**Benthic Macroinvertebrate Bioassessment Exercise using the Chesapeake Bay and New River Virginia Streams as example data.**

* Code was created by Emma Jones, Water Team Leader, at Virginia Department of Environmental Quality
* Code was edited, data source and cleaned and questions created by Sergio Sabat-Bonilla, PhD candidate at Virginia Tech.

**File names and descriptions:**

1. Please read this first. **SCI\_Calculation\_Guide.md**: This guide walks you through calculating Stream Condition Index (SCI) using two related indices: Virginia Stream Condition Index (VSCI) and Virginia Coastal Plain Macroinvertebrate Index (VCPMI). This file will step you through how to set up your data, where to save your files, what each file in the folder does and what data are required. \*Scroll down to see all file content in case you can’t open the associated .md file type.
2. Once you have run the code and generated scores, you can add context and questions to help students learn more about their streams. Here is an example from our Freshwater Biomonitoring Class at Virginia Tech:

**Example questions for students:**

* Virginia Stream Condition Index (VSCI) Scores: what is the average and variance associated with each of the 3 sites?  You can display this as a table or as a figure.
* What sites are showing an average that is above the VSCI threshold for impairment?
* What metrics are most different across the 3 sites?
* What metrics are most variable within the same sites?
* What are the taxa at the Family Level that are most responsible for influencing the differences in VSCI scores?
* Explain how total abundance is affecting the VSCI and explain.
* Using <https://wikiwatershed.org/model/> to model your watershed and generate the land cover by % - what are differences in the surrounding land use among your sites?
* Use the Composite VSCI scores and compare the average VSCI or a site with the composite site. Then, explain what metrics were different that likely were responsible for the differences in VSCI Score. Are there shared characteristics among the taxa driving the VSCI scores like tracheated gills, long life cycle, or strong fliers?

**Supportive literature:**

**SCI\_Calculation\_Guide.md copied below**

## \*\*2. Install Required R Packages\*\*

Open R or RStudio and run:

```r

install.packages(c("tidyverse", "lubridate", "lazyeval"))

```

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## \*\*3. Place All Required Files in the Same Folder\*\*

The following files are \*\*mandatory\*\* for the script to run:

1. \*\*Updated\_SCI Calculation 3 ways.Rmd\*\* – Main analysis script.

2. \*\*Updated\_rarifyFunction.R\*\* – Function to rarefy counts to 110.

3. \*\*VCPMI\_metrics\_GENUS.R\*\* – Metric calculation script for VCPMI.

4. \*\*VSCI\_metrics\_GENUS.R\*\* – Metric calculation script for VSCI.

5. \*\*masterTaxaGenus.csv\*\* – Master taxa list with tolerance values and traits.

6. \*\*stationInfoBenSampsTESTSITE.csv\*\* – Station metadata (site, collection date, etc.).

7. \*\*stationBenthicsTESTSITE.csv\*\* – Benthic macroinvertebrate data.

> \*\*Tip:\*\* Keep them all in one folder to avoid path issues.

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## \*\*4. Open and Edit the Script\*\*

1. Open \*\*Updated\_SCI Calculation 3 ways.Rmd\*\* in RStudio.

2. Check that all file paths in the script match your folder structure.

- For example:

```r

masterTaxaGenus <- read.csv("masterTaxaGenus.csv")

stationBenSamps <- read\_csv("stationInfoBenSampsTESTSITE.csv")

stationBenthics <- read\_csv("stationBenthicsTESTSITE.csv")

```

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## \*\*5. Source the Required Scripts\*\*

The main R Markdown file automatically loads:

```r

source("VSCI\_metrics\_GENUS.R")

source("VCPMI\_metrics\_GENUS.R")

source("Updated\_rarifyFunction.R")

```

Ensure these files are present in the working directory.

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## \*\*6. Run the Script\*\*

You have two options:

### \*\*Option A: Run Entire Script\*\*

- In RStudio, click \*\*Knit\*\* → \*\*Knit to HTML\*\* to generate a report with results.

### \*\*Option B: Run Line by Line\*\*

- Highlight and run each chunk (`Ctrl + Enter`) to inspect outputs at each stage.

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## \*\*7. Output Files\*\*

- The script saves results to CSV files:

- `VASCI\_rarefied.csv` (example output for VSCI)

- Similar CSV outputs will be generated for VCPMI +63 and VCPMI -65.

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## \*\*8. Troubleshooting\*\*

- If you get a "file not found" error → check that all required CSV and R scripts are in the same folder.

- If you get a "package not found" error → install the missing package using `install.packages()`.

- If column names in your data differ from the template, match them exactly to avoid errors.

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## \*\*Contact\*\*

For questions on SCI methodology, contact \*\*Emma Jones\*\* (emma.jones@deq.virginia.gov).