Quick tutorial
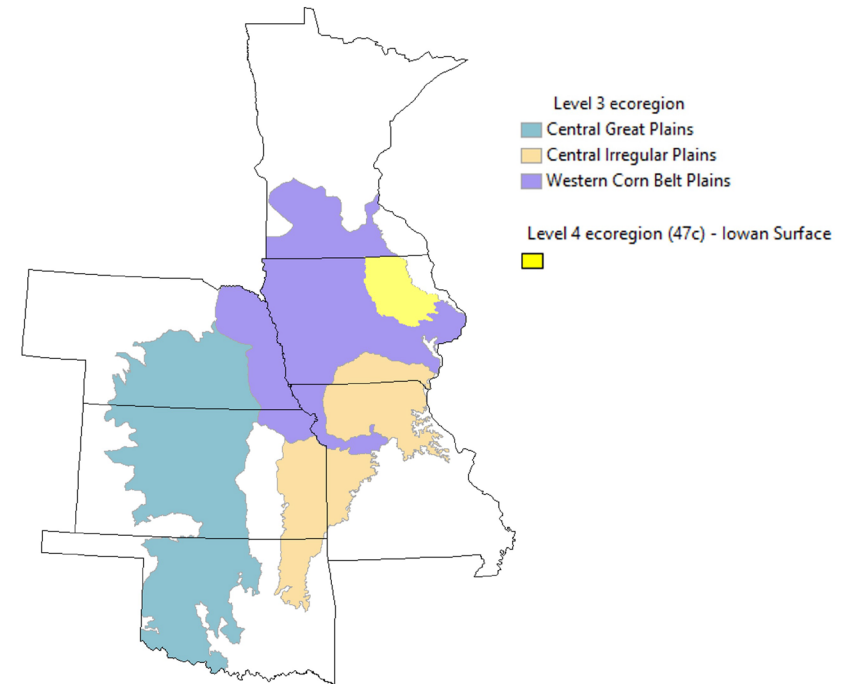
Great Plains Shiny app

https://tetratech-wtr-wne.shinyapps.io/GreatPlainsBCGCalc/

This R-based tool calculates Biological Condition Gradient (BCG) scores for macroinvertebrate and fish assemblages in Great Plains streams.

Level 3 ecoregion
Central Great Plains
Central Irregular Plains
Western Corn Belt Plains

Level 4 ecoregion (47c) - Iowan Surface

Requirements

Users do not need R on their computers to run the Shiny app, nor do they need to have any familiarity with R.

To run the Shiny app you need:

- Internet access*
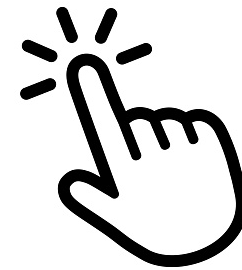- Intermediate-level computer skills (need to be able to browse, upload and download files, unzip files)

For those who prefer to work with R, the functions are carried out by the BCGcalc and BioMonTools R packages, which are available on GitHub and were developed by Erik W. Leppo from Tetra Tech (Erik.Leppo@tetratech.com).

*If using the R code instead of the Shiny app, you won't need internet access if you have R installed on your computer and have downloaded all the necessary packages.
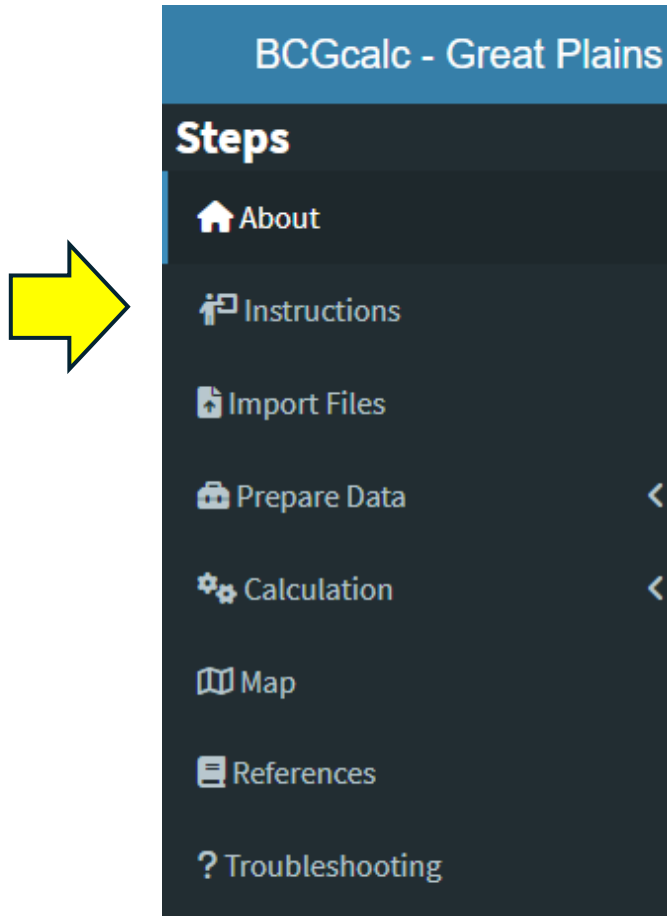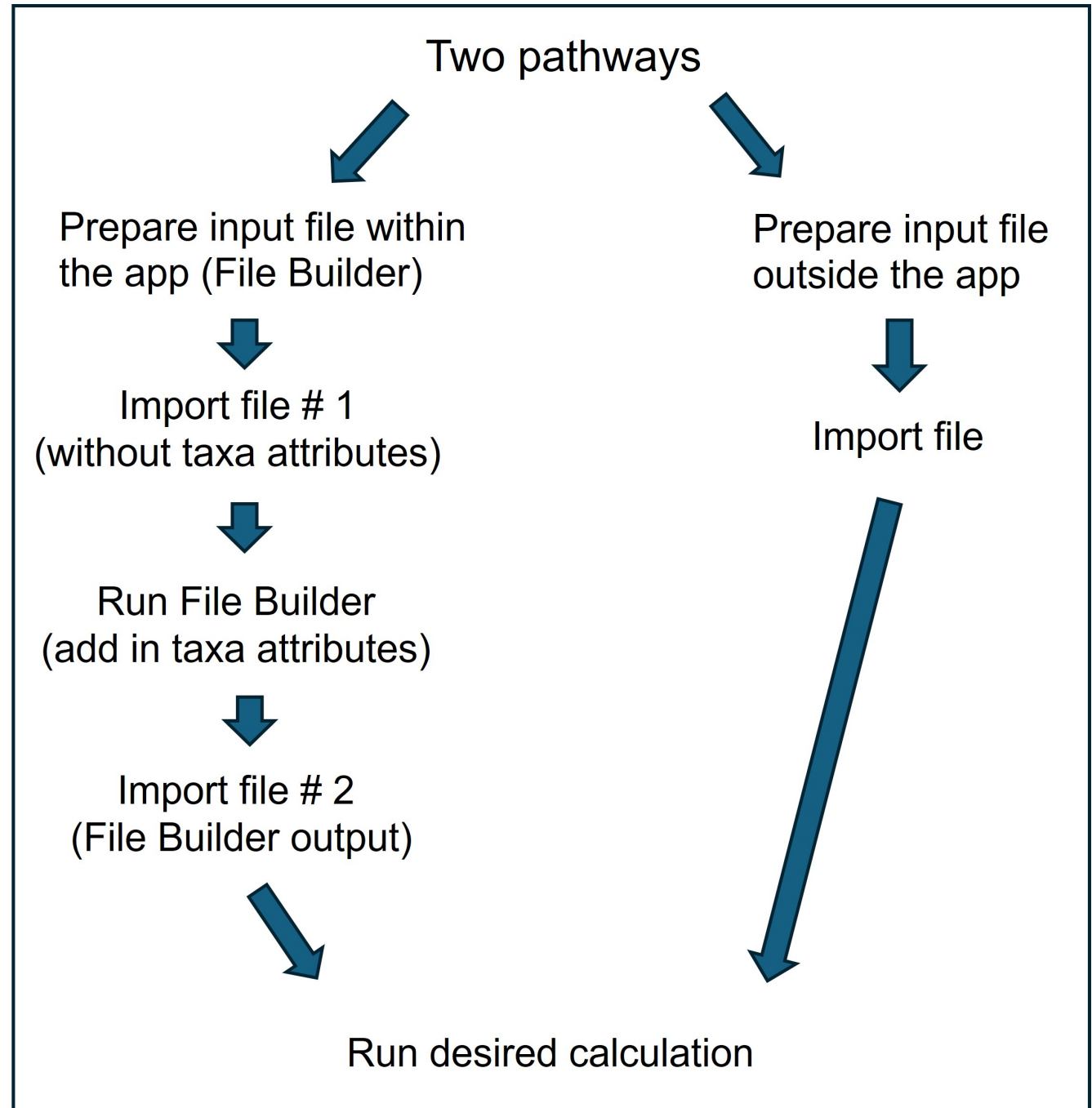
How the app works

Click buttons to
- Upload files
- Run the calculators
- Download results
- Unzip results

Instructions, test files and metadata

Workflow

Two pathways

Prepare input file within the app (File Builder)

Import file # 1
(without taxa attributes)

Run File Builder
(add in taxa attributes)

Import file # 2
(File Builder output)

Prepare input file outside the app

Import file

Run desired calculation

Time saver tip

Some internet browsers, like Google Chrome and Mozilla Firefox, allow you to change settings so that you can select which folder to download files to (versus files going to the default Download folder).

- Mozilla Firefox: go to Settings > General > Files and Applications > Check box for "always ask where to save files."

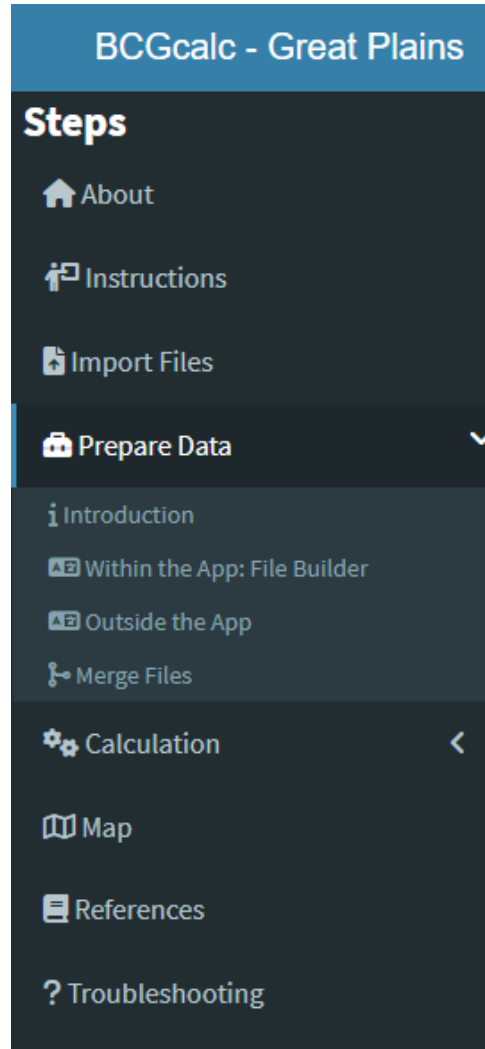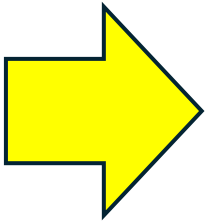- [Google Chrome file saving tip](#) [PDF]

Step 1: Set up a directory

This is the folder where you'll be saving your files

Step 2: Prepare input file

Steps
- About
- Instructions
- Import Files
- **Prepare Data**
  - Introduction
  - Within the App: File Builder
  - Outside the App
  - Merge Files
- Calculation
- Map
- References
- Troubleshooting

These pages contains instructions

Decide on a pathway

Option 1: Use the **Within the App: File Builder** function. Why?
- Fewer required fields
- Ensures use of proper Operational Taxonomic Units (OTUs) and attributes for the calculations
- More flexibility on names of column headings

Option 2: Generate a file **Outside of the app** that is ready to go (i.e., has all the required fields, with exact column heading names).

If using **Option 2 (Outside the app)**, skip to the Calculation step below.

Step 2: Prepare input file with File Builder

What does File Builder do?

The File Builder joins the taxon name in the input file with the 'original taxaID' column in the Taxa Translator table and performs two functions:

- Translates the original taxon name to the proper Operational Taxonomic Unit (OTU) for the calculation (for example, collapses worms to Oligochaeta).

- Adds in new columns with taxa attributes and hierarchy (e.g., Order, Family) that are needed for the metric calculations.

File Builder input file – required content

Required fields for all calculations. *Column names are flexible (use drop-down menus to match).*

Column Name	Domain (allowable entries)	Description
Index_Name	GP_Fish_BCG, IA_Bugs_BCG, KS_Bugs_BCG, MO_Bugs_BCG, NE_Bugs_BCG	Tells R which calculation to run
Index_Class	see table below for list of options	Tells R which rules and metrics to apply, based on class
SampleID	NA (flexible)	Unique sample identifier (typically comprised of the site name, sample date, and replicate number)
TaxaID	NA (flexible)	Taxon name, using the BCG Operational Taxonomic Unit (OTU)
N_Taxa	non-negative real numbers; for large/rare entries, -99, 0 or blank	Number of individuals

There is **one additional required field for the Iowa bug BCG** (column name must match exactly):

- BugGear (text entries: Qualitative, Surber, Hess, Artificial Substrate, Low-Flow Artificial Substrate and Anchored Artifical Substrate)

Optional fields (e.g., SiteID, latitude, longitude, collection date) can be selected as well and will be carried through into the output file.

IMPORTANT! When selecting optional fields, do not include Life Stage or other fields that would cause a taxon to occur in more than one row for a given sample (which could lead to double-counting of that taxon in the richness metrics).

Step 3: Import File # 1

Must be a comma-separated file (CSV). It can include **data for multiple samples, sites and Index Classes** (versus being limited to one sample at a time).
File uploads are limited to a maximum of 200 MB in size.
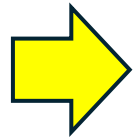
Step 4: Run File Builder

The name of the file that you uploaded will appear here. Confirm that it is the correct file.

IMPORTANT! The BCG models are calibrated for specific collection and processing protocols. Make sure you are using the Great Plains BCG model that is appropriate for your samples.

File Builder – enter required fields

BCGcalc - Great Plains

Steps

- About
- Instructions
- Import Files
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  - Within the App: File Builder
  - Outside the App
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- Calculation
- Map
- References
- Troubleshooting

File Builder: Taxa Translate and Attribute Assignment

Only columns specified below will be carried through into the output file.

A. Upload a File

If no file name showing below repeat 'Import File' in the left sidebar.

'BugBCG_Iowa_FileBuilder_Test1_20240730.csv'

B. Select Calculation.

Calculation

Great Plains BCG (IA Bugs)   ← ==Select calculation==

C. User File Column Names

Required Fields

If the default values are present they will be auto-populated.

Column, Unique Sample Identifier (e.g., SampleID)

BugSeriesID

Column, TaxaID (Scientific Name)

FinalID

Column, Taxa Count (number of individuals or N_Taxa)

SumOfIndiv

Column, Index Class (e.g., Index_Class)

INDEX_CLASS

Prepare an input file with *File Builder*

The BCG models are calibrated for specific collection and processing protocols. Make sure you are using the BCG model tha...

- Bug methods [PDF]
- Fish methods [PDF]

EXAMPLE INPUT FILES

- Bugs [ZIP]
- Fish [ZIP]

The File Builder joins the taxon name in the input file with the 'original taxaID' column in the Taxa Translator table and per...

- Translates the original taxon name to the proper OTU for the calculation.
- ...utes and hierarchy (e.g., Order, Family) that are needed for the metric calculatio...

The input file must be a comma-separated file (CSV).

Index Name and Index Class are required for all calculations (they tell R which BCG rules and IBI metrics to apply). See tabl...

The input file must be a comma-separated file (CSV). It can include data for multiple samples, sites and Index Classes.

Required fields for all calculations. Column names are flexible (use drop-down menus to match).

==Enter the **required fields**==
==Drop-down boxes allow for flexibility with==
==column names (match with the appropriate==
==columns in the input file).==

Column	Data			Description
		ntries)		
				...ch calculation to ...
				...s and metr...
				Unique sample identifier (ty... sample date, and replicate n...
TaxaID	flexible	text	NA (flexible)	Taxon name, using the BCG...

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File Builder – enter required fields continued...

B. Select Calculation.

Calculation

Great Plains BCG (IA Bugs) ▼

C. User File Column Names

Required Fields

If the default values are present they will be auto-populated.

Column, Unique Sample Identifier (e.g., SampleID)

BugSeriesID ▼

Column, TaxaID (Scientific Name)

FinalID ▼

Column, Taxa Count (number of individuals or N_Taxa)

SumOfIndiv ▼

Column, Index Class (e.g., Index_Class)

INDEX_CLASS ▼

Additional Fields

There is one additional required field (BugGear) for Iowa bug samples. Optional fields (e.g., SiteID, collection date) can be selected as well. IMPORTANT! Do not include Life Stage or other fields that might cause a taxon to occur in more than one row for a given sample (which could lead to double-counting of that taxon in the richness metrics).

Columns to Keep in Output

BugGear ← **BugGear (Iowa bugs only)**

D. Run Operation

This button will merge the user file with the official taxa file

Run Operation

E. Download Output

The File Builder joins the taxon name in the input file with the 'original taxaID' column in the Taxa Translator table and perform

- Translates the original taxon name to the proper OTU for the calculation.
- Adds in new columns with taxa attributes and hierarchy (e.g., Order, Family) that are needed for the metric calculations.

The input file must be a comma-separated file (CSV).

Index Name and Index Class are required for all calculations (they tell R which BCG rules and IBI metrics to apply). See tables a

The input file must be a comma-separated file (CSV). It can include data for multiple samples, sites and Index Classes.

Required fields for all calculations. Column names are flexible (use drop-down menus to match).

Column Name	Name	Data Type	Domain (allowable entries)	Description
Index_Name	flexible	text	GP_Fish_BCG, IA_Bugs_BCG, KS_Bugs_BCG,	Tells R which calculation to run

There is **one additional required field for the Iowa bug BCG** (column name must match exactly): BugGear

Optional fields (e.g., SiteID, collection date) can be selected under 'Columns to Keep in Output' as well.
IMPORTANT! Do not include Life Stage or other fields that might cause a taxon to occur in more than one row for a given sample (which could lead to double-counting of that taxon in the richness metrics).

Optional fields (e.g., SiteID, latitude, longitude, collection date) can be selected as well and will be carried through into the File taxon to occur in more than one row for a given sample

Below are the unique combinations of INDEX_NAME and INDEX_CLASS and descriptions of how sites should be correctly assig

Fish

Index_Name	INDEX_CLASS	Description

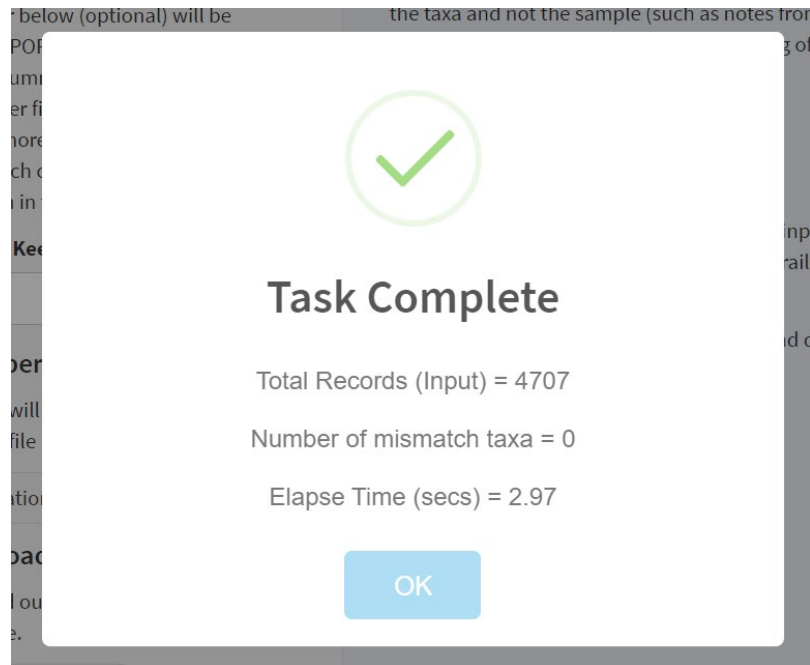# File Builder – Run Operation

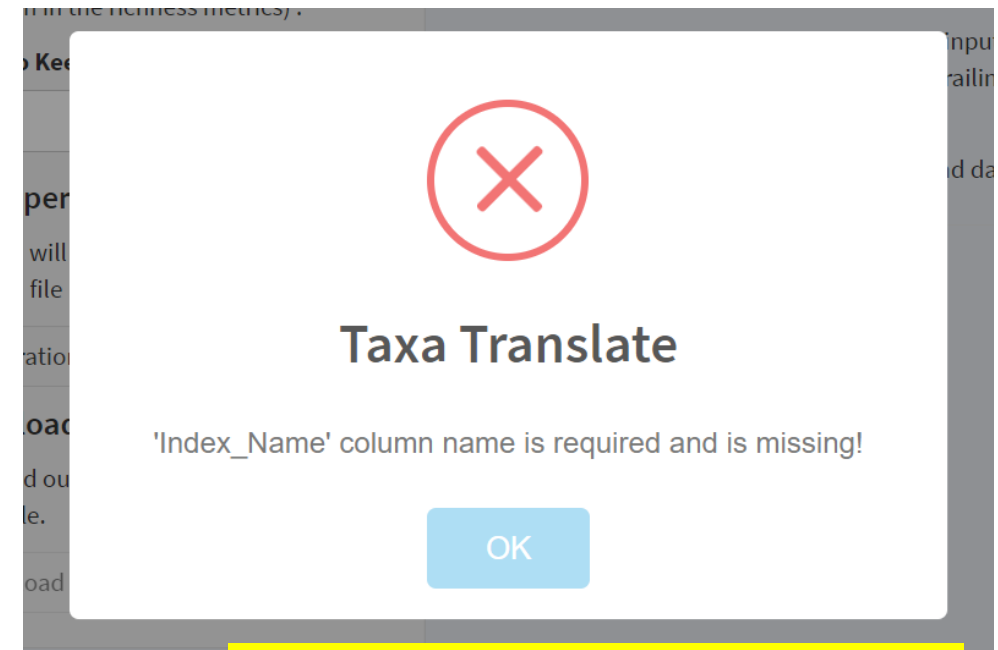**Click on the Run Operation button**

File Builder – prompt box

When the File Builder has finished running, **a prompt box will appear**. It will notify you if your File Builder run was successful or failed.
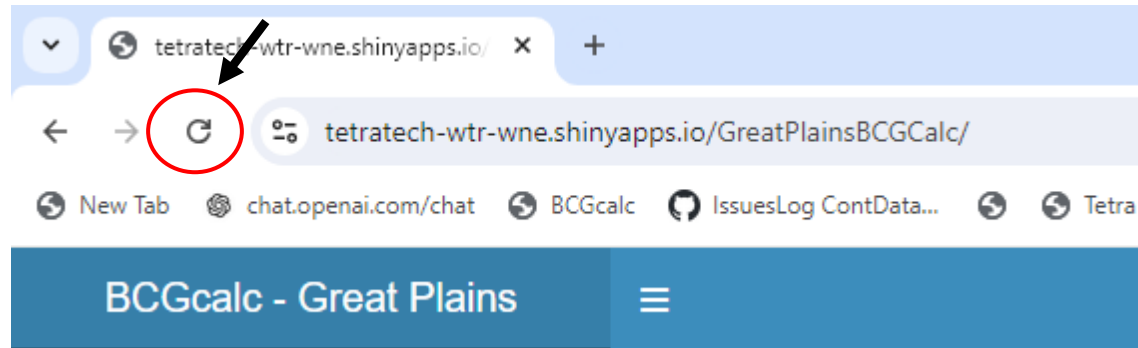
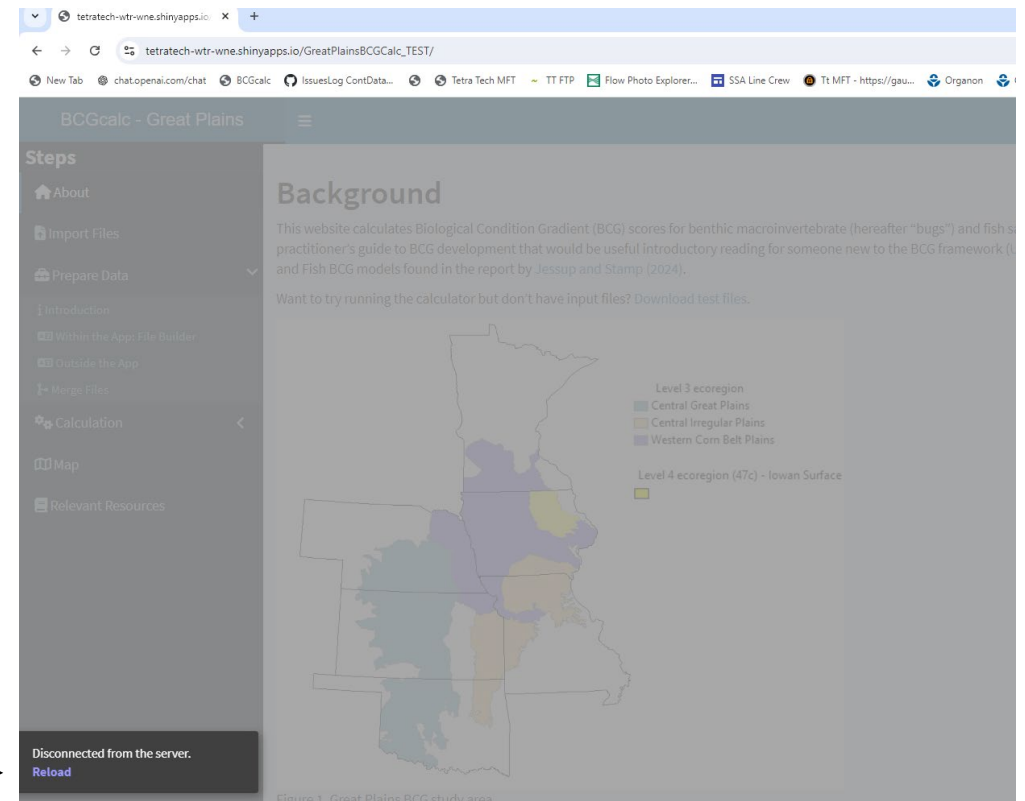Success!

Failure!

Will alert you to missing columns

Refresh the Shiny app

In some cases, the screen will gray out (meaning the Shiny app has crashed or timed out) and you'll have to refresh or reload the app, investigate potential problems with your input file, and try again.

Refresh button (upper left corner)

Reload if app crashes (gray screen)

File Builder – Download Results

Index_Class ▾

Select Additional Required Fields (which vary by Calculation – see table on right).

Columns need to be named exactly as shown on the right. Optional fields (e.g., SiteID, collection date) can be selected as well. IMPORTANT! Do not include the same field twice and do not include Life Stage or other fields that might cause a taxon to occur in more than one row for a given sample (which could lead to double-counting of that taxon in the richness metrics).

Columns to Keep in Output

GP.RR

D. Run Operation

This button will merge the user file with the official taxa file

Run Operation

E. Download Output

All input and output files will be available in a single zip file.

⭳ Download Results ⟵ The 'Download Results' button will become clickable when the files are ready to download. Click the button and save the zipped file to the directory. The file will either automatically go to the Download folder or, if you use the Time Saver tip with Google Chrome or Mozilla Firefox (see slide 6), you can browse to the desired folder and save it there.

Unzip
File Builder results

Subfolders within the 'results' folder

Unzip the file
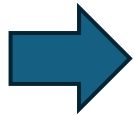
A 'results' folder will appear

_user_input ← original input file

reference ← taxa translator and taxa attributes tables, list of index names and classes

results_Bugs_IA_BCG

results_Bugs_KS_BCG

results_Bugs_MO_BCG

results_Bugs_NE_BCG

results_Fish_BCG

File Builder & Calculation results. These subfolders will vary depending on selected calculation(s).

Users must unzip/extract the files or else the files won't be seen as an option to upload for the next step. After files are unzipped, the original zipped files can be deleted if desired.

Unzipping files

For whatever reason, 7zip (free) seems to work better than the Microsoft default zip extractor with our Shiny apps (but if you can't get 7zip, the Microsoft option should work ok).

7zip (https://www.7-zip.org/)

File Builder outputs

Output file	Description
BCG_TaxaTranslator_modify	see which taxa names were modified during the Taxa Translation process (filter by Modified_woCAPS = TRUE)
BCG_TaxaTranslator_nonmatch	taxa in your input file that don't match with the taxa list in the Taxa Translator table
BCG_TaxaTranslator_source	shows which calculation was selected, which Operational Taxonomic Unit (OTU) column was used, and which versions of the Taxa Translator and Attribute tables were used
BCG_TaxaTranslator_TAXAATTR	input file is now ready to go! The taxa names have been translated to the proper OTU and attributes and hierarchy added in. Import this file into the Shiny app and run the desired calculation.

Non-matching taxa

Task Complete

Total Records (Input) = 4707

Number of mismatch taxa = 0

Elapse Time (secs) = 2.97

OK
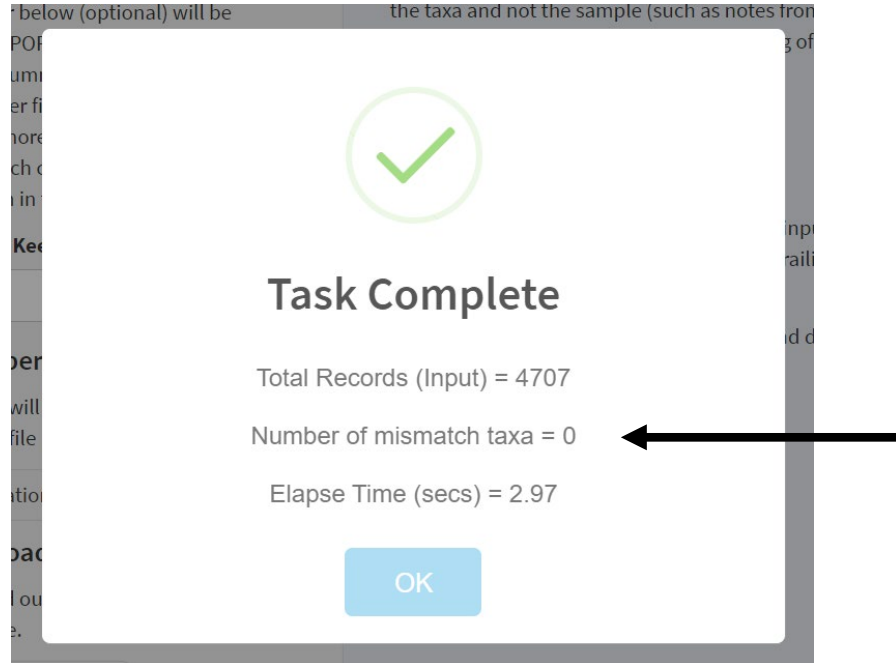
What if there are non-matching taxa?
Open the 'BCG_TaxaTranslator_nonmatch' file and view the list of non-matching taxa. If the non-matches are due to a misspelling, extra space or other small issue, fix the non-matching taxa in your input file, re-upload the file via the 'Import File' tab, and rerun the File Builder (and to prevent confusion, delete the first set of output files with the non-matching taxa). If the non-matching taxa are legitimate taxa that need to be added to the Taxa Translator table, notify Jen.Stamp@tetratech.com and Tetra Tech will update the Taxa Translator table as soon as resources permit.

Example 📁 results_Fish_BCG ⟶

BCG_TaxaTranslator_modify.csv
BCG_TaxaTranslator_nonmatch.csv
BCG_TaxaTranslator_source.csv
BCG_TaxaTranslator_TAXAATTR.csv

Step 5: Import File #2

Import the newly created 'BCG_TaxaTranslator_TAXAATTR' file

BCG_TaxaTranslator_modify.csv
BCG_TaxaTranslator_nonmatch.csv
BCG_TaxaTranslator_source.csv
BCG_TaxaTranslator_TAXAATTR.csv

Example   results_Fish_BCG ⟶

1. Browse to the file

2. Status bar will tell you when the upload is complete

3. A file preview will appear. Check to make sure everything looks ok.

Step 6: Run desired calculation

BCGcalc - Great Plains

Steps
- About
- Instructions
- Import Files
- Prepare Data
- Calculation
- BCG Models
- Map
- References
- Troubleshooting

Calculate BCG Models

This function will render all steps and make available files for download.

A. Upload a file

If no file name showing below repeat 'Import File' in the left sidebar.

'BugBCG_KDHE_Formatted_Test1_20240730.csv'

B. Define Community (for metrics)

Community

Bugs_KS

C. Mark Redundant (Non-Distinct) Taxa

Download RedundantTaxa.docx

☑ Generate Redundant Taxa Column

D. Define BCG Model

Determined by Community chosen in Step B.

E. Run Calculations

This button will calculate metrics values, metric memberships, level membership, and level assignment.

Run Calculations

F. Download Results

All input and output files will be available in a single zip file.

⬇ Download Results

The name of the file that you uploaded will appear here. Confirm that it is the correct file.

Select model

Default is for R/Shiny app to mark redundant taxa

Click Run Calculation button

The 'Download Results' button will become clickable when the files are ready to download
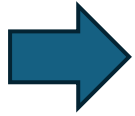
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BCG calculator workflow

✓ Mark non-distinct taxa (excluded from richness metrics)
✓ Calculate metric values each sample
✓ Calculate metric membership values for each sample
✓ Assign membership in each BCG level

Unzip Calculation results

Unzip
the file

Subfolders within the 'results' folder
(depending on which calculation(s) you run)

results_Bugs_IA_BCG

results_Bugs_KS_BCG

results_Bugs_MO_BCG

results_Bugs_NE_BCG

results_Fish_BCG

_BCG_RESULTS.csv
_BCG_RESULTS.html
BCG_1markexcl.csv
BCG_2metval_BCG.csv
BCG_2metvall_all.csv
BCG_3metmemb.csv
BCG_3metrules.csv
BCG_4levmemb.csv
BCG_5levassign.csv
BCG_6levflags.csv
BCG_6metflags.csv

Calculation
output files

BCG_TaxaTranslator_modify.csv
BCG_TaxaTranslator_nonmatch.csv
BCG_TaxaTranslator_source.csv
BCG_TaxaTranslator_TAXAATTR.csv

File
Builder
files

After files are unzipped, the original zipped files can be deleted if desired.

Unzip Calculation results

You will receive a prompt like this when you unzip the Calculation results file.

Click 'Yes to All'
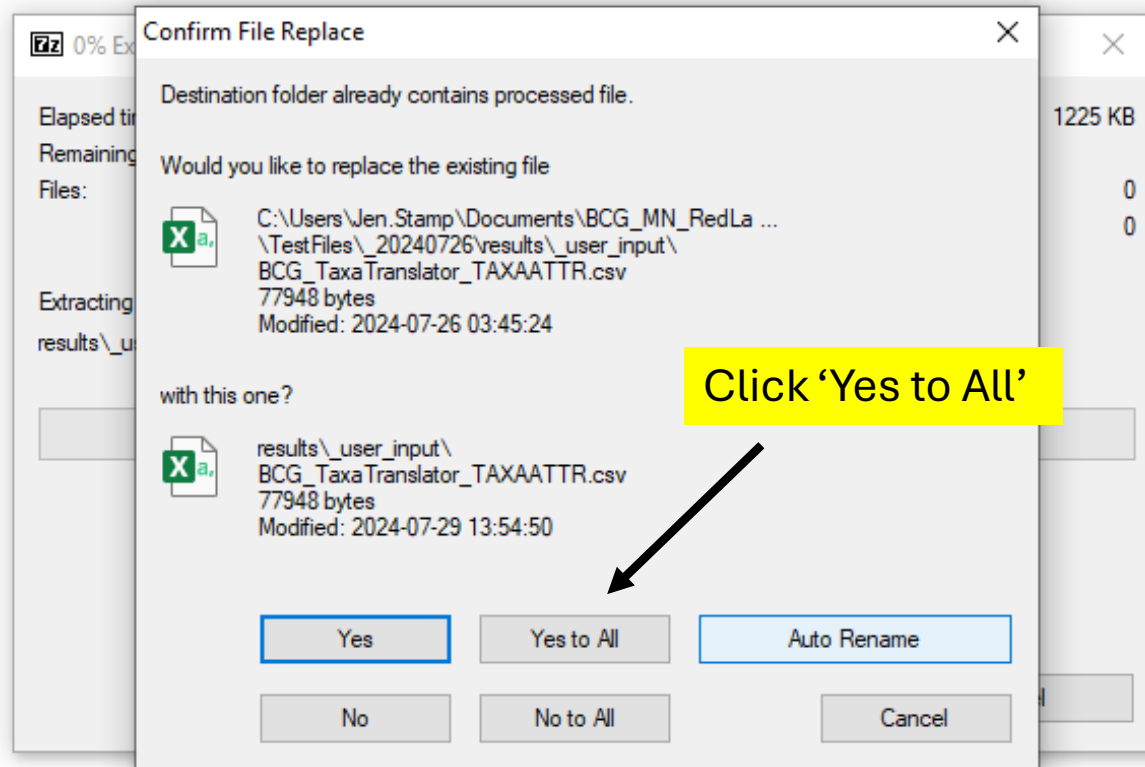
See Instructions page
for guidance on interpreting the results

Metadata for interpreting output files

Questions?
Comments?

We're always looking for feedback on ways we can improve the Shiny app.

Jen.Stamp@tetratech.com