**DRAFT**

**Fine Sediment Biotic Index (FSBI) Calculator User Guide**

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**Tool Description**

The Fine Sediment Biotic Index (FSBI) calculator is an R software tool for calculating FSBI values for macroinvertebrate samples. The Idaho Department of Environmental Quality (DEQ) Lewiston Regional Office developed this tool to calculate FSBI from external macroinvertebrate data.

**Fine Sediment Biotic Index**

FSBI is a macroinvertebrate index for assessing stream substrate fine sediment (< 2 mm) impacts on macroinvertebrate community composition in northwest U.S. streams (Relyea et al. 2012). FSBI was developed and validated using macroinvertebrate and stream substrate fine sediment data from multiple government agency monitoring programs in northwest. Relyea et al. (2012) assigned taxa-level FSBI scores reflecting taxa sensitivity to substrate fine sediment for taxa common in the northwest U.S. Taxa-level FSBI scores were assigned based on the % fines < 2 mm values for the taxa’s 75th percentile occurrence (Table 1). FSBI values for a macroinvertebrate sample are calculated as the sum of taxa FSBI values across all unique taxa present in a sample. Sample FSBI values are based on taxa occurrence only and are not based on taxa abundance.

Table 1. Taxa-level FSBI scores and basis from Relyea et al. (2012)

|  |  |  |
| --- | --- | --- |
| **% fines < 2 mm at 75th Occurrence Percentile** | **Category** | **Taxon FSBI score** |
| 0-20% | Extremely fine sediment sensitive | 20 |
| 21-30% | Very fine sediment sensitive | 15 |
| 31-40% | Moderately fine sediment sensitive | 10 |
| 41-50% | Slightly fine sediment sensitive | 5 |

In Relyea et al. 2012, sample FSBI values ranged from 0 to ~350, and FSBI values decrease as % fines < 2 mm increases. High FSBI scores indicate many sediment-sensitive taxa are present, whereas low FSBI scores indicate few sediment-sensitive taxa are present.

**Software Requirements**

The tool requires R, R Studio, and Microsoft Excel software. The ‘renv’ R package also must be installed and loaded. The R scripts use ‘renv’ to manage package dependencies and ensure the exact R package versions used to develop the tool are applied when using the tool.

**Instructions**

1. **Download and save the tool.** Download and save the tool into a folder. The tool includes R scripts, an ‘fsbI\_calculator\_inputs’ folder, and an ‘fsbi\_calculator\_output’ folder. Do not change the file organization structure.
2. **Open ‘FSBI\_calculator.Rproj’.** This requires R studio.
3. **Populate excel input template.** Enter data into the ‘sample\_taxa’ and ‘taxa\_fsbi’ tabs in the excel file within the ‘fsbi\_calculator\_inputs’ folder. Use ‘Save As’ to change the file name if desired.
   1. **sample\_taxa tab.** Data in the sample\_taxa tab should be one row per sample/taxa combination. Agency, project, and site values should be the same for each unique sample. The tool will calculate sample FSBI values for each unique agency/project/site/sample combination.
      1. agency - organization that collected data
      2. project - data collection project name
      3. site - site name associated with sample
      4. sample - unique sample identifier
      5. taxa - name of taxa observed
      6. additional columns can be added if desired.
   2. **taxa\_fsbi tab.** This tab should include taxa FSBI scores for each unique taxa in the ‘sample\_taxa’ tab. The tool user must assign taxa-level FSBI scores to each unique taxa, where applicable. Users should assign taxa FSBI scores only for taxa that match those in Relyea et al. 2012 or are equivalent to those in Relyea et al. 2012 after nomenclature changes. In cases where Relyea et al. 2012 assigned a taxa FSBI score to a genus (ex: *Megarcys*), one should NOT assume all species within the genus have the same taxa FSBI score. Use the taxa resolution at which Relyea et al. 2012 developed FSBI taxa scores. The tool will screen for and identify taxa that are in the ‘sample\_taxa’ tab, but not in the ‘taxa\_fsbi’ tab.
   3. **relyea\_fsbi.** This tab does not require any user input and should not be modified. It is a list of taxa-level FSBI scores from Relyea et al. 2012 for reference.
4. **R script user inputs.** Open the R script ‘user\_input\_for\_FSBI\_calculator.R’ and specify a name for the calculation to be conducted, the name of the input excel file, and the name of the tabs from steps 3a and 3b above.
5. **Run the tool.** Open ‘calculates\_sample\_FSBI.R’ and run the script (In R studio, click ‘Source’).
6. **Outputs.** An excel file with tool outputs will be saved in the ‘fsbi\_calculator\_output’ folder. Output tabs include:
   1. **user\_inputs -** inputs entered into the R script and date/time the calculation was run
   2. **input\_macro\_data - ­**same as ‘sample\_taxa’ input tab
   3. **input\_taxa\_fsbi -** same as ‘taxa\_fsbi’ input tab
   4. **Relyea\_taxa\_fsbi** - same as ‘relyea\_fsbi’ input tab
   5. **Merged -** data from ‘input\_macro\_data’ tab plus, assigned FSBI taxa score for each taxa. The ‘taxa\_missing\_flag’ column has value “Y” if a taxa is present in ‘input\_macro\_data’, but not in ‘input\_taxa\_fsbi’.
   6. **Calculated\_sample\_fsbi** - calculated sample FSBI values. ‘n\_FSBI\_taxa’ indicates the number of taxa in the sample with a taxa-level FSBI score.
   7. **Duplicate sample taxa -** lists duplicate sample/taxa combinations in input data. The tool filters for unique sample/taxa combinations, and only uses unique sample/taxa values for sample FSBI calculations. The list of duplicates is provided as an FYI.
7. **User Checks.** Generally, running the tool will be an iterative process. Users should check outputs for issues (taxa\_missing\_flag values or ‘NA’ site values in ‘merged’ tab, duplicate sample taxa, etc.), modify the input data as needed, and then re-run the script.

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**References**

Relyea, C.D., Minshall, W., Danehy, R.J. 2012. Development and validation of an aquatic fine sediment biotic index. *Environmental Management*. 49: 242-252.