fresh	Land-Based	5	2	Yes	1.08	0.65	3.67
UU	Medium	Marine	Land-Based	5	4	Yes	1.49	1.37	12.42
UU	Medium	Marine	Shipboard	3	0	No	0.20		
UU	Medium	Brackish	Land-Based	5	4	Yes	0.76	1.47	4.86
UU	Medium	Brackish	Shipboard	2	1	No	0.26		
UU	Medium	Fresh	Land-Based	5	5	Yes	8.97	0.55	73.78
UUU	Large	Marine	Land-Based	5	0	No	5.00		
UUU	Large	Marine	Shipboard	5	5	Yes	2.54	0.59	11.82
UUU	Large	Brackish	Land-Based	5	0	No	5.00		
UUU	Large	Fresh	Land-Based	5	1	No	4.52		
UUU	Medium	Marine	Land-Based	5	0	No	0.15		
UUU	Medium	Marine	Shipboard	5	0	No	0.20		
UUU	Medium	Brackish	Land-Based	5	2	No	0.13		
UUU	Medium	Fresh	Land-Based	5	1	No	0.14		
VVV	Large	Marine	Land-Based	5	2	Yes	0.80	0.20	1.18
VVV	Large	Marine	Shipboard	4	1	No	0.72		
VVV	Large	Brackish	Land-Based	5	4	Yes	1.34	0.49	3.94
VVV	Large	Brackish	Shipboard	1	0	No	0.30		
VVV	Large	Fresh	Land-Based	7	4	Yes	1.41	0.70	5.88
VVV	Medium	Marine	Land-Based	5	4	Yes	1.79	1.79	20.88
VVV	Medium	Marine	Shipboard	4	2	Yes	1.13	2.93	16.30
VVV	Medium	Brackish	Land-Based	5	4	Yes	1.31	1.77	13.21
VVV	Medium	Brackish	Shipboard	1	1	No	0.17		
VVV	Medium	Fresh	Land-Based	7	7	Yes	4.21	0.38	16.42
XXX	Large	Marine	Land-Based	5	1	No	0.87		
XXX	Large	Marine	Shipboard	8	7	Yes	13.92	1.03	232.70
XXX	Large	Brackish	Land-Based	6	2	Yes	0.90	1.60	6.80
XXX	Large	Brackish	Shipboard	1	1	No	9.50		

Table C-1. All sets, their numbers of trials, and calculated parameters.

For sets containing at least two distinct detected trials, the mean, sigma, and 99th percentiles were calculated based on a left-censored IG distribution; for the other sets, the arithmetic mean was calculated. These parameters' units are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Test Platform	Number of Trials	Number of Detected Trials	Contains ≥2 Distinct Detected Trials	Mean (org./ volume)	Sigma (org./ volume)	99th Percentile (org./ volume)
XXX	Medium	Marine	Land-Based	5	5	Yes	0.93	1.45	6.51
XXX	Medium	Marine	Shipboard	8	8	Yes	2.57	1.14	23.39
XXX	Medium	Brackish	Land-Based	6	6	Yes	2.33	1.36	23.95
XXX	Medium	Brackish	Shipboard	1	1	No	2.80		
XXX1	Large	Marine	Land-Based	3	1	No	1.10		
XXX1	Large	Brackish	Land-Based	3	2	No	0.53		
XXX1	Large	Fresh	Land-Based	3	1	No	0.90		
XXX1	Medium	Marine	Land-Based	3	3	Yes	0.43	0.37	0.73
XXX1	Medium	Brackish	Land-Based	3	3	Yes	1.17	0.84	5.26
XXX1	Medium	Fresh	Land-Based	3	3	No	0.30		
Z	Large	Marine	Land-Based	5	2	Yes	0.18	2.75	1.08
Z	Large	Marine	Shipboard	5	5	Yes	4.34	0.30	13.97
Z	Large	Brackish	Land-Based	5	3	Yes	0.91	3.09	12.60
Z	Medium	Marine	Land-Based	5	0	No	0.20		
Z	Medium	Marine	Shipboard	5	4	Yes	2.43	1.48	27.37
Z	Medium	Brackish	Land-Based	5	4	Yes	0.40	2.10	2.66
ZZZ	Large	Marine	Land-Based	5	1	No	1.14		
ZZZ	Large	Marine	Shipboard	3	0	No	0.30		
ZZZ	Large	Brackish	Land-Based	7	6	Yes	8.14	0.71	81.41
ZZZ	Large	Brackish	Shipboard	3	3	Yes	2.50	0.60	11.92
ZZZ	Large	Fresh	Land-Based	9	4	Yes	13.01	1.82	266.92
ZZZ	Medium	Marine	Land-Based	5	3	Yes	0.44	2.33	3.36
ZZZ	Medium	Marine	Shipboard	3	2	Yes	0.32	1.57	1.43
ZZZ	Medium	Brackish	Land-Based	7	5	Yes	0.40	1.64	2.06
ZZZ	Medium	Brackish	Shipboard	3	2	Yes	0.72	1.78	5.40
ZZZ	Medium	Fresh	Land-Based	9	8	Yes	0.51	1.62	2.96

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./ volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
C	Large	Marine	77.8%	0.93	6.63	7.14
C	Large	Brackish	62.5%	1.14	8.29	7.27
C	Large	Fresh	100.0%	0.48	1.58	3.28
C	Medium	Marine	77.8%	0.64	3.13	4.86
C	Medium	Brackish	62.5%	0.52		
C	Medium	Fresh	100.0%	0.40		
C1	Large	Marine	100.0%	0.83		
C1	Large	Brackish	100.0%	0.69	4.23	6.10
C1	Large	Fresh	100.0%	1.73	16.11	9.33
C1	Medium	Marine	100.0%	0.40		
C1	Medium	Brackish	100.0%	0.40		
C1	Medium	Fresh	100.0%	2.15	17.95	8.35
CC	Large	Marine	58.3%	66.60	1330.64	19.98
CC	Large	Brackish	100.0%	4.84	10.78	2.23
CC	Large	Fresh	100.0%	1.99	5.39	2.70
CC	Medium	Marine	58.3%	0.41	3.01	7.38
CC	Medium	Brackish	100.0%	0.54	4.04	7.50
CC	Medium	Fresh	100.0%	0.24		
CC1	Large	Brackish	100.0%	2.15	3.45	1.60
CC1	Large	Fresh	100.0%	3.76	9.24	2.46
CC1	Medium	Brackish	100.0%	0.50	1.94	3.86
CC1	Medium	Fresh	100.0%	0.30	0.49	1.63
CC2	Large	Marine	100.0%	3.47		
CC2	Large	Brackish	100.0%	5.00		
CC2	Large	Fresh	100.0%	3.80		
CC2	Medium	Marine	100.0%	0.72		
CC2	Medium	Brackish	100.0%	0.15		
CC2	Medium	Fresh	100.0%	1.03	10.16	9.86
CCCC	Large	Marine	60.0%	0.12	0.72	6.01
CCCC	Large	Brackish	85.7%	0.12	0.86	7.16
CCCC	Large	Fresh	100.0%	0.16	0.72	4.43
CCCC	Medium	Marine	60.0%	0.38	0.99	2.62
CCCC	Medium	Brackish	85.7%	1.15	8.88	7.74
CCCC	Medium	Fresh	100.0%	3.29	42.68	12.99
CCCC1	Large	Marine	100.0%	1.56	15.21	9.75
CCCC1	Large	Brackish	100.0%	11.22	157.85	14.06
CCCC1	Medium	Marine	100.0%	2.88	14.96	5.19

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m³.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
CCCC1	Medium	Brackish	100.0%	1.66	9.10	5.48
DD	Large	Marine	63.6%	1.11	21.35	19.29
DD	Large	Brackish	100.0%	1.00		
DD	Large	Fresh	100.0%	0.84	1.22	1.45
DD	Medium	Marine	63.6%	4.31	36.04	8.35
DD	Medium	Brackish	100.0%	0.15	0.38	2.55
DD	Medium	Fresh	100.0%	7.42	81.83	11.03
DD1	Large	Brackish	100.0%	1.53	5.11	3.34
DD1	Large	Fresh	100.0%	0.67		
DD1	Medium	Brackish	100.0%	2.42	7.12	2.93
DD1	Medium	Fresh	100.0%	2.98	12.18	4.08
DDDD	Large	Marine	100.0%	0.35		
DDDD	Large	Brackish	55.6%	1.50	10.23	6.80
DDDD	Large	Fresh	83.3%	0.39		
DDDD	Medium	Marine	100.0%	1.44	8.32	5.79
DDDD	Medium	Brackish	55.6%	1.02	6.49	6.39
DDDD	Medium	Fresh	83.3%	1.60	13.16	8.24
E	Large	Marine	100.0%	2.40	17.10	7.13
E	Large	Brackish	50.0%	2.07	15.71	7.60
E	Large	Fresh	100.0%	2.88	15.12	5.25
E	Medium	Marine	100.0%	0.63	4.49	7.07
E	Medium	Brackish	50.0%	0.89	11.86	13.30
E	Medium	Fresh	100.0%	2.37	21.26	8.97
FFFF	Large	Marine	50.0%	1.61	4.87	3.02
FFFF	Large	Brackish	100.0%	1.00		
FFFF	Large	Fresh	100.0%	0.49	1.01	2.05
FFFF	Medium	Marine	50.0%	0.35	1.38	3.93
FFFF	Medium	Brackish	100.0%	0.74	1.05	1.43
FFFF	Medium	Fresh	100.0%	4.12	19.84	4.82
FFFF1	Large	Marine	100.0%	6.46	82.55	12.77
FFFF1	Large	Brackish	100.0%	0.55		
FFFF1	Large	Fresh	100.0%	1.40		
FFFF1	Medium	Marine	100.0%	0.92	16.34	17.83
FFFF1	Medium	Brackish	100.0%	0.41	2.56	6.31
FFFF1	Medium	Fresh	100.0%	0.14		
G	Large	Marine	80.0%	1.38	13.08	9.46
G	Large	Brackish	72.7%	1.71	14.42	8.46

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./ volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
G	Large	Fresh	100.0%	3.01	31.57	10.49
G	Medium	Marine	80.0%	1.73	12.15	7.04
G	Medium	Brackish	72.7%	1.63	16.03	9.85
G	Medium	Fresh	100.0%	2.67	8.54	3.20
HH	Large	Marine	55.6%	1.97	8.12	4.13
HH	Large	Brackish	83.3%	0.69	1.55	2.23
HH	Large	Fresh	100.0%	1.18	7.13	6.04
HH	Medium	Marine	55.6%	1.40	18.15	12.93
HH	Medium	Brackish	83.3%	4.88	11.74	2.41
HH	Medium	Fresh	100.0%	9.02	66.78	7.41
HH1	Large	Marine	100.0%	1.58	4.96	3.15
HH1	Large	Brackish	100.0%	1.24	5.36	4.31
HH1	Large	Fresh	100.0%	4.33	53.50	12.37
HH1	Medium	Marine	100.0%	0.68	2.00	2.96
HH1	Medium	Brackish	100.0%	1.41	6.72	4.77
HH1	Medium	Fresh	100.0%	1.62	12.07	7.47
HH2	Large	Marine	100.0%	0.72		
HH2	Large	Brackish	100.0%	0.66		
HH2	Large	Fresh	100.0%	0.53	1.22	2.29
HH2	Medium	Marine	100.0%	5.70	6.97	1.22
HH2	Medium	Brackish	100.0%	4.06	26.63	6.55
HH2	Medium	Fresh	100.0%	7.10	12.87	1.81
HHHH	Large	Marine	62.5%	1.32	5.31	4.03
HHHH	Large	Brackish	71.4%	1.99	15.77	7.94
HHHH	Large	Fresh	100.0%	0.57	1.55	2.70
HHHH	Medium	Marine	62.5%	1.43	8.28	5.81
HHHH	Medium	Brackish	71.4%	1.64	11.24	6.85
HHHH	Medium	Fresh	100.0%	1.22	7.14	5.84
HHHH1	Large	Marine	100.0%	0.30		
HHHH1	Large	Brackish	100.0%	0.80	1.83	2.28
HHHH1	Large	Fresh	100.0%	0.30		
HHHH1	Medium	Marine	100.0%	0.25	0.39	1.57
HHHH1	Medium	Brackish	100.0%	1.05	1.79	1.70
HHHH1	Medium	Fresh	100.0%	0.25	0.39	1.57
III	Large	Marine	62.5%	3.22		
III	Large	Brackish	71.4%	3.93		
III	Large	Fresh	100.0%	5.00		

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m³.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
III	Medium	Marine	62.5%	0.16		
III	Medium	Brackish	71.4%	0.37	2.97	8.02
III	Medium	Fresh	100.0%	0.15	0.30	2.05
J	Large	Marine	54.5%	3.76	13.45	3.58
J	Large	Brackish	100.0%	1.68	5.60	3.33
J	Large	Fresh	100.0%	5.36		
J	Medium	Marine	54.5%	0.16		
J	Medium	Brackish	100.0%	0.13		
J	Medium	Fresh	100.0%	0.14		
J1	Large	Marine	100.0%	7.22	41.40	5.73
J1	Large	Brackish	100.0%	3.90		
J1	Large	Fresh	100.0%	2.80		
J1	Medium	Marine	100.0%	0.15	0.30	2.05
J1	Medium	Brackish	100.0%	0.13		
J1	Medium	Fresh	100.0%	0.12		
JJ	Large	Marine	100.0%	0.22		
JJ	Large	Brackish	100.0%	5.24	12.29	2.35
JJ	Large	Fresh	100.0%	0.50	0.78	1.57
JJ	Medium	Marine	100.0%	0.34	1.11	3.31
JJ	Medium	Brackish	100.0%	0.20	0.38	1.95
JJ	Medium	Fresh	100.0%	3.42	11.76	3.44
JJJJ	Large	Marine	66.7%	0.76		
JJJJ	Large	Brackish	83.3%	0.88		
JJJJ	Medium	Marine	66.7%	1.84	7.38	4.00
JJJJ	Medium	Brackish	83.3%	3.19	14.69	4.60
K	Large	Marine	66.7%	1.67	15.11	9.07
K	Large	Brackish	83.3%	0.42		
K	Large	Fresh	100.0%	1.01	5.48	5.41
K	Medium	Marine	66.7%	48.11	976.24	20.29
K	Medium	Brackish	83.3%	2.37	8.05	3.39
K	Medium	Fresh	100.0%	10.96	131.23	11.97
K1	Large	Marine	100.0%	1.00		
K1	Large	Brackish	100.0%	1.00		
K1	Large	Fresh	100.0%	1.00		
K1	Medium	Marine	100.0%	0.45	1.53	3.40
K1	Medium	Brackish	100.0%	0.25	0.39	1.57
K1	Medium	Fresh	100.0%	0.75	4.03	5.37

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
KKKK	Large	Marine	50.0%	1.45	8.43	5.82
KKKK	Large	Brackish	100.0%	2.07	7.61	3.68
KKKK	Large	Fresh	100.0%	1.03	2.57	2.51
KKKK	Medium	Marine	50.0%	2.59	15.90	6.15
KKKK	Medium	Brackish	100.0%	3.88	52.52	13.52
KKKK	Medium	Fresh	100.0%	2.69	11.34	4.21
L	Large	Marine	83.3%	1.42		
L	Large	Brackish	100.0%	0.50	1.47	2.94
L	Large	Fresh	100.0%	0.72		
L	Medium	Marine	83.3%	0.53		
L	Medium	Brackish	100.0%	0.30		
L	Medium	Fresh	100.0%	0.50		
LLL/LLLL	Large	Marine	50.0%	2.69	1.26	0.47
LLL/LLLL	Large	Brackish	100.0%	5.00		
LLL/LLLL	Large	Fresh	100.0%	3.29	17.97	5.46
LLL/LLLL	Medium	Marine	50.0%	0.17		
LLL/LLLL	Medium	Brackish	100.0%	0.13		
LLL/LLLL	Medium	Fresh	100.0%	0.15		
M	Large	Marine	38.5%	2.78	9.55	3.44
M	Large	Brackish	100.0%	5.00		
M	Large	Fresh	100.0%	5.00		
M	Medium	Marine	38.5%	0.62	11.47	18.64
M	Medium	Brackish	100.0%	5.83	95.89	16.44
M	Medium	Fresh	100.0%	0.16	0.33	2.06
MMM	Large	Marine	50.0%	9.74	76.28	7.83
MMM	Large	Brackish	71.4%	2.10	5.83	2.78
MMM	Medium	Marine	50.0%	1.80	15.71	8.71
MMM	Medium	Brackish	71.4%	0.55	0.72	1.31
NNNN	Large	Marine	100.0%	0.80	1.18	1.48
NNNN	Large	Brackish	55.6%	2.78	15.49	5.57
NNNN	Large	Fresh	83.3%	1.48	5.19	3.50
NNNN	Medium	Marine	100.0%	1.19	11.28	9.45
NNNN	Medium	Brackish	55.6%	1.94	13.47	6.93
NNNN	Medium	Fresh	83.3%	4.58	73.95	16.13
PP	Large	Marine	50.0%	0.82	4.78	5.82
PP	Large	Brackish	100.0%	3.15	14.42	4.57
PP	Large	Fresh	100.0%	1.93	5.68	2.94

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
PP	Medium	Marine	50.0%	0.49	7.80	15.79
PP	Medium	Brackish	100.0%	0.13		
PP	Medium	Fresh	100.0%	1.00	4.03	4.04
PP1	Large	Marine	100.0%	0.68	1.91	2.81
PP1	Large	Brackish	100.0%	0.36		
PP1	Large	Fresh	100.0%	2.45	2.82	1.15
PP1	Medium	Marine	100.0%	0.17		
PP1	Medium	Brackish	100.0%	0.21		
PP1	Medium	Fresh	100.0%	0.87	4.45	5.09
PPPP	Large	Marine	100.0%	2.70	20.68	7.67
PPPP	Large	Brackish	63.6%	2.04	7.86	3.85
PPPP	Large	Fresh	90.9%	45.93	1001.20	21.80
PPPP	Medium	Marine	100.0%	4.40	15.08	3.42
PPPP	Medium	Brackish	63.6%	2.12	14.23	6.71
PPPP	Medium	Fresh	90.9%	3.18	29.88	9.39
QQ	Large	Marine	100.0%	1.36	3.14	2.31
QQ	Large	Brackish	70.0%	0.46	1.46	3.19
QQ	Large	Fresh	71.4%	1.43		
QQ	Medium	Marine	100.0%	1.68	15.91	9.47
QQ	Medium	Brackish	70.0%	0.82	5.66	6.89
QQ	Medium	Fresh	71.4%	0.96	3.13	3.27
QQQ	Large	Marine	54.5%	0.68		
QQQ	Large	Brackish	100.0%	1.33		
QQQ	Large	Fresh	100.0%	1.00		
QQQ	Medium	Marine	54.5%	4.16	24.62	5.92
QQQ	Medium	Brackish	100.0%	14.17	148.90	10.51
QQQ	Medium	Fresh	100.0%	2.50	17.08	6.82
RR	Large	Marine	61.1%	23.72	427.34	18.02
RR	Large	Brackish	73.3%	3.73	48.55	13.03
RR	Large	Fresh	100.0%	3.77	43.69	11.60
RR	Medium	Marine	61.1%	4.96	79.59	16.03
RR	Medium	Brackish	73.3%	0.99	8.09	8.17
RR	Medium	Fresh	100.0%	2.87	17.16	5.99
RR1	Large	Marine	100.0%	1.00		
RR1	Large	Brackish	100.0%	1.00		
RR1	Large	Fresh	100.0%	5.00		
RR1	Medium	Marine	100.0%	0.30		

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m³.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
RR1	Medium	Brackish	100.0%	0.30		
RR1	Medium	Fresh	100.0%	2.83	28.58	10.09
RRR	Large	Marine	56.2%	5.52	93.86	17.02
RRR	Large	Brackish	100.0%	0.61	1.46	2.39
RRR	Large	Fresh	83.3%	0.80	1.61	2.00
RRR	Medium	Marine	56.2%	3.50	32.30	9.22
RRR	Medium	Brackish	100.0%	1.81	17.47	9.68
RRR	Medium	Fresh	83.3%	1.78	19.87	11.16
RRRR	Large	Marine	100.0%	3.55	43.41	12.24
RRRR	Large	Brackish	100.0%	0.41	0.80	1.94
RRRR	Large	Fresh	100.0%	1.71	6.37	3.72
RRRR	Medium	Marine	100.0%	5.17	89.77	17.38
RRRR	Medium	Brackish	100.0%	0.23		
RRRR	Medium	Fresh	100.0%	1.73	20.13	11.64
SS/R	Large	Marine	73.7%	3.15	41.19	13.09
SS/R	Large	Brackish	100.0%	27.10	498.57	18.40
SS/R	Large	Fresh	100.0%	0.60		
SS/R	Medium	Marine	73.7%	14.86	82.70	5.57
SS/R	Medium	Brackish	100.0%	6.56	56.62	8.63
SS/R	Medium	Fresh	100.0%	9.50	27.14	2.86
UU	Large	Marine	62.5%	0.74		
UU	Large	Brackish	71.4%	0.48	1.10	2.29
UU	Large	Fresh	100.0%	1.08	3.67	3.41
UU	Medium	Marine	62.5%	1.00	12.42	12.36
UU	Medium	Brackish	71.4%	0.62	4.86	7.85
UU	Medium	Fresh	100.0%	8.97	73.78	8.23
UUU	Large	Marine	50.0%	3.77	11.82	3.14
UUU	Large	Brackish	100.0%	5.00		
UUU	Large	Fresh	100.0%	4.52		
UUU	Medium	Marine	50.0%	0.17		
UUU	Medium	Brackish	100.0%	0.13		
UUU	Medium	Fresh	100.0%	0.14		
VVV	Large	Marine	55.6%	0.76	1.18	1.54
VVV	Large	Brackish	83.3%	1.16	3.94	3.38
VVV	Large	Fresh	100.0%	1.41	5.88	4.17
VVV	Medium	Marine	55.6%	1.50	18.84	12.60
VVV	Medium	Brackish	83.3%	1.12	13.21	11.76

Table C-2. Sets with test platforms combined using weighted means and percentiles.

Sets in which at least one platform had two or more distinct detected organism concentrations have weighted 99th percentiles and variability factors. Means and percentiles are in medium organisms/mL, and large organisms/m^3.

BWMS	Organism Size Class	Salinity Category	Percentage of Trials that are Land-Based	Weighted Mean (org./ volume)	Weighted 99th Percentile (org./volume)	Variability Factor (unitless)
VVV	Medium	Fresh	100.0%	4.21	16.42	3.90
XXX	Large	Marine	38.5%	8.90	232.70	26.15
XXX	Large	Brackish	85.7%	2.13	6.80	3.19
XXX	Medium	Marine	38.5%	1.94	16.89	8.69
XXX	Medium	Brackish	85.7%	2.40	23.95	9.98
XXX1	Large	Marine	100.0%	1.10		
XXX1	Large	Brackish	100.0%	0.53		
XXX1	Large	Fresh	100.0%	0.90		
XXX1	Medium	Marine	100.0%	0.43	0.73	1.69
XXX1	Medium	Brackish	100.0%	1.17	5.26	4.51
XXX1	Medium	Fresh	100.0%	0.30		
Z	Large	Marine	50.0%	2.26	7.52	3.33
Z	Large	Brackish	100.0%	0.91	12.60	13.87
Z	Medium	Marine	50.0%	1.31	27.37	20.84
Z	Medium	Brackish	100.0%	0.40	2.66	6.63
ZZZ	Large	Marine	62.5%	0.82		
ZZZ	Large	Brackish	70.0%	6.45	60.57	9.39
ZZZ	Large	Fresh	100.0%	13.01	266.92	20.52
ZZZ	Medium	Marine	62.5%	0.39	2.64	6.70
ZZZ	Medium	Brackish	70.0%	0.49	3.06	6.19
ZZZ	Medium	Fresh	100.0%	0.51	2.96	5.78