

**APPENDIX C**  
**DIRECT EFFECTS STATION ASSESSMENT**  
**EXAMPLE CALCULATION**

## **Direct Effects Station Assessment Example Calculation**

This document describes the calculations needed to evaluate sediment with respect to the sediment quality objective for aquatic life-benthic community protection. The evaluation process consists of 5 steps, as shown below. Step 1 consists of sediment sampling and laboratory measurement of three Lines of Evidence (LOE): chemistry, toxicity, and abundance of benthic infauna. The data from each LOE are then summarized, interpreted using multiple indices, and integrated in Steps 2-4 in order to determine a LOE condition category. The final step of the evaluation process is to combine the three LOE category classifications to determine the station assessment category.

The data used in the example are typical of those likely to be encountered in California embayments. Steps 2-4 are described separately for each LOE. The thresholds used to evaluate the data were obtained from Appendix A (Draft Enclosed Bays and Estuaries Sediment Quality Plan). The data analyses described in this example have been broken down into a number of intermediate steps to allow the reader who is unfamiliar with these analyses to follow the calculations. In practice, many of these steps are accomplished with a single calculation and the calculations are easily automated using readily available computer software.

### **Step 1**

Collect and analyze samples  
Chemistry, Toxicity, Benthos

### **Step 2**

Compile and summarize data  
QA review, means, sums

### **Step 3**

Apply Indicators for each LOE  
Indices and thresholds

### **Step 4**

Determine LOE Category  
Integrate indicators

### **Step 5**

Station impact assessment  
Integrate LOEs

## Sediment Chemistry

The steps involved in analysis of the chemistry LOE are gathering the data and getting them into the appropriate units, calculating the Logistic Regression Model values, calculating the Chemical Score Index values, and integrating these values to determine the chemistry LOE category. All of the calculations can be done with a standard desk calculator, but can be more easily accomplished using a spreadsheet program, such as Excel.

### Data preparation

The first step in the process is to gather the appropriate sediment chemistry data and put it into the proper units for analysis. The chemical constituents needed for the chemistry LOE analysis and the sample data are listed in Table 1. Note that all constituents are expressed on a dry weight basis, metals in mg/dry kg and organic constituents in µg/dry kg. For any chemicals that were measured but not detected, an estimated concentration (e.g., ½ of the detection limit) should be used for calculation purposes.

### California Logistic Regression Model Calculation

The California Logistic Regression Model (CA LRM) uses logistic regression models to predict the probability of sediment toxicity based on chemical concentration. The concentration data for each chemical, along with chemical-specific regression slope and intercept are used in the following equation to predict the probability of toxicity ( $p$ ).

$$p = e^{B_0 + B_1(x)} / (1 + e^{B_0 + B_1(x)})$$

Where:  $p$  = probability of observing a toxic effect;

$e$  = base of the natural logarithm, approximately 2.718;

$B_0$  = intercept parameter;

$B_1$  = slope parameter; and,

$x$  = log of the chemical concentration

For example, the following results are obtained using the cadmium data from Table 1 in the equation:

$$p = e^{0.2894 + 3.1764 \times \log(0.15)} / (1 + e^{0.2894 + 3.1764 \times \log(0.15)})$$

$$p = e^{-2.328} / (1 + e^{-2.328})$$

$$p = 0.09749 / 1.09749$$

$$p = 0.09$$

Figure 2 shows the regression curve and sample results for cadmium.

The regression parameters and results for the sample data are shown in Table 2. Note that the data for gamma chlordane, total DDDs, total DDEs and total DDTs are not used, because CA LRM approach does not include regressions for these chemicals. The

maximum  $p$  value for any of the chemicals in the sample is termed the  $P_{max}$ . The  $P_{max}$  value is then compared to a set of thresholds (Table 3) to determine the CA LRM category for the sample. The maximum value for this data set is 0.58 (mercury), which places the sample in the Moderate Exposure category, corresponding to a category score of 3.

**Table 1. Chemistry data used in the example.**

Chemical	Concentration
Cadmium (mg/kg)	0.15
Copper (mg/kg)	43.6
Lead (mg/kg)	33.5
Mercury (mg/kg)	1.37
Zinc (mg/kg)	45.4
HPAH <sup>1</sup> (ug/kg)	1672
LPAH <sup>2</sup> (ug/kg)	261
Alpha Chlordane (ug/kg)	3.1
Gamma Chlordane (ug/kg)	2.4
Dieldrin (ug/kg)	1.7
Trans Nonachlor (ug/kg)	2.5
DDD <sub>s</sub> , total (ug/kg)	6.7
DDE <sub>s</sub> , total (ug/kg)	2.7
DDT <sub>s</sub> , total (ug/kg)	10.6
PCBs, total (ug/kg)	22.7
4,4'-DDT (ug/kg)	2.5

1. Total high molecular weight PAH.

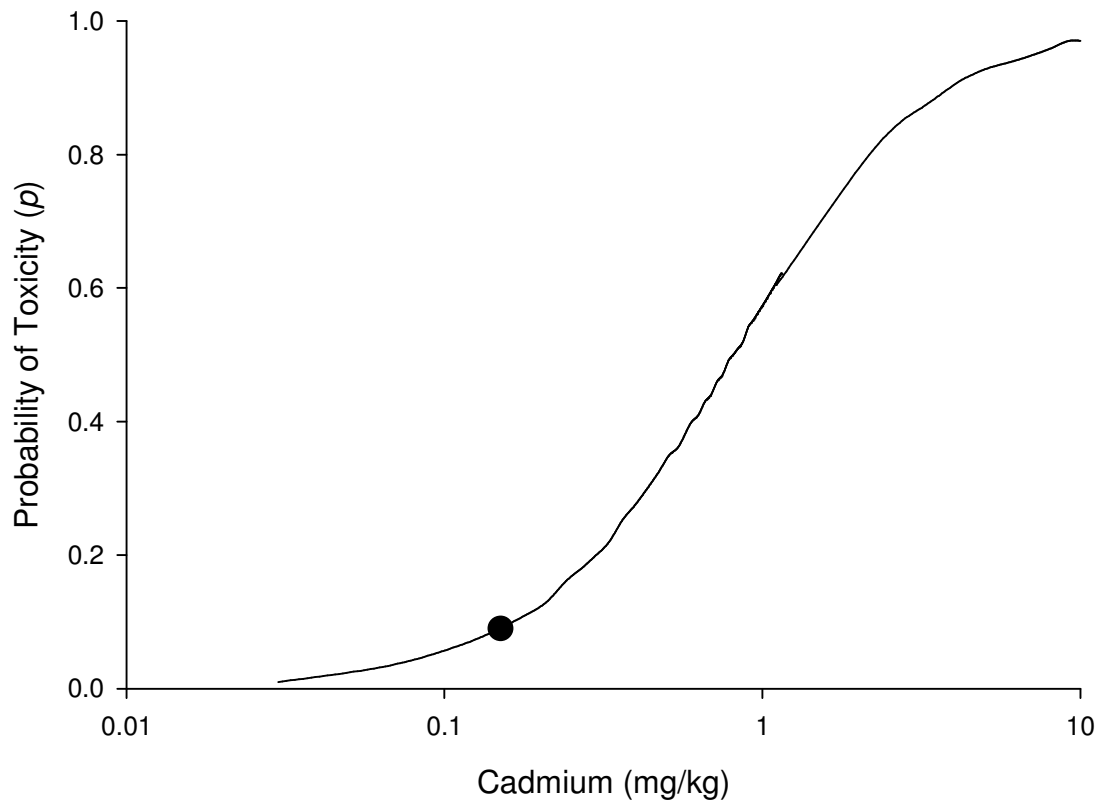
2. Total low molecular weight PAH.

**Table 2. CA LRM parameters and results for the sample data set. Highest probability of toxicity ( $P_{max}$ ) is in bold type.**

Chemical	B0	B1	P value
Cadmium	0.2894	3.1764	0.09
Copper	-5.5931	2.5885	0.21
Lead	-4.7228	2.8404	0.40
Mercury	-0.0618	2.6837	<b>0.58</b>
Zinc	-5.1337	2.4205	0.25
HPAH	-8.1922	1.9995	0.15
LPAH	-6.8071	1.8827	0.09
Alpha Chlordane	-3.4080	4.4570	0.23
Dieldrin	-1.8344	2.5890	0.22
Trans Nonachlor	-4.2590	5.3135	0.10
PCBs, total	-4.4144	1.4837	0.08
4,4'-DDT	-3.5531	3.2621	0.09

**Table 3. Threshold values of Pmax values for CA LRM calculation.**

Category	Pmax	Category Score
Minimal Exposure	< 0.33	1
Low Exposure	≥ 0.33 to ≤ 0.49	2
Moderate Exposure	> 0.49 to ≤ 0.66	3
High Exposure	> 0.66	4



**Figure 2. Plot of the logistic regression curve for cadmium. The circle shows the calculated probability of toxicity for cadmium.**

#### Chemical Score Index Calculation

The Chemical Score Index (CSI) uses the chemistry data to predict the occurrence of benthic community disturbance. The concentration data for each chemical are compared to a series of chemical-specific thresholds-concentration ranges and combined with weighting factors to calculate the mean CSI value. The following equation is used to calculate the mean CSI:

$$\text{Mean CSI} = \frac{\sum(w_i \times \text{cat}_i)}{\sum w}$$

Where:  $\text{cat}_i$  = predicted benthic disturbance category for chemical  $i$ ;  
 $w_i$  = weight factor for chemical  $i$ ;  
 $\sum w$  = sum of all weights.

This equation can be broken down into three parts. First, the concentration of each chemical is compared to a series of thresholds-ranges (Table 4) to determine the benthic disturbance category. The categories for each chemical in the sample dataset are shown in Table 5. Note that ~~cadmium~~, dieldrin, trans nonachlor and 4,4' DDT are not used in the CSI calculation ~~because these chemicals were not included in the development of the CSI approach~~. The second step is to calculate the CSI value for each chemical. This is achieved by multiplying the category value by the weight factor for each chemical (Table 5). The weight factor is proportional to the strength of association (correlation) observed between the chemical concentration and benthic community disturbance. The final step is to sum the CSI values for all chemicals and divide by the sum of all the weights (Table 5).

The final part of the process is to compare the mean CSI value to a series of thresholds to determine the CSI chemical exposure category (Table 6). The mean CSI value for the sample data is 2.04, which places it in the Low Exposure category, corresponding to a category score of 2.

**Table 4. Thresholds-Chemical concentration ranges for the predicted benthic disturbance categories used in the CSI calculation.**

Chemical	Benthic Disturbance Category			
	1	2	3	4
<del>Cadmium</del>	<del>≤ 0.09</del>	<del>&gt; 0.09 ≤ 0.22</del>	<del>&gt; 0.22 ≤ 1.66</del>	<del>&gt; 1.66</del>
Copper	≤ 52.8	> 52.8 ≤ 96.5	> 96.5 ≤ 406	> 406
Lead	≤ 26.4	> 26.4 ≤ 60.8	> 60.8 ≤ 154	> 154
Mercury	≤ 0.09	> 0.09 ≤ 0.45	> 0.45 ≤ 2.18	> 2.18
Zinc	≤ 112	> 112 ≤ 200	> 200 ≤ 629	> 629
HPAH	≤ 312	> 312 ≤ 1325	> 1325- 9320	> 9320
LPAH	≤ 85.4	> 85.4 ≤ 312	> 312 ≤ 2471	> 2471
Alpha Chlordane	≤ 0.50	> 0.50 ≤ 1.23	> 1.23 ≤ 11.1	> 11.1
Gamma Chlordane	≤ 0.54	> 0.54 ≤ 1.45	> 1.45 ≤ 14.5	> 14.5
DDD <sub>s</sub> , total	≤ 0.50	> 0.50 ≤ 2.69	> 2.69 ≤ 117	> 117
DDE <sub>s</sub> , total	≤ 0.50	> 0.50 ≤ 4.15	> 4.15 ≤ 154	> 154
DDT <sub>s</sub> , total	≤ 0.50	> 0.50 ≤ 1.52	> 1.52 ≤ 89.3	> 89.3
PCB <sub>s</sub> , total	≤ 11.9	> 11.9 ≤ 24.7	> 24.7 ≤ 288	> 288

**Table 5. Results of CSI calculations using the sample dataset.**

Chemical	Category	Weight	CSI
<del>Cadmium</del>	<del>2</del>	<del>38</del>	<del>76</del>
Copper	1	100	100
Lead	2	88	176
Mercury	3	30	90
Zinc	1	98	98
HPAH	3	16	48
LPAH	2	5	10
Alpha Chlordane	3	55	165
Gamma Chlordane	3	58	174
DDD <sub>s</sub> , total	3	46	138
DDE <sub>s</sub> , total	2	31	62
DDT <sub>s</sub> , total	3	16	48
PCBs, total	2	55	110
Sum		<del>636598</del>	<del>12951219</del>
Weighted Mean (CSI Sum/weight Sum)			2.04

**Table 6. Threshold values for CSI interpretation.**

Category	Mean CSI	Category Score
Minimal Exposure	< 0.1.69	1
Low Exposure	≥ 1.69 to ≤ 2.33	2
Moderate Exposure	> 2.33 to ≤ 2.99	3
High Exposure	> 2.99	4

#### Chemistry Indicator Integration

The final step in calculating the chemistry LOE is to integrate the results for the two sediment chemistry indicators: CA LRM and CSI. This is achieved by taking the average of the two category scores. If the average falls between two adjacent scores, the value is rounded up. The numeric average can then be converted back to a descriptive category. For the sample data, the category score for the CA LRM was 3 and for the CSI was 2. The average is 2.5, which rounds to 3 giving a chemistry LOE category of Moderate Exposure.

## Sediment Toxicity

The steps for calculating the sediment toxicity LOE are data preparation, comparison of toxicity endpoints to thresholds, and integration of the multiple toxicity test results. Once the data is formatted, no special calculation tools are needed for the sediment toxicity LOE calculations.

### Data preparation

The raw data from at least two toxicity test methods are compiled and the mean response (e.g., % survival) for each sample is calculated. The response data must be control normalized ((data from assessment station/control data)x100). T-tests must be performed on the raw data from the assessment station versus control response.

A sample data set containing results from two tests, the amphipod *Eohaustorius estuarius* survival test and sediment-water interface test using the mussel *Mytilus galloprovincialis* embryo development, is shown in Table 7.

### Individual Toxicity Test Result Classification

The data from each toxicity test is compared to a series of thresholds, which are unique to each test method (Table 8). Note that for the low threshold, the raw mean response for the assessment station is compared to the threshold. For the moderate and high thresholds, the control normalized response is compared to the thresholds. The flowchart in Figures 2 and 3 can be used as an aid in assigning categories. Note that the toxicity category is based on both the response level whether a statistically significant difference is present.

The raw *Eohaustorius* survival value being 90% puts that test in the nontoxic category (Figure 2). The *Mytilus* percent normal-alive value of 62% (control normalized) puts that test in the moderate category (Figure 3).

**Table 7. Toxicity data used in the example.**

Test Method	<i>E. estuarius</i> survival	<i>M. galloprovincialis</i> embryo development
Raw Station Response	90%	57%
Raw Control Response	92%	92%
Control Normalized Response	98%	62%
Statistical Difference from Control	No	Yes



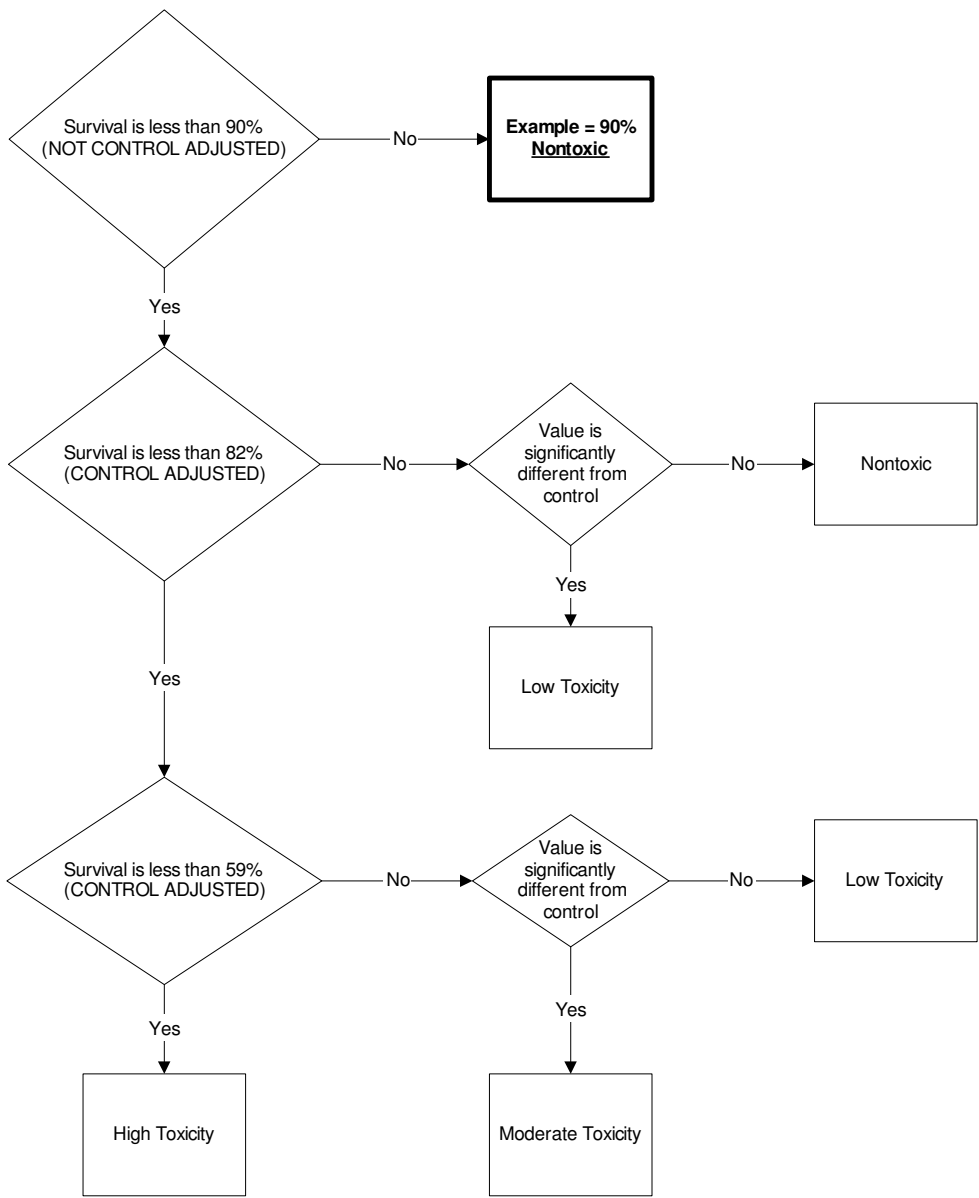
**Table 8. Threshold values for sediment toxicity test response.**

Test species/endpoint	Statistical Significance	Nontoxic (%)	Low Toxicity (% Control)	Moderate Toxicity (% Control)	High Toxicity (% Control)
<i>E. estuarius</i> Survival	Significant	90 to 100	82 to 89	59 to 81	< 59
	Not Sig.	82 to 100	59 to 81		< 59
<i>M. galloprovincialis</i> Normal Development	Significant	80 to 100	77 to 79	42 to 76	< 42
	Not Sig.	77 to 79	42 to 76		< 42

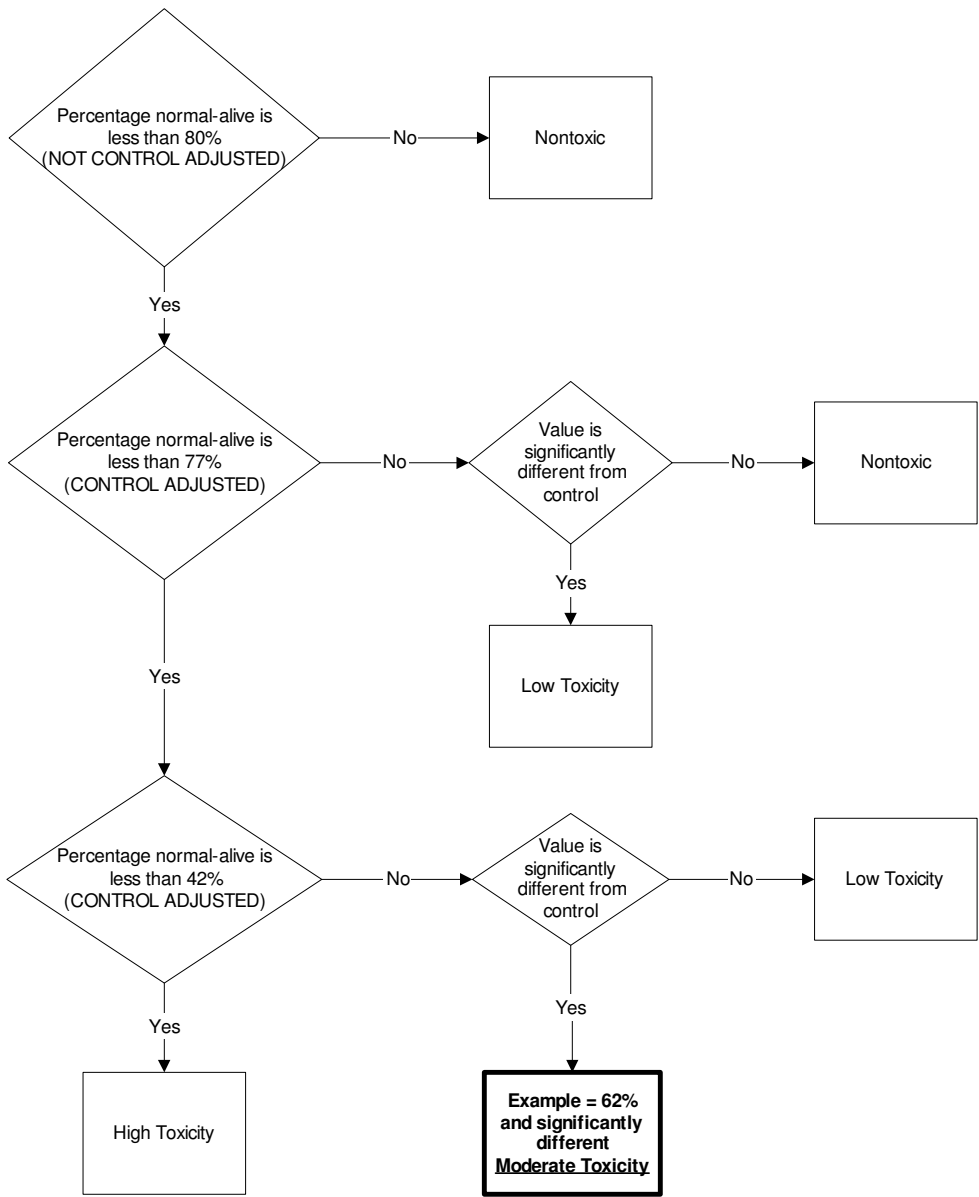
Integration of toxicity test results

The final step in determining the toxicity LOE is to integrate the toxicity test results. This is accomplished by averaging the category scores for all of the tests (nontoxic=1, low toxicity=2, moderate toxicity=3, high toxicity=4). If only two tests are used, and the average falls between two adjacent categories, the value is rounded up. If more than two tests are used and average falls between numbers, those that are 0.5 and above are rounded up, less than 0.5 are rounded down.

For the example data, the *Eohaustorius* data was in the non-toxic (1) category and the *Mytilus* data was in the moderate (3) category. Therefore, the final toxicity LOE for this station would be Low Toxicity.



**Figure 2. Flow chart for assignment of toxicity LOE category for *E. estuarius* example data.**



**Figure 3. Flow chart for assignment of toxicity LOE category for *M. galloprovincialis* example data.**

## Benthic Invertebrate Community Condition

For the benthic community LOE, the steps involved are gathering the data, calculating benthic community indices, comparing the index values to thresholds, and integrating the individual index results into a single benthic community LOE. While the general process of calculating the indices is similar between habitat types, the details may differ between habitats. The following example calculations are for the Southern California Marine Bays habitat. Most of the benthic index calculations can be made with a hand calculator, but it is simpler to use a spreadsheet program such as Excel.

### Data preparation

The raw data needed for the analyses include the abundance of each species (or lowest possible taxon) and station depth, latitude, and longitude. Data for several metrics must be also calculated from the raw data in order to compute some of the indices. Table 9 lists the metrics needed and the indices to which they apply.

**Table 9. Metrics used in calculation of benthic community indices.**

Metric	Index Where Used
Total number of taxa	IBI, RBI
Number of mollusc taxa	IBI, RBI
Number of sensitive taxa	IBI
Number of crustacean taxa	RBI
Abundance of Crustacea	RBI

A sample data set is shown in Table 10. This table presents species abundances for all the benthic organisms found at the station. Each species is designated as sensitive or not, based on to a list of sensitive species for the habitat, and identified as to whether it is a mollusc or crustacean.

**Table 10. Example benthic community data set.**

Species Name	Abundance	Sensitive	Mollusc	Crustacean
<i>Acteocina inculta</i>	296	Yes	Yes	No
<i>Ampithoe valida</i>	9	Yes	No	Yes
<i>Capitella capitata</i> Cmplx	764	No	No	No
Chironomidae	17	No	No	No
Dipolydora sp	73	No	No	No
<i>Exogone lourei</i>	5	Yes	No	No
<i>Geukensia demissa</i>	1	No	Yes	No
<i>Grandidierella japonica</i>	1116	No	No	Yes
Harpacticoida	1	No	No	Yes
<i>Hemigrapsus oregonensis</i>	1	No	No	Yes
Lineidae	1	No	No	No
<i>Marphysa angelensis</i>	9	No	No	No
<i>Marphysa stylobranchiata</i>	2	No	No	No
<i>Mayerella acanthopoda</i>	1	No	No	Yes
<i>Mediomastus</i> sp	2	No	No	No
<i>Monocorophium insidiosum</i>	3	Yes	No	Yes
<i>Musculista senhousia</i>	27	No	Yes	No
Oligochaeta	1584	No	No	No
Podocopida	1	No	No	Yes
<i>Polydora nuchalis</i>	73	No	No	No
<i>Protothaca</i> sp	1	No	Yes	No
<i>Pseudopolydora paucibranchiata</i>	60	No	No	No
<i>Streblospio benedicti</i>	1459	No	No	No
<i>Tagelus subteres</i>	4	Yes	Yes	No
<i>Tryonia</i> sp	2	No	Yes	No
<i>Tubulanus</i> sp	1	No	No	No
Turbellaria	1	No	No	No

### Index of biotic integrity (IBI)

The IBI compares the values of four different metrics to the ranges expected under reference conditions. Each metric that is outside of the reference range increases the IBI score by one. Therefore, if all four metrics were inside the reference range, the score would be 0. Conversely, if all four were outside the reference range, the value would be 4.

The specific data needed to calculate the IBI are the total number of taxa, number of mollusc taxa, abundance of *Notomastus* sp., and number of sensitive taxa. The sensitive species list should be from the list for the station's habitat.

The first step is to calculate the percentage of sensitive taxa present. This is calculated as:

$$\% \text{ sensitive taxa} = (\text{number of sensitive taxa} / \text{total number of taxa}) \times 100$$

The IBI metric values for the sample data set are presented in Table 11. There were 27 different taxa represented in the sample, 6 of which were molluscs. There were no occurrences of the polychaete, *Notomastus sp.* Finally, there were 5 sensitive species in the sample, which represents 18.5% of the taxa.

**Table 11. IBI metrics for sample data set.**

Metric	Value
Total Number of Taxa	27
Number of Mollusc Taxa	6
Abundance of <i>Notomastus sp.</i>	0
Percentage of Sensitive Taxa	18.5

The next step is to compare the values for each of the metrics to a reference range for that specific metric (Table 12). The IBI score is set to zero before comparison to the thresholds. For each metric that is out of the reference range (above or below), the IBI score goes up by one.

For the sample data set, the total number of taxa, number of mollusc taxa and abundance of *Notomastus sp.* all fell within their reference ranges and therefore did not cause the IBI score to rise. However, the percentage of sensitive taxa was below the reference range and therefore caused the IBI score to rise by 1. The final IBI score for this data set is thus 1.

**Table 12. Reference ranges for IBI metrics.**

Metric	Reference Range
Total Number of Taxa	13 to 99
Number of Mollusc Taxa	2 to 25
Abundance of <i>Notomastus sp.</i>	0 to 59
Percentage of Sensitive Taxa	19 to 47.1

The final step is to compare the IBI score to the category thresholds (Table 13) in order to determine the IBI category and score. For the example, the IBI score of 1 corresponds to the Low Disturbance category with a category score of 2.

**Table 13. IBI category thresholds.**

IBI Score	Category	Category Score
0	Reference	1
1	Low Disturbance	2
2	Moderate Disturbance	3
3 or 4	High Disturbance	4

### Relative Benthic Index (RBI)

The RBI is the weighted sum of: (a) several community metrics, (b) the abundances of three positive indicator species, and (c) the presence of two negative indicator species.

The data needed to calculate the RBI are: total number of taxa, number of mollusc taxa, number of crustacean taxa, number of crustacean individuals, number of individuals of *Monocorophium insidiosum*, *Asthenothaerus diegensis*, and *Goniada littorea*, presence of *Capitella capitata* complex and presence of Oligochaeta.

The first step is to normalize the values for the benthic community metrics relative to the test sample habitat type. In the case of this example the data come from the Southern California Marine Bays habitat. These values are referred to as the scaled values. The calculations use the following four equations:

$$\begin{aligned} & \text{Total number of taxa}/99 \\ & \text{Number of mollusc taxa}/28 \\ & \text{Number of crustacean taxa}/29 \\ & \text{Abundance of Crustacea}/1693 \end{aligned}$$

The results of these calculations using the sample data set are shown in Table 14.

**Table 14. Raw and scaled RBI metrics.**

RBI Metric	Raw	Scaled
Total number of taxa	27	0.272727
Number of Mollusc taxa	6	0.214286
Number of Crustacean taxa	7	0.241379
Abundance of Crustacea	1132	0.668636

The next step is to calculate the Taxa Weighted Value (TWV). This is calculated by the equation:

$$\text{TWV} = \text{Scaled total number of taxa} + \text{Scaled number of mollusc taxa} + \text{Scaled number of crustacean taxa} + (0.25 \times \text{Scaled abundance of Crustacea})$$

For the sample data set the TWV= 0.89555.

Next, the value for the two negative indicator taxa (NIT) is calculated. The two negative indicator taxa are *Capitella capitata* complex and Oligochaeta. For each of these taxa that are present, in any abundance whatsoever, the NIT is decreased by 0.1. Therefore, if neither were found the NIT=0, if both are found the NIT=-0.2. For our example data, both taxa were present, so the NIT=-0.2.

The next step is to calculate the value for the three positive indicator taxa (PIT). The positive indicator taxa are *Monocorophium insidiosum*, *Asthenothaerus diegensis*, and *Goniada littorea*. First, the PIT value is calculated for each species using the following equations:

$$\frac{\sqrt[4]{\text{Abundance of } M.\text{insidiosum}}}{\sqrt[4]{473}}$$

$$\frac{\sqrt[4]{\text{Abundance of } A.\text{diegensis}}}{\sqrt[4]{27}}$$

$$\frac{\sqrt[4]{\text{Abundance of } G.\text{littorea}}}{\sqrt[4]{15}}$$

The three species PIT values are then summed to calculate the PIT value for the sample. If none of the three species is present, then the sample PIT = 0. For the example data, only *M. insidiosum* was present and the result of its calculation was 0.282205, which in the absence of the other species is also the PIT value.

The next step is to calculate the Raw RBI:

$$\text{Raw RBI} = \text{TWV} + \text{NIT} + (2 \times \text{PIT})$$

For the sample data set:

$$\text{Raw RBI} = 0.89555 + (-0.2) + (2 \times 0.282205) = 1.25996$$

The final calculation is for the RBI Score:

$$\text{RBI Score} = (\text{Raw RBI} - 0.03)/4.69$$

For the sample data set:

$$\text{RBI Score} = (1.25996 - 0.03)/4.69 = 0.26$$

The last step in the RBI process is to compare the RBI Score to a set of thresholds to determine the RBI category (Table 15). For the example, the RBI score falls into the Low Disturbance category, with a category score of 2.

**Table 15. RBI category thresholds.**

RBI Score	Category	Category Score
> 0.27	Reference	1
> 0.16 - ≤ 0.27	Low Disturbance	2
> 0.08 - ≤ 0.16	Moderate Disturbance	3
≤ 0.08	High Disturbance	4

Benthic Response Index (BRI)



The BRI is the abundance weighted pollution tolerance score of the organisms present in a given benthic community sample. The higher the BRI score, the more degraded the benthic community present in the sample.

Two types of data are needed to calculate the BRI, the abundance of each species and its pollution tolerance score, P. P values are not available for all species, only for species that were sufficiently abundant and occurred with sufficient frequency for calculation of P values in the BRI development data set. Only species for which P values are available are used in the BRI calculations. P values should be obtained for the appropriate habitat and from the most up-to-date list available.

The first step in the BRI calculation is to compute the 4<sup>th</sup> root of the abundance of each taxon in the sample for which P values are available. For the sample data set, the calculated values are found in Table 16. The next step is to multiply the 4<sup>th</sup> root abundance value by the P value, for each taxon (Table 16).

Next, separately sum all of the 4<sup>th</sup> roots of the abundances and all of the products of the 4<sup>th</sup> roots of abundance and P values (Table 16). Any taxa that lack P values are not included in either sum.

The next step is to calculate the BRI score as:

$$\frac{\sum (\sqrt[4]{Abundance}) \times P}{\sum \sqrt[4]{Abundance}}$$

For the sample data set the BRI score is 82.56.

The last step is to compare the BRI score to BRI threshold values in Table 17 to determine the BRI category and category score. For the example, the BRI corresponds to the High Disturbance category, with a category score of 4.

**Table 16. BRI component calculations for the sample data set.**

Taxon Name	Abundance	P	Abundance 4 <sup>th</sup> root	Abundance 4 <sup>th</sup> root x P
<i>Acteocina inculta</i>	296	110.15	4.1478	456.88
<i>Ampithoe valida</i>	9	90.96	1.7321	157.56
<i>Capitella capitata</i> Cmplx	764	130.84	5.2574	687.90
Chironomidae	17	138.87	2.0305	281.99
<i>Dipolydora sp</i>	73	56.56	2.9230	165.33
<i>Exogone lourei</i>	5	41.86	1.4953	62.59
<i>Geukensia demissa</i>	1	na <sup>1</sup>	na	na
<i>Grandidierella japonica</i>	1116	105.98	5.7798	612.57
Harpacticoida	1	32.91	1	32.91
<i>Hemigrapsus oregonensis</i>	1	60.70	1	60.70
Lineidae	1	3.96	1	3.96
<i>Marphysa angelensis</i>	9	97.82	1.7321	169.43
<i>Marphysa stylobranchiata</i>	2	94.27	1.1892	112.10
<i>Mayerella acanthopoda</i>	1	22.26	1	22.26
<i>Mediomastus sp</i>	2	57.84	1.1892	68.78
<i>Monocorophium insidiosum</i>	3	103.42	1.3161	136.11
<i>Musculista senhousia</i>	27	68.05	2.2795	155.12
Oligochaeta	1584	69.96	6.3087	441.35
Podocopida	1	na	na	na
<i>Polydora nuchalis</i>	73	108.42	2.9230	316.91
<i>Protothaca sp</i>	1	55.94	1	55.94
<i>Pseudopolydora paucibranchiata</i>	60	81.68	2.7832	227.34
<i>Streblospio benedicti</i>	1459	61.83	6.1804	382.11
<i>Tagelus subteres</i>	4	37.28	1.4142	52.73
<i>Tryonia sp</i>	2	127.95	1.1892	152.16
<i>Tubulanus sp</i>	1	0.61	1	0.61
Turbellaria	1	44.95	1	44.95
Sum			58.8708	4860.23

<sup>1</sup> P value not available for taxon.

**Table 17. BRI category thresholds and category scores**

BRI Score	Category	Category Score
< 39.96	Reference	1
≥ 39.96 - < 49.15	Low Disturbance	2
≥ 49.15 - < 73.27	Moderate Disturbance	3
≥ 73.27	High Disturbance	4

#### River Invertebrate Prediction and Classification System (RIVPACS)

The RIVPACS index calculates the number of reference taxa present in the test sample (observed or “O”) and compares it to the number expected to be present (“E”) in a reference sample from the same habitat. Calculation of the RIVPACS score is a three-step process. The first step consists of determining the reference station group within the

Southern California Marine Bays habitat to which the station belongs. This determination is made based on the station's bottom depth, latitude, and longitude. These three parameters are used with a discriminant function to estimate the probability that the station belongs to each reference station group.

The expected number of reference site species for the station is calculated in the second step. Since each reference station group may contain a different number of reference species, the expected number of reference species for the test station example is determined using the probabilities of reference group membership calculated in step 1. The expected number of reference site species (E) for the sample data set is 4.447.

The final step consists of calculating the RIVPACS score (O/E). The number of reference site species present in the sample data set (O) is five. The RIVPACS score is therefore 1.124 (5/4.447).

The score is then compared to the thresholds in Table 18 to determine the RIVPACS category and category score. For the example, the RIVPACS score corresponds to the Low Disturbance category, with a category score of 2.

**Table 18. RIVPACS category thresholds and category scores.**

RIVPACS Score	Category	Category Score
> 0.90 - < 1.10	Reference	1
> 0.74 - ≤ 0.90 or ≥ 1.10 - < 1.26	Low Disturbance	2
> 0.32 to ≤ 0.74 or ≥ 1.26	Moderate Disturbance	3
≤ 0.32	High Disturbance	4

#### Benthic Community Index Integration

The benthic community LOE category is based on the integration of the four benthic index category scores. The integration is accomplished by calculating the median of the four individual index category scores. If the median falls between two adjacent categories, the value is rounded up. For the sample data set, the index category scores were 2, 2, 2 and 4 for the IBI, RBI, RIVPACS, and BRI, respectively. The median for those values is 2. Therefore, the benthic community LOE for the example is Low Disturbance.

## Final Station Assessment

The final station assessment is determined by the combination of the three LOE categories. There are 64 possible LOE combinations, each of which corresponds to one of six station assessments: Unimpacted, Likely Unimpacted, Possibly Impacted, Likely Impacted, Clearly Impacted, and Inconclusive (Table 19). To determine the station assessment, simply match each of the LOE categories for the sample to those in the table. For the example, the chemistry LOE was Moderate Exposure, the benthic community LOE was Low Disturbance and toxicity LOE was Low Toxicity. These categories correspond to combination number 38 in Table 19 and a station assessment of Possibly Impacted.

**Table 19. Final station assessment categories and LOE combinations. Results corresponding to the sample data are in bold text.**

Combination	Chemistry LOE	Benthic Community LOE	Toxicity LOE	Station Assessment
1	Minimal	Reference	Nontoxic	Unimpacted
2	Minimal	Reference	Low	Unimpacted
3	Minimal	Reference	Moderate	Unimpacted
4	Minimal	Reference	High	Inconclusive
5	Minimal	Low	Nontoxic	Unimpacted
6	Minimal	Low	Low	Likely unimpacted
7	Minimal	Low	Moderate	Likely unimpacted
8	Minimal	Low	High	Possibly impacted
9	Minimal	Moderate	Nontoxic	Likely unimpacted
10	Minimal	Moderate	Low	Likely unimpacted
11	Minimal	Moderate	Moderate	Possibly impacted
12	Minimal	Moderate	High	Likely impacted
13	Minimal	High	Nontoxic	Likely unimpacted
14	Minimal	High	Low	Inconclusive
15	Minimal	High	Moderate	Possibly impacted
16	Minimal	High	High	Likely impacted
17	Low	Reference	Nontoxic	Unimpacted
18	Low	Reference	Low	Unimpacted
19	Low	Reference	Moderate	Likely unimpacted
20	Low	Reference	High	Possibly impacted
21	Low	Low	Nontoxic	Unimpacted
22	Low	Low	Low	Likely unimpacted
23	Low	Low	Moderate	Possibly impacted
24	Low	Low	High	Possibly impacted
25	Low	Moderate	Nontoxic	Likely unimpacted
26	Low	Moderate	Low	Possibly impacted
27	Low	Moderate	Moderate	Likely impacted
28	Low	Moderate	High	Likely impacted
29	Low	High	Nontoxic	Likely unimpacted
30	Low	High	Low	Possibly impacted
31	Low	High	Moderate	Likely impacted
32	Low	High	High	Likely impacted
33	Moderate	Reference	Nontoxic	Unimpacted

Combination	Chemistry LOE	Benthic Community LOE	Toxicity LOE	Station Assessment
34	Moderate	Reference	Low	Likely unimpacted
35	Moderate	Reference	Moderate	Likely unimpacted
36	Moderate	Reference	High	Possibly impacted
37	Moderate	Low	Nontoxic	Unimpacted
<b>38</b>	<b>Moderate</b>	<b>Low</b>	<b>Low</b>	<b>Possibly impacted</b>
39	Moderate	Low	Moderate	Possibly impacted
40	Moderate	Low	High	Possibly impacted
41	Moderate	Moderate	Nontoxic	Possibly impacted
42	Moderate	Moderate	Low	Likely impacted
43	Moderate	Moderate	Moderate	Likely impacted
44	Moderate	Moderate	High	Likely impacted
45	Moderate	High	Nontoxic	Possibly impacted
46	Moderate	High	Low	Likely impacted
47	Moderate	High	Moderate	Likely impacted
48	Moderate	High	High	Likely impacted
49	High	Reference	Nontoxic	Likely unimpacted
50	High	Reference	Low	Likely unimpacted
51	High	Reference	Moderate	Inconclusive
52	High	Reference	High	Likely impacted
53	High	Low	Nontoxic	Likely unimpacted
54	High	Low	Low	Possibly impacted
55	High	Low	Moderate	Likely impacted
56	High	Low	High	Likely impacted
57	High	Moderate	Nontoxic	Likely impacted
58	High	Moderate	Low	Likely impacted
59	High	Moderate	Moderate	Clearly impacted
60	High	Moderate	High	Clearly impacted
61	High	High	Nontoxic	Likely impacted
62	High	High	Low	Likely impacted
63	High	High	Moderate	Clearly impacted
64	High	High	High	Clearly impacted