Quick tutorial

MN Shiny app

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

This R-based tool calculates Biological Condition Gradient (BCG) and Index of Biological Integrity (IBI) scores for macroinvertebrate and fish assemblages in Minnesota streams.

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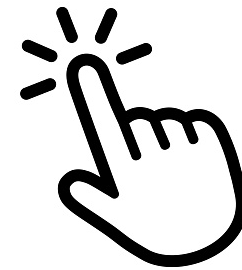- Intermediate-level computer skills (need to be able to browse, upload and download files, unzip files)

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.
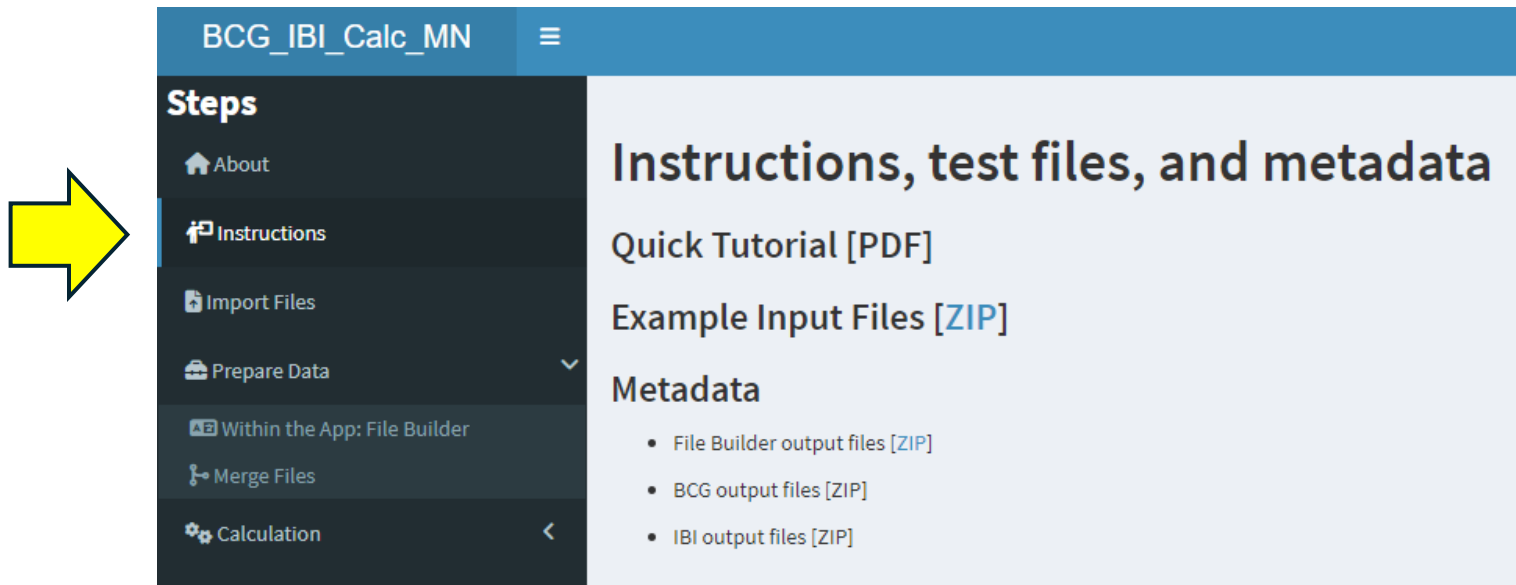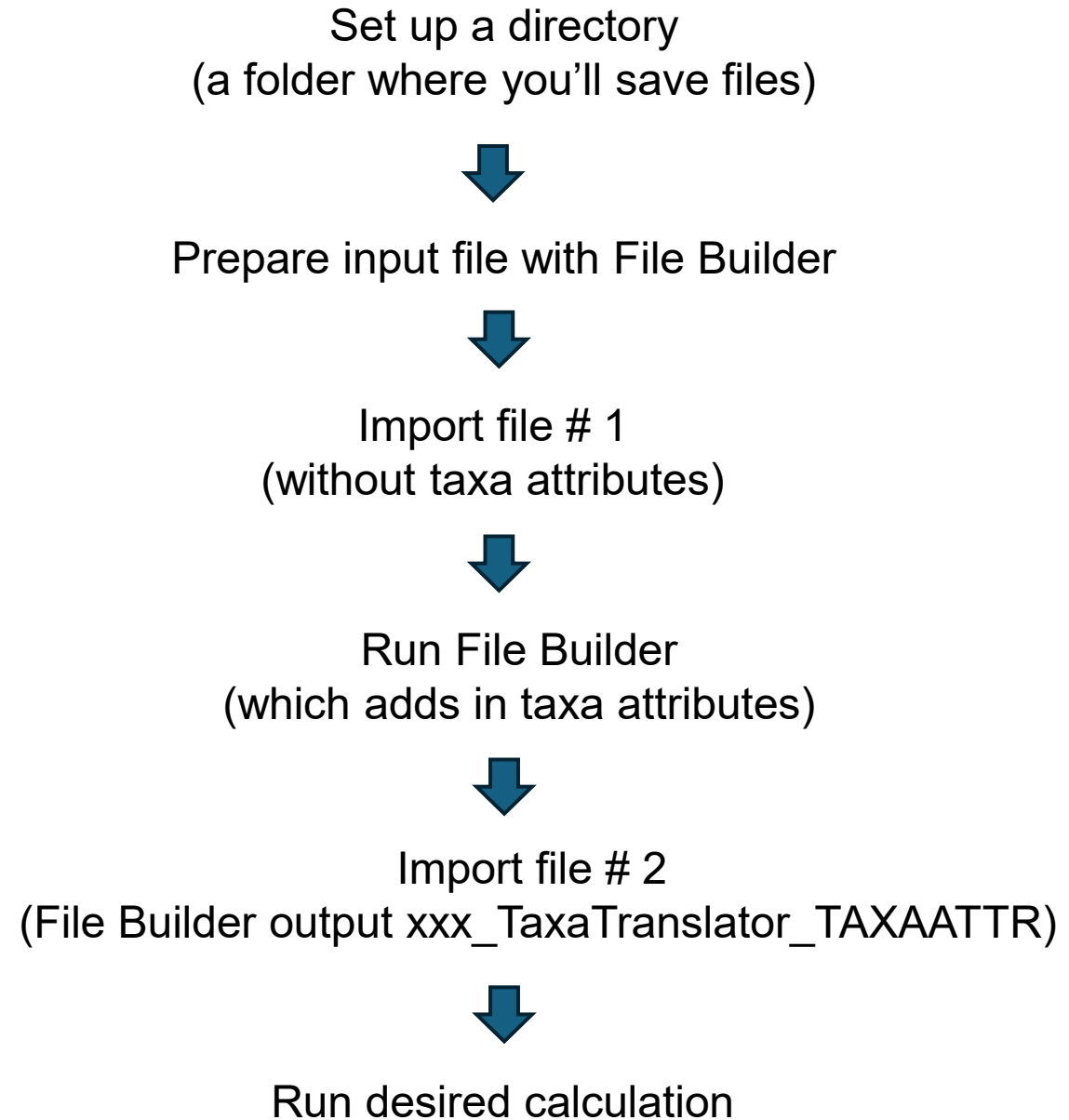
How the app works

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

Instructions, test files and metadata

Workflow

Set up a directory
(a folder where you'll save files)

⬇

Prepare input file with File Builder

⬇

Import file # 1
(without taxa attributes)

⬇

Run File Builder
(which adds in taxa attributes)

⬇

Import file # 2
(File Builder output xxx_TaxaTranslator_TAXAATTR)

⬇

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."

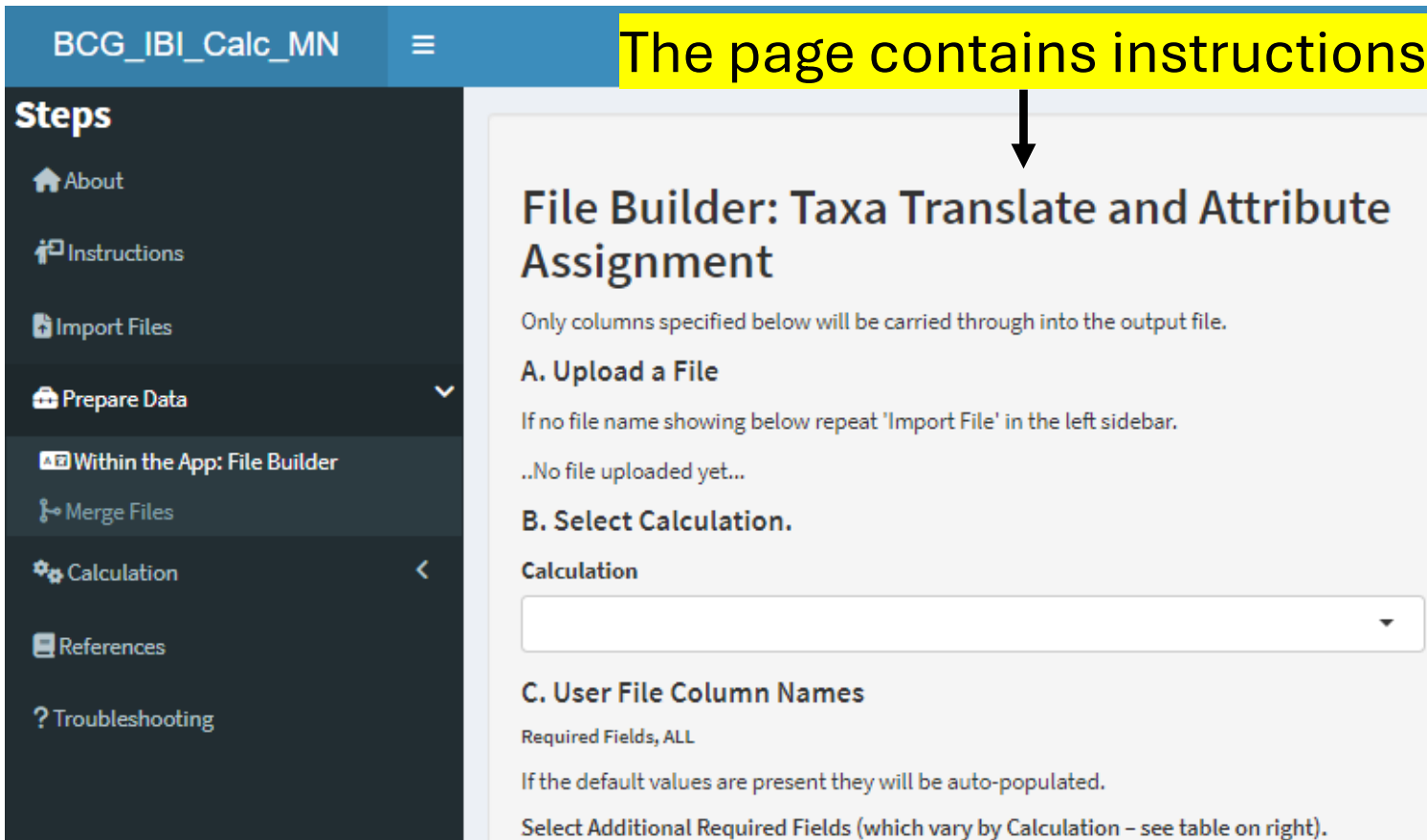- [Google Chrome file saving tip](#) [PDF]

Step 1: Set up a directory

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

Step 2: Prepare File Builder input file

IMPORTANT: the input file **can include data for multiple samples, sites and Index Classes** (versus being limited to one sample at a time).

The page contains instructions

BCG_IBI_Calc_MN ≡

Steps

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🧰 Prepare Data ⌄

🔤 Within the App: File Builder

⌿ Merge Files

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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.

..No file uploaded yet...

B. Select Calculation.

Calculation

[▼]

C. User File Column Names

Required Fields, ALL

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

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

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

Some columns are required for all calculations, and others are specific to a particular calculation.

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

Column name (flexible)	MN_BCG_Bugs	MN_IBI_Bugs	MN_BCG_Fish	MN_IBI_Fish
Unique sample ID (e.g., SampleID)	x	x	x	x
Taxon name (e.g., TaxaID)	x	x	x	x
Count (e.g., N_Taxa)	x	x	x	x
Index_Name (MN_IBI_Bugs, MN_IBI_Fish, MN_BCG)	x	x	x	x
Index_Class (e.g., fish5)	x	x	x	x

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

Additional required fields for specific calculations . Column names must match exactly with what is shown here.

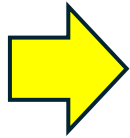| Column name (must match exactly)	MN_BCG_Bugs	MN_IBI_Bugs	MN_BCG_Fish	MN_IBI_Fish
GP.RR	x			
LargeRareCount		x		
N_Anomalies				x
DRAINSQMI		x	x	x
GRADIENT				x
Distance_m				x

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).
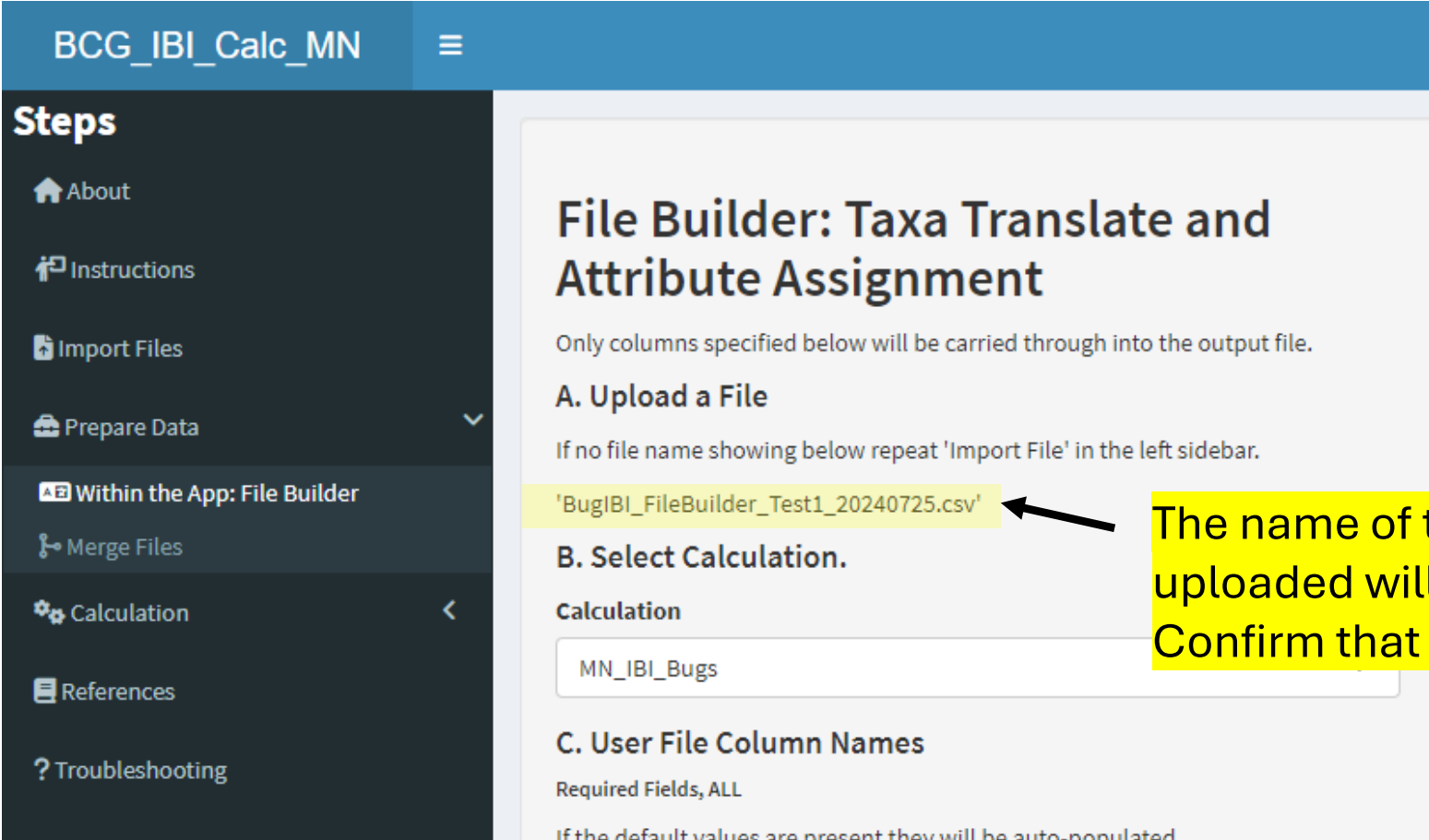File uploads are limited to a maximum of 200 MB in size.

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 4: Run File Builder

File Builder – enter required fields

A. Upload a File

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

'BugBCG_FileBuilder_Test1_20240725.csv'

B. Select Calculation.

Calculation

MN_BCG_Bugs ← Select calculation

C. User File Column Names

Required Fields, ALL

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

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

SampleID

Column, TaxaID

Taxonomic.Name

Column, Taxa Count (number of individuals or N_Taxa)

Count

Column, Index Name (e.g., Index_Name)

Index_Name

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

Index_Class

- Translates the original taxon name to the proper 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

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).

Some columns are required for all calculations, and others are specific to a particular calculation. Allowable entries are shown

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

Column name (flexible)	MN_BCG_Bugs	MN_IBI_Bugs	MN_BCG_Fish	MN_IBI_Fish
Unique sample ID (e.g., SampleID)	x	x	x	x
Taxon name (e.g., TaxaID)	x	x	x	x
Count (e.g., N_Taxa)	x	x	x	x
Index_Name (MN_IBI_Bugs, MN_IBI_Fish, MN_BCG)	x	x	x	x
MRCA Class (e.g., Index_Class)	x	x	x	x

wn here.

| DRAINSQMI | x | x | x | |
| GRADIENT | | | | x |

Enter the required fields
Ones with drop-down boxes are required for all calculations and can have flexible column names (use drop-downs to match with the appropriate columns in the input file).

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File Builder – enter required fields continued...

Column, Taxa Count (number of individuals or N_Taxa)

Count

Column, Index Name (e.g., Index_Name)

Index_Name

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

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. I... same field twice and do not include Life Stage o... taxon to occur in more than one row for a given s... double-counting of that taxon in the richness me...

Columns to Keep in Output

GP.RR

D. Run Operation

This button will merge the user file with the offic...

Run Operation

E. Download Output

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

Download Results

Additional required fields for specific calculations . Column names must match exactly with what is shown here.

Column name (must match exactly)	MN_BCG_Bugs	MN_IBI_Bugs	MN_BCG_Fish	MN_IBI_Fish
GP.RR	x			
LargeRareCount		x		
N_Anomalies				x
DRAINSQMI		x	x	x
GRADIENT				x
Distance_m				x

...de, collection date) ...n be carried through into the output file.

...e.g., do not include Samp...D and Taxon Name twice), and do not include Life Stage or other fields tha... ...ch could lead to double-... ...nting of that taxon in the richness metrics).

...ith each column liste... ...e previous tables.

Fields that are only required for specific calculations do NOT have flexible column names. They need to be named exactly as shown in the instructions.

			Domain (a... ...ntri	Description
		...e)		Unique sample identifier (typically comprised of the site name, samp...
TaxaID	flexible	text	NA (flexible)	Taxon name, using the BCG Operational Taxonomic Unit (OTU)
N_Taxa	flexible	numeric	non-negative real number	Number of individuals
Index_Name	flexible	text	MN_IBI_Bugs, MN_IBI_Fish, MN_BCG	Tells R which calculation to run
Index_Class	flexible	text	list of options [CSV]	Tells R which rules and metrics to apply, based on class (e.g., northe...

File Builder – Run Operation

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

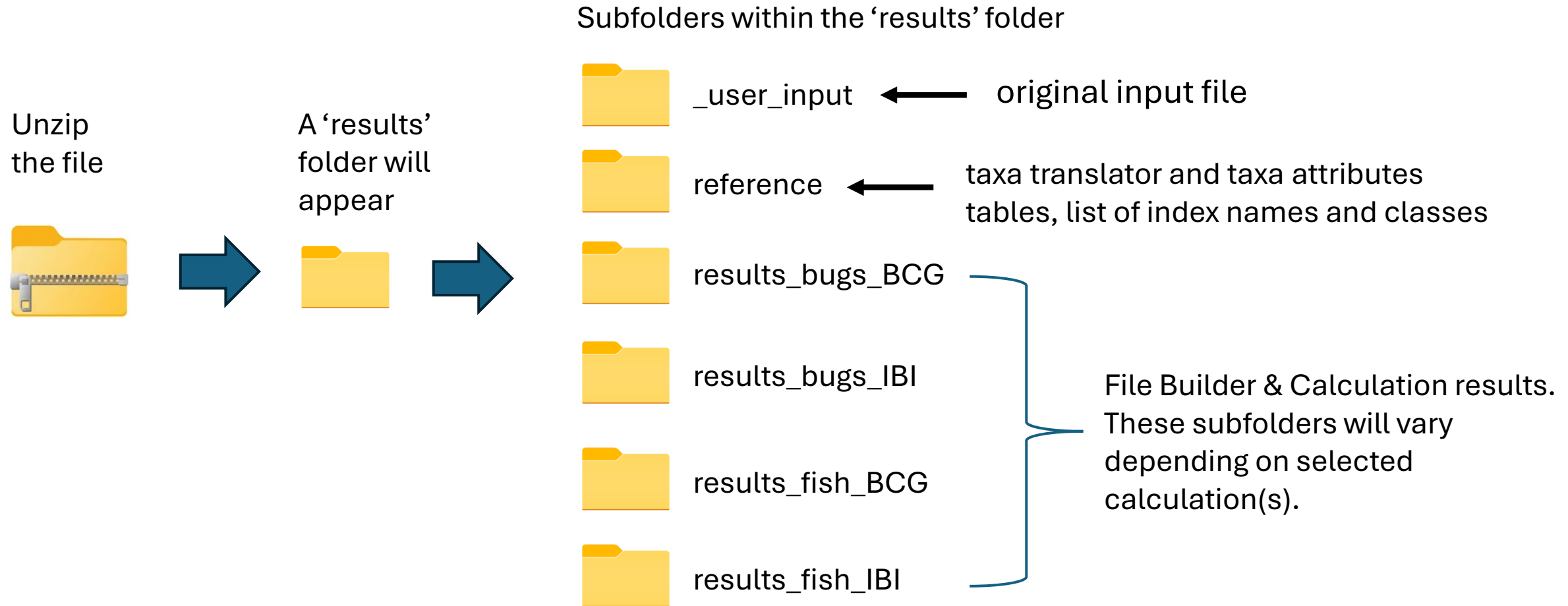This button will merge the user file with the official taxa file

Run Operation ←——————— **Click on the Run Operation button**

E. _____ **Output**

All _____ put files will be available in a single zip file.

⬇ Download Results

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!
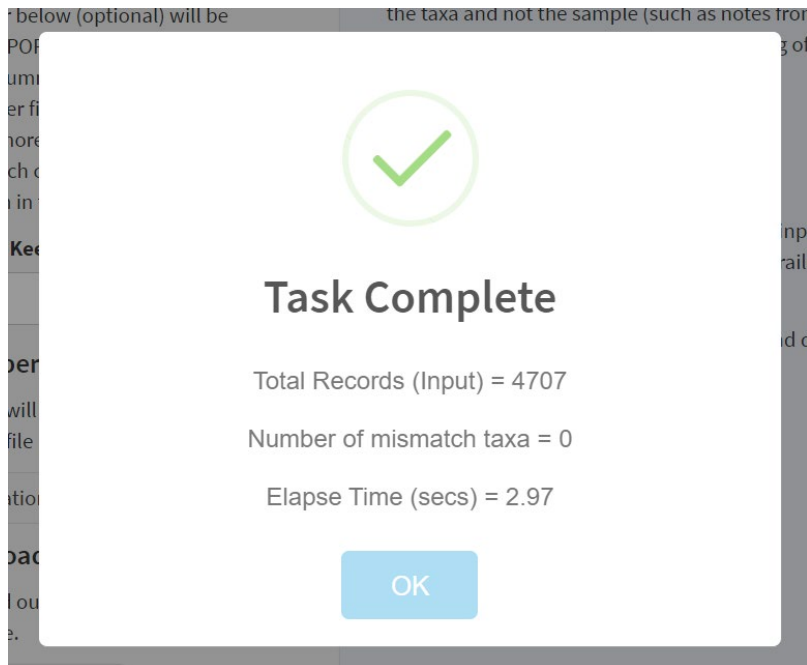
Failure!
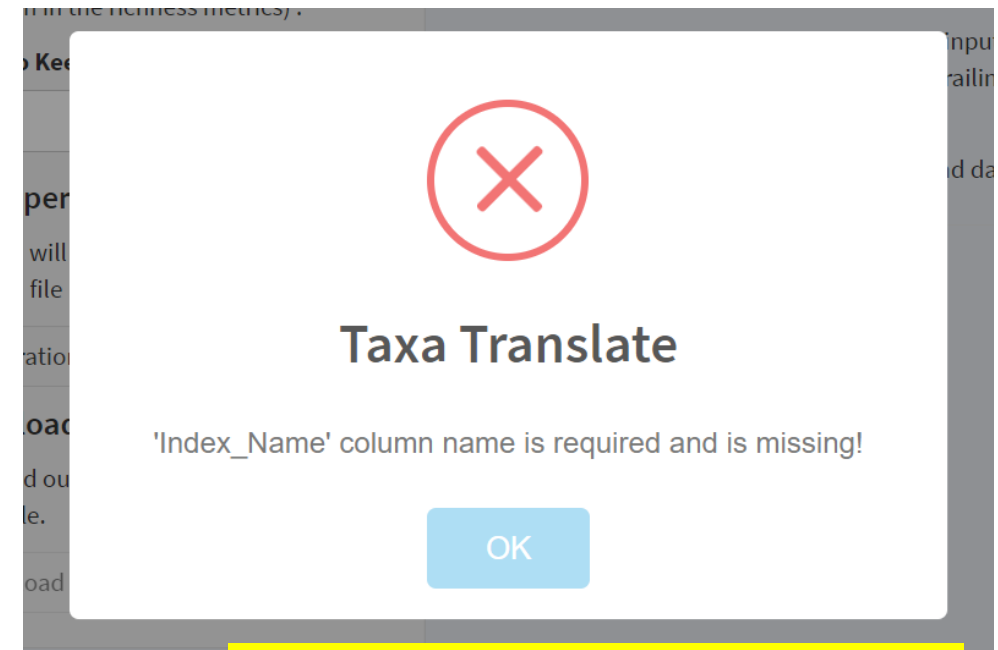
Will alert you to missing columns

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 the app, investigate potential problems with your input file, and try again.

Refresh button (upper left corner)

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.

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Unzip File Builder results

Unzip
the file

A 'results'
folder will
appear

Subfolders within the 'results' folder

📁 _user_input ← original input file

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

📁 results_bugs_BCG

📁 results_bugs_IBI

📁 results_fish_BCG

📁 results_fish_IBI

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
XXX_TaxaTranslator_modify	see which taxa names were modified during the Taxa Translation process (filter by Modified_woCAPS = TRUE)
XXX_TaxaTranslator_nonmatch	taxa in your input file that don't match with the taxa list in the Taxa Translator table
XXX_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
XXX_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

Total Records (Input) = 4707

Number of mismatch taxa = 0

Elapse Time (secs) = 2.97
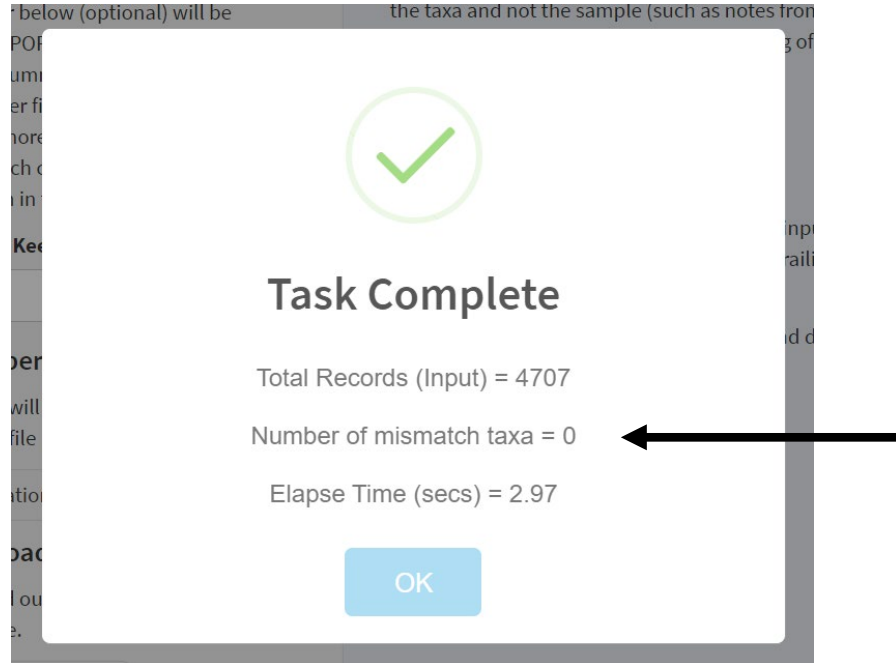
What if there are non-matching taxa?
Open the 'XXX_TaxaTranslator_nonmatch' file and view the list of non-matching taxa. If the non-matches are due to a misspelling, extra space or other small issue, fix the non-matching taxa in your input file, re-upload the file via the 'Import File' tab, and rerun 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_bugs_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 'XXX_TaxaTranslator_TAXAATTR' file

BCG_TaxaTranslator_modify.csv

BCG_TaxaTranslator_nonmatch.csv

BCG_TaxaTranslator_source.csv

Example   📁   results_bugs_BCG   ➡   BCG_TaxaTranslator_TAXAATTR.csv

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

BCG_IBI_Calc_MN ☰

Steps
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- ⚙ Calculation ⌄
- 🏅 BCG Models
- 👥 IBI Models
- 📕 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.

'BCG_TaxaTranslator_TAXAATTR.csv'

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

B. Define Community (for metrics)

Community

bugs ▼

Select assemblage

C. Mark Redundant (Non-Distinct) Taxa

Download RedundantTaxa.docx

☑ Generate Redundant Taxa Column

Default is for R/Shiny app to mark redundant taxa

D. Define BCG Model

Determined by INDEX_NAME and INDEX_CLASS in data input file.

E. Run Calculations

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

Run Calculations

Click Run Calculation button

F. Download Results

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

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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

IBI calculator workflow

- ✓ Mark non-distinct taxa (excluded from richness metrics)
- ✓ Calculate metric values for each sample
- ✓ Calculate metric scores for each sample
- ✓ Calculate overall IBI score for each sample

Unzip Calculation results

Unzip
the file
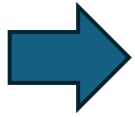
Subfolders within the 'results' folder

results_bugs_BCG

results_bugs_IBI

results_fish_BCG

results_fish_IBI

_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
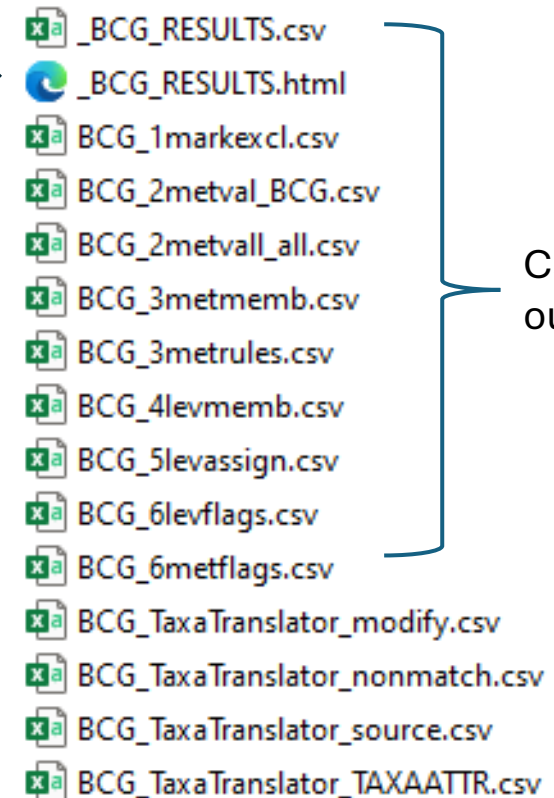
Calculation output files

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

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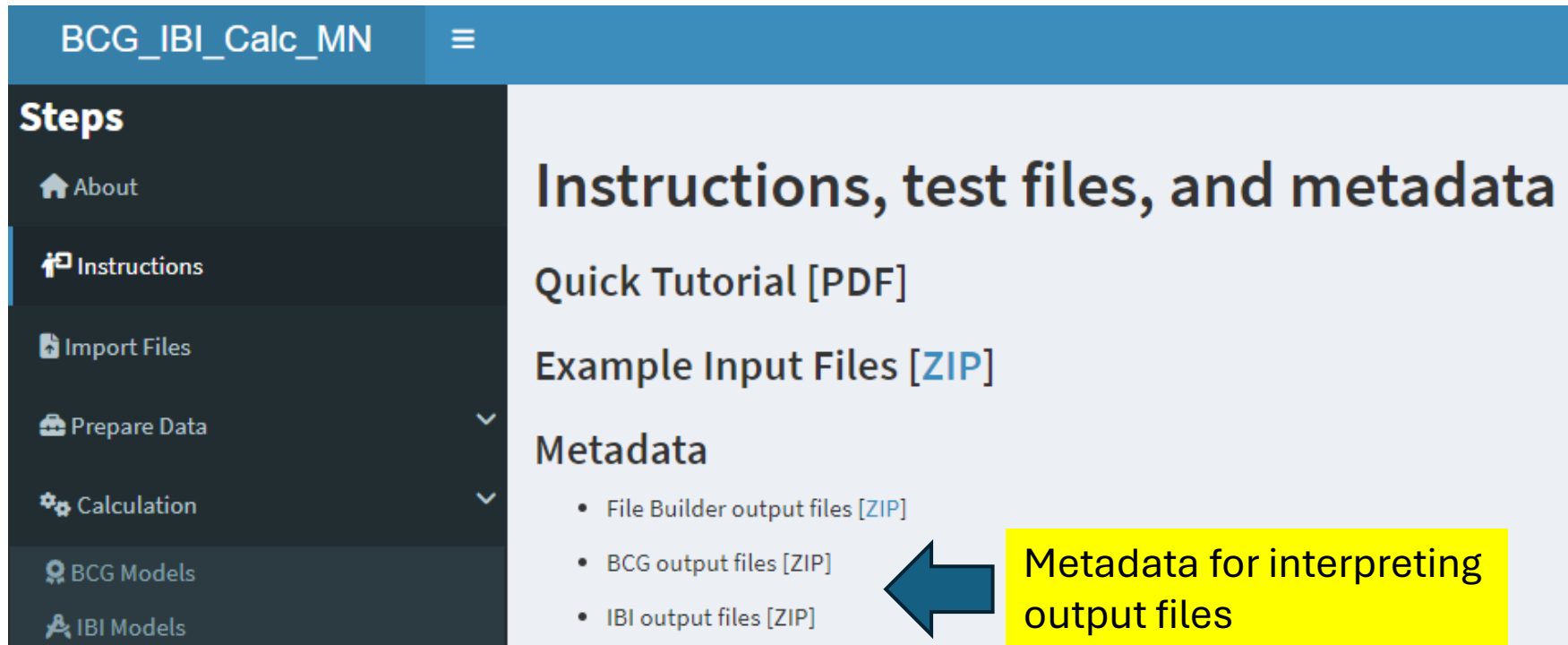
After files are unzipped, the original zipped files can be deleted if desired.

Unzip Calculation results

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

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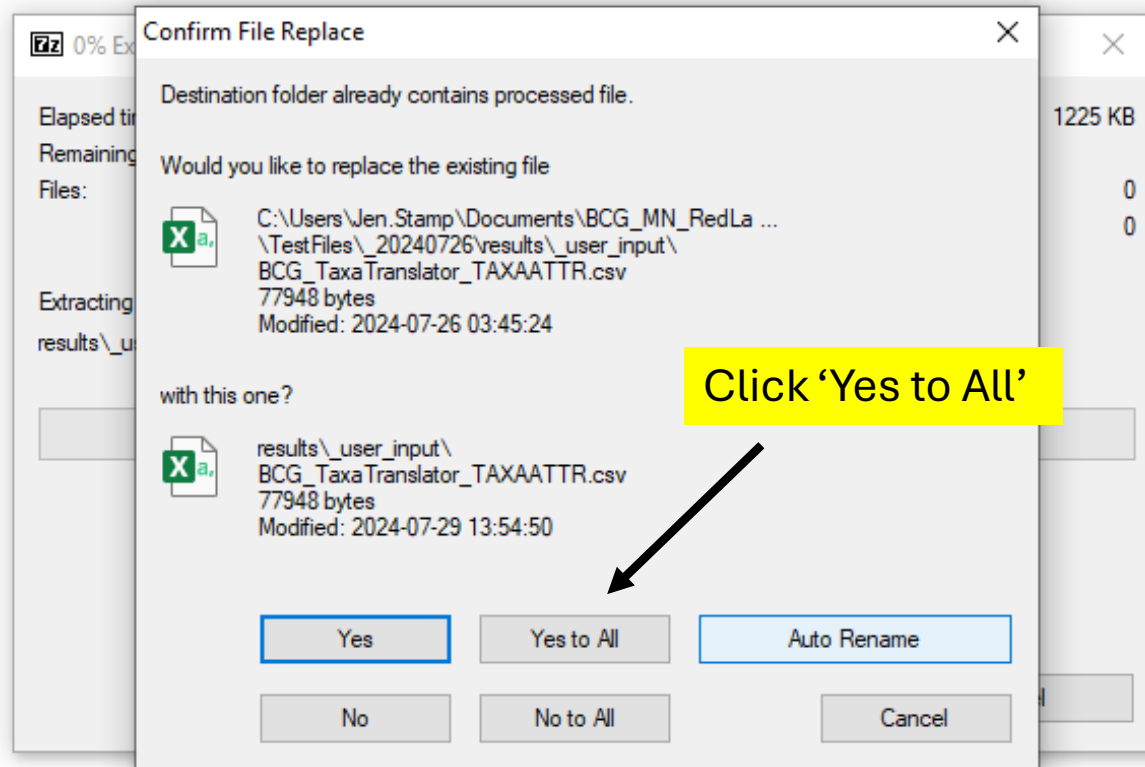
See Instructions page
for guidance on interpreting the results

Questions?
Comments?

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

Email Jen.Stamp@tetratech.com